

Table 2

Gene set	CK1α KO vs. Ctrl up			CK1α OE vs. Ctrl down		
	ES	NES	NOM p-val	ES	NES	NOM p-val
HALLMARK_E2F_TARGETS	0.58	2.25	0	-0.66	-2.75	0
HALLMARK_G2M_CHECKPOINT	0.56	2.22	0	-0.55	-2.33	0
HALLMARK_MITOTIC_SPINDLE	0.35	1.35	0.022	-0.3	-1.26	0.049
HALLMARK_MYC_TARGETS_V1	0.36	1.42	0.002	-0.56	-2.32	0
KEGG_CELL_CYCLE	0.47	1.72	0	-0.49	-1.86	0
KEGG_DNA_REPLICATION	0.56	1.65	0.004	-0.75	-2.3	0
KEGG_HOMOLOGOUS_RECOMBINATION	0.54	1.53	0.033	-0.67	-1.99	0
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	0.41	1.49	0.006	-0.36	-1.38	0.011
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	0.55	1.65	0.008	-0.7	-2.22	0
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	0.56	1.65	0.02	-0.79	-2.35	0
REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS	0.42	1.46	0.012	-0.47	-1.79	0
REACTOME_CELL_CYCLE_CHECKPOINTS	0.42	1.68	0	-0.55	-2.37	0
REACTOME_CELL_CYCLE_MITOTIC	0.38	1.61	0	-0.5	-2.29	0
REACTOME_CHROMOSOME_MAINTENANCE	0.52	1.79	0	-0.59	-2.24	0
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	0.61	1.72	0.008	-0.65	-1.96	0
REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	0.42	1.55	0.002	-0.54	-1.92	0
REACTOME_DNA_REPLICATION	0.42	1.53	0.004	-0.62	-2.41	0
REACTOME_DNA_STRAND_ELONGATION	0.63	1.83	0	-0.78	-2.38	0
REACTOME_EXTENSION_OF_TELOMERES	0.55	1.73	0.002	-0.62	-2.09	0
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVELOPE	0.64	1.96	0	-0.53	-1.73	0.005
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	0.55	1.55	0.021	-0.7	-2.07	0
REACTOME_G2_M_CHECKPOINTS	0.42	1.56	0	-0.54	-2.12	0
REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT	0.51	1.69	0	-0.51	-1.76	0
REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR	0.46	1.56	0.006	-0.54	-1.93	0
REACTOME_HDR_THROUGH_SINGLE_STRAND_ANNEALING_SSA	0.5	1.53	0.017	-0.57	-1.8	0.002
REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE	0.57	1.74	0.004	-0.61	-2.01	0
REACTOME_HOMOLOGY_DIRECTED_REPAIR	0.43	1.55	0.008	-0.53	-2.01	0
REACTOME_KERATINIZATION	0.63	1.97	0	-0.53	-1.72	0.002
REACTOME_LAGGING_STRAND_SYNTHESIS	0.61	1.58	0.019	-0.76	-2.06	0
REACTOME_M_PHASE	0.35	1.45	0.004	-0.45	-1.99	0
REACTOME_MEIOTIC_RECOMBINATION	0.62	1.69	0.008	-0.54	-1.55	0.031
REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION	0.38	1.45	0.011	-0.55	-2.18	0
REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	0.37	1.46	0.004	-0.5	-2.13	0
REACTOME_MITOTIC_PROMETAPHASE	0.43	1.69	0	-0.48	-2.01	0
REACTOME_MITOTIC_SPINDLE_CHECKPOINT	0.5	1.81	0	-0.59	-2.24	0
REACTOME_POLO LIKE_KINASE_MEDIATED_EVENTS	0.63	1.57	0.029	-0.7	-1.84	0
REACTOME_POLYMERASE_SWITCHING_ON_THE_C_STRAND_OF_THE_TELOMERE	0.54	1.48	0.041	-0.68	-1.94	0.002
REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS	0.46	1.53	0.012	-0.45	-1.8	0
REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND	0.6	1.48	0.044	-0.74	-1.86	0
REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES	0.52	1.53	0.023	-0.61	-1.88	0.002
REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES_THROUGH_SYNTHESIS_DEPENDENT_STRAND_ANNEA	0.63	1.73	0.004	-0.68	-1.99	0
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	0.46	1.7	0.002	-0.55	-2.13	0
REACTOME_RHO_GTPASE_EFFECTORS	0.31	1.26	0.026	-0.39	-1.65	0
REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	0.41	1.54	0.004	-0.52	-2.04	0
REACTOME_SEPARATION_OF_SISTER_CHROMATIDS	0.4	1.53	0.004	-0.49	-2.02	0
REACTOME_TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS	0.55	1.6	0.026	-0.71	-2.18	0
REACTOME_TELOMERE_MAINTENANCE	0.47	1.55	0.006	-0.59	-2.08	0

Gene set	CK1α OE vs. Ctrl up			CK1α KO vs. Ctrl down		
	ES	NES	NOM p-val	ES	NES	NOM p-val
KEGG_ABC_TRANSPORTERS	0.59	1.71	0.002	-0.51	-1.46	0.035
KEGG_RETINOL_METABOLISM	0.61	1.76	0.005	-0.56	-1.58	0.006
KEGG_STARCH_AND_SUCROSE_METABOLISM	0.57	1.66	0.015	-0.64	-1.87	0.002
REACTOME_BIOLOGICAL_OXIDATIONS	0.44	1.6	0.003	-0.44	-1.64	0