

Table S6: GSEA in the high-risk score cohort

Name	SIZE	ES	NES	NOM p-val	FDR q-val	RANK AT MAX
Cell cycle	124	0.726	2.291	< 0.001	0.001	6262
RNA degradation	59	0.641	2.120	< 0.001	0.005	6462
Base excision repair	35	0.714	2.057	< 0.001	0.005	5618
DNA replication	36	0.861	2.069	< 0.001	0.006	2715
Nucleotide excision repair	44	0.66	2.009	0.002	0.007	9025
Homologous recombination	28	0.759	1.996	0.002	0.007	8306
Pentose phosphate pathway	27	0.655	1.923	< 0.001	0.010	4301
Mismatch repair	23	0.788	1.955	< 0.001	0.011	2312
RNA polymerase	28	0.624	1.820	0.010	0.022	7635