

Table S1: Parameters of the cancer datasets analyzed.

dataset	num. patients	% censoring	num. mut. genes	num. genes: 1% < mut. freq. < 10%.
COADREAD	188	92%	2716	1090
GBM	268	30%	3702	1686
KIRC	292	74%	4448	1873
LUSC	175	60%	8465	5646
OV	315	43%	3740	664
UCEC	235	93%	8304	5770

For each dataset we show: the number of patients with both mutation and survival data; the percentage of patients with censored survival data; the number of (meta)genes mutated in at least one sample; the number of (meta)genes mutated in more than 1% and less than 10% of all samples.