

Table S4b: Gene sets enriched in untreated cells

GENE SET NAME	SIZE	ES	NES	NOM p-val	FDR q-val
PROTEIN TARGETING TO MITOCHONDRION GO GO:0006626	47	-0.72	-2.56	0.000	0.000
PROTEIN LOCALIZATION TO MITOCHONDRION GO GO:0070585	49	-0.70	-2.56	0.000	0.000
ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION GO GO:0072655	48	-0.71	-2.52	0.000	0.000
DNA STRAND ELONGATION REACTOME REACT_932.5	30	-0.77	-2.50	0.000	0.000
GLUTATHIONE METABOLISM KEGG HSA00480	44	-0.70	-2.45	0.000	0.000
MITOCHONDRIAL TRANSPORT GO GO:0006839	87	-0.61	-2.45	0.000	0.000
S PHASE REACTOME REACT_899.4	110	-0.58	-2.42	0.000	0.000
MITOCHONDRION ORGANIZATION GO GO:0007005	150	-0.55	-2.41	0.000	0.000
DESTABILIZATION OF MRNA BY KSRP REACTOME REACT_25042.1	17	-0.85	-2.36	0.000	0.000
NUCLEOSIDE PHOSPHATE BIOSYNTHETIC PROCESS GO GO:1901293	98	-0.57	-2.33	0.000	0.000
NCRNA METABOLIC PROCESS GO GO:0034660	182	-0.52	-2.33	0.000	0.000
DNA REPLICATION KEGG HSA03030	35	-0.70	-2.32	0.000	0.000
MITOCHONDRIAL MATRIX GO GO:0005759	235	-0.50	-2.32	0.000	0.000
S PHASE OF MITOTIC CELL CYCLE GO GO:0000084	114	-0.54	-2.30	0.000	0.000
NUCLEOSIDE MONOPHOSPHATE METABOLIC PROCESS GO GO:0009123	25	-0.74	-2.30	0.000	0.000
NUCLEOTIDE METABOLISM REACTOME REACT_1698.10	70	-0.59	-2.29	0.000	0.000
MITOCHONDRIAL PROTEIN IMPORT REACTOME REACT_118595.3	51	-0.64	-2.28	0.000	0.000
ACTIVATION OF THE PRE-REPLICATIVE COMPLEX REACTOME REACT_1095.2	29	-0.71	-2.28	0.000	0.000
TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING GO GO:0010833	34	-0.68	-2.27	0.000	0.000
SYNTHESIS OF DNA REACTOME REACT_2014.2	95	-0.55	-2.26	0.000	0.000
MRNA DECAY BY 3' TO 5' EXORIBONUCLEASE REACTOME REACT_20619.1	11	-0.92	-2.26	0.000	0.000
G1 S TRANSITION REACTOME REACT_1783.2	106	-0.55	-2.26	0.000	0.000
U12 DEPENDENT SPLICING REACTOME REACT_1753.2	42	-0.65	-2.26	0.000	0.000
DNA STRAND ELONGATION GO GO:0022616	36	-0.66	-2.25	0.000	0.000
DNA STRAND ELONGATION INVOLVED IN DNA REPLICATION GO GO:0006271	34	-0.68	-2.24	0.000	0.000
PURINE NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS GO GO:0009127	13	-0.85	-2.24	0.000	0.000
S PHASE GO GO:0051320	126	-0.52	-2.24	0.000	0.000
MITOTIC RECOMBINATION GO GO:0006312	32	-0.68	-2.23	0.000	0.000
M G1 TRANSITION REACTOME REACT_1725.1	81	-0.56	-2.22	0.000	0.000
PURINE RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHESIS REACTOME REACT_1776.3	11	-0.89	-2.22	0.000	0.000
TRNA METABOLIC PROCESS GO GO:0006399	70	-0.58	-2.22	0.000	0.000
NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS GO GO:0009124	18	-0.79	-2.21	0.000	0.000
PURINE RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS GO GO:0009168	13	-0.85	-2.21	0.000	0.000
TELOMERE C-STRAND (LAGGING STRAND) SYNTHESIS REACTOME REACT_7961.4	22	-0.73	-2.21	0.000	0.000
ANATOMICAL STRUCTURE HOMEOSTASIS GO GO:0060249	111	-0.53	-2.20	0.000	0.000
TELOMERE MAINTENANCE VIA RECOMBINATION GO GO:0000722	26	-0.71	-2.20	0.000	0.000
PURINE NUCLEOTIDES <i>DE NOVO</i> <i>BIOSYNTHESIS II HUMANCYC PWY-841</i>	11	-0.89	-2.20	0.000	0.000
DNA REPLICATION PRE-INITIATION REACTOME REACT_734.2	81	-0.56	-2.19	0.000	0.000
RIBONUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS GO GO:0009156	17	-0.78	-2.19	0.000	0.000
ONE CARBON POOL BY FOLATE KEGG HSA00670	18	-0.78	-2.19	0.000	0.000