



Mutational Data

CancerHubs Data Explorer: A Web Application for Investigating Mutation-Enriched Protein Interaction Hubs in Human Cancers

1 Summary Table

Cancer Type	Sample Size	Sequencing Method	Population	Depth
Multiple myeloma[1]	203	WES + WGS	Adult	89x-30x
Prostate cancer [2]	680	WES	Adult	104x
Breast cancer 1 [3]	216	WES	Adult	122x
Breast cancer 2 [4]	108	WES + WGS	Adult	100x-30x
Pancreatic cancer 1[5]	456	WES + WGS	Adult	400x-75x
Pancreatic cancer 2 [6]	142	WES	Adult	65x/104x/205x
Pancreatic cancer 3 [7]	109	WES	Adult	123x
Colorectal cancer [8]	~13000	NA	Adult	NA
Ovarian cancer [9]	316	WES	Adult	~400x
Small cell lung cancer [10]	110	WGS	Adult	30x
B-ALL [11]	2288	WES + WGS	Pediatric	50x-72x
Burkitt lymphoma [12]	91	WGS	Pediatric	82x
Gastric cancer [13]	100	WGS	Adult	84x
Melanoma [14]	75	WGS	Adult	85x

Table 1: Overview of selected cancer genomic studies

2 Bibliography

- [1] Jens G Lohr et al. “Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy”. In: *Cancer cell* 25.1 (2014), pp. 91–101.
- [2] Joshua Armenia et al. “The long tail of oncogenic drivers in prostate cancer”. In: *Nature genetics* 50.5 (2018), pp. 645–651.
- [3] Celine Lefebvre et al. “Mutational profile of metastatic breast cancers: a retrospective analysis”. In: *PLoS medicine* 13.12 (2016), e1002201.
- [4] Shantanu Banerji et al. “Sequence analysis of mutations and translocations across breast cancer subtypes”. In: *Nature* 486.7403 (2012), pp. 405–409.
- [5] Peter Bailey et al. “Genomic analyses identify molecular subtypes of pancreatic cancer”. In: *Nature* 531.7592 (2016), pp. 47–52.
- [6] Andrew V Biankin et al. “Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes”. In: *Nature* 491.7424 (2012), pp. 399–405.
- [7] Agnieszka K Witkiewicz et al. “Whole-exome sequencing of pancreatic cancer defines genetic diversity and therapeutic targets”. In: *Nature communications* 6.1 (2015), p. 6744.
- [8] David Chisanga et al. “Colorectal cancer atlas: an integrative resource for genomic and proteomic annotations from colorectal cancer cell lines and tissues”. In: *Nucleic acids research* 44.D1 (2016), pp. D969–D974.
- [9] Cancer Genome Atlas Research Network et al. “Integrated genomic analyses of ovarian carcinoma”. In: *Nature* 474.7353 (2011), p. 609.
- [10] Julie George et al. “Comprehensive genomic profiles of small cell lung cancer”. In: *Nature* 524.7563 (2015), pp. 47–53.
- [11] Samuel W Brady et al. “The genomic landscape of pediatric acute lymphoblastic leukemia”. In: *Nature genetics* 54.9 (2022), pp. 1376–1389.
- [12] Bruno M Grande et al. “Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma”. In: *Blood, The Journal of the American Society of Hematology* 133.12 (2019), pp. 1313–1324.
- [13] Kai Wang et al. “Whole-genome sequencing and comprehensive molecular profiling identify new driver mutations in gastric cancer”. In: *Nature genetics* 46.6 (2014), pp. 573–582.
- [14] Nicholas K Hayward et al. “Whole-genome landscapes of major melanoma subtypes”. In: *Nature* 545.7653 (2017), pp. 175–180.