













18. Polak, P., Karlić, R., Koren, A., Thurman, R., Sandstrom, R., et al. (2015). Cell-of-origin chromatin organization shapes the mutational landscape of cancer. *Nature* **518**(7539), 360-364. <https://dx.doi.org/10.1038/nature14221>
19. Jiao, W., Atwal, G., Polak, P., Karlic, R., Cuppen, E., et al. (2019). A deep learning system can accurately classify primary and metastatic cancers based on patterns of passenger mutations. *bioRxiv*. <https://dx.doi.org/10.1101/214494>
20. Poulos, R., Wong, Y., Ryan, R., Pang, H., Wong, J. (2018). Analysis of 7,815 cancer exomes reveals associations between mutational processes and somatic driver mutations. *PLOS Genetics* **14**(11), e1007779. <https://dx.doi.org/10.1371/journal.pgen.1007779>
21. Henderson, S., Chakravarthy, A., Su, X., Boshoff, C., Fenton, T. (2014). APOBEC-Mediated Cytosine Deamination Links PIK3CA Helical Domain Mutations to Human Papillomavirus-Driven Tumor Development. *Cell Reports* **7**(6), 1833-1841. <https://dx.doi.org/10.1016/j.celrep.2014.05.012>
22. Fredriksson, N., Elliott, K., Filges, S., Eynden, J., Ståhlberg, A., Larsson, E. (2017). Recurrent promoter mutations in melanoma are defined by an extended context-specific mutational signature. *PLOS Genetics* **13**(5), e1006773. <https://dx.doi.org/10.1371/journal.pgen.1006773>