

Table 1 Cancer genome–sequencing studies

Study type	Number of genes screened	Total number of mutations	Number of genes mutated	Average number of mutations per tumor	Estimated number of driver mutations	Reference(s)
Exomic						
Breast (<i>n</i> = 11)	18,191	1243	1137	84	140	87, 88
Colorectal (<i>n</i> = 11)	18,191	942	848	76	140	87, 88
Diverse (<i>n</i> = 210)	518	798	581	–	119	94
Pancreatic (<i>n</i> = 24)	20,661	1163	1007	48	160	98
Glioblastoma (<i>n</i> = 21)	20,661	748	685	47	155	102
Glioblastoma (<i>n</i> = 91)	601	453	223	–	8	103
Lung (<i>n</i> = 188)	623	1013	348	–	26	108
Genomic						
Acute myeloid leukemia (<i>n</i> = 1)	–	500–1000	10	Not applicable	10	82

82. Ley TJ, Mardis E, Ding L, Fulton B, McLellan M, et al. 2008. DNasequencing of a cytogenetically normal acute myeloid leukaemia genome. *Nature* 456:66–72
87. Sjöblom T, Jones S, Wood LD, Parsons DW, Lin J, et al. 2006. The consensus coding sequences of human breast and colorectal cancers. *Science* 314:268–74
88. Wood LD, Parsons DW, Jones S, Lin J, Sjöblom T, et al. 2007. The genomic landscapes of human breast and colorectal cancers. *Science* 318:1108–13
94. Greenman C, Stephens P, Smith R, Dalgliesh GL, Hunter C, et al. 2007. Patterns of somatic mutation in human cancer genomes. *Nature* 446:153–58
98. Jones S, Zhang X, Parsons D, Lin J, Leary R, et al. 2008. Core signaling pathways in human pancreatic cancers revealed by global genomic analyses. *Science* 321:1801–6
102. Parsons DW, Jones S, Zhang X, Lin JC, Leary RJ, et al. 2008. An integrated genomic analysis of human glioblastoma multiforme. *Science* 321:1807–12
103. Cancer Genome Atlas Network. 2008. Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature* 455:1061–68
108. Ding L, Getz G, Wheeler DA, Mardis ER, McLellan MD, et al. 2008. Somatic mutations affect key pathways in lung adenocarcinoma. *Nature* 455:1069–75