

LIST OF REFERENCES CORRESPONDING TO THE SUPPLEMENTARY TABLE

Sorted as they appear in the supplementary table.

TCGA

1. McLendon, R., Friedman, A., Bigner, D., Van Meir, E. G., Brat, D. J., M. Mastrogiannis, G., ... Thomson, E. (2008). Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*, 455(7216), 1061–1068. <https://doi.org/10.1038/nature07385>
2. Verhaak, R. G. W., Hoadley, K. A., Purdom, E., Wang, V., Qi, Y., Wilkerson, M. D., ... Hayes, D. N. (2010). Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. *Cancer Cell*, 17(1), 98–110. <https://doi.org/10.1016/j.ccr.2009.12.020>
3. Noshmehr, H., Weisenberger, D. J., Diefes, K., Phillips, H. S., Pujara, K., Berman, B. P., ... Aldape, K. (2010). Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. *Cancer Cell*, 17(5), 510–522. <https://doi.org/10.1016/j.ccr.2010.03.017>
4. Bell, D., Berchuck, A., Birrer, M., Chien, J., Cramer, D. W., Dao, F., ... Thomson, E. (2011). Integrated genomic analyses of ovarian carcinoma. *Nature*, 474(7353), 609–615. <https://doi.org/10.1038/nature10166>
5. Muzny, D. M., Bainbridge, M. N., Chang, K., Dinh, H. H., ... Thomson, E. (2012). Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, 487(7407), 330–337. <https://doi.org/10.1038/nature11252>
6. Hammerman, P. S., Lawrence, M. S., Voet, D., Jing, R., Cibulskis, K., ... Meyerson, M. (2012). Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, 489(7417), 519–525. <https://doi.org/10.1038/nature11404>
7. Koboldt, D. C., Fulton, R. S., McLellan, M. D., Schmidt, H., Kalicki-Veizer, J., McMichael, J. F., ... Palchik, J. D. (2012). Comprehensive molecular portraits of human breast tumours. *Nature*, 490(7418), 61–70. <https://doi.org/10.1038/nature11412>
8. Ley, T. J., Miller, C., Ding, L., Raphael, B. J., Mungall, A. J., ... Wilson, R. K. (2013). Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. *New England Journal of Medicine*, 368(22), 2059–2074. <https://doi.org/10.1056/nejmoa1301689>
9. Getz, G., Gabriel, S. B., Cibulskis, K., Lander, E., Sivachenko, A., Sougnez, C., ... Levine, D. A. (2013). Integrated genomic characterization of endometrial carcinoma. *Nature*, 497(7447), 67–73. <https://doi.org/10.1038/nature12113>
10. Creighton, C. J., Morgan, M., Gunaratne, P. H., Wheeler, D. A., Gibbs, R. A., ... Sofia, H. J. (2013). Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, 499(7456), 43–49. <https://doi.org/10.1038/nature12222>

11. Brennan, C. W., Verhaak, R. G. W., McKenna, A., Campos, B., Noushmehr, H., Salama, S. R., ... McLendon, R. (2013). The Somatic Genomic Landscape of Glioblastoma. *Cell*, 155(2), 462–477. <https://doi.org/10.1016/j.cell.2013.09.034>
12. Weinstein, J. N., Akbani, R., Broom, B. M., Wang, W., Verhaak, R. G. W., ... Eley, G. (2014). Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, 507(7492), 315–322. <https://doi.org/10.1038/nature12965>
13. Collisson, E. A., Campbell, J. D., Brooks, A. N., Berger, A. H., Lee, W., Chmielecki, J., ... Tsao, M.-S. (2014). Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, 511(7511), 543–550. <https://doi.org/10.1038/nature13385>
14. Bass, A. J., Thorsson, V., Shmulevich, I., Reynolds, S. M., Miller, M., Bernard, B., ... Liu, J. (2014). Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, 513(7517), 202–209. <https://doi.org/10.1038/nature13480>
15. Hoadley, K. A., Yau, C., Wolf, D. M., Cherniack, A. D., Tamborero, D., Ng, S., ... Stuart, J. M. (2014). Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. *Cell*, 158(4), 929–944. <https://doi.org/10.1016/j.cell.2014.06.049>
16. Davis, C. F., Ricketts, C. J., Wang, M., Yang, L., Cherniack, A. D., Shen, H., ... Sofia, H. J. (2014). The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. *Cancer Cell*, 26(3), 319–330. <https://doi.org/10.1016/j.ccr.2014.07.014>
17. Agrawal, N., Akbani, R., Aksoy, B. A., Ally, A., Arachchi, H., Asa, S. L., ... Zou, L. (2014). Integrated Genomic Characterization of Papillary Thyroid Carcinoma. *Cell*, 159(3), 676–690. <https://doi.org/10.1016/j.cell.2014.09.050>
18. Lawrence, M. S., Sougnez, C., Lichtenstein, L., Cibulskis, K., Lander, E., ... Yarbrough, W. G. (2015). Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*, 517(7536), 576–582. <https://doi.org/10.1038/nature14129>
19. Brat, D. J., Verhaak, R. G. W., Aldape, K. D., ... Zhang, J. (2015). Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, 372(26), 2481–2498. <https://doi.org/10.1056/nejmoa1402121>
20. Akbani, R., Akdemir, K. C., Aksoy, B. A., Albert, M., Ally, A., Amin, S. B., ... Zou, L. (2015). Genomic Classification of Cutaneous Melanoma. *Cell*, 161(7), 1681–1696. <https://doi.org/10.1016/j.cell.2015.05.044>
21. Ciriello, G., Gatza, M. L., Beck, A. H., Wilkerson, M. D., Rhie, S. K., Pastore, A., ... Zmuda, E. (2015). Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, 163(2), 506–519. <https://doi.org/10.1016/j.cell.2015.09.033>
22. Linehan, W. M., Spellman, P. T., Ricketts, C. J., Creighton, C. J., ... Zuna, R. (2016). Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma.

New England Journal of Medicine, 374(2), 135–145.
<https://doi.org/10.1056/nejmoa1505917>

23. Abeshouse, A., Ahn, J., Akbani, R., Ally, A., Amin, S., Andry, C. D., ... Zmuda, E. (2015). The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, 163(4), 1011–1025.
<https://doi.org/10.1016/j.cell.2015.10.025>

24. Ceccarelli, M., Barthel, F. P., Malta, T. M., Sabedot, T. S., Salama, S. R., Murray, B. A., ... Zmuda, E. (2016). Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell*, 164(3), 550–563.
<https://doi.org/10.1016/j.cell.2015.12.028>

25. Zheng, S., Cherniack, A. D., Dewal, N., Moffitt, R. A., Danilova, L., Murray, B. A., ... Defreitas, T. (2016). Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, 29(5), 723–736.
<https://doi.org/10.1016/j.ccell.2016.04.002>

26. Kim, J., Bowlby, R., Mungall, A. J., Robertson, A. G., Odze, R. D., Cherniack, A. D., ... Zhang, J. (2017). Integrated genomic characterization of oesophageal carcinoma. *Nature*, 541(7636), 169–175. <https://doi.org/10.1038/nature20805>

27. Burk, R. D., Chen, Z., Saller, C., Tarvin, K., Carvalho, A. L., Scapulatempo-Neto, C., ... Mutch, D. (2017). Integrated genomic and molecular characterization of cervical cancer. *Nature*, 543(7645), 378–384. <https://doi.org/10.1038/nature21386>

28. Fishbein, L., Leshchiner, I., Walter, V., Danilova, L., Robertson, A. G., Johnson, A. R., ... Zmuda, E. (2017). Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. *Cancer Cell*, 31(2), 181–193.
<https://doi.org/10.1016/j.ccell.2017.01.001>

29. Cherniack, A. D., Shen, H., Walter, V., Stewart, C., Murray, B. A., Bowlby, R., ... Zuna, R. E. (2017). Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, 31(3), 411–423. <https://doi.org/10.1016/j.ccell.2017.02.010>

30. Farshidfar, F., Zheng, S., Gingras, M.-C., Newton, Y., Shih, J., Robertson, A. G., ... Zmuda, E. (2017). Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH -Mutant Molecular Profiles. *Cell Reports*, 18(11), 2780–2794.
<https://doi.org/10.1016/j.celrep.2017.02.033>

31. Ally, A., Balasundaram, M., Carlsen, R., Chuah, E., Clarke, A., Dhalla, N., ... Laird, P. W. (2017). Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, 169(7), 1327–1341.e23.
<https://doi.org/10.1016/j.cell.2017.05.046>

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32. Ciriello, G., Miller, M. L., Aksoy, B. A., Senbabaoglu, Y., Schultz, N., & Sander, C. (2013). Emerging landscape of oncogenic signatures across human cancers. *Nature Genetics*, 45(10), 1127–1133. <https://doi.org/10.1038/ng.2762>

33. Zack, T. I., Schumacher, S. E., Carter, S. L., Cherniack, A. D., Saksena, G., Tabak, B., ... Beroukhi, R. (2013). Pan-cancer patterns of somatic copy number alteration. *Nature Genetics*, 45(10), 1134–1140. <https://doi.org/10.1038/ng.2760>
34. Lawrence, M. S., Stojanov, P., Polak, P., Kryukov, G. V., Cibulskis, K., Sivachenko, A., ... Getz, G. (2013). Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature*, 499(7457), 214–218. <https://doi.org/10.1038/nature12213>
35. Kandoth, C., McLellan, M. D., Vandin, F., Ye, K., Niu, B., Lu, C., ... Ding, L. (2013). Mutational landscape and significance across 12 major cancer types. *Nature*, 502(7471), 333–339. <https://doi.org/10.1038/nature12634>
36. Tang, K.-W., Alaei-Mahabadi, B., Samuelsson, T., Lindh, M., & Larsson, E. (2013). The landscape of viral expression and host gene fusion and adaptation in human cancer. *Nature Communications*, 4(1). <https://doi.org/10.1038/ncomms3513>
37. Yoshihara, K., Shahmoradgoli, M., Martínez, E., Vegesna, R., Kim, H., Torres-Garcia, W., ... Verhaak, R. G. W. (2013). Inferring tumour purity and stromal and immune cell admixture from expression data. *Nature Communications*, 4(1). <https://doi.org/10.1038/ncomms3612>
38. Jacobsen, A., Silber, J., Harinath, G., Huse, J. T., Schultz, N., & Sander, C. (2013). Analysis of microRNA-target interactions across diverse cancer types. *Nature Structural & Molecular Biology*, 20(11), 1325–1332. <https://doi.org/10.1038/nsmb.2678>
39. Reimand, J., Wagih, O., & Bader, G. D. (2013). The mutational landscape of phosphorylation signaling in cancer. *Scientific Reports*, 3(1). <https://doi.org/10.1038/srep02651>
40. Hofree, M., Shen, J. P., Carter, H., Gross, A., & Ideker, T. (2013). Network-based stratification of tumor mutations. *Nature Methods*, 10(11), 1108–1115. <https://doi.org/10.1038/nmeth.2651>
41. Burns, M. B., Temiz, N. A., & Harris, R. S. (2013). Evidence for APOBEC3B mutagenesis in multiple human cancers. *Nature Genetics*, 45(9), 977–983. <https://doi.org/10.1038/ng.2701>
42. Roberts, S. A., Lawrence, M. S., Klimczak, L. J., Grimm, S. A., Fargo, D., Stojanov, P., ... Gordenin, D. A. (2013). An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. *Nature Genetics*, 45(9), 970–976. <https://doi.org/10.1038/ng.2702>
43. Tamborero, D., Gonzalez-Perez, A., Perez-Llamas, C., Deu-Pons, J., Kandoth, C., Reimand, J., ... Lopez-Bigas, N. (2013). Comprehensive identification of mutational cancer driver genes across 12 tumor types. *Scientific Reports*, 3(1). <https://doi.org/10.1038/srep02650>

ALGORITHMS

ABSOLUTE. Carter, S. L., Cibulskis, K., Helman, E., McKenna, A., Shen, H., Zack, T., ... Getz, G. (2012). Absolute quantification of somatic DNA alterations in human cancer. *Nature Biotechnology*, 30(5), 413–421. <https://doi.org/10.1038/nbt.2203>

ActiveDriver. Reimand, J., & Bader, G. D. (2014). Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. *Molecular Systems Biology*, 9(1), 637–637. <https://doi.org/10.1038/msb.2012.68>

BamBam. Sanborn, J. Z., Salama, S. R., Grifford, M., Brennan, C. W., Mikkelsen, T., Jhanwar, S., ... Haussler, D. (2013). Double Minute Chromosomes in Glioblastoma Multiforme Are Revealed by Precise Reconstruction of Oncogenic Amplicons. *Cancer Research*, 73(19), 6036–6045. <https://doi.org/10.1158/0008-5472.can-13-0186>

BLAST. Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990). Basic local alignment search tool. *Journal of Molecular Biology*, 215(3), 403–410. [https://doi.org/10.1016/s0022-2836\(05\)80360-2](https://doi.org/10.1016/s0022-2836(05)80360-2)

BreakDancer. Chen, K., Wallis, J. W., McLellan, M. D., Larson, D. E., Kalicki, J. M., Pohl, C. S., ... Mardis, E. R. (2009). BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. *Nature Methods*, 6(9), 677–681. <https://doi.org/10.1038/nmeth.1363>

CC. Monti, S., Tamayo, P., Mesirov, J., & Golub, T. (2003). Consensus Clustering: A Resampling-Based Method for Class Discovery and Visualization of Gene Expression Microarray Data. *Machine Learning*, 52(1/2), 91–118. <https://doi.org/10.1023/a:1023949509487>

CHASM. Carter, H., Samayoa, J., Hruban, R. H., & Karchin, R. (2010). Prioritization of driver mutations in pancreatic cancer using cancer-specific high-throughput annotation of somatic mutations (CHASM). *Cancer Biology & Therapy*, 10(6), 582–587. <https://doi.org/10.4161/cbt.10.6.12537>

ClaNC. Dabney, A. R. (2005). ClaNC: point-and-click software for classifying microarrays to nearest centroids. *Bioinformatics*, 22(1), 122–123. <https://doi.org/10.1093/bioinformatics/bti756>

ElasticNet. Zou, H., & Hastie, T. (2005). Regularization and variable selection via the elastic net. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 67(2), 301–320. <https://doi.org/10.1111/j.1467-9868.2005.00503.x>

GISTIC. Beroukhi, R., Getz, G., Nghiemphu, L., Barretina, J., Hsueh, T., Linhart, D., ... Sellers, W. R. (2007). Assessing the significance of chromosomal aberrations in cancer: Methodology and application to glioma. *Proceedings of the National Academy of Sciences*, 104(50), 20007–20012. <https://doi.org/10.1073/pnas.0710052104>

GISTIC 2.0. Mermel, C. H., Schumacher, S. E., Hill, B., Meyerson, M. L., Beroukhi, R., & Getz, G. (2011). GISTIC2.0 facilitates sensitive and confident localization of the

targets of focal somatic copy-number alteration in human cancers. *Genome Biology*, 12(4), R41. <https://doi.org/10.1186/gb-2011-12-4-r41>

GTS. Wiedemeyer, R., Brennan, C., Heffernan, T. P., Xiao, Y., Mahoney, J., Protopopov, A., ... Chin, L. (2008). Feedback Circuit among INK4 Tumor Suppressors Constrains Human Glioblastoma Development. *Cancer Cell*, 13(4), 355–364. <https://doi.org/10.1016/j.ccr.2008.02.010>

HOTNET. Vandin, F., Upfal, E., & Raphael, B. J. (2011). Algorithms for Detecting Significantly Mutated Pathways in Cancer. *Journal of Computational Biology*, 18(3), 507–522. <https://doi.org/10.1089/cmb.2010.0265>

HOTNET2. Leiserson, M. D. M., Vandin, F., Wu, H.-T., Dobson, J. R., Eldridge, J. V., Thomas, J. L., ... Raphael, B. J. (2014). Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *Nature Genetics*, 47(2), 106–114. <https://doi.org/10.1038/ng.3168>

iCluster. Shen, R., Olshen, A. B., & Ladanyi, M. (2009). Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. *Bioinformatics*, 25(22), 2906–2912. <https://doi.org/10.1093/bioinformatics/btp543>

InVEx. Hodis, E., Watson, I. R., Kryukov, G. V., Arold, S. T., Imielinski, M., Theurillat, J.-P., ... Chin, L. (2012). A Landscape of Driver Mutations in Melanoma. *Cell*, 150(2), 251–263. <https://doi.org/10.1016/j.cell.2012.06.024>

ISOPure. Quon, G., Haider, S., Deshwar, A. G., Cui, A., Boutros, P. C., & Morris, Q. (2013). Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. *Genome Medicine*, 5(3), 29. <https://doi.org/10.1186/gm433>

LRT. Chun, S., & Fay, J. C. (2009). Identification of deleterious mutations within three human genomes. *Genome Research*, 19(9), 1553–1561. <https://doi.org/10.1101/gr.092619.109>

MEMo. Ciriello, G., Cerami, E., Sander, C., & Schultz, N. (2011). Mutual exclusivity analysis identifies oncogenic network modules. *Genome Research*, 22(2), 398–406. <https://doi.org/10.1101/gr.125567.111>

Meerkat. Yang, L., Luquette, L. J., Gehlenborg, N., Xi, R., Haseley, P. S., Hsieh, C.-H., ... Park, P. J. (2013). Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. *Cell*, 153(4), 919–929. <https://doi.org/10.1016/j.cell.2013.04.010>

MuSiC. Dees, N. D., Zhang, Q., Kandoth, C., Wendl, M. C., Schierding, W., Koboldt, D. C., ... Ding, L. (2012). MuSiC: Identifying mutational significance in cancer genomes. *Genome Research*, 22(8), 1589–1598. <https://doi.org/10.1101/gr.134635.111>

MutationAssesor. Reva, B., Antipin, Y., & Sander, C. (2011). Predicting the functional impact of protein mutations: application to cancer genomics. *Nucleic Acids Research*, 39(17), e118–e118. <https://doi.org/10.1093/nar/gkr407>

MutationDriver. Reimand, J., & Bader, G. D. (2014). Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. *Molecular Systems Biology*, 9(1), 637–637. <https://doi.org/10.1038/msb.2012.68>

MutationTaster. Schwarz, J. M., Rödelberger, C., Schuelke, M., & Seelow, D. (2010). MutationTaster evaluates disease-causing potential of sequence alterations. *Nature Methods*, 7(8), 575–576. <https://doi.org/10.1038/nmeth0810-575>

MutSig. Chapman, M. A., Lawrence, M. S., Keats, J. J., Cibulskis, K., Sougnez, C., Schinzel, A. C., ... Golub, T. R. (2011). Initial genome sequencing and analysis of multiple myeloma. *Nature*, 471(7339), 467–472. <https://doi.org/10.1038/nature09837>

MutSigCV. Lawrence, M. S., Stojanov, P., Polak, P., Kryukov, G. V., Cibulskis, K., Sivachenko, A., ... Getz, G. (2013). Mutational heterogeneity in cancer and the search for new cancer-associated genes. *Nature*, 499(7457), 214–218. <https://doi.org/10.1038/nature12213>

MutSig2CV. Lawrence, M. S., Stojanov, P., Mermel, C. H., Robinson, J. T., Garraway, L. A., Golub, T. R., ... Getz, G. (2014). Discovery and saturation analysis of cancer genes across 21 tumour types. *Nature*, 505(7484), 495–501. <https://doi.org/10.1038/nature12912>

MuTect. Cibulskis, K., Lawrence, M. S., Carter, S. L., Sivachenko, A., Jaffe, D., Sougnez, C., ... Getz, G. (2013). Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nature Biotechnology*, 31(3), 213–219. <https://doi.org/10.1038/nbt.2514>

NSC. Tibshirani, R., Hastie, T., Narasimhan, B., & Chu, G. (2002). Diagnosis of multiple cancer types by shrunken centroids of gene expression. *Proceedings of the National Academy of Sciences*, 99(10), 6567–6572. <https://doi.org/10.1073/pnas.082099299>

OncoDriveCIS. Tamborero, D., Lopez-Bigas, N., & Gonzalez-Perez, A. (2013). Oncodrive-CIS: A Method to Reveal Likely Driver Genes Based on the Impact of Their Copy Number Changes on Expression. *PLoS ONE*, 8(2), e55489. <https://doi.org/10.1371/journal.pone.0055489>

OncoDriveClust. Tamborero, D., Gonzalez-Perez, A., & Lopez-Bigas, N. (2013). OncodriveCLUST: exploiting the positional clustering of somatic mutations to identify cancer genes. *Bioinformatics*, 29(18), 2238–2244. <https://doi.org/10.1093/bioinformatics/btt395>

OncoDriveFM. Gonzalez-Perez, A., & Lopez-Bigas, N. (2012). Functional impact bias reveals cancer drivers. *Nucleic Acids Research*, 40(21), e169–e169. <https://doi.org/10.1093/nar/gks743>

OncoSign. Ciriello, G., Miller, M. L., Aksoy, B. A., Senbabaoglu, Y., Schultz, N., & Sander, C. (2013). Emerging landscape of oncogenic signatures across human cancers. *Nature Genetics*, 45(10), 1127–1133. <https://doi.org/10.1038/ng.2762>

PAM50. Parker, J. S., Mullins, M., Cheang, M. C. U., Leung, S., Voduc, D., Vickery, T., ... Bernard, P. S. (2009). Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes. *Journal of Clinical Oncology*, 27(8), 1160–1167. <https://doi.org/10.1200/jco.2008.18.1370>

PARADIGM. Vaske, C. J., Benz, S. C., Sanborn, J. Z., Earl, D., Szeto, C., Zhu, J., ... Stuart, J. M. (2010). Inference of patient-specific pathway activities from multi-dimensional cancer genomics data using PARADIGM. *Bioinformatics*, 26(12), i237–i245. <https://doi.org/10.1093/bioinformatics/btq182>

PARADIGM-SHIFT. Ng, S., Collisson, E. A., Sokolov, A., Goldstein, T., Gonzalez-Perez, A., Lopez-Bigas, N., ... Stuart, J. M. (2012). PARADIGM-SHIFT predicts the function of mutations in multiple cancers using pathway impact analysis. *Bioinformatics*, 28(18), i640–i646. <https://doi.org/10.1093/bioinformatics/bts402>

PHIAL. Van Allen, E. M., Wagle, N., Sucker, A., Treacy, D. J., Johannessen, C. M., ... Goetz, E. M. (2013). The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. *Cancer Discovery*, 4(1), 94–109. <https://doi.org/10.1158/2159-8290.cd-13-0617>

PolyPhen-2. Adzhubei, I. A., Schmidt, S., Peshkin, L., Ramensky, V. E., Gerasimova, A., Bork, P., ... Sunyaev, S. R. (2010). A method and server for predicting damaging missense mutations. *Nature Methods*, 7(4), 248–249. <https://doi.org/10.1038/nmeth0410-248>

RAE. Taylor, B. S., Barretina, J., Socci, N. D., DeCarolis, P., Ladanyi, M., Meyerson, M., ... Sander, C. (2008). Functional Copy-Number Alterations in Cancer. *PLoS ONE*, 3(9), e3179. <https://doi.org/10.1371/journal.pone.0003179>

SAM. Tusher, V. G., Tibshirani, R., & Chu, G. (2001). Significance analysis of microarrays applied to the ionizing radiation response. *Proceedings of the National Academy of Sciences*, 98(9), 5116–5121. <https://doi.org/10.1073/pnas.091062498>

SIFT. Kumar, P., Henikoff, S., & Ng, P. C. (2009). Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. *Nature Protocols*, 4(7), 1073–1081. <https://doi.org/10.1038/nprot.2009.86>

SigClust. Liu, Y., Hayes, D. N., Nobel, A., & Marron, J. S. (2008). Statistical Significance of Clustering for High-Dimension, Low-Sample Size Data. *Journal of the American Statistical Association*, 103(483), 1281–1293. <https://doi.org/10.1198/016214508000000454>

SOAPdenovo2. Luo, R., Liu, B., Xie, Y., Li, Z., Huang, W., Yuan, J., ... Wang, J. (2012). SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. *GigaScience*, 1(1). <https://doi.org/10.1186/2047-217x-1-18>