

Supplementary Table 1. Detail of the Gene Set Enrichment Analysis for all six lncRNAs

Gene set	Gene	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	38	0.68	2.24	0.00E+00	9.59E-04	8.00E-03
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	35	0.76	2.23	0.00E+00	9.60E-04	9.00E-03
REACTOME_MITOTIC_M_M_G1_PHASES	137	0.66	2.26	0.00E+00	1.04E-03	6.00E-03
REACTOME_G1_S_TRANSITION	93	0.70	2.24	0.00E+00	1.05E-03	8.00E-03
REACTOME_TRANSCRIPTION	165	0.58	2.22	0.00E+00	1.13E-03	1.00E-02
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	57	0.66	2.24	0.00E+00	1.15E-03	8.00E-03
REACTOME_HIV_LIFE_CYCLE	108	0.60	2.21	0.00E+00	1.18E-03	1.20E-02
REACTOME_DNA_REPLICATION	156	0.66	2.26	0.00E+00	1.19E-03	6.00E-03
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	96	0.60	2.21	0.00E+00	1.26E-03	1.20E-02
REACTOME_CELL_CYCLE_CHECKPOINTS	94	0.70	2.24	0.00E+00	1.28E-03	8.00E-03
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	186	0.57	2.28	0.00E+00	1.30E-03	4.00E-03
REACTOME_CELL_CYCLE_MITOTIC	253	0.61	2.26	0.00E+00	1.39E-03	6.00E-03
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	153	0.59	2.29	0.00E+00	1.40E-03	3.00E-03
REACTOME_HIV_INFECTION	182	0.61	2.27	0.00E+00	1.67E-03	6.00E-03
REACTOME_CELL_CYCLE	322	0.60	2.31	0.00E+00	1.98E-03	2.00E-03
REACTOME_RNA_POL_II_TRANSCRIPTION	84	0.64	2.30	0.00E+00	2.10E-03	3.00E-03
REACTOME_M_G1_TRANSITION	67	0.71	2.17	0.00E+00	2.54E-03	2.30E-02
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	114	0.62	2.16	0.00E+00	2.57E-03	2.50E-02
REACTOME_MITOTIC_G1_G1_S_PHASES	112	0.64	2.15	0.00E+00	2.81E-03	3.20E-02
REACTOME_DNA_REPAIR	92	0.58	2.16	0.00E+00	2.96E-03	3.20E-02
REACTOME_S_PHASE	93	0.69	2.15	0.00E+00	3.15E-03	4.00E-02
REACTOME_MITOTIC_PROMETAPHASE	66	0.62	2.12	0.00E+00	3.68E-03	5.20E-02
REACTOME_MRNA_SPLICING	71	0.62	2.12	0.00E+00	3.72E-03	5.40E-02
KEGG_BASAL_TRANSCRIPTION_FACTORS	31	0.61	2.14	0.00E+00	3.74E-03	4.80E-02
REACTOME_SYNTHESIS_OF_DNA	78	0.70	2.12	0.00E+00	3.83E-03	5.20E-02
REACTOME_CHROMOSOME_MAINTENANCE	93	0.62	2.12	0.00E+00	3.86E-03	5.40E-02
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	51	0.74	2.11	0.00E+00	3.88E-03	5.90E-02
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	69	0.71	2.13	0.00E+00	3.90E-03	5.10E-02
KEGG_CELL_CYCLE	105	0.56	2.11	0.00E+00	3.91E-03	5.70E-02
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	73	0.66	2.13	0.00E+00	3.97E-03	5.10E-02
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	58	0.72	2.07	0.00E+00	4.32E-03	8.80E-02
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX	41	0.65	2.08	0.00E+00	4.53E-03	8.80E-02
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	47	0.60	2.08	0.00E+00	4.64E-03	8.80E-02
REACTOME_MRNA_PROCESSING	114	0.57	2.10	0.00E+00	4.64E-03	6.90E-02
KEGG_HUNTINGTONS_DISEASE	151	0.56	2.07	0.00E+00	4.73E-03	9.40E-02
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION	60	0.71	2.10	0.00E+00	4.75E-03	6.80E-02
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	56	0.71	2.08	0.00E+00	4.75E-03	8.80E-02
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1	58	0.72	2.08	0.00E+00	4.85E-03	8.70E-02
KEGG_SPLICEOSOME	84	0.63	2.08	0.00E+00	4.95E-03	8.60E-02
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	51	0.73	2.06	0.00E+00	4.95E-03	9.80E-02
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	99	0.58	2.08	0.00E+00	5.05E-03	8.60E-02
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	50	0.71	2.08	0.00E+00	5.08E-03	8.40E-02
REACTOME_METABOLISM_OF_NON_CODING_RNA	39	0.65	2.05	0.00E+00	5.14E-03	1.06E-01
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION	27	0.68	2.08	0.00E+00	5.18E-03	8.40E-02
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	17	0.75	2.05	0.00E+00	5.19E-03	1.04E-01
KEGG_PARKINSONS_DISEASE	96	0.64	2.05	0.00E+00	5.30E-03	1.09E-01
REACTOME_APOPTOSIS	128	0.52	2.08	0.00E+00	5.33E-03	8.40E-02
REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	42	0.62	2.08	0.00E+00	5.34E-03	8.00E-02
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	47	0.75	2.04	0.00E+00	5.39E-03	1.12E-01
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	54	0.71	2.04	0.00E+00	5.76E-03	1.27E-01
REACTOME_SIGNALING_BY_WNT	59	0.67	2.03	0.00E+00	5.95E-03	1.30E-01

(Continued to the next page)

Supplementary Table 1. Continued

Gene set	Gene	ES	NES	NOM <i>p</i> -val	FDR <i>q</i> -val	FWER <i>p</i> -val
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	56	0.69	2.03	0.00E+00	5.96E-03	1.33E-01
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	44	0.74	2.03	0.00E+00	6.02E-03	1.37E-01
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	103	0.66	2.03	0.00E+00	6.02E-03	1.37E-01
REACTOME_SCF_BETA_TROP_MEDIATED_DEGRADATION_OF_EMI1	46	0.74	2.02	0.00E+00	6.63E-03	1.52E-01
PID_BARD1_PATHWAY	28	0.62	2.02	0.00E+00	6.78E-03	1.61E-01
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	108	0.48	2.01	0.00E+00	6.88E-03	1.69E-01
REACTOME_TRNA_AMINOACYLATION	29	0.69	1.97	0.00E+00	8.05E-03	2.35E-01
REACTOME_REGULATION_OF_APOPTOSIS	51	0.67	1.98	0.00E+00	8.11E-03	2.24E-01
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	21	0.62	1.97	0.00E+00	8.12E-03	2.35E-01
REACTOME_MRNA_CAPPING	27	0.65	1.98	0.00E+00	8.13E-03	2.24E-01
REACTOME_REGULATORY_RNA_PATHWAYS	21	0.64	1.97	0.00E+00	8.16E-03	2.33E-01
REACTOME_PURINE_METABOLISM	27	0.64	1.98	0.00E+00	8.17E-03	2.27E-01
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	45	0.73	1.98	0.00E+00	8.21E-03	2.18E-01
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	44	0.73	1.98	0.00E+00	8.24E-03	2.21E-01
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	46	0.72	1.97	0.00E+00	8.24E-03	2.32E-01
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	95	0.57	1.99	0.00E+00	8.26E-03	2.04E-01
REACTOME_FORMATION_OF_TRANSCRIPTION_COUPLED_NER_TC_NER_REPAIR_COMPLEX	27	0.61	1.98	0.00E+00	8.32E-03	2.18E-01
REACTOME_FORMATION_OF_THE_HIV1_EARLY_ELONGATION_COMPLEX	31	0.65	1.96	0.00E+00	8.39E-03	2.45E-01
REACTOME_ELONGATION_ARREST_AND_RECOVERY	31	0.64	1.98	0.00E+00	8.55E-03	2.18E-01
REACTOME_METABOLISM_OF_NUCLEOTIDES	56	0.57	1.98	0.00E+00	8.61E-03	2.16E-01
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	46	0.73	1.98	0.00E+00	8.71E-03	2.15E-01
KEGG_OXIDATIVE_PHOSPHORYLATION	98	0.63	1.98	0.00E+00	8.79E-03	2.14E-01
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	26	0.73	1.96	0.00E+00	9.10E-03	2.63E-01
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	78	0.58	1.95	0.00E+00	9.15E-03	2.76E-01
REACTOME_G2_M_CHECKPOINTS	31	0.71	1.95	0.00E+00	9.29E-03	2.75E-01
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	60	0.56	2.05	1.96E-03	5.08E-03	1.04E-01
REACTOME_ER_PHAGOSOME_PATHWAY	56	0.69	1.99	1.96E-03	8.10E-03	2.01E-01
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS	72	0.69	1.95	1.96E-03	9.44E-03	2.74E-01
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	47	0.72	1.97	1.98E-03	8.09E-03	2.35E-01
KEGG_PROTEASOME	41	0.78	2.01	1.98E-03	6.86E-03	1.64E-01
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	68	0.63	2.00	1.99E-03	7.80E-03	1.92E-01
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	40	0.63	1.97	2.05E-03	7.99E-03	2.35E-01
REACTOME_TELOMERE_MAINTENANCE	60	0.65	1.98	2.08E-03	8.44E-03	2.18E-01
KEGG_DNA_REPLICATION	32	0.73	2.08	2.09E-03	4.42E-03	8.80E-02
KEGG_PYRIMIDINE_METABOLISM	73	0.54	1.95	2.09E-03	9.24E-03	2.76E-01
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	20	0.74	2.00	2.10E-03	7.91E-03	1.92E-01
REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	45	0.65	1.95	2.13E-03	9.35E-03	2.74E-01
REACTOME_MICRORNA_MIRNA_BIOGENESIS	20	0.65	1.96	2.20E-03	8.46E-03	2.49E-01
PID_FANCONI_PATHWAY	37	0.63	2.06	2.21E-03	4.84E-03	9.80E-02
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	31	0.60	1.98	2.25E-03	8.15E-03	2.22E-01

lncRNA = long noncoding RNA; ES = enrichment score; NES = normalized enrichment score; NOM *p*-val = nominal *p*-value; FDR *q*-val = false discovery rate *q*-value; FWER *p*-val = familywise-error rate *p*-value.