Publications

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Fortes-Lima, C. A., Burgarella, C., Hammarén, R., Eriksson, A., Vicente, M., Jolly, C., Semo, A., Gunnink, H., Pacchiarotti, S., Mundeke, L., Matonda, I., Muluwa, J. K., Coutros, P., Nyambe, T. S., Cikomola, J. C., Coetzee, V., de Castro, M., Ebbesen, P., Delanghe, J., Stoneking, M., Barham, L., Lombard, M., Meyer, A., Steyn, M., Malmström, H., Rocha, J., Soodyall, H., Pakendorf, B., Bostoen, K., & Schlebusch, C. M. (2024). The genetic legacy of the expansion of Bantu-speaking peoples in Africa. Nature, 625, 540-547.

Mylopotamitaki, D., Weiss, M., Fewlass, H., Zavala, E. I., Rougier, H., Sümer, A., Hajdinjak, M., Smith, G. M., Ruebens, K., Sinet-Mathiot, V., Pederzani, S., Essel, E., Harking, F. S., Xia, H., Hansen, J., Kirchner, A., Lauer, T., Stahlschmidt, M., Hein, M., Talamo, S., Wacker, L., Meller, H., Dietl, H., Orschiedt, J., Olsen, J. V., Zeberg, H., Prüfer, K., Krause, J., Meyer, M., Welker, F., McPherron, S. P., Schüler, T., & Hublin, J.-J. (2024). Homo sapiens reached the higher latitudes of Europe by 45,000 years ago. Nature, 626, 341-346.

Pederzani, S., Britton, K., Trost, M., Fewlass, H., Bourgon, N., McCormack, J., Jaouen, K., Dietl, H., Döhle, H.-J., Kirchner, A., Lauer, T., Le Corre, M., McPherron, S. P., Meller, H., Mylopotamitaki, D., Orschiedt, J., Rougier, H., Ruebens, K., Schüler, T., Sinet-Mathiot, V., Smith, G. M., Talamo, S., Tütken, T., Welker, F., Zavala, E. I., Weiss, M., & Hublin, J.-J. (2024). Stable isotopes show Homo sapiens dispersed into cold steppes ~45,000 years ago at Ilsenhöhle in Ranis, Germany. Nature Ecology & Evolution.

Smith, G. M., Ruebens, K., Zavala, E. I., Sinet-Mathiot, V., Fewlass, H., Pederzani, S., Jaouen, K., Mylopotamitaki, D., Britton, K., Rougier, H., Stahlschmidt, M., Meyer, M., Meller, H., Dietl, H., Orschiedt, J., Krause, J., Schüler, T., McPherron, S. P., Weiss, M., Hublin, J.-J., & Welker, F. (2024). The ecology, subsistence and diet of ~45,000-year-old Homo sapiens at Ilsenhöhle in Ranis, Germany. Nature Ecology & Evolution.

Zeberg, H., Jakobsson, M., & Pääbo, S. (2024). [Review] The genetic changes that shaped Neandertals, Denisovans, and modern humans. Cell, 187, 1047-1058.

2023

Ågren, R., Patil, S., Zhou, X., Sahlholm, K., Pääbo, S., & Zeberg, H. (2023). Major genetic risk factors for Dupuytren's disease are inherited from Neandertals. Molecular Biology and Evolution, 40(6): msad130.

Arias, L., Emlen, N. Q., Norder, S., Julmi, N., Lemus Serrano, M., Chacon, T., Wiegertjes, J., Howard, A., Azevedo, M. C. B. C., Caine, A., Dunn, S., Stoneking, M., & Van Gijn, R. (2023). Interpreting mismatches between linguistic and genetic patterns among speakers of Tanimuka (Eastern Tukanoan) and Yukuna (Arawakan). Interface Focus, 13(1): 20220056.

Bornschein, U., Zeberg, H., Enard, W., Hevers, W., & Pääbo, S. (2023). Functional dissection of two amino acid substitutions unique to the human FOXP2 protein. Scientific Reports, 13(1): 3747.

Breitfeld, J., Horn, K., Le Duc, D., Velluva, A., Marzi, C., Grallert, H., Friedrich, N., Pietzner, M., Völker, U., Völzke, H., Ahlqvist, E., Aly, D. M., Tuomi, T., Baber, R., Kratzsch, J., Thiery, J., Isermann, B., Loeffler, M., Klöting, N., Blüher, M., Stumvoll, M., Heiker, J. T., Tönjes, A., Scholz, M., & Kovacs, P. (2023). Genetic dissection of serum vaspin highlights its causal role in lipid metabolism. Obesity, 31(11), 2862-2874.

Bundalian, L., Su, Y.-Y., Chen, S., Velluva, A., Kirstein, A. S., Garten, A., Biskup, S., Battke, F., Lal, D., Heyne, H. O., Platzer, K., Lin, C.-C., Lemke, J. R., & Le Duc, D. (2023). Epilepsies of presumed genetic etiology show enrichment of rare variants that occur in the general population. The American Journal of

Human Genetics, 110, 1110-1122.

Cahan, P., & Treutlein, B. (2023). A conversation with ChatGPT on the role of computational systems biology in stem cell research [Editorial]. Stem Cell Reports, 18, 1-2.

Carlhoff, S., Kutanan, W., Rohrlach, A. B., Posth, C., Stoneking, M., Nägele, K., Shoocongdej, R., & Krause, J. (2023). Genomic portrait and relatedness patterns of the Iron Age Log Coffin culture in northwestern Thailand. Nature Communications, 14(1): 8527.

Cauret, C. M. S., Jordan, D. C., Kukoly, L. M., Burton, S. R., Anele, E. U., Kwiecien, J. M., Gansauge, M.-T., Senthillmohan, S., Greenbaum, E., Meyer, M., Horb, M. E., & Evans, B. J. (2023). Functional dissection and assembly of a small, newly evolved, W chromosome-specific genomic region of the African clawed frog Xenopus laevis. PLoS Genetics, 19(10): e1010990.

Emlen, N. Q., Arias, L., & van Gijn, R. (2023). Multidisciplinary approaches to the Amazonian past: Introduction to the theme issue. Interface Focus, 13(1): 2022.0068.

Essel, E. (2023). Releasing secrets bound to ancient remains with modern DNA extraction techniques: An interview with Elena Essel. BioTechniques, 75(2), 42-46.

Essel, E., Zavala, E. I., Schulz-Kornas, E., Kozlikin, M. B., Fewlass, H., Vernot, B., Shunkov, M. V., Derevianko, A. P., Douka, K., Barnes, I., Soulier, M.-C., Schmidt, A., Szymanski, M., Tsanova, T., Sirakov, N., Endarova, E., McPherron, S. P., Hublin, J.-J., Kelso, J., Pääbo, S., Hajdinjak, M., Soressi, M., & Meyer, M. (2023). Ancient human DNA recovered from a Palaeolithic pendant. Nature, 618, 328-332.

Fleck, J. S., Jansen, S. M. J., Wollny, D., Zenk, F., Seimiya, M., Jain, A., Okamoto, R., Santel, M., He, Z., Camp, J. G., & Treutlein, B. (2023). Inferring and perturbing cell fate regulomes in human brain organoids. Nature, 621, 365-372.

Lackner, M., Helmbrecht, N., Pääbo, S., & Riesenberg, S. (2023). Detection of unintended on-target effects in CRISPR genome editing by DNA donors carrying diagnostic substitutions. Nucleic Acids Research, 51(5): gkac1254.

Lauterbur, M. E., Cavassim, M. I. A., Gladstein, A. L., Gower, G., Pope, N. S., Tsambos, G., Adrion, J., Belsare, S., Biddanda, A., Caudill, V., Cury, J., Echevarria, I., Haller, B. C., Hasan, A. R., Huang, X., Iasi, L. N., Noskova, E., Obsteter, J., Pavinato, V. A. C., Pearson, A., Peede, D., Perez, M. F., Rodrigues, M. F., Smith, C. C., Spence, J. P., Teterina, A., Tittes, S., Unneberg, P., Vazquez, J. M., Waples, R. K., Wohns, A. W., Wong, Y., Baumdicker, F., Cartwright, R. A., Gorjanc, G., Gutenkunst, R. N., Kelleher, J., Kern, A. D., Ragsdale, A. P., Ralph, P. L., Schrider, D. R., & Gronau, I. (2023). Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. eLife, 12: RP84874.

Liu, D., Min-Shan Ko, A., & Stoneking, M. (2023). The genomic diversity of Taiwanese Austronesian groups: Implications for the “Into- and Out-of-Taiwan” models. PNAS Nexus, 2(5): pgad122.

Murat, F., Mbengue, N., Winge, S. B., Trefzer, T., Leushkin, E., Sepp, M., Cardoso-Moreira, M., Schmidt, J., Schneider, C., Mößinger, K., Brüning, T., Lamanna, F., Belles, M. R., Conrad, C., Kondova, I., Bontrop, R., Behr, R., Khaitovich, P., Pääbo, S., Marques-Bonet, T., Grützner, F., Almstrup, K., Schierup, M. H., & Kaessmann, H. (2023). The molecular evolution of spermatogenesis across mammals. Nature, 613, 308-316.

Oliveira, S., Fehn, A.-M., Amorim, B., Stoneking, M., & Rocha, J. (2023). Genome-wide variation in the Angolan Namib Desert reveals unique pre-Bantu ancestry. Science Advances, 9(38): eadh3822.

Parker, C. E., Hiss, A. N., Spyrou, M. A., Neumann, G. U., Slavin, P., Nelson, E. A., Nagel, S., Dalidowski, X., Friederich, S., Krause, J., Herbig, A., Haak, W., & Bos, K. I. (2023). 14th century Yersinia pestis genomes support emergence of pestis secunda within Europe. PLoS Pathogens, 19(7): e1011404.

Penner-Goeke, S., Bothe, M., Rek, N., Kreitmaier, P., Pöhlchen, D., Kühnel, A., Glaser, L. V., Kaya, E., Krontira, A. C., Röh, S., Czamara, D., Ködel, M., Monteserin-Garcia, J., Diener, L., Wölfel, B., Sauer, S., Rummel, C., Riesenberg, S., Arloth-Knauer, J., Ziller, M., Labeur, M., Meijsing, S., & Binder, E. B. (2023). High-throughput screening of glucocorticoid-induced enhancer activity reveals mechanisms of stress-related psychiatric disorders. PNAS, 120(49): e2305773120.

Peyrégne, S., Slon, V., & Kelso, J. (2023). More than a decade of genetic research on the Denisovans. Nature Reviews Genetics, 25(2), 83-103.

Popli, D., Peyrégne, S., & Peter, B. M. (2023). Estimating genetic relatedness from ancient DNA. In H. Meller, J. Krause, W. Haak, & R. Risch (Eds.), Kinship, sex, and biological relatedness: the contribution of archaeogenetics to the understanding of social and biological relations: 15. Mitteldeutscher Archäologentag vom 6. bis 8. Oktober 2022 in Halle (Saale) (pp. 95-99). Halle (Saale): Landesamt für Denkmalpflege und Archäologie Sachsen-Anhalt - Landesmuseum für Vorgeschichte.

Popli, D., Peyrégne, S., & Peter, B. M. (2023). KIN: a method to infer relatedness from low-coverage ancient DNA. Genome Biology, 24: 10.

Riesenberg, S., Kanis, P., Macak, D., Wollny, D., Düsterhöft, D., Kowalewski, J., Helmbrecht, N., Maricic, T., & Pääbo, S. (2023). Efficient high-precision homology-directed repair-dependent genome editing by HDRobust. Nature Methods, 20, 1388-1399.

Safrastyan, A., zu Siederdissen, C. H., & Wollny, D. (2023). Decoding cell-type contributions to the cfRNA transcriptomic landscape of liver cancer. Human Genomics, 17(1): 90.

Soressi, M., & Hajdinjak, M. (2023). Ancient woman's DNA recovered from a 20,000-year-old pendant. Nature, 618, 328-332.

Stoneking, M., Arias, L., Liu, D., Oliveira, S., Pugach, I., & Rodriguez, J. (2023). Genomic perspectives on human dispersals during the Holocene. Proceedings of the National Academy of Sciences, 120(4): e22094751.

Swali, P., Schulting, R., Gilardet, A., Kelly, M., Anastasiadou, K., Glocke, I., McCabe, J., Williams, M., Audsley, T., Loe, L., Fernández-Crespo, T., Ordoño, J., Walker, D., Clare, T., Cook, G., Hodkinson, I., Simpson, M., Read, S., Davy, T., Silva, M., Hajdinjak, M., Bergström, A., Booth, T., & Skoglund, P. (2023). Yersinia pestis genomes reveal plague in Britain 4000 years ago. Nature Communications, 14: 2930.

The COVID-19 Host Genetics Initiative, including authors, Zeberg, H., & Maricic, T. (2023). A second update on mapping the human genetic architecture of COVID-19. Nature, 621, E7-E26.

Tkaczynski, P. J., Mafessoni, F., Girard-Buttoz, C., Samuni, L., Ackermann, C. Y., Fedurek, P., Gomes, C., Hobaiter, C., Löhrich, T., Manin, V., Preis, A., Valé, P. D., Wessling, E. G., Wittiger, L., Zommers, Z., Zuberbuehler, K., Vigilant, L., Deschner, T., Wittig, R. M., & Crockford, C. (2023). Shared community effects and the non-genetic maternal environment shape cortisol levels in wild chimpanzees. Communications Biology, 6(1): 565.

Van Gijn, R., Norder, S., Arias, L., Emlen, N. Q., Azevedo, M. C. B. C., Caine, A., Dunn, S., Howard, A., Julmi, N., Krasnoukhova, O., Stoneking, M., & Wiegertjes, J. (2023). The social lives of isolates (and small language families): The case of the Northwest Amazon. Interface Focus, 13(1).

Wang, K., Yu, H., Radzeviciute, R., Kiryushin, Y. F., Tishkin, A. A., Frolov, Y. V., Stepanova, N. F.,

Kiryushin, K. Y., Kungurov, A. L., Shnaider, S. V., Tur, S. S., Tiunov, M. P., Zubova, A. V., Pevzner, M., Karimov, T., Buzhilova, A., Slon, V., Jeong, C., Krause, J., & Posth, C. (2023). Middle Holocene Siberian genomes reveal highly connected gene pools throughout North Asia. Current Biology, 33(3), 423-433, e1-e5.

Westerich, K. J., Reinecke, S., Emich, J., Wyrwoll, M. J., Stallmeyer, B., Meyer, M., Oud, M. S., Fietz, D., Pilatz, A., Kliesch, S., Reichman-Fried, M., Tarbashevich, K., Limon, T., Stehling, M., Friedrich, C., Tüttelmann, F., & Raz, E. (2023). Linking human Dead end 1 (DND1) variants to male infertility employing zebrafish embryos. Human Reproduction, 38(4): dead031, pp. 655-670.

Woravatin, W., Stoneking, M., Srikummool, M., Kampuansai, J., Arias, L., & Kutanan, W. (2023). South Asian maternal and paternal lineages in southern Thailand and the role of sex-biased admixture. PLoS One, 18: e0291547.

Yoshiji, S., Butler-Laporte, G., Lu, T., Willett, J. D. S., Su, C.-Y., Nakanishi, T., Morrison, D. R., Chen, Y., Liang, K., Hultström, M., Ilboudo, Y., Afrasiabi, Z., Lan, S., Duggan, N., DeLuca, C., Vaezi, M., Tselios, C., Xue, X., Bouab, M., Shi, F., Laurent, L., Münter, H. M., Afilalo, M., Afilalo, J., Mooser, V., Timpson, N. J., Zeberg, H., Zhou, S., Forgetta, V., Farjoun, Y., & Richards, J. B. (2023). Proteome-wide Mendelian randomization implicates nephronectin as an actionable mediator of the effect of obesity on COVID-19 severity. Nature Metabolism, 5, 248-264.

2022

Alva, O., Leroy, A., Heiske, M., Pereda-Loth, V., Tisseyre, L., Boland, A., Deleuze, J.-F., Rocha, J., Schlebusch, C., Fortes-Lima, C., Stoneking, M., Radimilahy, C., Rakotoarisoa, J.-A., Letellier, T., & Pierron, D. (2022). The loss of biodiversity in Madagascar is contemporaneous with major demographic events. Current Biology, 32, 4997-5007, e1-e5.

Barth, L. A. G., Nebe, M., Kalwa, H., Velluva, A., Kehr, S., Kolbig, F., Prabutzki, P., Kiess, W., Le Duc, D., Garten, A., & Kirstein, A. S. (2022). Phospholipid Scramblase 4 (PLSCR4) Regulates Adipocyte Differentiation via PIP3-Mediated AKT Activation. International Journal of Molecular Sciences, 23(17): 9787.

Brown, S., Massilani, D., Kozlikin, M. B., Shunkov, M. V., Derevianko, A. P., Stoessel, A., Jope-Street, B., Meyer, M., Kelso, J., Pääbo, S., Higham, T., & Douka, K. (2022). The earliest Denisovans and their cultural adaptation. Nature Ecology & Evolution, 6, 28-35.

Coppo, L., Mishra, P., Siefert, N., Holmgren, A., Pääbo, S., & Zeberg, H. (2022). A substitution in the glutathione reductase lowers electron leakage and inflammation in modern humans. Science Advances, 8(1): eabm1148.

COVID-19 Genetics Initiative, including authors, Zeberg, H., & Maricic, T. (2022). A first update on mapping the human genetic architecture of COVID-19. Nature, 608, E1-E10.

Cruz, R., Diz-de Almeida, S., López de Heredia, M., Quintela, I., Ceballos, F. C., Pita, G., Lorenzo-Salazar, J. M., González-Montelongo, R., Gago-Domínguez, M., Sevilla Porras, M., Tenorio Castaño, J. A., Nevado, J., Aguado, J. M., Aguilar, C., Aguilera-Albesa, S., Almadana, V., Almoguera, B., Alvarez, N., Andreu-Bernabeu, Á., Arana-Arri, E., Arango, C., Arranz, M. J., Artiga, M.-J., Baptista-Rosas, R. C., Barreda-Sánchez, M., Belhassen-Garcia, M., Bezerra, J. F., Bezerra, M. A. C., Boix-Palop, L., Brion, M., Brugada, R., Bustos, M., Calderón, E. J., Carbonell, C., Castano, L., Castelao, J. E., Conde-Vicente, R., Cordero-Lorenzana, M. L., Cortes-Sanchez, J. L., Corton, M., Darnaude, M. T., De Martino-Rodríguez, A., del Campo-Pérez, V., Diaz de Bustamante, A., Domínguez-Garrido, E., Luchessi, A. D., Eiros, R., Estigarribia Sanabria, G. M., Carmen Fariñas, M., Fernández-Robelo, U., Fernández-Rodríguez, A.,

Fernández-Villa, T., Gil-Fournier, B., Gómez-Arrue, J., González Álvarez, B., Gonzalez Bernaldo de Quirós, F., González-Peñas, J., Gutiérrez-Bautista, J. F., Herrero, M. J., Herrero-Gonzalez, A., Jimenez-Sousa, M. A., Lattig, M. C., Liger Borja, A., Lopez-Rodriguez, R., Mancebo, E., Martín-López, C., Martín, V., Martinez-Nieto, O., Martinez-Lopez, I., Martinez-Resendez, M. F., Martinez-Perez, A., Mazzeu, J. F., Merayo Macías, E., Minguez, P., Moreno Cuerda, V., Silbiger, V. N., Oliveira, S. F., Ortega-Paino, E., Parellada, M., Paz-Artal, E., Santos, N. P. C., Pérez-Matute, P., Perez, P., Pérez-Tomás, M. E., Perucho, T., Pinsach-Abuin, M. L., Pompa-Mera, E. N., Porras-Hurtado, G. L., Pujol, A., Ramiro León, S., Resino, S., Fernandes, M. R., Rodríguez-Ruiz, E., Rodriguez-Artalejo, F., Rodriguez-Garcia, J. A., Ruiz Cabello, F., Ruiz-Hornillos, J., Ryan, P., Soria, J. M., Souto, J. C., Tamayo, E., Tamayo-Velasco, A., Taracido-Fernandez, J. C., Teper, A., Torres-Tobar, L., Urioste, M., Valencia-Ramos, J., Yáñez, Z., Zarate, R., Nakanishi, T., Pigazzini, S., Degenhardt, F., Butler-Laporte, G., Maya-Miles, D., Bujanda, L., Bouysran, Y., Palom, A., Ellinghaus, D., Martínez-Bueno, M., Rolker, S., Amitrano, S., Roade, L., Fava, F., Spinner, C. D., Prati, D., Bernardo, D., Garcia, F., Darcis, G., Fernández-Cadenas, I., Holter, J. C., Banales, J. M., Frithiof, R., Duga, S., Asselta, R., Pereira, A. C., Romero-Gómez, M., Nafría-Jiménez, B., Hov, J. R., Migeotte, I., Renieri, A., Planas, A. M., Ludwig, K. U., Buti, M., Rahmouni, S., Alarcón-Riquelme, M. E., Schulte, E. C., Franke, A., Karlsen, T. H., Valenti, L., Zeberg, H., Richards, B., Ganna, A., Boada, M., de Rojas, I., Ruiz, A., Sánchez-Juan, P., Real, L. M., SCOURGE Cohort Group, HOSTAGE Cohort Group, GRA@CE Cohort Group, Guillen-Navarro, E., Ayuso, C., González-Neira, A., Riancho, J. A., Rojas-Martinez, A., Flores, C., Lapunzina, P., & Carracedo, A. (2022). Novel genes and sex differences in COVID-19 severity. Human Molecular Genetics, 31(22), 3789-3806.

Dannemann, M., Milaneschi, Y., Yermakovich, D., Stiglbauer, V., Kariis, H. M., Krebs, K., Friese, M. A., Otte, C., Esko, T., Metspalu, A., Milani, L., Mägi, R., Nelis, M., Lehto, K., Penninx, B. W. J. H., Kelso, J., Gold, S. M., & Team, E. B. R. (2022). Neandertal introgression partitions the genetic landscape of neuropsychiatric disorders and associated behavioral phenotypes. Translational Psychiatry, 12: 433.

Fast, L., Ågren, R., & Zeberg, H. (2022). Fluorescence-based measurements of membrane-bound angiotensin converting enzyme 2 activity using Xenopus Laevis Oocytes. Biosensors, 12(8): 601.

Gerber, T., Loureiro, C., Schramma, N., Chen, S., Jain, A., Weber, A., Weigert, A., Santel, M., Alim, K., Treutlein, B., & Camp, J. G. (2022). Spatial transcriptomic and single-nucleus analysis reveals heterogeneity in a gigantic single-celled syncytium. eLife, 11: e69745.

Haeggström, S., Ingelman-Sundberg, M., Pääbo, S., & Zeberg, H. (2022). The clinically relevant CYP2C8*3 and CYP2C9*2 haplotype is inherited from Neandertals. The Pharmacogenomics Journal, 22, 247-249.

He, Z., Maynard, A., Jain, A., Gerber, T., Petri, R., Lin, H.-C., Santel, M., Ly, K., Dupré, J.-S., Sidow, L., Sanchis Calleja, F., Jansen, S. M. J., Riesenberg, S., Camp, J. G., & Treutlein, B. (2022). Lineage recording in human cerebral organoids. Nature Methods, 19(1), 90-99.

Jagoda, E., Xue, J. R., Reilly, S. K., Dannemann, M., Racimo, F., Huerta-Sanchez, E., Sankararaman, S., Kelso, J., Pagani, L., Sabeti, P. C., & Capellini, T. D. (2022). Detection of Neanderthal adaptively introgressed genetic variants that modulate reporter gene expression in human immune cells. Molecular Biology and Evolution, 39(1): msab304.

Kilpatrick, A. M., Rahman, F., Anjum, A., Shome, S., Andalib, K. M. S., Banik, S., Chowdhury, S. F., Coombe, P., Astroz, Y. C., Douglas, J. M., Eranti, P., Kiran, A. D., Kumar, S., Lim, H., Lorenzi, V., Lubiana, T., Mahmud, S., Puche, R., Rybarczyk, A., Sium, A., Muktadir, S., Twesigomwe, D., Zok, T., Orengo, C. A., Friedberg, I., Kelso, J., & Welch, L. (2022). Characterizing domain-specific open educational resources by linking ISCB Communities of Special Interest to Wikipedia. Bioinformatics, 38(Supplement_1), i19-i27.

Körner, M. B., Velluva, A., Bundalian, L., Radtke, M., Lin, C.-C., Zacher, P., Bartolomaeus, T., Kirstein, A. S., Mrestani, A., Scholz, N., Platzer, K., Teichmann, A.-C., Hentschel, J., Langenhan, T., Lemke, J. R., Garten, A., Abou Jamra, R., & Le Duc, D. (2022). Altered gene expression profiles impair the nervous system development in individuals with 15q13.3 microdeletion. Scientific Reports, 12(1): 13507.

Krumm, J., Sekine, K., Samaras, P., Brazovskaja, A., Breunig, M., Yasui, R., Kleger, A., Taniguchi, H., Wilhelm, M., Treutlein, B., Camp, J. G., & Kuster, B. (2022). High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development. Cell Reports, 38: 110604.

Le Duc, D., Velluva, A., Cassatt-Johnstone, M., Olsen, R.-A., Baleka, S., Lin, C.-C., Lemke, J. R., Southon, J. R., Burdin, A., Wang, M.-S., Grunewald, S., Rosendahl, W., Joger, U., Rutschmann, S., Hildebrandt, T. B., Fritsch, G., Estes, J. A., Kelso, J., Dalén, L., Hofreiter, M., Shapiro, B., & Schöneberg, T. (2022). Genomic basis for skin phenotype and cold adaptation in the extinct Steller's sea cow. Science Advances, 8(5).

Liu, D., Peter, B. M., Schiefenhövel, W., Kayser, M., & Stoneking, M. (2022). Assessing human genome-wide variation in the Massim region of Papua New Guinea and implications for the Kula trading tradition. Molecular Biology and Evolution, 39(8): msac165.

Liu, Q., Iqbal, M. F., Yaqub, T., Firyal, S., Zhao, Y., Stoneking, M., & Li, M. (2022). The transmission of human mitochondrial DNA in four-generation pedigrees. Human Mutation, 43(9), 1259-1267.

Massilani, D., Morley, M. W., Mentzer, S. M., Aldeias, V., Vernot, B., Miller, C., Stahlschmidt, M., Kozlikin, M. B., Shunkov, M. V., Derevianko, A. P., Conard, N. J., Wurz, S., Henshilwood, C. S., Vasquez, J., Essel, E., Nagel, S., Richter, J., Nickel, B., Roberts, R. G., Pääbo, S., Slon, V., Goldberg, P., & Meyer, M. (2022). Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments. Proceedings of the National Academy of Sciences, 119(1): e2113666118.

Mora-Bermúdez, F., Kanis, P., Macak, D., Peters, J., Naumann, R., Xing, L., Sarov, M., Winkler, S., Oegema, C. E., Haffner, C., Wimberger, P., Riesenberg, S., Maricic, T., Huttner, W. B., & Pääbo, S. (2022). Longer metaphase and fewer chromosome segregation errors in modern human than Neanderthal brain development. Science Advances, 8: eabn7702.

Mora-Bermúdez, F., Taverna, E., & Huttner, W. B. (2022). From stem and progenitor cells to neurons in the developing neocortex: Key differences among hominids. The FEBS Journal, 289(6), 1524-1535.

Nebe, M., Kehr, S., Schmitz, S., Breitfeld, J., Lorenz, J., Le Duc, D., Stadler, P. F., Meiler, J., Kiess, W., Garten, A., & Kirstein, A. S. (2022). Small integral membrane protein 10 like 1 downregulation enhances differentiation of adipose progenitor cells. Biochemical and Biophysical Research Communications, 604, 57-62.

Oliveira, S., Nägele, K., Carlhoff, S., Pugach, I., Koesbardiati, T., Hübner, A., Meyer, M., Oktaviana, A. A., Takenaka, M., Katagiri, C., Murti, D. B., Putri, R. S., Mahirta, Petchey, F., Higham, T., Higham, C., O'Connor, S., Hawkins, S., Kinaston, R., Bellwood, P., Ono, R., Powell, A., Krause, J., Posth, C., & Stoneking, M. (2022). Ancient genomes from the last three millennia support multiple human dispersals into Wallacea. Nature Ecology & Evolution, 6, 1024-1034.

Oskolkov, N., Santel, M., Parikh, H. M., Ekström, O., Camp, J. G., Miyamoto-Mikami, E., Ström, K., Mir, B. A., Kryvokhyzha, D., Lehtovirta, M., Kobayashi, H., Kakigi, R., Naito, H., Eriksson, K.-F., Nystedt, B., Fuku, N., Treutlein, B., Pääbo, S., & Hansson, O. (2022). High-throughput muscle fiber typing from RNA sequencing data. Skeletal Muscle, 12: 16.

Oxilia, G., Bortolini, E., Marciani, G., Menghi Sartorio, J. C., Vazzana, A., Bettuzzi, M., Panetta, D., Arrighi, S., Badino, F., Figus, C., Lugli, F., Romandini, M., Silvestrini, S., Sorrentino, R., Moroni, A., Donadio, C.,

Morigi, M. P., Slon, V., Piperno, M., Talamo, S., Collina, C., & Benazzi, S. (2022). Direct evidence that late Neanderthal occupation precedes a technological shift in southwestern Italy. American Journal of Biological Anthropology, 179(1), 18-30.

Peter, B. M. (2022). A geometric relationship of F2, F3 and F4-statistics with principal component analysis. Philosophical Transactions of the Royal Society B: Biological Sciences, 377(1852): 20200413.

Peyrégne, S., Kelso, J., Peter, B. M., & Pääbo, S. (2022). The evolutionary history of human spindle genes includes back-and-forth gene flow with Neandertals. eLife, 11: e75464.

Pietzner, M., Chua, R. L., Wheeler, E., Jechow, K., Willett, J. D. S., Radbruch, H., Trump, S., Heidecker, B., Zeberg, H., Heppner, F. L., Eils, R., Mall, M. A., Richards, J. B., Sander, L.-E., Lehmann, I., Lukassen, S., Wareham, N. J., Conrad, C., & Langenberg, C. (2022). ELF5 is a potential respiratory epithelial cell-specific risk gene for severe COVID-19. Nature Communications, 13: 4484.

Pinson, A., Xing, L., Namba, T., Kalebic, N., Peters, J., Oegema, C. E., Traikov, S., Reppe, K., Riesenberg, S., Maricic, T., Derihaci, R., Wimberger, P., Pääbo, S., & Huttner, W. B. (2022). Human TKTL1 implies greater neurogenesis in frontal neocortex of modern humans than Neanderthals. Science, 377(6611): eabl6422, pp. 1170.

Riesenberg, S., Helmbrecht, N., Kanis, P., Maricic, T., & Pääbo, S. (2022). Improved gRNA secondary structures allow editing of target sites resistant to CRISPR-Cas9 cleavage. Nature Communications, 13: 489.

Rocha, J. L., Vaz Pinto, P., Siegismund, H. R., Meyer, M., Jansen van Vuuren, B., Veríssimo, L., Ferrand, N., & Godinho, R. (2022). African climate and geomorphology drive evolution and ghost introgression in sable antelope. Molecular Ecology, 31(10), 2968-2984.

Rodriguez, J., Cuales, J. M. D., Herrera, M. J. B., Zubiri, L. A. M., Muallil, R. N., Ishmael, A. I., Jimenez, E. B., Stoneking, M., & De Ungria, M. C. A. (2022). Ethical challenges in genetic research among Philippine Indigenous Peoples: Insights from fieldwork in Zamboanga and the Sulu Archipelago. Frontiers in Genetics, 13: 901515.

Silén, C., Karlgren, K., Hjelmqvist, H., Meister, B., Zeberg, H., & Pettersson, A. (2022). Three-dimensional visualisation of authentic cases in anatomy learning – An educational design study. BMC Medical Education, 22(477).

Slon, V., Clark, J. L., Friesem, D. E., Orbach, M., Porat, N., Meyer, M., Kandel, A. W., & Shimelmitz, R. (2022). Extended longevity of DNA preservation in Levantine Paleolithic sediments, Sefunim Cave, Israel. Scientific Reports, 12: 14528.

Wollny, D., Vernot, B., Wang, J., Hondele, M., Safrastyan, A., Aron, F., Micheel, J., He, Z., Hyman, A., Weis, K., Camp, J. G., Tang, T. D., & Treutlein, B. (2022). Characterization of RNA content in individual phase-separated coacervate microdroplets. Nature Communications, 13: 2626.

Yu, H., Loosdrecht, M. S. v. d., Mannino, M. A., Talamo, S., Rohrlach, A. B., Childebayeva, A., Villalba-Mouco, V., Aron, F., Brandt, G., Burri, M., Freund, C., Radzeviciute, R., Stahl, R., Wissgott, A., Fewlass, H., Tagliacozzo, A., Piperno, M., Tusa, S., Collina, C., Schimmenti, V., Di Salvo, R., Prüfer, K., Posth, C., Hublin, J.-J., Gronenborn, D., Binder, D., Jeong, C., Haak, W., & Krause, J. (2022). Genomic and dietary discontinuities during the Mesolithic and Neolithic in Sicily. iScience, 5(25): 104244.

Zavala, E. I., Thomas, J. T., Sturk-Andreaggi, K., Daniels-Higginbotham, J., Meyers, K. K., Barrit-Ross, S.,

Ayinuer-Petri, A., Richter, J., Nickel, B., Berg, G. E., McMahon, T. P., Meyer, M., & Marshall, C. (2022). Ancient DNA methods improve forensic DNA profiling of Korean War and World War II unknowns. Genes, 13(129).

Zeberg, H. (2022). The major genetic risk factor for severe COVID-19 is associated with protection against HIV. Proceedings of the National Academy of Sciences of the United States of America, 119(9): e2116435119.

2021

Alpaslan-Roodenberg, S., Anthony, D., Babiker, H., Bánffy, E., Booth, T., Capone, P., Deshpande-Mukherjee, A., Eisenmann, S., Fehren-Schmitz, L., Frachetti, M., Fujita, R., Frieman, C. J., Fu, Q., Gibbon, V., Haak, W., Hajdinjak, M., Hofmann, K. P., Holguin, B., Inomata, T., Kanzawa-Kiriyama, H., Keegan, W., Kelso, J., Krause, J., Kumaresan, G., Kusimba, C., Kusimba, S., Lalueza-Fox, C., Llamas, B., MacEachern, S., Mallick, S., Matsumura, H., Morales-Arce, A. Y., Matuzeviciute, G. M., Mushrif-Tripathy, V., Nakatsuka, N., Nores, R., Ogola, C., Okumura, M., Patterson, N., Pinhasi, R., Prasad, S. P. R., Prendergast, M. E., Punzo, J. L., Reich, D., Sawafuji, R., Sawchuk, E., Schiffels, S., Sedig, J., Shnaider, S., Sirak, K., Skoglund, P., Slon, V., Snow, M., Soressi, M., Spriggs, M., Stockhammer, P. W., Szécsényi-Nagy, A., Thangaraj, K., Tiesler, V., Tobler, R., Wang, C.-C., Warinner, C., Yasawardene, S., & Zahir, M. (2021). Ethics of DNA research on human remains: Five globally applicable guidelines. Nature, 599, 41-46.

Berger, C., Heyne, H. O., Heiland, T., Dommel, S., Höfling, C., Guiu-Jurado, E., Lorenz, J., Roßner, S., Dannemann, M., Kelso, J., Kovacs, P., Blüher, M., & Klöting, N. (2021). A novel compound heterozygous leptin receptor mutation causes more severe obesity than in Lepr mice. Journal of Lipid Research, 62: 100105.

Bokelmann, L., Nickel, O., Maricic, T., Pääbo, S., Meyer, M., Borte, S., & Riesenberg, S. (2021). Point-of-care bulk testing for SARS-CoV-2 by combining hybridization capture with improved colorimetric LAMP. Nature Communications, 12(1): 1467.

Carlhoff, S., Duli, A., Nägele, K., Nur, M., Skov, L., Sumantri, I., Oktaviana, A. A., Hakim, B., Burhan, B., Syahdar, F. A., McGahan, D. P., Bulbeck, D., Perston, Y. L., Newman, K., Saiful, A. M., Ririmasse, M., Chia, S., Hasanuddin, Pulubuhu, D. A. T., Suryatman, Supriadi, Jeong, C., Peter, B. M., Prüfer, K., Powell, A., Krause, J., Posth, C., & Brumm, A. (2021). Genome of a middle Holocene hunter-gatherer from Wallacea. Nature, 596, 543-547.

Choin, J., Mendoza-Revilla, J., Arauna, L. R., Cuadros-Espinoza, S., Cassar, O., Larena, M., Ko, A.-M.-S., Harmant, C., Laurent, R., Verdu, P., Laval, G., Boland, A., Olaso, R., Deleuze, J.-F., Valentin, F., Ko, Y.-C., Jakobsson, M., Gessain, A., Excoffier, L., Stoneking, M., Patin, E., & Quintana-Murci, L. (2021). Genomic insights into population history and biological adaptation in Oceania. Nature, 592(7855), 583-589.

Devièse, T., Abrams, G., Hajdinjak, M., Pirson, S., De Groote, I., Di Modica, K., Toussaint, M., Fischer, V., Comeskey, D., Spindler, L., Meyer, M., Semal, P., & Higham, T. (2021). Reevaluating the timing of Neanderthal disappearance in Northwest Europe. Proceedings of the National Academy of Sciences, 118(12): e2022466118.

Devièse, T., Abrams, G., Hajdinjak, M., Pirson, S., De Groote, I., Di Modica, K., Toussaint, M., Fischer, V., Comeskey, D., Spindler, L., Meyer, M., Semal, P., & Higham, T. (2021). Reply to Van Peer: Direct radiocarbon dating and ancient genomic analysis reveal the true age of the Neanderthals at Spy Cave. Proceedings of the National Academy of Sciences of the United States of America, 118(26): e2107116118.

Evans, B. J., Peter, B., Melnick, D. J., Andayani, N., Supriatna, J., Zhu, J., & Tosi, A. J. (2021). Mitonuclear interactions and introgression genomics of macaque monkeys (Macaca) highlight the influence of behaviour on genome evolution. Proceedings of the Royal Society B: Biological Sciences, 288(1960): 20211756.

Fellows Yates, J. A., Andrades Valtueña, A., Vågene, A. J., Cribdon, B., Velsko, I. M., Borry, M., Bravo-López, M. J., Fernandez-Guerra, A., Green, E. J., Ramachandran, S. L., Heintzman, P. D., Spyrou, M. A., Hübner, A., Gancz, A. S., Hider, J., Allshouse, A. F., & Warinner, C. G. (2021). Community-curated and standardised metadata of published ancient metagenomic samples with AncientMetagenomeDir. Scientific Data, 8: 31.

Fleck, J. S., Sanchís-Calleja, F., He, Z., Santel, M., Boyle, M. J., Camp, J. G., & Treutlein, B. (2021). Resolving organoid brain region identities by mapping single-cell genomic data to reference atlases. Cell Stem Cell, 28, 1148-1159.

Gjermeni, E., Kirstein, A. S., Kolbig, F., Kirchhof, M., Bundalian, L., Katzmann, J. L., Laufs, U., Blüher, M., Garten, A., & Le Duc, D. (2021). Obesity – an update on the basic pathophysiology and review of recent therapeutic advances. Biomolecules, 11(10): 1426.

Guo, S., Huang, S., Jiang, X., Hu, H., Han, D., Moreno, C. S., Fairbrother, G. L., hughes, D. A., Stoneking, M., & Khaitovich, P. (2021). Variation of microRNA expression in the human placenta driven by population identity and sex of the newborn. BMC Genomics, 22: 286.

Hajdinjak, M., Mafessoni, F., Skov, L., Vernot, B., Hübner, A., Fu, Q., Essel, E., Nagel, S., Nickel, B., Richter, J., Moldovan, O. T., Constantin, S., Endarova, E., Zahariev, N., Spasov, R., Welker, F., Smith, G. M., Sinet-Mathiot, V., Paskulin, L., Fewlass, H., Talamo, S., Rezek, Z., Sirakova, S., Sirakov, N., McPherron, S. P., Tsanova, T., Hublin, J.-J., Peter, B., Meyer, M., Skoglund, P., Kelso, J., & Pääbo, S. (2021). Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. Nature, 592, 253-257.

Hodgkins, J., Orr, C. M., Gravel-Miguel, C., Riel-Salvatore, J., Miller, C. E., Bondioli, L., Nava, A., Lugli, F., Talamo, S., Hajdinjak, M., Cristiani, E., Romandini, M., Meyer, D., Drohobytsky, D., Kuester, F., Pothier-Bouchard, G., Buckley, M., Mancini, L., Baruffaldi, F., Silvestrini, S., Arrighi, S., Keller, H. M., Griggs, R. B., Peresani, M., Strait, D. S., Benazzi, S., & Negrino, F. (2021). An infant burial from Arma Veirana in northwestern Italy provides insights into funerary practices and female personhood in early Mesolithic Europe. Scientific Reports, 11: 23735.

Hou, Q.-Q., Xiao, Q., Sun, X.-Y., Ju, X.-C., & Luo, Z.-G. (2021). TBC1D3 promotes neural progenitor proliferation by suppressing the histone methyltransferase G9a. Science Advances, 7: eaba8053.

Iasi, L. N., Ringbauer, H., & Peter, B. (2021). An extended admixture pulse model reveals the limitations to human-Neandertal introgression dating. Molecular Biology and Evolution, 38(11), 5156-5174.

Jauss, R.-T., Nowack, A., Walden, S., Wolf, R., Schaffer, S., Schellbach, B., Bonkowski, M., & Schlegel, M. (2021). To the canopy and beyond: Air dispersal as a mechanism of ubiquitous protistan pathogen assembly in tree canopies. European Journal of Protistology, 80: 125805.

Kirstein, A. S., Kehr, S., Nebe, M., Hanschkow, M., Barth, L. A., Lorenz, J., Penke, M., Breitfeld, J., Le Duc, D., Landgraf, K., Körner, A., Kovacs, P., Stadler, P. F., Kiess, W., & Garten, A. (2021). PTEN regulates adipose progenitor cell growth, differentiation, and replicative aging. Journal of Biological Chemistry, 297(2): 100968.

Kutanan, W., Liu, D., Kampuansai, J., Srikummool, M., Srithawong, S., Shoocongdej, R., Sangkhano, S., Ruangchai, S., Pittayaporn, P., Arias, L., & Stoneking, M. (2021). Reconstructing the human genetic history

of mainland Southeast Asia: Insights from genome-wide data from Thailand and Laos. Molecular Biology and Evolution, 38(8), 3459-3477.

Kyrousi, C., O'Neill, A. C., Brazovskaja, A., He, Z., Kielkowski, P., Coquand, L., Di Giaimo, R., D' Andrea, P., Belka, A., Forero Echeverry, A., Mei, D., Lenge, M., Cruceanu, C., Buchsbaum, I. Y., Khattak, S., Fabien, G., Binder, E., Elmslie, F., Guerrini, R., Baffet, A. D., Sieber, S. A., Treutlein, B., Robertson, S. P., & Cappello, S. (2021). Extracellular LGALS3BP regulates neural progenitor position and relates to human cortical complexity. Nature Communications, 12(1): 6298.

Le Duc, D., Hentschel, J., Neuser, S., Stiller, M., Meier, C., Jäger, E., Abou Jamra, R., Platzer, K., Monecke, A., Ziemer, M., Markovic, A., Bläker, H., & Lemke, J. R. (2021). In cis TP53 and RAD51C pathogenic variants may predispose to sebaceous gland carcinomas. European Journal of Human Genetics, 29, 489-494.

Lin, H.-C., He, Z., Ebert, S., Schörnig, M., Santel, M., Nikolova, M. T., Weigert, A., Hevers, W., Kasri, N. N., Taverna, E., Camp, J. G., & Treutlein, B. (2021). NGN2 induces diverse neuron types from human pluripotency. Stem Cell Reports, 16, 2118-2127.

Lin, T.-Y., Gerber, T., Taniguchi-Sugiura, Y., Murawala, P., Hermann, S., Grosser, L., Shibata, E., Treutlein, B., & Tanaka, E. M. (2021). Fibroblast dedifferentiation as a determinant of successful regeneration. Developmental Cell, 56(10), 1541-1551.e6.

Mafessoni, F., Lachmann, M., & Gokhale, C. S. (2021). On the fitness of informative cues in complex environments. Journal of Theoretical Biology, 527: 110819.

Maricic, T., Helmbrecht, N., Riesenberg, S., Macak, D., Kanis, P., Lackner, M., Pugach-Matveeva, A. D., & Pääbo, S. (2021). Comment on "Reintroduction of the archaic variant of NOVA1 in cortical organoids alters neurodevelopment". Science, 374(6565), 269.

Martinón-Torres, M., d'Errico, F., Santos, E., Álvaro Gallo, A., Amano, N., Archer, W., Armitage, S. J., Arsuaga, J. L., de Castro, B., María, J., Blinkhorn, J., Crowther, A., Douka, K., Dubernet, S., Faulkner, P., Fernández-Colón, P., Kourampas, N., González García, J., Larreina, D., Le Bourdonnec, F.-X., MacLeod, G., Martín-Francés, L., Massilani, D., Mercader, J., Miller, J. M., Ndiema, E., Notario, B., Pitarch Martí, A., Prendergast, M. E., Queffelec, A., Rigaud, S., Roberts, P., Shoaee, M. J., Shipton, C., Simpson, I., Boivin, N., & Petraglia, M. D. (2021). Earliest known human burial in Africa. Nature, 593(7857), 95-100.

Matsumae, H., Ranacher, P., Savage, P. E., Blasi, D. E., Currie, T. E., Koganebuchi, K., Nishida, N., Sato, T., Tanabe, H., Tajima, A., Brown, S., Stoneking, M., Shimizu, K. K., Oota, H., & Bickel, B. (2021). Exploring correlations in genetic and cultural variation across language families in northeast Asia. Science Advances, 7(34): eabd9223.

Nakanishi, T., Pigazzini, S., Degenhardt, F., Cordioli, M., Butler-Laporte, G., Maya-Miles, D., Bujanda, L., Bouysran, Y., Niemi, M. E., Palom, A., Ellinghaus, D., Khan, A., Martínez-Bueno, M., Rolker, S., Amitrano, S., Tato, L. R., Fava, F., FinnGen, (HGI), T.-C.-1.-H.-G.-I., Spinner, C. D., Prati, D., Bernardo, D., Garcia, F., Darcis, G., Fernández-Cadenas, I., Holter, J. C., Banales, J. M., Frithiof, R., Kiryluk, K., Duga, S., Asselta, R., Pereira, A. C., Romero-Gómez, M., Nafría-Jiménez, B., Hov, J. R., Migeotte, I., Renieri, A., Planas, A. M., Ludwig, K. U., Buti, M., Rahmouni, S., Alarcón-Riquelme, M. E., Schulte, E. C., Franke, A., Karlsen, T. H., Valenti, L., Zeberg, H., Richards, J. B., & Ganna, A. (2021). Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. The Journal of Clinical Investigation, 131(23).

Overcast, I., Ruffley, M., Rosindell, J., Harmon, L., Borges, P. A. V., Emerson, B. C., Etienne, R. S., Gillespie, R., Krehenwinkel, H., Mahler, D. L., Massol, F., Parent, C. E., Patiño, J., Peter, B., Week, B., Wagner, C., Hickerson, M. J., & Rominger, A. (2021). A unified model of species abundance, genetic

diversity, and functional diversity reveals the mechanisms structuring ecological communities. Molecular Ecology Resources, 21(8), 2782-2800.

Pakendorf, B., & Stoneking, M. (2021). The genomic prehistory of peoples speaking Khoisan languages. Human Molecular Genetics, 30(2), R49-R55.

Picin, A., Benazzi, S., Blasco, R., Hajdinjak, M., Helgen, K. M., Hublin, J.-J., Rosell, J., Skoglund, P., Stringer, C., & Talamo, S. (2021). Comment on “A global environmental crisis 42,000 years ago”. Science, 374(6570): eabi8330.

Pugach, I., Hübner, A., Hung, H.-c., Meyer, M., Carson, M. T., & Stoneking, M. (2021). Ancient DNA from Guam and the peopling of the Pacific. Proceedings of the National Academy of Sciences, 118(1): e202211211.

Reinscheid, R. K., Mafessoni, F., Lüttjohann, A., Jüngling, K., Pape, H.-C., & Schulz, S. (2021). Neandertal introgression and accumulation of hypomorphic mutations in the neuropeptide S (NPS) system promote attenuated functionality. Peptides, 138: 170506.

Schörnig, M., & Taverna, E. (2021). A closer look to the evolution of neurons in humans and apes using stem-cell-derived model systems. Frontiers in Cell and Developmental Biology, 9: 661113.

Schörnig, M., Ju, X.-C., Fast, L., Weigert, A., Schaffer, T., Ebert, S., Treutlein, B., Kasri, N. N., Peter, B., Hevers, W., & Taverna, E. (2021). Comparison of induced neurons reveals slower structural and functional maturation in humans than in apes. eLife, 10: e59323.

Shull, G., Haffner, C., Huttner, W. B., Taverna, E., & Kodandaramaiah, S. B. (2021). Manipulation of Single Neural Stem Cells and Neurons in Brain Slices using Robotic Microinjection. Journal of Visualized Experiments, 167: e61599.

Silvestrini, S., Romandini, M., Marciani, G., Arrighi, S., Carrera, L., Fiorini, A., López-García, J. M., Lugli, F., Ranaldo, F., Slon, V., Tassoni, L., Higgins, O. A., Bortolini, E., Curci, A., Meyer, M., Meyer, M. C., Oxilia, G., Zerboni, A., Benazzi, S., & Spinapolice, E. E. (2021). Integrated multidisciplinary ecological analysis from the Uluzzian settlement at the Uluzzo C Rock Shelter, south-eastern Italy. Journal of Quaternary Science, 37(2): jqs.3341, pp. 235-256.

Srithawong, S., Muisuk, K., Srikummool, M., Kampuansai, J., Pittayaporn, P., Ruangchai, S., Liu, D., & Kutanan, W. (2021). Close genetic relationship between central Thai and Mon people in Thailand revealed by autosomal microsatellites. International Journal of Legal Medicine, 135, 445-448.

Stepanova, V., Moczulska, K., Vacano, G. N., Kurochkin, I., Ju, X.-C., Riesenberg, S., Macak, D., Maricic, T., Dombrowski, L., Schörnig, M., Anastassiadis, K., Baker, O., Naumann, R., Khrameeva, E., Vanushkina, A., Stekolschikova, E., Egorova, A., Nkatchev, A., Mazzarino, R., Duval, N., Zubkov, D., Giavalisco, P., Wilkinson, T. G., Patterson, D., Khaitovich, P., & Pääbo, S. (2021). Reduced purine biosynthesis in humans after their divergence from Neandertals. eLife, 10: e58741.

Stoneking, M. (2021). Genomic insights into the Out-of-Africa dispersal(s) of modern humans. In M. d. L. Muñoz-Moreno, & M. H. Crawford (Eds.), Human migration: Biocultural perspectives (pp. 9-19). Oxford: Oxford University Press.

Suchý, T., Kaczmarek, I., Maricic, T., Zieschang, C., Schöneberg, T., Thor, D., & Liebscher, I. (2021). Evaluating the feasibility of Cas9 overexpression in 3T3-L1 cells for generation of genetic knock-out adipocyte cell lines. Adipocyte, 10(1), 631-645.

Trucchi, E., Gratton, P., Mafessoni, F., Motta, S., Cicconardi, F., Bertorelle, G., D’Annessa, I., & Marino, D.

D. (2021). Population dynamics and structural effects at short and long range support the hypothesis of the selective advantage of the G614 SARS-CoV-2 spike variant. Molecular Biology and Evolution, 38(5), 1966-1979.

Velluva, A., Radtke, M., Horn, S., Popp, B., Platzer, K., Gjermeni, E., Lin, C.-C., Lemke, J. R., Garten, A., Schöneberg, T., Blüher, M., Abou Jamra, R., & Le Duc, D. (2021). Phenotype-tissue expression and exploration (PTEE) resource facilitates the choice of tissue for RNA-seq-based clinical genetics studies. BMC Genomics, 22(802).

Vernot, B., Zavala, E. I., Gómez-Olivencia, A., Jacobs, Z., Slon, V., Mafessoni, F., Romagné, F., Pearson, A., Petr, M., Sala, N., Pablos, A., Aranburu, A., de Castro, J. M. B., Carbonell, E., Li, B., Krajcarz, M. T., Krivoshapkin, A. I., Kolobova, K. A., Kozlikin, M. B., Shunkov, M. V., Derevianko, A. P., Viola, B., Grote, S., Essel, E., López Herráez, D., Nagel, S., Nickel, B., Richter, J., Schmidt, A., Peter, B., Kelso, J., Roberts, R. G., Arsuaga, J.-L., & Meyer, M. (2021). Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments. Science, eabf1667.

Zavala, E. I., Jacobs, Z., Vernot, B., Shunkov, M. V., Kozlikin, M. B., Derevianko, A. P., Essel, E., de Filippo, C., Nagel, S., Richter, J., Romagné, F., Schmidt, A., Li, B., O'Gorman, K., Slon, V., Kelso, J., Pääbo, S., Roberts, R. G., & Meyer, M. (2021). Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave. Nature, 595, 399-403.

Zeberg, H., & Pääbo, S. (2021). A genomic region associated with protection against severe COVID-19 is inherited from Neandertals. Proceedings of the National Academy of Sciences, 118(9): e2026309118.

2020

Balzeau, A., Turq, A., Talamo, S., Daujeard, C., Guérin, G., Welker, F., Crevecoeur, I., Fewlass, H., Hublin, J.-J., Lahaye, C., Maureille, B., Meyer, M., Schwab, C., & Gómez-Olivencia, A. (2020). Pluridisciplinary evidence for burial for the La Ferrassie 8 Neandertal child. Scientific Reports, 10: 21230.

Bokelmann, L., Glocke, I., & Meyer, M. (2020). Reconstructing double-stranded DNA fragments on a single-molecule level reveals patterns of degradation in ancient samples. Genome Research, 30(10), 1449-1457.

Braadbaart, F., Reidsma, F., Roebroeks, W., Chiotti, L., Slon, V., Meyer, M., Théry-Parisot, I., van Hoesel, A., Nierop, K., Kaal, J., van Os, B., & Marquer, L. (2020). Heating histories and taphonomy of ancient fireplaces: A multi-proxy case study from the Upper Palaeolithic sequence of Abri Pataud (Les Eyzies-de-Tayac, France). Journal of Archaeological Science: Reports, 33: 102468.

Cauret, C. M. S., Gansauge, M.-T., Tupper, A. S., Furman, B. L. S., Knytl, M., Song, X., Greenbaum, E., Meyer, M., & Evans, B. J. (2020). Developmental systems drift and the drivers of sex chromosome evolution. Molecular Biology and Evolution, 37(3), 799-808.

Dannemann, M., He, Z., Heide, C., Vernot, B., Sidow, L., Kanton, S., Weigert, A., Treutlein, B., Pääbo, S., Kelso, J., & Camp, J. G. (2020). Human stem cell resources are an inroad to Neandertal DNA functions. Stem Cell Reports, 15, 214-225.

Evans, B. J., Gansauge, M.-T., Tocheri, M. W., Schillaci, M. A., Sutikna, T., Jatmiko, Saptomo, E. W., Klegarth, A., Tosi, A. J., Melnick, D. J., & Meyer, M. (2020). Mitogenomics of macaques (Macaca) across Wallace's Line in the context of modern human dispersals. Journal of Human Evolution, 146: 102852.

Gansauge, M.-T., Aximu-Petri, A., Nagel, S., & Meyer, M. (2020). Manual and automated preparation of single-stranded DNA libraries for the sequencing of DNA from ancient biological remains and other sources

of highly degraded DNA. Nature Protocols, 15, 2279-2300.

Gunnarsdottir, E. D., & Stoneking, M. (2020). Genetic Landscape of Present-Day Hunter-Gatherer Groups. In T. Güldemann (Ed.), Language of Hunter-Gatherers (pp. 49-75). Cambridge: Cambridge University Press.

He, Z., Brazovskaja, A., Ebert, S., Camp, J. G., & Treutlein, B. (2020). CSS: Cluster similarity spectrum integration of single-cell genomics data. Genome Biology, 21: 224.

Hublin, J.-J., Sirakov, N., Aldeias, V., Bailey, S., Bard, E., Delvigne, V., Endarova, E., Fagault, Y., Fewlass, H., Hajdinjak, M., Kromer, B., Krumov, I., Marreiros, J., Martisius, N. L., Paskulin, L., Sinet-Mathiot, V., Meyer, M., Pääbo, S., Popov, V., Rezek, Z., Sirakova, S., Skinner, M. M., Smith, G. M., Spasov, R., Talamo, S., Tuna, T., Wacker, L., Welker, F., Wilcke, A., Zahariev, N., McPherron, S. P., & Tsanova, T. (2020). Initial Upper Palaeolithic Homo sapiens from Bacho Kiro Cave, Bulgaria. Nature, 581(7808), 299-302.

Kanton, S., Treutlein, B., & Camp, J. G. (2020). Single-cell genomic analysis of human cerebral organoids. In J. R. Spence (Ed.), Human Pluripotent Stem Cell Derived Organoid Models (pp. 229-256). Elsevier.

Key, F. M., Posth, C., Esquivel-Gomez, L. R., Hübler, R., Spyrou, M. A., Neumann, G., Furtwängler, A., Sabin, S., Burri, M., Wissgott, A., Lankapalli, A. K., Vågene, Å. J., Meyer, M., Nagel, S., Tukhbatova, R. I., Khokhlov, A., Chizhevsky, A., Hansen, S., Belinsky, A. B., Kalmykov, A., Kantorovich, A. R., Maslov, V. E., Stockhammer, P. W., Vai, S., Zavattaro, M., Riga, A., Caramelli, D., Skeates, R., Beckett, J., Gradoli, M. G., Steuri, N., Hafner, A., Ramstein, M., Siebke, I., Lösch, S., Erdal, Y. S., Alikhan, N.-F., Zhou, Z., Achtman, M., Bos, K. I., Reinhold, S., Haak, W., Kühnert, D., Herbig, A., & Krause, J. (2020). Emergence of human-adapted Salmonella enterica is linked to the Neolithization process. Nature Ecology & Evolution, 4, 324-333.

Khan, N., de Manuel, M., Peyrégne, S., Do, R., Prüfer, K., Marques-Bonet, T., Varki, N., Gagneux, P., & Varki, A. (2020). Multiple Genomic Events Altering Hominin SIGLEC Biology and Innate Immunity Predated the Common Ancestor of Humans and Archaic Hominins. Genome Biology and Evolution, 12(7), 1040-1050.

Khrameeva, E., Kurochkin, I., Han, D., Guijarro, P., Kanton, S., Santel, M., Qian, Z., Rong, S., Mazin, P., Sabirov, M., Bulat, M., Efimova, O., Tkachev, A., Guo, S., Sherwood, C. C., Camp, J. G., Pääbo, S., Treutlein, B., & Khaitovich, P. (2020). Single-cell-resolution transcriptome map of human, chimpanzee, bonobo, and macaque brains. Genome Research, 30(5), 776-789.

Kutanan, W., Shoocongdej, R., Srikummool, M., Hübner, A., Suttipai, T., Srithawong, S., Kampuansai, J., & Stoneking, M. (2020). Cultural variation impacts paternal and maternal genetic lineages of the Hmong-Mien and Sino-Tibetan groups from Thailand. European Journal of Human Genetics, 28, 1563-1579.

Lang, P. L. M., Weiß, C. L., Kersten, S., Latorre, S. M., Nagel, S., Nickel, B., Meyer, M., & Burbano, H. A. (2020). Hybridization ddRAD-sequencing for population genomics of nonmodel plants using highly degraded historical specimen DNA. Molecular Ecology Resources, 20(5), 1228-1247.

Liu, D., Duong, N. T., Ton, N. D., Van Phong, N., Pakendorf, B., Van Hai, N., & Stoneking, M. (2020). Extensive ethnolinguistic diversity in Vietnam reflects multiple sources of genetic diversity. Molecular Biology and Evolution, 37(9): msaa099, pp. 2503-2519.

Mafessoni, F., Grote, S., de Filippo, C., Slon, V., Kolobova, K. A., Viola, B., Markin, S. V., Chintalapati, M., Peyrégne, S., Skov, L., Skoglund, P., Krivoshapkin, A. I., Derevianko, A. P., Meyer, M., Kelso, J., Peter, B., Prüfer, K., & Pääbo, S. (2020). A high-coverage Neandertal genome from Chagyrskaya Cave. Proceedings of the National Academy of Sciences, 117(26), 15132-15136.

Maricic, T., Nickel, O., Ayinuer-Petri, A., Essel, E., Gansauge, M.-T., Kanis, P., Macak, D., Riesenberg, S., Bokelmann, L., Zeberg, H., Meyer, M., Borte, S., & Pääbo, S. (2020). A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. PLoS One, 15(12): e0244824.

Massilani, D., Skov, L., Hajdinjak, M., Gunchinsuren, B., Tseveendorj, D., Yi, S., Lee, J., Nagel, S., Nickel, B., Devièse, T., Higham, T., Meyer, M., Kelso, J., Peter, B., & Pääbo, S. (2020). Denisovan ancestry and population history of early East Asians. Science, 370(6516), 579-583.

Miller, A. J., Yu, Q., Czerwinski, M., Tsai, Y.-H., Conway, R. F., Wu, A., Holloway, E. M., Walker, T., Glass, I. A., Treutlein, B., Camp, J. G., & Spence, J. R. (2020). In vitro and in vivo development of the human airway at single-cell resolution. Developmental Cell, 53(1): e6, pp. 117-128.

Mitina, A., Mazin, P., Vanyushkina, A., Anikanov, N., Mair, W., Guo, S., & Khaitovich, P. (2020). Lipidome analysis of milk composition in humans, monkeys, bovids, and pigs. BMC Evolutionary Biology, 20(70).

Ou, M.-Y., Ju, X.-C., Cai, Y.-J., Sun, X.-Y., Wang, J.-F., Fu, X.-Q., Sun, Q., & Luo, Z.-G. (2020). Heterogeneous nuclear ribonucleoprotein A3 controls mitotic progression of neural progenitors via interaction with cohesin. Development, 147: dev185132.

Parker, E. C., Rohrlach, A. B., Friederich, S., Nagel, S., Meyer, M., Krause, J., Bos, K. I., & Haak, W. (2020). A systematic investigation of human DNA preservation in medieval skeletons. Scientific Reports, 10(1): 18225.

Pedro, N., Brucato, N., Fernandes, V., André, M., Saag, L., Pomat, W., Besse, C., Boland, A., Deleuze, J.-F., Clarkson, C., Sudoyo, H., Metspalu, M., Stoneking, M., Cox, M. P., Leavesley, M., Pereira, L., & Ricaut, F.-X. (2020). Papuan mitochondrial genomes and the settlement of Sahul. Journal of Human Genetics, 65(875), 887.

Peter, B. M., Petkova, D., & Novembre, J. (2020). Genetic landscapes reveal how human genetic diversity aligns with geography. Molecular Biology and Evolution, 37(4), 943-951.

Petr, M., Hajdinjak, M., Fu, Q., Essel, E., Rougier, H., Crevecoeur, I., Semal, P., Golovanova, L. V., Doronichev, V. B., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Shunkov, M. V., Kozlikin, M. B., Derevianko, A. P., Vernot, B., Meyer, M., & Kelso, J. (2020). The evolutionary history of Neanderthal and Denisovan Y chromosomes. Science, 369(6511), 1653-1656.

Peyrégne, S. (2020). Tracing the ancestral roots of Neandertals. The Science Breaker, 6(1).

Peyrégne, S., & Peter, B. M. (2020). AuthentiCT: A model of ancient DNA damage to estimate the proportion of present-day DNA contamination. Genome Biology, 21: 246.

Peyrégne, S., & Prüfer, K. (2020). Present-Day DNA contamination in ancient DNA datasets. BioEssays, 42: 2000081.

Romandini, M., Gregorio, O., Bortolini, E., Peyrégne, S., Delpiano, D., Nava, A., Panetta, D., Domenico, G. D., Martini, P., Arrighi, S., Badino, F., Figus, C., Lugli, F., Marciani, G., Silvestrini, S., Sartorio, J. C. M., Terlato, G., Hublin, J.-J., Meyer, M., Bondioli, L., Higham, T., Slon, V., Peresani, M., & Benazzi, S. (2020). A late Neanderthal tooth from northeastern Italy. Journal of Human Evolution, 147: 102867.

Semo, A., Gayà-Vidal, M., Fortes-Lima, C., Alard, B., Oliveira, S., Almeida, J., Prista, A., Damasceno, A., Fehn, A., Schlebusch, C., & Rocha, J. (2020). Along the Indian Ocean coast: Genomic variation in Mozambique provides new insights into the Bantu expansion. Molecular Biology and Evolution, 37(2), 406-416.

Skov, L., Macià, M. C., Sveinbjörnsson, G., Mafessoni, F., Lucotte, E. A., Einarsdóttir, M. S., Jonsson, H., Halldorsson, B., Gudbjartsson, D. F., Helgason, A., Schierup, M. H., & Stefansso, K. (2020). The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. Nature, 582, 78-83.

Telford, M., Hughes, D. A., Juan, D., Stoneking, M., Navarro, A., & Santpere, G. (2020). Expanding the Geographic Characterisation of Epstein–Barr Virus Variation through Gene-Based Approaches. Microorganisms, 8: 1686.

Voiculescu, S. E., Le Duc, D., Rosca, A. E., & Zagrean, A.-M. (2020). The pineal gland development and its physiology in fetus and neonate. In C. S. Kovacs, & C. L. Deal (Eds.), Maternal-Fetal and Neonatal Endocrinology: Physiology, Pathophysiology, and Clinical Management (pp. 547-561). Academic Press.

Weiß, C. L., Gansauge, M.-T., Aximu-Petri, A., Meyer, M., & Burbano, H. A. (2020). Mining ancient microbiomes using selective enrichment of damaged DNA molecules. BMC Genomics, 21: 432.

Yang, M. A., Fan, X., Sun, B., Chen, C., Lang, J., Ko, Y.-C., Tsang, C.-h., Chiu, H., Wang, T., Bao, Q., Wu, X., Hajdinjak, M., Ko, A.-M.-S., Ding, M., Cao, P., Yang, R., Liu, F., Nickel, B., Dai, Q., Feng, X., Zhang, L., Sun, C., Ning, C., Zeng, W., Zhao, Y., Zhang, M., Gao, X., Cui, Y., Reich, D., Stoneking, M., & Fu, Q. (2020). Ancient DNA indicates human population shifts and admixture in northern and southern China. Science, 369(6501), 282-288.

Zeberg, H., & Pääbo, S. (2020). The major genetic risk factor for severe COVID-19 is inherited from Neanderthals. Nature, 587(7835), 610-612.

Zeberg, H., Dannemann, M., Sahlholm, K., Tsuo, K., Maricic, T., Wiebe, V., Hevers, W., Robinson, H. P., Kelso, J., & Pääbo, S. (2020). A Neandertal sodium channel increases pain sensitivity in present-day humans. Current Biology, 30(17), 3465-3469.

Zeberg, H., Kelso, J., & Pääbo, S. (2020). The Neandertal progesterone receptor. Molecular Biology and Evolution, 37(9): msaa119, pp. 2655-2660.

Zhang, D., Xia, H., Chen, F., Li, B., Slon, V., Cheng, T., Yang, R., Jacobs, Z., Dai, Q., Massilani, D., Shen, X., Wang, J., Feng, X., Cao, P., Yang, M. A., Yao, J., Yang, J., Madsen, D. B., Han, Y., Ping, W., Liu, F., Perreault, C., Chen, X., Meyer, M., Kelso, J., Pääbo, S., & Fu, Q. (2020). Denisovan DNA in Late Pleistocene sediments from Baishiya Karst Cave on the Tibetan Plateau. Science, 370(6516), 584-587.

2019

Barbieri, C., Barquera, R., Arias, L., Sandoval, J. R., Acosta, O., Zurita, C., Aguilar-Campos, A., Tito-Álvarez, A. M., Serrano-Osuna, R., Gray, R. D., Mafessoni, F., Heggarty, P., Shimizu, K. K., Fujita, R., Stoneking, M., Pugach, I., & Fehren-Schmitz, L. (2019). The current genomic landscape of Western South America: Andes, Amazonia, and Pacific Coast. Molecular Biology and Evolution, 36(12), 2698-2713.

Bokelmann, L., Hajdinjak, M., Peyrégne, S., Brace, S., Essel, E., de Filippo, C., Glocke, I., Grote, S., Mafessoni, F., Nagel, S., Kelso, J., Prüfer, K., Vernot, B., Barnes, I., Pääbo, S., Meyer, M., & Stringer, C. (2019). A genetic analysis of the Gibraltar Neanderthals. Proceedings of the National Academy of Sciences, 116(31), 15610-15615.

Brazovskaja, A., Treutlein, B., & Camp, J. G. (2019). High-throughput single-cell transcriptomics on organoids. Current Opinion in Biotechnology, 55, 167-171.

Bücking, R., Cox, M. P., Hudjashov, G., Saag, L., Sudoyo, H., & Stoneking, M. (2019). Archaic

mitochondrial DNA inserts in modern day nuclear genomes. BMC Genomics, 20: 1017.

Dabney, J., & Meyer, M. (2019). Extraction of highly degraded DNA from ancient bones and teeth. In B. Shapiro, A. Barlow, P. D. Heintzman, M. Hofreiter, J. L. A. Paijmans, & A. E. R. Soares (Eds.), Ancient DNA: Methods and Protocols (2nd ed., pp. 25-29). New York, NY: Springer.

Dannemann, M. (2019). Der Neandertaler in uns. BIOspektrum, 25(5), 497-499.

Devièse, T., Massilani, D., Yi, S., Comeskey, D., Nagel, S., Nickel, B., Ribechini, E., Lee, J., Tseveendorj, D., Gunchinsuren, B., Meyer, M., Pääbo, S., & Higham, T. (2019). Compound-specific radiocarbon dating and mitochondrial DNA analysis of the Pleistocene hominin from Salkhit Mongolia. Nature Communications, 10(10): 274.

Douka, K., Brown, S., Higham, T., Pääbo, S., Derevianko, A., & Shunkov, M. (2019). FINDER project: Collagen fingerprinting (ZooMS) for the identification of new human fossils. Antiquity, 93(367): e1.

Douka, K., Slon, V., Jacobs, Z., Ramsey, C. B., Shunkov, M. V., Derevianko, A. P., Mafessoni, F., Kozlikin, M. B., Li, B., Grün, R., Comeskey, D., Devièse, T., Brown, S., Viola, B., Kinsley, L., Buckley, M., Meyer, M., Roberts, R. G., Pääbo, S., Kelso, J., & Higham, T. (2019). Age estimates for hominin fossils and the onset of the Upper Palaeolithic at Denisova Cave. Nature, 565(7741), 640-644.

Drukewitz, S. H., Bokelmann, L., Undheim, E. A. B., & von Reumont, B. M. (2019). Toxins from scratch? Diverse, multimodal gene origins in the predatory robber fly Dasypogon diadema indicate a dynamic venom evolution in dipteran insects. GigaScience, 8(7): giz081.

Drukewitz, S. H., Jauss, R.-T., Bokelmann, L., & von Reumont, B. M. (2019). The complete mitochondrial genome of the hymenopteran hunting robber fly Dasypogon diadema. Mitochondrial DNA Part B, 4(1), 1584-1585.

Evans, B. J., Gansauge, M.-T., Stanley, E. L., Furman, B. L. S., Cauret, C. M. S., Ofori-Boateng, C., Gvoždík, V., Streicher, J. W., Greenbaum, E., Tinsley, R. C., Meyer, M., & Blackburn, D. C. (2019). Xenopus fraseri: Mr. Fraser, where did your frog come from? PLoS One, 14(9): e0220892.

Ezra, D., Hershkovitz, I., Salame, K., Alperovitch-Najenson, D., & Slon, V. (2019). Osteophytes in the Cervical Vertebral Bodies (C3–C7)—Demographical Perspectives. The Anatomical Record, 302(2), 226-231.

Ezra, D., Slon, V., Kedar, E., Masharawi, Y., Salame, K., Alperovitch-Najenson, D., & Hershkovitz, I. (2019). The torg ratio of C3-C7 in African Americans and European Americans: A skeletal study. Clinical Anatomy, 32(1), 84-89.

Gansauge, M.-T., & Meyer, M. (2019). A method for single-stranded ancient DNA library preparation. In B. Shapiro, A. Barlow, P. D. Heintzman, M. Hofreiter, J. L. A. Paijmans, & A. E. R. Soares (Eds.), Ancient DNA: Methods and Protocols (2nd ed., pp. 75-83). New York, NY: Springer.

Giner-Delgado, C., Villatoro, S., Lerga-Jaso, J., Gayà-Vidal, M., Oliva, M., Castellano, D., Pantano, L., Bitarello, B. D., Izquierdo, D., Noguera, I., Olalde, I., Delprat, A., Blancher, A., Lalueza-Fox, C., Esko, T., O'Reilly, P. F., Andrés, A. M., Ferretti, L., Puig, M., & Cáceres, M. (2019). Evolutionary and functional impact of common polymorphic inversions in the human genome. Nature Communications, 10(4222).

Gunz, P., Tilot, A. K., Wittfeld, K., Teumer, A., Shapland, C. Y., van Erp, T. G. M., Dannemann, M., Vernot, B., Neubauer, S., Guadalupe, T., Fernández, G., Brunner, H. G., Enard, W., Fallon, J., Hosten, N., Völker, U., Profico, A., Di Vincenzo, F., Manzi, G., Kelso, J., St. Pourcain, B., Hublin, J.-J., Franke, B., Pääbo, S., Macciardi, F., Grabe, H. J., & Fisher, S. E. (2019). Neandertal introgression sheds light on modern human endocranial globularity. Current Biology, 29(1), 120-127.e5.

Han, S., Andrés, A. M., & Marques-Bonet, T. (2019). Genetic variation in Pan species is shaped by demographic history and harbors lineage-specific functions. Genome Biology and Evolution, 11(4), 1178-1191.

Hübner, A., Wachsmuth, M., Schröder, R., Li, M., Eis-Hübinger, A. M., Madea, B., & Stoneking, M. (2019). Sharing of heteroplasmies between human liver lobes varies across the mtDNA genome. Scientific Reports, 9: 11219.

Jacobs, G. S., Hudjashov, G., Saag, L., Kusuma, P., Darusallam, C. C., Lawson, D. J., Mondal, M., Pagani, L., Ricaut, F.-X., Stoneking, M., Metspalu, M., Sudoyo, H., Lansing, J. S., & Cox, M. P. (2019). Multiple deeply divergent Denisovan ancestries in Papuans. Cell, 117(4), 1010-1021.

Kanton, S., Boyle, M. J., He, Z., Santel, M., Weigert, A., Sanchís-Calleja, F., Guijarro, P., Sidow, L., Fleck, J. S., Han, D., Qian, Z., Heide, M., Huttner, W. B., Khaitovich, P., Pääbo, S., Treutlein, B., & Camp, J. G. (2019). Organoid single-cell genomic atlas uncovers human-specific features of brain development. Nature, 574(7778), 418-422.

Klaus, J., Kanton, S., Kyrousi, C., Ayo-Martin, A. C., Giaimo, R. D., Riesenberg, S., O'Neill, A. C., Camp, J. G., Tocco, C., Santel, M., Rusha, E., Drukker, M., Schroeder, M., Götz, M., Robertson, S. P., Treutlein, B., & Cappello, S. (2019). Altered neuronal migratory trajectories in human cerebral organoids derived from individuals with neuronal heterotopia. Nature Medicine, 25, 561-568.

Klein, A. M., & Treutlein, B. (2019). Single cell analyses of development in the modern era. Development, 146(12): dev181396.

Kutanan, W., Kampuansai, J., Srikummool, M., Brunelli, A., Ghirotto, S., Arias, L., Macholdt, E., Hübner, A., Schröder, R., & Stoneking, M. (2019). Contrasting paternal and maternal genetic histories of Thai and Lao populations. Molecular Biology and Evolution, 36(7): msz083, pp. 1490-1506.

Laval, G., Peyrégne, S., Zidane, N., Harmant, C., Renaud, F., Patin, E., Prugnolle, F., & Quintana-Murci, L. (2019). Recent adaptive acquisition by African rainforest hunter-gatherers of the late Pleistocene sickle-cell mutation suggests past differences in malaria exposure. The American Journal of Human Genetics, 104(3), 553-561.

Macholdt, E., Arias, L., Duong, N. T., Ton, N. D., Van Phong, N., Schröder, R., Pakendorf, B., Van Hai, N., & Stoneking, M. (2019). The paternal and maternal genetic history of Vietnamese populations. European Journal of Human Genetics, 28(5), 636-645.

Mafessoni, F. (2019). Encounters with archaic hominins. Nature Ecology and Evolution, 3, 14-15.

Mafessoni, F., & Lachmann, M. (2019). The complexity of understanding others as the evolutionary origin of empathy and emotional contagion. Scientific Reports, 9: 5794.

Narasimhan, V. M., Patterson, N., Moorjani, P., Rohland, N., Bernardos, R., Mallick, S., Lazaridis, I., Nakatsuka, N., Olalde, I., Lipson, M., Kim, A. M., Olivieri, L. M., Coppa, A., Vidale, M., Mallory, J., Moiseyev, V., Kitov, E., Monge, J., Adamski, N., Alex, N., Broomandkhoshbacht, N., Candilio, F., Callan, K., Cheronet, O., Culleton, B. J., Ferry, M., Fernandes, D., Freilich, S., Gamarra, B., Gaudio, D., Hajdinjak, M., Harney, É., Harper, T. K., Keating, D., Lawson, A. M., Mah, M., Mandl, K., Michel, M., Novak, M., Oppenheimer, J., Rai, N., Sirak, K., Slon, V., Stewardson, K., Zalzala, F., Zhang, Z., Akhatov, G., Bagashev, A. N., Bagnera, A., Baitanayev, B., Bendezu-Sarmiento, J., Bissembaev, A. A., Bonora, G. L., Chargynov, T. T., Chikisheva, T., Dashkovskiy, P. K., Derevianko, A., Dobeš, M., Douka, K., Dubova, N., Duisengali, M. N., Enshin, D., Epimakhov, A., Fribus, A. V., Fuller, D., Goryachev, A., Gromov, A., Grushin, S. P., Hanks, B., Judd, M., Kazizov, E., Khokhlov, A., Krygin, A. P., Kupriyanova, E., Kuznetsov, P., Luiselli,

D., Maksudov, F., Mamedov, A. M., Mamirov, T. B., Meiklejohn, C., Merrett, D. C., Micheli, R., Mochalov, O., Mustafokulov, S., Nayak, A., Pettener, D., Potts, R., Razhev, D., Rykun, M., Sarno, S., Savenkova, T. M., Sikhymbaeva, K., Slepchenko, S. M., Soltobaev, O. A., Stepanova, N., Svyatko, S., Tabaldiev, K., Teschler-Nicola, M., Tishkin, A. A., Tkachev, V. V., Vasilyev, S., Velemínský, P., Voyakin, D., Yermolayeva, A., Zahir, M., Zubkov, V. S., Zubova, A., Shinde, V. S., Lalueza-Fox, C., Meyer, M., Anthony, D., Boivin, N., Thangaraj, K., Kennett, D. J., Frachetti, M., Pinhasi, R., & Reich, D. (2019). The formation of human populations in South and Central Asia. Science, 365(6457): eaat7487.

Nersisyan, L., Nikoghosyan, M., Arakelyan, A., Genome of the Netherlands Consortium, including authors, Stoneking, M., Li, M., & others (2019). WGS-based telomere length analysis in Dutch family trios implicates stronger maternal inheritance and a role for RRM1 gene. Scientific Reports, 9: 18758.

Oliveira, S., Hübner, A., Fehn, A.-M., Aço, T., Lages, F., Pakendorf, B., Stoneking, M., & Rocha, J. (2019). The role of matrilineality in shaping patterns of Y chromosome and mtDNA sequence variation in southwestern Angola. European Journal of Human Genetics, 27, 475-483.

Pääbo, S. (2019). Lessons from our inner Neanderthal: How extinct hominins live on in people today; the genomes of now-extinct archaic humans can help us understand more about what makes us modern-day humans truly unique. In S. Shuzhen, & B. Seet (Eds.), Sydney Brenner's 10-on-10: the chronicles of evolution (pp. 129-137). Singapore: Wildtype Books.

Parra, R. G., Papadopoulos, N., Ahumada-Arranz, L., El Kholtei, J., Mottelson, N., Horokhovsky, Y., Treutlein, B., & Soeding, J. (2019). Reconstructing complex lineage trees from scRNA-seq data using MERLoT. Nucleic Acids Research, 47(17), 8961-8974.

Petr, M., Pääbo, S., Kelso, J., & Vernot, B. (2019). Limits of long-term selection against Neandertal introgression. Proceedings of the National Academy of Sciences, 116(5), 1639-1644.

Petr, M., Vernot, B., & Kelso, J. (2019). admixr – R package for reproducible analyses using ADMIXTOOLS. Bioinformatics, 35(17): btz030, pp. 3194-3195.

Peyrégne, S., Slon, V., Mafessoni, F., de Filippo, C., Hajdinjak, M., Nagel, S., Nickel, B., Essel, E., Le Cabec, A., Wehrberger, K., Conard, N. J., Kind, C. J., Posth, C., Krause, J., Abrams, G., Bonjean, D., Di Modica, K., Toussaint, M., Kelso, J., Meyer, M., Pääbo, S., & Prüfer, K. (2019). Nuclear DNA from two early Neandertals reveals 80,000 years of genetic continuity in Europe. Science Advances, 5(6): eaaw5873.

Reher, D., Key, F. M., Andrés, A. M., & Kelso, J. (2019). Immune gene diversity in archaic and present-day humans. Genome Biology and Evolution, 11(1), 232-241.

Riesenberg, S., Chintalapati, M., Macak, D., Kanis, P., Maricic, T., & Pääbo, S. (2019). Simultaneous precise editing of multiple genes in human cells. Nucleic Acids Research, 47(19): e116.

Schmidt, J., de Manuel, M., Marques-Bonet, T., Castellano, S., & Andrés, A. M. (2019). The impact of genetic adaptation on chimpanzee subspecies differentiation. PLOS Genetics, 15(11), 1-32.

Shinde, V., Narasimhan, V. M., Rohland, N., Mallick, S., Mah, M., Lipson, M., Nakatsuka, N., Adamski, N., Broomandkhoshbacht, N., Ferry, M., Lawson, A. M., Michel, M., Oppenheimer, J., Stewardson, K., Jadhav, N., Kim, Y. J., Chatterjee, M., Munshi, A., Panyam, A., Waghmare, P., Yadav, Y., Patel, H., Kaushik, A., Thangaraj, K., Meyer, M., Patterson, N., Rai, N., & Reich, D. (2019). An ancient Harappan genome lacks ancestry from Steppe pastoralists or Iranian farmers. Cell, 179(3), 729-735.e10.

Shull, G., Haffner, C., Huttner, W. B., Kodandaramaiah, S. B., & Taverna, E. (2019). Robotic platform for microinjection into single cells in brain tissue. EMBO reports, 20(10): e47880.

Shvetsova, E., Sofronova, A., Monajemi, R., Gagalova, K., Draisma, H. H. M., White, S. J., Santen, G. W.

E., Chuva de Sousa Lopes, S. M., Heijmans, B. T., van Meurs, J., Jansen, R., Franke, L., Kielbasa, S. M., den Dunnen, J. T., ´t Hoen, P. A. C., BIOS consortium, GoNL consortium, including authors, Li, M., Stoneking, M., & & others (2019). Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 27, 455-465.

Slon, V., & Pääbo, S. (2019). Rendezvous in der Steinzeit. In Highlights 2018 aus dem Jahrbuch der Max-Planck-Gesellschaft (pp. 32-34). München: Max-Planck-Gesellschaft zur Förderung der Wissenschaften e. V.

Spataru, A., Le Duc, D., Zagrean, L., & Zagrean, A.-M. (2019). Ethanol exposed maturing rat cerebellar granule cells show impaired energy metabolism and increased cell death after oxygen-glucose deprivation. Neural Regeneration Research, 14(3), 485-490.

Swift, J. A., Bunce, M., Dortch, J., Douglass, K., Faith, J. T., Fellows Yates, J. A., Field, J., Haberle, S. G., Jacob, E., Johnson, C. N., Lindsey, E., Lorenzen, E. D., Louys, J., Miller, G., Mychajliw, A. M., Slon, V., Villavicencio, N. A., Waters, M. R., Welker, F., Wood, R., Petraglia, M. D., Boivin, N., & Roberts, P. (2019). Micro methods for megafauna: novel approaches to late quaternary extinctions and their contributions to faunal conservation in the anthropocene. Bioscience, 69(11): biz105, pp. 877-887.

Taverna, E., & Huttner, W. B. (2019). The Golgi apparatus in polarized neuroepithelial stem cells and their progeny: Canonical and noncanonical features. In M. Kloc (Ed.), The Golgi Apparatus and Centriole: Functions, Interactions and Role in Disease (pp. 359-375). Cham: Springer International Publishing.

Tkachev, A., Stepanova, V., Zhang, L., Khrameeva, E., Zubkov, D., Giavalisco, P., & Khaitovich, P. (2019). Differences in lipidome and metabolome organization of prefrontal cortex among human populations. Scientific Reports, 9: 18348.

Tyshkovskiy, A., Bozaykut, P., Borodinova, A. A., Gerashchenko, M. V., Ables, G. P., Garratt, M., Khaitovich, P., Clish, C. B., Miller, R. A., & Gladyshev, V. N. (2019). Identification and application of gene expression signatures associated with lifespan extension. Cell Metabolism, 30(3): e8, pp. 573-593.

Vai, S., Sarno, S., Lari, M., Luiselli, D., Manzi, G., Gallinaro, M., Mataich, S., Hübner, A., Modi, A., Pilli, E., Tafuri, M. A., Caramelli, D., & di Lernia, S. (2019). Ancestral mitochondrial N lineage from the Neolithic 'green' Sahara. Scientific Reports, 9(1): 3530.

Wiedenhoeft, J., Cagan, A., Kozhemyakina, R., Gulevich, R., & Schliep, A. (2019). Bayesian localization of CNV candidates in WGS data within minutes. Algorithms for Molecular Biology, 14: 20.

Wren, J. D., Valencia, A., & Kelso, J. (2019). Reviewer-coerced citation: Case report, update on journal policy and suggestions for future prevention. Bioinformatics, 35(18), 3217-3218.

2018

Arias, L., Barbieri, C., Barreto, G., Stoneking, M., & Pakendorf, B. (2018). High-resolution mitochondrial DNA analysis sheds light on human diversity, cultural interactions, and population mobility in Northwestern Amazonia. American Journal of Physical Anthropology, 165(2), 238-255.

Arias, L., Schröder, R., Hübner, A., Barreto, G., Stoneking, M., & Pakendorf, B. (2018). Cultural innovations influence patterns of genetic diversity in Northwestern Amazonia. Molecular Biology and Evolution, 35(11), 2719-2735.

Ayabe, H., Anada, T., Kamoya, T., Sato, T., Kimura, M., Yoshizawa, E., Kikuchi, S., Ueno, Y., Sekine, K., Camp, J. G., Treutlein, B., Ferguson, A., Suzuki, O., Takebe, T., & Taniguchi, H. (2018). Optimal hypoxia regulates human iPSC-derived liver bud differentiation through intercellular TGFB signaling. Stem Cell

Reports, 11(2), 306-316.

Bajic, V., Barbieri, C., Hübner, A., Güldemann, T., Naumann, C., Gerlach, L., Berthold, F., Nakagawa, H., Mpoloka, S. W., Roewer, L., Purps, J., Stoneking, M., & Pakendorf, B. (2018). Genetic structure and sex-biased gene flow in the history of southern African populations. American Journal of Physical Anthropology, 167(3): 23694, pp. 656-671.

Barlow, A., Cahill, J. A., Hartmann, S., Theunert, C., Xenikoudakis, G., Fortes, G. G., Paijmans, J. L. A., Rabeder, G., Frischauf, C., Grandal-d'Anglade, A., García-Vázquez, A., Murtskhvaladze, M., Saarma, U., Anijalg, P., Skrbinšek, T., Bertorelle, G., Gasparian, B., Bar-Oz, G., Pinhasi, R., Slatkin, M., Dalén, L., Shapiro, B., & Hofreiter, M. (2018). Partial genomic survival of cave bears in living brown bears. Nature Ecology & Evolution, 2, 1563-1570.

Battlay, P., Leblanc, P. B., Green, L., Garud, N. R., Schmidt, J., Fournier-Level, A., & Robin, C. (2018). Structural variants and selective sweep Foci contribute to insecticide resistance in the Drosophila genetic reference panel. G3: Genes, Genomes, Genetics, 8(11), 3489-3497.

Bitarello, B. D., de Filippo, C., Teixeira, J. C., Schmidt, J. M., Kleinert, P., Meyer, D., & Andrés, A. M. (2018). Signatures of long-term balancing selection in human genomes. Genome Biology and Evolution, 10(3), 939-955.

Brucato, N., Fernandes, V., Mazières, S., Kusuma, P., Cox, M. P., Ng'ang'a, J. W., Omar, M., Simeone-Senelle, M.-C., Frassati, C., Alshamali, F., Fin, B., Boland, A., Deleuze, J.-F., Stoneking, M., Adelaar, A., Crowther, A., Boivin, N., Pereira, L., Bailly, P., Chiaroni, J., & Ricaut, F.-X. (2018). The Comoros show the earliest Austronesian gene flow into the Swahili corridor. The American Journal of Human Genetics, 102(1), 58-68.

Camp, J. G., Wollny, D., & Treutlein, B. (2018). Single-cell genomics to guide human stem cell and tissue engineering. Nature Methods, 15(9), 661-667.

Dannemann, M., & Racimo, F. (2018). Something old, something borrowed: Admixture and adaptation in human evolution. Current Opinion in Genetics & Development, 53, 1-8.

de Filippo, C., Meyer, M., & Prüfer, K. (2018). Quantifying and reducing spurious alignments for the analysis of ultra-short ancient DNA sequences. BMC Biology, 16: 121.

Duong, N. T., Macholdt, E., Ton, N. D., Arias, L., Schröder, R., Phong, N. V., Thuy, V. T. B., Ha, N. H., Hue, H. T. T., Xuan, N. T., Oanh, K. T. P., Hien, L. T. T., Hoang, N. H., Pakendorf, B., Stoneking, M., & Hai, N. V. (2018). Complete human mtDNA genome sequences from Vietnam and the phylogeography of Mainland Southeast Asia. Scientific Reports, 8: 11651.

Fei, J.-F., Lou, W.-P.-K., Knapp, D., Murawala, P., Gerber, T., Taniguchi, Y., Nowoshilow, S., Khattak, S., & Tanaka, E. M. (2018). Application and optimization of CRISPR–Cas9-mediated genome engineering in axolotl (Ambystoma mexicanum). Nature Protocols, 13, 2908-2943.

Gayk, Z. G., Le Duc, D., Horn, J., & Lindsay, A. R. (2018). Genomic insights into natural selection in the common loon (Gavia immer): evidence for aquatic adaptation. BMC Evolutionary Biology, 18: 64.

Gerber, T., Murawala, P., Knapp, D., Masselink, W., Schuez, M., Hermann, S., Gac-Santel, M., Nowoshilow, S., Kageyama, J., Khattak, S., Currie, J. D., Camp, J. G., Tanaka, E. M., & Treutlein, B. (2018). Single-cell analysis uncovers convergence of cell identities during axolotl limb regeneration. Science, 362(6413): eaaq0681.

Hajdinjak, M., Fu, Q., Hübner, A., Petr, M., Mafessoni, F., Grote, S., Skoglund, P., Narasimham, V., Rougier, H., Crevecoeur, I., Semal, P., Soressi, M., Talamo, S., Hublin, J.-J., Gušic, I., Kucan, Ž., Rudan,

P., Golovanova, L. V., Doronichev, V. B., Posth, C., Krause, J., Korlevic, P., Nagel, S., Nickel, B., Slatkin, M., Patterson, N., Reich, D., Prüfer, K., Meyer, M., Pääbo, S., & Kelso, J. (2018). Reconstructing the genetic history of late Neanderthals. Nature, 555(7698), 652-656.

He, Z., & Yu, Q. (2018). Identification and characterization of functional modules reflecting transcriptome transition during human neuron maturation. BMC Genomics, 19: 262.

Heide, M., Huttner, W. B., & Mora-Bermúdez, F. (2018). Brain organoids as models to study human neocortex development and evolution. Current Opinion in Cell Biology, 55, 8-16.

Helm, C., Beckers, P., Bartolomaeus, T., Drukewitz, S. H., Kourtesis, I., Weigert, A., Purschke, G., Worsaae, K., Struck, T. H., & Bleidorn, C. (2018). Convergent evolution of the ladder-like ventral nerve cord in Annelida. Frontiers in Zoology, 15: 36.

Henne, K., Schilling, H., Stoneking, M., Conrads, G., & Horz, H.-P. (2018). Sex-specific differences in the occurrence of Fusobacterium nucleatum subspecies and Fusobacterium periodonticum in the oral cavity. Oncotarget, 9(29), 20631-20639.

Hernandez-Rodriguez, J., Arandjelovic, M., Lester, J. D., de Filippo, C., Weihmann, A., Meyer, M., Angedakin, S., Casals, F., Navarro, A., Vigilant, L., Kühl, H. S., Langergraber, K., Boesch, C., Hughes, D., & Marques-Bonet, T. (2018). The impact of endogenous content, replicates and pooling on genome capture from faecal samples. Molecular Ecology Resources, 18(2), 319-333.

Hershkovitz, I., & Slon, V. (2018). Levantine fossil record. In W. Trevathan (Ed.), The International Encyclopedia of Biological Anthropology (pp. 946-950). Hoboken, New Jersey: Wiley.

Hu, H., Liu, J.-M., Hu, Z., Jiang, X., Yang, X., Li, J., Zhang, Y., Yu, H., & Khaitovich, P. (2018). Recently evolved tumor suppressor transcript TP73-AS1 functions as sponge of human-specific miR-941. Molecular Biology and Evolution, 35(5), 1063-1077.

Kageyama, J., Wollny, D., Treutlein, B., & Camp, J. G. (2018). ShinyCortex: Exploring single-cell transcriptome data from the developing human cortex. Frontiers in Neuroscience, 12: 315.

Karow, M., Camp, J. G., Falk, S., Gerber, T., Pataskar, A., Gac-Santel, M., Kageyama, J., Brazovskaja, A., Garding, A., Fan, W., Riedemann, T., Casamassa, A., Smiyakin, A., Schichor, C., Goetz, M., Tiwari, V. K., Treutlein, B., & Berninger, B. (2018). Direct pericyte-to-neuron reprogramming via unfolding of a neural stem cell-like program. Nature Reviews Neurology, 21, 932-940.

Key, F. M., Abdul-Aziz, M. A., Mundry, R., Peter, B. M., Sekar, A., D'Amato, M., Dennis, M. Y., Schmidt, J. M., & Andrés, A. M. (2018). Human local adaptation of the TRPM8 cold receptor along a latitudinal cline. PLoS Genetics, 14(5): e1007298.

Khrameeva, E., Kurochkin, I., Bozek, K., Giavalisco, P., & Khaitovich, P. (2018). Lipidome Evolution in Mammalian Tissues. Molecular Biology and Evolution, 35(8), 1947-1957.

Klotz, B., Kneitz, S., Regensburger, M., Hahn, L., Dannemann, M., Kelso, J., Nickel, B., Lu, Y., Boswell, W., Postlethwait, J., Warren, W., Kunz, M., Walter, R. B., & Schartl, M. (2018). Expression signatures of early-stage and advanced medaka melanomas. Comparative Biochemistry and Physiology Part C: Toxicology & Pharmacology, 208, 20-28.

Kolora, S. R. R., Weigert, A., Saffari, A., Kehr, S., Walter Costa, M. B., Spröer, C., Indrischek, H., Chintalapati, M., Lohse, K., Doose, G., Overmann, J., Bunk, B., Bleidorn, C., Grimm-Seyfarth, A., Henle, K., Nowick, K., Faria, R., Stadler, P. F., & Schlegel, M. (2018). Divergent evolution in the genomes of closely related lacertids, Lacerta viridis and L. bilineata, and implications for speciation. GigaScience, 8(2): giy160.

Korlevic, P., Talamo, S., & Meyer, M. (2018). A combined method for DNA analysis and radiocarbon dating

from a single sample. Scientific Reports, 8(1): 4127.

Kunz, M., Löffler-Wirth, H., Dannemann, M., Willscher, E., Doose, G., Kelso, J., Kottek, T., Nickel, B., Hopp, L., Landsberg, J., Hoffmann, S., Tüting, T., Zigrino, P., Mauch, C., Utikal, J., Ziemer, M., Schulze, H.-J., Hölzel, M., Roesch, A., Kneitz, S., Meierjohann, S., Bosserhoff, A., Binder, H., & Schartl, M. (2018). RNA-seq analysis identifies different transcriptomic types and developmental trajectories of primary melanomas. Oncogene, 37, 6136-6151.

Kutanan, W., Kampuansai, J., Brunelli, A., Ghirotto, S., Pittayaporn, P., Ruangchai, S., Schröder, R., Macholdt, E., Srikummool, M., Kangwanpong, D., Hübner, A., Arias, L., & Stoneking, M. (2018). New insights from Thailand into the maternal genetic history of Mainland Southeast Asia. European Journal of Human Genetics, 26, 898-911.

Kutanan, W., Kampuansai, J., Changmai, P., Flegontov, P., Schröder, R., Macholdt, E., Hübner, A., Kangwanpong, D., & Stoneking, M. (2018). Contrasting maternal and paternal genetic variation of hunter-gatherer groups in Thailand. Scientific Reports, 8: 1536.

Lamnidis, T. C., Majander, K., Jeong, C., Salmela, E., Wessman, A., Moiseyev, V., Khartanovich, V., Balanovsky, O., Ongyerth, M., Weihmann, A., Sajantila, A., Kelso, J., Pääbo, S., Onkamo, P., Haak, W., Krause, J., & Schiffels, S. (2018). Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe. Nature Communications, 9: 5018.

Loosdrecht, M. v. d., Bouzouggar, A., Humphrey, L., Posth, C., Barton, N., Ayinuer-Petri, A., Nickel, B., Nagel, S., Talbi, E. H., Hajraoui, M. A. E., Amzazi, S., Hublin, J.-J., Pääbo, S., Schiffels, S., Meyer, M., Haak, W., Jeong, C., & Krause, J. (2018). Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. Science, 360(6388), 548-552.

Mafessoni, F., Prasad, R. B., Groop, L., Hansson, O., & Prüfer, K. (2018). Turning Vice into Virtue: Using Batch-Effects to Detect Errors in Large Genomic Data Sets. Genome Biology and Evolution, 10(10), 2697-2708.

Mazin, P. V., Jiang, X., Fu, N., Han, D., Guo, M., Gelfand, M. S., & Khaitovich, P. (2018). Conservation, evolution, and regulation of splicing during prefrontal cortex development in humans, chimpanzees, and macaques. RNA, 24(4), 585-596.

Meyer, D., Aguiar, V. R. C., Bitarello, B. D., Brandt, D. Y. C., & Nunes, K. (2018). A genomic perspective on HLA evolution. Immunogenetics, 70(1), 5-27.

Oliveira, S., Fehn, A.-M., Aço, T., Lages, F., Gayà-Vidal, M., Pakendorf, B., Stoneking, M., & Rocha, J. (2018). Matriclans shape populations: Insights from the Angolan Namib Desert into the maternal genetic history of southern Africa. American Journal of Physical Anthropology, 165(3), 518-535.

Paijmans, J. L. A., Barlow, A., Förster, D. W., Henneberger, K., Meyer, M., Nickel, B., Nagel, D., Havmøller, R. W., Baryshnikov, G. F., Joger, U., Rosendahl, W., & Hofreiter, M. (2018). Historical biogeography of the leopard (Panthera pardus) and its extinct Eurasian populations. BMC Evolutionary Biology, 18: 156.

Pierron, D., Heiske, M., Razafindrazaka, H., Pereda-loth, V., Sanchez, J., Alva, O., Arachiche, A., Boland, A., Olaso, R., Deleuze, J.-F., Ricaut, F.-X., Rakotoarisoa, J.-A., Radimilahy, C., Stoneking, M., & Letellier, T. (2018). Strong selection during the last millennium for African ancestry in the admixed population of Madagascar. Nature Communications, 9: 932.

Prüfer, K. (2018). snpAD: An ancient DNA genotype caller. Bioinformatics, 34(24), 4165-4171.

Pugach, I., Duggan, A. T., Merriwether, D. A., Friedlaender, F. R., Friedlaender, J. S., & Stoneking, M. (2018). The gateway from near into remote Oceania: New insights from genome-wide data. Molecular

Biology and Evolution, 35(4), 871-886.

Renaud, G. (2018). glactools: A command-line toolset for the management of genotype likelihoods and allele counts. Bioinformatics, 34(8), 1398-1400.

Riesenberg, S., & Maricic, T. (2018). Targeting repair pathways with small molecules increases precise genome editing in pluripotent stem cells. Nature Communications, 9: 2164.

Rohland, N., Glocke, I., Ayinuer-Petri, A., & Meyer, M. (2018). Extraction of highly degraded DNA from ancient bones, teeth and sediments for high-throughput sequencing. Nature Protocols, 13, 2447-2461.

Sarangi, G. K., Romagné, F., & Castellano, S. (2018). Distinct patterns of selection in selenium-dependent genes between land and aquatic vertebrates. Molecular Biology and Evolution, 35(7), 1744-1756.

Slon, V., Mafessoni, F., Vernot, B., de Filippo, C., Grote, S., Viola, T. B., Hajdinjak, M., Peyrégne, S., Nagel, S., Brown, S., Douka, K., Higham, T., Kozlikin, M. B., Shunkov, M. V., Derevianko, A. P., Kelso, J., Meyer, M., Prüfer, K., & Pääbo, S. (2018). The genome of the offspring of a Neanderthal mother and a Denisovan father. Nature, 561(7721), 113-116.

Stoneking, M. (2018). Mitochondrial DNA. In W. Trevathan (Ed.), The International Encyclopedia of Biological Anthropology (pp. 1020-1023). Hoboken, New Jersey: Wiley.

Tavano, S., Taverna, E., Kalebic, N., Haffner, C., Namba, T., Dahl, A., Wilsch-Bräuninger, M., Paridaen, J. T. M. L., & Huttner, W. B. (2018). Insm1 Induces Neural Progenitor Delamination in Developing Neocortex via Downregulation of the Adherens Junction Belt-Specific Protein Plekha7. Neuron, 97(6): e8, pp. 1299-1314.

Tucci, S., Vohr, S. H., McCoy, R. C., Vernot, B., Robinson, M. R., Barbieri, C., Nelson, B. J., Fu, W., Purnomo, G. A., Sudoyo, H., Eichler, E. E., Barbujani, G., Visscher, P. M., Akey, J. M., & Green, R. E. (2018). Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. Science, 361(6401), 511-516.

Vaid, S., Camp, J. G., Hersemann, L., Oegema, C. E., Heninger, A.-K., Winkler, S., Brandl, H., Sarov, M., Treutlein, B., Huttner, W. B., & Namba, T. (2018). A novel population of Hopx-dependent basal radial glial cells in the developing mouse neocortex. Development, 145(20): dev169276.

Van Laer, B., Kapp, U., Soler-Lopez, M., Moczulska, K., Pääbo, S., Leonard, G., & Mueller-Dieckmann, C. (2018). Molecular comparison of Neanderthal and Modern Human adenylosuccinate lyase. Scientific Reports, 8: 18008.

Vernot, B., & Pääbo, S. (2018). The predecessors within.. (Commentary). Cell, 173(1), 6-7.

Xiong, J., Jiang, X., Ditsiou, A., Gao, Y., Sun, J., Lowenstein, E. D., Huang, S., & Khaitovich, P. (2018). Predominant patterns of splicing evolution on human, chimpanzee and macaque evolutionary lineages. Human Molecular Genetics, 27(8), 1474-1485.

Yu, Q., He, Z., Zubkov, D., Huang, S., Kurochkin, I., Yang, X., Halene, T., Willmitzer, L., Giavalisco, P., Akbarian, S., & Khaitovich, P. (2018). Lipidome alterations in human prefrontal cortex during development, aging, and cognitive disorders. Molecular Psychiatry, 25, 2952-2969.

2017

Arai, Y., & Taverna, E. (2017). Neural progenitor cell polarity and cortical development. Frontiers in Cellular Neuroscience, 11: 384.

Barbieri, C., Sandoval, J. R., Valqui, J., Shimelman, A., Ziemendorff, S., Schröder, R., Geppert, M., Roewer, L., Gray, R., Stoneking, M., Fujita, R., & Heggarty, P. (2017). Enclaves of genetic diversity resisted Inca impacts on population history. Scientific Reports, 7: 17411.

Bozek, K., Khrameeva, E. E., Reznick, J., Omerbašic, D., Bennett, N. C., Lewin, G. R., Azpurua, J., Gorbunova, V., Seluanov, A., Regnard, P., Wanert, F., Marchal, J., Pifferi, F., Aujard, F., Liu, Z., Shi, P., Pääbo, S., Schröder, F., Willmitzer, L., Giavalisco, P., & Khaitovich, P. (2017). Lipidome determinants of maximal lifespan in mammals. Scientific Reports, 7: 5.

Camp, J. G., & Treutlein, B. (2017). Advances in mini-brain technology. Nature, 545(7652), 39-40.

Camp, J. G., & Treutlein, B. (2017). Human organomics: A fresh approach to understanding human development using single-cell transcriptomics. Development, 144(9), 1584-1587.

Camp, J. G., Sekine, K., Gerber, T., Loeffler-Wirth, H., Binder, H., Gac, M., Kanton, S., Kageyama, J., Damm, G., Seehofer, D., Belicova, L., Bickle, M., Barsacchi, R., Okuda, R., Yoshizawa, E., Kimura, M., Ayabe, H., Taniguchi, H., Takebe, T., & Treutlein, B. (2017). Multilineage communication regulates human liver bud development from pluripotency. Nature, 546(7659), 533-538.

Chang, D., Knapp, M., Enk, J., Lippold, S., Kircher, M., Lister, A., MacPhee, R. D. E., Widga, C., Czechowski, P., Sommer, R., Hodges, E., Stümpel, N., Barnes, I., Dalén, L., Derevianko, A., Germonpré, M., Hillebrand-Voiculescu, A., Constantin, S., Kuznetsova, T., Mol, D., Rathgeber, T., Rosendahl, W., Tikhonov, A. N., Willerslev, E., Hannon, G., Lalueza-Fox, C., Joger, U., Poinar, H., Hofreiter, M., & Shapiro, B. (2017). The evolutionary and phylogeographic history of woolly mammoths: A comprehensive mitogenomic analysis. Scientific Reports, 7: 44585.

Chintalapati, M., Dannemann, M., & Prüfer, K. (2017). Using the Neandertal genome to study the evolution of small insertions and deletions in modern humans. BMC Evolutionary Biology, 17: 179.

Cohen, H., Kugel, C., May, H., Medlej, B., Stein, D., Slon, V., Brosh, T., & Hershkovitz, I. (2017). The effect of impact tool geometry and soft material covering on long bone fracture patterns in children. International Journal of Legal Medicine, 131(4), 1011-1021.

Cohen, H., Kugel, C., May, H., Medlej, B., Stein, D., Slon, V., Brosh, T., & Hershkovitz, I. (2017). The influence of impact direction and axial loading on the bone fracture pattern. Forensic Science International, 277, 197-206.

Dannemann, M., & Kelso, J. (2017). The contribution of Neanderthals to phenotypic variation in modern humans. The American Journal of Human Genetics, 101(4), 578-589.

Dannemann, M., Prüfer, K., & Kelso, J. (2017). Functional implications of Neandertal introgression in modern humans. Genome Biology, 18: 61.

Devièse, T., Karavanic, I., Comeskey, D., Kubiak, C., Korlevic, P., Hajdinjak, M., Radovic, S., Procopio, N., Buckley, M., Pääbo, S., & Higham, T. (2017). Direct dating of Neanderthal remains from the site of Vindija Cave and implications for the Middle to Upper Paleolithic transition. Proceedings of the National Academy of Sciences of the United States of America, 114(40), 10606-10611.

Dönertas, H. M., Izgi, H., Kamacioglu, A., He, Z., Khaitovich, P., & Somel, M. (2017). Gene expression reversal toward pre-adult levels in the aging human brain and age-related loss of cellular identity. Scientific Reports, 7(1): 5894.

Douka, K., Slon, V., Stringer, C., Potts, R., Hübner, A., Meyer, M., Spoor, F., Pääbo, S., & Higham, T. (2017). Direct radiocarbon dating and DNA analysis of the Darra-i-Kur (Afghanistan) human temporal bone. Journal of Human Evolution, 107, 86-93.

Francioli, L. C., Cretu-Stancu, M., Garimella, K. V., Fromer, M., Kloosterman, W. P., Genome of the Netherlands consortium, including, Li, M., Stoneking, M., Samocha, K. E., Neale, B. M., Daly, M. J., Banks, E., DePristo, M. A.., & de Bakker, P. I. (2017). A framework for the detection of de novo mutations in family-based sequencing data. European Journal of Human Genetics, 25, 227-223.

Froese, D., Stiller, M., Heintzman, P. D., Reyes, A. V., Zazula, G. D., Soares, A. E. R., Meyer, M., Hall, E., Jensen, B. J. L., Arnold, L. J., MacPhee, R. D. E., & Shapiro, B. (2017). Fossil and genomic evidence constrains the timing of bison arrival in North America. Proceedings of the National Academy of Sciences of the United States of America, 114(13), 3457-3462.

Gansauge, M.-T., Gerber, T., Glocke, I., Korlevic, P., Lippik, L., Nagel, S., Riehl, L. M., Schmidt, A., & Meyer, M. (2017). Single-stranded DNA library preparation from highly degraded DNA using T4 DNA ligase. Nucleic Acids Research, 45(10): e79.

Gerber, T., Willscher, E., Loeffler-Wirth, H., Hopp, L., Schadendorf, D., Schartl, M., Anderegg, U., Camp, G., Treutlein, B., Binder, H., & Kunz, M. (2017). Mapping heterogeneity in patient-derived melanoma cultures by single-cell RNA-seq. Oncotarget, 8(1), 846-862.

Glocke, I., & Meyer, M. (2017). Extending the spectrum of DNA sequences retrieved from ancient bones and teeth. Genome Research, 27, 1230-1237.

He, Z., Han, D., Efimova, O., Guijarro, P., Yu, Q., Oleksiak, A., Jiang, S., Anokhin, K., Velichkovsky, B., Grünewald, S., & Khaitovich, P. (2017). Comprehensive transcriptome analysis of neocortical layers in humans, chimpanzees and macaques. Nature Neuroscience, 20(6), 886-895.

Jinam, T. A., Phipps, M. E., Aghakhanian, F., Majumder, P. P., Datar, F., Stoneking, M., Sawai, H., Nishida, N., Tokunaga, K., Kawamura, S., Omoto, K., & Saitou, N. (2017). Discerning the origins of the Negritos, first Sundaland people: Deep divergence and archaic admixture. Genome Biology and Evolution, 9(8), 2013-2022.

Kelso, J., Kovats, D. E., Leard, S., & Orengo, C. (2017). ISMB/ECCB 2017 proceedings paper comitee. Bioinformatics, 33, I3-I4.

Kolora, S. R., Faria, R., Weigert, A., Schaffer, S., Grimm, A., Henle, K., Sahyoun, A. H., Stadler, P. F., Nowick, K., Bleidorn, C., & Schlegel, M. (2017). The complete mitochondrial genome of Lacerta bilineata and comparison with its closely related congener L. Viridis. Mitochondrial DNA Part A, 28(1), 116-118.

Kozhemyakina, R. V., Shikhevich, S. G., Cagan, A., & Gulevich, R. G. (2017). Effect of single ethanol administration on the behavior, consumption, and preference of ethanol in tame and aggressive rats. Russian Journal of Genetics: Applied Research, 7(1), 93-99.

Kuo, T.-M., Huang, C.-M., Tu, H.-P., Ko, A.-M.-S., Wang, S.-J., Lee, C.-P., & Ko, Y.-C. (2017). URAT1 inhibition by ALPK1 is associated with uric acid homeostasis. Rheumatology, 56(4), 654-659.

Kupczik, K., Cagan, A., Brauer, S., & Fischer, M. S. (2017). The dental phenotype of hairless dogs with FOXI3 haploinsufficiency. Scientific Reports, 7: 5459.

Kutanan, W., Kampuansai, J., Srikummool, M., Kangwanpong, D., Ghirotto, S., Brunelli, A., & Stoneking, M. (2017). Complete mitochondrial genomes of Thai and Lao populations indicate an ancient origin of Austroasiatic groups and demic diffusion in the spread of Tai–Kadai languages. Human Genetics, 136(1), 85-98.

Kutanan, W., Kampuansai, J., Srikummool, M., Kangwanpong, D., Ghirotto, S., Brunelli, A., & Stoneking, M. (2017). Erratum to: Complete mitochondrial genomes of Thai and Lao populations indicate an ancient origin of Austroasiatic groups and demic diffusion in the spread of Tai–Kadai languages. Human Genetics,

136(6), 803-803.

Li, Q., Bozek, K., Xu, C., Guo, Y., Sun, J., Pääbo, S., Sherwood, C. C., Hof, P. R., Ely, J. J., Li, Y., Willmitzer, L., Giavalisco, P., & Khaitovich, P. (2017). Changes in lipidome composition during brain development in humans, chimpanzees, and macaque monkeys. Molecular Biology and Evolution, 34(5), 1155-1166.

Mafessoni, F., & Prüfer, K. (2017). Better support for a small effective population size of Neandertals and a long shared history of Neandertals and Denisovans. Proceedings of the National Academy of Sciences, 114(48), E10256-E10257.

Martin, M. D., Jay, F., Castellano, S., & Slatkin, M. (2017). Determination of genetic relatedness from low-coverage human genome sequences using pedigree simulations. Molecular Ecology, 26(16), 4145-4157.

Meyer, M., Palkopoulou, E., Baleka, S., Stiller, M., Penkman, K. E. H., Alt, K. W., Ishida, Y., Mania, D., Mallick, S., Meijer, T., Meller, H., Nagel, S., Nickel, B., Ostritz, S., Rohland, N., Schauer, K., Schüler, T., Roca, A. L., Reich, D., Shapiro, B., & Hofreiter, M. (2017). Palaeogenomes of Eurasian straight-tusked elephants challenge the current view of elephant evolution. eLife, e25413.

Nissen, J. D., Lykke, K., Bryk, J., Stridh, M. H., Zaganas, I., Skytt, D. M., Schousboe, A., Bak, L. K., Enard, W., Pääbo, S., & Waagepetersen, H. S. (2017). Expression of the human isoform of glutamate dehydrogenase, hGDH2, augments TCA cycle capacity and oxidative metabolism of glutamate during glucose deprivation in astrocytes. Glia, 65(3), 474-488.

Noureen, A., Ronke, C., Khalifa, M., Halbwax, M., Fischer, A., Andre, C., Atencia, R., Garriga, R., Mugisha, L., Ceglarek, U., Thiery, J., Utermann, G., & Schmidt, K. (2017). Significant differentiation in the apolipoprotein(a)/lipoprotein(a) trait between chimpanzees from Western and Central Africa. American Journal of Primatology, 79(9): e22683.

Peyrégne, S., Dannemann, M., & Prüfer, K. (2017). Detecting ancient positive selection in humans using extended lineage sorting. Genome Research, 27(9), 1563-1572.

Pierron, D., Heiske, M., Razafindrazaka, H., Rakoto, I., Rabetokotany, N., Ravololomanga, B., Rakotozafy, L.-M.-A., Rakotomalala, M. M., Razafiarivony, M., Rasoarifetra, B., Raharijesy, M. A., Razafindralambo, L., Ramilisonina,.-., Fanony, F., Lejamble, S., Thomas, O., Abdallah, A. M., Rocher, C., Arachiche, A., Tonaso, L., Pereda-loth, V., Schiavinato, S., Brucato, N., Ricaut, F.-X., Kusuma, P., Sudoyo, H., Ni, S., Boland, A., Deleuze, J.-F., Beaujard, P., Grange, P., Adelaar, S., Stoneking, M., Rakotoarisoa, J.-A., Radimilahy, C., & Letellier, T. (2017). Genomic landscape of human diversity across Madagascar. Proceedings of the National Academy of Sciences of the United States of America, 114(32), E6498-E6506.

Prüfer, K., Filippo, C. d., Grote, S., Mafessoni, F., Korlevic, P., Hajdinjak, M., Vernot, B., Skov, L., Hsieh, P., Peyrégne, S., Reher, D., Hopfe, C., Nagel, S., Maricic, T., Fu, Q., Theunert, C., Rogers, R., Skoglund, P., Chintalapati, M., Dannemann, M., Nelson, B. J., Key, F. M., Rudan, P., Kucan, Ž., Gušic, I., Golovanova, L. V., Doronichev, V. B., Patterson, N., Reich, D., Eichler, E. E., Slatkin, M., Schierup, M. H., Andrés, A. M., Kelso, J., Meyer, M., & Pääbo, S. (2017). A high-coverage Neandertal genome from Vindija Cave in Croatia. Science, 358(6363), 655-658.

Reher, D., Klink, B., Deutsch, A., & Voss-Böhme, A. (2017). Cell adhesion heterogeneity reinforces tumour cell dissemination: Novel insights from a mathematical model. Biology Direct, 12: 18.

Santika, T., Ancrenaz, M., Wilson, K. A., Spehar, S., Abram, N., Banes, G. L., Campbell-Smith, G., Curran, L., d'Arcy, L., Delgado, R. A., Erman, A., Goossens, B., Hartanto, H., Houghton, M., Husson, S. J., Kühl, H. S., Lackman, I., Leiman, A., Sanchez, K. L., Makinuddin, N., Marshall, A. J., Meididit, A., Mengersen, K.,

Musnanda, Nardiyono, Nurcahyo, A., Odom, K., Panda, A., Prasetyo, D., Purnomo, Rafiastanto, A., Raharjo, S., Ratnasari, D., Russon, A. E., Santana, A. H., Santoso, E., Sapari, I., Sihite, J., Suyoko, A., Tjiu, A., Utami-Atmoko, S. S., Schaik, C. P. v., Voigt, M., Wells, J., Wich, S. A., Willems, E. P., & Meijaard, E. (2017). First integrative trend analysis for a great ape species in Borneo. Scientific Reports, 7(1): 4839.

Sarangi, G. K., White, L., & Castellano, S. (2017). Genetic adaptation and Selenium uptake in vertebrates. In Encyclopedia of the Life Sciences. Chichester [u.a.]: Wiley.

Sarkar, A., Stoneking, M., & Nandineni, M. R. (2017). Unraveling the human salivary microbiome diversity in Indian populations. PLoS One, 12(9): e0184515.

Schmidt, J. M., Battlay, P., Gledhill-Smith, R. S., Good, R. T., Lumb, C., Fournier-Level, A., & Robin, C. (2017). Insights into DDT resistance from the drosophila melanogaster genetic reference panel. Genetics, 207(3), 1181-1193.

Singh, N., Albert, F. W., Plyusnina, I., Trut, L., Pääbo, S., & Harvati, K. (2017). Facial shape differences between rats selected for tame and aggressive behaviors. PLoS One, 12(4): e0175043.

Skoglund, P., Thompson, J. C., Prendergast, M. E., Mittnik, A., Sirak, K., Hajdinjak, M., Salie, T., Rohland, N., Mallick, S., Peltzer, A., Heinze, A., Olalde, I., Ferry, M., Harney, E., Michel, M., Stewardson, K., Cerezo-Román, J. I., Chiumia, C., Crowther, A., Gomani-Chindebvu, E., Gidna, A. O., Grillo, K. M., Helenius, I. T., Hellenthal, G., Helm, R., Horton, M., López, S., Mabulla, A. Z. P., Parkington, J., Shipton, C., Thomas, M. G., Tibesasa, R., Welling, M., Hayes, V. M., Kennett, D. J., Ramesar, R., Meyer, M., Pääbo, S., Patterson, N., Morris, A. G., Boivin, N., Pinhasi, R., Krause, J., & Reich, D. (2017). Reconstructing prehistoric African population structure. Cell, 171(1), 59-71.e21.

Slon, V., Hopfe, C., Weiß, C. L., Mafessoni, F., de la Rasilla, M., Lalueza-Fox, C., Rosas, A., Soressi, M., Knul, M. V., Miller, R., Stewart, J. R., Derevianko, A. P., Jacobs, Z., Li, B., Roberts, R. G., Shunkov, M. V., de Lumley, H., Perrenoud, C., Gušic, I., Kucan, Ž., Rudan, P., Ayinuer-Petri, A., Essel, E., Nagel, S., Nickel, B., Schmidt, A., Prüfer, K., Kelso, J., Burbano, H. A., Pääbo, S., & Meyer, M. (2017). Neandertal and Denisovan DNA from Pleistocene sediments. Science, 356(6338), 605-608.

Slon, V., Viola, B., Renaud, G., Gansauge, M.-T., Benazzi, S., Sawyer, S., Hublin, J.-J., Shunkov, M. V., Derevianko, A. P., Kelso, J., Prüfer, K., Meyer, M., & Pääbo, S. (2017). A fourth Denisovan individual. Science Advances, 3(7): e1700186.

Sohail, M., Vakhrusheva, O. A., Sul, J. H., Pulit, S. L., Francioli, L. C., Genome of the Netherlands Consortium, including, Li, M., Stoneking, M., Alzheimer's Disease Neuroimaging Initiative, van den Berg, L. H., Veldink, J. H., de Bakker, P. I. W., Bazykin, G. A., Kondrashov, A. S., & Sunyaev, S. R. (2017). Negative selection in humans and fruit flies involves synergistic epistasis. Science, 356(6337), 539-542.

Stoneking, M. (2017). An introduction to molecular anthropology. New York [u.a.]: Wiley.

Stoneking, M. (2017). Genes, culture, and human evolution. OBM Genetics, 1(2).

Sundaramoorthy, R., Hughes, A. L., Singh, V., Wiechens, N., Ryan, D. P., El-Mkami, H., Petoukhov, M., Svergun, D. I., Treutlein, B., Quack, S., Fischer, M., Michaelis, J., Böttcher, B., Norman, D. G., & Owen-Hughes, T. (2017). Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. eLife, 6: e22510.

Theunert, C., & Slatkin, M. (2017). Distinguishing recent admixture from ancestral population structure. Genome Biology and Evolution, 9(3), 427-437.

Theunert, C., Racimo, F., & Slatkin, M. (2017). Joint estimation of relatedness coefficients and allele frequencies from ancient samples. Genetics, 206(2), 1025-1035.

Wapinski, O. L., Lee, Q. Y., Chen, A. C., Li, R., Corces, M. R., Ang, C. E., Treutlein, B., Xiang, C., Baubet, V., Suchy, F. P., Sankar, V., Sim, S., Quake, S. R., Dahmane, N., Wernig, M., & Chang, H. Y. (2017). Rapid chromatin switch in the direct reprogramming of fibroblasts to neurons. Cell Reports, 20(13), 3236-3247.

Yang, M. A., Gao, X., Theunert, C., Tong, H., Ayinuer-Petri, A., Nickel, B., Slatkin, M., Meyer, M., Pääbo, S., Kelso, J., & Fu, Q. (2017). 40,000-year-old individual from Asia provides insight into early population structure in Eurasia. Current Biology, 27(20), 3202-3208.

2016

Barbieri, C., Hübner, A., Macholdt, E., Ni, S., Lippold, S., Schröder, R., Mpoloka, S. W., Purps, J., Roewer, L., Stoneking, M., & Pakendorf, B. (2016). Refining the Y chromosome phylogeny with southern African sequences. Human Genetics, 135(5), 541-553.

Brown, S., Higham, T., Slon, V., Pääbo, S., Meyer, M., Douka, K., Brock, F., Comeskey, D., Procopio, N., Shunkov, M., Derevianko, A., & Buckley, M. (2016). Identification of a new hominin bone from Denisova Cave, Siberia using collagen fingerprinting and mitochondrial DNA analysis. Scientific Reports, 6: 23559.

Cagan, A., & Blass, T. (2016). Identification of genomic variants putatively targeted by selection during dog domestication. BMC Evolutionary Biology, 16: 10.

Cagan, A., Theunert, C., Laayouni, H., Santpere, G., Pybus, M., Casals, F., Prüfer, K., Navarro, A., Marques-Bonet, T., Bertranpetit, J., & Andrés, A. M. (2016). Natural selection in the great apes. Molecular Biology and Evolution, 33(12), 3268-3283.

Carmody, R. N., Dannemann, M., Briggs, A. W., Nickel, B., Groopman, E. E., Wrangham, R. W., & Kelso, J. (2016). Genetic evidence of human adaptation to a cooked diet. Genome biology and evolution, 8(4), 1091-1103.

Chen, Y.-C., Kuo, H.-Y., Bornschein, U., Takahashi, H., Chen, S.-Y., Lu, K.-M., Yang, H.-Y., Chen, G.-M., Lin, J.-R., Lee, Y.-H., Chou, Y.-C., Cheng, S.-J., Chien, C.-T., Enard, W., Hevers, W., Pääbo, S., Graybiel, A. M., & Liu, F.-C. (2016). Foxp2 controls synaptic wiring of corticostriatal circuits and vocal communication by opposing Mef2c. Nature Neuroscience, 19(11), 1513-1522.

Cohen, H., Kugel, C., May, H., Medlej, B., Stein, D., Slon, V., Hershkovitz, I., & Brosh, T. (2016). The impact velocity and bone fracture pattern: Forensic perspective. Forensic Science International, 266, 54-62.

Dannemann, M., Andrés, A. M., & Kelso, J. (2016). Introgression of Neandertal- and Denisovan-like haplotypes contributes to adaptive variation in human toll-like receptors. The American Journal of Human Genetics, 98(1), 22-33.

de Filippo, C., Key, F. M., Ghirotto, S., Benazzo, A., Meneu, J. R., Weihmann, A., NISC Comparative Sequence Program, Parra, G., Green, E. D., & Andrés, A. M. (2016). Recent selection changes in human genes under long-term balancing selection. Molecular Biology and Evolution, 33(6), 1435-1447.

de Manuel, M., Kuhlwilm, M., Frandsen, P., Sousa, V. C., Desai, T., Prado-Martinez, J., Hernandez-Rodriguez, J., Dupanloup, I., Lao, O., Hallast, P., Schmidt, J. M., Heredia-Genestar, J. M., Benazzo, A., Barbujani, G., Peter, B. M., Kuderna, L. F. K., Casals, F., Angedakin, S., Arandjelovic, M., Boesch, C., Kühl, H. S., Vigilant, L., Langergraber, K., Novembre, J., Gut, M., Gut, I., Navarro, A., Carlsen, F., Andrés, A. M., Siegismund, H. R., Scally, A., Excoffier, L., Tyler-Smith, C., Castellano, S., Xue, Y., Hvilsom, C., & Marques-Bonet, T. (2016). Chimpanzee genomic diversity reveals ancient admixture with

bonobos. Science, 354(6311), 477-481.

Engelken, J., Espadas, G., Mancuso, F. M., Bonet, N., Scherr, A.-L., Jímenez-Álvarez, V., Codina-Solà, M., Medina-Stacey, D., Spataro, N., Stoneking, M., Calafell, F., Sabidó, E., & Bosch, E. (2016). Signatures of evolutionary adaptation in quantitative trait loci influencing trace element homeostasis in liver. Molecular Biology and Evolution, 33(3), 738-754.

Fournier-Level, A., Neumann-Mondlak, A., Good, R., Green, L., Schmidt, J. M., & Robin, C. (2016). Behavioural response to combined insecticide and temperature stress in natural populations of Drosophila melanogaster. Journal of Evolutionary Biology, 29(5), 1030-1044.

Fu, Q., Posth, C., Hajdinjak, M., Petr, M., Mallick, S., Fernandes, D., Furtwängler, A., Haak, W., Meyer, M., Mittnik, A., Nickel, B., Peltzer, A., Rohland, N., Slon, V., Talamo, S., Lazaridis, I., Lipson, M., Mathieson, I., Schiffels, S., Skoglund, P., Derevianko, A. P., Drozdov, N., Slavinsky, V., Tsybankov, A., Cremonesi, R. G., Mallegni, F., Gély, B., Vacca, E., Morales, M. R. G., Straus, L. G., Neugebauer-Maresch, C., Teschler-Nicola, M., Constantin, S., Moldovan, O. T., Benazzi, S., Peresani, M., Coppola, D., Lari, M., Ricci, S., Ronchitelli, A., Valentin, F., Thevenet, C., Wehrberger, K., Grigorescu, D., Rougier, H., Crevecoeur, I., Flas, D., Semal, P., Mannino, M. A., Cupillard, C., Bocherens, H., Conard, N. J., Harvati, K., Moiseyev, V., Drucker, D. G., Svoboda, J., Richards, M. P., Caramelli, D., Pinhasi, R., Kelso, J., Patterson, N., Krause, J., Pääbo, S., & Reich, D. (2016). The genetic history of Ice Age Europe. Nature, 534(7606), 200-205.

Gladyshev, V. N., Arnér, E. S., Berry, M. J., Brigelius-Flohé, R., Bruford, E. A., Burk, R. F., Carlson, B. A., Castellano, S., Chavatte, L., Conrad, M., Copeland, P. R., Diamond, A. M., Driscoll, D. M., Ferreiro, A., Flohé, L., Green, F. R., Guigó, R., Handy, D. E., Hatfield, D. L., Hesketh, J., Holmgren, A., Hoffmann, P. R., Hondal, R. J., Howard, M. T., Huang, K., Kim, H.-Y., Köhrle, J., Kim, I. Y., Krol, A., Kryukov, G. V., Lee, B. J., Lee, B. C., Lei, X. G., Liu, Q., Lescure, A., Lobanov, A. V., Loscalzo, J., Maiorino, M., Mariotti, M., Prabhu, K. S., Rayman, M. P., Rozovsky, S., Salinas, G., Schmidt, E. E., Schomburg, L., Schweizer, U., Simonovic, M., Sunde, R. A., Tsuji, P. A., Tweedie, S., Ursini, F., Whanger, P. D., & Zhang, Y. (2016). Selenoprotein Gene Nomenclature. The Journal of Biological Chemistry, 291(46), 24036-24040.

Gokce, O., Stanley, G. M., Treutlein, B., Neff, N. F., Camp, J. G., Malenka, R. C., Rothwell, P. E., Fuccillo, M. V., Südhof, T. C., & Quake, S. R. (2016). Cellular taxonomy of the mouse striatum as revealed by single-cell RNA-seq. Cell Reports, 16(4), 1126-1137.

Grote, S., Prüfer, K., Kelso, J., & Dannemann, M. (2016). ABAEnrichment: An R package to test for gene set expression enrichment in the adult and developing human brain. Bioinformatics, 32(20), 3201-3203.

Key, F. M., Fu, Q., Romagné, F., Lachmann, M., & Andrés, A. M. (2016). Human adaptation and population differentiation in the light of ancient genomes. Nature Communications, 7: 10775.

Kozhemyakina, R. V., Shikhevich, S. G., Cagan, A., & Gulevich, R. G. (2016). Vlijanie odnokratnogo vvedenija etanola na poredenie, ego potredlenie i predpochtenie u krys, selekcioniruemych ne ruchnoe i agressivnoe povedenie po otnoshenija k cheloveku = Effect of single ethanol administration on behavior and the consumption and preference of ethanol in tame and aggressive rats. Vavilovskij Žurnal Genetiki i Selekcii = Vavilov Journal of Genetics and Breeding, 20(2), 165-171.

Krause, J., & Pääbo, S. (2016). Genetic time travel. Genetics, 203(1), 9-12.

Kuhlwilm, M., Gronau, I., Hubisz, M. J., de Filippo, C., Prado-Martinez, J., Kircher, M., Fu, Q., Burbano, H. A., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Rudan, P., Brajkovic, D., Kucan, Ž., Gušic, I., Marques-Bonet, T., Andrés, A. M., Viola, B., Pääbo, S., Meyer, M., Siepel, A., & Castellano, S. (2016). Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 530(7591), 429-433.

Lazaridis, I., Nadel, D., Rollefson, G., Merrett, D. C., Rohland, N., Mallick, S., Fernandes, D., Novak, M., Gamarra, B., Sirak, K., Connell, S., Stewardson, K., Harney, E., Fu, Q., Gonzalez-Fortes, G., Jones, E. R., Roodenberg, S. A., Lengyel, G., Bocquentin, F., Gasparian, B., Monge, J. M., Gregg, M., Eshed, V., Mizrahi, A.-S., Meiklejohn, C., Gerritsen, F., Bejenaru, L., Blüher, M., Campbell, A., Cavalleri, G., Comas, D., Froguel, P., Gilbert, E., Kerr, S. M., Kovacs, P., Krause, J., McGettigan, D., Merrigan, M., Merriwether, D. A., O'Reilly, S., Richards, M. B., Semino, O., Shamoon-Pour, M., Stefanescu, G., Stumvoll, M., Tönjes, A., Torroni, A., Wilson, J. F., Yengo, L., Hovhannisyan, N. A., Patterson, N., Pinhasi, R., & Reich, D. (2016). Genomic insights into the origin of farming in the ancient Near East. Nature, 536(7617), 419-424.

Le Duc, D., & Schöneberg, T. (2016). Adaptation to nocturnality – learning from avian genomes. BioEssays, 38(7), 694-703.

Lee, C.-P., Chiang, S.-L., Ko, A.-M.-S., Liu, Y.-F., Ma, C., Lu, C.-Y., Huang, C.-M., Chang, J.-G., Kuo, T.-M., Chen, C.-L., Tsai, E.-M., & Ko, Y.-C. (2016). ALPK1 phosphorylates myosin IIA modulating TNF-alpha trafficking in gout flares. Scientific Reports, 6: 25740.

Li, M., Rothwell, R., Vermaat, M., Wachsmuth, M., Schröder, R., Laros, J. F., Oven, M. v., Bakker, P. I. d., Bovenberg, J. A., Duijn, C. M. v., Ommen, G.-J.-B.-v., Slagboom, P. E., Swertz, M. A., Wijmenga, C., Genome of the Netherlands Consortium, Kayser, M., Boomsma, D. I., Zöllner, S., Knijff, P. d., & Stoneking, M. (2016). Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: Support for a variable-size bottleneck. Genome Research, 26(4), 417-426.

Li, Q., Guo, S., Jiang, X., Bryk, J., Naumann, R., Enard, W., Tomita, M., Sugimoto, M., Khaitovich, P., & Pääbo, S. (2016). Mice carrying a human GLUD2 gene recapitulate aspects of human transcriptome and metabolome development. Proceedings of the National Academy of Sciences of the United States of America, 113(19), 5358-5363.

Liu, X., Han, D., Somel, M., Jiang, X., Hu, H., Guijarro, P., Zhang, N., Mitchell, A., Halene, T., Ely, J. J., Sherwood, C. C., Hof, P. R., Qiu, Z., Pääbo, S., Akbarian, S., & Khaitovich, P. (2016). Disruption of an evolutionarily novel synaptic expression pattern in autism. PLoS Biology, 14(9): e1002558.

Liu, Y.-F., Chiang, S.-L., Lin, C.-Y., Chang, J.-G., Chung, C.-M., Ko, A.-M.-S., Lin, Y.-Z., Lee, C.-H., Lee, K.-W., Chen, M.-K., Hua, C.-H., Tsai, M.-H., Chen, Y.-C., & Ko, Y.-C. (2016). Somatic mutations and genetic variants of NOTCH1 in head and neck squamous cell carcinoma occurrence and development. Scientific Reports, 6: 24014.

Lobon, I., Tucci, S., de Manuel, M., Ghirotto, S., Benazzo, A., Prado-Martinez, J., Lorente-Galdos, B., Nam, K., Dabad, M., Hernandez-Rodriguez, J., Comas, D., Navarro, A., Schierup, M. H., Andrés, A. M., Barbujani, G., Hvilsom, C., & Marques-Bonet, T. (2016). Demographic history of the genus Pan inferred from whole mitochondrial genome reconstructions. Genome Biology and Evolution, 8(10), 2020-2030.

Malaspinas, A.-S., Westaway, M. C., Muller, C., Sousa, V. C., Lao, O., Alves, I., Bergström, A., Athanasiadis, G., Cheng, J. Y., Crawford, J. E., Heupink, T. H., Macholdt, E., Peischl, S., Rasmussen, S., Schiffels, S., Subramanian, S., Wright, J. L., Albrechtsen, A., Barbieri, C., Dupanloup, I., Eriksson, A., Margaryan, A., Moltke, I., Pugach, I., Korneliussen, T. S., Levkivskyi, I. P., Moreno-Mayar, J. V., Ni, S., Racimo, F., Sikora, M., Xue, Y., Aghakhanian, F. A., Brucato, N., Brunak, S., Campos, P. F., Clark, W., Ellingvåg, S., Fourmile, G., Gerbault, P., Injie, D., Koki, G., Leavesley, M., Logan, B., Lynch, A., Matisoo-Smith, E. A., McAllister, P. J., Mentzer, A. J., Metspalu, M., Migliano, A. B., Murgha, L., Phipps, M. E., Pomat, W., Reynolds, D., Ricaut, F.-X., Siba, P., Thomas, M. G., Wales, T., Wall, C. M., Oppenheimer, S. J., Tyler-Smith, C., Durbin, R., Dortch, J., Manica, A., Schierup, M. H., Foley, R. A., Lahr, M. M., Bowern, C., Wall, J. D., Mailund, T., Stoneking, M., Nielsen, R., Sandhu, M. S., Excoffier, L., Lambert, D. M., & Willerslev, E. (2016). A genomic history of Aboriginal Australia. Nature, 538(7624), 207-214.

Mallick, S., Li, H., Lipson, M., Mathieson, I., Gymrek, M., Racimo, F., Zhao, M., Chennagiri, N., Nordenfelt,

S., Tandon, A., Skoglund, P., Lazaridis, I., Sankararaman, S., Fu, Q., Rohland, N., Renaud, G., Erlich, Y., Willems, T., Gallo, C., Spence, J. P., Song, Y. S., Poletti, G., Balloux, F., van Driem, G., de Knijff, P., Romero, I. G., Jha, A. R., Behar, D. M., Bravi, C. M., Capelli, C., Hervig, T., Moreno-Estrada, A., Posukh, O. L., Balanovska, E., Balanovsky, O., Karachanak-Yankova, S., Sahakyan, H., Toncheva, D., Yepiskoposyan, L., Tyler-Smith, C., Xue, Y., Abdullah, M. S., Ruiz-Linares, A., Beall, C. M., Rienzo, A. D., Jeong, C., Starikovskaya, E. B., Metspalu, E., Parik, J., Villems, R., Henn, B. M., Hodoglugil, U., Mahley, R., Sajantila, A., Stamatoyannopoulos, G., Wee, J. T. S., Khusainova, R., Khusnutdinova, E., Litvinov, S., Ayodo, G., Comas, D., Hammer, M. F., Kivisild, T., Klitz, W., Winkler, C. A., Labuda, D., Bamshad, M., Jorde, L. B., Tishkoff, S. A., Watkins, W. S., Metspalu, M., Dryomov, S., Sukernik, R., Singh, L., Thangaraj, K., Pääbo, S., Kelso, J., Patterson, N., & Reich, D. (2016). The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature, 538(7624), 201-206.

Mendez, F. L., Poznik, G. D., Castellano, S., & Bustamante, C. D. (2016). The divergence of Neandertal and modern human Y chromosomes. The American Journal of Human Genetics, 98(4), 728-734.

Meyer, M., Arsuaga, J.-L., de Filippo, C., Nagel, S., Aximu-Petri, A., Nickel, B., Martínez, I., Gracia, A., Bermúdez de Castro, J. M., Carbonell, E., Viola, B., Kelso, J., Prüfer, K., & Pääbo, S. (2016). Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. Nature, 531(7595), 504-507.

Mora-Bermúdez, F., Badsha, F., Kanton, S., Camp, J. G., Vernot, B., Köhler, K., Voigt, B., Okita, K., Maricic, T., He, Z., Lachmann, R., Pääbo, S., Treutlein, B., & Huttner, W. B. (2016). Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. eLife, e18683.

Ni, S., & Stoneking, M. (2016). Improvement in detection of minor alleles in next generation sequencing by base quality recalibration. BMC Genomics, 17: 139.

Posth, C., Renaud, G., Mittnik, A., Drucker, D. G., Rougier, H., Cupillard, C., Valentin, F., Thevenet, C., Furtwängler, A., Wißing, C., Francken, M., Malina, M., Bolus, M., Lari, M., Gigli, E., Capecchi, G., Crevecoeur, I., Beauval, C., Flas, D., Germonpré, M., van der Plicht, J., Cottiaux, R., Gély, B., Ronchitelli, A., Wehrberger, K., Grigorescu, D., Svoboda, J., Semal, P., Caramelli, D., Bocherens, H., Harvati, K., Conard, N. J., Haak, W., Powell, A., & Krause, J. (2016). Pleistocene mitochondrial genomes suggest a single major dispersal of non-Africans and a late glacial population turnover in Europe. Current Biology, 26(6), 827-833.

Prasad, R. B., Lessmark, A., Almgren, P., Kovacs, G., Hansson, O., Oskolkov, N., Vitai, M., Ladenvall, C., Kovacs, P., Fadista, J., Lachmann, M., Zhou, Y., Sonestedt, E., Poon, W., Wollheim, C. B., Orho-Melander, M., Stumvoll, M., Tuomi, T., Pääbo, S., Koranyi, L., & Groop, L. (2016). Excess maternal transmission of variants in the THADA gene to offspring with type 2 diabetes. Diabetologia, 59(8), 1702-1713.

Pugach, I., Matveev, R., Spitsyn, V., Makarov, S., Novgorodov, I., Osakovsky, V., Stoneking, M., & Pakendorf, B. (2016). The complex admixture history and recent southern origins of Siberian populations. Molecular Biology and Evolution, 33(7), 1777-1795.

Quach, H., Rotival, M., Pothlichet, J., Loh, Y.-H.-E., Dannemann, M., Zidane, N., Laval, G., Patin, E., Harmant, C., Lopez, M., Deschamps, M., Naffakh, N., Duffy, D., Coen, A., Leroux-Roels, G., Clément, F., Boland, A., Deleuze, J.-F., Kelso, J., Albert, M. L., & Quintana-Murci, L. (2016). Genetic adaptation and neandertal admixture shaped the immune system of human populations. Cell, 167(3), 643-656.

Racimo, F., Renaud, G., & Slatkin, M. (2016). Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans. PLoS Genetics, 12(4): e1005972.

Skoglund, P., Posth, C., Sirak, K., Spriggs, M., Valentin, F., Bedford, S., Clark, G. R., Reepmeyer, C., Petchey, F., Fernandes, D., Fu, Q., Harney, E., Lipson, M., Mallick, S., Novak, M., Rohland, N.,

Stewardson, K., Abdullah, S., Cox, M. P., Friedlaender, F. R., Friedlaender, J. S., Kivisild, T., Koki, G., Kusuma, P., Merriwether, D. A., Ricaut, F.-X., Wee, J. T. S., Patterson, N., Krause, J., Pinhasi, R., & Reich, D. (2016). Genomic insights into the peopling of the Southwest Pacific. Nature, 538(7626), 510-513.

Slon, V., Glocke, I., Barkai, R., Gopher, A., Hershkovitz, I., & Meyer, M. (2016). Mammalian mitochondrial capture, a tool for rapid screening of DNA preservation in faunal and undiagnostic remains, and its application to Middle Pleistocene specimens from Qesem Cave (Israel). Quaternary International, 398, 210-218.

Stiller, M., Sucker, A., Griewank, K., Aust, D., Baretton, G. B., Schadendorf, D., & Horn, S. (2016). Single-strand DNA library preparation improves sequencing of formalin-fixed and paraffin-embedded (FFPE) cancer DNA. Oncotarget, 7(37), 59115-59128.

Stoneking, M. (2016). Archaic genomes and the peopling of South Asia. In G. R. Schug, & S. R. Walimbe (Eds.), A companion to South Asia in the past (pp. 51-59). Malden, MA: Wiley Blackwell.

Stoneking, M. (2016). The contribution of genetic ancestry from archaic humans to modern humans. In M. Tibayrenc, & F. J. Ayala (Eds.), On human nature: Biology, psychology, ethics, politics, and religion (pp. 55-61). San Diego [u.a.]: Elsevier.

Suh, A., Witt, C. C., Menger, J., Sadanandan, K. R., Podsiadlowski, L., Gerth, M., Weigert, A., McGuire, J. A., Mudge, J., Edwards, S. V., & Rheindt, F. E. (2016). Ancient horizontal transfers of retrotransposons between birds and ancestors of human pathogenic nematodes. Nature Communications, 7: 11396.

Talamo, S., Hajdinjak, M., Mannino, M. A., Fasani, L., Welker, F., Martini, F., Romagnoli, F., Zorzin, R., Meyer, M., & Hublin, J.-J. (2016). Direct radiocarbon dating and genetic analyses on the purported Neanderthal mandible from the Monti Lessini (Italy). Scientific Reports, 6: 29144.

Treutlein, B., Lee, Q. Y., Camp, J. G., Mall, M., Koh, W., Shariati, S. A. M., Sim, S., Neff, N. F., Skotheim, J. M., Wernig, M., & Quake, S. R. (2016). Dissecting direct reprogramming from fibroblast to neuron using single-cell RNA-seq. Nature, 534(7607), 391-395.

Tu, H.-P., Chung, C.-M., Ko, A.-M.-S., Lee, S.-S., Lai, H.-M., Lee, C.-H., Huang, C.-M., Liu, C.-S., & Ko, Y.-C. (2016). Additive composite ABCG2, SLC2A9 and SLC22A12 scores of high-risk alleles with alcohol use modulate gout risk. Journal of Human Genetics, 61(9), 803-810.

Vernot, B., Tucci, S., Kelso, J., Schraiber, J., Wolf, A., Gittelman, R., Dannemann, M., Grote, S., McCoy, R., Norton, H., Scheinfeldt, L., Merriwether, D., Koki, G., Friedlaender, J., Wakefield, J., Pääbo, S., & Akey, J. (2016). Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. Science, 352(6282), 235-239.

Voiculescu, S. E., Le Duc, D., Rosca, A. E., Zeca, V., Chitimus, D. M., Arsene, A. L., Dragoi, C. M., Crenguta Nicolae, A., Zagrean, L., Schöneberg, T., & Zagrean, A.-M. (2016). Behavioral and molecular effects of prenatal continuous light exposure in the adult rat. Brain Research, 1650, 51-59.

Wachsmuth, M., Hübner, A., Li, M., Madea, B., & Stoneking, M. (2016). Age-Related and Heteroplasmy-Related Variation in Human mtDNA Copy Number. PLoS Genetics, 12(3): e1005939.

Weigert, A., Golombek, A., Gerth, M., Schwarz, F., Struck, T. H., & Bleidorn, C. (2016). Evolution of mitochondrial gene order in Annelida. Molecular Phylogenetics and Evolution, 94(Part A), 196-206.

Welker, F., Hajdinjak, M., Talamo, S., Jaouen, K., Dannemann, M., David, F., Julien, M., Meyer, M., Kelso, J., Barnes, I., Braces, S., Kamminga, P., Fischer, R., Kessler, B., Stewart, J. R., Pääbo, S., Collins, M. J., & Hublin, J.-J. (2016). Palaeoproteomic evidence identifies archaic hominins associated with the Châtelperronian at the Grotte du Renne. Proceedings of the National Academy of Sciences of the United

States of America, 113(44), 11162-11167.

Weyer, S., & Pääbo, S. (2016). Functional analyses of transcription factor binding sites that differ between present-day and archaic humans. Molecular Biology and Evolution, 33(2), 316-322.

White, L., & Castellano, S. (2016). The role of selenium in human evolution. In D. Hatfield, & V. Gladyshev (Eds.), Selenium: Its molecular biology and role in human health (4th ed., pp. 59-71). New York [u.a.]: Springer.

White, L., & Castellano, S.(2016). Genetische Anpassung an den Selengehalt von Nahrung in der jüngsten Menschheitsgeschichte.

Zhang, B., Han, D., Korostelev, Y., Yan, Z., Shao, N., Khrameeva, E., Velichkovsky, B. M., Chen, Y.-P.-P., Gelfand, M. S., & Khaitovich, P. (2016). Changes in snoRNA and snRNA abundance in the human, chimpanzee, macaque, and mouse brain. Genome Biology and Evolution, 8(3), 840-850.

2015

Aguado, M. T., Glasby, C. J., Schroeder, P. C., Weigert, A., & Bleidorn, C. (2015). The making of a branching annelid: An analysis of complete mitochondrial genome and ribosomal data of Ramisyllis multicaudata. Scientific Reports, 5: 12072.

Alter, S. E., Meyer, M., Post, K., Czechowski, P., Gravlund, P., Gaines, C., Rosenbaum, H. C., Kaschner, K., Turvey, S. T., van der Plicht, J., Shapiro, B., & Hofreiter, M. (2015). Climate impacts on transocean dispersal and habitat in gray whales from the Pleistocene to 2100. Molecular Ecology, 24(7), 1510-1522.

Benazzi, S., Slon, V., Talamo, S., Negrino, F., Peresani, M., Bailey, S. E., Sawyer, S., Panetta, D., Vicino, G., Starnini, E., Mannino, M. A., Salvadori, P. A., Meyer, M., Pääbo, S., & Hublin, J.-J. (2015). The makers of the Protoaurignacian and implications for Neandertal extinction. Science, 348(6236), 793-796.

Bozek, K., Wei, Y., Yan, Z., Liu, X., Xiong, J., Sugimoto, M., Tomita, M., Pääbo, S., Sherwood, C. C., Hof, P. R., Ely, J. J., Li, Y., Steinhauser, D., Willmitzer, L., Giavalisco, P., & Khaitovich, P. (2015). Organization and evolution of brain lipidome revealed by large-scale analysis of human, chimpanzee, macaque, and mouse tissues. Neuron, 85(4), 695-702.

Cahill, J. A., Stirling, I., Kistler, L., Salamzade, R., Ersmark, E., Fulton, T. L., Stiller, M., Green, R. E., & Shapiro, B. (2015). Genomic evidence of geographically widespread effect of gene flow from polar bears into brown bears. Molecular Ecology, 24(6), 1205-1217.

Camp, J. G., Badsha, F., Florio, M., Kanton, S., Gerber, T., Wilsch-Bräuninger, M., Lewitus, E., Sykes, A., Hevers, W., Lancaster, M., Knoblich, J. A., Lachmann, R., Pääbo, S., Huttner, W. B., & Treutlein, B. (2015). Human cerebral organoids recapitulate gene expression programs of fetal neocortex development. Proceedings of the National Academy of Sciences of the United States of America, 112(51), 15672-15677.

Cao, Q., Didelot, X., Wu, Z., Li, Z., He, L., Li, Y., Ni, M., You, Y., Lin, X., Li, Z., Gong, Y., Zheng, M., Zhang, M., Liu, J., Wang, W., Bo, X., Falush, D., Wang, S., & Zhang, J. (2015). Progressive genomic convergence of two Helicobacter pylori strains during mixed infection of a patient with chronic gastritis. Gut, 64(4), 554-561.

de Boer, M., Tzur, S., van Leeuwen, K., Dencher, P. C., Skorecki, K., Wolach, B., Gavrieli, R., Nasidze, I., Stoneking, M., Tanck, M. W., & Roos, D. (2015). A founder effect for p47phoxTrp193Ter chronic granulomatous disease in Kavkazi Jews. Blood Cells, Molecules, and Diseases, 55(4), 320-327.

Fanti, S. D., Barbieri, C., Sarno, S., Sevini, F., Vianello, D., Tamm, E., Metspalu, E., van Oven, M., Hübner,

A., Sazzini, M., Franceschi, C., Pettener, D., & Luiselli, D. (2015). Fine dissection of human mitochondrial DNA haplogroup HV lineages reveals paleolithic signatures from European glacial refugia. PLoS One, 10(12): e0144391.

Florio, M., Albert, M., Taverna, E., Namba, T., Brandl, H., Lewitus, E., Haffner, C., Sykes, A., Wong, F. K., Peters, J., Guhr, E., Klemroth, S., Prüfer, K., Kelso, J., Naumann, R., Nüsslein, I., Dahl, A., Lachmann, R., Pääbo, S., & Huttner, W. B. (2015). Human-specific gene ARHGAP11B promotes basal progenitor amplification and neocortex expansion. Science, 347(6229), 1465-1470.

Frantz, L. A., Schraiber, J. G., Madsen, O., Megens, H.-J., Cagan, A., Bosse, M., Paudel, Y., Crooijmans, R. P., Groenen, G. L., & Groenen, M. A. (2015). Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. Nature Genetics, 47(10), 1141-1148.

Fu, Q., Hajdinjak, M., Moldovan, O., Constantin, S., Mallick, S., Skoglund, P., Patterson, N., Rohland, N., Lazaridis, I., Nickel, B., Viola, B., Prüfer, K., Meyer, M., Kelso, J., Reich, D., & Pääbo, S. (2015). An early modern human from Romania with a recent Neanderthal ancestor. Nature, 524(7564), 216-219.

Germonpré, M., Sablin, M. V., Láznicková-Galetová, M., Després, V., Stevens, R. E., Stiller, M., & Hofreiter, M. (2015). Palaeolithic dogs and Pleistocene wolves revisited: A reply to Morey (2014). Journal of Archaeological Science, 54, 210-216.

Haak, W., Lazaridis, I., Patterson, N., Rohland, N., Mallick, S., Llamas, B., Brandt, G., Nordenfelt, S., Harney, E., Stewardson, K., Fu, Q., Mittnik, A., Bánffy, E., Economou, C., Francken, M., Friederich, S., Pena, R. G., Hallgren, F., Khartanovich, V., Khokhlov, A., Kunst, M., Kuznetsov, P., Meller, H., Mochalov, O., Moiseyev, V., Nicklisch, N., Pichler, S. L., Risch, R., Guerra, M. A. R., Roth, C., Szécsényi-Nagy, A., Wahl, J., Meyer, M., Krause, J., Brown, D., Anthony, D., Cooper, A., Alt, K. W., & Reich, D. (2015). Massive migration from the steppe was a source for Indo-European languages in Europe. Nature, (522), 207-211.

Hammerschmidt, K., Schreiweis, C., Minge, C., Pääbo, S., Fischer, J., & Enard, W. (2015). A humanized version of Foxp2 does not affect ultrasonic vocalization in adult mice. Genes, Brain and Behavior, 14(8), 583-590.

Hughes, D. A., Kircher, M., He, Z., Guo, S., Fairbrother, G. L., Moreno, C. S., Khaitovich, P., & Stoneking, M. (2015). Evaluating intra- and inter-individual variation in the human placental transcriptome. Genome Biology, 16: 54.

Le Duc, D., Renaud, G., Krishnan, A., Almén, M. S., Huynen, L., Prohaska, S. J., Ongyerth, M., Bitarello, B. D., Schiöth, H. B., Hofreiter, M., Stadler, P. F., Prüfer, K., Lambert, D., Kelso, J., & Schöneberg, T. (2015). Kiwi genome provides insights into evolution of a nocturnal lifestyle. Genome Biology, 16: 147.

Li, M., Schröder, R., Ni, S., Madea, B., & Stoneking, M. (2015). Extensive tissue-related and allele-related mtDNA heteroplasmy suggests positive selection for somatic mutations. Proceedings of the National Academy of Sciences of the United States of America, 112(8), 2491-2496.

Macholdt, E., Slatkin, M., Pakendorf, B., & Stoneking, M. (2015). New insights into the history of the C-14010 lactase persistence variant in Eastern and Southern Africa. American Journal of Physical Anthropology, 156(4), 661-664.

MacLarnon, A. M., Sommer, V., Goffe, A. S., Higham, J. P., Lodge, E., Tkaczynski, P. J., & Ross, C. (2015). Assessing adaptability and reactive scope: Introducing a new measure and illustrating its use through a case study of environmental stress in forest-living baboons. General and Comparative Endocrinology, 215, 10-24.

Mafessoni, F., & Lachmann, M. (2015). Selective strolls: Fixation and extinction in diploids are slower for weakly selected mutations than for neutral ones. Genetics, 201(4), 1581-1589.

Nogueiro, I., Teixeira, J. C., Amorim, A., Gusmão, L., & Alvarez, L. (2015). Portuguese crypto-Jews: The genetic heritage of a complex history. Frontiers in Genetics, 6: 12.

Nogueiro, I., Teixeira, J. C., Amorim, A., Gusmão, L., & Alvarez, L. (2015). Reply to letter from Felice L. Bedford and Doron Yacobi. European journal of human genetics, 23(8), 994-995.

Nogueiro, I., Teixeira, J., Amorim, A., Gusmão, L., & Alvarez, L. (2015). Echoes from Sepharad: Signatures on the maternal gene pool of crypto-Jewish descendants. European Journal of Human Genetics, 23, 693-699.

Pääbo, S. (2015). Dorcas Cummings Lecture: The Genetic Legacy of Neanderthals. In T. Grodzicker, D. Stewart, & B. Stillman (Eds.), 21st Century Genetics: Genes at Work (pp. 291-294). Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press.

Pääbo, S. (2015). Genomy drevnich gominin iz Sibiri = Genomes of ancient hominins from Siberia. In Vestnik Rossijskoj Akademii Nauk 85 (10): Doklady Laureatov Bol'shoj Zolotoj Medali imeni M. V. Lomonosova Rossijskoj Akademii Nauk 2014 goda (pp. 879-884). Moscow: Nauka.

Pääbo, S. (2015). The contribution of ancient hominin genomes from Siberia to our understanding of human evolution. In Herald of the Russian Academy of Sciences 85 (5): Papers by Laureates of the 2014 Lomonosov Grand Gold Medal of the Russian Academy of Sciences (pp. 392-396). Moscow: IAPC «Nauka/Interperiodica».

Pääbo, S. (2015). The diverse origins of the human gene pool (Commentary). Nature Reviews Genetics, 16, 313-314.

Palamara, P. F., Francioli, L. C., Wilton, P. R., Genovese, G., Gusev, A., Finucane, H. K., Sankararaman, S., Genome of the Netherlands Consortium, including authors, Stoneking, M., Li, M., & others, Sunyaev, S. R., de Bakker, P. I., Wakeley, J., Pe'er, I., & Price, A. L. (2015). Leveraging distant relatedness to quantify human mutation and gene-conversion rates. The American Journal of Human Genetics, 97(6), 775-789.

Prüfer, K., & Meyer, M. (2015). Comment on "Late Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americans". Science, 347(6224), 835-835.

Pugach, I., & Stoneking, M. (2015). Genome-wide insights into the genetic history of human populations. Investigative Genetics, 6: 6.

Qin, P., & Stoneking, M. (2015). Denisovan Ancestry in East Eurasian and Native American Populations. Molecular Biology and Evolution, 32(10), 2665-2674.

Renaud, G., Slon, V., Duggan, A. T., & Kelso, J. (2015). Schmutzi: Estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. Genome Biology, 16: 224.

Renaud, G., Stenzel, U., Maricic, T., Wiebe, V., & Kelso, J. (2015). deML: Robust demultiplexing of Illumina sequences using a likelihood-based approach. Bioinformatics, 31(5), 770-772.

Ronke, C., Dannemann, M., Halbwax, M., Fischer, A., Helmschrodt, C., Brügel, M., André, C., Atencia, R., Mugisha, L., Scholz, M., Ceglarek, U., Thiery, J., Pääbo, S., Prüfer, K., & Kelso, J. (2015). Lineage-specific changes in biomarkers in great apes and humans. PLoS One, 10(8): e0134548.

Savage, P. E., Matsumae, H., Oota, H., Stoneking, M., Currie, T. E., Tajima, A., Gillan, M., & Brown, S. (2015). How 'circumpolar' is Ainu music? Musical and genetic perspectives on the history of the Japanese archipelago. Ethnomusicology Forum, 24(3), 443-467.

Sawyer, S., Renaud, G., Viola, B., Hublin, J.-J., Gansauge, M.-T., Shunkov, M. V., Derevianko, A. P., Prüfer, K., Kelso, J., & Pääbo, S. (2015). Nuclear and mitochondrial DNA sequences from two Denisovan individuals. Proceedings of the National Academy of Sciences of the United States of America, 112(51), 15696-15700.

Strehlow, V., Heyne, H. O., & Lemke, J. R. (2015). The spectrum of GRIN2A-associated disorders. Epileptologie, 32(3), 147-151.

Struck, T. H., Golombek, A., Weigert, A., Franke, F. A., Westheide, W., Purschke, G., Bleidorn, C., & Halanych, K. M. (2015). The evolution of annelids reveals two adaptive routes to the interstitial realm. Current Biology, 25(15), 1993-1999.

Teixeira, J. C., de Filippo, C., Weihmann, A., Meneu, J. R., Racimo, F., Dannemann, M., Nickel, B., Fischer, A., Halbwax, M., Andre, C., Atencia, R., Meyer, M., Parra, G., Pääbo, S., & Andrés, A. M. (2015). Long-term balancing selection in LAD1 maintains a missense trans-species polymorphism in humans, chimpanzees and bonobos. Molecular Biology and Evolution, 32(5), 1186-1196.

Valverde, G., Zhou, H., Lippold, S., de Filippo, C., Tang, K., Herráez, D. L., Li, J., & Stoneking, M. (2015). A novel candidate region for genetic adaptation to high altitude in Andean populations. PLoS One, 10(5): e0125444.

van Leeuwen, E. M., Kanterakis, A., Deelen, P., Kattenberg, M. V., The Genome the Netherlands Consortium, including authors, Stoneking, M., Li, M., & others, Slagboom, P. E., de Bakker, P. I., Wijmenga, C., Swertz, M. A., Boomsma, D. I., van Duijn, C. M., Karrsen, L. C., & Hottenga, J. J. (2015). Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 10(9), 1285-1296.

van Leeuwen, E. M., Karssen, L. C., Deelen, J., Isaacs, A., Medina-Gomez, C., Mbarek, H., Kanterakis, A., Trompet, S., Postmus, I., Verweij, N., van Enckevort, D. J., Huffman, J. E., White, C. C., Feitosa, M. F., Bartz, T. M., Manichaikul, A., Joshi, P. K., Peloso, G. M., Deelen, P., van Dijk, F., Willemsen, G., de Geus, E. J., Milaneschi, Y., Penninx, B. W., Francioli, L. C., Menelaou, A., Pulit, S. L., Rivadeneira, F., Hofman, A., Oostra, B. A., Franco, O. H., Leach, I. M., Beekman, M., de Craen, A. J., Uh, H.-W., Trochet, H., Hocking, L. J., Porteous, D. J., Sattar, N., Packard, C. J., Buckley, B. M., Brody, J. A., Bis, J. C., Rotter, J. I., Mychaleckyj, J. C., Campbell, H., Duan, Q., Lange, L. A., Wilson, J. F., Hayward, C., Polasek, O., Vitart, V., Rudan, I., Wright, A. F., Rich, S. S., Psaty, B. M., Borecki, I. B., Kearney, P. M., Stott, D. J., Cupples, L. A., The Genome of the Netherlands Consortium, including authors, Stoneking, M., Li, M., & others, Jukema, J. W., van der Harst, P., Sijbrands, E. J., Hottenga, J.-J., Uitterlinden, A. G., Swertz, M. A., van Ommen, G.-J.-B., de Bakker, P. I., Slagboom, P. E., Boomsma, D. I., Wijmenga, C., & van Duijn, C. M. (2015). Genome of the Netherlands population - specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 6: 6065.

Vaughan, A. E., Brumwell, A. N., Xi, Y., Gotts, J. E., Brownfield, D. G., Treutlein, B., Tan, K., Tan, V., Liu, F. C., Looney, M. R., Matthay, M. A., Rock, J. R., & Chapman, H. A. (2015). Lineage-negative progenitors mobilize to regenerate lung epithelium after major injury. Nature, 517(7536), 621-625.

Wei, Y.-N., Hu, H.-Y., Xie, G.-C., Fu, N., Ning, Z.-B., Zeng, R., & Khaitovich, P. (2015). Transcript and protein expression decoupling reveals RNA binding proteins and miRNAs as potential modulators of human aging. Genome Biology, 16: 41.

Weiß, C. L., Dannemann, M., Prüfer, K., & Burbano, H. A. (2015). Contesting the presence of wheat in the British Isles 8,000 years ago by assessing ancient DNA authenticity from low-coverage data. eLife, 4: e10005.

White, L., Romagné, F., Müller, E., Erlebach, E., Weihmann, A., Parra, G., Andrés, A. M., & Castellano, S. (2015). Genetic adaptation to levels of dietary selenium in recent human history. Molecular Biology and

Evolution, 32(6), 1507-1518.

2014

Andrés, A. M., & Nowick, K. (Eds.). (2014). Genetics of human evolution [Special Issue]. Current Opinion in Genetics & Development, 29.

Andrés, A. M., & Nowick, K. (2014). Editorial overview: Genetics of human evolution: The genetics of human origins. Current Opinion in Genetics & Development, 29, v-vii.

Barbieri, C., Güldemann, T., Naumann, C., Gerlach, L., Berthold, F., Nakagawa, H., Mpoloka, S. W., Stoneking, M., & Pakendorf, B. (2014). Unraveling the complex maternal history of Southern African Khoisan populations. American Journal of Physical Anthropology, 153(3), 435-448.

Barbieri, C., Vicente, M., Oliveira, S., Bostoen, K., Rocha, J., Stoneking, M., & Pakendorf, B. (2014). Migration and interaction in a contact zone: mtDNA variation among Bantu-speakers in southern Africa. PLoS One, 9(6): e9911.

Benazzi, S., Peresani, M., Talamo, S., Fu, Q., Mannino, M. A., Richards, M. P., & Hublin, J.-J. (2014). A reassessment of the presumed Neandertal remains from San Bernardino Cave, Italy. Journal of Human Evolution, 66(1), 89-94.

Bozek, K., Wei, Y., Yan, Z., Liu, X., Xiong, J., Sugimoto, M., Tomita, M., Pääbo, S., Pieszek, R., Sherwood, C. C., Hof, P. R., Ely, J. J., Steinhauser, D., Bangsbo, J., Willmitzer, L., Hansson, O., Call, J., Giavalisco, P., & Khaitovich, P. (2014). Exceptional evolutionary divergence of human muscle and brain metabolomes parallels human cognitive and physical uniqueness. PLoS Biology, 12(5): e1001871.

Brown, S., Savage, P. E., Ko, A.-M.-S., Stoneking, M., Ko, Y.-C., Loo, J.-H., & Trejaut, J. A. (2014). Correlations in the population structure of music, genes and language. Proceedings of the Royal Society of London. Series B: Biological Sciences, 281(1774): 20132072.

Carneiro, M., Albert, F. W., Afonso, S., Pereira, R. J., Burbano, H. A., Campos, R., Melo-Ferreira, J., Blanco-Aguiar, J. A., Villafuerte, R., Nachman, M. W., Good, J. M., & Ferrand, N. (2014). The genomic architecture of population divergence between subspecies of the European rabbit. PLoS Genetics, 10(8): e1003519.

Carneiro, M., Rubin, C.-J., Palma, F. D., Albert, F. W., Alföldi, J., Barrio, A. M., Pielberg, G., Rafati, N., Sayyab, S., Turner-Maier, J., Younis, S., Afonso, S., Aken, B., Alves, J. M., Barrell, D., Bolet, G., Boucher, S., Burbano, H. A., Campos, R., Chang, J. L., Duranthon, V., Fontanesi, L., Garreau, H., Heiman, D., Johnson, J., Mage, R. G., Peng, Z., Queney, G., Rogel-Gaillard, C., Ruffier, M., Searle, S., Villafuerte, R., Xiong, A., Young, S., Forsberg-Nilsson, K., Good, J. M., Lander, E. S., Ferrand, N., Lindblad-Toh, K., & Andersson, L. (2014). Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. Science, 345(6200), 1074-1079.

Castellano, S., Parra, G., Sánchez-Quinto, F. A., Racimo, F., Kuhlwilm, M., Kircher, M., Sawyer, S., Fu, Q., Heinze, A., Nickel, B., Dabney, J., Siebauer, M. F., White, L., Burbano, H. A., Renaud, G., Stenzel, U., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Rudan, P., Brajkovic, D., Kucan, Ž., Gušic, I., Shunkov, M. V., Derevianko, A. P., Viola, B., Meyer, M., Kelso, J., Andrés, A. M., & Pääbo, S. (2014). Patterns of coding variation in the complete exomes of three Neandertals. Proceedings of the National Academy of Sciences of the United States of America, 111(18), 6666-6671.

Dabney, J., Meyer, M., & Pääbo, S. (2014). Ancient DNA damage. In E. C. Friedberg, S. J. Elledge, A. R. Lehmann, T. Lindahl, & M. Muzi-Falconi (Eds.), DNA Repair, Mutagenesis, and Other Responses to DNA

Damage: A subject collection from Cold Spring Harbor Perspectives in Biology (pp. 19-26). New York: Cold Spring Harbor Laboratory Pr.

Deelen, P., Menelaou, A., van Leeuwen, E. M., Kanterakis, A., van Dijk, F., Medina-Gomez, C., Francioli, L. C., Hottenga, J. J., Karssen, L. C., Estrada, K., Kreiner-Møller, E., Rivadeneira, F., van Setten, J., Gutierrez-Achury, J., Westra, H.-J., Franke, L., van Enckevort, D., Dijkstra, M., Byelas, H., van Duijn, C. M., Genome of the Netherlands Consortium, including authors, Stoneking, M., Li, M., & others, de Bakker, P. I. W., Wijmenga, C., & Swertz, M. A. (2014). Improved imputation quality of low-frequency and rare variants in European samples using the 'Genome of The Netherlands'. European Journal of Human Genetics, 22(11), 1321-1326.

Delfin, F. S., Ko, A.-M.-S., Li, M., Gunnarsdóttir, E. D., Tabbada, K. A., Salvador, J. M., Calacal, G. C., Sagum, M. S., Datar, F. A., Padilla, S. G., Ungria, M. C. A. D., & Stoneking, M. (2014). Complete mtDNA genomes of Filipino ethnolinguistic groups: A melting pot of recent and ancient lineages in the Asia-Pacific region. European journal of human genetics, 22(2), 228-237.

Duggan, A. T., & Stoneking, M. (2014). Recent developments in the genetic history of East Asia and Oceania. Current Opinion in Genetics & Development, 29, 9-14.

Duggan, A. T., Evans, B., Friedlaender, F. R., Friedlaender, J. S., Koki, G., Merriwether, D. A., Kayser, M., & Stoneking, M. (2014). Maternal history of Oceania from complete mtDNA genomes: Contrasting ancient diversity with recent homogenization due to the Austronesian expansion. The American Journal of Human Genetics, 94(5), 721-733.

Engelken, J., Carnero-Montoro, E., Pybus, M., Andrews, G. K., Lalueza-Fox, C., Comas, D., Sekler, I., de la Rasilla, M., Rosas, A., Stoneking, M., Valverde, M. A., Vicente, R., & Bosch, E. (2014). Extreme population differences in the human zinc transporter ZIP4 (SLC39A4) are explained by positive selection in Sub-Saharan Africa. PLoS Genetics, 10(2): e1004128.

Francioli, L. C., Menelaou, A., Pulit, S. L., van Dijk, F., Palamara, P. F., Elbers, C. C., Neerincx, P. B. T., Ye, K., Guryev, V., Kloosterman, W. P., Deelen, P., Abdellaoui, A., van Leeuwen, E. M., van Oven, M., Vermaat, M., Li, M., Laros, J. F. J., Karssen, L. C., Kanterakis, A., Amin, N., Hottenga, J. J., Lameijer, E.-W., Kattenberg, M., Dijkstra, M., Byelas, H., van Setten, J., van Schaik, B. D. C., Bot, J., Nijman, I. J., Renkens, I., Marschall, T., Schönhuth, A., Hehir-Kwa, J. Y., Handsaker, R. E., Polak, P., Sohail, M., Vuzman, D., Hormozdiari, F., van Enckevort, D., Mei, H., Koval, V., Moed, M. H., van der Velde, K. J., Rivadeneira, F., Estrada, K., Medina-Gomez, C., Isaacs, A., McCarroll, S. A., Beekman, M., de Craen, A. J. M., Suchiman, H. E. D., Hofman, A., Oostra, B., Uitterlinden, A. G., Willemsen, G., Study, L. C., Platteel, M., Veldink, J. H., van den Berg, L. H., Pitts, S. J., Potluri, S., Sundar, P., Cox, D. R., Sunyaev, S. R., den Dunnen, J. T., Stoneking, M., de Knijff, P., Kayser, M., Li, Q., Li, Y., Du, Y., Chen, R., Cao, H., Li, N., Cao, S., Wang, J., Bovenberg, J. A., Pe'er, I., Slagboom, P. E., van Duijn, C. M., Boomsma, D. I., van Ommen, G.-J.-B., de Bakker, P. I. W., Swertz, M. A., Wijmenga, C., & Genome of the Netherlands Consortium, The (2014). Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 46(8), 818-825.

Fu, Q., Li, H., Moorjani, P., Jay, F., Slepchenko, S. M., Bondarev, A. A., Johnson, P. L. F., Ayinuer-Petri, A., Prüfer, K., de Filippo, C., Meyer, M., Zwyns, N., Salazar García, D. C., Kuzmin, Y. V., Keates, S. G., Kosintsev, P. A., Razhev, D. I., Richards, M. P., Peristov, N. V., Lachmann, M., Douka, K., Higham, T. F. G., Slatkin, M., Hublin, J.-J., Reich, D., Kelso, J., Viola, B., & Pääbo, S. (2014). Genome sequence of a 45,000-year-old modern human from western Siberia. Nature, 514(7523), 445-449.

Gansauge, M.-T., & Meyer, M. (2014). Selective enrichment of damaged DNA molecules for ancient genome sequencing. Genome Research, 24(9), 1543-1549.

Gerth, M., Gansauge, M.-T., Weigert, A., & Bleidorn, C. (2014). Phylogenomic analyses uncover origin and

spread of the Wolbachia pandemic. Nature Communications, 5: 5117.

Giuliani, C., Barbieri, C., Li, M., Bucci, L., Monti, D., Passarino, G., Luiselli, D., Franceschi, C., Stoneking, M., & Garagnani, P. (2014). Transmission from centenarians to their offspring of mtDNA heteroplasmy revealed by ultra-deep sequencing. Aging, 6(6), 454-467.

Gokhman, D., Lavi, E., Prüfer, K., Fraga, M. F., Riancho, J. A., Kelso, J., Pääbo, S., Meshorer, E., & Carmel, L. (2014). Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. Science, 344(6183), 523-527.

Guo, J., Tan, J., Yang, Y., Zhou, H., Hu, S., Hashan, A., Bahaxar, N., Xu, S., Weaver, T. D., Jin, L., Stoneking, M., & Tang, K. (2014). Variation and signatures of selection on the human face. Journal of Human Evolution, 75, 143-152.

Gustavino, B., Meschini, R., Franzetti, G., Gratton, P., Allegrucci, G., & Sbordoni, V. (2014). Genotoxicity testing for radon exposure: Dolichopoda (Orthoptera, Rhaphidophoridae) as potential bio-indicator of confined environments. Current Zoology, 60(2), 299-307.

He, Z., Bammann, H., Han, D., Xie, G., & Khaitovich, P. (2014). Conserved expression of lincRNA during human and macaque prefrontal cortex development and maturation. RNA, 20(7), 1103-1111.

Hellenthal, G., Busby, G. B. J., Band, G., Wilson, J. F., Capelli, C., Falush, D., & Myers, S. (2014). A genetic atlas of human admixture history. Science, 373(6172), 747-751.

Henne, K., Li, J., Stoneking, M., Kessler, O., Schilling, H., Sonanini, A., Conrads, G., & Horz, H.-P. (2014). Global analysis of saliva as a source of bacterial genes for insights into human population structure and migration studies. BMC Evolutionary Biology, 14: 190.

Heyn, P., Kircher, M., Dahl, A., Kelso, J., Tomancak, P., Kalinka, A. T., & Neugebauer, K. M. (2014). The earliest transcribed zygotic genes are short, newly evolved and different across species. Cell Reports, 6(2), 285-292.

Heyne, H. O., Lautenschläger, S., Nelson, R., Besnier, F., Rotival, M., Cagan, A., Kozhemyakina, R., Plyusnina, I. Z., Trut, L., Carlborg, Ö., Petretto, E., Kruglyak, L., Pääbo, S., Schöneberg, T., & Albert, F. W. (2014). Genetic influences on brain gene expression in rats selected for tameness and aggression. Genetics, 198(3), 1277-1290.

Horn, S. (2014). TERT-Promoter-Mutationen im familiären und sporadischen Melanom. In Lebendige Wissenschaft: Spitzenforschung in der Dermatologie - Innovationen und Auszeichnungen 2014 (pp. 52-57). Lampertheim: Alpha-Informations-GmbH.

Horn, S., Prost, S., Stiller, M., Makowiecki, D., Kuznetsova, T., Benecke, N., Pucher, E., Hufthammer, A. K., Schouwenburg, C., Shapiro, B., & Hofreiter, M. (2014). Ancient mitochondrial DNA and the genetic history of Eurasian beaver (Castor fiber) in Europe. Molecular Ecology, 23(7), 1717-1729.

Hu, H. Y., He, L., & Khaitovich, P. (2014). Deep sequencing reveals a novel class of bidirectional promoters associated with neuronal genes. BMC Genomics, 15: 457.

Kelso, J., & Prüfer, K. (2014). Ancient humans and the origin of modern humans. Current Opinion in Genetics & Development, 29, 133-138.

Key, F. M., Peter, B., Dennis, M. Y., Huerta-Sanchez, E., Tang, W., Prokunina-Olsson, L., Nielsen, R., & Andrés, A. M. (2014). Selection on a variant associated with improved viral clearance drives local, adaptive pseudogenization of Interferon Lambda 4 (IFNL 4). PLoS Genetics, 10(10): e1004681.

Key, F. M., Teixeira, J. C., de Filippo, C., & Andrés, A. M. (2014). Advantageous diversity maintained by

balancing selection in humans. Current Opinion in Genetics & Development, 29, 45-51.

Khrameeva, E. E., Bozek, K., He, L., Yan, Z., Jiang, X., Wei, Y., Tang, K., Gelfand, M. S., Prüfer, K., Kelso, J., Pääbo, S., Giavalisco, P., Lachmann, M., & Khaitovich, P. (2014). Neanderthal ancestry drives evolution of lipid catabolism in contemporary Europeans. Nature Communications, 5: 3584.

Ko, A.-M.-S., Chen, C.-Y., Fu, Q., Delfin, F. S., Li, M., Chiu, H.-L., Stoneking, M., & Ko, Y.-C. (2014). Early Austronesians: Into and out of Taiwan. The American Journal of Human Genetics, 94(3), 426-436.

Lazaridis, I., Patterson, N., Mittnik, A., Renaud, G., Mallick, S., Kirsanow, K., Sudmant, P. H., Schraiber, J. G., Castellano, S., Lipson, M., Berger, B., Economou, C., Bollongino, R., Fu, Q., Bos, K. I., Nordenfelt, S., Li, H., de Filippo, C., Prüfer, K., Sawyer, S., Posth, C., Haak, W., Hallgren, F., Fornander, E., Rohland, N., Delsate, D., Francken, M., Guinet, J.-M., Wahl, J., Ayodo, G., Babiker, H. A., Bailliet, G., Balanovska, E., Balanovsky, O., Barrantes, R., Bedoya, G., Ben-Ami, H., Bene, J., Berrada, F., Bravi, C. M., Brisighelli, F., Busby, G. B. J., Cali, F., Churnosov, M., Cole, D. E. C., Corach, D., Damba, L., van Driem, G., Dryomov, S., Dugoujon, J.-M., Fedorova, S. A., Romero, I. G., Gubina, M., Hammer, M., Henn, B. M., Hervig, T., Hodoglugil, U., Jha, A. R., Karachanak-Yankova, S., Khusainova, R., Khusnutdinova, E., Kittles, R., Kivisild, T., Klitz, W., Kucinskas, V., Kushniarevich, A., Laredj, L., Litvinov, S., Loukidis, T., Mahley, R. W., Melegh, B., Metspalu, E., Molina, J., Mountain, J., Näkkäläjärvi, K., Nesheva, D., Nyambo, T., Osipova, L., Parik, J., Platonov, F., Posukh, O., Romano, V., Rothhammer, F., Rudan, I., Ruizbakiev, R., Sahakyan, H., Sajantila, A., Salas, A., Starikovskaya, E. B., Tarekegn, A., Toncheva, D., Turdikulova, S., Uktveryte, I., Utevska, O., Vasquez, R., Villena, M., Voevoda, M., Winkler, C. A., Yepiskoposyan, L., Zalloua, P., Zemunik, T., Cooper, A., Capelli, C., Thomas, M. G., Ruiz-Linares, A., Tishkoff, S. A., Singh, L., Thangaraj, K., Villems, R., Comas, D., Sukernik, R., Metspalu, M., Meyer, M., Eichler, E. E., Burger, J., Slatkin, M., Pääbo, S., Kelso, J., Reich, D., & Krause, J. (2014). Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature, 513(7518), 409-413.

Lee, C.-H., Chiang, S.-L., Ko, A.-M.-S., Hua, C.-H., Tsai, M.-H., Warnakulasuriya, S., Ibrahim, S. O., Sunarjo,.-., Zain, R. B., Ling, T.-Y., Huang, C.-L., Lane, H.-Y., Lin, C.-C., & Ko, Y.-C. (2014). Betel-quid dependence domains and syndrome associated with betel-quid ingredients among chewers: An Asian multi-country evidence. Addiction, 109(7), 1194-1204.

Li, J., Quinque, D., Horz, H.-P., Li, M., Rzhetskaya, M., Raff, J. A., Hayes, M. G., & Stoneking, M. (2014). Comparative analysis of the human saliva microbiome from different climate zones: Alaska, Germany, and Africa. BMC Microbiology, 14: 316.

Lindskog, C., Kuhlwilm, M., Davierwala, A., Fu, N., Hegde, G., Uhlén, M., Navani, S., Pääbo, S., & Pontén, a. F. (2014). Analysis of candidate genes for lineage-specific expression changes in humans and primates. Journal of Proteome Research, 13(8), 3596-3606.

Lippold, S., Xu, H., Ko, A., Li, M., Renaud, G., Butthoff, A., Schröder, R., & Stoneking, M. (2014). Human paternal and maternal demographic histories: Insights from high-resolution Y chromosome and mtDNA sequences. Investigative Genetics, 5: 13.

Lipson, M., Loh, P.-R., Patterson, N., Moorjani, P., Ko, Y.-C., Stoneking, M., Berger, B., & Reich, D. (2014). Reconstructing Austronesian population history in Island Southeast Asia. Nature Communications, 5: 4689.

Macholdt, E., Lede, V., Barbieri, C., Mpoloka, S. W., Chen, H., Slatkin, M., Pakendorf, B., & Stoneking, M. (2014). Tracing pastoralist migrations to Southern Africa with lactase persistence alleles. Current Biology, 24(8), 875-879.

Malaspinas, A.-S., Lao, O., Schroeder, H., Rasmussen, M., Raghavan, M., Moltke, I., Campos, P. F., Sagredo, F. S., Rasmussen, S., Gonçalves, V. F., Albrechtsen, A., Allentoft, M. E., Johnson, P. L., Li, M.,

Reis, S., Bernardo, D. V., DeGiorgio, M., Duggan, A. T., Bastos, M., Wang, Y., Stenderup, J., Moreno-Mayar, J. V., Brunak, S., Sicheritz-Ponten, T., Hodges, E., Hannon, G. J., Orlando, L., Price, T. D., Jensen, J. D., Nielsen, R., Heinemeier, J., Olsen, J., Rodrigues-Carvalho, C., Lahr, M. M., Neves, W. A., Kayser, M., Higham, T., Stoneking, M., Pena, S. D., & Willerslev, E. (2014). Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 24(21), R1035-R1037.

Meyer, M., Fu, Q., Ayinuer-Petri, A., Glocke, I., Nickel, B., Arsuaga, J.-L., Martínez, I., Gracia, A., de Castro, J. M. B., Carbonell, E., & Pääbo, S. (2014). A mitochondrial genome sequence of a hominin from Sima de los Huesos. Nature, 505(7483), 403-406.

Mitchell, K. J., Pratt, R. C., Watson, L. N., Gibb, G. C., Llamas, B., Kasper, M., Edson, J., Hopwood, B., Male, D., Armstrong, K. N., Meyer, M., Hofreiter, M., Austin, J., Donnellan, S. C., Lee, M. S. Y., Phillips, M. J., & Cooper, A. (2014). Molecular phylogeny, biogeography, and habitat preference evolution of marsupials. Molecular Biology and Evolution, 31(9), 2322-2330.

Morris, A. G., Heinze, A., Chan, E. K., Smith, A. B., & Hayes, V. M. (2014). First ancient mitochondrial human genome from a prepastoralist southern African. Genome biology and evolution, 6(10), 2647-2653.

Nigst, P. R., Haesaerts, P., Damblon, F., Frank-Fellner, C., Mallol, C., Viola, B., Götzinger, M., Niven, L., Trnka, G., & Hublin, J.-J. (2014). Early modern human settlement of Europe north of the Alps occurred 43,500 years ago in a cold steppe-type environment. Proceedings of the National Academy of Sciences of the United States of America, 111(40), 14394-14399.

O'Brien, J., Didelot, X., Iqbal, Z., Amenga-Etego, L., Ahiska, B., & Falush, D. (2014). A Bayesian approach to inferring the phylogenetic structure of communities from metagenomic data. Genetics, 197(3), 925-937.

Oven, M. v., Brauer, S., Choi, Y., Ensing, J., Schiefenhövel, W., Stoneking, M., & Kayser, M. (2014). Human genetics of the Kula Ring: Y-chromosome and mitochondrial DNA variation in the Massim of Papua New Guinea. European journal of human genetics, 22, 1393-1403.

Pääbo, S. (2014). Die Neandertaler und wir: Meine Suche nach den Urzeit-Genen. Frankfurt a.M.: S. Fischer.

Pääbo, S. (2014). Neanderthal man: In search of lost genomes (Translated into 14 languages). New York: Basic Books.

Pääbo, S. (2014). The human condition: A molecular approach (Review). Cell, 157(1), 216-226.

Pfefferle, D., Kazem, A. J. N., Brockhausen, R. R., Ruiz-Lambides, A., & Widdig, A. (2014). Monkeys spontaneously discriminate their unfamiliar paternal relatives under natural conditions using facial cues. Current Biology, 24(15), 1806-1810.

Pickrell, J. K., Patterson, N., Loh, P.-R., Lipson, M., Berger, B., Stoneking, M., Pakendorf, B., & Reich, D. (2014). Ancient west Eurasian ancestry in southern and eastern Africa. Proceedings of the National Academy of Sciences of the United States of America, 111(7), 2632 -2637.

Prüfer, K., Racimo, F., Patterson, N., Jay, F., Sankararaman, S., Sawyer, S., Heinze, A., Renaud, G., Sudmant, P. H., de Filippo, C., Li, H., Mallick, S., Dannemann, M., Fu, Q., Kircher, M., Kuhlwilm, M., Lachmann, M., Meyer, M., Ongyerth, M., Siebauer, M. F., Theunert, C., Tandon, A., Moorjani, P., Pickrell, J., Mullikin, J. C., Vohr, S. H., Green, R. E., Hellmann, I., Johnson, P. L. F., Blanche, H., Cann, H., Kitzman, J. O., Shendure, J., Eichler, E. E., Lein, E. S., Bakken, T. E., Golovanova, L. V., Doronichev, V. B., Shunkov, M. V., Derevianko, A. P., Viola, B., Slatkin, M., Reich, D., Kelso, J., & Pääbo, S. (2014). The complete genome sequence of a Neanderthal from the Altai Mountains. Nature, 505(7481), 43-49.

Pybus, M., Dall'Olio, G. M., Luisi, P., Uzkudun, M., Carreño-Torres, A., Pavlidis, P., Laayouni, H., Bertranpetit, J., & Engelken, J. (2014). 1000 genomes selection browser 1.0: A genome browser dedicated to signatures of natural selection in modern humans. Nucleic Acids Research, 42(D1), D903-D909.

Racimo, F., Kuhlwilm, M., & Slatkin, M. (2014). A test for ancient selective sweeps and an application to candidate sites in modern humans. Molecular Biology and Evolution, 31(12), 3344-3358.

Renaud, G., LaFave, M. C., Liang, J., Wolfsberg, T. G., & Burgess, S. M. (2014). trieFinder: an efficient program for annotating Digital Gene Expression (DGE) tags. BMC Bioinformatics, 15: 329.

Renaud, G., Stenzel, U., & Kelso, J. (2014). leeHom: adaptor trimming and merging for Illumina sequencing reads. Nucleic Acids Research (London), 42(18): e141.

Rieux, A., Eriksson, A., Li, M., Sobkowiak, B., Weinert, L. A., Warmuth, V., Ruiz-Linares, A., Manica, A., & Balloux, F. (2014). Improved calibration of the human mitochondrial clock using ancient genomes. Molecular Biology and Evolution, 31(10), 2780-2792.

Romagné, F., Santesmasses, D., White, L., Sarangi, G. K., Mariotti, M., Hübler, R., Weihmann, A., Parra, G., Gladyshev, V. N., Guigó, R., & Castellano, S. (2014). SelenoDB 2.0: Annotation of selenoprotein genes in animals and their genetic diversity in humans. Nucleic Acids Research, 42(D1), D437-D443.

Sankararaman, S., Mallick, S., Dannemann, M., Prüfer, K., Kelso, J., Pääbo, S., Patterson, N., & Reich, D. (2014). The genomic landscape of Neanderthal ancestry in present-day humans. Nature, 507(7492), 354-357.

Schreiweis, C., Bornschein, U., Burguière, E., Kerimoglu, C., Schreiter, S., Dannemann, M., Goyal, S., Rea, E., French, C. A., Puliyadi, R., Groszer, M., Fisher, S. E., Mundry, R., Winter, C., Hevers, W., Pääbo, S., Enard, W., & Graybiel, A. M. (2014). Humanized Foxp2 accelerates learning by enhancing transitions from declarative to procedural performance. Proceedings of the National Academy of Sciences of the United States of America, 111(39), 14253-14258.

Skoglund, P., Northoff, B. H., Shunkov, M. V., Derevianko, A. P., Pääbo, S., Krause, J., & Jakobsson, M. (2014). Separating endogenous ancient DNA from modern day contamination in a Siberian Neandertal. Proceedings of the National Academy of Sciences of the United States of America, 111(6), 2229-2234.

Stiller, M., Molak, M., Prost, S., Rabeder, G., Baryshnikov, G., Rosendahl, W., Münzel, S., Bocherens, H., Grandal-d'Anglade, A., Hilpert, B., Germonpré, M., Stasyk, O., Pinhasi, R., Tintori, A., Rohland, N., Mohandesan, E., Ho, S. Y., Hofreiter, M., & Knapp, M. (2014). Mitochondrial DNA diversity and evolution of the Pleistocene cave bear complex. Quaternary International, 339-340, 224-231.

The SIGMA Type 2 Diabetes Consortium, including authors, Prüfer, K., Sawyer, S., Stenzel, U., Kelso, J., Pääbo, S., & and others (2014). Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. Nature, 506, 97-101.

Tu, H.-P., Ko, A.-M.-S., Chiang, S.-L., Lee, S.-S., Lai, H.-M., Chung, C.-M., Huang, C.-M., Lee, C.-H., Kuo, T.-M., Hsieh, M.-J., & Ko, Y.-C. (2014). Joint effects of alcohol consumption and ABCG2 Q141K on chronic tophaceous gout risk. Journal of Rheumatology, 41(4), 749-758.

Vilardell, M., Parra, G., & Civit, S. (2014). WISCOD: A statistical web-enabled tool for the identification of significant protein coding regions. BioMed Research International, 2014: 282343.

Weigert, A., Helm, C., Meyer, M., Nickel, B., Arendt, D., Hausdorf, B., Santos, S. R., Halanych, K. M., Purschke, G., Bleidorn, C., & Struck, T. H. (2014). Illuminating the base of the annelid tree using transcriptomics. Molecular Biology and Evolution, 31(6), 1391-1401.

Wunderlich, S., Kircher, M., Vieth, B., Haase, A., Merkert, S., Beier, J., Göhring, G., Glage, S., Schambach,

A., Curnow, E. C., Pääbo, S., Martin, U., & Enard, W. (2014). Primate iPS cells as tools for evolutionary analyses. Stem Cell Research, 12(3), 622-629.

Yahara, K., Didelot, X., Ansari, M. A., Sheppard, S. K., & Falush, D. (2014). Efficient inference of recombination hot regions in bacterial genomes. Molecular Biology and Evolution, 31(6), 1593-1605.

Zhao, G., Guo, S., Somel, M., & Khaitovich, P. (2014). Evolution of human longevity uncoupled from caloric restriction mechanisms. PLoS One, 9(1): e84117.

Zwyns, N., & Viola, B. (2014). L'Asie centrale et la Sibérie durant le pléistocène supérieur. In M. Otte (Ed.), Néandertal / Cro-Magnon: La rencontre (pp. 267-294). Paris: Ed. Errance.

2013

Barbieri, C., Butthoff, A., Bostoen, K., & Pakendorf, B. (2013). Genetic perspectives on the origin of clicks in Bantu languages from southwestern Zambia. European journal of human genetics: EJHG; the official journal of the European Society of Human Genetics, 21, 430-436.

Barbieri, C., Vicente, M., Rocha, J., Mpoloka, S. W., Stoneking, M., & Pakendorf, B. (2013). Ancient substructure in early mtDNA lineages of southern Africa. American Journal of Human Genetics, 92, 285-292.

Bonazzi, M., Le Cabec, A., Schünemann, V., Viola, B., Harvati, K., Pääbo, S., Hublin, J.-J., Tafforeau, P., & Krause, J. (2012). Evaluation of the influence of computed tomography imaging on ancient DNA recovery. Talk presented at German Society of Anthropology (GfA) 10th International Meeting. Bolzano. 2012-09-02 - 2013-09-06.

Brandariz-Fontes, C., Leonard, J. A., Vega-Pla, J. L., Backström, N., Lindgren, G., Lippold, S., & Rico, C. (2013). Y-Chromosome Analysis in Retuertas Horses. PLoS One, 8(5): e64985.

Bruche, S., Gusset, M., Lippold, S., Barnett, R., Eulenberger, K., Junhold, J., Driscoll, C. A., & Hofreiter, M. (2013). A genetically distinct lion (Panthera leo) population from Ethiopia. European Journal of Wildlife Research, 59(2), 215-225.

Bryk, J., Somel, M., Lorenc, A., & Teschke, M. (2013). Early gene expression divergence between allopatric populations of the house mouse (Mus musculus domesticus). Ecology and Evolution, 3(3), 558-568.

Dabney, J., Knapp, M., Glocke, I., Gansauge, M.-T., Weihmann, A., Nickel, B., Valdiosera, C., García, N., Pääbo, S., Arsuaga, J.-L., & Meyer, M. (2013). Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments. Proceedings of the National Academy of Sciences of the United States of America, 110(39), 15758-15763.

Dabney, J., Meyer, M., & Pääbo, S. (2013). Ancient DNA damage. Cold Spring Harbor Perspectives in Biology, 5(7): a012567.

Donaldson-Matasci, M. C., Bergstrom, C. T., & Lachmann, M. (2013). When unreliable cues are good enough. American Naturalist, 182(3), 313-327.

Duggan, A. T., & Stoneking, M. (2013). A highly unstable recent mutation in human mtDNA. American Journal of Human Genetics, 92(2), 279-284.

Duggan, A. T., Whitten, C. M., Wiebe, V., Crawford, M., Butthoff, A., Spitsyn, V., Makarov, S., Novgorodov, I., Osakovsky, V., & Pakendorf, B. (2013). Investigating the prehistory of Tungusic peoples of Siberia and the Amur-Ussuri region with complete mtDNA genome sequences and Y-chromosomal markers. PLoS One, 8(12): e83570.

Ferreira, Z., Hurle, B., Andrés, A. M., Kretzschmar, W. W., Mullikin, J. C., Cherukuri, P. F., Cruz, P., Gonder, M. K., Stone, A. C., Tishkoff, S., Swanson, W. J., NISC Comparative Sequencing Program, Green, E. D., Clark, A. G., & Seixas, S. (2013). Sequence diversity of Pan troglodytes subspecies and the impact of WFDC6 selective constraints in reproductive immunity. Genome Biology and Evolution, 5(12), 2512-2523.

Ferreira, Z., Seixas, S., Andrés, A. M., Kretzschmar, W. W., Mullikin, J. C., Cherukuri, P. F., Cruz, P., Swanson, W. J., Clark, A. G., Green, E. D., & Hurle, B. (2013). Reproduction and immunity-driven natural selection in the human WFDC locus. Molecular Biology and Evolution, 30(4), 938-950.

Finstermeier, K., Zinner, D., Brameier, M., Meyer, M., Kreuz, E., Hofreiter, M., & Roos, C. (2013). A mitogenomic phylogeny of living primates. PLoS One, 8(7): e69504.

Fu, Q., Meyer, M., Gao, X., Stenzel, U., Burbano, H. A., Kelso, J., & Pääbo, S. (2013). DNA analysis of an early modern human from Tianyuan Cave, China. Proceedings of the National Academy of Sciences of the United States of America, 110(6), 2223-2227.

Fu, Q., Mittnik, A., Johnson, P. L., Bos, K., Lari, M., Bollongino, R., Sun, C., Giemsch, L., Schmitz, R., Burger, J., Ronchitelli, A. M., Martini, F., Cremonesi, R. G., Svoboda, J., Bauer, P., Caramelli, D., Castellano, S., Reich, D., Pääbo, S., & Krause, J. (2013). A revised timescale for human evolution based on ancient mitochondrial genomes. Current Biology, 23(7), 553-559.

Gansauge, M.-T., & Meyer, M. (2013). Single-stranded DNA library preparation for the sequencing of ancient or damaged DNA. Nature Protocols, 8(4), 737-748.

Good, J. M., Wiebe, V., Albert, F., Burbano, H. A., Kircher, M., Green, R. E., Halbwax, M., André, C., Atencia, R., Fischer, A., & Pääbo, S. (2013). Comparative population genomics of the ejaculate in humans and the great apes. Molecular Biology and Evolution, 30(4), 964-976.

Grossmann, T., Vaish, A., Franz, J., Schroeder, R., Stoneking, M., & Friederici, A. D. (2013). Emotional voice processing: Investigating the role of genetic variation in the serotonin transporter across development. PLoS One, 8(7): e68377.

Guschanski, K., Krause, J., Sawyer, S., Valente, L. M., Bailey, S., Finstermeier, K., Sabin, R., Gilissen, E., Sonet, G., Nagy, Z. T., Lenglet, G., Mayer, F., & Savolainen, V. (2013). Next-generation museomics disentangles one of the largest primate radiations. Systematic Biology, 62(4), 539-554.

Ka, S., Markljung, E., Ring, H., Albert, F. W., Harun-Or-Rashid, M., Wahlberg, P., Garcia-Roves, P. M., Zierath, J. R., Denbow, D. M., Pääbo, S., Siegel, P. B., Andersson, L., & Hallbook, F. (2013). Expression of carnitine palmitoyl-CoA transferase-1B is influenced by a cis-acting eQTL in two chicken lines selected for high and low body weight. Physiological Genomics, 45(9), 367-376.

Ko, A.-M.-S., Tu, H.-P., Liu, T.-T., Chang, J.-G., Yuo, C.-Y., Chiang, S.-L., Chang, S.-J., Liu, Y.-F., Ko, A.-M.-J., Lee, C.-H., Lee, C.-P., Chang, C.-M., Tsai, S.-F., & Ko, Y.-C. (2013). ALPK1 genetic regulation and risk in relation to gout. International Journal of Epidemiology, 42(2), 466-474.

Kuhlwilm, M., Davierwala, A., & Pääbo, S. (2013). Identification of putative target genes of the transcription factor RUNX2. PLoS One, 8(12): e83218.

Kunz, M., Dannemann, M., & Kelso, J. (2013). High-throughput sequencing of the melanoma genome. Experimental Dermatology, 22(1), 10-17.

Lachmann, M. (2013). The value of information in signals and cues. In U. E. Stegmann (Ed.), Animal Communication Theory: Information and Influence (pp. 357-376). Cambridge: Cambridge University Press.

Li, J., Nasidze, I., Quinque, D., Li, M., Horz, H.-P., Andre, C., Garriga, R. M., Halbwax, M., Fischer, A., &

Stoneking, M. (2013). The saliva microbiome of Pan and Homo. BMC Microbiology, 13: 204.

Li, Z., Bammann, H., Li, M., Liang, H., Yan, Z., Chen, Y.-P.-P., Zhao, M., & Khaitovich, P. (2013). Evolutionary and ontogenetic changes in RNA editing in human, chimpanzee, and macaque brains. RNA, 19(12), 1693-1702.

Maricic, T., Günther, V., Georgiev, O., Gehre, S., Curlin, M., Schreiweis, C., Naumann, R., Burbano, H. A., Meyer, M., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Gajovic, S., Kelso, J., Enard, W., Schaffner, W., & Pääbo, S. (2013). A recent evolutionary change affects a regulatory element in the human FOXP2 gene. Molecular Biology and Evolution, 30(4), 844-852.

Mazin, P., Xiong, J., Liu, X., Yan, Z., Zhang, X., Li, M., He, L., Somel, M., Yuan, Y., Chen, Y.-P.-P., Li, N., Hu, Y., Fu, N., Ning, Z., Zeng, R., Yang, H., Chen, W., Gelfand, M., & Khaitovich, P. (2013). Widespread splicing changes in human brain development and aging. Molecular Systems Biology, 9: 663.

Oña Bubach, L. (2013). On the role of resonance in drug failure under HIV treatment interruption. Theoretical Biology & Medical Modelling, 10: 44.

Prado-Martinez, J., Hernando-Herraez, I., Lorente-Galdos, B., Dabad, M., Ramirez, O., Baeza-Delgado, C., Morcillo-Suarez, C., Alkan, C., Hormozdiari, F., Raineri, E., Estellé, J., Fernandez-Callejo, M., Valles, M., Ritscher, L., Schöneberg, T., de la Calle-Mustienes, E., Casillas, S., Rubio-Acero, R., Melé, M., Engelken, J., Caceres, M., Gomez-Skarmeta, J. L., Gut, M., Bertranpetit, J., Gut, I. G., Abello, T., Eichler, E. E., Mingarro, I., Lalueza-Fox, C., Navarro, A., & Marques-Bonet, T. (2013). The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 14: 363.

Prado-Martinez, J., Sudmant, P. H., Kidd, J. M., Li, H., Kelley, J. L., Lorente-Galdos, B., Veeramah, K. R., Woerner, A. E., O'Connor, T. D., Santpere, G., Cagan, A., Theunert, C., Casals, F., Laayouni, H., Munch, K., Hobolth, A., Halager, A. E., Malig, M., Hernandez-Rodriguez, J., Hernando-Herraez, I., Prüfer, K., Pybus, M., Johnstone, L., Lachmann, M., Alkan, C., Twigg, D., Petit, N., Baker, C., Hormozdiari, F., Fernandez-Callejo, M., Dabad, M., Wilson, M. L., Stevison, L., Camprubí, C., Carvalho, T., Ruiz-Herrera, A., Vives, L., Mele, M., Abello, T., Kondova, I., Bontrop, R. E., Pusey, A., Lankester, F., Kiyang, J. A., Bergl, R. A., Lonsdorf, E., Myers, S., Ventura, M., Gagneux, P., Comas, D., Siegismund, H., Blanc, J., Agueda-Calpena, L., Gut, M., Fulton, L., Tishkoff, S. A., Mullikin, J. C., Wilson, R. K., Gut, I. G., Gonder, M. K., Ryder, O. A., Hahn, B. H., Navarro, A., Akey, J. M., Bertranpetit, J., Reich, D., Mailund, T., Schierup, M. H., Hvilsom, C., Andrés, A. M., Wall, J. D., Bustamante, C. D., Hammer, M. F., Eichler, E. E., & Marques-Bonet, T. (2013). Great ape genetic diversity and population history. Nature, 499, 471-475.

Prüfer, K., Langergraber, K. E., Pääbo, S., & Vigilant, L. (2013). Reply to Gibb and Hills: Divergence times, generation lengths and mutation rates in great apes and humans. Proceedings of the National Academy of Sciences of the United States of America, 110(8): E612.

Pugach, I., & Stoneking, M. (2013). Reply to Price and Bird: No inconsistency between the date of gene flow from India and the Australian archaeological record. Proceedings of the National Academy of Sciences of the United States of America, 110(32): E2949.

Pugach, I., Delfin, F., Gunnarsdóttir, E., Kayser, M., & Stoneking, M. (2013). Genome-wide data substantiate Holocene gene flow from India to Australia. Proceedings of the National Academy of Sciences of the United States of America, 110(5), 1803-1808.

Renaud, G., Kircher, M., Stenzel, U., & Kelso, J. (2013). freeIbis: An efficient basecaller with calibrated quality scores for Illumina sequencers. Bioinformatics, 29(9), 1208-1209.

Sheppard, S. K., Didelot, X., Meric, G., Torralbo, A., Jolley, K. A., Kelly, D. J., Bentley, S. D., Maiden, M. C. J., Parkhill, J., & Falush, D. (2013). Genome-wide association study identifies vitamin B5 biosynthesis as a

host specificity factor in Campylobacter. Proceedings of the National Academy of Sciences of the United States of America, 110(29), 11923-11927.

Somel, M., Liu, X., & Khaitovich, P. (2013). Human brain evolution: transcripts, metabolites and their regulators. Nature Reviews Neuroscience, 14(2), 112-127.

Stiller, M., & Hofreiter, M. (2013). An ancient DNA perspective on the cave bears from Pestera cu Oase, Romani. In E. Trinkaus, S. Constantin, & J. Zilhão (Eds.), Life and Death at the Pestera cu Oase: a setting for modern human emergence (pp. 159-167). New York: Oxford University Press.

Stoneking, M. (2013). Mitochondrial genome: Evolution. In Encyclopedia of the Life Sciences. Chichester [u.a.]: Wiley.

Stoneking, M., & Harvati, K. (2013). Early Old World migrations of Homo sapiens: human biology. In The Encyclopedia of Global Human Migration, P. I. Hoboken, NJ: Wiley-Backwell.

Thalmann, O., Shapiro, B., Cui, P., Schuenemann, V. J., Sawyer, S., Greenfield, D. L., Germonpré, M. B., Sablin, M. V., López-Giráldez, F., Domingo-Roura, X., Napierala, H., Uerpmann, H.-P., Loponte, D. M., Acosta, A. A., Giemsch, L., Schmitz, R. W., Worthington, B., Buikstra, J. E., Druzhkova, A., Graphodatsky, A. S., Ovodov, N. D., Wahlberg, N., Freedman, A. H., Schweizer, R. M., Koepfli, K.-P., Leonard, J. A., Meyer, M., Krause, J., Pääbo, S., Green, R. E., & Wayne, R. K. (2013). Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. Science, 342(6160), 871-874.

Viola, B., & Pääbo, S. (2013). What's new in Central Asia? In M. V. Shunkov, & V. Molodin (Eds.), Fundamental'nye problemy archeologii anthropogii i etnografii evrazii: k 70. letiju akademika A. P. Derevjanko = Basic Issues in Archaeology, Anthropology and Ethnography of Eurasia: Festschrift on the occasion of Anatoly Derevianko's 70th birthday (pp. 555-565). Novosibirsk: SB RAS Press.

Yahara, K., Furuta, Y., Oshima, K., Yoshida, M., Azuma, T., Hattori, M., Uchiyama, I., & Kobayashi, I. (2013). Chromosome Painting In Silico in a Bacterial Species Reveals Fine Population Structure. Molecular Biology and Evolution, 30(6), 1454-1464.

2012

Albert, F. W., Somel, M., Carneiro, M., Aximu-Petri, A., Halbwax, M., Thalmann, O., Blanco-Aguiar, J. A., Plyusnina, I. Z., Trut, L., Villafuerte, R., Ferrand, N., Kaiser, S., Jensen, P., & Pääbo, S. (2012). A comparison of brain gene expression levels in domesticated and wild animals. PLoS Genetics, 8(9): e1002962.

Ballantyne, K. N., van Oven, M., Ralf, A., Stoneking, M., Mitchell, R. J., van Oorschot, R. A., & Kayser, M. (2012). MtDNA SNP multiplexes for efficient inference of matrilineal genetic ancestry within Oceania. Forensic Science International: Genetics, 6(4), 425-436.

Barbieri, C., Whitten, M., Beyer, K., Schreiber, H., Li, M., & Pakendorf, B. (2012). Contrasting maternal and paternal histories in the linguistic context of Burkina Faso. Molecular Biology and Evolution, 29(4), 1213 -1223.

Burbano, H. A., Green, R. E., Maricic, T., Lalueza-Fox, C., de la Rasilla, M., Rosas, A., Kelso, J., Pollard, K. S., Lachmann, M., & Pääbo, S. (2012). Analysis of human accelerated DNA regions using archaic hominin genomes. PLoS One, 7(3): e32877.

Carneiro, M., Albert, F. W., Melo-Ferreira, J., Galtier, N., Gayral, P., Blanco-Aguiar, J. A., Villafuerte, R., Nachman, M. W., & Ferrand, N. (2012). Evidence for Widespread Positive and Purifying Selection Across the European Rabbit (Oryctolagus cuniculus) Genome. Molecular Biology and Evolution, 29(7), 1837-1849.

Carnero-Montoro, E., Bonet, L., Engelken, J., Bielig, T., Martínez-Florensa, M., Lozano, F., & Bosch, E. (2012). Evolutionary and functional evidence for positive selection at the human CD5 immune receptor gene. Molecular Biology and Evolution, 29(2), 811-823.

Clovis, Y. M., Enard, W., Marinaro, F., Huttner, W. B., & Tonelli, D. D. P. (2012). Convergent repression of Foxp2 3'UTR by miR-9 and miR-132 in embryonic mouse neocortex: implications for radial migration of neurons. Development, 139(18), 3332-3342.

Dabney, J., & Meyer, M. (2012). Length and GC-biases during sequencing library amplification: A comparison of various polymerase-buffer systems with ancient and modern DNA sequencing libraries. BioTechniques, 52(2), 87-94.

Dannemann, M., Lachmann, M., & Lorenc, A. (2012). 'maskBAD' – a package to detect and remove Affymetrix probes with binding affinity differences. BMC Bioinformatics, 13: 56.

Dannemann, M., Nickel, B., Lizano, E., Burbano, H., & Kelso, J. (2012). Annotation of primate miRNAs by high throughput sequencing of small RNA libraries. BMC Genomics, 13(Suppl. 3): 116.

Dannemann, M., Prüfer, K., Lizano, E., Nickel, B., Burbano, H. A., & Kelso, J. (2012). Transcription factors are targeted by differentially expressed miRNAs in primates. Genome biology and evolution, 4(4), 552-564.

de Filippo, C., Bostoen, K., Stoneking, M., & Pakendorf, B. (2012). Bringing together linguistic and genetic evidence to test the Bantu expansion. Proceedings of the Royal Society B: Biological Sciences, 279(1741), 3256-3263.

Delfin, F., Myles, S., Choi, Y., Hughes, D., Illek, R., van Oven, M., Pakendorf, B., Kayser, M., & Stoneking, M. (2012). Bridging Near and Remote Oceania: mtDNA and NRY Variation in the Solomon Islands. Molecular Biology and Evolution, 29(2), 545-564.

Didelot, X., Méric, G., Falush, D., & Darling, A. E. (2012). Impact of homologous and non-homologous recombination in the genomic evolution of Escherichia coli. BMC Genomics, 13: 256.

Enard, W. (2012). Functional primate genomics - leveraging the medical potential. Journal of Molecular Medicine, 90(5), 471-480.

Fietz, S. A., Lachmann, R., Brandl, H., Kircher, M., Samusik, N., Schröder, R., Lakshmanaperumal, N., Henry, I., Vogt, J., Riehn, A., Distler, W., Nitsch, R., Enard, W., Pääbo, S., & Huttner, W. B. (2012). Transcriptomes of germinal zones of human and mouse fetal neocortex suggest a role of extracellular matrix in progenitor self-renewal. Proceedings of the National Academy of Sciences of the United States of America, 109(29), 11836-11841.

Fu, Q., Rudan, P., Pääbo, S., & Krause, J. (2012). Complete mitochondrial genomes reveal neolithic expansion into Europe. PLoS One, 7(3): e32473.

Gravlund, P., Aaris-Sørensen, K., Hofreiter, M., Meyer, M., Bollback, J. P., & Noe-Nygaar, N. (2012). Ancient DNA extracted from Danish aurochs (Bos primigenius): Genetic diversity and preservation. Annals of Anatomy - Anatomischer Anzeiger, 194(1), 103-111.

Groß, A., Hartung, M., Prüfer, K., Kelso, J., & Rahm, E. (2012). Impact of ontology evolution on functional analyses. Bioinformatics, 28(20), 2671-2677.

Han, Y., Han, D., Yan, Z., Boyd-Kirkup, J. D., Green, C. D., Khaitovich, P., & Han, J.-D.-J. (2012). Stress-associated H3K4 methylation accumulates during postnatal development and aging of rhesus macaque brain. Aging Cell, 11(6), 1055-1064.

Hartmann, S., Helm, C., Nickel, B., Meyer, M., Struck, T. H., Tiedemann, R., Selbig, J., & Bleidorn, C.

(2012). Exploiting gene families for phylogenomic analysis of myzostomid transcriptome data. PLoS One, 7(1): e29843.

Helm, C., Bernhart, S. H., Siederdissen, C. H. z., Nickel, B., & Bleidorn, C. (2012). Deep sequencing of small RNAs confirms an annelid affinity of Myzostomida. Molecular Phylogenetics and Evolution, 64(1), 198-203.

Hering, L., Henze, M. J., Kohler, M., Kelber, A., Bleidorn, C., Leschke, M., Nickel, B., Meyer, M., Kircher, M., Sunnucks, P., & Mayer, G. (2012). Opsins in onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods. Molecular Biology and Evolution, 29(11), 3451-3458.

Hevers, W., & Lüddens, H. (2012). Pharmakologische und präklinische Grundlagen: Aminosäuren. In Handbuch der Psychopharmakotherapie (2. Aufl., pp. 169-184). Berlin [u.a.]: Springer.

Horn, S. (2012). Case study: enrichment of ancient mitochondrial DNA by hybridization capture. In B. Shapiro, & M. Hofreiter (Eds.), Ancient DNA (pp. 189-195). New York: Humana Press.

Horn, S. (2012). Target Enrichment via DNA Hybridization Capture. In B. Shapiro, & M. Hofreiter (Eds.), Ancient DNA (pp. 177-188). New York: Humana Press.

Hu, H. Y., He, L., Fominykh, K., Yan, Z., Guo, S., Zhang, X., Taylor, M. S., Tang, L., Li, J., Liu, J., Wang, W., Yu, H., & Khaitovich, P. (2012). Evolution of the human-specific microRNA miR-941. Nature Communications, 3: 1145.

Jinam, T. A., Hong, L.-C., Phipps, M. E., Stoneking, M., Ameen, M., Edo, J., HUGO Pan-Asian SNP Consortium, & Saitou, N. (2012). Evolutionary history of continental South East Asians: "Early Train" hypothesis based on genetic analysis of mitochondrial and autosomal DNA data. Molecular Biology and Evolution, 29(11), 3513-3527.

Kenny, E. E., Timpson, N. J., Sikora, M., Yee, M.-C., Moreno-Estrada, A., Eng, C., Huntsman, S., Burchard, E. G., Stoneking, M., Bustamante, C. D., & Myles, S. (2012). Melanesian blond hair is caused by an amino acid change in TYRP1. Science, 336(6081), 554-554.

Khrameeva, E. E., Mironov, A. A., Fedonin, G. G., Khaitovich, P., & Gelfand, M. S. (2012). Spatial proximity and similarity of the epigenetic state of genome domains. PLoS One, 7(4): e33947.

Kircher, M. (2012). Analysis of high-throughput ancient DNA sequencing data. In B. Shapiro, & M. Hofreiter (Eds.), Ancient DNA (pp. 197-228). New York: Humana Press.

Kircher, M., Sawyer, S., & Meyer, M. (2012). Double indexing overcomes inaccuracies in multiplex sequencing on the Illumina platform. Nucleic Acids Research, 40(1): e3.

Knapp, M., Stiller, M., & Meyer, M. (2012). Generating barcoded libraries for multiplex high-throughput sequencing. In B. Shapiro, & M. Hofreiter (Eds.), Ancient DNA (pp. 155-170). New York: Humana Pr.

Langergraber, K., Pruefer, K., Rowney, C., Boesch, C., Crockford, C., Fawcett, K., Inoue, E., Inoue-Muruyama, M., Mitani, J. C., Muller, M. N., Robbins, M. M., Schubert, G., Stoinski, T. S., Viola, B., Watts, D., Wittig, R., Wrangham, R. W., Zuberbühler, K., Pääbo, S., & Vigilant, L. (2012). Generation times in wild chimpanzees and gorillas suggest earlier divergence times in great ape and human evolution. Proceedings of the National Academy of Sciences of the United States of America, 109(39), 15716-15721.

Lawson, D. J., & Falush, D. (2012). Population identification using genetic data. Annual Review of Genomics and Human Genetics, 13, 337-361.

Lawson, D. J., Hellenthal, G., Myers, S., & Falush, D. (2012). Inference of Population Structure using

Dense Haplotype Data. PLoS Genetics, 8(1): e1002453.

Lee, C.-H., Ko, A.-M.-S., Yen, C.-F., Chu, K.-S., Gao, Y.-J., Warnakulasuriya, S., Sunarjo,.-., Ibrahim, S. O., Zain, R. B., Patrick, W. K., & Ko, Y.-C. (2012). Betel-quid dependence and oral potentially malignant disorders in six Asian countries. British Journal of Psychiatry, 201(5), 383-391.

Li, J., Menard, V., Benish, R. L., Jurevic, R. J., Guillemette, C., Stoneking, M., Zimmerman, P. A., & Mehlotra, R. K. (2012). Worldwide variation in human drug-metabolism enzyme genes CYP2B6 and UGT2B7: implications for HIV/AIDS treatment. Pharmacogenomics, 13(5), 555-570.

Li, M., & Stoneking, M. (2012). A new approach for detecting low-level mutations in next-generation sequence data. Genome Biology, 13(5): R34.

Li, M., Schröder, R., Ko, A.-M.-S., & Stoneking, M. (2012). Fidelity of capture-enrichment for mtDNA genome sequencing: influence of NUMTs. Nucleic Acids Research, 40(18): e137.

Liu, X., Somel, M., Tang, L., Yan, Z., Jiang, X., Guo, S., Yuan, Y., He, L., Oleksiak, A., Zhang, Y., Li, N., Hu, Y., Chen, W., Qiu, Z., Pääbo, S., & Khaitovich, P. (2012). Extension of cortical synaptic development distinguishes humans from chimpanzees and macaques. Genome Research, 22(4), 611-622.

Mailund, T., Halager, A. E., Westergaard, M., Dutheil, J. Y., Munch, K., Andersen, L. N., Lunter, G., Pruefer, K., Scally, A., Hobolth, A., & Schierup, M. H. (2012). A new isolation with migration model along complete genomes infers very different divergence processes among closely related great ape species. PLoS Genetics, 8(12): e1003125.

Meyer, M., Kircher, M., Gansauge, M.-T., Li, H., Racimo, F., Mallick, S., Schraiber, J. G., Jay, F., Prüfer, K., Filippo, C. d., Sudmant, P. H., Alkan, C., Fu, Q., Do, R., Rohland, N., Tandon, A., Siebauer, M., Green, R. E., Bryc, K., Briggs, A. W., Stenzel, U., Dabney, J., Shendure, J., Kitzman, J., Hammer, M. F., Shunkov, M. V., Derevianko, A. P., Patterson, N., Andrés, A. M., Eichler, E. E., Slatkin, M., Reich, D., Kelso, J., & Pääbo, S. (2012). A high-coverage genome sequence from an archaic Denisovan individual. Science, 338(6104), 222-226.

Pickrell, J. K., Patterson, N., Berthold, F., Barbieri, C., Gerlach, L., Gueldemann, T., Kure, B., Mpoloka, S. W., Nakagawa, H., Naumann, C., Lipson, M., Loh, P.-R., Lachance, J., Mountain, J., Bustamante, C. D., Berger, B., Tishkoff, S. A., Henn, B. M., Stoneking, M., Reich, D., & Pakendorf, B. (2012). The genetic prehistory of southern Africa. Nature Communications, 3: 1143.

Prüfer, K., Munch, K., Hellmann, I., Akagi, K., Miller, J. R., Walenz, B., Koren, S., Sutton, G., Kodira, C., Winer, R., Knight, J. R., Mullikin, J. C., Meader, S. J., Ponting, C. P., Lunter, G., Higashino, S., Hobolth, A., Dutheil, J., Karakoç, E., Alkan, C., Sajjadian, S., Catacchio, C. R., Ventura, M., Marques-Bonet, T., Eichler, E. E., André, C., Atencia, R., Mugisha, L., Junhold, J., Patterson, N., Siebauer, M., Good, J. M., Fischer, A., Ptak, S. E., Lachmann, M., Symer, D. E., Mailund, T., Schierup, M. H., Andrés, A. M., Kelso, J., & Pääbo, S. (2012). The bonobo genome compared with the chimpanzee and human genomes. Nature, 486(7404), 527-531.

Quillen, E. E., Bauchet, M., Bigham, A. W., Delgado-Burbano, M. E., Faust, F. X., Klimentidis, Y. C., Mao, X., Stoneking, M., & Shriver, M. D. (2012). OPRM1 and EGFR contribute to skin pigmentation differences between Indigenous Americans and Europeans. Human Genetics, 131(7), 1073-1080.

Ratikainen, I. I., Sødal, L. R. H., Kazem, A., & Wright, J. (2012). Private and public information use strategies by foraging groups of wild Siberian jays. Animal Behaviour, 83(5), 1243-1251.

Rost, B., Gaasterland, T., Lengauer, T., Linial, M., Markel, S., McKay, B. M., Schneider, R., Horton, P., & Kelso, J. (2012). Paving the future: finding suitable ISMB venues. Bioinformatics, 28(19), 2556-2559.

Sankararaman, S., Patterson, N., Li, H., Pääbo, S., & Reich, D. (2012). The date of interbreeding between Neandertals and modern humans. PLoS Genetics, 8(10): e1002947.

Sawyer, S., Krause, J., Guschanski, K., Savolainen, V., & Pääbo, S. (2012). Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. PLoS One, 7(3): e34131.

Schmidt, M., Horn, S., Flieger, K., Ehlers, K., Wilhelm, C., & Schnetter, R. (2012). Synchroma pusillum sp. nov. and other New Algal Isolates with Chloroplast Complexes Confirm the Synchromophyceae (Ochrophyta) as a Widely Distributed Group of Amoeboid Algae. Protist, 163(4), 544-559.

Stoneking, M. (2012). Genetic evidence concerning the origins and dispersals of modern humans. In M. H. Crawford, & B. C. Campbell (Eds.), Causes and Consequences of Human Migration: An Evolutionary Perspective (pp. 11-20). Cambridge: Cambridge Univ. Pr.

Theunert, C., Tang, K., Lachmann, M., Hu, S., & Stoneking, M. (2012). Inferring the history of population size change from genome-wide SNP data. Molecular Biology and Evolution, 29(2), 3653-3667.

Weng, K., Hu, H., Xu, G. A., Khaitovich, P., & Somel, M. (2012). Mechanisms of Dietary Response in Mice and Primates: A Role for EGR1 in Regulating the Reaction to Human-Specific Nutritional Content. PLoS One, 7(8): e43915.

White, L., & Castellano, S. (2012). Evolutionary basis for the use of selenocysteine. In D. L. Hatfield, M. J. Berry, & V. N. Gladyshev (Eds.), Selenium: Its Molecular Biology and Role in Human Health (3, pp. 85-93). New York [u.a.]: Springer.

Xu, S., & Stoneking, M. (2012). Reply to Denham and Donohue: Asian-Papuan genetic admixture is in excellent agreement with Austronesian dispersal in eastern Indonesia. Proceedings of the National Academy of Sciences of the United States of America, 109(39): E2578.

Xu, S., Pugach, I., Stoneking, M., Kayser, M., Jina, L., & The HUGO Pan-Asian SNP Consortium (2012). Genetic dating indicates that the Asian–Papuan admixture through Eastern Indonesia corresponds to the Austronesian expansion. Proceedings of the National Academy of Sciences of the United States of America, 109(12), 4574-4579.

Yuan, Y., Chen, Y.-P.-P., Boyd-Kirkup, J., Khaitovich, P., & Somel, M. (2012). Accelerated aging-related transcriptome changes in the female prefrontal cortex. Aging Cell, 11(5), 894-901.

2011

Abramson, G., Trejo Soto, C. A., & Oña Bubach, L. (2011). The role of asymmetric interactions on the effect of habitat destruction in mutualistic networks. PLoS ONE, 6(6): e21028.

Albert, F. W., Hodges, E., Jensen, J. D., Besnier, F., Xuan, Z., Rooks, M., Bhattacharjee, A., Brizuela, L., Good, J. M., Green, R. E., Burbano, H. A., Plyusnina, I. Z., Trut, L., Andersson, L., Schöneberg, T., Carlborg, Ö., Hannon, G. J., & Pääbo, S. (2011). Targeted resequencing of a genomic region influencing tameness and aggression reveals multiple signals of positive selection. Heredity, 107(3), 205-214.

Andrés, A. M. (2011). Balancing selection in the human genome. In Encyclopedia of Life Sciences. Chichester [u.a.]: Wiley.

Benazzi, S., Viola, B., Kullmer, O., Fiorenza, L., Harvati, K., Paul, T., Gruppioni, G., Weber, G. W., & Mallegni, F. (2011). A reassessment of the Neanderthal teeth from Taddeo cave (southern Italy). Journal of Human Evolution, 61(4), 377-387.

Bos, K. I., Schuenemann, V. J., Golding, G. B., Burbano, H. A., Waglechner, N., Coombes, B. K., McPhee,

J. B., DeWitte, S. N., Meyer, M., Schmedes, S., Wood, J., Earn, D. J. D., Herring, D. A., Bauer, P., Poinar, H. N., & Krause, J. (2011). A draft genome of Yersinia pestis from victims of the Black Death. Nature, 478(7370), 506-510.

Brawand, D., Soumillon, M., Necsulea, A., Julien, P., Csárdi, G., Harrigan, P., Weier, M., Liechti, A., Aximu-Petri, A., Kircher, M., Albert, F. W., Zeller, U., Khaitovich, P., Grützner, F., Bergmann, S., Nielsen, R., Pääbo, S., & Kaessmann, H. (2011). The evolution of gene expression levels in mammalian organs. Nature, 478(7369), 343-348.

de Filippo, C., Barbieri, C., Whitten, M., Mpoloka, S. W., Gunnarsdóttir, E. D., Bostoen, K., Nyambe, T., Beyer, K., Schreiber, H., Knijff, P. d., Luiselli, D., Stoneking, M., & Pakendorf, B. (2011). Y-chromosomal variation in sub-saharan Africa: Insights into the history of Niger-Congo groups. Molecular Biology and Evolution, 28(3): msq312v1, pp. 1255-1269.

Delfin, F., Salvador, J. M., Calacal, G. C., Perdigon, H. B., Tabbada, K. A., Villamor, L. P., Halos, S. C., Gunnarsdóttir, E., Myles, S., Hughes, D. A., Xu, S., Jin, L., Lao, O., Kayser, M., Hurles, M. E., Stoneking, M., & Ungria, M. C. A. d. (2011). The Y-chromosome landscape of the Philippines: extensive heterogeneity and varying genetic affinities of Negrito and non-Negrito groups. European Journal of Human Genetics, 19(2), 224-230.

Didelot, X., Bowden, R., Street, T., Golubchik, T., Spencer, C., McVean, G., Sangal, V., Anjum, M. F., Achtman, M., Falush, D., & Donelly, P. (2011). Recombination and population structure in Salmonella enterica. PLoS Genetics, 7(7): e1002191.

Döppes, D., Rabeder, G., & Stiller, M. (2011). Was the Middle Würmian in the High Alps warmer than today? Quaternary International, 245(2), 193-200.

Enard, W. (2011). FOXP2 and the role of cortico-basal ganglia circuits in speech and language evolution. Current Opinion in Neurobiology, 21(3), 415-424.

Fiorenza, L., Benazzi, S., Viola, B., Kullmer, O., & Schrenk, F. (2011). Relationship Between Cusp Size and Occlusal Wear Pattern in Neanderthal and Homo sapiens First Maxillary Molars. The Anatomical Record: Advances in Integrative Anatomy and Evolutionary Biology, 294(3), 453-461.

Fischer, A., Prüfer, K., Good, J. M., Halbwax, M., Wiebe, V., André, C., Atencia, R., Mugisha, L., Ptak, S. E., & Pääbo, S. (2011). Bonobos fall within the genomic variation of chimpanzees. PLoS One, 6(6): e21605.

Fu, X., Giavalisco, P., Liu, X., Catchpole, G., Fu, N., Ning, Z.-B., Guo, S., Yan, Z., Somel, M., Pääbo, S., Zeng, R., Willmitzer, L., & Khaitovich, P. (2011). Rapid metabolic evolution in human prefrontal cortex. Proceedings of the National Academy of Sciences of the United States of America, 108(15), 6181-6186.

Gaudet, P., Bairoch, A., Field, D., Sansone, S.-A., Taylor, C., Attwood, T. K., Bateman, A., Blake, J. A., Bult, C. J., Cherry, J. M., Chrisholm, R. L., Cochrane, G., Cook, C. E., Eppig, J. T., Galperin, M. Y., Gentleman, R., Goble, C. A., Gojobori, T., Hancock, J. M., Howe, D. G., Imanishi, T., Kelso, J., Landsman, D., Lewis, S. E., Karsch-Mizrachi, I., Orchard, S., Ouellette, B. F. F., Ranganathan, S., Richardson, L., Rocca-Serra, P., Schofield, P. N., Smedley, D., Southan, C., Tan, T. W., Tatusova, T., Whetzel, P. L., White, O., & Yamasaki, C. (2011). Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 39(Suppl. 1).

Gaudet, P., Bairoch, A., Field, D., Sansone, S.-A., Taylor, C., Attwood, T. K., Bateman, A., Blake, J. A., Bult, C. J., Cherry, J. M., Chrisholm, R. L., Cochrane, G., Cook, C. E., Eppig, J. T., Galperin, M. Y., Gentleman, R., Goble, C. A., Gojobori, T., Hancock, J. M., Howe, D. G., Imanishi, T., Kelso, J., Landsman, D., Lewis, S. E., Mizrachi, I. K., Orchard, S., Ouellette, B. F. F., Ranganathan, S., Richardson, L.,

Rocca-Serra, P., Schofield, P. N., Smedley, D., Southan, C., Tan, T. W., Tatusova, T., Whetzel, P. L., White, O., & Yamasaki, C. (2011). Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011: baq027, pp. 1-6.

Gralle, M., & Pääbo, S. (2011). A comprehensive functional analysis of ancestral human signal peptides. Molecular Biology and Evolution, 28(1), 25-28.

Gross, A., Tönjes, A., Kovacs, P., Veeramah, K. R., Ahnert, P., Roshyara, N. R., Gieger, C., Rueckert, I.-M., Loeffler, M., Stoneking, M., Wichmann, H.-E., Novembre, J., Stumvoll, M., & Scholz, M. (2011). Population-genetic comparison of the Sorbian isolate population in Germany with the German KORA population using genome-wide SNP arrays. BMC Genetics, 12: 67.

Grossmann, T., Johnson, M. H., Vaish, A., Hughes, D. A., Quinque, D., Stoneking, M., & Friederici, A. D. (2011). Genetic and neural dissociation of individual responses to emotional expressions in human infants. Developmental Cognitive Neuroscience, 1(1), 57-66.

Gunnarsdóttir, E. D., Li, M., Bauchet, M., Finstermeier, K., & Stoneking, M. (2011). High-throughput sequencing of complete human mtDNA genomes from the Philippines. Genome Research, 21(1), 1-11.

Gunnarsdóttir, E. D., Nandineni, M. R., Li, M., Myles, S., Gil, D., Pakendorf, B., & Stoneking, M. (2011). Larger mitochondrial DNA than Y-chromosome differences between matrilocal and patrilocal groups from Sumatra. Nature Communications, 2: 228.

Harrison, A., Lemey, P., Hurles, M., Moyes, C., Horn, S., Pryor, J., Malani, J., Supuri, M., Masta, A., Teriboriki, B., Toatu, T., Penny, D., Rambaut, A., & Shapiro, B. (2011). Genomic Analysis of Hepatitis B Virus Reveals Antigen State and Genotype as Sources of Evolutionary Rate Variation. Viruses, 3(2), 83-101.

Herre, H., Hoehndorf, R., Kelso, J., Loebe, F., & Schulz, S. (2011). OBML – Ontologies in biomedicine and life sciences. Journal of Biomedical Semantics, 2(Suppl. 4): I1, pp. 1-6.

Horn, S., Durka, W., Wolf, R., Ermala, A., Stubbe, A., Stubbe, M., & Hofreiter, M. (2011). Mitochondrial Genomes Reveal Slow Rates of Molecular Evolution and the Timing of Speciation in Beavers (Castor), One of the Largest Rodent Species. PLoS ONE, 6(1): e14622.

Hu, H. Y., Guo, S., Xi, J., Yan, Z., Fu, N., Zhang, X., Menzel, C., Liang, H., Yang, H., Zhao, M., Zeng, R., Chen, W., Pääbo, S., & Khaitovich, P. (2011). MicroRNA expression and regulation in human, chimpanzee, and macaque brains. PLoS Genetics, 7(10): e1002327, pp. 1-14.

Jin, C., Li, J., Green, C. D., Yu, X., Tang, X., Han, D., Xian, B., Wang, D., Huang, X., Cao, X., Yan, Z., Hou, L., Liu, J., Shukeir, N., Khaitovich, P., Chen, C. D., Zhang, H., Jenuwein, T., & Han, J.-D.-J. (2011). Histone Demethylase UTX-1 Regulates C. elegans Life Span by Targeting the Insulin/IGF-1 Signaling Pathway. Cell Metabolism, 14(2), 161-172.

Jordan, S., Krause, J., Prager, A., Mitrovic, M., Jonjic, S., Koszinowski, U. H., & Adler, B. (2011). Virus progeny of murine cytomegalovirus bacterial artificial chromosome pSM3fr show reduced growth in salivary glands due to a fixed mutation of MCK-2. Journal of Virology, 85(19), 10346-10353.

Ka, S., Albert, F. W., Denbow, D. M., Pääbo, S., Siegel, P. B., Andersson, L., & Hallböök, F. (2011). Differentially expressed genes in hypothalamus in relation to genomic regions under selection in two chicken lines resulting from divergent selection for high or low body weight. Neurogenetics, 12(3), 211-221.

Kircher, M., Heyn, P., & Kelso, J. (2011). Addressing challenges in the production and analysis of illumina sequencing data. BMC Genomics, 12: 382.

Lehnertz, B., Rogalski, J. C., Schulze, F. M., Yi, L., Lin, S., Kast, J., & Rossi, F. M. (2011). p53-dependent

transcription and tumor suppression are not affected in set7/9-deficient mice. Molecular Cell, 43(4), 673-680.

Lerner, H. R. L., Meyer, M., James, H. F., Hofreiter, M., & Fleischer, R. C. (2011). Multilocus resolution of phylogeny and timescale in the extant adaptive radiation of Hawaiian honeycreepers. Current Biology, 21(21), 1838-1844.

Li, J., Zhang, L., Zhou, H., Stoneking, M., & Tang, K. (2011). Global patterns of genetic diversity and signals of natural selection for human ADME genes. Human Molecular Genetics, 20(3), 528-540.

Li, M., & Chen, S.-S. (2011). The tendency to recreate ancestral CG dinucleotides in the human genome. BMC Evolutionary Biology, 11: 3.

Liebscher, I., Müller, U., Teupser, D., Engemaier, E., Engel, K. M. Y., Ritscher, L., Thor, D., Sangkuhl, K., Ricken, A., Wurm, A., Piehler, D., Schmutzler, S., Fuhrmann, H., Albert, F. W., Reichenbach, A., Thiery, J., Schöneberg, T., & Schulz, A. (2011). Altered Immune Response in Mice Deficient for the G Protein-coupled Receptor GPR34. The Journal of Biological Chemistry, 286(3), 2101-2110.

Lippold, S., Knapp, M., Kuznetsova, T., Leonard, J. A., Benecke, N., Ludwig, A., Rasmussen, M., Cooper, A., Weinstock, J., Willerslev, E., Shapiro, B., & Hofreiter, M. (2011). Discovery of lost diversity of paternal horse lineages using ancient DNA. Nature Communications, 2: 450, pp. 1-6.

Lippold, S., Matzke, N. J., Reissmann, M., & Hofreiter, M. (2011). Whole mitochondrial genome sequencing of domestic horses reveals incorporation of extensive wild horse diversity during domestication. BMC Evolutionary Biology, 11: 328.

Liu, Y., Han, D., Han, Y., Yan, Z., Xie, B., Li, J., Qiao, N., Hu, H., Khaitovich, P., Gao, Y., & Han, J.-D.-J. (2011). Ab initio identification of transcription start sites in the Rhesus macaque genome by histone modification and RNA-Seq. Nucleic Acids Research, 39(4), 1408-1418.

Myles, S., Lea, R. A., Ohashi, J., Chambers, G. K., Weiss, J. G., Hardouin, E., Engelken, J., Macartney-Coxson, D. P., Eccles, D. A., Naka, I., Kimura, R., Inaoka, T., Matsumura, Y., & Stoneking, M. (2011). Testing the thrifty gene hypothesis: the Gly482Ser variant in PPARGC1A is associated with BMI in Tongans. BMC Medical Genetics, 12(1): 10, pp. 1-7.

Nagaraj, N., Wisniewski, J. R., Geiger, T., Cox, J., Kircher, M., Kelso, J., Pääbo, S., & Mann, M. (2011). Deep proteome and transcriptome mapping of a human cancer cell line. Molecular Systems Biology, 7: 548.

Nasidze, I., & Stoneking, M. (2011). Microbiome diversity in human saliva. In F. J. d. Bruijn (Ed.), Handbook of Molecular Microbial Ecology II: Metagenomics in Different Habitats (pp. 335-339). New York: Wiley.

Nasidze, I., Li, J., Schroeder, R., Creasey, J. L., Li, M., & Stoneking, M. (2011). High diversity of the saliva microbiome in Batwa pygmies. PLoS ONE, 6(8): e23352.

Oña, L., & Lachmann, M. (2011). Ant aggression and evolutionary stability in plant–ant and plant–pollinator mutualistic interactions. Journal of Evolutionary Biology, 24(3), 617-629.

Oota, H., & Stoneking, M. (2011). Effect of human migration on genome diversity in East Asia. In Y. Takezawa (Ed.), Racial representations in Asia (pp. 173-187). Kyoto: Kyoto Univ. Press.

Pugach, I., Matveyev, R., Wollstein, A., Kayser, M., & Stoneking, M. (2011). Dating the age of admixture via wavelet transform analysis of genome-wide data. Genome Biology, 12(2): R19, pp. 1-18.

Ranganathan, S., Schönbach, C., Kelso, J., Rost, B., Nathan, S., & Tan, T. W. (2011). Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. BMC

Bioinformatics, 12(Suppl. 13): S1.

Reich, D., Patterson, N., Kircher, M., Delfin, F., Nandineni, M. R., Pugach, I., Ko, A.-M.-S., Ko, Y.-C., Jinam, T. A., Phipps, M. E., Saitou, N., Wollstein, A., Kayser, M., Pääbo, S., & Stoneking, M. (2011). Denisova admixture and the first modern human dispersals into southeast Asia and Oceania. The American Journal of Human Genetics, 89(4), 516-528.

Reimers-Kipping, S., Hevers, W., Pääbo, S., & Enard, W. (2011). Humanized Foxp2 specifically affects cortico-basal ganglia circuits. Neuroscience, 175, 75-84.

Reinartz, R., Lippold, S., Lieckfeldt, D., & Ludwig, A. (2011). Population genetic analyses of Acipenser ruthenus as a prerequisite for the conservation of the uppermost Danube population. Journal of Applied Ichthyology, 27(2), 477-483.

Schönbach, C., Tan, T. W., Kelso, J., Rost, B., Nathan, S., & Ranganathan, S. (2011). InCoB celebrates its tenth anniversary as first joint conference with ISCB-Asia. BMC Genomics, 12(Suppl. 3): S1.

Schönberg, A., Theunert, C., Li, M., Stoneking, M., & Nasidze, I. (2011). High-throughput sequencing of complete human mtDNA genomes from the Caucasus and West Asia: High diversity and demographic inferences. European Journal of Human Genetics, 19(9), 988-994.

Scott, N. A., & Murphy, T. H. (2011). Glial laminar cortical architecture matches metabolic demand. Journal of Cerebral Blood Flow & Metabolism, 31(3), 793-794.

Somel, M., Liu, X., Tang, L., Yan, Z., Hu, H., Guo, S., Jiang, X., Zhang, X., Xu, G., Xie, G., Li, N., Hu, Y., Chen, W., Pääbo, S., & Khaitovich, P. (2011). MicroRNA-driven developmental remodeling in the brain distinguishes humans from other primates. PLoS Biology, 9(12): e1001214.

Stewart, J. R., Aspinall, S., Beech, M., Fenberg, P., Hellyer, P., Larkin, N., Lokier, S. W., Marx, F. G., Meyer, M., Miller, R., Rainbow, P. S., Taylor, J. D., Whittaker, J. E., Al-Mehsin, K., & Strohmenger, C. J. (2011). Biotically constrained palaeoenvironmental conditions of a mid-Holocene intertidal lagoon on the southern shore of the Arabian Gulf: Evidence associated with a whale skeleton at Musaffah, Abu Dhabi, UAE. Quaternary Science Reviews, 30(25-26), 3675-3690.

Stoneking, M., & Krause, J. (2011). Learning about human population history from ancient and modern genomes. Nature Reviews Genetics, 12(9), 603-614.

Stoneking, M.(2011). Was wir von Spucke lernen können: Diversität im Mikrobiom des menschlichen Speichels. Retrieved from https://www.mpg.de/1262166/Mikrobiom_Speichel?c=1070738.

Thalmann, O., Wegmann, D., Spitzner, M., Arandjelovic, M., Guschanski, K., Leuenberger, C., Bergl, R. A., & Vigilant, L. (2011). Historical sampling reveals dramatic demographic changes in western gorilla populations. BMC Evolutionary Biology, 11: 85, pp. 1-10.

Wang, S.-J., Tu, H.-P., Ko, A.-M.-S., Chiang, S.-L., Chiou, S.-J., Lee, S.-S., Tsai, Y.-S., Lee, C.-P., & Ko, Y.-C. (2011). Lymphocyte alpha-kinase is a gout-susceptible gene involved in monosodium urate monohydrate-induced inflammatory responses. Journal of Molecular Medicine, 89(12), 1241-1251.

Yan, Z., Hu, H. Y., Jiang, X., Maierhofer, V., Neb, E., He, L., Hu, Y., Hu, H., Li, N., Chen, W., & Khaitovich, P. (2011). Widespread expression of piRNA-like molecules in somatic tissues. Nucleic Acids Research, 39(15), 6596-6607.

Yuan, Y., Chen, Y.-P.-P., Ni, S., Xu, G. A., Tang, L., Vingron, M., Somel, M., & Khaitovich, P. (2011). Development and application of a modified dynamic time warping algorithm (DTW-S) to analyses of primate brain expression time series. BMC Bioinformatics, 12: 347.

2010

Addis, L., Friederici, A. D., Kotz, S. A., Sabisch, B., Barry, J., Richter, N., Ludwig, A. A., Rübsamen, R., Albert, F. W., Pääbo, S., Newbury, D. F., & Monaco, A. P. (2010). A locus for an auditory processing deficit and language impairment in an extended pedigree maps to 12p13.31-q14.3. Genes, Brain & Behavior, 9(6), 545-561.

Andrés, A. M., Dennis, M. Y., Kretzschmar, W. W., Cannons, J. L., Lee-Lin, S.-Q., Hurle, B., NISC Comparative Sequencing Program, Schwartzberg, P. L., Williamson, S. H., Bustamante, C. D., Nielsen, R., Clark, A. G., & Green, E. D. (2010). Balancing selection maintains a form of ERAP2 that undergoes nonsense-mediated decay and affects antigen presentation. PLoS Genetics, 6(10): e1001157.

Asher, R. J., Maree, S., Bronner, G., Bennett, N. C., Bloomer, P., Czechowski, P., Meyer, M., & Hofreiter, M. (2010). A phylogenetic estimate for golden moles (Mammalia, Afrotheria, Chrysochloridae). BMC Evolutionary Biology, 10: 69.

Athanasiadis, G., Esteban, E., Gayà-Vidal, M., Dugoujon, J.-M., Moschonas, N., Chaabani, H., Bissar-Tadmouri, N., Harich, N., Stoneking, M., & Moral, P. (2010). Different evolutionary histories of the coagulation factor VII gene in human populations? Annals of Human Genetics, 74(1), 34-45.

Athanasiadis, G., González-Pérez, E., Esteban, E., Dugoujon, J.-M., Stoneking, M., & Moral, P. (2010). The Mediterranean Sea as a barrier to gene flow: Evidence from variation in and around the F7 and F12 genomic regions. BMC Evolutionary Biology, 10: 84.

Bigham, A., Pinto, D., Bauchet, M., Mao, X., Akey, J. M., Mei, R., Scherer, S. W., Julian, C. G., Wilson, M. J., Herráez, D. L., Brutsaert, T., Parra, E. J., Moore, L. G., & Shriver, M. D. (2010). Identifying signatures of natural selection in Tibetan and Andean populations using dense genome scan data. PLoS Genetics, 6(9): e1001116, pp. 1-14.

Bower, M. A., Campana, M. G., Whitten, M., Edwards, C. J., Jones, H., Barrett, E., Cassidy, R., Nisbet, R. E. R., Hill, E. W., Howe, C. J., & Binns, M. (2010). The cosmopolitan maternal heritage of the Thoroughbred racehorse breed shows a significant contribution from British and Irish native mares. Biology Letters, 7(2), 316-320.

Briggs, A. W., Stenzel, U., Meyer, M., Krause, J., Kircher, M., & Pääbo, S. (2010). Removal of deaminated cytosines and detection of in vivo methylation in ancient DNA. Special Issue on Synthetic Biology, e87, pp. 1-12.

Burbano, H. A., Hodges, E., Green, R. E., Briggs, A. W., Krause, J., Meyer, M., Good, J. M., Maricic, T., Johnson, P. L. F., Xuan, Z., Rooks, M., Bhattacharjee, A., Brizuela, L., Albert, F. W., Rasilla, M. d. l., Fortea, J., Rosas, A., Lachmann, M., Hannon, G. J., & Pääbo, S. (2010). Targeted investigation of the Neandertal genome by array-based sequence capture. Science, 328(5979), 723-725.

Campana, M. G., Whitten, C. M., Edwards, C. J., Stock, F., Murphy, A. M., Binns, M. M., Barker, G. W. W., & Bower, M. A. (2010). Accurate determination of phenotypic information from historic thoroughbred horses by single base extension. PLoS ONE, 5(12): e15172.

Campbell, K. L., Roberts, J. E. E., Watson, L. N., Stetefeld, J., Sloan, A. M., Signore, A. V., Howatt, J. W., Tame, J. R. H., Rohland, N., Shen, T.-J., Austin, J. J., Hofreiter, M., Ho, C., Weber, R. E., & Cooper, A. (2010). Substitutions in woolly mammoth hemoglobin confer biochemical properties adaptive for cold tolerance. Nature Genetics, 42(6), 536-540.

Campos, P. F., Kristensen, T., Orlando, L., Sher, A., Kholodova, M. V., Götherström, A., Hofreiter, M., Drucker, D. G., Kosintsev, P., Tikhonov, A., Baryshnikov, G. F., Willerslev, E., & Gilbert, M. T. P. (2010).

Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope (Saiga tatarica) since the Pleistocene. Molecular Ecology, 19(22), 4863-4875.

Campos, P. F., Willerslev, E., Mead, J. I., Hofreiter, M., & Gilbert, M. T. P. (2010). Molecular identification of the extinct mountain goat, Oreamnos harringtoni (Bovidae). Boreas, 39(1), 18-23.

Cieslak, M., Pruvost, M., Benecke, N., Hofreiter, M., Morales, A., Reissmann, M., & Ludwig, A. (2010). Origin and history of mitochondrial DNA lineages in domestic horses. PLoS ONE, 5(12): e15311.

de Filippo, C., Heyn, P., Barham, L., Stoneking, M., & Pakendorf, B. (2010). Genetic perspectives on forager-farmer interaction in the Luangwa Valley of Zambia. American Journal of Physical Anthropology, 141(3), 382-394.

Donaldson-Matasci, M. C., Bergstrom, C. T., & Lachmann, M. (2010). The fitness value of information. Oikos, 119(2), 219-230.

Fuselli, S., de Filippo, C., Stefano, M., Sistonen, J., Fariselli, P., Destro-Bisol, G., Barbujani, G., Bertorelle, G., & Sajantila, A. (2010). Evolution of detoxifying systems: the role of environment and population history in shaping genetic diversity at human CYP2D6 locus. Pharmacogenetics & Genomics, 20(8), 485-499.

Giger, T., Khaitovich, P., Somel, M., Lorenc, A., Lizano, E., Harris, L. W., Ryan, M. M., Lan, M., Wayland, M. T., Bahn, S., & Pääbo, S. (2010). Evolution of neuronal and endothelial transcriptomes in primates. Genome Biology and Evolution, 2, 284-292.

Good, J. M., Giger, T., Dean, M. D., & Nachman, M. W. (2010). Widespread Over-Expression of the X Chromosome in Sterile F1 Hybrid Mice. PLoS Genetics, 6(9): e1001148, pp. 1-13.

Gralle, M., Schäfer, I., Seibel, P., & Pääbo, S. (2010). A functional test of Neandertal and modern human mitochondrial targeting sequences. Biochemical and Biophysical Research Communications, 402(4), 747-749.

Green, R. E., Krause, J., Briggs, A. W., Maricic, T., Stenzel, U., Kircher, M., Patterson, N., Li, H., Zhai, W., Fritz, M.-H.-Y., Hansen, N. F., Durand, E. Y., Malaspinas, A.-S., Jensen, J. D., Marques-Bonet, T., Alkan, C., Prüfer, K., Meyer, M., Burbano, H. A., Good, J. M., Schultz, R., Aximu-Petri, A., Butthoff, A., Höber, B., Höffner, B., Siegemund, M., Weihmann, A., Nusbaum, C., Lander, E. S., Russ, C., Novod, N., Affourtit, J., Egholm, M., Verna, C., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Doronichev, V. B., Golovanova, L. V., Lalueza-Fox, C., Rasilla, M. d. l., Fortea, J., Rosas, A., Schmitz, R. W., Johnson, P. L. F., Eichler, E. E., Falush, D., Birney, E., Mullikin, J. C., Slatkin, M., Nielsen, R., Kelso, J., Lachmann, M., Reich, D., & Pääbo, S. (2010). A draft sequence of the Neandertal genome. Science, 328(5979), 710-722.

Heyn, P., Stenzel, U., Briggs, A. W., Kircher, M., Hofreiter, M., & Meyer, M. (2010). Road blocks on paleogenomes - polymerase extension profiling reveals the frequency of blocking lesions in ancient DNA. Nucleic Acids Research, 38(16): e161.

Hoehndorf, R., Ngonga Ngomo, A.-C., & Kelso, J. (2010). Applying the functional abnormality ontology pattern to anatomical functions. Journal of biomedical semantics, 1(1): 4, pp. 1-15.

Hoehndorf, R., Ngonga Ngomo, A.-C., Dannemann, M., & Kelso, J. (2010). Statistical tests for associations between two directed acyclic graphs. PLoS ONE, 5(6): e10996, pp. 1-8.

Hoehndorf, R., Oellrich, A., Dumontier, M., Kelso, J., Rebholz-Schuhmann, D., & Herre, H. (2010). Relations as patterns: bridging the gap between OBO and OWL. BMC Bioinformatics, 11: 441.

Hofreiter, M. (2010). Human Evolution. In M. R. Speicher, S. E. Antonarakis, A. G. Motulsky (Ed.), Vogel and Motulsky's Human Genetics (pp. 529-555). Heidelberg: Springer.

Hofreiter, M., & Römpler, H. (2010). Polymerase chain reaction: a blessing and a curse for ancient deoxyribonucleic acid research. In Stephen A. Bustin (Ed.), The PCR revolution: basic technologies and applications (pp. 284-299). Cambridge: Cambridge University Press.

Hofreiter, M., & Schöneberg, T. (2010). The genetic and evolutionary basis of colour variation in vertebrates. Cellular and Molecular Life Sciences, 67(15), 2591-2603.

Hofreiter, M., Kreuz, E., Eriksson, J., Schubert, G., & Hohmann, G. (2010). Vertebrate DNA in fecal samples from bonobos and gorillas: Evidence for meat consumption or artefact? PLoS One, 5(2): e9419.

Kelso, J., Hoehndorf, R., & Prüfer, K. (2010). Ontologies in biology. In R. Poli, M. Healy, & A. Kameas (Eds.), Theory and applications of ontology: Computer applications (pp. 347-371). New York [u.a.]: Springer.

Khaitovich, P. (2010). Annotating conserved and novel features of primate transcriptomes using sequencing. Genome Biology, 11(7): 125, pp. 1-3.

Kircher, M., & Kelso, J. (2010). High-throughput DNA sequencing - concepts and limitations. BioEssays, 32(6), 524-536.

Knapp, M., Finstermeier, K., Horn, S., Stiller, M., & Hofreiter, M. (2010). Neue PCR-Technologien für alte DNA. Biospektrum, 16(5), 531-535.

Krause, J., Briggs, A. W., Kircher, M., Maricic, T., Zwyns, N., Derevianko, A. P., & Pääbo, S. (2010). A complete mtDNA genome of an early modern human from Kostenki, Russia. Current Biology, 20(3), 231-236.

Krause, J., Fu, Q., Good, J. M., Viola, B., Shunkov, M. V., Derevianko, A. P., & Pääbo, S. (2010). The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. Nature, 464(7290), 894-897.

Krief, S., Escalante, A. A., Pacheco, M. A., Mugisha, L., André, C., Halbwax, M., Fischer, A., Krief, J.-M., Kasenene, J. M., Crandfield, M., Cornejo, O. E., Chavatte, J.-M., Lin, C., Letourneur, F., Grüner, A. C., McCutchan, T. F., Rénia, L., & Snounou, G. (2010). On the Diversity of Malaria Parasites in African Apes and the Origin of Plasmodium falciparum from Bonobos. PLoS Pathogens, 7(2): e1000765, pp. 1-12.

Li, M., Schönberg, A., Schaefer, M., Schroeder, R., Nasidze, I., & Stoneking, M. (2010). Detecting heteroplasmy from high-throughput sequencing of complete human mitochondrial DNA genomes. The American Journal of Human Genetics, 87(2), 237-249.

Maricic, T., Whitten, M., & Pääbo, S. (2010). Multiplexed DNA sequence capture of mitochondrial genomes using PCR products. PLoS ONE, 5(11): e14004, pp. 1-5.

Meyer, M., & Kircher, M. (2010). Illumina sequencing library preparation for highly multiplexed target capture and sequencing. Cold Spring Harbor Protocols, 2010(6): prot5448.

Pääbo, S. (2010). Analyses of pleistocene genomes. Talk presented at 35th FEBS Congress. Gothenburg, Sweden. 2010-06-26 - 2010-07-01.

Prost, S., Knapp, M., Flemmig, J., Hufthammer, A. K., Kosintsev, P., Stiller, M., & Hofreiter, M. (2010). A phantom extinction? New insights into extinction dynamics of the Don-hare Lepus tanaiticus. Journal of Evolutionary Biology, 23(9), 2022-2029.

Prost, S., Smirnov, N., Fedorov, V. B., Sommer, R. S., Stiller, M., Nagel, D., Knapp, M., & Hofreiter, M. (2010). Influence of climate warming on arctic mammals? New insights from ancient DNA studies of the Collared Lemming Dicrostonyx torquatus. PLoS ONE, 5(5): e10447, pp. 1-11.

Prüfer, K., Stenzel, U., Hofreiter, M., Pääbo, S., Kelso, J., & Green, R. E. (2010). Computational challenges in the analysis of ancient DNA. Genome Biology, 11(5): R47.

Pulvers, J. N., Bryk, J., Fish, J. L., Wilsch-Bräuninger, M., Arai, Y., Schreier, D., Naumann, R., Helppi, J., Habermann, B., Vogt, J., Nitsch, R., Tóth, A., Enard, W., Pääbo, S., & Huttner, W. B. (2010). Mutations in mouse Aspm (abnormal spindle-like microcephaly associated) cause not only microcephaly but also major defects in the germline. Proceedings of the National Academy of Sciences of the United States of America, 107(38), 16595-16600.

Ratikainen, I. I., Wright, J., & Kazem, A. J. N. (2010). Social class influences degree of variance sensitivity in wild Siberian jays. Behavioral Ecology, 21(5), 1067-1072.

Reich, D., Green, R. E., Kircher, M., Krause, J., Patterson, N., Durand, E. Y., Viola, B., Briggs, A. W., Stenzel, U., Johnson, P. L. F., Maricic, T., Good, J. M., Marques-Bonet, T., Alkan, C., Fu, Q., Mallick, S., Li, H., Meyer, M., Eichler, E. E., Stoneking, M., Richards, M., Talamo, S., Shunkov, M. V., Derevianko, A. P., Hublin, J.-J., Kelso, J., Slatkin, M., & Pääbo, S. (2010). Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 468(7327), 1053-1060.

Rohland, N., Reich, D., Mallick, S., Meyer, M., Green, R. E., Georgiadis, N. J., Roca, A. L., & Hofreiter, M. (2010). Genomic DNA sequences from mastodon and woolly mammoth reveal deep speciation of forest and savanna elephants. PLoS Biology, 8(12): e1000564.

Rohland, N., Siedel, H., & Hofreiter, M. (2010). A rapid column-based ancient DNA extraction method for increased sample throughput. Molecular Ecology Resources, 10(4), 677-683.

Somel, M., Guo, S., Fu, N., Yan, Z., Hu, H. Y., Xu, Y., Yuan, Y., Ning, Z., Hu, Y., Menzel, C., Hu, H., Lachmann, M., Zeng, R., Chen, W., & Khaitovich, P. (2010). MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain. Genome Research, 20(9), 1207-1218.

Stäubert, C., Böselt, I., Bohnekamp, J., Römpler, H., Enard, W., & Schöneberg, T. (2010). Structural and functional evolution of the trace amine-associated receptors TAAR3, TAAR4 and TAAR5 in primates. PLoS ONE, 5(6): e11133.

Stiller, M., Baryshnikov, G., Bocherens, H., d'Anglade, A. G., Hilpert, B., Münzel, S. C., Pinhasi, R., Rabeder, G., Rosendahl, W., Trinkaus, E., Hofreiter, M., & Knapp, M. (2010). Withering Away - 25,000 Years of Genetic Decline Preceded Cave Bear Extinction. Molecular Biology and Evolution, 27(5), 975-978.

Stoneking, M., & Delfin, F. S. (2010). The human genetic history of East Asia: Weaving a complex tapestry. Current Biology, 20(4), R188-R193.

Wollstein, A., Lao, O., Becker, C., Brauer, S., Trent, R. J., Nürnberg, P., Stoneking, M., & Kayser, M. (2010). Demographic history of Oceania inferred from genome-wide data. Current Biology, 20, 1983-1992.

Xu, G., He, L., Li, Z., Xu, Y., Li, M., Fu, X., Yan, Z., Yuan, Y., Menzel, C., Li, N., Somel, M., Hu, H., Chen, W., Pääbo, S., & Khaitovich, P. (2010). Intergenic and repeat transcription in human, chimpanzee and macaque brains measured by RNA-seq. PLoS Computational Biology, 6(7): e1000843.

2009

Albert, F. W., Carlborg, O., Plyusnina, I. Z., Besnier, F., Hedwig, D., Lautenschläger, S., Lorenz, D., McIntosh, J., Neumann, C., Richter, H., Zeising, C., Kozhemyakina, T., Shchepina, O., Kratzsch, J., Trut, L. N., Teupser, D., Thiery, J., Schöneberg, T., Andersson, L., & Pääbo, S. (2009). Genetic architecture of tameness in a rat model of animal domestication. Genetics, 182(2), 541-554.

Balaresque, P., Parkin, E. J., Roewer, L., Carvalho-Silva, D. R., Mitchell, R. J., Oorschot, R. A. H. v., Henke, J., Stoneking, M., Nasidze, I., Wetton, J., Knijff, P. d., Tyler-Smith, C., & Jobling, M. A. (2009). Genomic complexity of the Y-STR DYS19: inversions, deletions and founder lineages carrying duplications. International Journal of Legal Medicine, 123(1), 15-23.

Blanchette, M., Green, R. E., MacArthur, S., Brooks, A. N., Brenner, S. E., Eisen, M. B., & Rio, D. C. (2009). Genome-wide Analysis of Alternative Pre-mRNA Splicing and RNA-Binding Specificities of the Drosophila hnRNP A/B Family Members. Molecular Cell, 33(4), 438-449.

Briggs, A. W., Good, J. M., Green, R. E., Krause, J., Maricic, T., Stenzel, U., & Pääbo, S. (2009). Primer extension capture: Targeted sequence retrieval from heavily degraded DNA sources (Videodocumentation). Journal of Visualized Experiments, (31).

Briggs, A. W., Good, J. M., Green, R. E., Krause, J., Maricic, T., Stenzel, U., Lalueza-Fox, C., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Schmitz, R. W., Doronichev, V. B., Golovanova, L. V., de la Rasilla, M., Fortea, J., Rosas, A., & Pääbo, S. (2009). Targeted retrieval and analysis of five Neandertal mtDNA genomes. Science, 325(5938), 318-321.

Castellano, S. (2009). On the unique function of selenocysteine - insights from the evolution of selenoproteins. Biochimica et Biophysica Acta, 1790, 1463-1470.

Collins, M. J., Penkman, K. E. H., Rohland, N., Shapiro, B., Dobberstein, R. C., Ritz-Timme, S., & Hofreiter, M. (2009). Is amino acid racemization a useful tool for screening for ancient DNA in bone? Proceedings of the Royal Society of London, B, Biological Sciences, 276(1669), 2971-2977.

Dannemann, M., Lorenc, A., Hellmann, I., Khaitovich, P., & Lachmann, M. (2009). The effects of probe binding affinity differences on gene expression measurements and how to deal with them. Bioinformatics, 25(21), 2772-2779.

De Pietri Tonelli, D., Enard, W., & Huttner, W. B. (2009). 01-P003 The role of miRNAs in mouse neocortical development. Mechanisms of Development, 126(Supplement 1), S51-S52.

Enard, W. (2009). The phenotype in high dimensions. Trends in Ecology & Evolution, 24(2), 70-71.

Enard, W., Gehre, S., Hammerschmidt, K., Hölter, S. M., Blass, T., Somel, M., Brückner, M. K., Schreiweis, C., Winter, C., Sohr, R., Becker, L., Wiebe, V., Nickel, B., Müller, U., Groszer, M., Adler, T., Aguilar, A., Bolle, I., Calzada-Wack, J., Dalke, C., Erhardt, N., Favor, J., Fuchs, H., Gailus-Durner, V., Hans, W., Hölzlwimmer, G., Javaheri, A., Kalaydjiev, S., Kallnik, M., Kling, E., Kunder, S., Moßbrugger, I., Naton, B., Racz, I., Rathkolb, B., Rozman, J., Schrewe, A., Busch, D. H., Graw, J., Ivandic, B., Klingenspor, M., Klopstock, T., Ollert, M., Quintanilla-Martinez, L., Schulz, H., Wolf, E., Wurst, W., Zimmer, A., Fisher, S. E., Morgenstern, R., Arendt, T., Hrabé de Angelis, M., Fischer, J., Schwarz, J., & Pääbo, S. (2009). A humanized version of Foxp2 affects cortico-basal ganglia circuits in mice. Cell, 137(5), 961-971.

Germonpre, M., Sabli, M. V., Stevens, R. E., Hedges, R. E. M., Hofreiter, M., Stiller, M., & Després, V. R. (2009). Fossil dogs and wolves from Palaeolithic sites in Belgium, the Ukraine and Russia: osteometry, ancient DNA and stable isotopes. Journal of Archaeological Science, 36(2), 473-490.

Gilbert, M. T. P., Jenkins, D. L., Higham, T. F. G., Rasmussen, M., Malmström, H., Svensson, E. M., Sanchez, J. J., Cummings, L. S., Yohe, R. M., Hofreiter, M., Götherström, A., & Willerslev, E. (2009). Response to Comment by Poinar et al. on "DNA from Pre-Clovis Human Coprolites in Oregon, North America". Science, 325(5937), 148-148.

Gralle, M., Gralle Botelho, M., & Wouters, F. S. (2009). Neuroprotective Secreted Amyloid Precursor Protein Acts by Disrupting Amyloid Precursor Protein Dimers. Journal of Biological Chemistry, 284(22), 15016-15025.

Green, R. E., Briggs, A. W., Krause, J., Prüfer, K., Burbano, H. A., Siebauer, M., Lachmann, M., & Pääbo, S. (2009). The Neandertal genome and ancient DNA authenticity. EMBO Journal, 28(17), 2494-2502.

Halbwax, M., Mahamba, C. K., Ngalula, A.-M., & André, C. (2009). Placental retention in a bonobo (Pan paniscus). Journal of Medical Primatology, 38(3), 171-174.

Hansen, K. D., Lareau, L. F., Blanchette, M., Green, R. E., Meng, Q., Rehwinkel, J., Gallusser, F. L., Izaurralde, E., Rio, D. C., & Dudoit, S. (2009). Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in Drosophila. PLoS Genetics, 6(5): e1000525.

Harris, L. W., Lockstone, H. E., Khaitovich, P., Weickert, C. S., Webster, M. J., & Bahn, S. (2009). Gene expression in the prefrontal cortex during adolescence: implications for the onset of schizophrenia. BMC Medical Genomics, 2: 28.

Haussler, D., O'Brien, S. J., Ryder, O. A., Barker, F. K., Clamp, M., Crawford, A. J., Hanner, R., Hanotte, O., Johnson, W. E., McGuire, J. A., Miller, W., Murphy, R. W., Murphy, W. J., Sheldon, F. H., Sinervo, B., Venkatesh, B., Wiley, E. O., Allendorf, F. W., Amato, G., Baker, C. S., Bauer, A., Beja-Pereira, A., Bermingham, E., Bernardi, G., Bonvicino, C. R., Brenner, S., Burke, T., Cracraft, J., Diekhans, M., Edwards, S., Ericson, P. G. P., Estes, J., Fjelsda, J., Flesness, N., Gamble, T., Gaubert, P., Graphodatsky, A. S., Graves, J. A., Green, E. D., Green, R. E., Hackett, S., Hebert, P., Helgen, K. M., Joseph, L., Kessing, B., Kingsley, D. M., Lewin, H. A., Luikart, G., Martelli, P., Moreira, M. A., Nguyen, N., Orti, G., Pike, B. L., Rawson, D. M., Schuster, S. C., Seuanez, H. N., Shaffer, H. B., Springer, M. S., Stuart, J. M., Sumner, J., Teeling, E., Vrijenhoek, R. C., Ward, R. D., Warren, W. C., Wayne, R. K., Williams, T. M., Wolfe, N. D., Zhang, Y.-P., Felsenfeld, A., & Turner, S. (2009). Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10 000 Vertebrate Species. Journal of Heredity, 100(6), 659-674.

Hillmer, A. M., Freudenberg, J., Myles, S., Herms, S., Tang, K., Hughes, D. A., Brockschmidt, F. F., Ruan, Y., Stoneking, M., & Nöthen, M. M. (2009). Recent positive selection of a human androgen receptor/ectodysplasin A2 receptor haplotype and its relationship to male pattern baldness. Human Genetics, 126(2), 223-232.

Hoehndorf, R., Bacher, J., Backhaus, M., Gregorio, S. E. J., Loebe, F., Pruefer, K., Uciteli, A., Visagie, J., Herre, H., & Kelso, J. (2009). BOWiki: An ontology-based wiki for annotation of data and integration of knowledge in biology. BMC Bioinformatics, 10: S5.

Hoehndorf, R., Kelso, J., & Herre, H. (2009). The ontology of biological sequences. BMC Bioinformatics, 10: 377.

Hoehndorf, R., Ngomo, A.-C.-N., & Herre, H. (2009). Developing Consistent and Modular Software Models with Ontologies. In H. Fujita and V. Marík (Ed.), New Trends in Software Methodologies, Tools and Techniques (pp. 399-412). Amsterdam: IOS Press.

Hofreiter, M. (2009). Gene data for endangered species have limitations. Nature, 459(7248), 774-774.

Hofreiter, M. (2009). Gene der Vergangenheit - DNS-Analysen. In Rau, Susanne [Hrsg.] (Ed.), Eiszeit: Kunst und Kultur; Begleitband zur Großen Landesausstellung Eiszeit - Kunst und Kultur, im Kunstgebäude Stuttgart, 18. September 2009 - 10. Januar 2010 (pp. 51-51). Ostfildern: Thorbecke.

Hofreiter, M. (2009). Spurensuche in alter DNA. Evolutionsforschung, 176-184.

Hofreiter, M., & Stewart, J. (2009). Ecological Change, Range Fluctuations and Population Dynamics during the Pleistocene. Current Biology, 19(14), R584-R594.

Hughes, D. A., Hinney, A., Brumm, H., Wermter, A.-K., Biebermann, H., Hebebrand, J., & Stoneking, M. (2009). Increased constraints on MC4R during primate and human evolution. Human Genetics, 124(6),

633-647.

Hughes, D. A., Jastroch, M., Stoneking, M., & Klingenspor, M. (2009). Molecular evolution of UCP1 and the evolutionary history of mammalian non-shivering thermogenesis. BMC Evolutionary Biology, 9: 4.

Kircher, M., Stenzel, U., & Kelso, J. (2009). Improved base calling for the Illumina Genome Analyzer using machine learning strategies. Genome Biology, 10(8): R83, pp. 1-9.

Knapp, M., Rohland, N., Weinstock, J., Baryshnikov, G. F., Sher, A., Nagel, D., Rabeder, G., Pinhasi, R., Schmidt, H. A., & Hofreiter, M. (2009). First DNA sequences from Asian cave bear fossils reveal deep divergences and complex phylogeographic patterns. Molecular Ecology, 18(6), 1225-1238.

Landsman, D., Gentleman, R., Kelso, J., & Ouellette, B. F. F. (2009). DATABASE: A new forum for biological databases and curation. Database: the Journal of Biological Databases and Curation, 2009: bap002, pp. 1-2.

López Herráez, D., Bauchet, M., Tang, K., Theunert, C., Pugach, I., Li, J., Nandineni, M. R., Gross, A., Scholz, M., & Stoneking, M. (2009). Genetic variation and recent positive selection in worldwide human populations: Evidence from nearly 1 million SNPs. PLoS ONE, 4(11): e7888.

Ludwig, A., Lippold, S., Debus, L., & Reinartz, R. (2009). First evidence of hybridization between endangered sterlets (Acipenser ruthenus) and exotic Siberian sturgeons (Acipenser baerii) in the Danube River. Biological Invasions, 11(3), 753-760.

Ludwig, A., Pruvost, M., Reissmann, M., Benecke, N., Brockmann, G. A., Castanos, P., Cieslak, M., Lippold, S., Llorente, L., Malaspinas, A.-S., Slatkin, M., & Hofreiter, M. (2009). Coat Color Variation at the Beginning of Horse Domestication. Science, 324(5926), 485-485.

Maricic, T., & Pääbo, S. (2009). Optimization of 454 sequencing library preparation from small amounts of DNA permits sequence determination of both DNA strands. BioTechniques, 46(1), 51-57.

McIntyre, M. H., Herrmann, E., Wobber, V., Halbwax, M., Mohamba, C., de Sousa, N., Atencia, R., Cox, D., & Hare, B. (2009). Bonobos have a more human-like second-to-fourth finger length ratio (2D:4D) than chimpanzees: a hypothesized indication of lower prenatal androgens. Journal of Human Evolution, 56(4), 361-365.

Mona, S., Grunz, K. E., Brauer, S., Pakendorf, B., Castrì, L., Sudoyo, H., Marzuki, S., Barnes, R. H., Schmidtke, J., Stoneking, M., & Kayser, M. (2009). Genetic admixture history of Eastern Indonesia as revealed by Y-chromosome and mitochondrial DNA analysis. Molecular Biology and Evolution, 26(8), 1865-1877.

Moreno-Estrada, A., Tang, K., Sikora, M., Marquès-Bonet, T., Casals, F., Navarro, A., Calafell, F., Bertranpetit, J., Stoneking, M., & Bosch, E. (2009). Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. Molecular Biology and Evolution, 26(10), 2285-2297.

Myles, S., Stoneking, M., & Timpson, N. (2009). An assessment of the portability of ancestry informative markers between human populations. BMC Medical Genomics, 2: 45.

Nasidze, I., Li, J., Quinque, D., Tang, K., & Stoneking, M. (2009). Global diversity in the human salivary microbiome. Genome Research, 19(4), 636-643.

Nasidze, I., Quinque, D., Li, J., Li, M., Tang, K., & Stoneking, M. (2009). Comparative analysis of human saliva microbiome diversity by barcoded pyrosequencing and cloning approaches. Analytical Biochemistry, 391(1), 64-68.

Nasidze, I., Quinque, D., Rahmani, M., Alemohamad, S. A., Asadova, P., Zhukova, O., & Stoneking, M. (2009). MtDNA and Y-chromosome variation in the Talysh of Iran and Azerbaijan. American Journal of Physical Anthropology, 138(1), 82-89.

Ptak, S. E., Enard, W., Wiebe, V., Hellmann, I., Krause, J., Lachmann, M., & Pääbo, S. (2009). Linkage disequilibrium extends across putative selected sites in FOXP2. Molecular Biology and Evolution, 26(10), 2181-2184.

Roewer, L., Willuweit, S., Stoneking, M., & Nasidze, I. (2009). A Y-STR database of Iranian and Azerbaijanian minority populations. Forensic Science International: Genetics, 4(1), e53-e55.

Ryan, A. W., Hughes, D. A., Tang, K., Kelleher, D. P., Ryan, T., McManus, R., & Stoneking, M. (2009). Natural selection and the molecular basis of electrophoretic variation at the coagulation F13B locus. European Journal of Human Genetics, 17(2), 219-227.

Somel, M., Franz, H., Yan, Z., Lorenc, A., Guo, S., Giger, T., Kelso, J., Nickel, B., Dannemann, M., Bahn, S., Webster, M. J., Weickert, C. S., Pääbo, S., & Khaitovich, P. (2009). Transcriptional neoteny in the human brain. PNAS - Proceedings of the National Academy of Sciences, 106(14), 5743-5748.

Stiller, M., Knapp, M., Stenzel, U., Hofreiter, M., & Meyer, M. (2009). Direct multiplex sequencing (DMPS): A novel method for targeted high-throughput sequencing of ancient and highly degraded DNA. Genome Research, 19(10), 1843-1848.

Stoneking, M. (2009). Humans as second orangutans: sense or nonsense? BioEssays, 31(10), 1010-1012.

Weickert, C. S., Elashof, M., Richards, A. B., Sinclair, D., Bahn, S., Pääbo, S., Khaitovich, P., & Webster, M. J. (2009). Transcriptome analysis of male–female differences in prefrontal cortical development. Molecular Psychiatry, 14(6), 558-561.

2008

Albert, F. W. (2008). Uncovering the genetic basis for tameness - a research strategy. Vestnik Vogis, 12, 19-23.

Albert, F. W., Shchepina, O., Winter, C., Römpler, H., Teupser, D., Palme, R., Ceglarek, U., Kratzsch, J., Sohr, R., Trut, L. N., Thiery, J., Morgenstern, R., Plyusnina, I. Z., Schöneberg, T., & Pääbo, S. (2008). Phenotypic differences in behavior, physiology and neurochemistry between rats selected for tameness and for defensive aggression towards humans. Hormones and Behavior, 53(3), 413-421.

Balaresque, P., Bowden, G. R., Parkin, E. J., Omran, G. A., Heyer, E., Quintana-Murci, L., Roewer, L., Stoneking, M., Nasidze, I., Carvalho-Silva, D. R., Tyler-Smith, C., de Knijff, P., & Jobling, M. A. (2008). Dynamic nature of the proximal AZFc region of the human Y chromosome: Multiple independent deletion and duplication events revealed by microsatellite analysis. Human Mutation, 29(10), 1171-1180.

Bergstrom, C. T., Kerr, B., & Lachmann, M. (2008). Building trust by wasting time. In Paul J. Zak (Ed.), Moral Markets: The Critical Role of Values in the Economy (pp. 142-156). Princeton: Princeton University Press.

Bryk, J., Hardouin, E., Pugach, I., Hughes, D. A., Strotmann, R., Stoneking, M., & Myles, S. (2008). Positive selection in East Asians for an EDAR allele that enhances NF-kappaB activation. PLoS ONE, 3(5): e2209.

Castellano, S. (2008). Little biological and statistical support for hundreds of selenoproteins in mouse pseudo-messenger RNAs [A critical assessment of PLoS Genetics, 2, e3 (2006)]. PLoS Genetics.

Castellano, S., Gladyshev, V. N., Guigó, R., & Berry, M. J. (2008). SelenoDB 1.0: A database of

selenoprotein genes, proteins and SECIS elements. Nucleic Acids Research, 36(Suppl. 1), D332-D338.

Chaix, R., Somel, M., Kreil, D. P., Khaitovich, P., & Lunter, G. A. (2008). Evolution of Primate Gene Expression: Drift and Corrective Sweeps? Genetics, 180(3), 1379-1389.

Donaldson-Matasci, M. C., Lachmann, M., & Bergstrom, C. T. (2008). Phenotypic Diversity as an Adaptation to Environmental Uncertainty. Evolutionary Ecology Research, 10(4), 493-515. Retrieved from http://www.evolutionary-ecology.com/.

Farkas, L. M., Haffner, C., Giger, T., Khaitovich, P., Nowick, K., Birchmeier, C., Pääbo, S., & Huttner, W. B. (2008). Insulinoma-associated 1 has a panneurogenic role and promotes the generation and expansion of basal progenitors in the developing mouse neocortex. Neuron, 60(1), 40-55.

Fechner, A., Quinque, D., Rychkov, S., Morozowa, I., Naumova, O., Schneider, Y., Willuweit, S., Zhukova, O., Roewer, L., Stoneking, M., & Nasidze, I. (2008). Boundaries and clines in the West Eurasian Y-chromosome landscape: Insights from the European part of Russia. American Journal of Physical Anthropology, 137(1), 41-47.

Giger, T., Excoffier, L., Amstutz, U., Day, P. J. R., Champigneulle, A., Hansen, M. M., Kelso, J., & Largiadèr, C. R. (2008). Population transcriptomics of life-history variation in the genus Salmo. Molecular Ecology, 17(13), 3095-3108.

Green, R. E., Malaspinas, A.-S., Krause, J., Briggs, A. W., Johnson, P. L. F., Uhler, C., Meyer, M., Good, J. M., Maricic, T., Stenzel, U., Prüfer, K., Siebauer, M., Burbano, H. A., Ronan, M. T., Rothberg, J. M., Egholm, M., Rudan, P., Brajkovic, D., Kucan, Z., Gusic, I., Wikström, M., Laakkonen, L., Kelso, J., Slatkin, M., & Pääbo, S. (2008). A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. Cell, 134(3), 416-426.

Groszer, M., Keays, D. A., Deacon, R. M., de Bono, J. P., Prasad-Mulcare, S., Gaub, S., Baum, M. G., French, C. A., Nicod, J., Coventry, J. A., Enard, W., Fray, M., Brown, S. D. M., Nolan, P. M., Pääbo, S., Channon, K. M., Costa, R. M., Eilers, J., Ehret, G., Rawlins, J. N. P., & Fisher, S. E. (2008). Impaired synaptic plasticity and motor learning in mice with a point mutation implicated in human speech deficits. Current Biology, 18(5), 354-362.

Güldemann, T., & Stoneking, M. (2008). A historical appraisal of clicks: A linguistic and genetic population perspective. Annual Review of Anthropology, 37, 93-109.

Herráez, D. L., & Stoneking, M. (2008). High fractions of exogenous DNA in human buccal samples reduce the quality of large-scale genotyping. Analytical Biochemistry, 383(2), 329-331.

Hoehndorf, R., Loebe, F., Poli, R., Herre, H., & Kelso, J. (2008). GFO-Bio: A biological core ontology. Applied ontology, 3(4), 219-227.

Hofreiter, M. (2008). DNA sequencing mammoth genomics. Nature, 456(7220), 330-331.

Hofreiter, M. (2008). Long DNA sequences and large data sets: Investigating the quaternary via ancient DNA. Quaternary Science Reviews, 27(2), 2586-2592.

Hofreiter, M. (2008). Palaeogenomics. Comptes Rendus Palevol, 7(2-3), 113-124.

Hublin, J.-J., Pääbo, S., Derevianko, A. P., Doronichev, V. B., Golovanova, L. V., Friess, M., Froment, A., Hoffmann, A., Kachache, N. E. J., Kullmer, O., Lordkipanidze, D., Moncel, M.-H., Potts, R., Méndez, J. R., Rosas, A., Schmauder, M., Schmitz, R. W., Semal, P., Smith, T. M., Tafuri, M. A., Tattersall, I., Tournepiche, J.-F., Toussaint, M., Vassiliev, S., Vialet, A., Richards, M. P., Radovcic, J., Rak, Y. Z., White, T., & Ziegler, R. (2008). Suggested guidelines for invasive sampling of hominid remains. Journal of Human Evolution, 55(4), 756-757.

Hughes, D. A., Tang, K., Strotmann, R., Schöneberg, T., Prenen, J., Nilius, B., & Stoneking, M. (2008). Parallel selection on TRPV6 in human populations. PLoS One, 3(3): e1686.

Kayser, M., Choi, Y., Oven, M. v., Mona, S., Brauer, S., Trent, R. J., Suarkia, D., Schiefenhövel, W., & Stoneking, M. (2008). The impact of the Austronesian expansion: Evidence from mtDNA and Y chromosome diversity in the Admiralty Islands of Melanesia. Molecular Biology and Evolution, 25(7), 1362-1374.

Kayser, M., Lao, O., & Stoneking, M. (2008). Reply to Hedrick: East Asian and Melanesian ancestry in Polynesians. American Journal of Human Genetics, 83(1), 140-142.

Kayser, M., Lao, O., Saar, K., Brauer, S., Wang, X., Nürnberg, P., Trent, R. J., & Stoneking, M. (2008). Genome-wide analysis indicates more Asian than Melanesian ancestry of Polynesians. American Journal of Human Genetics, 82(1), 194-198.

Khaitovich, P., Lockstone, H. E., Wayland, M. T., Tsang, T. M., Jayatilaka, S. D., Guo, A. J., Zhou, J., Somel, M., Harris, L. W., Holmes, E., Pääbo, S., & Bahn, S. (2008). Metabolic changes in schizophrenia and human brain evolution. Genome Biology, 9(8): R124.

Kircher, M., Bock, C., & Paulsen, M. (2008). Structural conservation versus functional divergence of maternally expressed microRNAs in the Dlk1/Gtl2 imprinting region. BMC Genomics, 9: 346.

Klingenspor, M., Fromme, T., Hughes, D. A., Manzke, L., Polymeropoulos, E., Riemann, T., Trzcionka, M., Hirschberg, V., & Jastroch, M. (2008). An ancient look at UCP1. Biochimica et Biophysica Acta (BBA) - Bioenergetics, 1777(7-8), 637-641.

Klingenspor, M., Fromme, T., Hughes, D. A., Manzke, L., Polymeropoulos, E., Riemann, T., Trzcionka, M., Hirschberg, V., & Jastroch, M. (2008). S3/1 An ancient look at UCP1. Biochimica et Biophysica Acta (BBA) - Bioenergetics, 1777(Supplement 1), S24-S24.

Knapp, M., Vigilant, L., & Hofreiter, M. (2008). Ancient DNA: Phylogenetic applications. In Encyclopedia of Life Sciences. New York: Wiley.

Krause, J., Unger, T., Noçon, A., Malaspinas, A.-S., Kolokotronis, S.-O., Stiller, M., Soibelzon, L., Spriggs, H., Dear, P. H., Briggs, A. W., Bray, S. C. E., O'Brien, S. J., Rabeder, G., Matheus, P., Cooper, A., Slatkin, M., Pääbo, S., & Hofreiter, M. (2008). Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary. BMC Evolutionary Biology, 8: 220.

Lalueza-Fox, C., Gigli, E., de la Rasilla, M., Fortea, J., Rosas, A., Bertranpetit, J., & Krause, J. (2008). Genetic characterization of the ABO blood group in Neandertals. BMC Evolutionary Biology, 8: 342.

Mehlotra, R. K., Mattera, G., Bockarie, M. J., Maguire, J. D., Baird, J. K., Sharma, Y. D., Alifrangis, M., Dorsey, G., Rosenthal, P. J., Fryauff, D. J., Kazura, J. W., Stoneking, M., & Zimmerman, P. A. (2008). Discordant patterns of genetic variation at two chloroquine resistance loci in worldwide populations of the malaria parasite Plasmodium falciparum. Antimicrobial Agents and Chemotherapy, 52(6), 2212-2222.

Meyer, M., Briggs, A. W., Maricic, T., Höber, B., Höffner, B., Krause, J., Weihmann, A., Pääbo, S., & Hofreiter, M. (2008). From micrograms to picograms: Quantitative PCR reduces the material demands of high-throughput sequencing. Nucleic Acids Research, 36(1): e5.

Meyer, M., Stenzel, U., & Hofreiter, M. (2008). Parallel tagged sequencing on the 454 platform. Nature Protocols, 3, 267-278.

Mohandesan, E., Mowla, S. J., Noobari, A. H., & Hofreiter, M. (2008). Ancient DNA from human and animal remains from North-West Iran. Journal of Sciences, Islamic Republic of Iran, 19(1), 3-8. Retrieved from http://www.sid.ir/En/ViewPaper.asp?ID=106036&varStr=3;MOHANDESAN%20E.,MOULA%20S.J.,HAZHA

BRI%20NOUBARI%20A.R.,HOFREITER%20M.;JOURNAL%20OF%20SCIENCES%20ISLAMIC%20REPUBLIC%20OF%20IRAN;WINTER%202008;19;1;3;8.

Myles, S., Davison, D., Barrett, J., Stoneking, M., & Timpson, N. (2008). Worldwide population differentiation at disease-associated SNPs. BMC Medical Genomics, 1: 22.

Myles, S., Tang, K., Somel, M., Green, R. E., Kelso, J., & Stoneking, M. (2008). Identification and analysis of genomic regions with large between-population differentiation in humans. Annals of Human Genetics, 72(1), 99-110.

Nasidze, I., Quinque, D., Rahmani, M., Alemohamad, S. A., & Stoneking, M. (2008). Close genetic relationship between Semitic-speaking and Indo-European-speaking groups in Iran. Annals of Human Genetics, 72(2), 241-252.

Prüfer, K., Stenzel, U., Dannemann, M., Green, R. E., Lachmann, M., & Kelso, J. (2008). PatMaN: Rapid alignment of short sequences to large databases. Bioinformatics, 24(13), 1530-1533.

Rabeder, G., Debeljak, I., Hofreiter, M., & Withalm, G. (2008). Morphological responses of cave bears (Ursus spelaeus group) to high-alpine habitats. Die Höhle, 59, 59-72. Retrieved from http://homepage.univie.ac.at/gerhard.withalm/downloads/Rabeder_etal_2008.pdf.

Richards, M. P., Pacher, M., Stiller, M., Quilès, J., Hofreiter, M., Constantin, S., Zilhão, J., & Trinkaus, E. (2008). Isotopic evidence for omnivory among European cave bears: Late Pleistocene Ursus spelaeus from the Pestera cu Oase, Romania. Proceedings of the National Academy of Sciences of the United States of America (PNAS), 105(2), 600-604.

Roewer, L., Willuweit, S., Krüger, C., Nagy, M., Rychkov, S., Morozowa, I., Naumova, O., Schneider, Y., Zhukova, O., Stoneking, M., & Nasidze, I. (2008). Analysis of Y chromosome STR haplotypes in the European part of Russia reveals high diversities but non-significant genetic distances between populations. International Journal of Legal Medicine, 122(3), 219-223.

Somel, M., Creely, H., Franz, H., Müller, U., Lachmann, M., Khaitovich, P., & Pääbo, S. (2008). Human and chimpanzee gene expression differences replicated in mice fed different diets. PLoS ONE, 3(1): e1504.

Stoneking, M. (2008). Human origins - the molecular perspective. EMBO Reports, 9(Supplement 1), S46-S50.

Stoneking, M. (2008). Mitochondrial genome: Evolution. In Encyclopedia of Life Sciences (ELS). Chichester: Wiley.

Thomas, M., Gilbert, M. T. P., Jenkins, D. L., Götherström, A., Naveran, N., Sanchez, J. J., Hofreiter, M., Thomsen, P. F., Binladen, J., Higham, T. F. G., Vohe II, R. M., Parr, R., Cummings, L. S., & Willerslev, E. (2008). DNA from Pre-Clovis Human Coprolites in Oregon, North America. Science, 320(5877), 786-789. Retrieved from http://search.ebscohost.com/login.aspx?direct=true&db=aph&AN=32102830&site=ehost-live.

Valdiosera, C. E., García-Garitagoitia, J. L., García, N., Doadrio, I., Thomas, M. G., Hänni, C., Arsuaga, J.-L., Barnes, I., Hofreiter, M., Orlando, L., & Götherström, A. (2008). Surprising migration and population size dynamics in ancient Iberian brown bears (Ursus arctos). Proceedings of the National Academy of Sciences, 115(13), 5123-5128.

2007

Bradley, B. J., Stiller, M., Doran-Sheehy, D. M., Harris, T. R., Chapman, C. A., Vigilant, L., & Poinar, H. N.

(2007). Plant DNA sequences from feces: Potential means for assessing diets of wild primates. American Journal of Primatology, 69(6), 699-705.

Briggs, A. W., Stenzel, U., Johnson, P. L. F., Green, R. E., Kelso, J., Prüfer, K., Meyer, M., Krause, J., Ronan, M. T., Lachmann, M., & Pääbo, S. (2007). Patterns of damage in genomic DNA sequences from a Neandertal. Proceedings of the National Academy of Sciences of the United States of America, 104(37), 14616-14621.

Chen, H., Green, R. E., Pääbo, S., & Slatkin, M. (2007). The joint allele-frequency spectrum in closely related species. Genetics, 177(1), 387-398.

Clark, V. J., Ptak Tamarlin, S. E., Tiemann, I., Qian, Y., Coop, G., Stone, A. C., Przeworski, M., Arnheim, N., & Di Rienzo, A. (2007). Combining Sperm Typing and Linkage Disequilibrium Analysis Reveals Differences in Selective Pressures or Recombination rates across Human Populations. Genetics, 175(2), 795-804.

Cordaux, R., Srikanta, D., Lee, J., Stoneking, M., & Batzer, M. A. (2007). In search of polymorphic alu insertions with restricted geographic distributions. Genomics, 90(1), 154-158.

d'Abbadie, M., Hofreiter, M., Vaisman, A., Loakes, D., Gasparutto, D., Cadet, J., Woodgate, R., Pääbo, S., & Holliger, P. (2007). Molecular breeding of polymerases for amplification of ancient DNA. Nature Biotechnology, 25(8), 939-943.

DaRe, J. T., Mehlotra, R. K., Michon, P., Mueller, I., Reeder, J. C., Sharma, Y. D., Stoneking, M., & Zimmerman, P. A. (2007). Microsatellite polymorphism within pfcrt provides evidence of continuing evolution of chloroquine-resistant alleles in Papua New Guinea. Malaria Journal, 6: 34.

Donaldson, M. C., Lachmann, M., & Bergstrom, C. T. (2007). The evolution of functionally referential meaning in a structured world. Journal of Theoretical Biology, 246(2), 225-233.

Francks, C., Maegawa, S., Lauren, J., Abrahams, B. S., Velayos-Baeza, A., Medland, S. E., Colella, S., Groszer, M., McAuley, E. Z., Caffrey, T. M., Timmusk, T., Pruunsild, P., Koppel, I., Lind, P. A., Matsumoto-Itaba, N., Nicod, J., Xiong, L., Joober, R., Enard, W., Krinsky, B., Nanba, E., Richardson, A. J., Riley, B. P., Martin, N. G., Strittmatter, S. M., Möller, H.-J., Rujescu, D., Clair, D. S., Muglia, P., Roos, L., Fisher, S. E., Wade-Martins, R., Rouleau, G. A., Stein, J. F., Karayiorgou, M., Geschwind, D. H., Ragoussis, J., Kendler, K. S., Airaksinen, M. S., Oshimura, M., DeLisi, L. E., & Monaco, A. P. (2007). LRRTM1 on chromosome 2p12 is a maternally suppressed gene that is associated paternally with handedness and schizophrenia. Molecular Psychiatry, 12(12), 1129-1139.

Fu, N., Drinnenberg, I., Kelso, J. F., Wu, J.-R., Pääbo, S., Zeng, R., & Khaitovich, P. (2007). Comparison of protein and mRNA expression evolution in humans and chimpanzees. PLoS One, 2(2): e216, pp. e216.

Hoehndorf, R., Loebe, F., Kelso, J., & Herre, H. (2007). Representing default knowledge in biomedical ontologies: Application to the integration of anatomy and phenotype ontologies. BMC Bioinformatics, 8: 377.

Hofreiter, M. (2007). Pleistocene extinctions: haunting the survivors. Current Biology, 17(15), R609-R611.

Hofreiter, M., Münzel, S., Conard, N. J., Pollack, J. L., Slatkin, M., Weiss, G., & Pääbo, S. (2007). Sudden replacement of cave bear mitochondrial DNA in the late Pleistocene. Current Biology, 17(4), R122-R123.

Khaitovich, P. (2007). Brain expression—is it all in our SNPs? Molecular Systems Biology, (3): 155.

Knapp, M., Mudaliar, R., Havell, D., Wagstaff, S. J., & Lockhart, P. J. (2007). The Drowning of New Zealand and the Problem of Agathis. Systematic Biology, 56(5), 862-870.

Krause, J., Lalueza-Fox, C., Ludovic, O., Enard, W., Green, R. E., Burbano, H. A., Hublin, J.-J., Hänni, C., Fortea, J., de la Rasilla, M., Bertranpetit, J., Rosas, A., & Pääbo, S. (2007). The derived FOXP2 variant of modern humans was shared with Neandertals. Current Biology, 17(21), 1908-1912.

Krause, J., Orlando, L., Serre, D., Viola, B., Prüfer, K., Richards, M. P., Hublin, J.-J., Hänni, C., Derevianko, A. P., & Pääbo, S. (2007). Neanderthals in central Asia and Siberia. Nature, 449(7164), 902-904.

Kuch, M., Gröcke, D. R., Knyf, M. C., Gilbert, M. T. P., Younghusband, B., Young, T., Marshall, I., Willerslev, E., Stoneking, M., & Poinar, H. N. (2007). A preliminary analysis of the DNA and diet of the extinct Beothuk: A systematic approach to ancient human DNA. American Journal of Physical Anthropology, 132(4), 594-604.

Lalueza-Fox, C., Römpler, H., Caramelli, D., Stäubert, C., Catalano, G., Hughes, D. A., Rohland, N., Pilli, E., Longo, L., Condemi, S., de la Rasilla, M., Fortea, J., Rosas, A., Stoneking, M., Schöneberg, T., Bertranpetit, J., & Hofreiter, M. (2007). A melanocortin 1 receptor allele suggests varying pigmentation among Neanderthals. Science, 318(5855), 1453-1455.

Leonard, J. A., Shanks, O., Hofreiter, M., Kreuz, E., Hodges, L., Ream, W., Wayne, R. K., & Fleischer, R. C. (2007). Animal DNA in PCR reagents plagues ancient DNA research. Journal of Archaeological Science, 34(9), 1361-1366.

Lizano, E., Schuster, M., Müller, M., Kelso, J., & Mörl, M. (2007). A splice variant of the human CCA-adding enzyme with modified activity. Journal of Molecular Biology (London), 366, 1258-1265.

Meyer, M., Stenzel, U., Myles, S., Prüfer, K., & Hofreiter, M. (2007). Targeted high-throughput sequencing of tagged nucleic acid samples. Nucleic Acids Research, 35(15): e97.

Morin, P. A., Aitken, N. C., Rubio-Cisneros, N., Dizon, A. E., & Mesnick, S. (2007). Characterization of 18 SNP markers for sperm whale (Physeter macrocephalus). Molecular Ecology Notes, 7(4), 626-630.

Müller, G. A., Heißig, F., & Engeland, K. (2007). Chimpanzee, Orangutan, Mouse, and Human Cell Cycle Promoters Exempt CCAAT Boxes and CHR Elements from Interspecies Differences. Molecular Biology and Evolution, 24(3), 814-826.

Myles, S., Hradetzky, E., Engelken, J., Lao, O., Nürnberg, P., Trent, R. J., Wang, X., Kayser, M., & Stoneking, M. (2007). Identification of a candidate genetic variant for the high prevalence of type II diabetes in Polynesians. European Journal of Human Genetics, 15, 584-589.

Myles, S., Hughes, D., & Stoneking, M. (2007). Detecting local selection in human populations. In C. Santos, & M. Lima (Eds.), Recent Advances in Molecular Biology and Evolution: Applications to Biological Anthropolgy (pp. 65-81). Trivandrum, India: Research Signpost.

Myles, S., Somel, M., Tang, K., Kelso, J., & Stoneking, M. (2007). Identifying genes underlying skin pigmentation differences among human populations. Human Genetics, 120(5), 613-621.

Nasidze, I., Quinque, D., Udina, I., Kunizheva, S., & Stoneking, M. (2007). The Gagauz, a linguistic enclave, are not a genetic isolate. Annals of Human Genetics, 71(3), 379-389.

Pakendorf, B., Novgorodov, I. N., Osakovskij, V. L., & Stoneking, M. (2007). Mating patterns amongst Siberian reindeer herders: Inferences from mtDNA and Y-chromosomal analyses. American Journal of Physical Anthropology, 133(3), 1013-1027.

Prüfer, K., Muetzel, B., Do, H.-H., Weiss, G., Khaitovich, P., Rahm, E., Pääbo, S., Lachmann, M., & Enard, W. (2007). FUNC: A package for detecting significant associations between gene sets and ontological annotations. BMC Bioinformatics, 8: 41.

Rhesus Macaque Genome Sequencing and Analysis Consortium, Gibbs, R. A., Rogers, J., Katze, M. G., Bumgarner, R., Weinstock, G. M., Mardis, E. R., Remington, K. A., Strausberg, R. L., Venter, J. C., Wilson, R. K., Batzer, M. A., Bustamante, C. D., Eichler, E. E., Hahn, M. W., Hardison, R. C., Makova, K. D., Miller, W., Milosavljevic, A., Palermo, R. E., Siepel, A., Sikela, J. M., Attaway, T., Bell, S., Bernard, K. E., Buhay, C. J., Chandrabose, M. N., Dao, M., Davis, C., Delehaunty, K. D., Ding, Y., Dinh, H. H., Dugan-Rocha, S., Fulton, L. A., Gabisi, R. A., Garner, T. T., Godfrey, J., Hawes, A. C., Hernandez, J., Hines, S., Holder, M., Hume, J., Jhangiani, S. N., Joshi, V., Khan, Z. M., Kirkness, E. F., Cree, A., Fowler, R. G., Lee, S., Lewis, L. R., Li, Z., Liu, Y.-s., Moore, S. M., Muzny, D., Nazareth, L. V., Ngo, D. N., Okwuonu, G. O., Pai, G., Parker, D., Paul, H. A., Pfannkoch, C., Pohl, C. S., Rogers, Y.-H., Ruiz, S. J., Sabo, A., Santibanez, J., Schneider, B. W., Smith, S. M., Sodergren, E., Svatek, A. F., Utterback, T. R., Vattathil, S., Warren, W., White, C. S., Chinwalla, A. T., Feng, Y., Halpern, A. L., Hillier, L. W., Huang, X., Minx, P., Nelson, J. O., Pepin, K. H., Qin, X., Sutton, G. G., Venter, E., Walenz, B. P., Wallis, J. W., Worley, K. C., Yang, S.-P., Jones, S. M., Marra, M. A., Rocchi, M., Schein, J. E., Baertsch, R., Clarke, L., Csürös, M., Glasscock, J., Harris, R. A., Havlak, P., Jackson, A. R., Jiang, H., Liu, Y., Messina, D. N., Shen, Y., Song, H.-X.-Z., Wylie, T., Zhang, L., Birney, E., Han, K., Konkel, M. K., Lee, J., Smit, A. F. A., Ullmer, B., Wang, H., Xing, J., Burhans, R., Cheng, Z., Karro, J. E., Ma, J., Raney, B., She, X., Cox, M. J., Demuth, J. P., Dumas, L. J., Han, S.-G., Hopkins, J., Karimpour-Fard, A., Kim, Y. H., Pollack, J. R., Vinar, T., Addo-Quaye, C., Degenhardt, J., Denby, A., Hubisz, M. J., Indap, A., Kosiol, C., Lahn, B. T., Lawson, H. A., Marklein, A., Nielsen, R., Vallender, E. J., Clark, A. G., Ferguson, B., Hernandez, R. D., Hirani, K., Kehrer-Sawatzki, H., Kolb, J., Patil, S., Pu, L.-L., Ren, Y., Smith, D. G., Wheeler, D. A., Schenck, I., Ball, E. V., Chen, R., Cooper, D. N., Giardine, B., Hsu, F., Kent, W. J., Lesk, A., Nelson, D. L., O'Brien, W. E., Prüfer, K., Stenson, P. D., Wallace, J. C., Ke, H., Liu, X.-M., Wang, P., Xiang, A. P., Yang, F., Barber, G. P., Haussler, D., Karolchik, D., Kern, A. D., Kuhn, R. M., Smith, K. E., & Zwieg, A. S. (2007). Evolutionary and biomedical insights from the rhesus macaque genome. Science, 316(5822), 222-234.

Roewer, L., Krüger, C., Willuweit, S., Nagy, M., Rodig, H., Kokshunova, L., Rothämel, T., Kravchenko, S. A., Jobling, M. A., Stoneking, M., & Nasidze, I. (2007). Y-chromosomal STR haplotypes in Kalmyk population samples. Forensic Science International, 173(2-3), 204-209.

Rohland, N., & Hofreiter, M. (2007). Ancient DNA extraction from bones and teeth. Nature Protocols, 2(7), 1756-1762.

Rohland, N., & Hofreiter, M. (2007). Comparison and optimization of ancient DNA extraction. BioTechniques, 42(3), 343-352.

Rohland, N., Malaspinas, A.-S., Pollack, J. L., Slatkin, M., Matheus, P., & Hofreiter, M. (2007). Proboscidean mitogenomics: Chronology and mode of elephant evolution using mastodon as outgroup. PLoS Biology, 5(8): e207.

Römpler, H., Stäubert, C., Thor, D., Schulz, A., Hofreiter, M., & Schöneberg, T. (2007). G Protein-Coupled Time Travel: Evolutionary Aspects of GPCR Research. Molecular Interventions, 7(1), 17-25.

Rootsi, S., Zhivotovsky, L. A., Baldovic, M., Kayser, M., Kutuev, I. A., Khusainova, R., Bermisheva, M. A., Gubina, M., Fedorova, S. A., Ilumäe, A.-M., Khusnutdinova, E., Voevoda, M. I., Osipova, L. P., Stoneking, M., Lin, A. A., Ferak, V., Parik, J., Kivisild, T., Underhill, P. A., & Villems, R. (2007). A counter-clockwise northern route of the Y-chromosome haplogroup N from Southeast Asia towards Europe. European Journal of Human Genetics, 15(2), 204-211.

Schöneberg, T., Hofreiter, M., Schulz, A., & Römpler, H. (2007). Learning from the past: evolution of GPCR functions. Trends in Pharmacological Sciences, 28(3), 117-121.

Somel, M., Somel, R. N. O., & Kence, A. (2007). Turks fighting back against anti-evolution forces. Nature, 445(7124), 147-147.

Stoneking, M., & Kayser, M. (2007). Genealogical markers: mtDNA and the Y-chromosome. In Michael P. Weiner, Stacey B. Gabriel, J. Claiborne Stephens (Ed.), Genetic Variation: A Laboratory Manual (pp. 421-436). New York: Cold Spring Harbor Laborarory Press.

Stoneking, M., & Nasidze, I. (2007). Reply to Parson: The art of reading sequence electropherograms. Annals of Human Genetics, 71(2), 279-280.

Tang, K., Thornton, K. R., & Stoneking, M. (2007). A new approach for using genome scans to detect recent positive selection in the human genome. PLoS Biology, 5(7): e171.

Thalmann, O., Fischer, A., Lankester, F., Pääbo, S., & Vigilant, L. (2007). The complex evolutionary history of gorillas: Insights from genomic data. Molecular Biology and Evolution, 24(1), 146-158.

Timpson, N., Heron, J., Smith, G. D., & Enard, W. (2007). Comment on Papers by Evans et al. and Mekel-Bobrov et al. on Evidence for Positive Selection of MCPH1 and ASPM. Science, 317(5841), 1036-1036.

Unterseher, M., Reiher, A., Finstermeier, K., Otto, P., & Morawetz, W. (2007). Species richness and distribution patterns of leaf-inhabiting endophytic fungi in a temperate forest canopy. Mycological Progress, 6(3), 201-212.

Valdiosera, C. E., García, N., Anderung, C., Dalén, L., Crégut-Bonnoure, E., Kahlke, R.-D., Stiller, M., Brandström, M., Thomas, M. G., Arsuaga, J.-L., Götherström, A., & Barnes, I. (2007). Staying out in the cold: glacial refugia and mitochondrial DNA phylogeography in ancient European brown bears. Molecular Ecology, 16(24), 5140-5148.

Weber, M., Hellmann, I., Stadler, M. B., Ramos, L., Pääbo, S., Rebhan, M., & Schübeler, D. (2007). Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome. Nature Genetics, 39(4), 457-466.

Willerslev, E., Cappellini, E., Boomsma, W., Nielsen, R., Hebsgaard, M. B., Brand, T. B., Hofreiter, M., Bunce, M., Poinar, H. N., Dahl-Jensen, D., Johnsen, S., Steffensen, J. P., Bennike, O., Schwenninger, J.-L., Nathan, R. P., Armitage, S., Hoog, C.-J.-d., Alfimov, V., Christl, M., Beer, J., Muscheler, R., Barker, J., Sharp, M., Penkman, K. E. H., Haile, J., Taberlet, P., Gilbert, M. T. P., Casoli, A., Campani, E., & Collins, M. J. (2007). Ancient Biomolecules from Deep Ice Cores Reveal a Forested Southern Greenland. Science, 317(5834), 111-114.

2006

Asher, R., & Hofreiter, M. (2006). Tenrec phylogeny and the non-invasive extraction of nuclear DNA. Systematic Biology, 55(2), 184-194.

Burek, P., Hoehndorf, R., Loebe, F., Visagie, J., Herre, H., & Kelso, J. (2006). A top-level ontology of functions and its application in the Open Biomedical Ontologies. Bioinformatics, 22(14), e66-e73.

Creely, H., & Khaitovich, P. (2006). Human Brain Evolution. Prog Brain Res, 158, 295-309.

Eriksson, J., Siedel, H., Lukas, D., Kayser, M., Erler, A., Hashimoto, C., Hohmann, G., Boesch, C., & Vigilant, L. (2006). Y-chromosome analysis confirms highly sex-biased dispersal and suggests a low male effective population size in bonobos (Pan paniscus). Molecular Ecology, 15(4), 939-949.

Fischer, A., Pollack, J. L., Thalmann, O., Nickel, B., & Pääbo, S. (2006). Demographic history and genetic differentiation in apes. Current Biology, 16(11), 1133-1138.

Fish, J. L., Kosodo, Y., Enard, W., Pääbo, S., & Huttner, W. B. (2006). Aspm specifically maintains

symmetric proliferative divisions of neuroepithelial cells. Proceedings of the National Academy of Sciences of the United States of America, 103(27), 10438-10443.

Goidts, V., Armengol, L., Schempp, W., Conroy, J., Nowak, N., Muller, S., Cooper, D. N., Estivill, X., Enard, W., Szamalek, J. M., Hameister, H., & Kehrer-Sawatzki, H. (2006). Identification of large-scale human-specific copy number differences by inter-species array comparative genomic hybridization. Human Genetics, 119(1-2), 185-198.

Green, R. E., Krause, J., Ptak, S. E., Briggs, A. W., Ronan, M. T., Simons, J. F., Du, L., Egholm, M., Rothberg, J. M., Paunovic, M., & Pääbo, S. (2006). Analysis of one million base pairs of Neanderthal DNA. Nature, 444, 330-336.

Hammer, M. F., Karafet, H., Park, H.-S., Omoto, K., Harihara, S., Stoneking, M., & Horai, S. (2006). Dual origins of the Japanese: common ground for hunter-gatherer and farmer Y chromosomes. Journal of Human Genetics, 51, 47-58.

Hoehndorf, R., Prüfer, K., Backhaus, M., Herre, H., Kelso, J., Loebe, F., & Visagie, J. (2006). A proposal for a gene functions wiki. In R. Meersman, Z. Tari, & P. Herrero (Eds.), On the move to meaningful internet systems 2006: OTM 2006 workshops (pp. 669-678). New York [u.a.]: Springer.

Hofreiter, M. (2006). Die Analyse alter DNA. In Uelsberg, Gabriele, & Rheinisches LandesMuseum Bonn (Eds.), Roots: Wurzeln der Menschheit [Katalog zur Ausstellung Rheinisches LandesMuseum Bonn: 8.7. - 19.11.2006] (pp. 175-182). Mainz: Zabern.

Hofreiter, M., & Lister, A. M. (2006). Mammoths. Current Biology, 16(10), R347-R348.

Hublin, J.-J., & Pääbo, S. (2006). Neandertals. Current Biology, 16(4), R113-R114.

Jänicke-Després, V. R., & Smith, B. D. (2006). Ancient DNA and the Integration of Archaeological and Genetic Approaches to the Study of Maize Domestication. In Staller, John E. (Ed.), Histories of maize (pp. 83-95). Amsterdam [u.a.]: Elsevier.

Kayser, M., Brauer, S., Cordaux, R., Casto, A., Lao, O., Zhivotovsky, L. A., Moyse-Faurie, C., Rutledge, R., Schiefenhövel, W., Gil, D., Lin, A. A., Underhill, P. A., Oefner, P. J., Trent, R. J., & Stoneking, M. (2006). Melanesian and Asian origins of Polynesians: mtDNA and Y-chromosome gradients across the Pacific. Molecular Biology and Evolution, 23(11), 2234-2244.

Kayser, M., Vowles, E. J., Kappei, D., & Amos, W. (2006). Microsatellite length differences between humans and chimpanzees at autosomal loci are not found at equivalent haploid Y chromosomal loci. Genetics, 173(4), 2179-2186.

Khaitovich, P., Enard, W., Lachmann, M., & Pääbo, S. (2006). Evolution of primate gene expression. Nature Reviews Genetics, 7, 693-702.

Khaitovich, P., Kelso, J., Franz, H., Visagie, J., Giger, T., Joerchel, S., Petzold, E., Green, R. E., Lachmann, M., & Pääbo, S. (2006). Functionality of intergenic transcription: An evolutionary comparison. PLoS Genetics, 2(10): e171, pp. 1590-1598.

Khaitovich, P., Tang, K., Franz, H., Kelso, J., Hellmann, I., Enard, W., Lachmann, M., & Pääbo, S. (2006). Positive selection on gene expression in the human brain. Current Biology, 16(10), R356-R358.

Krause, J., Dear, P. H., Pollack, J. L., Slatkin, M., Spriggs, H., Barnes, I., Lister, A. M., Ebersberger, I., Pääbo, S., & Hofreiter, M. (2006). Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae. Nature, 439(7077), 724-727.

Lachmann, M.(2006). Die Evolution der mRNS-Expression bei Mensch und Schimpanse. Retrieved from

https://www.mpg.de/351269/forschungsSchwerpunkt1?c=166410.

Lalueza-Fox, C., Krause, J., Caramelli, D., Catalano, G., Milani, L., Sampietro, M. L., Calafell, F., Martinez-Maza, C., Bastir, M., García-Tabernero, A., de la Rasilla, M., Fortea, J., Pääbo, S., Bertranpetit, J., & Rosas, A. (2006). Mitochondrial DNA of an Iberian neandertal suggests a population affinity with other European neandertals. Current Biology, 16(16), R629-R630.

Lizano, E., & Mörl, M. (2006). tRNA. In D. Ganten; K. Ruckpaul (Ed.), Encyclopedic Reference of Genomics and Proteomics in Molecular Medicine (pp. 1920-1924). Heidelberg: Springer.

Mehlotra, R. K., Stoneking, M., & Zimmerman, P. A. (2006). Paleoparasite populations from archived sera: Insights into chloroquine drug resistance in Papua New Guinea - Reply to Chan et al. Journal of Infectious Diseases, 194(7), 1024-1025.

Nasidze, I., & Stoneking, M. (2006). Mother tongue: Concomitant replacement of language and mtDNA in South Caspian populations of Iran. In Cangelosi, A.; Smith, A.; (Ed.), Evolution of Language: Proceedings of the 6th international conference EVOLANG6, Rome, Italy, 12-15 April 2006 (pp. 432-433). New Jersey: World Scientific.

Nasidze, I., Quinque, D., Rahmani, M., Alemohamad, S. A., & Stoneking, M. (2006). Concomitant replacement of language and mtDNA in South Caspian populations of Iran. Current Biology, 16(7), 668-673.

Noonan, J. P., Coop, G., Kudaravalli, S., Smith, D., Krause, J., Alessi, J., Chen, J., Platt, D., Pääbo, S., Pritchard, J. K., & Rubin, E. M. (2006). Sequencing and analysis of Neanderthal genomic DNA. Science, 314, 1113-1118.

Pakendorf, B., Novgorodov, I. N., Osakovskij, V. L., Danilova, A. P., Protod´jakonov, A., & Stoneking, M. (2006). Investigating the effects of prehistoric migrations in Siberia: genetic variation and the origins of Yakuts. Human Genetics, 120(3), 334-353.

Prabhakar, S., Noonan, J. P., Pääbo, S., & Rubin, E. M. (2006). Accelerated evolution of conserved noncoding sequences in humans. Science, 314, 786-786.

Quinque, D., Kittler, R., Kayser, M., Stoneking, M., & Nasidze, I. (2006). Evaluation of saliva as a source of human DNA for population and association studies. Analytical Biochemistry, 353(2), 272-277.

Römpler, H., Dear, P. H., Krause, J., Meyer, M., Rohland, N., Schöneberg, T., Spriggs, H., Stiller, M., & Hofreiter, M. (2006). Multiplex amplification of ancient DNA. Nature Protocols, 1(2), 720-728.

Römpler, H., Rohland, N., Lalueza-Fox, C., Willerslev, E., Kuznetsova, T., Rabeder, G., Betranpetit, J., Schöneberg, T., & Hofreiter, M. (2006). Nuclear Gene Indicates Coat-Color Polymorphism in Mammoths. Science, 313, 62-62.

Serre, D., & Pääbo, S. (2006). The fate of European Neanderthals. In Katerina Harvati & Terry Harrison (Ed.), Neanderthals revisited: new approaches and perspectives (pp. 211-219). Berlin: Springer.

Serre, D., Langaney, A., Chech, M., Teschler-Nicola, M., Paunovic, M., Mennecier, P., Hofreiter, M., Possnert, G., & Pääbo, S. (2006). No evidence of Neandertal mtDNA contribution to early modern humans. In M. Teschler-Nicola (Ed.), Early modern humans and the Moravian Gate: Mladec caves and their remains (pp. 491-503). Berlin: Springer.

Serre, D., Schmitz, R. W., & Pääbo, S. (2006). Genetic analyses of the Neanderthals from the Feldhofer Caves. Neanderthal 1856-2006, 329-333.

Somel, M., Khaitovich, P., Bahn, S., Pääbo, S., & Lachmann, M. (2006). Gene expression becomes

heterogeneous with age. Current Biology, 16(10), R359-R360.

Stiller, M., Green, R. E., Ronan, M. T., Simons, J. F., Du, L., Egholm, M., Rothberg, J. M., Keats, S. G., Ovodov, N. D., Antipina, E. E., Baryshnikov, G. F., Kuzmin, Y. V., Vasilevski, A. A., Wuenschell, G. E., Termini, J., Hofreiter, M., Jänicke-Després, V. R., Pääbo, S., & He, W. (2006). Patterns of nucleotide misincorporations during enzymatic amplification and direct large-scale sequencing of ancient DNA. Proceedings of the National Academy of Sciences of the United States of America, 103(37), 13578-13584.

Stoneking, M. (2006). Genetic evidence for our recent African ancestry. In Soodyall, Himla (Ed.), Prehistory of Africa (pp. 24-36). Johannesburg: Ball.

Stoneking, M. (2006). Investigating the health of our ancestors: Insights from the evolutionary genetic consequences of prehistoric diseases. In Bromage, Timothy (Ed.), Integrative Approaches to Human Health and Evolution: proceedings.. (pp. 106-114). Amsterdam [u.a.]: Elsevier.

Stoneking, M., & Nasidze, I. (2006). The patient is not dead yet: Premature autopsy of an mtDNA data set. Annals Human Genetics, 70(3), 327-331.

Stroud, J. C., Wu, Y. Q., Bates, D. L., Han, A. D., Nowick, K., Pääbo, S., Tong, H., & Chen, L. (2006). Structure of the forkhead domain of FOXP2 bound to DNA. Structure, 14(1), 159-166.

2005

Beauval, C., Maureille, B., Lacrampe-Cuyaubere, F., Serre, D., Peressinotto, D., Bordes, J. G., Cochard, D., Couchoud, I., Dubrasquet, D., Laroulandie, W., Lenoble, A., Mallye, J. B., Pasty, S., Primault, J., Rohland, N., Pääbo, S., & Trinkaus, E. (2005). A late Neandertal femur from Les Rochers-de-Villeneuve, France. Proceedings of the National Academy of Sciences of the United States of America, 102(20), 7085-7090.

Bull, J. J., Meyers, L. A., & Lachmann, M. (2005). Quasispecies made simple. PLoS Computational Biology, 1(6): e61, pp. 450-460.

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impiombato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Crowe, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Gatta, G. D., Bernardo, D. d., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Huminiecki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S. P. T., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Babu, M. M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schönbach, C., Sekiguchi, K., Semple, C. A. M., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlestedt, C.,

Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J., Hayashizaki, Y., FANTOM Consortium, & RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group) (2005). The transcriptional landscape of the mammalian genome. Science, 309(5740), 1559-1563.

Castellano, S., Lobanov, A. V., Chapple, C., Novoselov, S. V., Albrecht, M., Hua, D., Lescure, A., Lengauer, T., Krol, A., Gladyshev, V. N., & Guigó, R. (2005). Diversity and functional plasticity of eukaryotic selenoproteins: Identification and characterization of the SelJ family. Proceedings of the National Academy of Sciences of the United States of America, 102(45), 16188-16193.

Cheng, Z., Ventura, M., She, X., Khaitovich, P., Graves, T. A., Osoegawa, K., Church, D., de Jong, P., Wilson, R. K., Pääbo, S., Rocchi, M., & Eichler, E. E. (2005). A genome-wide comparison of recent chimpanzee and human segmental duplications. Nature, 437(7055), 88-93.

Cox, J., Stern, R., Springell, K., Lindsay, S., Scott, S., Bond, J., Enard, W., & Woods, C. G. (2005). Primary microcephaly: a centrosomal disease? Journal of Medical Genetics, 42, S34-S34.

Ebersberger, I., & Meyer, M. (2005). A genomic region evolving toward different GC contents in humans and chimpanzees indicates a recent and regionally limited shift in the mutation pattern. Molecular Biology and Evolution, 22(5), 1240-1245.

Enard, W. (2005). Mensch und Schimpanse: Ein genetischer Vergleich. In Kleeberg, Bernhard; Walter, Tilmann; Crivellari, Fabio (Ed.), Urmensch und Wissenschaften: eine Bestandsaufnahme; [Festschrift für Dieter Groh] (pp. 125-136). Darmstadt: Wiss. Buchges.

Fischer, A., Gilad, Y., Man, O., & Pääbo, S. (2005). Evolution of bitter taste receptors in humans and apes. Molecular Biology and Evolution, 22(3), 432-436.

Franz, H., Ullmann, C., Becker, A., Ryan, M., Bahn, S., Arendt, T., Simon, M., Pääbo, S., & Khaitovich, P. (2005). Systematic analysis of gene expression in human brains before and after death. Genome Biology, 6(13): R112, pp. R112.1-R112.9.

Fraser, H. B., Khaitovich, P., Plotkin, J. B., Pääbo, S., & Eisen, M. B. (2005). Aging and gene expression in the primate brain. PLoS Biology, 3(9): e274, pp. 1653-1661.

Gilbert, M. T. P., Bandelt, H. J., Hofreiter, M., & Barnes, I. (2005). Assessing ancient DNA studies. Trends in Ecology & Evolution, 20(10), 541-544.

Gilbert, M. T. P., Barnes, I., Collins, M. J., Smith, C. I., Eklund, J., Goudsmit, J., Poinar, H. N., & Cooper, A. (2005). Long-term survival of ancient DNA in Egypt: Response to Zink and Nerlich (2003). American Journal of Physical Anthropology, 128(1), 110-114.

Hamilton, G., Stoneking, M., & Excoffier, L. (2005). Molecular analysis reveals tighter social regulation of immigration in patrilocal populations than in matrilocal populations. Proceedings of the National Academy of Sciences of the United States of America, 102(21), 7476-7480.

Heißig, F., Krause, J., Bryk, J., Khaitovich, P., Enard, W., & Pääbo, S. (2005). Functional analysis of human and chimpanzee promoters. Genome Biology, 6: R57.

Hellmann, I., Prüfer, K., Ji, H. K., Zody, M. C., Pääbo, S., & Ptak, S. E. (2005). Why do human diversity levels vary at a megabase scale? Genome Research, 15(9), 1222-1231.

Hofreiter, M. (2005). Book Review: Ancient DNA typing. Hournal of Comparative Human Biology, 55(3),

298-300.

Hofreiter, M. (2005). Evolutionsgeschichte alpiner Höhlenbären aus molekulargenetischer Sicht. Mitteilungen der Kommission für Quartärforschung der Österreichischen Akademie der Wissenschaften, 14, 67-72.

Iyengar, A., Babu, V. N., Hedges, S., Venkataraman, B., Maclean, N., & Morin, P. A. (2005). Phylogeography, genetic structure, and diversity in the dhole (Cuon alpinus). Molecular Ecology, 14(8), 2281-2297.

Kayser, M., Lao, O., Anslinger, K., Augustin, C., Bargel, G., Edelmann, J., Elias, S., Heinrich, M., Henke, J., Henke, L., Hohoff, C., Illing, A., Jonkisz, A., Kuzniar, P., Lebioda, A., Lessig, R., Lewicki, S., Maciejewska, A., Monies, D. M., Pawlowski, R., Poetsch, M., Schmid, D., Schmidt, U., Schneider, P. M., Stradmann-Bellinghausen, B., Szibor, R., Wegener, R., Wozniak, M., Zoledziewska, M., Roewer, L., Dobosz, T., & Ploski, R. (2005). Significant genetic differentiation between Poland and Germany follows present-day political borders, as revealed by Y-chromosome analysis. Human Genetics, 117(5), 428-443.

Khaitovich, P., Hellmann, I., Enard, W., Nowick, K., Leinweber, M., Franz, H., Weiss, G., Lachmann, M., & Pääbo, S. (2005). Parallel patterns of evolution in the genomes and transcriptomes of humans and chimpanzees. Science, 309(5742), 1850-1854.

Khaitovich, P., Pääbo, S., & Weiss, G. (2005). Toward a neutral evolutionary model of gene expression. Genetics, 170(2), 929-939.

Laan, M., Wiebe, V., Khusnutdinova, E., Remm, M., & Pääbo, S. (2005). X-chromosome as a marker for population history: Linkage disequilibrium and haplotype study in Eurasian populations. European Journal of Human Genetics, 13(4), 452-462.

Leonard, J. A., Rohland, N., Glaberman, S., Fleischer, R. C., Caccone, A., & Hofreiter, M. (2005). A rapid loss of stripes: the evolutionary history of the extinct quagga. Biology Letters, 1(3), 291-295.

Lohmann, H., Tomasello, M., & Meyer, S. (2005). Linguistic Communication and Social Understanding. In J. W. Astington, & J. A. Baird (Eds.), Why language matters for theory of mind (pp. 245-265). Oxford: Oxford Univ. Press.

Mehlotra, R. K., Mattera, G., Bhatia, K., Reeder, J. C., Stoneking, M., & Zimmerman, P. A. (2005). Insight into the early spread of chloroquine resistant Plasmodium falciparum infections in Papua New Guinea. Journal of Infectious Diseases, 192(12), 2174-2179.

Meyers, L. A., Ancel, F. D., & Lachmann, M. (2005). Evolution of Genetic Potential. PLoS Computational Biology, 1(3): e32, pp. 0236-0243.

Mörl, M., Lizano, E., Willkomm, D. K., & Hartmann, R. K. (2005). Production of RNAs with homogeneous 5'- and 3'-ends. In Hartmann, R.K.; Bindereif, A.; Schön, A. Westhof, E. (Ed.), Handbook of RNA Biochemistry (pp. 22-35). Weinheim: Wiley-VCH.

Myles, S., Bouzekri, N., Haverfield, E., Cherkaoui, M., Dugoujon, J.-M., & Ward, R. D. (2005). Genetic evidence in support of a shared Eurasian-North African dairying origin. Human Genetics, 117(1), 34-42.

Nasidze, I., Quinque, D., Dupanloup, I., Cordaux, R., Kokshunova, L., & Stoneking, M. (2005). Genetic evidence for the Mongolian ancestry of Kalmyks. American Journal of Physical Anthropology, 128(4), 846-854.

Nasidze, I., Quinque, D., Ozturk, M., Bendukidze, N., & Stoneking, M. (2005). MtDNA and Y-chromosome variation in Kurdish groups. Annals of Human Genetics, 69(4), 401-412.

Nielsen-Marsh, C. M., Richards, M. P., Hauschka, P. V., Thomas-Oates, J. E., Trinkaus, E., Pettitt, P. B., Karavanic, I., Poinar, H. N., & Collins, M. J. (2005). Osteocalcin protein sequences of Neanderthals and modern primates. Proceedings of the National Academy of Sciences of the United States of America, 102(12), 4409-4413.

Noonan, J. P., Hofreiter, M., Smith, D., Priest, J. R., Rohland, N., Rabeder, G., Krause, J., Detter, J. C., Pääbo, S., & Rubin, E. M. (2005). Genomic sequencing of Pleistocene cave bears. Science, 309(5734), 597-599.

Oota, H., Pakendorf, B., Weiss, G., von Haeseler, A., Pookajorn, S., Settheetham-Ishida, W., Tiwawech, D., Ishida, T., & Stoneking, M. (2005). Recent origin and cultural reversion of a hunter–gatherer group. PLoS Biology, 3(3): e71.

Pääbo, S. (2005). Was ist Forschung? In H. Braun, & D. Grömling (Eds.), Entwurfsatlas Forschungs- und Technologiebau (pp. 10-11). Basel: Birkhäuser.

Pakendorf, B., & Stoneking, M. (2005). Mitochondrial DNA and human evolution. Annual Review of Genomics and Human Genetics, 6, 165-183.

Ptak, S. E., Hinds, D. A., Köhler, K., Nickel, B., Patil, N., Ballinger, D. G., Przeworski, M., Frazer, K. A., & Pääbo, S. (2005). Fine-scale recombination patterns differ between chimpanzees and humans. Nature Genetics, 37(4), 429-434.

Rabeder, G., Hofreiter, M., & Wild, E. M. (2005). Die Bären der Brieglersberghöhle. Die Höhle, 56, 36-43.

Roewer, L., Croucher, P. J. P., Willuweit, S., Lu, T. T., Kayser, M., Lessig, R., de Knijff, P., Jobling, M. A., Tyler-Smith, C., & Krawczak, M. (2005). Signature of recent historical events in the European Y-chromosomal STR haplotype distribution. Human Genetics, 116(4), 279-291.

Rohland, N., Pollack, J. L., Nagel, D., Beauval, C., Airvaux, J., Pääbo, S., & Hofreiter, M. (2005). The population history of extant and extinct hyenas. Molecular Biology and Evolution, 22(12), 2435-2443.

Römpler, H., Schulz, A., Pitra, C., Coop, G., Przeworski, M., Pääbo, S., & Schöneberg, T. (2005). The rise and fall of the chemoattractant receptor GPR33. Journal of Biological Chemistry, 280(35), 31068-31075.

Schuster, J., Betat, H., & Mörl, M. (2005). Is yeast on its way to evolving tRNA editing?: Corrigendum. EMBO Reports, 6(5), 487-487.

Schuster, J., Betat, H., & Mörl, M. (2005). Is yeast on its way to evolving tRNA editing? EMBO Reports, 6(4), 367-372.

Smith, S., & Morin, P. A. (2005). Optimal storage conditions for highly dilute DNA samples: A role for trehalose as a preserving agent. Journal of Forensic Sciences, 50(5), 1101-1108.

Somel, M. (2005). Turkish science needs more than membership of the EU. Nature, 438(7069), 738-738.

Stoneking, M. (2005). Gene, Geographie und Sprache. In Günter Hauska (Ed.), Gene, Sprachen und ihre Evolution: wie verwandt sind die Menschen - wie verwandt sind ihre Sprachen? (pp. 133-140). Regensburg: Universitätsverlag Regensburg.

Stoneking, M., Pakendorf, B., & Oota, H. (2005). Authors' reply. PLoS Biol, 3(8): e270, pp. 1354-1355.

Tanino, M., Debily, M.-A., Tamura, T., Hishiki, T., Ogasawara, O., Murakawa, K., Kawamoto, S., Itoh, K., Watanabe, S., de Souza, S. J., Imbeaud, S., Graudens, E., Eveno, E., Hilton, P., Sudo, Y., Kelso, J., Ikeo, K., Imanishi, T., Gojobori, T., Auffray, C., Hide, W., & Okubo, K. (2005). The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate

technologies and platforms. Nucleic Acids Research (London), 33(Suppl. 1 Database Issue), D567-D572.

Taskov, K., Chapple, C., Kryukov, G. V., Castellano, S., Lobanov, A. V., Korotkov, K. V., Guigó, R., & Gladyshev, V. N. (2005). Nematode selenoproteome: The use of the selenocysteine insertion system to decode one codon in an animal genome? Nucleic Acids Research, 33(7), 2227-2238.

Thalmann, O., Serre, D., Hofreiter, M., Lukas, D., Eriksson, J., & Vigilant, L. (2005). Nuclear insertions help and hinder inference of the evolutionary history of gorilla mtDNA. Molecular Ecology, 14(1), 179-188.

The Chimpanzee Sequencing and Analysis Consortium, Mikkelsen, T. S., Hillier, L. W., Eichler, E. E., Zody, M. C., Jaffe, D. B., Yang, S.-P., Enard, W., Hellmann, I., Lindblad-Toh, K., Altheide, T. K., Archidiacono, N., Bork, P., Butler, J., Chang, J. L., Cheng, Z., Chinwalla, A. T., de Jong, P., Delehaunty, K. D., Fronick, C. C., Fulton, L. L., Gilad, Y., Glusman, G., Gnerre, S., Graves, T. A., Hayakawa, T., Hayden, K. E., Huang, X., Ji, H., Kent, W. J., King, M.-C., Kulbokasl, E. J., Lee, M. K., Liu, G., Lopez-Otin, C., Makova, K. D., Man, O., Mardis, E. R., Mauceli, E., Miner, T. L., Nash, W. E., Nelson, J. O., Pääbo, S., Patterson, N. J., Pohl, C. S., Pollard, K. S., Prüfer, K., Puente, X. S., Reich, D., Rocchi, M., Rosenbloom, K., Ruvolo, M., Richter, D. J., Schaffner, S. F., Smit, A. F. A., Smith, S. M., Suyama, M., Taylor, J., Torrents, D., Tuzun, E., Varki, A., Velasco, G., Ventura, M., Wallis, J. W., Wendl, M. C., Wilson, R. K., Lander, E. S., & Waterston, R. H. (2005). Initial sequence of the chimpanzee genome and comparison with the human genome. Nature, 437(7055), 69-87.

Tiffin, N., Kelso, J., Powell, A. R., Hong, P., Bajic, V. B., & Hide, W. A. (2005). Integration of text- and data-mining using ontologies successfully selects disease gene candidates. Nucleic Acids Research, 33(5), 1544-1552.

Vigilant, L., Eriksson, J., Siedel, H., Lang, C., Erler, A., & Kayser, M. (2005). Contrasting patterns, of male, and female-mediated gene flow in wild bonobo populations.

Willerslev, E., Hansen, A. J., & Poinar, H. N. (2005). Theoretical and experimental considerations on the recovery of DNA and viable organisms from ancient ice and permafrost. In Life in ancient ice. Princeton: Princeton Univ. Press.

Woods, C. G., Bond, J., & Enard, W. (2005). Autosomal Recessive Primary Microcephaly (MCPH): A Review of Clinical, Molecular, and Evolutionary Findings. The American Journal of Human Genetics, 76, 717-728.

Yohn, C. T., Jiang, Z., McGrath, S. D., Hayden, K. E., Khaitovich, P., Johnson, M. E., Eichler, M. Y., McPerson, J. D., Zhao, S., Pääbo, S., & Eichler, E. E. (2005). Lineage-specific expansions of retroviral insertions within the genomes of African great apes but not humans and orangutans. PLoS Biology, 3(4): e110.

2004

Aitken, N. C., Smith, S., Schwarz, C., & Morin, P. A. (2004). Single nucleotide polymorphism (SNP) discovery in mammals: a targeted-gene approach. Molecular Ecology, 13(6), 1423-1431.

Bergstrom, C., & Lachmann, M. (2004). Shannon information and biological fitness. In Institute of Electrical and Electronics Engineers (Ed.), Information theory workshop, 2004. IEEE (pp. 50-54).

Betat, H., Rammelt, C., Martin, G., & Mörl, M. (2004). Exchange of Regions between Bacterial Poly(A) Polymerase and the CCA-Adding Enzyme Generates Altered Specificities. Molecular Cell, 15, 329-398.

Castellano, S., Novoselov, S. V., Kryukov, G. V., Lescure, A., Blanco, E., Krol, A., Gladyshev, V. N., & Guigó, R. (2004). Reconsidering the evolution of eukaryotic selenoproteins: A novel nonmammalian family

with scattered phylogenetic distribution. EMBO Reports, 5(1), 71-77.

Cordaux, R., Aunger, R., Bentley, G. R., Nasidze, I., Sirajuddin, S. M., & Stoneking, M. (2004). Independent origins of Indian caste and tribal paternal lineages. Current Biology, 14(3), 231-235.

Cordaux, R., Bentley, G. R., Aunger, R., Sirajuddin, S. M., & Stoneking, M. (2004). Y-STR haplotypes from eight south Indian groups based on five loci. Journal of Forensic Sciences, 49(4), 847-848.

Cordaux, R., Edwin, D., Vishwanathan, H., & Stoneking, M. (2004). Genetic evidence for the demic diffusion of agriculture to India. Science, 304(5674), 1125-1125.

Cordaux, R., Weiss, G., Saha, N., & Stoneking, M. (2004). The northeast Indian passageway: A barrier or corridor for human migrations? Molecular Biology and Evolution, 21(8), 1525-1533.

Enard, W., & Pääbo, S. (2004). Comparative primate genomics. Annual Review of Genomics and Human Genetics, 5, 351-378.

Enard, W., Fassbender, A., Model, F., Adorján, P., Pääbo, S., & Olek, A. (2004). Differences in DNA methylation patterns between humans and chimpanzees. Current Biology, 14(4), R148-R149.

Erler, A., Stoneking, M., & Kayser, M. (2004). Development of Y-chromosomal microsatellite markers for non-human primates. Molecular Ecology, 13(10), 2921-2930.

Fischer, A., Wiebe, V., Pääbo, S., & Przeworski, M. (2004). Evidence for a complex demographic history of chimpanzees. Molecular Biology and Evolution, 21(5), 799-808.

Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D., & Pääbo, S. (2004). Loss of olfactory receptor genes coincides with the acquisition of full trichromatic vision in primates. PLoS Biology, 2(1): e5 [V. Wiebe and S. Pääbo retracted authorship].

Hartmann, R. K., Mörl, M., & Sprinzl, M. (2004). The tRNA world. RNA, 10(3), 344-349.

Hofreiter, M., & Pacher, M. (2004). Using ancient DNA to elucidate raw material origin of bone points from Potocka Zijalka (Slovenia): Preliminary results. In M. Pacher (Ed.), Potochka zijalka: Palaeontological and archaeological results of the campaigns 1997-2000 (pp. 201-210). Wien: Verlag der österreichischen Akademie der Wissenschaften.

Hofreiter, M., Loreille, O., Ferriola, D., & Parsons, T. J. (2004). Ongoing Controversy over Romanov Remains: Letter. Science, 306, 407-408.

Hofreiter, M., Rabeder, G., Jänicke-Després, V. R., Withalm, G., Nagel, D., Paunovic, M., Jambresic, G., & Pääbo, S. (2004). Evidence for reproductive isolation between cave bear populations. Current Biology, 14(1), 40-43.

Hofreiter, M., Serre, D., Rohland, N., Rabeder, G., Nagel, D., Conard, N. J., Münzel, S., & Pääbo, S. (2004). Lack of phylogeography in European mammals before the last glaciation. PNAS, 101(35), 12963-12968.

Hughes, D. A., Cordaux, R., & Stoneking, M. (2004). Humans. Current Biology, 14, R367-R369.

Imanishi, T., Itoh, T., Suzuki, Y., O'Donovan, C., Fukuchi, S., Koyanagi, K. O., Barrero, R. A., Tamura, T., Yamaguchi-Kabata, Y., Tanino, M., Yura, K., Miyazaki, S., Ikeo, K., Homma, K., Kasprzyk, A., Nishikawa, T., Hirakawa, M., Thierry-Mieg, J., Thierry-Mieg, D., Ashurst, J., Jia, L., Nakao, M., Thomas, M. A., Mulder, N., Karavidopoulou, Y., Jin, L., Kim, S., Yasuda, T., Lenhard, B., Eveno, E., Suzuki, Y., Yamasaki, C., Takeda, J.-i., Gough, C., Hilton, P., Fujii, Y., Sakai, H., Tanaka, S., Amid, C., Bellgard, M., de Bonaldo, M. F., Bono, H., Bromberg, S. K., Brookes, A. J., Bruford, E., Carninci, P., Chelala, C., Couillault, C., de

Souza, S. J., Debily, M.-A., Devignes, M.-D., Dubchak, I., Endo, T., Estreicher, A., Eyras, E., Fukami-Kobayashi, K., Gopinath, G. R., Graudens, E., Hahn, Y., Han, M., Han, Z.-G., Hanada, K., Hanaoka, H., Harada, E., Hashimoto, K., Hinz, U., Hirai, M., Hishiki, T., Hopkinson, I., Imbeaud, S., Inoko, H., Kanapin, A., Kaneko, Y., Kasukawa, T., Kelso, J., Kersey, P., Kikuno, R., Kimura, K., Korn, B., Kuryshev, V., Makalowska, I., Makino, T., Mano, S., Mariage-Samson, R., Mashima, J., Matsuda, H., Mewes, H.-W., Minoshima, S., Nagai, K., Nagasaki, H., Nagata, N., Nigam, R., Ogasawara, O., Ohara, O., Ohtsubo, M., Okada, N., Okido, T., Oota, S., Ota, M., Ota, T., Otsuki, T., Piatier-Tonneau, D., Poustka, A., Ren, S.-X., Saitou, N., Sakai, K., Sakamoto, S., Sakate, R., Schupp, I., Servant, F., Sherry, S., Shiba, R., Shimizu, N., Shimoyama, M., Simpson, A. J., Soares, B., Steward, C., Suwa, M., Suzuki, M., Takahashi, A., Tamiya, G., Tanaka, H., Taylor, T., Terwilliger, J. D., Unneberg, P., Veeramachaneni, V., Watanabe, S., Wilming, L., Yasuda, N., Yoo, H.-S., Stodolsky, M., Makalowski, W., Go, M., Nakai, K., Takagi, T., Kanehisa, M., Sakaki, Y., Quackenbush, J., Okazaki, Y., Hayashizaki, Y., Hide, W., Chakraborty, R., Nishikawa, K., Sugawara, H., Tateno, Y., Chen, Z., Oishi, M., Tonellato, P., Apweiler, R., Okubo, K., Wagner, L., Wiemann, S., Strausberg, R. L., Isogai, T., Auffray, C., Nomura, N., Gojobori, T., & Sugano, S. (2004). Integrative annotation of 21,037 human genes validated by full-length cDNA clones. PLoS Biology, 2(6): e162.

International Chicken Genome Sequencing Consortium, & Castellano, S. (2004). Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 432, 695-716.

Iyengar, A., Stockwell, A., Layfield, D., & Morin, P. A. (2004). Characterization of microsatellite markers in a threatened species, the White Sands pupfish (Cyprinodon tularosa). Molecular Ecology Notes, 4, 191-193.

Jaillon, O., Aury, J.-M., Brunet, F., Petit, J.-L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Biémont, C., Skalli, Z., Cattolico, L., Poulain, J., de Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.-P., Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K. J., McEwan, P., Bosak, S., Kellis, M., Volff, J.-N., Guigó, R., Zody, M. C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quétier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E. S., & Crollius, J. W. H. R. (2004). Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. Nature, 431, 946-957.

Kasperaviciute, D., Kucinskas, V., & Stoneking, M. (2004). Y chromosome and mitochondrial DNA variation in Lithuanians. Annals of Human Genetics, 68(5), 438-452.

Kayser, M., Kittler, R., Erler, A., Hedman, M., Lee, A. C., Mohyuddin, A., Mehdi, S. Q., Rosser, Z. H., Stoneking, M., Jobling, M. A., Sajantila, A., & Tyler-Smith, C. (2004). A comprehensive survey of human Y-chromosomal microsatellites. American Journal of Human Genetics, 74(6), 1183-1197.

Kelso, J. (2004). EST resources, clone sets, and databases. In L. B. Jorde (Ed.), Encyclopedia of genetics, genomics, proteomics and bioinformatics. Wiley.

Khaitovich, P., Muetzel, B., She, X., Lachmann, M., Hellmann, I., Dietzsch, J., Steigele, S., Do, H.-H., Weiss, G., Enard, W., Heißig, F., Arendt, T., Nieselt-Struwe, K., Eichler, E. E., & Pääbo, S. (2004). Regional patterns of gene expression in human and chimpanzee brains. Genome Research, 14, 1462-1473.

Khaitovich, P., Weiss, G., Lachmann, M., Hellmann, I., Enard, W., Muetzel, B., Wirkner, U., Ansorge, W., & Pääbo, S. (2004). A neutral model of transcriptome evolution. PLoS Biology, 2(5): e132, pp. 0682-0689.

Lachmann, M., & Bergstrom, C. T. (2004). The disadvantage of combinatorial communication. Proceedings of the Royal Society of London - Series B: Biological Sciences, 271, 2337-2343.

Lachmann, M., Newman, M. E. J., & Moore, C. (2004). The physical limits of communication or Why any sufficiently advanced technology is indistinguishable from noise. American Journal of Physics, 72(10), 1290-1293.

Levinger, L., Mörl, M., & Florentz, C. (2004). Mitochondrial tRNA 3' end metabolism and human disease. Nucleic Acids Research, 32, 5430-5441.

Levinger, L., Mörl, M., & Florentz, C. (2004). Reduced efficiency of 3´end cleavage and CCA addition with mutant human mitochondrial tRNAs could contribute to pathogenesis. Biochimica et Biophysica Acta (BBA) - Bioenergetics, 1657(Suppl. 1), 54-54.

Levinger, L., Oestreich, I., Florentz, C., & Mörl, M. (2004). A pathogenesis-associated mutation in human mitochondrial tRNA Leu(UUR) leads to reduced 3'-end processing and CCA addition. Journal of Molecular Biology, 337(3), 535-544.

Matheus, P., Burns, J., Weinstock, J., & Hofreiter, M. (2004). Pleistocene brown bears in the midcontinent of North America. Science, 306, 1150-1150.

Morin, P. A., & Goldberg, T. L. (2004). Determination of genealogical relationships from genetic data: a review of methods and applications. In B. Chapais, C. M. Berman (Ed.), Kinship and Behavior in Primates (pp. 15-45). New York: Oxford Univ. Press.

Morin, P. A., Luikart, G., & Wayne, R. K. (2004). SNPs in ecology, evolution and conservation. Trends in Ecology and Evolution, 19(4), 208-216.

Nasidze, I., Ling, E. Y., Quinque, D., Dupanloup, I., Cordaux, R., Rychkov, S., Naumova, O., Zhukova, O., Sarraf-Zadegan, N., Naderi, G. A., Asgary, S., Sardas, S., Farhud, D. D., Sarkisian, T., Asadov, C., Kerimov, A., & Stoneking, M. (2004). Mitochondrial DNA and Y-chromosome variation in the Caucasus. Annals of Human Genetics, 68(3), 205-221.

Nasidze, I., Quinque, D., Dupanloup, I., Rychkov, S., Naumova, O., Zhukova, O., & Stoneking, M. (2004). Genetic evidence concerning the origins of South and North Ossetians. Annals of Human Genetics, 68(6), 588-599.

Nembaware, V., Wolfe, K. H., Bettoni, F., Kelso, J., & Seoighe, C. (2004). Allele-specific transcript isoforms in human. FEBS Letters, 577(1-2), 233-238.

Nsubuga, A. M., Robbins, M. M., Roeder, A. D., Morin, P. A., Boesch, C., & Vigilant, L. (2004). Factors affecting the amount of genomic DNA extracted from ape faeces and the identification of an improved sample storage method. Molecular Ecology, 13(7), 2089-2094.

Pääbo, S. (2004). Ancient DNA. In Krude, T. (Ed.), DNA - Changing Science and Society (pp. 68-87). Cambridge: Cambridge University Press.

Pääbo, S., Poinar, H. N., Serre, D., Jänicke-Després, V. R., Hebler, J., Rohland, N., Kuch, M., Krause, J., Vigilant, L., & Hofreiter, M. (2004). Genetic analyses from ancient DNA. Annual Review of Genetics, 38, 645-679.

Ptak, S. E., Roeder, A. D., Stephens, M., Gilad, Y., Pääbo, S., & Przeworski, M. (2004). Absence of the TAP2 human recombination hotspot in chimpanzees. PLoS Biology, 2(6), 0849-0855.

Ptak, S. E., Voelpel, K., & Przeworski, M. (2004). Insights Into Recombination From Patterns of Linkage Disequilibrium in Humans. Genetics, 167, 387-397.

Rabeder, G., & Hofreiter, M. (2004). Der neue Stammbaum der alpinen Höhlenbären. Die Höhle, 55(1-4), 58-77.

Rabeder, G., Hofreiter, M., & Withalm, G. (2004). The systematic position of cave bears from Potocka Zijalka. In M. Pacher (Ed.), Potocka Zijalka: Palaeontological and archaeological results of the campaigns 1997-2000 (pp. 197-200). Wien: Verlag der österreichischen Akademie der Wissenschaften.

Rabeder, G., Hofreiter, M., Nagel, D., & Withalm, G. (2004). New Taxa of Alpine Cave Bears (Ursidae, Carnivora). Cahiers scientifiques. Hors série, 2, 49-67.

Roeder, A. D., Archer, F. I., Poinar, H. N., & Morin, P. A. (2004). A novel method for collection and preservation of faeces for genetic studies. Molecular Ecology Notes, 4, 761-764.

Rohland, N., Siedel, H., & Hofreiter, M. (2004). Nondestructive DNA extraction method for mitochondrial DNA analyses of museum specimens. BioTechniques, 36(5), 814-821.

Schuster, J., & Mörl, M. (2004). Mitochondrial tRNA editing. Topics in Current Genetics, 8, 81-96.

Serre, D., & Pääbo, S. (2004). Evidence for gradients of human genetic diversity within and among continents. Genome Research, 14, 1679-1685.

Serre, D., Hofreiter, M., & Pääbo, S. (2004). Mutations induced by ancient DNA extracts? Molecular Biology and Evolution, 21(8), 1463-1467.

Serre, D., Langaney, A., Chell, M., Teschler-Nicola, M., Paunovic, M., Mennecier, P., Hofreiter, M., Possnert, G., & Pääbo, S. (2004). No evidence of Neandertal mtDNA contribution to early modern humans. PLoS Biology, 2(3): e57, pp. 313-317.

Smith, S., Aitken, N. C., Schwarz, C., & Morin, P. A. (2004). Characterization of 15 single nucleotide polymorphism markers for chimpanzees (Pan troglodytes). Molecular Ecology Notes, 4(3), 348-351.

Thalmann, O., Hebler, J., Poinar, H. N., Pääbo, S., & Vigilant, L. (2004). Unreliable mtDNA data due to nuclear insertions: A cautionary tale from analysis of humans and other great apes. Molecular Ecology, 13(2), 321-335.

The international Chimpanzee Chromosome 22 Consortium, Watanabe, H., Fujiyama, A., Hattory, M., Taylor, T. D., Toyoda, A., Kuroki, Y., Noguchi, H., BenKahla, A., Lehrach, H., Sudbrak, R., Kube, M., Taenzer, S., Galgoczy, P., Platzer, M., Scharfe, M., Nordsiek, G., Blöcker, H., Hellmann, I., Khaitovich, P., Pääbo, S., Reinhardt, R., Zheng, H.-J., Zhang, X.-L., Zhu, G.-F., Wang, B.-F., Fu, G., Ren, S.-X., Zhao, G.-P., Chen, Z., Lee, Y.-S., Cheong, J.-E., Choi, S.-H., Wu, K.-M., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Kim, C.-G., Oota, S., Kitano, T., Kohora, Y., Saitou, N., Park, H.-S., Wang, S.-Y., Yaspo, M.-L., & Sakaki, Y. (2004). DNA sequence and comparative analysis of chimpanzee chromosome 22. Nature, 429, 382-388.

Vishwanathan, H., Deepa, E., Cordaux, R., Stoneking, M., Usha Rani, M. V., & Majumder, P. P. (2004). Genetic structure and affinities among tribal populations of southern India: a study of 24 autosomal DNA markers. Annals Human Genetics, 68(2), 128-138.

Zhivotovsky, L. A., Underhill, P. A., Cinnioglu, C., Kayser, M., Morar, B., Kivisild, T., Scozzari, R., Cruciani, F., Destro-Bisol, G., Spedini, G., Chambers, G. K., Herrera, R. J., Yong, K. K., Gresham, D., Tournev, I., Feldman, M. W., & Kalaydjieva, L. (2004). The effective mutation rate at Y chromosome short tandem repeats, with application to human population-divergence time. American Journal of Human Genetics, 74(1), 50-61.

2003

Augustin, M. A., Reichert, A. S., Betat, H., Huber, R., & Mörl, M. (2003). Crystal structure of the human CCA-adding enzyme: insights into template-independent polymerization. Journal of Molecular Biology, 328,

985-994.

Betat, H., & Mörl, M. (2003). tRNA Import in Mitochondrien. Biospektrum, 9, 33-35.

Brentani, H., Caballero, O. L., Camargo, A. A., da Silva, A. M., da Silva, W. A., Neto, E. D., Grivet, M., Gruber, A., Guimaraes, P. E. M., Hide, W., Iseli, C., Jongeneel, C. V., Kelso, J., Nagai, M. A., Ojopi, E. P. B., Osorio, E. C., Reis, E. M. R., Riggins, G. J., Simpson, A. J. G., de Souza, S., Stevenson, B. J., Strausberg, R. L., Tajara, E. H., Verjovski-Almeida, S., The Human Cancer Genome Project Cancer Genome Anatomy Project Annotation Consortium, & The Human Cancer Genome Project Sequencing Consortium (2003). The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. Proceedings of the National Academy of Sciences of the United States of America, 100(23), 13418-13423.

Cordaux, R., & Stoneking, M. (2003). South Asia: the Andamanese and the genetic evidence for an "early" human dispersal out of Africa. American Journal of Human Genetics, 72(6), 1586-1590.

Cordaux, R., Saha, N., Bentley, G. R., Aunger, A., Sirajuddin, S. M., & Stoneking, M. (2003). Mitochondrial DNA analysis reveals diverse histories of tribal populations of India. European Journal of Human Genetics, 11(3), 253-264.

Enard, W. (2003). All that jazz.. Nature's insight into what makes scientists tick. Nature, 421(6920), 215-215.

Gilad, Y., Bustamante, C. D., Lancet, D., & Pääbo, S. (2003). Natural selection on the olfactory receptor gene family in humans and chimpanzees. The American Journal of Human Genetics, 73(3), 489-501.

Gilad, Y., Man, O., Pääbo, S., & Lancet, D. (2003). Human specific loss of olfactory receptor genes. Proceedings of the National Academy of Sciences of the United States of America, 100(6), 3324-3327.

Hellmann, I., Ebersberger, I., Ptak, S. E., Pääbo, S., & Przeworski, M. (2003). A neutral explanation for the correlation of diversity with recombination rates in humans. American Journal of Human Genetics, 72(6), 1527-1535.

Hellmann, I., Zöllner, S., Enard, W., Ebersberger, I., Nickel, B., & Pääbo, S. (2003). Selection on human genes as revealed by comparisons to chimpanzee cDNA. Genome Research, 13, 831-837.

Hide, W., Smedley, D., McCarthy, M., & Kelso, J. (2003). Application of eVOC: Controlled vocabularies for unifying gene expression data. Comptes Rendus Biologies, 326(10-11), 1089-1096.

Hofreiter, M., & Vigilant, L. (2003). Ancient human DNA: Phylogenetic applications. In David N. Cooper (Ed.), Nature encyclopedia of the human genome: vol. 1 (ABS - DIG) (pp. 116-119). London [et al]: Nature Publishers Group.

Hofreiter, M., Betancourt, J. L., Pelliza Sbriller, A., Markgraf, V., & McDonald, H. G. (2003). Phylogeny, diet, and habitat of an extinct ground sloth from Cuchillo Curá, Neuquén Province, southwest Argentina. Quaternary Research, 59(3), 364-378.

Hofreiter, M., Mead, J. I., Martin, P. S., & Poinar, H. N. (2003). Molecular caving. Current Biology, 13(18), R693-R695.

Hofreiter, M., Siedel, H., van Neer, W., & Vigilant, L. (2003). Mitochondrial DNA sequence from an enigmatic gorilla population (Gorilla gorilla uellensis). American Journal of Physical Anthropology, 121(4), 361-368.

Jänicke-Després, V. R., Buckler, E. S., Smith, B. D., Gilbert, M. T. P., Cooper, A., Doebley, J., & Pääbo, S. (2003). Early allelic selection in maize as revealed by ancient DNA. Science, 302(5648), 1206-1208.

Kaessmann, H. (2003). Human and Chimpanzee Nucleotide Diversity. In David N. Cooper (Ed.), Nature encyclopedia of the human genome: vol. 3 (GEN - MIT) (pp. 293-298). London [et al]: Nature Publishers Group.

Kayser, M. (2003). The human Y-chromosome: introduction into genetics and applications. Forensic Science Review, 15(2), 77-89.

Kayser, M., Brauer, S., & Stoneking, M. (2003). A genome scan to detect candidate regions influenced by local natural selection in human populations. Molecular Biology and Evolution, 20(6), 893-900.

Kayser, M., Brauer, S., Schädlich, H., Prinz, M., Batzer, M. A., Zimmerman, P. A., Boatin, B. A., & Stoneking, M. (2003). Y chromosome STR haplotypes and the genetic structure of U.S. populations of African, European, and Hispanic ancestry. Genome Research, 13, 624-634.

Kayser, M., Brauer, S., Weiss, G., Schiefenhövel, W., Underhill, P. A., Shen, P. D., Oefner, P. J., Tommaseo-Ponzetta, M., & Stoneking, M. (2003). Reduced Y-chromosome, but not mitochondrial DNA, diversity in human populations from West New Guinea. American Journal of Human Genetics, 72(2), 281-302.

Kelso, J., Visagie, J., Theiler, G., Christoffels, A., Bardien, S., Smedley, D., Otgaar, D., Greyling, G., Jongeneel, C. V., McCarthy, M. I., Hide, T., & Hide, W. (2003). eVOC: A controlled vocabulary for unifying gene expression data. Genome Research, 13(6a), 1222-1230.

Kitano, T., Schwarz, C., Nickel, B., & Pääbo, S. (2003). Gene diversity patterns at 10 X-chromosomal loci in humans and chimpanzees. Molecular Biology and Evolution, 20(8), 1281-1289.

Kittler, R., Erler, A., Brauer, S., Stoneking, M., & Kayser, M. (2003). Apparent intra-chromosomal exchange on the human Y chromosome explained by population history. European Journal of Human Genetics, 11, 304-314.

Kittler, R., Kayser, M., & Stoneking, M. (2003). Molecular evolution of Pediculus humanus and the origin of clothing. Current Biology, 13(16), 1414-1417.

Kryukov, G. V., Castellano, S., Novoselov, S. V., Lobanov, A. V., Zehtab, O., Guigó, R., & Gladyshev, V. N. (2003). Characterization of mammalian selenoproteomes. Science, 300(5624), 1439-1443.

Lessig, R., Willuweit, S., Krawczak, M., Wu, F.-C., Pu, C.-E., Kim, W., Henke, L., Henke, J., Miranda, J., Hidding, M., Benecke, M., Schmitt, C., Magno, M., Calacal, G., Delfin, F. C., de Ungria, M. C. A., Elias, S., Augustin, C., Tun, Z., Honda, K., Kayser, M., Gusmao, L., Amorim, A., Alves, C., Hou, Y., Keyser, C., Ludes, B., Klintschar, M., Immel, U. D., Reichenpfader, B., Zaharova, B., & Roewer, L. (2003). Asian online Y-STR Haplotype Reference Database. Legal Medicine, 5(Suppl.1), S160-S163.

Meyer, S., & von Haeseler, A. (2003). Identifying site-specific substitution rates. Molecular Biology and Evolution, 20(2), 182-189.

Motz, M., Sagner, G., Pääbo, S., & Kilger, C. (2003). Sequential DEXAS: A method for obtaining DNA sequences from genomic DNA and blood in one reaction. Nucleic Acids Research, 31(20): e121, pp. 1-8.

Nasidze, I., Sarkisian, T., Kerimov, A., & Stoneking, M. (2003). Testing hypotheses of language replacement in the Caucasus: Evidence from the Y-chromosome. Human Genetics, 112(3), 255-261.

Nasidze, I., Schädlich, H., & Stoneking, M. (2003). Haplotypes from the Caucasus, Turkey and Iran for nine Y-STR loci. Forensic Science International, 137(1), 85-93.

Otte, K., Kranz, H., Kober, I., Thompson, P., Hoefer, M., Haubold, B., Remmel, B., Voss, H., Kaiser, C., Albers, M., Cheruvallath, Z., Jackson, D., Casari, G., Koegl, M., Pääbo, S., Mous, J., Kremoser, C., &

Deuschle, U. (2003). Identification of Farnesoid X Receptor ß as a Novel Mammalian Nuclear Receptor Sensing Lanosterol. Molecular and Cellular Biology, 23(3), 864-872.

Pääbo, S. (2003). The mosaic that is our genome. Nature, 421(6921), 409-412.

Pakendorf, B., Wiebe, V., Tarskaia, L. A., Spitsyn, V. A., Soodyall, H., Rodewald, A., & Stoneking, M. (2003). Mitochondrial DNA evidence for admixed origins of central Siberian populations. American Journal of Physical Anthropology, 120(3), 211-224.

Poinar, H. N., Kuch, M., McDonald, H. G., Martin, P. S., & Pääbo, S. (2003). Nuclear gene sequences from a late Pleistocene sloth coprolite. Current Biology, 13(13), 1150-1152.

Przeworski, M. (2003). Estimating the Time Since the Fixation of a Beneficial Allele. Genetics, 164(4), 1667-1676.

Sharov, A. A., Piao, Y., Matoba, R., Dudekula, D. B., Qian, Y., VanBuren, V., Falco, G., Martin, P. R., Stagg, C. A., Bassey, U. C., Wang, Y., Carter, M. G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T. S., Kimber, W. L., Yoshikawa, T., Jaradat, S. A., Pantano, S., Nagaraja, R., Boheler, K. R., Taub, D., Hodes, R. J., Longo, D. L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A. L., Rossant, J., Kunath, T., Hogan, B. L. M., Curci, A., D'Urso, M., Kelso, J., Hide, W., & Ko, M. S. H. (2003). Transcriptome analysis of mouse stem cells and early embryos. PLoS Biology, 1(3): e74.

Stoneking, M. (2003). Mitochondrial genome: Evolution. In David N. Cooper (Ed.), Nature encyclopedia of the human genome: vol. 3 (GEN - MIT) (pp. 1019-1023). London [et al]: Nature Publishing Group.

Stoneking, M. (2003). Widespread prehistoric human cannibalism: Easier to swallow? Trends in Ecology & Evolution, 18(10), 489-490.

Strimmer, K., & von Haeseler, A. (2003). Nucleotide substitution models. In Marco Salemi and Anne-Mieke Vandamme (Ed.), The Phylogenetic Handbook (pp. 72-87). Cambridge: Cambridge University Press.

von Haeseler, A., & Strimmer, K. (2003). Phylogeny inference based on maximum-likelihood methods with Tree-Puzzle. In Marco Salemi and Anne-Mieke Vandamme (Ed.), The Phylogenetic Handbook (pp. 137-159). Cambridge: Cambridge University Press.

Wandeler, P., Smith, S., Morin, P. A., Pettifor, R. A., & Funk, S. M. (2003). Patterns of nuclear DNA degeneration over time - a case study in historic teeth samples. Molecular Ecology, 12(4), 1087-1093.

Weiss, G., & von Haeseler, A. (2003). Testing substitution models within a phylogenetic tree. Molecular Biology and Evolution, 20(4), 572-578.

Zöllner, S., & von Haeseler, A. (2003). Population History and Linkage Disequilibrium. In David N. Cooper (Ed.), Nature encyclopedia of the human genome: vol. 4 (MIT - REL) (pp. 628-632). London [et al]: Nature Publishing Group.

2002

Chou, H. H., Hayakawa, T., Diaz, S., Krings, M., Indriati, E., Leakey, M., Pääbo, S., Satta, Y., Takahata, N., & Varki, A. (2002). Inactivation of CMP-N-acetylneuraminic acid hydroxylase occurred prior to brain expansion during human evolution. Proceedings of the National Academy of Sciences of the United States of America, 99(18), 11736-11741.

Ebersberger, I., Metzler, D., Schwarz, C., & Pääbo, S. (2002). Genomewide comparison of DNA sequences between humans and chimpanzees. American Journal of Human Genetics, 70(6), 1490-1497.

Enard, W., & Pääbo, S. (2002). Funktionelle Genanalyse im Schimpansen. GenomXPress: Informationen aus der Deutschen Genomforschung, (3), 3-5. Retrieved from http://www.genomxpress.de/seiten/archivdetail-ausgabe-2002-3.php.

Enard, W., Ebersberger, I., Fischer, A., Heißig, F., Hellmann, I., Höffner, B., Khaitovich, P., Kitano, T., Köhler, K., Metzler, D., Nickel, B., Przeworski, M., Schwarz, C., Nowick, K., Wiebe, V., Winkler, M., Zöllner, S., & Pääbo, S.(2002). Functional genomics in the chimpanzee.

Enard, W., Khaitovich, P., Klose, J., Zöllner, S., Heißig, F., Giavalisco, P., Nieselt-Struwe, K., Muchmore, E., Varki, A., Ravid, R., Doxiadis, G. M., Bontrop, R. E., & Pääbo, S. (2002). Intra- and interspecific variation in primate gene expression patterns. Science, 296(5566), 340-343.

Enard, W., Przeworski, M., Fisher, S. E., Lai, C. S. L., Wiebe, V., Kitano, T., Monaco, A. P., & Pääbo, S. (2002). Molecular evolution of FOXP2, a gene involved in speech and language. Nature, 418(6900), 869-872.

Gilad, Y., Rosenberg, S., Przeworski, M., Lancet, D., & Skorecki, K. (2002). Evidence for positive selection and population structure at the human MAO-A gene. Proceedings of the National Academy of Sciences, 99, 862-867.

Hofreiter, M. (2002). Genetic stability and replacement in the late Pleistocene cave bear populations. In Verband der Deutschen Höhlen- und Karstforscher, & W. Rosendahl (Eds.), Cave-Bear-Researches / Höhlen-Bären-Forschungen. - (Abhandlungen zur Karst- und Höhlenkunde; 34) (pp. 64-67). München: Verb. der Dt. Höhlen- und Karstforscher.

Hofreiter, M., Capelli, C., Krings, M., Waits, L., Conard, N. J., Munzel, S., Rabeder, G., Nagel, D., Paunovic, M., Jambresic, G., Meyer, S., Weiss, G., & Pääbo, S. (2002). Ancient DNA analyses reveal high mitochondrial DNA sequence diversity and parallel morphological evolution of late pleistocene cave bears. Molecular Biology and Evolution, 19(8), 1244-1250.

Kaessmann, H., & Pääbo, S. (2002). The genetical history of humans and the great apes. Journal of Internal Medicine, 251(1), 1-18.

Kaessmann, H., Zöllner, S., Gustafsson, A. C., Wiebe, V., Laan, M., Lundeberg, J., Uhlen, M., & Pääbo, S. (2002). Extensive linkage disequilibrium in small human populations in Eurasia. American Journal of Human Genetics, 70(3), 673-685.

Kayser, M., Brauer, S., Willuweit, S., Schädlich, H., Batzer, M. A., Zawacki, J., Prinz, M., Roewer, L., & Stoneking, M. (2002). Online Y-chromosomal short tandem repeat haplotype reference database (YHRD) for US populations. Journal of Forensic Sciences, 47(3), 513-519.

Kelso, J. (2002). Transcript reconstruction and analysis using STACKdb and stackPACK. EMBnet.news, 8(1), 8-11. Retrieved from http://journal.embnet.org/index.php/embnetnews/article/view/106/132.

Kittler, R., Stoneking, M., & Kayser, M. (2002). A whole genome amplification method to generate long fragments from low quantities of genomic DNA. Analytical Biochemistry, 300(2), 237-244.

Kuch, M., Rohland, N., Betancourt, J. L., Latorre, C., Steppan, S., & Poinar, H. N. (2002). Molecular analysis of a 11 700-year-old rodent midden from the Atacama Desert, Chile. Molecular Ecology, 11(5), 913-924.

Liebers, D., & Helbig, A. J. (2002). Phylogeography and colonization history of Lesser Black-backed Gulls (Larus fuscus) as revealed by mtDNA sequences. Journal of Evolutionary Biology, 15(6), 1021-1033.

Mattiangeli, V., Galvin, P., Ryan, A. W., Mork, J., & Cross, T. F. (2002). VNTR variability in Atlantic poor cod (Trisopterus minutus minutus) throughout its range: single locus minisatellite data suggest reproductive

isolation for the Faroe Bank population. Fisheries Research, 58(2), 185-191.

Nasidze, I., & Stoneking, M. (2002). Genetic variation among human populations from the Caucasus. In Shumny, V. K.; Kolchanov, N. A.; Fedotov, A. M. (Ed.), The First Workshop on Information Techologies Application to Problems of Biodiversity and Dynamics (pp. 272-278). Novosibirsk, Russia: Russian Academy od Sciences.

Nembaware, V., Crum, K., Kelso, J., & Seoighe, C. (2002). Impact of the presence of paralogs on sequence divergence in a set of mouse-human orthologs. Genome Research, 12(9), 1370-1376.

Oota, H., Kitano, T., Jin, F., Yuasa, I., Wang, L., Ueda, S., Saitou, N., & Stoneking, M. (2002). Extreme mtDNA homogeneity in continental Asian populations. American Journal of Physical Anthropology, 118(2), 146-153.

Pääbo, S. (2002). Die Wurzeln der Menschheit - die Evolution des humanen Genoms. In M. Lessl, & G. Stock (Eds.), Die Architektur des Lebens - über Gene, Organismen und Personen: Symposium anlässlich des 10-jährigen Bestehens der Schering-Forschungsgesellschaft, November 2001 (pp. 39-72). Berlin: Springer.

Pakendorf, B., Morar, B., Tarskaia, L. A., Kayser, M., Soodyall, H., Rodewald, A., & Stoneking, M. (2002). Y-chromosomal evidence for a strong reduction in male population size of Yakuts. Human Genetics, 110(2), 198-200.

Partecke, J., von Haeseler, A., & Partecke, M. (2002). Territory establishment in lekking marine iguanas, Amblyrhynchus cristatus: support for the hotshot mechanism. Behavioral Ecology and Sociobiology, 51(6), 579-587.

Ploski, R., Wozniak, M., Pawlowski, R., Monies, D. M., Branicki, W., Kupiec, T., Kloosterman, A., Dobosz, T., Bosch, E., Nowak, M., Lessig, R., Jobling, M. A., Roewer, L., & Kayser, M. (2002). Homogeneity and distinctiveness of Polish paternal lineages revealed by Y chromosome microsatellite haplotype analysis. Human Genetics, 110(6), 592-600.

Poinar, H. N. (2002). DNA chemical instability. In eLS (Encyclopedia of Life Sciences). Wiley.

Poinar, H. N. (2002). The genetic secrets some fossils hold. Accounts of Chemical Research, 35(8), 676-684.

Presser, J., Deverell, A., Redd, A., & Stoneking, M. (2002). Tasmanian aborigines and DNA. Papers and Proceedings of the the Royal Society of Tasmania, 136, 35-38.

Przeworski, M. (2002). The signature of positive selection at randomly chosen loci. Genetics, 160(3), 1179-1189.

Ptak, S. E., & Petrov, D. A. (2002). How intron splicing affects the deletion and insertion profile in Drosophila melanogaster. Genetics, 162(3), 1233-1244.

Ptak, S. E., & Przeworski, M. (2002). Evidence for population growth in humans is confounded by fine-scale population structure. Trends in Genetics, 18(11), 559-563.

Rabeder, G., Hofreiter, M., Nagel, D., Pääbo, S., & Withalm, G. (2002). Die neue Taxonomy der Höhlenbären. In W. Rosendahl, M. Morgan, & M. Correa (Eds.), Cave Bear Researches (pp. 68-69). München: Verband der Dt. Höhlen- und Karstforscher.

Romualdi, C., Balding, D., Nasidze, I., Risch, G. M., Robichaux, M., Sherry, S. T., Stoneking, M., Batzer, M. A., & Barbujani, G. (2002). Patterns of human diversity, within and among continents, inferred from biallelic DNA polymorphisms. Genome Research, 12(4), 602-612.

Schmidt, H. A., Strimmer, K., Vingron, M., & von Haeseler, A. (2002). TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. Bioinformatics, 18(3), 502-504.

Schmitz, R. W., Serre, D., Bonani, G., Feine, S., Hillgruber, F., Krainitzki, H., Pääbo, S., & Smith, F. H. (2002). The Neandertal type site revisited: Interdisciplinary investigations of skeletal remains from the Neander Valley, Germany. Proceedings of the National Academy of Sciences of the United States of America, 99(20), 13342-13347.

Schurer, H., Lang, K., Schuster, J., & Mörl, M. (2002). A universal method to produce in vitro transcripts with homogeneous 3 ' ends. Nucleic Acids Research, 30(12): e56.

Smith, S., Vigilant, L., & Morin, P. A. (2002). The effects of sequence length and oligonucleotide mismatches on 5 ' exonuclease assay efficiency. Nucleic Acids Research, 30(20): e111.

VanBuren, V., Piao, Y., Dudekula, D. B., Qian, Y., Carter, M. G., Martin, P. R., Stagg, C. A., Bassey, U. C., Aiba, K., Hamatani, T., Kargul, G. J., Luo, A. G., Kelso, J., Hide, W., & Ko, M. S. (2002). Assembly, verification, and initial annotation of the NIA mouse 7.4K cDNA clone set. Genome Research, 12(12), 1999-2003.

Wall, J. D., Andolfatto, P., & Przeworski, M. (2002). Testing models of selection and demography in Drosophila simulans. Genetics, 162, 203-216.

2001

Andolfatto, P., & Przeworski, M. (2001). Regions of lower recombination harbor more rare variants in African populations of Drosophila melanogaster. Genetics, 158, 657-665.

Begovich, A. B., Moonsamy, P. V., Mack, S. J., Barcellos, L. F., Steiner, L. L., Grams, S., Suraj-Baker, V., Hollenbach, J., Trachtenberg, E., Louie, L., Zimmerman, P. A., Hill, A. V. S., Stoneking, M., Sasazuki, T., Konenkov, V. I., Sartakova, M. L., Titanji, V. P. K., Rickards, O., & Klitz, W. (2001). Genetic variability and linkage disequilibrium within the DP region: Analysis of 15 different populations. Tissue Antigens, 57(5), 424-439.

Castellano, S., Morozova, N., Morey, M., Berry, M. J., Serras, F., Corominas, M., & Guigó, R. (2001). In silico identification of novel selenoproteins in the Drosophila melanogaster genome. EMBO Reports, 2(8), 697-702.

Donnelly, P., Foley, R., Stoneking, M., Deininger, P. L., & Batzer, M. A. (2001). Alu insertion polymorphisms in humans: A review. In Genes, Fossils and Behaviour (pp. 111-121). Amsterdam: IOS Press.

Dörner, M., Altmann, M., Pääbo, S., & Mörl, M. (2001). Evidence for import of a lysyl-tRNA into marsupial mitochondria. Molecular Biology of the Cell, 12(9), 2688-2698.

Enard, W. (2001). Anmerkungen zum aktuellen Stand der Humangenetik. In B. Kleeberg (Ed.), Die List der Gene (pp. 15-19). Tübingen: Narr.

Enard, W. (2001). Evolution des menschlichen Transkriptoms. In Max-Planck-Gesellschaft: Jahrbuch 2001 (pp. 707-711). München: Max-Planck-Gesellschaft.

Gagneux, P., Gonder, M. K., Goldberg, T. L., & Morin, P. A. (2001). Gene flow in wild chimpanzee populations: what genetic data tell us about chimpanzee movement over space and time. Philosophical Transactions of the Royal Society of London B, 356, 889-896.

Gill, P., Brenner, C., Brinkmann, B., Budowle, B., Carracedo, A., Jobling, M. A., de Knijff, P., Kayser, M., Krawczak, M., Mayr, W. R., Morling, N., Olaisen, B., Pascali, V., Prinz, M., Roewer, L., Schneider, P. M.,

Sajantila, A., & Tyler-Smith, C. (2001). DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y- chromosome STRs. Forensic Science International, 124(1), 5-10.

Gill, P., Brenner, C., Brinkmann, B., Budowle, B., Mayr, E., Jobling, M. A., de Knijff, P., Kayser, M., Krawczak, M., Morling, N., Olaisen, B., Pascali, V., Prinz, M., Roewer, L., Schneider, P. M., Sajantila, A., & Tyler-Smith, C. (2001). International Society of Forensic Genetics recommendations on forensic analysis using Y-chromosome STRs. International Journal of Legal Medicine, 114, 305-309.

Greenwood, A. D., Castresana, J., Feldmaier-Fuchs, G., & Pääbo, S. (2001). A molecular phylogeny of two extinct sloths. Molecular Phylogenetics and Evolution, 18(1), 94-103.

Henke, J., Henke, L., Chatthopadhyay, P. K., Kayser, M., Dülmer, M., Cleef, S., Pöche, H., & Felske-Zech, H. (2001). Application of Y-chromosomal STR haplotypes to Forensic Genetics. Croatian Medical Journal, 42, 292-297.

Hide, W. A., Babenko, V. N., van Heusden, P. A., Seoighe, C., & Kelso, J. (2001). The contribution of exon-skipping events on chromosome 22 to protein coding diversity. Genome Research, 11(11), 1848-1853.

Hide, W., Mizrahi, V., Venkatesh, B., Brenner, S., Simpson, A., Blatch, G., Soodyall, H., Denby, K., Wingfield, M., Wingfield, B., van Helden, P., Ramesar, R., Dorrington, R., Kelso, J., Oppon, E., Goyvaerts, E., Ramsay, M., de Villiers, E., van Heerden, C., Allsopp, B., & Seoighe, C. (2001). A platform for genomics in South Africa. South African Medical Journal, 91(12), 1006-1007. Retrieved from http://archive.samj.org.za/2001%20VOL%2091%20Jan-Dec/Articles/12%20December/1.1%20LETTERS.pdf.

Hofreiter, M. (2001). Analyse alter DNA. Höhlenbärspuren, 5.

Hofreiter, M., Jänicke, V. R., Serre, D., Haeseler, A. v., & Pääbo, S. (2001). DNA sequences from multiple amplifications reveal artifacts induced by cytosine deamination in ancient DNA. Nucleic Acids Research, 29(23), 4793-4799.

Hofreiter, M., Serre, D., Poinar, H. N., Kuch, M., & Pääbo, S. (2001). Ancient DNA. Nature Reviews Genetics, 2, 353-359.

Justice, C. M., Den, Z., Nguyen, S. V., Stoneking, M., Deininger, P. L., Batzer, M. A., & Keats, B. J. B. (2001). Phylogenetic analysis of the Friedreich ataxia GAA trinucleotide repeat. Journal of Molecular Evolution, 52(3), 232-238.

Kaessmann, H., Wiebe, V., Weiss, G., & Pääbo, S. (2001). Great ape DNA sequences reveal a reduced diversity and an expansion in humans. Nature Genetics, 27, 155-156.

Kayser, M., & Sajantila, A. (2001). Mutations at Y-STR loci: implications for paternity testing and forensic analysis. Forensic Science International, 118, 116-121.

Kayser, M., Brauer, S., Weiss, G., Schiefenhövel, W., Underhill, P. A., & Stoneking, M. (2001). Independent histories of human Y chromosomes from Melanesia and Australia. American Journal of Human Genetics, 68(1), 173-190.

Kayser, M., Krawczak, M., Excoffier, L., Dieltjes, P., Corach, D., Cagliá, A., Gehrig, C., Bernini, L. F., Jespersen, J., Bakker, E., Roewer, L., & de Knijff, P. (2001). Extensive analysis of chromosome Y microsatellite haplotypes in globally dispersed human populations. American Journal of Human Genetics, 68, 990-1018.

Koller, D. L., Liu, G., Econs, M. J., Hui, S. L., Morin, P. A., Joslyn, G., Rodriguez, L. A., Conneally, P. M.,

Christian, J. C., Johnston Jr., C. C., Foroud, T., & Peacock, M. (2001). Genome screen for quantitative trait loci underlying normal variation in femoral structure. Journal of Bone and Mineral Research, 16, 985-991.

Liebers, D., Helbig, A. J., & de Knijff, P. (2001). Genetic differentiation and phylogeography of gulls in the Larus cachinnans-fuscus group (Aves: Charadriiformes). Molecular Ecology, 10, 2447-2462.

Martin, L. J., Blangero, J., Rogers, J., Mahaney, M. C., Hixson, J. E., Carey, K. D., Morin, P. A., & Comuzzie, A. G. (2001). A quantitative trait locus influencing estrogen levels maps to a region homologous to human chromosome 20. Physiological Genomics, 5, 75-80.

Melton, T., Clifford, S., Kayser, M., Nasidze, I., Batzer, M. A., & Stoneking, M. (2001). Diversity and heterogeneity in mitochondrial DNA of North American populations. Journal of Forensic Sciences, 46(1), 46-52.

Metzler, D., Fleissner, R., Wakolbinger, A., & Haeseler, A. v. (2001). Assessing variability by joint sampling of alignments and mutation rates. Journal of Molecular Evolution, 53, 660-669.

Morin, P. A., Chambers, K. E., Boesch, C., & Vigilant, L. (2001). Quantitative polymerase chain reaction analysis of DNA from noninvasive samples for accurate microsatellite genotyping of wild chimpanzees (Pan troglodytes verus). Molecular Ecology, 10(7), 1835-1844.

Mörl, M., & Marchfelder, A. (2001). The final cut: The importance of tRNA 3'- processing. EMBO Reports, 2, 17-20.

Mühlen, D. G. v., Barrett-Connor, E., Schneider, D. L., Morin, P. A., & Parry, P. (2001). Osteoporosis and apolipoprotein E genotype in older adults: The Rancho Bernardo study. Osteoporosis International, 12, 332-335.

Nasidze, I., & Stoneking, M. (2001). Mitochondrial DNA variation and language replacements in the Caucasus. Proceedings of the Royal Society of London B, 268(1472), 1197-1206.

Nasidze, I., Risch, G. M., Robichaux, M., Sherry, S. T., Batzer, M. A., & Stoneking, M. (2001). Alu insertion polymorphisms and the genetic structure of human populations from the Caucasus. European Journal of Human Genetics, 9, 267-272.

Nieselt-Struwe, K., & Haeseler, A. v. (2001). Quartet mapping, a generalization of the likelihood mapping procedure. Molecular Biology and Evolution, 18, 1204-1219.

Oota, H., Settheetham-Ishida, W., Tiwawech, D., Ishida, T., & Stoneking, M. (2001). Human mtDNA and Y-chromosome variation is correlated with matrilocal vs. patrilocal residence. Nature Genetics, 29, 20-21.

Pääbo, S. (2001). The human genome and our view of ourselves. Science, 291(5507), 1219-1220.

Poinar, H. N., & Pääbo, S. (Eds.). (2001). DNA. In D. E. G. Briggs, & P. R. Crowther (Eds.), Palaeobiology II (pp. 241-245). Oxford: Blackwell Science.

Poinar, H. N., Kuch, M., & Pääbo, S. (2001). Molecular analyses of oral polio vaccine samples. Science, 292(5517), 743-744.

Poinar, H. N., Kuch, M., Sobolik, K. D., Barnes, I., Stankiewicz, A. B., Kuder, T., Spaulding, W. G., Bryant, V. M., Cooper, A., & Pääbo, S. (2001). A molecular analysis of dietary diversity for three archaic Native Americans. Proceedings of the National Academy of Sciences USA, 98(8), 4317-4322.

Pritchard, J. K., & Przeworski, M. (2001). Linkage Disequlibrium in Humans: Models and Data. American Journal of Human Genetics, 69, 1-14.

Przeworski, M., & Wall, J. D. (2001). Why is there so little intragenic linkage disequlibrium in humans?

Genetical Research, 77, 143-151.

Przeworski, M., Wall, J. D., & Andolfatto, P. (2001). Recombination and the frequency spectrum in Drosophila melanogaster and D. simulans. Molecular Biology and Evolution, 18, 291-298.

Reichert, A. S., Thurlow, D. L., & Mörl, M. (2001). A eubacterial origin for the human tRNA nucleotidyltransferase? Biological Chemistry, 382, 1431-1438.

Roewer, L., Krawczak, M., Willuweit, S., Nagy, M., Alves, C., Amorim, A., Anslinger, K., Augustin, C., Betz, A., Bosch, E., Cagliá, A., Carracedo, A., Corach, D., Dobosz, T., Dupuy, B. M., Furedi, S., Gehrig, C., Gusmao, L., Henke, J., Henke, L., Hidding, M., Hohoff, C., Hoste, B., Jobling, M. A., Kargel, H. J., de Knijff, P., Lessig, R., Liebherr, E., Lorente, M., Martinez-Jarreta, B., Nievas, P., Nowak, M., Parson, W., Pascali, V., Penacino, G., Ploski, R., Rolf, B., Salas, A., Schmidt, U., Schmitt, C., Schneider, P. M., Szibor, R., Teifel-Greding, J., & Kayser, M. (2001). Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. Forensic Science International, 118, 106-113.

Schürer, H., Schiffer, S., Marchfelder, A., & Mörl, M. (2001). This is the end: Processing, editing and repair at the tRNA 3'- Terminus. Biological Chemistry, 382, 1147-1156.

Stone, A. C., Starrs, J. E., & Stoneking, M. (2001). Mitochondrial DNA analysis of the presumptive remains of Jesse James. Journal of Forensic Sciences, 46(1), 173-176.

Stoneking, M. (2001). Single nucleotide polymorphisms: From the evolutionary past.. Nature, 409, 821-822.

Straube, A., Enard, W., Berner, A., Wedlich-Söldner, R., Kahmann, R., & Steinberg, G. (2001). A split motor domain in a cytoplasmic dynein. EMBO Journal, 20, 5091-5100.

Straube, A., Enard, W., Berner, A., Wedlich-Söldner, R., Kahmann, R., & Steinberg, G. (2001). A split motor domain in a cytoplasmic dynein. Molecular Biology of the Cell, 12(Suppl. S), 1714.

Tishkoff, S. A., Varkonyi, R., Cahinhinan, N., Abbes, S., Argyropoulos, G., Destro-Bisol, G., Drousiotou, A., Dangerfield, B., Lefranc, G., Loiselet, J., Piro, A., Stoneking, M., Tagarelli, A., Tagarelli, G., Touma, E. H., Williams, S. M., & Clark, A. G. (2001). Haplotype diversity and linkage disequilibrium at human G6PD recent origin of alleles that confer malarial resistance. Science, 293(5529), 455-462.

Vigilant, L., Hofreiter, M., Siedel, H., & Boesch, C. (2001). Paternity and relatedness in wild chimpanzee communities. Proceedings of the National Academy of Sciences USA, 98(23), 12890-12895.

Zhang, Y., Morin, P. A., Ryder, O. A., & Zhang, Y. (2001). A set of human tri- and tetra-nucleotide microsatellite loci useful for population analyses in gorillas (Gorilla gorilla gorilla) and orangutans (Pongo pygmaeus). Conservation Genetics, 2, 391-395.

Ziv, E., Cauley, J., Morin, P. A., Saiz, R., & Browner, W. S. (2001). Association between the T 29->C polymorphism in the transforming growth factor beta1 gene and breast cancer among elderly white women. Journal of the American Medical Association, 285, 2859-2863.

2000

Begovich, A. B., Klitz, W., Steiner, L. L., Grams, S., Suraj-Baker, V., Hollenbach, J., Trachtenberg, E., Louie, L., Zimmerman, P. A., Hill, A. V. S., Stoneking, M., Sasazuki, T., Rickards, O., Titanji, V. P. K., Konenkov, V. I., & Sartakova, M. L. (2000). HLA-DQ haplotypes in 15 different populations. In M. Kasahara (Ed.), The Major Histocompatibility Complex: Evolution, Structure and Function (pp. 412-426). Tokyo: Springer.

Börner, G. V., Zeviani, M., Tiranti, V., Carrara, F., Hoffmann, S., Gerbitz, K. D., Lochmüller, H., Klopstock, T., Pongratz, D., Melberg, A., Holme, E., & Pääbo, S. (2000). Decreased aminoacylation of mutant tRNAs in MELAS but not in MERRF patients. Human Molecular Genetics, 9(4), 467-475.

Clark, V. J., Sivendren, S., Saha, N., Bentley, G. R., Aunger, R., Sirajuddin, S. M., & Stoneking, M. (2000). The 9-bp deletion between the mitochondrial lysine tRNA and COII genes in tribal populations of India. Human Biology, 72(2), 273-285.

Comas, D., Calafell, F., Benchemsi, N., Helal, A., Lefranc, G., Stoneking, M., Batzer, M. A., Bertranpetit, J., & Sajantila, A. (2000). Alu insertion polymorphisms in Northwest Africa and the Iberian Peninsula: Evidence for a strong genetic boundary through the Gibraltar Straits. Human Genetics, 107(4), 312-319.

Cooper, A., & Poinar, H. N. (2000). Ancient DNA: Do it right or Not at all. Science, 289.

Di Benedetto, G., Nasidze, I., Stenico, M., Nigro, L., Krings, M., Lanzinger, M., Vigilant, L., Stoneking, M., Pääbo, S., & Barbujani, G. (2000). Mitochondrial DNA sequences in prehistoric human remains from the Alps. European Journal of Human Genetics, 8(9), 669-677.

Eppart, M., Krumbein, W. E., Haeseler, A. v., & Rhiel, E. (2000). Characterization and phylogeny of light-harvesting proteins of Cyclotella cryptica, Bacillariophyllae. Plant Biology, 49, 283-289.

Erlandsson, R., Wilson, J. F., & Pääbo, S. (2000). Sex chromosomal transposable element accumulation and male-driven substitutional evolution in humans. Molecular Biology and Evolution, 17(5), 804-812.

Fleissner, R., Metzler, D., & Haeseler, A. v. (2000). Can one estimate distances from pairwise alignment? In E. Bornberg-Bauer (Ed.), Proceedings of the German Conference on Bioinformatics (pp. 89-95). Berlin: Logos Verlag Berlin.

Grassly, N. C., Haeseler, A. v., & Krakauer, D. (2000). Error, population structure and the origin of diverse sign systems. Journal of Theoretical Biology, 206, 369-378.

Haeseler, A. v. (2000). Maximum likelihood tree reconstruction. Zoology - Analysis of Complex Systems, 102, 101-110.

Hofreiter, M., Poinar, H. N., Spaulding, W. G., Bauer, K., Martin, P. S., Possnert, G., & Pääbo, S. (2000). A molecular analysis of ground sloth diet through the last glaciation. Molecular Ecology, 9(12), 1975-1984.

Ingman, M., Kaessmann, H., Pääbo, S., & Gyllenstein, U. (2000). Mitochondrial genome variation and the origin of modern humans. Nature, 408, 708-713.

Kayser, M., Brauer, S., Weiss, G., Underhill, P. A., Roewer, L., Schiefenhövel, W., & Stoneking, M. (2000). Melanesian origin of Polynesian Y chromosomes. Current Biology, 10, 1237-1246.

Kayser, M., Roewer, L., Hedman, M., Henke, L., Henke, J., Brauer, S., Kruger, C., Krawczak, M., Nagy, M., Dobosz, T., Szibor, R., de Knijff, P., Stoneking, M., & Sajantila, A. (2000). Characteristics and frequency of germline mutations at microsatellite loci from the human Y chromosome revealed by direct observation in father/son pairs. American Journal of Human Genetics, 66(5), 1580-1588.

Krings, M., Capelli, C., Tschentscher, F., Geisert, H., Meyer, S., Haeseler, A. v., Grossschmidt, K., Possnert, G., Paunovic, M., & Pääbo, S. (2000). A view of Neandertal genetic diversity. Nature Genetics, 26, 144-146.

Kumar, S., Hedrick, P. W., Dowling, T., & Stoneking, M. (2000). Questioning evidence for recombination in human mitochondrial DNA. Science, 288(5473), 1931.

Kumar, S., Nasidze, I., Walimbe, S. R., & Stoneking, M. (2000). Brief communication: Discouraging

prospects for ancient DNA from India. American Journal of Physical Anthropology, 113(1), 129-133.

Mack, S. J., Bugawan, T. L., Moonsamy, P. V., Erlich, J. A., Trachtenberg, E., Paik, Y. K., Begovich, A. B., Saha, N., Beck, H. P., Stoneking, M., & Erlich, H. A. (2000). Evolution of Pacific/Asian populations inferred from HLA class II allele frequency distributions. Tissue Antigens, 55(5), 383-400.

Morin, P. A. (2000). Genetic resources: Opportunities and perspectives for the new century. Conservation Genetics, 1(3), 271-275.

Morin, P. A. (2000). Preservation of DNA from endangered species (letter). Science, 289, 725-726.

Motz, M., Pääbo, S., & Kilger, C. (2000). Improved cycle sequencing of GC-rich templates by a combination of nucleotide analogs. BioTechniques, 29(2), 268-270.

Olaisen, B., Roewer, L., Kayser, M., Anslinger, K., Augustin, C., Cagliá, A., Corach, D., Füredi, S., Geserick, G., Henke, L., Hidding, M., Kärgel, H. P., de Knijff, P., Lessing, R., Pascali, V., Parson, W., Prinz, M., Rolf, B., Schneider, P. M., Szibor, R., Teifel-Greding, J., & Krawczak, M. (2000). Caucasian Y-STR haplotype reference database for forensic application. In G. F. Sensabaugh; P. J. Linoln (Ed.), Progress in Forensic Genetics, Vol. 8 (pp. 613-615). Amsterdam: Elsevier Science.

Pääbo, S. (2000). Gene, Sprache und die Besiedelung des europäischen Nordens Europas - Zum Ursprung von Populationen aus molekulargenetischer Sicht. In Max-Planck-Gesellschaft (Ed.), Wie entstehen neue Qualitäten in komplexen Systemen? 50 Jahre Max-Planck-Gesellschaft 1948-1998. Dokumentation des Symposiums zum 50jährigen Gründungsjubiläum der Max-Planck-Gesellschaft am 18. Dezember 1998 in Berlin (pp. 49-56). Göttingen: Vandenhoeck & Ruprecht.

Pääbo, S. (2000). Of bears, conservation genetics, and the value of time travel (Commentary). Proceedings of the National Academy of Sciences USA, 97(4), 1320-1321.

Poinar, H. N. (2000). Preservation of DNA in the fossil record (Zugl.: München, Univ., Diss., 1999). Leipzig: Wodtke und Stegbauer.

Reichert, A. S., & Mörl, M. (2000). Repair of tRNAs in metazoan mitochondria. Nucleic Acids Research, 28, 2043-2048.

Roewer, L., Kayser, M., de Knijff, P., Anslinger, K., Corach, D., Füredi, S., Geserick, G., Henke, L., Hidding, M., Kärgel, H. J., Lessig, R., Nagy, M., Pascali, V., Parson, W., Rolf, B., Schmitt, C., Szibor, R., Teifel-Greding, J., & Krawczak, M. (2000). A new method for the evaluation of matches in non-recombining genomes: application to Y-chromosomal short tandem repeat (STR) haplotypes in European males. Forensic Science International, 114, 31-43.

Rogers, J., Mahaney, M. C., Witte, S. M., Nair, S., Newman, D., Wedel, S., Rodriguez, L. A., Rice, K. S., Slifer, S. H., Perelygin, A., Slifer, M., Palladino-Negro, P., Newman, T., Chambers, K. E., Joslyn, G., Parry, P., & Morin, P. A. (2000). A Genetic Linkage Map of the Baboon (Papio hamadryas) Genome Based on Human Microsatellite Polymorphisms. Genomics, 67(3), 237-247.

Rosser, Z. H., Zerjal, T., Hurles, M. E., Adojaan, M., Alavantic, D., Amorim, A., Amos, W., Armenteros, M., Arroyo, E., Barbujani, G., Beckamnn, L., Bertranpetit, J., Bosch, E., Bradley, D. G., Brede, G., Cooper, G. C., Corte-Real, H. B. S. M., de Knijff, P., Decorte, R., Dubrova, Y. E., Evgrafov, O., Gilissen, A., Glisic, S., Gölge, M., Hill, E. W., Jeziorowska, A., Kalaydjieva, L., Kayser, M., Kravchenko, S. A., Lavinha, J., Livshits, L. A., Maria, S., McElreavy, K., Meitinger, T. A., Melegh, B., Mitchell, R. J., Nicholson, J., Norby, S., Noveletto, A., Pandya, A., Parik, J., Patsalis, P. C., Pereira, L., Peterlin, B., Pielberg, G., Prata, M. J., Previdere, C., Rajczy, K., Roewer, L., Rootsi, S., Rubinsztein, D. C., Saillard, J., Santos, F. R., Shlumukova, M., Stefanescu, G., Sykes, B. C., Tolun, A., Villems, R., Tyler-Smith, C., & Jobling, M. A. (2000). Y-chromosomal diversity within Europe is clinal and influenced primarily by geography, rather than

by language. American Journal of Human Genetics, 67, 1526-1543.

Saas, J., Ziegelbauer, K., Haeseler, A. v., Fast, B., & Boshart, M. (2000). A developmentally regulated aconitase related to iron-regulatory protein 1 is localized in the cytoplasm and in the mitochondrion of Trypanosoma brucei. Journal of Biological Chemistry, 275, 2745-2755.

Santos, F. R., Pandya, A., Kayser, M., Mitchell, R. J., Liu, A., Singh, L., Destro-Bisol, G., Novelletto, A., Qamar, R., Mehdi, S. Q., Adhikari, R., de Knijff, P., & Tyler-Smith, C. (2000). A polymorphic L1 retroposon insertion in the centromere of the human Y chromosome. Human Molecular Genetics, 9, 421-430.

Sheen, F., Sherry, S. T., Risch, G. M., Robichaux, M., Nasidze, I., Stoneking, M., Batzer, M. A., & Swergold, G. D. (2000). Reading between the LINEs: Human genomic variation induced by LINE-1 retrotransposition. Genome Research, 10(10), 1496-1508.

Stoneking, M. (2000). Hypervariable sites in the mtDNA control region are mutational hotspots. American Journal of Human Genetics, 67(4), 1029-1032.

Szibor, R., Kayser, M., & Roewer, L. (2000). Identification of the human Y-chromosomal microsatellite locus DYS 19 from degraded DNA. American Journal of Forensic Medicine and Pathology, 21, 252-254.

Tishkoff, S. A., Pakstis, A. J., Stoneking, M., Kidd, J. R., Destro-Bisol, G., Sajantila, A., Deinard, A. S., Sirugo, G., Jenkins, T., Kidd, K. K., & Clark, A. G. (2000). Short tandem-repeat polymorphism/Alu haplotype variation at the PLAT locus: Implications for modern human origins. American Journal of Human Genetics, 67(4), 901-925.

Weiss, G. (2000). Maximum likelihood estimation of genetic diversity. In C. Renfrew, & K. Boyle (Eds.), Archaeogenetics: DNA and the population prehistory of Europe (pp. 279-283). Cambridge: McDonald Institute Monographs University of Cambridge.

Zöllner, S., & Haeseler, A. v. (2000). A coalescent approach to study linkage disequilibrium between between SNPs. American Journal of Human Genetics, 66, 615-628.

1999

Baake, E., & Haeseler, A. v. (1999). Distance Measures in Terms of Substitution Processes. Theoretical Population Biology, 55(2), 166-175.

Bugawan, T. L., Mack, S. J., Stoneking, M., Saha, N., Beck, H. P., & Erlich, H. A. (1999). HLA class I allele distributions in six Pacific/Asian populations: evidence of selection at the HLA-A locus. Tissue Antigens, 53, 311-319.

Burckhardt, F., von Haeseler, A., & Meyer, S. (1999). HvrBase: compilation of mtDNA control region sequences from primates. Nucleic Acids Research, 27(1), 138-142.

Deininger, P. L., Sherry, S. T., Risch, G. M., Donaldson, C., Robichaux, M., Soodyall, H., Jenkins, T., Sheen, S., Swergold, G. D., Stoneking, M., & Batzer, M. A. (1999). Interspersed repeat insertion polymorphisms for studies of human molecular anthropology. In Surinder S. Papiha, Ranjan Deka, and Ranajit Chakraborty (Ed.), Genomic diversity: applications in human population genetics (pp. 201-212). New York: Kluwer Academic/Plenum Publishers.

Fujino, T., Nararatnam, A., Jamuz, A., Haeseler, A. v., & Scott, J. (1999). C-->U editing of apolipoprotein B mRNA in marsupials: Identification and characterisation of APOBEC-1 from the American opossum Monodelphus domestica. Nucleic Acids Research, 27(13), 2662-2671.

Gagneux, P., Wills, C., Gerloff, U., Tautz, D., Morin, P. A., Boesch, C., Fruth, B., Hohmann, G., Ryder, O.

A., & Woodruff, D. (1999). Mitochondrial sequences show diverse evolutionary histories of African hominids. Proceedings of the National Academy of Sciences USA, 96(9), 5077-5082.

Greenwood, A. D., & Pääbo, S. (1999). Nuclear insertion sequences of mitochondrial DNA predominate in hair but not in blood of elephants. Molecular Ecology, 8(1), 133-137.

Greenwood, A. D., Capelli, C., Possnert, G., & Pääbo, S. (1999). Nuclear DNA sequences from late Pleistocene megafauna. Molecular Biology and Evolution, 16(11), 1466-1473.

Haeseler, A. v. (1999). Der Zufall in der Biologie: molekulare Evolutionstheorie. In Deutsche Akademie der Naturforscher Leopoldina, Halle (Saale) (Ed.), Der Zufall: Leopoldina-Meeting vom 17. bis 18. April 1998 in Halle (Saale) (pp. 79-90). Heidelberg: Barth.

Haeseler, A. v. (1999). Model based phylogenetic inference. In L. Lovasz (Ed.), Graph Theory and Combinatorial Biology: (International Colloquium on Combinatorics and Graph Theory, Balatonlelle, July 1996) (pp. 307-322). Budapest: János Bolyai Math. Soc.

Kaessmann, H., Heißig, F., Haeseler, A. v., & Pääbo, S. (1999). DNA sequence variation in a non-coding region of low recombination on the human X chromosome. Nature Genetics, 22(1), 78-81.

Kaessmann, H., Wiebe, V., & Pääbo, S. (1999). Extensive nuclear DNA sequence diversity among chimpanzees. Science, 286(5442), 1159-1162.

Krings, M., Geisert, H., Schmitz, R. W., Krainitzki, H., & Pääbo, S. (1999). DNA sequence of the mitochondrial hypervariable region II from the Neandertal type specimen. Proceedings of the National Academy of Sciences of the United States of America, 96(10), 5581-5585.

Krings, M., Salem, A.-e.-H., Bauer, K., Geisert, H., Malek, A. K., Chaix, L., Simon, C., Welsby, D., Di Rienzo, A., Utermann, G., Sajantila, A., Pääbo, S., & Stoneking, M. (1999). mtDNA analysis of Nile River Valley populations: A genetic corridor or a barrier to migration? American Journal of Human Genetics, 64(4), 1166-1176.

Meyer, S., Weiss, G., & von Haeseler, A. (1999). Pattern of Nucleotide Substitution and Rate Heterogeneity in the Hypervariable Regions I and II of Human mtDNA. Genetics, 152(3), 1103-1110. Retrieved from http://www.genetics.org/content/152/3/1103.abstract.

Nasidze, I., & Stoneking, M. (1999). Construction of larger-size sequencing templates from degraded DNA. BioTechniques, 27, 480-488.

Pääbo, S. (1999). Agriculture: Neolithic genetic engineering (News and Views). Nature, 398, 194-195.

Pääbo, S. (1999). Human evolution. Trends in Genetics, 15(12), M13-M16.

Poinar, H. N., & Stankiewicz, A. B. (1999). Protein Preservation and DNA Retrieval from Ancient Tissues. Proceedings of the National Academy of Sciences of the United States of America, 96(15), 8426-8431.

Redd, A. J., & Stoneking, M. (1999). Peopling of Sahul: mitochondrial DNA variation in Australian aboriginal and Papua New Guinean populations. American Journal of Human Genetics, 65, 808-828.

Schöniger, M., & von Haeseler, A. (1999). Toward Assigning Helical Regions in Alignments of Ribosomal RNA and Testing the Appropriateness of Evolutionary Models. Journal of Molecular Evolution, 49(5), 691-698.

Stone, A. C., & Stoneking, M. (1999). Analysis of ancient DNA from a prehistoric Amerindian cemetery. Philosophical Transactions of the Royal Society of London B, 354, 153-159.

Szabó, Z., Levi-Minzi, S. A., Christiano, A. M., Struminger, C., Stoneking, M., Batzer, M. A., & Boyd, C. D.

(1999). Sequential Loss of Two Neighboring Exons of the Tropoelastin Gene During Primate Evolution. Journal of Molecular Evolution, 49(5), 664-671.

Vigilant, L., & Pääbo, S. (1999). A chimpanzee millenium (Guest Editorial). Biological Chemistry, 380(12), 1353-1354.

Yokobori, S.-i., Ueda, T., Feldmaier-Fuchs, G., Pääbo, S., Kondow, A., Nishikawa, K., & Watanabe, K. (1999). Complete DNA sequence of the mitochondrial genome of the ascidian Halocynthia roretzi (Chordata, Urochordata). Genetics, 153(4), 1851-1862.

1998

Laan, M., & Pääbo, S. (1998). Mapping genes by drift-generated linkage disequilibrium. American Journal of Human Genetics, 63(2), 654-656.

Poinar, H. N., Hofreiter, M., Spaulding, W. G., Martin, P. S., Stankiewicz, A. B., Bland, H., Evershed, R. P., Possnert, G., & Pääbo, S. (1998). Molecular coproscopy: Dung and diet of the extinct ground sloth Nothrotheriops shastensis. Science, 281(5375), 402-406.

Reichert, A. S., Rothbauer, U., & Mörl, M. (1998). Processing and Editing of Overlapping tRNAs in Human Mitochondria. Journal of Biological Chemistry, 273(48), 31977-31984.

Updated: March 28th, 2024