

Supplementary Table 1: Top Altered Pathways (Hallmarks) Found by GSEA

NAME	ES	NES	NOM p-val	FDR q-val	FWER p-val
HALLMARK_MYC_TARGETS_V2	0.60538054	1.6276323	0	0.007223	0.008
HALLMARK_COAGULATION	0.5158395	1.4932013	0	0.040666	0.081
HALLMARK_DNA_REPAIR	0.45669493	1.33333	0.013319672	0.287705	0.612
HALLMARK_MYC_TARGETS_V1	0.4408033	1.3066767	0.009063444	0.304192	0.737
HALLMARK_IL2_STAT5_SIGNALING	0.40566048	1.2073549	0.064386316	0.870637	0.995
HALLMARK_ALLOGRAFT_REJECTION	0.39063314	1.1652709	0.11155779	1	1
HALLMARK_COMPLEMENT	0.38741273	1.1414809	0.15126903	1	1
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.37742546	1.121301	0.20101011	1	1
HALLMARK_APICAL_SURFACE	0.43187517	1.1201342	0.29477197	1	1
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSIT	0.37593582	1.1175237	0.21370968	1	1
HALLMARK_P53_PATHWAY	0.37350225	1.1085943	0.2201005	1	1
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0.39848816	1.1032214	0.29306722	0.962513	1
HALLMARK_APOPTOSIS	0.37412247	1.1029364	0.25583756	0.890098	1
HALLMARK_HYPOXIA	0.36348468	1.0855932	0.28241205	0.943208	1
HALLMARK_SPERMATOGENESIS	0.37099823	1.078535	0.3119266	0.925385	1
HALLMARK_INFLAMMATORY_RESPONSE	0.35054496	1.0518492	0.35656565	1	1
HALLMARK_PANCREAS_BETA_CELLS	0.40927812	1.0508529	0.4127708	0.984789	1
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHW	0.39641365	1.0387547	0.42857143	0.998277	1
HALLMARK_XENOBIOTIC_METABOLISM	0.347125	1.0330001	0.41893253	0.979746	1
HALLMARK_UV_RESPONSE_UP	0.35012487	1.0267731	0.4336373	0.963679	1
HALLMARK_ADIPOGENESIS	0.33963317	1.0117598	0.48738647	0.994493	1
HALLMARK_PEROXISOME	0.35077068	1.0042886	0.48715314	0.984671	1
HALLMARK_KRAS_SIGNALING_UP	0.33394197	0.98538816	0.5497487	1	1
HALLMARK_GLYCOLYSIS	0.3283518	0.97529405	0.582495	1	1
HALLMARK_APICAL_JUNCTION	0.324182	0.9622982	0.5866935	1	1
HALLMARK_KRAS_SIGNALING_DN	0.3181483	0.949984	0.6487854	1	1
HALLMARK_HEDGEHOG_SIGNALING	0.379662	0.94853055	0.58796823	1	1
HALLMARK_MITOTIC_SPINDLE	0.30376834	0.9016724	0.75075376	1	1
HALLMARK_IL6_JAK_STAT3_SIGNALING	0.31807417	0.89518476	0.68393236	1	1
HALLMARK_BILE_ACID_METABOLISM	0.29928148	0.8595257	0.7792746	1	1

HALLMARK_FATTY_ACID_METABOLISM	0.28964478	0.851636	0.8235294	1	1
HALLMARK_MYOGENESIS	0.28270015	0.841054	0.8663968	1	1
HALLMARK_WNT_BETA_CATENIN_SIGNALING	0.3243181	0.84052074	0.7394286	1	1
HALLMARK_UV_RESPONSE_DN	0.28026488	0.82431847	0.8575788	1	1
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.2771199	0.8241499	0.8891129	1	1
HALLMARK_PROTEIN_SECRETION	0.28308353	0.8005513	0.8543388	1	1
HALLMARK_E2F_TARGETS	0.26323238	0.77946323	0.9366197	1	1
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.2738264	0.77696174	0.8917526	1	1
HALLMARK_ESTROGEN_RESPONSE_EARLY	0.24998467	0.7386228	0.9769308	1	1
HALLMARK_ESTROGEN_RESPONSE_LATE	0.24042875	0.72114694	0.9757576	1	1
HALLMARK_TGF_BETA_SIGNALING	0.26075536	0.69803345	0.9256017	1	1
HALLMARK_PI3K_AKT_MTOR_SIGNALING	0.22416037	0.6395408	0.9927159	1	1
HALLMARK_MTORC1_SIGNALING	0.19858561	0.5916655	1	1	1
HALLMARK_G2M_CHECKPOINT	0.18722288	0.5564647	1	0.99861	1

Supplementary Table 2: Top Altered Pathways (All included) Found by GSEA

NAME	ES	NES	NOM p-val	FDR q-val	FWER p-val
REACTOME_PEPTIDE_CHAIN_ELONGATION	0.8821209	2.4668512	0	0	0
KEGG_RIBOSOME	0.85542816	2.3796058	0	0	0
REACTOME_SRP_DEPENDENT_COTRANSLATION	0.8228177	2.348257	0	0	0
REACTOME_3_UTR_MEDIATED_TRANSLATION	0.82671034	2.3478634	0	0	0
GCM_TPT1	0.856445	2.3263211	0	0	0
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION	0.8275831	2.3235037	0	0	0
REACTOME_NONSENSE_MEDIATED_DECAY_OF_MRNA	0.8144567	2.3197722	0	0	0
STRUCTURAL_CONSTITUENT_OF_RIBOSOME	0.8173651	2.2617867	0	0	0
BILANGES_SERUM_AND_RAPAMYCIN_SENSITIVITY	0.8415251	2.256115	0	0	0
REACTOME_TRANSLATION	0.7573706	2.2176175	0	0	0
GNF2_EIF3S6	0.7659197	2.1851923	0	0	0
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX	0.8296112	2.174116	0	0	0
REACTOME_INFLUENZA_LIFE_CYCLE	0.75449145	2.1721048	0	0	0
GNF2_ST13	0.785444	2.1223912	0	0	0
CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UI	0.8040925	2.1123197	0	0	0
GNF2_TPT1	0.85651046	2.1089988	0	0	0
MORF_TPT1	0.7476573	2.0991602	0	0	0
REACTOME_ACTIVATION_OF_THE_MRNA_UPSTREAM	0.77908516	2.095887	0	0	0
MODULE_29	0.87099814	2.083428	0	0	0
GCM_NPM1	0.73270184	2.0820324	0	0	0
GNF2_GLTSCR2	0.8589662	2.0524864	0	0	0
MORF_ACTG1	0.6982923	2.0117874	0	0	0
MORF_NPM1	0.68745464	2.0082934	0	0	0
GNF2_FBL	0.66961443	1.9675678	0	8.23E-05	0.002
REACTOME_METABOLISM_OF_MRNA	0.65269077	1.9490323	0	7.90E-05	0.002
BILANGES_SERUM_RESPONSE_TRANSLATION	0.765813	1.9243857	0	1.52E-04	0.004
HOLLEMAN_ASPARAGINASE_RESISTANCE_B	0.79257584	1.9107535	0	4.02E-04	0.011
MORF_JUND	0.70063734	1.8961203	0	6.34E-04	0.018
REACTOME_METABOLISM_OF_RNA	0.6146553	1.8456451	0	0.00210843	0.06
TRANSLATION	0.6125013	1.8189807	0	0.00394564	0.114

GSE2405_0H_VS_24H_A_PHAGOCYTOPHILUM	0.6084147	1.8166133	0	0.00404093	0.121
GNF2_DAP3	0.6324597	1.8057325	0	0.00465451	0.142
MORF_NME2	0.6180371	1.7984093	0	0.0053802	0.167
GSE2405_0H_VS_9H_A_PHAGOCYTOPHILUM_	0.60228866	1.7975248	0	0.00530902	0.17
CHR11Q11	0.6755318	1.7970518	0	0.00518557	0.171
MODULE_83	0.5812919	1.7621909	0	0.01131662	0.336
TIEN_INTESTINE_PROBIOTICS_6HR_UP	0.65977275	1.7475249	0	0.01482352	0.423
STRUCTURAL_MOLECULE_ACTIVITY	0.58592355	1.7454493	0	0.01497838	0.435
PECE_MAMMARY_STEM_CELL_UP	0.5975707	1.7446808	0	0.01477124	0.438
GCM_ACTG1	0.6102801	1.7434995	0	0.0148953	0.451
LUI_THYROID_CANCER_CLUSTER_3	0.71250176	1.7223192	0	0.02285601	0.602
FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONS	0.6448852	1.7111357	0	0.02750201	0.67
POMEROY_MEDULLOBLASTOMA_PROGNOSIS	0.65398914	1.7056035	0	0.02993678	0.701
YAMASHITA_LIVER_CANCER_WITH_EPCAM_U	0.6358509	1.6935279	0	0.03678644	0.788
MODULE_151	0.55775696	1.6934345	0	0.03603471	0.789
GSE14000_TRANSLATED_RNA_VS_MRNA_DC	0.5682297	1.693358	0	0.03529431	0.79
GCM_APEX1	0.58865047	1.6801664	0	0.04518152	0.875
MORF_EIF3S6	0.5792044	1.6773926	0	0.04664381	0.893
BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1	0.60306114	1.6718509	0	0.05068482	0.917
POMEROY_MEDULLOBLASTOMA_DESMOPLAS	0.622295	1.6709313	0	0.05049953	0.921
MODULE_114	0.55404806	1.6702026	0	0.05014738	0.923
MODULE_32	0.5592743	1.6692228	0	0.04999847	0.927
GSE41978_ID2_KO_VS_ID2_KO_AND_BIM_KC	0.561629	1.6688108	0	0.04940864	0.928
GNF2_NPM1	0.6011008	1.6640451	0.00107181	0.05254708	0.941
MORF_EIF4A2	0.5714935	1.6594828	0	0.05564504	0.953
MYC_UP.V1_UP	0.5573767	1.6494309	0	0.06493662	0.975
GCM_CSNK2B	0.5799508	1.6403692	0	0.07461243	0.986
GNF2_SPRR1B	0.71056086	1.6361141	0.0012285	0.0791752	0.99
RNA_BINDING	0.54184085	1.6335474	0	0.08127637	0.993
MCGOWAN_RSP6_TARGETS_UP	0.72852594	1.6301829	0.00125156	0.08440943	0.996
CARBOHYDRATE_TRANSPORT	0.7456734	1.6260619	0.00483092	0.08891249	0.996

HALLMARK_MYC_TARGETS_V2	0.60538054	1.6220471	0.00107181	0.09361915	0.997
GSE42088_UNINF_VS_LEISHMANIA_INF_DC_	0.54699755	1.621902	0	0.09233674	0.997
REACTOME_METABOLISM_OF_PROTEINS	0.5315821	1.6207446	0	0.09240431	0.997
MORF_UBE2I	0.5419062	1.6204833	0	0.09146821	0.997
SWEET_KRAS_ONCOGENIC_SIGNATURE	0.5705057	1.6023487	0	0.12394311	1
LUI_THYROID_CANCER_PAX8_PPARG_DN	0.60970944	1.6021744	0.00111732	0.12243166	1
GSE22886_NAIVE_TCELL_VS_DC_UP	0.5423759	1.5988914	0	0.12749194	1
JIANG_TIP30_TARGETS_DN	0.6939703	1.5919838	0.00363196	0.14093745	1
GSE13485_CTRL_VS_DAY7_YF17D_VACCINE_I	0.54482466	1.5904001	0	0.14267212	1
GSE3720_UNSTIM_VS_PMA_STIM_VD2_GAM	0.5375035	1.5879712	0	0.14583017	1
STEGER_ADIPOGENESIS_DN	0.6644432	1.5878977	0.00238379	0.14394176	1
MORF_CCNI	0.5654207	1.5873467	0	0.14298345	1
IRITANI_MAD1_TARGETS_DN	0.5996607	1.5854287	0	0.14550292	1
HOLLEMAN_ASPARAGINASE_RESISTANCE_AL	0.68996346	1.5842619	0.00241255	0.14632373	1
ABE_INNER_EAR	0.60904694	1.5826453	0.00448934	0.14800522	1
HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_	0.7115724	1.5802433	0.00369914	0.15160392	1
CHR4Q35	0.65230995	1.5773951	0	0.15632483	1
GSE42724_NAIVE_VS_B1_BCELL_DN	0.52969486	1.5757798	0	0.15857798	1
GCM_PSME1	0.5596052	1.574699	0.00210084	0.15912314	1
GSE22886_NAIVE_BCELL_VS_NEUTROPHIL_U	0.53098655	1.5729147	0	0.16130026	1
REACTOME_METAL_ION_SLC_TRANSPORTER:	0.6686739	1.5704443	0.00472255	0.16591242	1
HILLION_HMGA1_TARGETS	0.5547232	1.568255	0.00105042	0.16941547	1
CALCIUM_INDEPENDENT_CELL_CELL_ADHESIC	0.671338	1.5652384	0.00713436	0.1758639	1
GSE37532_TREG_VS_TCONV_CD4_TCELL_FRC	0.52696645	1.5647296	0	0.1749089	1
GSE21927_SPLEEN_C57BL6_VS_4T1_TUMOR_	0.5260873	1.5619605	0	0.1803051	1
GSE41978_KLRG1_HIGH_VS_LOW_EFFECTOR	0.52455604	1.5610679	0	0.1807718	1
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_D	0.566605	1.5595582	0.00106157	0.18265063	1
MACROMOLECULE_BIOSYNTHETIC_PROCESS	0.5144034	1.5585566	0	0.18364607	1
LIPOPROTEIN_BIOSYNTHETIC_PROCESS	0.64861053	1.558046	0.00473373	0.18286563	1
CHIARADONNA_NEOPLASTIC_TRANSFORMAT	0.5855788	1.5571196	0.00220264	0.18334933	1
APICOLATERAL_PLASMA_MEMBRANE	0.6190701	1.5523444	0.00800915	0.1955924	1

REACTOME_ABC_FAMILY_PROTEINS_MEDIAT	0.62543786	1.5480615	0.00451977	0.20623665	1
TIGHT_JUNCTION	0.62610644	1.5456564	0.0079636	0.21222499	1
CHRX21	0.66182864	1.5445017	0.00859951	0.21370725	1
NEWMAN_ERCC6_TARGETS_DN	0.613319	1.5437745	0.00683371	0.21402858	1
APICAL_JUNCTION_COMPLEX	0.6190701	1.5434597	0.00696056	0.2127474	1
CHR7Q11	0.5624893	1.5428807	0	0.21237777	1
DEVELOPMENT_OF_PRIMARY_SEXUAL_CHAR.	0.65302175	1.5397419	0.00358852	0.220613	1
HE_PTEN_TARGETS_UP	0.70413804	1.5394862	0.0122549	0.21931419	1

Supplementary Table 2: Genotyping Primers

Gene	Sequencing Primers (5' to 3')
<i>Cre</i>	GCT GCC ACG ACC AAG TGA CAG CAA TG GTA GTT ATT CGG ATC ATC AGC CAC AC
<i>Kras</i>	CTA GCC ACC ATG GCT TGA GT TCC GAA TTC AGT GAC TAC AGA TG ATG TCT TTC CCC AGC ACA GT
<i>Arid1a</i>	GTA ATG GGA AAG CGA CTA CTG GAG TGT TCA TTT TTG TGG CGG GAG
<i>Tp53</i>	GGT TAA ACC CAG CTT GAC CA GGA GGC AGA GAC AGT TGG AG
<i>tdTomato</i>	AAG GGA GCT GCA GTG GAG TA CCG AAA ATC TGT GGG AAG TC GGC ATT AAA GCA GCG TAT CC CTG TTC CTG TAC GGC ATG G

Supplementary Table 3: Primers used for qRT-PCR

Gene	Forward Sequence	Reverse Sequence
<i>Ii1b</i>	GGGCCTCAAAGGAAAGAATC	TACCAGTTGGGGAACCTCTGC
<i>Ii7</i>	ATTGCCCGAATAATGAACCA	TCACCAGTGTTTGTGTGCCT
<i>Tgfb1</i>	CTGAACCAAGGAGACGGAATAC	CTGAACCAAGGAGACGGAATAC
<i>Tnfa</i>	CTGAGGTCAATCTGCCCAAGTAC	CTTCACAGAGCAATGACTCCAAAG
<i>Ccl2</i>	CCCAATGAGTAGGCTGGAGA	TCTGGACCCATTCTTCTTG
<i>Ccl3</i>	ATGAAGGTCTCCACCACTGC	GATGAATTGGCGTGGAATCT
<i>Ccl5</i>	ATATGGCTCGGACACCACTC	TCCTTCGAGTGACAAACACG
<i>Fau</i>	GCCCAGGAACCTACACACC	AAGCACGACTTGATCTTCGGG
<i>Rps2</i>	GGGGCTCGTGGAGGTAAAG	TCTCAGACTCCTTAATGGGCAG
<i>Rps3</i>	ATGGCGGTGCAGATTTCCAA	GTAACCTCGGACTTCAACTCCAG
<i>Rps5</i>	TGGCAGAGACCCCTGACAT	GGGCAGGTACTTGGCATACT
<i>Rps7</i>	AGCGCCAAGATCGTGAAGC	CACCACCAACTTCGATTTCTT
<i>Rps9</i>	TTGTGCGAAAACCTATGTGACC	GCCGCCTTACGGATCTTGG
<i>Rps17</i>	CCAAGACCGTGAAGAAGGCTG	GCTGGGGATAATGGCGATCT
<i>Rpl11</i>	ATGGCGCAAGATCAAGGGG	GACTGTGCAGTGAACAGCAAT
<i>Rpl12</i>	ACTGGAAGGGTCTCAGAATTACA	TGCCGGGCAATGTTGACAA
<i>Rpl37a</i>	GCTAAACGCACCAAGAAGGTC	GCCACTGTTTTTCATGCAGGAA