

References

- 1 Kono, R. T. Molar enamel thickness and distribution patterns in extant great apes and humans: new insights based on a 3-dimensional whole crown perspective. *Anthropol Sci* **112**, 121-146 (2004).
- 2 Richmond, B. G. & Strait, D. S. Evidence that humans evolved from a knuckle-walking ancestor. *Nature* **404**, 382-385 (2000).
- 3 Thorpe, S. K. S., Holder, R. L. & Crompton, R. H. Origin of human bipedalism as an adaptation for locomotion on flexible branches. *Science* **16**, 1328-1331 (2007).
- 4 Yunis, J. J. & Sanchez, O. G-Banding and Chromosome Structure. *Chromosoma* **44**, 15-23 (1973).
- 5 Sarich, V. M. & Wilson, A. C. Immunological time-scale for Hominid evolution. *Science* **158**, 1200-1203 (1967).
- 6 Sibley, C. G. & Ahlquist, J. E. The phylogeny of the hominoid primates, as indicated by DNA-DNA hybridization. *J Mol Evol.* **20**, 2-15 (1984).
- 7 Chen, F.-C. & Li, W.-H. Genomic divergences between humans and other hominoids and the effective population size of the common ancestor of humans and chimpanzees. *Am J Hum Genet* **68**, 444-456 (2001).
- 8 The Chimpanzee Sequencing and Analysis Consortium. Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature* **437**, 69-87 (2005).
- 9 Scally, A. *et al.* Insights into hominid evolution from the gorilla genome sequence. *Nature* **483**, 169-175 (2012).
- 10 Fischer, A. *et al.* Bonobos Fall within the Genomic Variation of Chimpanzees. *PLoS ONE* **6**, e21605 (2011).
- 11 Hublin, J.-J. The origin of Neandertals. *Proc Natl Acad Sci USA* **106**, 16022-16027 (2009).
- 12 Reich, D. *et al.* Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature* **468**, 1053-1060 (2010).
- 13 Caramelli, D. *et al.* A highly divergent mtDNA sequence in a Neandertal individual from Italy. *Curr Biol* **16**, R630-R632 (2006).
- 14 Green, R. E. *et al.* A complete Neandertal mitochondrial genome sequence determined by high-throughput sequencing. *Cell* **134**, 416-426 (2008).
- 15 Briggs, A. W. *et al.* Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. *Science* **325**, 318-321 (2009).
- 16 Krause, J. *et al.* The complete mitochondrial DNA genome of an unknown hominin from southern Siberia. *Nature* **464**, 894-897 (2011).
- 17 Green, R. E. *et al.* A Draft Sequence of the Neandertal Genome. *Science* **328**, 710-722 (2010).
- 18 Reich, D. *et al.* Denisova admixture and the first modern human dispersals into southeast Asia and Oceania. *Am J Hum Genet* **89**, 516-528 (2011).
- 19 Eriksson, A. & Manica, A. Effect of ancient population structure on the degree of polymorphism shared between modern human populations and ancient hominins. *Proc Natl Acad Sci USA* (2012).

- 20 Wood, B. & Harrison, T. The evolutionary context of the first hominins. *Nature* **470**, 347-352 (2011).
- 21 Leakey, M. D. & Hay, R. L. Pliocene footprints in the Laetolil Beds at Laetoli, northern Tanzania. *Nature* **278**, 317 - 323 (1979).
- 22 Walker, A. & Leakey, R. E. F. *The Nariokatome Homo erectus skeleton* (Harvard University Press, Cambridge, 1993).
- 23 Ammerman, A. J. & Cavalli-Sforza, L. L. *The Neolithic Transition and the Genetics of Populations in Europe*. (Princeton University Press, Princeton, NJ, USA, 1984).
- 24 Ingman, M., Kaessmann, H., Pääbo, S. & Gyllensten, U. Mitochondrial genome variation and the origin of modern humans. *Nature* **408**, 708-713 (2000).
- 25 Thomson, R., Pritchard, J. K., Shen, P., Oefner, P. J. & Feldman, M. W. Recent common ancestry of human Y chromosomes: evidence from DNA sequence data. *Proc Natl Acad Sci USA* **97**, 7360-7365 (2000).
- 26 Schaffner, S. F. *et al.* Calibrating a coalescent simulation of human genome sequence variation. *Genome Res* **15**, 1576-1583 (2005).
- 27 Manica, A., Amos, W., Balloux, F. & Hanihara, T. The effect of ancient population bottlenecks on human phenotypic variation. *Nature* **448**, 346-348 (2007).
- 28 von Cramon-Taubadel, N. & Lycett, S. J. Brief communication: human cranial variation fits iterative founder effect model with African origin. *Am J Phys Anthropol* **136**, 108-113 (2008).
- 29 Liu, H., Prugnolle, F., Manica, A. & Balloux, F. A geographically explicit genetic model of worldwide human-settlement history. *Am J Hum Genet* **79**, 230-237 (2006).
- 30 Li, J. Z. *et al.* Worldwide human relationships inferred from genome-wide patterns of variation. *Science* **319**, 1100-1104.
- 31 Nachman, M. W. & Crowell, S. L. Estimate of the mutation rate per nucleotide in humans. *Genetics* **156**, 297-304 (2000).
- 32 Conrad, D. F. *et al.* Variation in genome-wide mutation rates within and between human families. *Nat Genet* **43**, 712-714 (2011).
- 33 Kong, A. *et al.* Rate of de novo mutations and the importance of father's age to disease risk. *Nature* **488**, 471-475 (2012).
- 34 Bailey, J. A. *et al.* Recent segmental duplications in the human genome. *Science* **297**, 1003-1007 (2002).
- 35 Tuzun, E. *et al.* Fine-scale structural variation of the human genome. *Nat Genet* **37**, 727-732 (2005).
- 36 Conrad, D. F. *et al.* Origins and functional impact of copy number variation in the human genome. *Nature* **464**, 704-712 (2009).
- 37 Stephens, M. & Donnelly, P. A comparison of bayesian methods for haplotype reconstruction from population genotype data. *Am J Hum Genet* **73**, 1162-1169 (2003).
- 38 Rapley, R. & Harbron, S. *Molecular Analysis and Genome Discovery*. (John Wiley & Sons Ltd, 2004).
- 39 The International HapMap Consortium *et al.* A second generation human haplotype map of over 3.1 million SNPs. *Nature* **449**, 851-861 (2007).

- 40 The 1000 Genomes Project Consortium. A map of human genome
variation from population-scale sequencing. *Nature* **467**, 1061-1073
(2010).
- 41 Xie, C. & Tammi, M. T. CNV-seq, a new method to detect copy number
variation using high-throughput sequencing. *BMC Bioinformatics* **10**, 80
(2009).
- 42 Xi, R. *et al.* Copy number variation detection in whole-genome sequencing
data using the Bayesian information criterion. *Proc Natl Acad Sci USA* **108**,
E1128-E1136 (2011).
- 43 Mills, R. E. *et al.* Mapping copy number variation by population-scale
genome sequencing. *Nature* **470**, 59-65 (2011).
- 44 Dohm, J. C., Lottaz, C., Borodina, T. & Himmelbauer, H. Substantial biases
in ultra-short read data sets from high-throughput DNA sequencing. *Nucl
Acids Res* **36**, e105 (2008).
- 45 Harismendy, O. *et al.* Evaluation of next generation sequencing platforms
for population targeted sequencing studies. *Genome Biol* **10**, R32 (2009).
- 46 Li, H., Ruan, J. & Durbin, R. Mapping short DNA sequencing reads and
calling variants using mapping quality scores. *Genome Res* **18**, 1851-1858
(2008).
- 47 Bentley, D. R. *et al.* Accurate whole human genome sequencing using
reversible terminator chemistry. *Nature* **456**, 53-59 (2008).
- 48 Ning, Z., Cox, A. J. & Mullikin, J. C. SSAHA: a fast search method for large
DNA databases. *Genome Res* **11**, 1725-1729 (2001).
- 49 Warren, R. L. & Holt, R. A. Targeted assembly of short sequence reads.
PLoS One **6**, e19816 (2011).
- 50 Li, H. & Homer, N. A survey of sequence alignment algorithms for next-
generation sequencing. *Brief Bioinform* **11**, 473-483 (2010).
- 51 Hardison, R. C. Conserved noncoding sequences are reliable guides to
regulatory elements. *Trend Genet* **16**, 369-372 (2000).
- 52 Frazer, K. A. *et al.* Noncoding sequences conserved in a limited number of
mammals in the SIM2 interval are frequently functional. *Genome Res* **14**,
367-372 (2004).
- 53 King, D. *et al.* Evaluation of regulatory potential and conservation scores
for detecting cis-regulatory modules in aligned mammalian genome
sequences. *Genome Res* **15**, 1051-1060 (2005).
- 54 Wang, Q. F. *et al.* Detection of weakly conserved ancestral mammalian
regulatory sequences by primate comparisons. *Genome Biol* **8**, R1 (2007).
- 55 Prabhakar, S. *et al.* Close sequence comparisons are sufficient to identify
human cis-regulatory elements. *Genome Res* **16**, 855-863 (2006).
- 56 The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science* **306**, 636-
640 (2004).
- 57 Birney, E. *et al.* Identification and analysis of functional elements in 1% of
the human genome by the ENCODE pilot project. *Nature* **447**, 799-816
(2007).
- 58 Wright, S. Classification of the factors of evolution. *Cold Spring Harb Symp
Quant Biol* **20**, 16-24 (1955).
- 59 Darwin, C. *On The Origin of Species*. (Oxford University Press, 1859).

- 60 Michon, P. *et al.* Duffy-null promoter heterozygosity reduces DARC
expression and abrogates adhesion of the *P. vivax* ligand required for
blood-stage infection. *FEBS Lett* **495**, 111-114 (2001).
- 61 Hamblin, M. T. & Di Rienzo, A. Detection of the signature of natural
selection in humans: evidence from the Duffy blood group locus. *Am J
Hum Genet* **66**, 1669-1679 (2000).
- 62 Hamblin, M. T., Thompson, E. E. & Di Rienzo, A. Complex signatures of
natural selection at the Duffy blood group locus. *Am J Hum Genet* **70**, 369-
383 (2002).
- 63 Bustamante, C. D. *et al.* Natural selection on protein-coding genes in the
human genome. *Nature* **437**, 1153-1157 (2005).
- 64 Lewontin, R. C. The interaction of selection and linkage. I. general
considerations; heterotic models. *Genetics* **49**, 49-67 (1964).
- 65 Sabeti, P. C. *et al.* Detecting recent positive selection in the human genome
from haplotype structure. *Nature* **419**, 832-837 (2002).
- 66 Sabeti, P. C. *et al.* Genome-wide detection and characterization of positive
selection in human populations. *Nature* **449**, 913-918 (2007).
- 67 Voight, B. F., Kudravalli, S., Wen, X. & Pritchard, J. K. A map of recent
positive selection in the human genome. *PLoS Biol* **4**, e72 (2006).
- 68 Grossman, S. R. *et al.* A composite of multiple signals distinguishes causal
variants in regions of positive selection. *Science* **327**, 883-886 (2010).
- 69 Hinds, D. A. *et al.* Whole-genome patterns of common DNA variation in
three human populations. *Science* **307**, 1072-1079 (2005).
- 70 Wang, E. T., Kodama, G., Baldi, P. & Moyzis, R. K. Global landscape of
recent inferred Darwinian selection for *Homo sapiens*. *Proc Natl Acad Sci
USA* **103**, 135-140 (2006).
- 71 Tajima, F. Statistical method for testing the neutral mutation hypothesis
by DNA polymorphism. *Genetics* **123**, 585-595 (1989).
- 72 Fay, J. C. & Wu, C. I. Hitchhiking under positive Darwinian selection.
Genetics **155**, 1405-1413 (2000).
- 73 Kim, Y. & Stephan, W. Detecting a local signature of genetic hitchhiking
along a recombining chromosome. *Genetics* **160**, 765-777 (2002).
- 74 Kim, Y. & Nielsen, R. Linkage disequilibrium as a signature of selective
sweeps. *Genetics* **167**, 1513-1524 (2004).
- 75 Jensen, J. D., Kim, Y., DuMont, V. B., Aquadro, C. F. & Bustamante, C. D.
Distinguishing between selective sweeps and demography using DNA
polymorphism data. *Genetics* **170**, 1401-1410 (2005).
- 76 Nielsen, R. *et al.* Genomic scans for selective sweeps using SNP data.
Genome Res **15**, 1566-1575 (2005).
- 77 Kelley, J. L., Madeoy, J., Calhoun, J. C., Swanson, W. & Akey, J. M. Genomic
signatures of positive selection in humans and the limits of outlier
approaches. *Genome Res* **16**, 980-989 (2006).
- 78 Williamson, S. H. *et al.* Localizing recent adaptive evolution in the human
genome. *PLoS Genet* **3**, e90 (2007).
- 79 Wright, S. Evolution in Mendelian populations. *Genetics* **16**, 97-159
(1931).
- 80 Akey, J. M., Zhang, G., Zhang, K., Jin, L. & Shriver, M. D. Interrogating a high-
density SNP map for signatures of natural selection. *Genome Res* **12**,
1805-1814 (2002).

- 81 Weir, B. S., Cardon, L. R., Anderson, A. D., Nielsen, D. M. & Hill, W. G. Measures of human population structure show heterogeneity among genomic regions. *Genome Res* **15**, 1468-1476 (2005).
- 82 Beaumont, M. A. & Balding, D. J. Identifying adaptive genetic divergence among populations from genome scans. *Mol Ecol* **13**, 969-980 (2004).
- 83 The International HapMap Consortium. A haplotype map of the human genome. *Nature* **437**, 1299-1320 (2005).
- 84 Oleksyk, T. K. *et al.* Identifying selected regions from heterozygosity and divergence using a light-coverage genomic dataset from two human populations. *PLoS ONE* **3**, e1712 (2008).
- 85 Kingman, J. F. C. The coalescent. *Stochastic Processes and Their Applications* **13**, 235-248 (1982).
- 86 R. C. Griffiths, S. T. Ancestral inference in population genetics. *Statistical Science* **9**, 307-319 (1994).
- 87 Harding, R. M. *et al.* Archaic African and Asian lineages in the genetic ancestry of modern humans. *Am J Hum Genet* **60**, 772-789 (1997).
- 88 Hudson, R. R. Generating samples under a Wright-Fisher neutral model of genetic variation. *Bioinformatics* **18**, 337-338 (2002).
- 89 Spencer, C. C. & Coop, G. SelSim: a program to simulate population genetic data with natural selection and recombination. *Bioinformatics* **20**, 3673-3675 (2004).
- 90 Mailund, T. *et al.* CoaSim: a flexible environment for simulating genetic data under coalescent models. *BMC bioinformatics* **6**, 252 (2005).
- 91 Marjoram, P. & Wall, J. D. Fast "coalescent" simulation. *BMC Genetics* **7**, 16 (2006).
- 92 Peng, B. & Kimmel, M. simuPOP: a forward-time population genetics simulation environment. *Bioinformatics* **21**, 3686-3687 (2005).
- 93 Hoggart, C. J. *et al.* Sequence-level population simulations over large genomic regions. *Genetics* **177**, 1725-1731 (2007).
- 94 Pickrell, J. K. *et al.* Signals of recent positive selection in a worldwide sample of human populations. *Genome Res* **19**, 826-837 (2009).
- 95 Harding, R. M. *et al.* Evidence for variable selective pressures at MC1R. *Am J Hum Genet* **66**, 1351-1361 (2000).
- 96 Soejima, M., Tachida, H., Ishida, T., Sano, A. & Koda, Y. Evidence for recent positive selection at the human *AIM1* locus in a European population. *Mol Biol Evol* **23**, 179-188 (2006).
- 97 Aoki, K. Sexual selection as a cause of human skin colour variation: Darwin's hypothesis revisited. *Ann Hum Biol* **29**, 589-608 (2002).
- 98 Juzeniene, A., Setlow, R., Porojnicu, A., Steindal, A. H. & Moan, J. Development of different human skin colors: a review highlighting photobiological and photobiophysical aspects. *J Photochem Photobiol B* **96**, 93-100 (2009).
- 99 Lamason, R. L. *et al.* SLC24A5, a putative cation exchanger, affects pigmentation in zebrafish and humans. *Science* **310**, 1782-1786 (2005).
- 100 Akey, J. M. Constructing genomic maps of positive selection in humans: Where do we go from here? *Genome Res* **19**, 711-722 (2009).
- 101 Akey, J. M. Constructing genomic maps of positive selection in humans: where do we go from here? *Genome Res* **19**, 711-722 (2009).

- 102 Hernandez, R. D. *et al.* Classic selective sweeps were rare in recent human evolution. *Science* **331**, 920-924 (2011).
- 103 Hu, M. *et al.* Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. *Hum Genet* **131**, 665-674 (2012).
- 104 Fisher, R. A. *Statistical Methods for Research Workers*. 12th edn, (Oliver and Boyd, 1954).
- 105 Xue, Y. *et al.* Spread of an inactive form of caspase-12 in humans is due to recent positive selection. *Am J Hum Genet* **78**, 659-670 (2006).
- 106 Mamanova, L. *et al.* Target-enrichment strategies for next-generation sequencing. *Nature Methods* **7**, 111-118 (2010).
- 107 Quail, M. A. *et al.* A large genome center's improvements to the Illumina sequencing system. *Nature Methods* **5**, 1005-1010 (2008).
- 108 Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079 (2009).
- 109 Guerra-Assuncao, J. A. & Enright, A. J. MapMi: automated mapping of microRNA loci. *BMC bioinformatics* **11**, 133 (2010).
- 110 Hofacker, I. L. *et al.* Fast folding and comparison of RNA secondary structures. *Monatshefte für Chemie* **125**, 167-188 (1994).
- 111 Heintzman, N. D. *et al.* Histone modifications at human enhancers reflect global cell-type-specific gene expression. *Nature* **459**, 108-112 (2009).
- 112 Xue, Y. *et al.* Population differentiation as an indicator of recent positive selection in humans: an empirical evaluation. *Genetics* **183**, 1065-1077 (2009).
- 113 Grossman, S. R. *et al.* A composite of multiple signals distinguishes causal variants in regions of positive selection. *Science* **327**, 883-886 (2010).
- 114 Veyrieras, J. B. *et al.* High-resolution mapping of expression-QTLs yields insight into human gene regulation. *PLoS Genet* **4**, e1000214 (2008).
- 115 Piriyaopongsa, J. & Jordan, I. K. A family of human microRNA genes from miniature inverted-repeat transposable elements. *PLoS ONE* **2**, e203 (2007).
- 116 King, M. C. & Wilson, A. C. Evolution at two levels in humans and chimpanzees. *Science* **188**, 107-116 (1975).
- 117 Quach, H. *et al.* Signatures of purifying and local positive selection in human miRNAs. *Am J Hum Genet* **84**, 316-327 (2009).
- 118 Neilson, L. I. *et al.* cDNA cloning and characterization of a human sperm antigen (SPAG6) with homology to the product of the *Chlamydomonas PF16* locus. *Genomics* **60**, 272-280 (1999).
- 119 Sapiro, R. *et al.* Male infertility, impaired sperm motility, and hydrocephalus in mice deficient in sperm-associated antigen 6. *Mol Cell Biol* **22**, 6298-6305 (2002).
- 120 Maine, G. N. & Burstein, E. COMMD proteins: COMMin'g to the scene. *Cell Mol Life Sci* **64**, 1997-2005 (2007).
- 121 Shakhova, O., Leung, C. & Marino, S. *Bmi1* in development and tumorigenesis of the central nervous system. *J. Mol. Med.* **83**, 596-600 (2005).
- 122 Schuringa, J. J. & Vellenga, E. Role of the polycomb group gene BMI1 in normal and leukemic hematopoietic stem and progenitor cells. *Curr Opin Hematol* **17**, 294-299 (2010).

- 123 Ginjala, V. *et al.* BMI1 is recruited to DNA breaks and contributes to DNA damage induced H2A ubiquitination and repair. *Mol Cell Biol* **31**, 1972-1982 (2011).
- 124 van der Lugt, N. M. *et al.* Posterior transformation, neurological abnormalities, and severe hematopoietic defects in mice with a targeted deletion of the *bmi-1* proto-oncogene. *Genes & Development* **8**, 757-769 (1994).
- 125 Zhang, J. & Sarge, K. D. Identification of a polymorphism in the RING finger of human Bmi-1 that causes its degradation by the ubiquitin-proteasome system. *FEBS Lett* **583**, 960-964 (2009).
- 126 Yngvadottir, B., Macarthur, D. G., Jin, H. & Tyler-Smith, C. The promise and reality of personal genomics. *Genome Biol* **10**, 237 (2009).
- 127 Hellenthal, G. & Stephens, M. msHOT: modifying Hudson's ms simulator to incorporate crossover and gene conversion hotspots. *Bioinformatics* **23**, 520-521 (2007).
- 128 Abdi, H. in *Encyclopedia of Measurement and Statistics* (ed Neil Salkind) (Sage, 2007).
- 129 Gonzalez-Perez, A. & Lopez-Bigas, N. Improving the assessment of the outcome of nonsynonymous SNVs with a consensus deleteriousness score, Condel. *Am J Hum Genet* **88**, 440-449 (2011).
- 130 Kumar, P., Henikoff, S. & Ng, P. C. Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. *Nature Protocols* **4**, 1073-1082 (2009).
- 131 Adzhubei, I. A. *et al.* A method and server for predicting damaging missense mutations. *Nature Methods* **7**, 248-249 (2010).
- 132 Mann, H. B. & whitney, D. R. On a Test of Whether one of Two Random Variables is Stochastically Larger than the Other. *Ann Math Statist* **18**, 50-60 (1947).
- 133 The 1000 Genomes Project Consortium. An integrated map of genetic variation from 1,092 human genomes. *Nature* **submitted** (2012).
- 134 Dennis, G., Jr. *et al.* DAVID: Database for Annotation, Visualization, and Integrated Discovery. *Genome Biol* **4**, P3 (2003).
- 135 Hindorff, L. A. *et al.* Potential etiologic and functional implications of genome-wide association loci for human diseases and traits. *Proc Natl Acad Sci USA* **106**, 9362-9367 (2009).
- 136 Yngvadottir, B. *et al.* A genome-wide survey of the prevalence and evolutionary forces acting on human nonsense SNPs. *Am J Hum Genet* **84**, 224-234 (2009).
- 137 Harvey, K. F., Dinudom, A., Cook, D. I. & Kumar, S. The Nedd4-like protein KIAA0439 is a potential regulator of the epithelial sodium channel. *J Biol Chem* **276**, 8597-8601 (2001).
- 138 Raikwar, N. S. & Thomas, C. P. Nedd4-2 isoforms ubiquitinate individual epithelial sodium channel subunits and reduce surface expression and function of the epithelial sodium channel. *Am J Physiol Renal Physiol.* **294**, 1157-1165 (2008).
- 139 Dahlberg, J., Nilsson, L.-O., Wowern, F. v. & Melander, O. Polymorphism in NEDD4L Is Associated with Increased Salt Sensitivity, Reduced Levels of P-renin and Increased Levels of Nt-proANP. *PLoS ONE* **2**, e432 (2007).

- 140 Fava, C. *et al.* 24-h ambulatory blood pressure is linked to chromosome 18q21–22 and genetic variation of NEDD4L associates with cross-sectional and longitudinal blood pressure in Swedes. *Kidney Int* **70**, 562-569 (2006).
- 141 Russo, C. J. *et al.* Association of NEDD4L ubiquitin ligase with essential hypertension. *Hypertension* **46**, 488-491 (2005).
- 142 Pucharcos, C., Estivill, X. & Luna, S. d. l. Intersectin 2, a new multimodular protein involved in clathrin-mediated endocytosis. *FEBS Lett* **478**, 43-51 (2000).
- 143 McGavin, M. K. H. *et al.* The Intersectin 2 Adaptor Links Wiskott Aldrich Syndrome Protein (WASp)-mediated Actin Polymerization to T Cell Antigen Receptor Endocytosis. *J Exp Med* **194**, 1777-1787 (2001).
- 144 Winther, M., Berezin, V. & Walmod, P. S. NCAM2/OCAM/RNCAM: cell adhesion molecule with a role in neuronal compartmentalization. *Int J Biochem Cell Biol* **44**, 441-446 (2012).
- 145 Kaufman, L., Hayashi, K., Ross, M. J., Ross, M. D. & Klotman, P. E. Sidekick-1 is upregulated in glomeruli in HIV-associated nephropathy. *J Am Soc Nephrol* **15**, 1721-1730 (2004).
- 146 Kaufman, L. *et al.* The homophilic adhesion molecule sidekick-1 contributes to augmented podocyte aggregation in HIV-associated nephropathy. *FASEB J* **21**, 1367-1375 (2007).
- 147 Oguri, M. *et al.* Assessment of a polymorphism of SDK1 with hypertension in Japanese Individuals. *Am J Hypertens* **23**, 70-77 (2010).
- 148 Levy, D. *et al.* Genome-wide association study of blood pressure and hypertension. *Nature Genet* **41**, 677-687 (2009).
- 149 Tang, K., Thornton, K. R. & Stoneking, M. A New Approach for Using Genome Scans to Detect Recent Positive Selection in the Human Genome. *PLoS Biol* **5**, e171 (2007).
- 150 Carlson, C. S. *et al.* Genomic regions exhibiting positive selection identified from dense genotype data. *Genome Res* **15**, 1553-1565 (2005).
- 151 Kelley, J. L., Madeoy, J., Calhoun, J. C., Swanson, W. & Akey, J. M. Genomic signatures of positive selection in humans and the limits of outlier approaches. *Genome Res* **16**, 980-989 (2006).
- 152 Akey, J. M. *et al.* Population history and natural selection shape patterns of genetic variation in 132 genes. *PLoS Biol* **2**, e286 (2004).
- 153 Bryk, J. *et al.* Positive selection in East Asians for an *EDAR* allele that enhances NF-kappaB activation. *PLoS ONE* **3**, e2209 (2008).
- 154 Hudson, R. R. in *Oxford Surveys in Evolutionary Biology* Vol. 7 (ed Douglas Futuyma and Janis Antonovics) 1-44 (Oxford University Press, 1991).
- 155 Levy, S. *et al.* The diploid genome sequence of an individual human. *PLoS Biol* **5**, e254 (2007).
- 156 Wheeler, D. A. *et al.* The complete genome of an individual by massively parallel DNA sequencing. *Nature* **452**, 872-876 (2007).
- 157 Wang, J. *et al.* The diploid genome sequence of an Asian individual. *Nature* **456**, 60-66 (2008).
- 158 Ahn, S.-M. *et al.* The first Korean genome sequence and analysis: Full genome sequencing for a socio-ethnic group. *Genome Res* **19**, 1622-1629 (2009).

- 159 Kim, J.-I. *et al.* A highly annotated whole-genome sequence of a Korean individual. *Nature* **460**, 1011-1016 (2009).
- 160 Drmanac, R. *et al.* Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays. *Science* **327**, 78-81 (2009).
- 161 Schuster, S. C. *et al.* Complete Khoisan and Bantu genomes from southern Africa. *Nature* **463**, 943-947 (2010).
- 162 Browning, S. R. & Browning, B. L. Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *Am J Hum Genet* **81**, 1084-1097 (2007).
- 163 Lenhard, J. Kritische Untersuchung einer Methode zur Schätzung Phylogenetischer Größen. *PhD thesis, Mathematics Department, Johann Wolfgang Goethe University* (1997).
- 164 R. C. Griffiths, S. T. Simulating probability distributions in the coalescent. *Theor Popn Biol* **46**, 131-159 (1994).
- 165 R. C. Griffiths, S. T. Sampling theory for neutral alleles in a varying environment. *Phil Trans R Soc Lond B* **344**, 403-410 (1994).
- 166 R. C. Griffiths, S. T. Unrooted genealogical tree probabilities in the infinitely-many-sites model. *Math Biosci* **127**, 77-98 (1995).
- 167 Harding, R. M. *et al.* Archaic African and Asian lineages in the genetic ancestry of modern humans. *Am J Hum Genet* **60**, 772-789 (1997).
- 168 Kong, A. *et al.* Fine-scale recombination rate differences between sexes, populations and individuals. *Nature* **467**, 1099-1103 (2010).
- 169 Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079 (2009).
- 170 Bandelt, H. J., Forster, P. & Röhl, A. Median-joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* **16**, 37-48 (1999).
- 171 Langergraber, K. E. *et al.* Generation times in wild chimpanzees and gorillas suggest earlier divergence times in great ape and human evolution. *Proc Natl Acad Sci USA* (2012).
- 172 Fimia, G. M. *et al.* Ambra1 regulates autophagy and development of the nervous system. *Nature* **447**, 1121-1125 (2007).
- 173 Benjamini, Y. & Hochberg, Y. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J Roy Stat Soc, Series B (Methodological)* **57**, 289-300 (1995).
- 174 Podlaha, O. & Zhang, J. Positive selection on protein-length in the evolution of a primate sperm ion channel. *Proc Natl Acad Sci USA* **100**, 12241-12246 (2003).
- 175 Tishkoff, S. A. *et al.* Haplotype diversity and linkage disequilibrium at human G6PD: recent origin of alleles that confer malarial resistance. *Science* **293**, 455-462 (2001).
- 176 Ayodo, G. *et al.* Combining evidence of natural selection with association analysis increases power to detect malaria-resistance variants. *Am J Hum Genet* **81**, 234-242 (2007).
- 177 Skarnes, W. C. *et al.* A conditional knockout resource for the genome-wide study of mouse gene function. *Nature* **474**, 337-342 (2011).
- 178 Freimer, N. & Sabatti, C. The human phenome project. *Nat Genet* **34**, 15-21 (2003).
- 179 Turchin, M. C. *et al.* Evidence of widespread selection on standing variation in Europe at height-associated SNPs. *Nat Genet* (2012).

- 180 Casals, F. *et al.* Genetic adaptation of the antibacterial human innate immunity network. *BMC Evol Biol* **11**, 202 (2011).
- 181 Dall'olio, G. M. *et al.* Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. *BMC Evol Biol* **12**, 98 (2012).
- 182 Szklarczyk, D. *et al.* The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. *Nucleic Acids Res* **39**, D561-568 (2011).
- 183 Xue, Y. *et al.* Adaptive evolution of UGT2B17 copy-number variation. *Am J Hum Genet* **83**, 337-346 (2008).