

References

1. Siegel, R. L., Miller, K. D., Jemal, A. (2015) Cancer statistics, 2015. *CA Cancer J Clin* 65(1):5-29.
2. Berndt, S. I., Carter, H. B., Schoenberg, M. P., Newschaffer, C. J. (2007) Disparities in treatment and outcome for renal cell cancer among older black and white patients. *J Clin Oncol* 25(24):3589-95.
3. Stafford, H. S., Saltzstein, S. L., Shimasaki, S., Sanders, C., Downs, T. M., Sadler, G. R. (2008) Racial/ethnic and gender disparities in renal cell carcinoma incidence and survival. *J Urol* 179(5):1704-8.
4. Vaishampayan, U. N., Do, H., Hussain, M., Schwartz, K. (2003) Racial disparity in incidence patterns and outcome of kidney cancer. *Urology* 62(6):1012-7.
5. Lipworth, L., Tarone, R. E., McLaughlin, J. K. (2011) Renal cell cancer among African Americans: an epidemiologic review. *BMC Cancer* 11():133.
6. Benichou, J., Chow, W. H., McLaughlin, J. K., Mandel, J. S., Fraumeni, Jr, J. F. (1998) Population attributable risk of renal cell cancer in Minnesota. *Am J Epidemiol* 148(5):424-30.
7. Chow, W. H., Devesa, S. S., Warren, J. L., Fraumeni, Jr, J. F. (1999) Rising incidence of renal cell cancer in the United States. *JAMA* 281(17):1628-31.
8. Ljungberg, B., Campbell, S. C., Choi, H. Y., Cho, H. Y., Jacqmin, D., Lee, J. E., Weikert, S., Kiemeney, L. A. (2011) The epidemiology of renal cell carcinoma. *Eur Urol* 60(4):615-21.
9. Chow, W.-H., Dong, L. M., Devesa, S. S. (2010) Epidemiology and risk factors for kidney cancer. *Nat Rev Urol* 7(5):245-57.
10. Cowey, C. L., Rathmell, W. K. (2009) VHL gene mutations in renal cell carcinoma: role as a biomarker of disease outcome and drug efficacy. *Curr Oncol Rep* 11(2):94-101.
11. Clark, P. E. (2009) The role of VHL in clear-cell renal cell carcinoma and its relation to targeted therapy. *Kidney Int* 76(9):939-45.
12. Moore, L. E., Nickerson, M. L., Brennan, P., Toro, J. R., Jaeger, E., Rinsky, J., Han, S., Zaridze, D., Matveev, V., Janout, V., Kollarova, H., Bencko, V., Navratilova, M., Szeszenia-Dabrowska, N., Mates, D., Schmidt, L. S., Lenz, P., Karami, S., Linehan, W. M., Merino, M., Chanock, S., Boffetta, P., Chow, W.-H., Waldman, F. M., Rothman, N. (2011) Von Hippel-Lindau (VHL) inactivation in sporadic clear cell renal cancer: associations with germline VHL polymorphisms and etiologic risk factors. *PLoS Genet* 7(10):e1002312.
13. Hakimi, A. A., Ostrovnaya, I., Jacobsen, A., Susztak, K., Coleman, J. A., Russo, P., Winer, A. G., Mano, R., Sankin, A. I., Motzer, R. J., Voss, M. H., Offit, K., Purdue, M., Pomerantz, M., Freedman, M., Choueiri, T. K., Hsieh, J. J., Klein, R. J. (2016) Validation and genomic interrogation of the MET variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma. *Cancer* 122(3):402-10.
14. Giubellino, A., Linehan, W. M., Bottaro, D. P. (2009) Targeting the Met signaling pathway in renal cancer. *Expert Rev Anticancer Ther* 9(6):785-93.
15. Salgia, R. (2017) MET in Lung Cancer: Biomarker Selection Based on Scientific Rationale. *Mol Cancer Ther* 16(4):555-565.
16. Knudson, Jr, A. G. (1971) Mutation and cancer: statistical study of retinoblastoma. *Proc Natl Acad Sci U S A* 68(4):820-3.
17. Bhardwaj, A., Srivastava, S. K., Khan, M. A., Prajapati, V. K., Singh, S., Carter, J. E.,

- Singh, A. P. (2017) Racial disparities in prostate cancer: a molecular perspective. *Front Biosci (Landmark Ed)* 22():772-782.
18. Cooperberg, M. R. (2013) Re-examining racial disparities in prostate cancer outcomes. *J Clin Oncol* 31(24):2979-80.
19. Krishnan, B., Rose, T. L., Kardos, J., Milowsky, M. I., Kim, W. Y. (2016) Intrinsic Genomic Differences Between African American and White Patients With Clear Cell Renal Cell Carcinoma. *JAMA Oncol* ():.
20. Huang, F. W., Mosquera, J. M., Garofalo, A., Oh, C., Baco, M., Amin-Mansour, A., Rabasha, B., Bahl, S., Mullane, S. A., Robinson, B. D., Aldubayan, S., Khani, F., Karir, B., Kim, E., Chimene-Weiss, J., Hofree, M., Romanel, A., Osborne, J. R., Kim, J. W., Azabdaftari, G., Woloszynska-Read, A., Sfanos, K., De Marzo, A. M., Demichelis, F., Gabriel, S., Van Allen, E. M., Mesirov, J., Tamayo, P., Rubin, M. A., Powell, I. J., Garraway, L. A. (2017) Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function ERF Mutations. *Cancer Discov* 7(9):973-983.
21. Mills, R. E., Walter, K., Stewart, C., Handsaker, R. E., Chen, K., Alkan, C., Abyzov, A., Yoon, S. C., Ye, K., Cheetham, R. K., Chinwalla, A., Conrad, D. F., Fu, Y., Grubert, F., Hajirasouliha, I., Hormozdiari, F., Iakoucheva, L. M., Iqbal, Z., Kang, S., Kidd, J. M., Konkel, M. K., Korn, J., Khurana, E., Kural, D., Lam, H. Y. K., Leng, J., Li, R., Li, Y., Lin, C.-Y., Luo, R., Mu, X. J., Nemesh, J., Peckham, H. E., Rausch, T., Scally, A., Shi, X., Stromberg, M. P., Stütz, A. M., Urban, A. E., Walker, J. A., Wu, J., Zhang, Y., Zhang, Z. D., Batzer, M. A., Ding, L., Marth, G. T., McVean, G., Sebat, J., Snyder, M., Wang, J., Ye, K., Eichler, E. E., Gerstein, M. B., Hurles, M. E., Lee, C., McCarroll, S. A., Korbel, J. O., 1000 Genomes Project (2011) Mapping copy number variation by population-scale genome sequencing. *Nature* 470(7332):59-65.
22. 1000 Genomes Project Consortium, Abecasis, G. R., Altshuler, D., Auton, A., Brooks, L. D., Durbin, R. M., Gibbs, R. A., Hurles, M. E., McVean, G. A. (2010) A map of human genome variation from population-scale sequencing. *Nature* 467(7319):1061-73.
23. 1000 Genomes Project Consortium, Abecasis, G. R., Auton, A., Brooks, L. D., DePristo, M. A., Durbin, R. M., Handsaker, R. E., Kang, H. M., Marth, G. T., McVean, G. A. (2012) An integrated map of genetic variation from 1,092 human genomes. *Nature* 491(7422):56-65.
24. DePristo, M. A., Banks, E., Poplin, R., Garimella, K. V., Maguire, J. R., Hartl, C., Philippakis, A. A., del Angel, G., Rivas, M. A., Hanna, M., McKenna, A., Fennell, T. J., Kernytsky, A. M., Sivachenko, A. Y., Cibulskis, K., Gabriel, S. B., Altshuler, D., Daly, M. J. (2011) A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nat Genet* 43(5):491-8.
25. Cancer Genome Atlas Research Network, Linehan, W. M., Spellman, P. T., Ricketts, C. J., Creighton, C. J., Fei, S. S., Davis, C., Wheeler, D. A., Murray, B. A., Schmidt, L., Vocke, C. D., Peto, M., Al Mamun, A. A. M., Shinbrot, E., Sethi, A., Brooks, S., Rathmell, W. K., Brooks, A. N., Hoadley, K. A., Robertson, A. G., Brooks, D., Bowlby, R., Sadeghi, S., Shen, H., Weisenberger, D. J., Bootwalla, M., Baylin, S. B., Laird, P. W., Cherniack, A. D., Saksena, G., Haake, S., Li, J., Liang, H., Lu, Y., Mills, G. B., Akbani, R., Leiserson, M. D. M., Raphael, B. J., Anur, P., Bottaro, D., Albiges, L., Barnabas, N., Choueiri, T. K., Czerniak, B., Godwin, A. K., Hakimi, A. A., Ho, T. H., Hsieh, J., Ittmann, M., Kim, W. Y., Krishnan, B., Merino, M. J., Mills Shaw, K. R., Reuter, V. E., Reznik, E., Shelley, C. S., Shuch, B.,

- Signoretti, S., Srinivasan, R., Tamboli, P., Thomas, G., Tickoo, S., Burnett, K., Crain, D., Gardner, J., Lau, K., Mallory, D., Morris, S., Paulauskis, J. D., Penny, R. J., Shelton, C., Shelton, W. T., Sherman, M., Thompson, E., Yena, P., Avedon, M. T., Bowen, J., Gastier-Foster, J. M., Gerken, M., Leraas, K. M., Lichtenberg, T. M., Ramirez, N. C., Santos, T., Wise, L., Zmuda, E., Demchok, J. A., Felau, I., Hutter, C. M., Sheth, M., Sofia, H. J., Tarnuzzer, R., Wang, Z., Yang, L., Zenklusen, J. C., Zhang, J., Ayala, B., Baboud, J., Chudamani, S., Liu, J., Lolla, L., Naresh, R., Pihl, T., Sun, Q., Wan, Y., Wu, Y., Ally, A., Balasundaram, M., Balu, S., Beroukhim, R., Bodenheimer, T., Buhay, C., Butterfield, Y. S. N., Carlsen, R., Carter, S. L., Chao, H., Chuah, E., Clarke, A., Covington, K. R., Dahdouli, M., Dewal, N., Dhalla, N., Doddapaneni, H. V., Drummond, J. A., Gabriel, S. B., Gibbs, R. A., Guin, R., Hale, W., Hawes, A., Hayes, D. N., Holt, R. A., Hoyle, A. P., Jefferys, S. R., Jones, S. J. M., Jones, C. D., Kalra, D., Kovar, C., Lewis, L., Li, J., Ma, Y., Marra, M. A., Mayo, M., Meng, S., Meyerson, M., Mieczkowski, P. A., Moore, R. A., Morton, D., Mose, L. E., Mungall, A. J., Muzny, D., Parker, J. S., Perou, C. M., Roach, J., Schein, J. E., Schumacher, S. E., Shi, Y., Simons, J. V., Sipahimalani, P., Skelly, T., Soloway, M. G., Sougnez, C., Tam, A., Tan, D., Thiessen, N., Veluvolu, U., Wang, M., Wilkerson, M. D., Wong, T., Wu, J., Xi, L., Zhou, J., Bedford, J., Chen, F., Fu, Y., Gerstein, M., Haussler, D., Kasaian, K., Lai, P., Ling, S., Radenbaugh, A., Van Den Berg, D., Weinstein, J. N., Zhu, J., Albert, M., Alexopoulou, I., Andersen, J. J., Auman, J. T., Bartlett, J., Bastacky, S., Bergsten, J., Blute, M. L., Boice, L., Bollag, R. J., Boyd, J., Castle, E., Chen, Y.-B., Cheville, J. C., Curley, E., Davies, B., DeVolk, A., Dhir, R., Dike, L., Eckman, J., Engel, J., Harr, J., Hrebinko, R., Huang, M., Huelsenbeck-Dill, L., Iacocca, M., Jacobs, B., Lobis, M., Maranchie, J. K., McMeekin, S., Myers, J., Nelson, J., Parfitt, J., Parwani, A., Petrelli, N., Rabeno, B., Roy, S., Salner, A. L., Slaton, J., Stanton, M., Thompson, R. H., Thorne, L., Tucker, K., Weinberger, P. M., Winemiller, C., Zach, L. A., Zuna, R. (2016) Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *N Engl J Med* 374(2):135-45.
26. Cibulskis, K., Lawrence, M. S., Carter, S. L., Sivachenko, A., Jaffe, D., Sougnez, C., Gabriel, S., Meyerson, M., Lander, E. S., Getz, G. (2013) Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nat Biotechnol* 31(3):213-9.
27. Saunders, C. T., Wong, W. S. W., Swamy, S., Becq, J., Murray, L. J., Cheetham, R. K. (2012) Strelka: accurate somatic small-variant calling from sequenced tumor-normal sample pairs. *Bioinformatics* 28(14):1811-7.
28. Lam, H. Y. K., Mu, X. J., Stütz, A. M., Tanzer, A., Cayting, P. D., Snyder, M., Kim, P. M., Korbel, J. O., Gerstein, M. B. (2010) Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. *Nat Biotechnol* 28(1):47-55.
29. Abyzov, A., Urban, A. E., Snyder, M., Gerstein, M. (2011) CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. *Genome Res* 21(6):974-84.
30. Abyzov, A., Gerstein, M. (2011) AGE: defining breakpoints of genomic structural variants at single-nucleotide resolution, through optimal alignments with gap excision. *Bioinformatics* 27(5):595-603.
31. Korbel, J. O., Abyzov, A., Mu, X. J., Carriero, N., Cayting, P., Zhang, Z., Snyder, M., Gerstein, M. B. (2009) PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data.

Genome Biol 10(2):R23.

32. Khurana, E., Fu, Y., Colonna, V., Mu, X. J., Kang, H. M., Lappalainen, T., Sboner, A., Lochovsky, L., Chen, J., Harmanci, A., Das, J., Abyzov, A., Balasubramanian, S., Beal, K., Chakravarty, D., Challis, D., Chen, Y., Clarke, D., Clarke, L., Cunningham, F., Evani, U. S., Flieck, P., Fragoza, R., Garrison, E., Gibbs, R., Gümüş, Z. H., Herrero, J., Kitabayashi, N., Kong, Y., Lage, K., Liliuashvili, V., Lipkin, S. M., MacArthur, D. G., Marth, G., Muzny, D., Pers, T. H., Ritchie, G. R. S., Rosenfeld, J. A., Sisu, C., Wei, X., Wilson, M., Xue, Y., Yu, F., 1000 Genomes Project Consortium, Dermitzakis, E. T., Yu, H., Rubin, M. A., Tyler-Smith, C., Gerstein, M. (2013) Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science* 342(6154):1235587.
33. Abyzov, A., Li, S., Kim, D. R., Mohiyuddin, M., Stütz, A. M., Parrish, N. F., Mu, X. J., Clark, W., Chen, K., Hurles, M., Korbel, J. O., Lam, H. Y. K., Lee, C., Gerstein, M. B. (2015) Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. *Nat Commun* 6():7256.
34. Wang, J., Mullighan, C. G., Easton, J., Roberts, S., Heatley, S. L., Ma, J., Rusch, M. C., Chen, K., Harris, C. C., Ding, L., Holmfeldt, L., Payne-Turner, D., Fan, X., Wei, L., Zhao, D., Obenauer, J. C., Naeve, C., Mardis, E. R., Wilson, R. K., Downing, J. R., Zhang, J. (2011) CREST maps somatic structural variation in cancer genomes with base-pair resolution. *Nat Methods* 8(8):652-4.
35. Habegger, L., Balasubramanian, S., Chen, D. Z., Khurana, E., Sboner, A., Harmanci, A., Rozowsky, J., Clarke, D., Snyder, M., Gerstein, M. (2012) VAT: a computational framework to functionally annotate variants in personal genomes within a cloud-computing environment. *Bioinformatics* 28(17):2267-9.
36. Balasubramanian, S., Fu, Y., Pawashe, M., McGillivray, P., Jin, M., Liu, J., Karczewski, K. J., MacArthur, D. G., Gerstein, M. (2017) Using ALoFT to determine the impact of putative loss-of-function variants in protein-coding genes. *Nat Commun* 8(1):382.
37. Clarke, D., Sethi, A., Li, S., Kumar, S., Chang, R. W. F., Chen, J., Gerstein, M. (2016) Identifying Allosteric Hotspots with Dynamics: Application to Inter- and Intra-species Conservation. *Structure* 24(5):826-837.
38. Kumar, S., Clarke, D., Gerstein, M. (2016) Localized structural frustration for evaluating the impact of sequence variants. *Nucleic Acids Res* 44(21):10062-10073.
39. Lochovsky, L., Zhang, J., Fu, Y., Khurana, E., Gerstein, M. (2015) LARVA: an integrative framework for large-scale analysis of recurrent variants in noncoding annotations. *Nucleic Acids Res* 43(17):8123-34.
40. Cancer Genome Atlas Research Network (2015) The Molecular Taxonomy of Primary Prostate Cancer. *Cell* 163(4):1011-25.
41. Davis, C. F., Ricketts, C. J., Wang, M., Yang, L., Cherniack, A. D., Shen, H., Buhay, C., Kang, H., Kim, S. C., Fahey, C. C., Hacker, K. E., Bhanot, G., Gordenin, D. A., Chu, A., Gunaratne, P. H., Biehl, M., Seth, S., Kaipparettu, B. A., Bristow, C. A., Donehower, L. A., Wallen, E. M., Smith, A. B., Tickoo, S. K., Tamboli, P., Reuter, V., Schmidt, L. S., Hsieh, J. J., Choueiri, T. K., Hakimi, A. A., The Cancer Genome Atlas Research Network, Chin, L., Meyerson, M., Kucherlapati, R., Park, W.-Y., Robertson, A. G., Laird, P. W., Henske, E. P., Kwiatkowski, D. J., Park, P. J., Morgan, M., Shuch, B., Muzny, D., Wheeler, D. A., Linehan, W. M., Gibbs, R. A., Rathmell, W. K., Creighton, C. J. (2014) The somatic genomic

- landscape of chromophobe renal cell carcinoma. *Cancer Cell* 26(3):319-330.
42. Leont'ev, A. P., Minchenkova, B. I., Osipov, V. T. (1973) [Emitters for the apparatus for ultrasonic therapy]. *Med Tekh* 5(0):23-5.
43. Bütler, R., Brunner, E. (1969) Inability of Ag-Anti-Ag complexes to fix complement and its significance. *Vox Sang* 17(5):462-4.
44. Kovac, M., Navas, C., Horswell, S., Salm, M., Bardella, C., Rowan, A., Stares, M., Castro-Giner, F., Fisher, R., de Bruin, E. C., Kovacova, M., Gorman, M., Makino, S., Williams, J., Jaeger, E., Jones, A., Howarth, K., Larkin, J., Pickering, L., Gore, M., Nicol, D., L., Hazell, S., Stamp, G., O'Brien, T., Challacombe, B., Matthews, N., Phillimore, B., Begum, S., Rabinowitz, A., Varela, I., Chandra, A., Horsfield, C., Polson, A., Tran, M., Bhatt, R., Terracciano, L., Eppenberger-Castori, S., Protheroe, A., Maher, E., El Bahrawy, M., Fleming, S., Ratcliffe, P., Heinemann, K., Swanton, C., Tomlinson, I. (2015) Recurrent chromosomal gains and heterogeneous driver mutations characterise papillary renal cancer evolution. *Nat Commun* 6():6336.
45. Durinck, S., Stawiski, E. W., Pavía-Jiménez, A., Modrusan, Z., Kapur, P., Jaiswal, B. S., Zhang, N., Toffessi-Tcheuyap, V., Nguyen, T. T., Pahuja, K. B., Chen, Y.-J., Saleem, S., Chaudhuri, S., Heldens, S., Jackson, M., Peña-Llopis, S., Guillory, J., Toy, K., Ha, C., Harris, C. J., Holloman, E., Hill, H. M., Stinson, J., Rivers, C. S., Janakiraman, V., Wang, W., Kinch, L. N., Grishin, N. V., Haverty, P. M., Chow, B., Gehring, J. S., Reeder, J., Pau, G., Wu, T. D., Margulis, V., Lotan, Y., Sagalowsky, A., Pedrosa, I., de Sauvage, F. J., Brugarolas, J., Seshagiri, S. (2015) Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. *Nat Genet* 47(1):13-21.
46. Cancer Genome Atlas Research Network (2013) Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature* 499(7456):43-9.
47. Sato, Y., Yoshizato, T., Shiraishi, Y., Maekawa, S., Okuno, Y., Kamura, T., Shimamura, T., Sato-Otsubo, A., Nagae, G., Suzuki, H., Nagata, Y., Yoshida, K., Kon, A., Suzuki, Y., Chiba, K., Tanaka, H., Niida, A., Fujimoto, A., Tsunoda, T., Morikawa, T., Maeda, D., Kume, H., Sugano, S., Fukayama, M., Aburatani, H., Sanada, M., Miyano, S., Homma, Y., Ogawa, S. (2013) Integrated molecular analysis of clear-cell renal cell carcinoma. *Nat Genet* 45(8):860-7.
48. Christinat, Y., Krek, W. (2015) Integrated genomic analysis identifies subclasses and prognosis signatures of kidney cancer. *Oncotarget* 6(12):10521-31.
49. Gulati, S., Cheng, T. M. K., Bates, P. A. (2013) Cancer networks and beyond: interpreting mutations using the human interactome and protein structure. *Semin Cancer Biol* 23(4):219-26.
50. Lawrence, M. S., Stojanov, P., Polak, P., Kryukov, G. V., Cibulskis, K., Sivachenko, A., Carter, S. L., Stewart, C., Mermel, C. H., Roberts, S. A., Kiezun, A., Hammerman, P. S., McKenna, A., Drier, Y., Zou, L., Ramos, A. H., Pugh, T. J., Stransky, N., Helman, E., Kim, J., Sougnez, C., Ambrogio, L., Nickerson, E., Shefler, E., Cortés, M. L., Auclair, D., Saksena, G., Voet, D., Noble, M., DiCara, D., Lin, P., Lichtenstein, L., Heiman, D. I., Fennell, T., Imielinski, M., Hernandez, B., Hodis, E., Baca, S., Dulak, A. M., Lohr, J., Landau, D.-A., Wu, C. J., Melendez-Zajgla, J., Hidalgo-Miranda, A., Koren, A., McCarroll, S. A., Mora, J., Crompton, B., Onofrio, R., Parkin, M., Winckler, W., Ardlie, K., Gabriel, S. B., Roberts, C. W. M., Biegel, J. A., Stegmaier, K., Bass, A. J., Garraway, L. A., Meyerson, M., Golub, T. R.,

- Gordenin, D. A., Sunyaev, S., Lander, E. S., Getz, G. (2013) Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature* 499(7457):214-218.
51. Lek, M., Karczewski, K. J., Minikel, E. V., Samocha, K. E., Banks, E., Fennell, T., O'Donnell-Luria, A. H., Ware, J. S., Hill, A. J., Cummings, B. B., Tukiainen, T., Birnbaum, D. P., Kosmicki, J. A., Duncan, L. E., Estrada, K., Zhao, F., Zou, J., Pierce-Hoffman, E., Berghout, J., Cooper, D. N., Deflaux, N., DePristo, M., Do, R., Flannick, J., Fromer, M., Gauthier, L., Goldstein, J., Gupta, N., Howrigan, D., Kiezun, A., Kurki, M. I., Moonshine, A. L., Natarajan, P., Orozco, L., Peloso, G. M., Poplin, R., Rivas, M. A., Ruano-Rubio, V., Rose, S. A., Ruderfer, D. M., Shakir, K., Stenson, P. D., Stevens, C., Thomas, B. P., Tiao, G., Tusie-Luna, M. T., Weisburd, B., Won, H.-H., Yu, D., Altshuler, D. M., Ardiissino, D., Boehnke, M., Danesh, J., Donnelly, S., Elosua, R., Florez, J. C., Gabriel, S. B., Getz, G., Glatt, S. J., Hultman, C. M., Kathiresan, S., Laakso, M., McCarroll, S., McCarthy, M. I., McGovern, D., McPherson, R., Neale, B. M., Palotie, A., Purcell, S. M., Saleheen, D., Scharf, J. M., Sklar, P., Sullivan, P. F., Tuomilehto, J., Tsuang, M. T., Watkins, H. C., Wilson, J. G., Daly, M. J., MacArthur, D. G., Exome Aggregation Consortium (2016) Analysis of protein-coding genetic variation in 60,706 humans. *Nature* 536(7616):285-91.
52. Locke, A. E., Kahali, B., Berndt, S. I., Justice, A. E., Pers, T. H., Day, F. R., Powell, C., Vedantam, S., Buchkovich, M. L., Yang, J., Croteau-Chonka, D. C., Esko, T., Fall, T., Ferreira, T., Gustafsson, S., Kutalik, Z., Luan, J., Mägi, R., Randall, J. C., Winkler, T. W., Wood, A. R., Workalemahu, T., Faul, J. D., Smith, J. A., Zhao, J. H., Zhao, W., Chen, J., Fehrman, R., Hedman, Å. K., Karjalainen, J., Schmidt, E. M., Absher, D., Amin, N., Anderson, D., Beekman, M., Bolton, J. L., Bragg-Gresham, J. L., Buyske, S., Demirkan, A., Deng, G., Ehret, G. B., Feenstra, B., Feitosa, M. F., Fischer, K., Goel, A., Gong, J., Jackson, A. U., Kanoni, S., Kleber, M. E., Kristiansson, K., Lim, U., Lotay, V., Mangino, M., Leach, I. M., Medina-Gomez, C., Medland, S. E., Nalls, M. A., Palmer, C. D., Pasko, D., Pechlivanis, S., Peters, M. J., Prokopenko, I., Shungin, D., Stančáková, A., Strawbridge, R. J., Sung, Y., J., Tanaka, T., Teumer, A., Trompet, S., van der Laan, S. W., van Setten, J., Van Vliet-Ostaptchouk, J. V., Wang, Z., Yengo, L., Zhang, W., Isaacs, A., Albrecht, E., Ärnlöv, J., Arscott, G. M., Attwood, A. P., Bandinelli, S., Barrett, A., Bas, I. N., Bellis, C., Bennett, A. J., Berne, C., Blagieva, R., Blüher, M., Böhringer, S., Bonnycastle, L. L., Böttcher, Y., Boyd, H. A., Bruinenberg, M., Caspersen, I. H., Chen, Y.-D. I., Clarke, R., Daw, E. W., de Craen, A. J. M., Delgado, G., Dimitriou, M., Doney, A. S. F., Eklund, N., Estrada, K., Eury, E., Folkersen, L., Fraser, R. M., Garcia, M. E., Geller, F., Giedraitis, V., Gigante, B., Go, A. S., Golay, A., Goodall, A. H., Gordon, S. D., Gorski, M., Grabe, H.-J., Grallert, H., Grammer, T. B., Gräßler, J., Grönberg, H., Groves, C. J., Gusto, G., Haessler, J., Hall, P., Haller, T., Hallmans, G., Hartman, C. A., Hassinen, M., Hayward, C., Heard-Costa, N. L., Helmer, Q., Hengstenberg, C., Holmen, O., Hottenga, J.-J., James, A. L., Jeff, J. M., Johansson, Å., Jolley, J., Juliusdottir, T., Kinnunen, L., Koenig, W., Koskenvuo, M., Kratzer, W., Laitinen, J., Lamina, C., Leander, K., Lee, N. R., Lichtner, P., Lind, L., Lindström, J., Lo, K. S., Lobbens, S., Lorbeer, R., Lu, Y., Mach, F., Magnusson, P. K. E., Mahajan, A., McArdle, W. L., McLachlan, S., Menni, C., Merger, S., Mihailov, E., Milani, L., Moayyeri, A., Monda, K. L., Morken, M. A., Mulas, A., Müller, G., Müller-Nurasyid, M., Musk, A. W., Nagaraja, R., Nöthen, M. M., Nolte, I. M., Pilz, S., Rayner, N. W., Renstrom, F., Rettig, R., Ried, J. S., Ripke, S., Robertson, N. R., Rose, L. M., Sanna, S., Scharnagl, H., Scholtens, S.,

Schumacher, F. R., Scott, W. R., Seufferlein, T., Shi, J., Smith, A. V., Smolonska, J., Stanton, A. V., Steinhorsdottir, V., Stirrups, K., Stringham, H. M., Sundström, J., Swertz, M. A., Swift, A. J., Syvänen, A.-C., Tan, S.-T., Tayo, B. O., Thorand, B., Thorleifsson, G., Tyrer, J. P., Uh, H.-W., Vandenput, L., Verhulst, F. C., Vermeulen, S. H., Verweij, N., Vonk, J. M., Waite, L. L., Warren, H. R., Waterworth, D., Weedon, M. N., Wilkens, L. R., Willenborg, C., Wilsgaard, T., Wojczynski, M. K., Wong, A., Wright, A. F., Zhang, Q., LifeLines Cohort Study, Brennan, E. P., Choi, M., Dastani, Z., Drong, A. W., Eriksson, P., Franco-Cereceda, A., Gådin, J. R., Gharavi, A. G., Goddard, M. E., Handsaker, R. E., Huang, J., Karpe, F., Kathiresan, S., Keildson, S., Kiryluk, K., Kubo, M., Lee, J.-Y., Liang, L., Lifton, R. P., Ma, B., McCarroll, S. A., McKnight, A. J., Min, J. L., Moffatt, M. F., Montgomery, G. W., Murabito, J. M., Nicholson, G., Nyholt, D. R., Okada, Y., Perry, J. R. B., Dorajoo, R., Reinmaa, E., Salem, R. M., Sandholm, N., Scott, R. A., Stolk, L., Takahashi, A., Tanaka, T., van 't Hooft, F. M., Vinkhuyzen, A. A. E., Westra, H.-J., Zheng, W., Zondervan, K. T., ADIPOGen Consortium, AGEN-BMI Working Group, CARDIOGRAMplusC4D Consortium, CKDGen Consortium, GLGC, ICBP, MAGIC Investigators, MuTHER Consortium, MiGen Consortium, PAGE Consortium, ReproGen Consortium, GENIE Consortium, International Endogene Consortium, Heath, A. C., Arveiler, D., Bakker, S. J. L., Beilby, J., Bergman, R. N., Blangero, J., Bovet, P., Campbell, H., Caulfield, M. J., Cesana, G., Chakravarti, A., Chasman, D. I., Chines, P. S., Collins, F. S., Crawford, D. C., Cupples, L. A., Cusi, D., Danesh, J., de Faire, U., den Ruijter, H. M., Dominiczak, A. F., Erbel, R., Erdmann, J., Eriksson, J. G., Farrall, M., Felix, S. B., Ferrannini, E., Ferrières, J., Ford, I., Forouhi, N. G., Forrester, T., Franco, O. H., Gansevoort, R. T., Gejman, P. V., Gieger, C., Gottesman, O., Gudnason, V., Gyllensten, U., Hall, A. S., Harris, T. B., Hattersley, A. T., Hicks, A. A., Hindorff, L. A., Hingorani, A. D., Hofman, A., Homuth, G., Hovingh, G. K., Humphries, S. E., Hunt, S. C., Hyppönen, E., Illig, T., Jacobs, K. B., Jarvelin, M.-R., Jöckel, K.-H., Johansen, B., Jousilahti, P., Jukema, J. W., Jula, A. M., Kaprio, J., Kastelein, J. J. P., Keinanen-Kiukaanniemi, S. M., Kiemeney, L. A., Knekt, P., Kooner, J. S., Kooperberg, C., Kovacs, P., Kraja, A. T., Kumari, M., Kuusisto, J., Lakka, T. A., Langenberg, C., Marchand, L. L., Lehtimäki, T., Lyssenko, V., Männistö, S., Marette, A., Matise, T. C., McKenzie, C. A., McKnight, B., Moll, F. L., Morris, A. D., Morris, A. P., Murray, J. C., Nelis, M., Ohlsson, C., Oldehinkel, A. J., Ong, K. K., Madden, P. A. F., Pasterkamp, G., Peden, J. F., Peters, A., Postma, D. S., Pramstaller, P. P., Price, J. F., Qi, L., Raitakari, O. T., Rankinen, T., Rao, D. C., Rice, T. K., Ridker, P. M., Rioux, J. D., Ritchie, M. D., Rudan, I., Salomaa, V., Samani, N. J., Saramies, J., Sarzynski, M. A., Schunkert, H., Schwarz, P. E. H., Sever, P., Shuldiner, A. R., Sinisalo, J., Stolk, R. P., Strauch, K., Tönjes, A., Tréguoët, D.-A., Tremblay, A., Tremoli, E., Virtamo, J., Vohl, M.-C., Völker, U., Waeber, G., Willemse, G., Witteman, J. C., Zillikens, M. C., Adair, L. S., Amouyel, P., Asselbergs, F. W., Assimes, T. L., Bochud, M., Boehm, B. O., Boerwinkle, E., Bornstein, S. R., Bottinger, E. P., Bouchard, C., Cauchi, S., Chambers, J. C., Chanock, S. J., Cooper, R. S., de Bakker, P. I. W., Dedoussis, G., Ferrucci, L., Franks, P. W., Froguel, P., Groop, L. C., Haiman, C. A., Hamsten, A., Hui, J., Hunter, D. J., Hveem, K., Kaplan, R. C., Kivimaki, M., Kuh, D., Laakso, M., Liu, Y., Martin, N. G., März, W., Melbye, M., Metspalu, A., Moebus, S., Munroe, P. B., Njølstad, I., Oostra, B. A., Palmer, C. N. A., Pedersen, N. L., Perola, M., Pérusse, L., Peters, U., Power, C., Quertermous, T., Rauramaa, R., Rivadeneira, F., Saaristo, T. E., Saleheen, D., Sattar, N., Schadt, E. E., Schlessinger, D., Slagboom, P. E., Snieder, H., Spector, T. D.,

- Thorsteinsdottir, U., Stumvoll, M., Tuomilehto, J., Uitterlinden, A. G., Uusitupa, M., van der Harst, P., Walker, M., Wallaschofski, H., Wareham, N. J., Watkins, H., Weir, D. R., Wichmann, H.-E., Wilson, J. F., Zanen, P., Borecki, I. B., Deloukas, P., Fox, C. S., Heid, I. M., O'Connell, J. R., Strachan, D. P., Stefansson, K., van Duijn, C. M., Abecasis, G. R., Franke, L., Frayling, T. M., McCarthy, M. I., Visscher, P. M., Scherag, A., Willer, C. J., Boehnke, M., Mohlke, K. L., Lindgren, C. M., Beckmann, J. S., Barroso, I., North, K. E., Ingelsson, E., Hirschhorn, J. N., Loos, R. J. F., Speliotes, E. K. (2015) Genetic studies of body mass index yield new insights for obesity biology. *Nature* 518(7538):197-206.
53. Warren, H. R., Evangelou, E., Cabrera, C. P., Gao, H., Ren, M., Mifsud, B., Ntalla, I., Surendran, P., Liu, C., Cook, J. P., Kraja, A. T., Drenos, F., Loh, M., Verweij, N., Marten, J., Karaman, I., Segura Lepe, M. P., O'Reilly, P. F., Knight, J., Snieder, H., Kato, N., He, J., Tai, E. S., Said, M. A., Porteous, D., Alver, M., Poulter, N., Farrall, M., Gansevoort, R. T., Padmanabhan, S., Mägi, R., Stanton, A., Connell, J., Bakker, S. J. L., Metspalu, A., Shields, D. C., Thom, S., Brown, M., Sever, P., Esko, T., Hayward, C., van der Harst, P., Saleheen, D., Chowdhury, R., Chambers, J. C., Chasman, D. I., Chakravarti, A., Newton-Cheh, C., Lindgren, C. M., Levy, D., Kooner, J. S., Keavney, B., Tomaszewski, M., Samani, N. J., Howson, J. M. M., Tobin, M. D., Munroe, P. B., Ehret, G. B., Wain, L. V., International Consortium of Blood Pressure (ICBP) 1000G Analyses, The CHD Exome+ Consortium, The ExomeBP Consortium The T2D-GENES Consortium The GoT2DGenes Consortium The Cohorts for Heart and Ageing Research in Genome Epidemiology (CHARGE) BP Exome Consortium The International Genomics of Blood Pressure (iGEN-BP) Consortium, Barnes, M. R., Tzoulaki, I., Caulfield, M. J., Elliott, P., UK Biobank CardioMetabolic Consortium BP working group (2017) Corrigendum: Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nat Genet* 49(10):1558.
54. Tobacco and Genetics Consortium (2010) Genome-wide meta-analyses identify multiple loci associated with smoking behavior. *Nat Genet* 42(5):441-7.
55. Wu, M. C., Lee, S., Cai, T., Li, Y., Boehnke, M., Lin, X. (2011) Rare-variant association testing for sequencing data with the sequence kernel association test. *Am J Hum Genet* 89(1):82-93.
56. 1000 Genomes Project Consortium, Auton, A., Brooks, L. D., Durbin, R. M., Garrison, E. P., Kang, H. M., Korbel, J. O., Marchini, J. L., McCarthy, S., McVean, G. A., Abecasis, G. R. (2015) A global reference for human genetic variation. *Nature* 526(7571):68-74.
57. Mu, X. J., Lu, Z. J., Kong, Y., Lam, H. Y. K., Gerstein, M. B. (2011) Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. *Nucleic Acids Res* 39(16):7058-76.
58. He, Z., Xu, B., Lee, S., Ionita-Laza, I. (2017) Unified Sequence-Based Association Tests Allowing for Multiple Functional Annotations and Meta-analysis of Noncoding Variation in Metabochip Data. *Am J Hum Genet* 101(3):340-352.
59. Srigley, J. R., Delahunt, B., Eble, J. N., Egevad, L., Epstein, J. I., Grignon, D., Hes, O., Moch, H., Montironi, R., Tickoo, S. K., Zhou, M., Argani, P., ISUP Renal Tumor Panel (2013) The International Society of Urological Pathology (ISUP) Vancouver Classification of Renal Neoplasia. *Am J Surg Pathol* 37(10):1469-89.
60. Tishkoff, S. A., Reed, F. A., Friedlaender, F. R., Ehret, C., Ranciaro, A., Froment, A.,

- Hirbo, J. B., Awomoyi, A. A., Bodo, J.-M., Doumbo, O., Ibrahim, M., Juma, A. T., Kotze, M. J., Lema, G., Moore, J. H., Mortensen, H., Nyambo, T. B., Omar, S. A., Powell, K., Pretorius, G. S., Smith, M. W., Thera, M. A., Wambebe, C., Weber, J. L., Williams, S. M. (2009) The genetic structure and history of Africans and African Americans. *Science* 324(5930):1035-44.
61. Bryc, K., Durand, E. Y., Macpherson, J. M., Reich, D., Mountain, J. L. (2015) The genetic ancestry of African Americans, Latinos, and European Americans across the United States. *Am J Hum Genet* 96(1):37-53.
62. Salichos, L., Stamatakis, A., Rokas, A. (2014) Novel information theory-based measures for quantifying incongruence among phylogenetic trees. *Mol Biol Evol* 31(5):1261-71.
63. Price, A. L., Patterson, N. J., Plenge, R. M., Weinblatt, M. E., Shadick, N. A., Reich, D. (2006) Principal components analysis corrects for stratification in genome-wide association studies. *Nat Genet* 38(8):904-9.
64. Zhang, K., Wiener, H., Aissani, B. (2015) Admixture mapping of genetic variants for uterine fibroids. *J Hum Genet* 60(9):533-8.
65. Wise, L. A., Ruiz-Narvaez, E. A., Palmer, J. R., Cozier, Y. C., Tandon, A., Patterson, N., Radin, R. G., Rosenberg, L., Reich, D. (2012) African ancestry and genetic risk for uterine leiomyomata. *Am J Epidemiol* 176(12):1159-68.
66. Dunn, P. K., Smyth, G. K. (1996) Randomized Quantile Residuals. *J. Comput. Graph. Stat* 5(3):236--244.
67. Schutz, F. A. B., Pomerantz, M. M., Gray, K. P., Atkins, M. B., Rosenberg, J. E., Hirsch, M. S., McDermott, D. F., Lampron, M. E., Lee, G.-S. M., Signoretti, S., Kantoff, P. W., Freedman, M. L., Choueiri, T. K. (2013) Single nucleotide polymorphisms and risk of recurrence of renal-cell carcinoma: a cohort study. *Lancet Oncol* 14(1):81-7.
68. Brooks, S. A., Brannon, A. R., Parker, J. S., Fisher, J. C., Sen, O., Kattan, M. W., Hakimi, A. A., Hsieh, J. J., Choueiri, T. K., Tamboli, P., Maranchie, J. K., Hinds, P., Miller, C. R., Nielsen, M. E., Rathmell, W. K. (2014) ClearCode34: A prognostic risk predictor for localized clear cell renal cell carcinoma. *Eur Urol* 66(1):77-84.
69. Gordan, J. D., Lal, P., Dondeti, V. R., Letrero, R., Parekh, K. N., Oquendo, C. E., Greenberg, R. A., Flaherty, K. T., Rathmell, W. K., Keith, B., Simon, M. C., Nathanson, K. L. (2008) HIF-alpha effects on c-Myc distinguish two subtypes of sporadic VHL-deficient clear cell renal carcinoma. *Cancer Cell* 14(6):435-46.