References:

- Gerlinger M, Rowan AJ, Horswell S, et al. Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. N Engl J Med. 2012;366(10):88392.
- Murali R, Soslow RA, Weigelt B. Classification of endometrial carcinoma: more than two types. Lancet Oncol. 2014;15(7):e26878.
- 3. Wu CJ. CLL clonal heterogeneity: an ecology of competing subpopulations. Blood. 2012;120(20):41178.
- 4. Schuh A, Becq J, Humphray S, et al. Monitoring chronic lymphocytic leukemia progression by whole genome sequencing reveals heterogeneous clonal evolution patterns. Blood. 2012;120(20):41916.
- Landau DA, Carter SL, Stojanov P, et al. Evolution and impact of subclonal mutations in chronic lymphocytic leukemia. Cell. 2013;152(4):71426.
- 6. Mroz EA, Tward AM, Hammon RJ, Ren Y, Rocco JW. Intratumor genetic heterogeneity and mortality in head and neck cancer: analysis of data from the Cancer Genome Atlas. PLoS Med. 2015;12(2):e1001786.
- 7. Shah SP, Roth A, Goya R, et al. The clonal and mutational evolution spectrum of primary triplenegative breast cancers. Nature. 2012;486(7403):3959.
- Ding L, Ley TJ, Larson DE, et al. Clonal evolution in relapsed acute myeloid leukaemia revealed by wholegenome sequencing. Nature. 2012;481(7382):50610.
- Mertens F, Johansson B, Höglund M, Mitelman F. Chromosomal imbalance maps of malignant solid tumors: a cytogenetic survey of 3185 neoplasms. Cancer Res. 1997;57(13):276580.
- 10. Mitelman F. Recurrent chromosome aberrations in cancer. Mutat Res. 2000;462(23):24753.
- Xi R, Hadjipanayis AG, Luquette LJ, et al. Copy number variation detection in whole genome sequencing data using the Bayesian information criterion. Proc Natl Acad Sci USA. 2011;108(46):E112836.
- 12. Patel AP, Tirosh I, Trombetta JJ, et al. Single cell RNAseq highlights intratumoral heterogeneity in primary glioblastoma. Science. 2014;344(6190):1396401.
- Deng Q, Ramsköld D, Reinius B, Sandberg R. Single cell RNAseq reveals dynamic, random monoallelic gene expression in mammalian cells. Science. 2014;343(6167):1936.
- 14. Borel C, Ferreira PG, Santoni F, et al. Biased allelic expression in human primary fibroblast single cells. Am J Hum Genet. 2015;96(1):7080.
- 15. Carter SL, Cibulskis K, Helman E, et al. Absolute quantification of somatic DNA alterations in human cancer. Nat Biotechnol. 2012;30(5):41321.
- 16. Trapnell C, Cacchiarelli D, Grimsby J, et al. The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. Nat Biotechnol. 2014;32(4):3816.
- 17. Kharchenko PV, Silberstein L, Scadden DT. Bayesian approach to single cell differential expression analysis. Nat Methods. 2014;11(7):7402.
- 18. Fan J, Salathia N, Liu R, Kaeser G, Yung Y, Herman J, Kaper F, Fan JB, Zhang K, Chun J, and Kharchenko PV. Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. Nature Methods (manuscript pending publication)
- 19. Ramsköld D, Luo S, Wang YC, et al. Full length mRNASeq from single cell levels of RNA and individual circulating tumor cells. Nat Biotechnol. 2012;30(8):77782.
- Buganim Y, Faddah DA, Cheng AW, et al. Singlecell expression analyses during cellular reprogramming reveal an early stochastic and a late hierarchic phase. Cell. 2012;150(6):120922.
- 21. Djebali S, Davis CA, Merkel A, et al. Landscape of transcription in human cells. Nature. 2012;489(7414): 1018.
- 22. Burger, JA, Landau DA, Taylor-Weiner A, et al. Clonal evolution in patients with chronic lymphocytic leukemia developing resistance to BTK inhibition. Cancer Discovery (manuscript pending publication)
- 23. Kawaguchi A, Ikawa T, Kasukawa T, et al. Single-cell gene profiling defines differential progenitor subclasses in mammalian neurogenesis. Development. 2008;135(18):311324.
- 24. Ma C, Fan R, Ahmad H, et al. A clinical microchip for evaluation of single immune cells reveals high functional heterogeneity in phenotypically similar T cells. Nat Med. 2011;17(6):73843.
- 25. Marinov GK, Williams BA, Mccue K, et al. From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. Genome Res. 2014;24(3):496510.
- 26. Wang L, Lawrence MS, Wan Y, et al. SF3B1 and other novel cancer genes in chronic lymphocytic leukemia. N Engl J Med. 2011;365(26):2497-506.
- 27. Boeva V, Popova T, Bleakley K, et al. Control-FREEC: a tool for assessing copy number and allelic content using next-generation sequencing data. Bioinformatics. 2012;28(3):423-5.
- 28. Cibulskis K, Lawrence MS,
- 29. Carter SL, et al. Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. Nat Biotechnol. 2013;31(3):213-9.
- 30. Mckenna A, Hanna M, Banks E, et al. The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. Genome Res. 2010;20(9):1297-303.

- 31. Felsenstein J. Evolutionary trees from DNA sequences: a maximum likelihood approach. J Mol Evol. 1981;17(6):368-76.
- 32. Huelsenbeck JP, Ronquist F. MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics. 2001;17(8):754-5.
- 33. Bouckaert R, Heled J, Kühnert D, et al. BEAST 2: a software platform for Bayesian evolutionary analysis. PLoS Comput Biol. 2014;10(4):e1003537.
- 34. Deshwar AG, Vembu S, Yung CK, Jang GH, Stein L, Morris Q. PhyloWGS: reconstructing subclonal composition and evolution from whole-genome sequencing of tumors. Genome Biol. 2015;16:35.
- 35. Subramanian A, Tamayo P, Mootha VK, et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc Natl Acad Sci USA. 2005;102(43):15545-50.
- 36. Irish JM, Myklebust JH, Alizadeh AA, et al. B-cell signaling networks reveal a negative prognostic human lymphoma cell subset that emerges during tumor progression. Proc Natl Acad Sci USA. 2010;107(29): 12747-54.
- 37. Wang L, Shalek AK, Lawrence M, et al. Somatic mutation as a mechanism of Wnt/β-catenin pathway activation in CLL. Blood. 2014;124(7):1089-98.