

Figure S1A

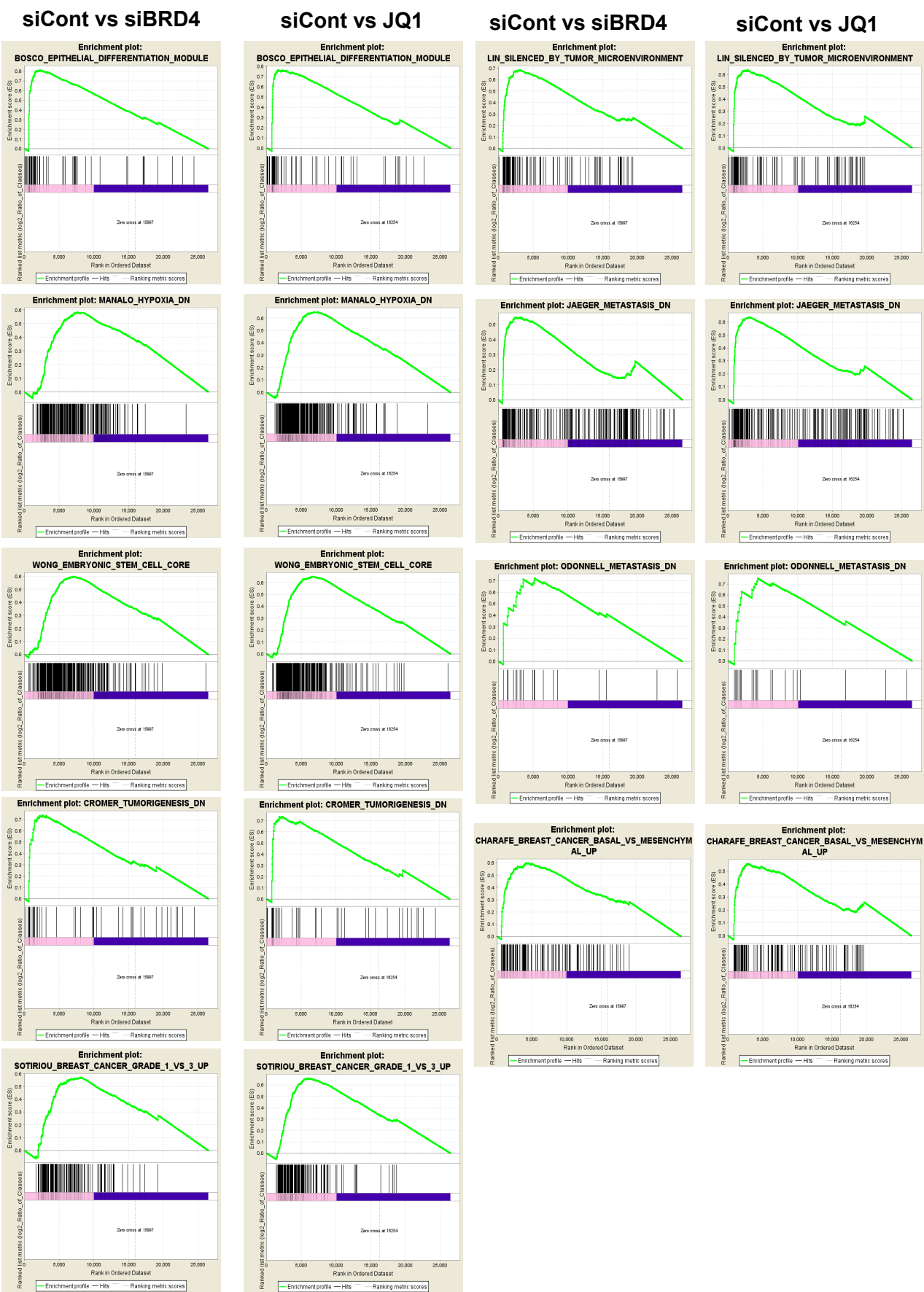


Figure S1B

GSEA- siCont vs siBRD4

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE	63	0.814977	2.853733	0	0
REACTOME_PEPTIDE_CHAIN_ELONGATION	76	0.751187	2.686106	0	0
KEGG_RIBOSOME	77	0.748261	2.681724	0	0
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS	77	0.738128	2.639164	0	0
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	92	0.720975	2.63175	0	0
RICKMAN_HEAD_AND_NECK_CANCER_E	83	0.72368	2.620103	0	0
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	61	0.73975	2.573976	0	0
LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT	105	0.684441	2.539676	0	1.27E-04
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	95	0.695614	2.532714	0	1.13E-04
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	97	0.689609	2.523994	0	1.02E-04
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	97	0.688278	2.50099	0	9.24E-05
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	112	0.669844	2.491455	0	1.69E-04
REACTOME_TRANSLATION	132	0.655036	2.464481	0	1.56E-04
CROMER_TUMORIGENESIS_DN	46	0.738976	2.455032	0	1.44E-04
REACTOME_INFLUENZA_LIFE_CYCLE	125	0.653445	2.449092	0	1.35E-04
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	44	0.72671	2.432371	0	1.90E-04
MOOTHA_VOXPPOS	84	0.668009	2.418099	0	4.16E-04
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	51	0.702599	2.395483	0	3.93E-04
WONG_EMBRYONIC_STEM_CELL_CORE	314	0.598805	2.349427	0	0.001221
ZHAN_MULTIPLE_MYELOMA_PR_UP	43	0.695864	2.342377	0	0.001311
REACTOME_MRNA_SPLICING	105	0.632875	2.336182	0	0.001488
BILANGES_SERUM_RESPONSE_TRANSLATION	32	0.732947	2.315992	0	0.001972
IRITANI_MAD1_TARGETS_DN	43	0.687387	2.306887	0	0.002237
KEGG_SPLICEOSOME	121	0.612888	2.287308	0	0.00269
HUMMERICH_BENIGN_SKIN_TUMOR_UP	18	0.842332	2.286632	0	0.002704
MANALO_HYPOXIA_DN	264	0.583874	2.276993	0	0.003143
GRAHAM_NORMAL QUIESCENT VS NORMAL DIVIDING_DN	80	0.628937	2.264085	0	0.003625
REACTOME_METABOLISM_OF_MRNA	185	0.590081	2.25952	0	0.003999
WONG_MITOCHONDRIA_GENE_MODULE	208	0.585477	2.259472	0	0.003895
KEGG_PARKINSONS_DISEASE	108	0.611671	2.252873	0	0.004068
YAMASHITA_LIVER_CANCER_WITH_EPCAM_UP	49	0.657166	2.247621	0	0.004294
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	129	0.595661	2.243494	0	0.004633
CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP	114	0.599718	2.234401	0	0.005379
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	116	0.597244	2.221554	0	0.006613
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	133	0.590556	2.220518	0	0.00654
REACTOME_METABOLISM_OF_RNA	229	0.570623	2.218254	0	0.006695
MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	80	0.616263	2.216265	0	0.006733
BENPORATH_PROLIFERATION	126	0.590461	2.211904	0	0.006927
DANG_MYC_TARGETS_UP	134	0.588041	2.208442	0	0.007112
WANG_BARRETTS_ESOPHAGUS_DN	22	0.75722	2.20654	0.001171	0.00711
JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_DN	42	0.661338	2.192359	0	0.008462
KEGG_OXIDATIVE_PHOSPHORYLATION	113	0.588467	2.191388	0	0.008429
MISSIAGLIA_REGULATED_BY_METHYLATION_DN	112	0.588073	2.186622	0	0.008913
MENSSEN_MYC_TARGETS	47	0.646513	2.177505	0	0.009603
REACTOME_DNA_REPLICATION	167	0.570669	2.176882	0	0.009502
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	42	0.661675	2.175316	0	0.00958
KEGG_RNA_POLYMERASE	29	0.702251	2.174562	0	0.009527
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP	80	0.603269	2.169469	0	0.009915
CHNG_MULTIPLE_MYELOMA_HYPERPLOID_UP	46	0.645121	2.162866	0	0.010823

Figure S1C

GSEA - siCont vs JQ1

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE	63	0.766355	2.579987	0	0	0
RICKMAN_HEAD_AND_NECK_CANCER_E	83	0.735326	2.559872	0	0	0
WONG_EMBRYONIC_STEM_CELL_CORE	314	0.650442	2.487749	0	3.35E-04	0.001
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	129	0.6799	2.477213	0	2.52E-04	0.001
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	78	0.71614	2.476781	0	2.01E-04	0.001
ONDER_CDH1_TARGETS_3_DN	55	0.752014	2.473961	0	1.68E-04	0.001
MANALO_HYPOXIA_DN	264	0.648934	2.463933	0	1.44E-04	0.001
WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN	34	0.781662	2.454889	0	1.26E-04	0.001
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR	116	0.687059	2.454298	0	1.12E-04	0.001
ZHAN_MULTIPLE_MYELOMA_PR_UP	43	0.754923	2.437968	0	1.01E-04	0.001
REACTOME_DNA_REPLICATION	167	0.652929	2.429175	0	9.15E-05	0.001
JAEGER_METASTASIS_DN	246	0.637101	2.422525	0	8.38E-05	0.001
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	138	0.659052	2.403524	0	2.32E-04	0.003
ISHIDA_E2F_TARGETS	49	0.728276	2.393639	0	2.15E-04	0.003
REACTOME_MITOTIC_M_M_G1_PHASES	152	0.649921	2.392601	0	2.01E-04	0.003
CROMER_TUMORIGENESIS_DN	46	0.736325	2.385485	0	1.88E-04	0.003
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN	80	0.680813	2.378308	0	2.96E-04	0.005
CHANG_IMMORTALIZED_BY_HPV31_DN	62	0.704211	2.366175	0	5.60E-04	0.01
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	77	0.689092	2.36342	0	5.30E-04	0.01
TARTE_PLASMA_CELL_VS_PLASMABLAST_DN	295	0.618513	2.362157	0	5.54E-04	0.011
BENPORATH_PROLIFERATION	126	0.648907	2.353695	0	6.24E-04	0.013
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_UP	166	0.632893	2.347211	0	6.41E-04	0.014
KEGG_PARKINSONS_DISEASE	108	0.653315	2.343537	0	6.13E-04	0.014
PUJANA_BRCA_CENTERED_NETWORK	110	0.651646	2.338067	0	6.29E-04	0.015
MOOTHA_VOXPPOS	84	0.66618	2.327467	0	6.04E-04	0.015
PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_UP	53	0.697604	2.317455	0	7.75E-04	0.02
SCHUHMACHER_MYC_TARGETS_UP	75	0.67315	2.312837	0	7.84E-04	0.021
REACTOME_BETA_DEFENSINS	34	0.737612	2.30273	0	9.71E-04	0.027
WHITEFORD_PEDIATRIC_CANCER_MARKERS	109	0.644644	2.302095	0	9.38E-04	0.027
HUPER_BREAST_BASAL_VS_LUMINAL_UP	52	0.692757	2.298434	0	0.001007	0.03
ZHANG_TLX_TARGETS_60HR_DN	257	0.604537	2.291765	0	0.001299	0.04
PUJANA_XPRSS_INT_NETWORK	159	0.621425	2.287156	0	0.001353	0.043
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	61	0.691601	2.283614	0	0.001403	0.046
LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT	105	0.639351	2.281149	0	0.001391	0.047
MISSIAGLIA_REGULATED_BY_METHYLATION_DN	112	0.640902	2.27949	0	0.00138	0.048
REACTOME_MITOTIC_G1_G1_S_PHASES	116	0.632988	2.277478	0	0.001342	0.048
KEGG_SPLICEOSOME	121	0.63328	2.277469	0	0.001306	0.048
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	133	0.623791	2.276691	0	0.001271	0.048
SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM	143	0.619335	2.274105	0	0.001265	0.049
MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	80	0.650796	2.273284	0	0.001233	0.049
REACTOME_MRNA_SPLICING	105	0.634219	2.267832	0	0.001252	0.051
MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN	66	0.662292	2.266465	0	0.001246	0.052
REACTOME_S_PHASE	88	0.644351	2.26362	0	0.001264	0.054
AMUNDSON_GAMMA_RADIATION_RESPONSE	39	0.70883	2.249826	0	0.001532	0.066
REACTOME_M_G1_TRANSITION	66	0.663042	2.24594	0	0.001565	0.068
REACTOME_TRANSLATION	132	0.621247	2.237778	0	0.001794	0.079
SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	29	0.754825	2.229646	0	0.002033	0.092
KOBAYASHI_EGFR_SIGNALING_24HR_DN	232	0.590549	2.228154	0	0.002075	0.094
WANG BARRETTS ESOPHAGUS DN	22	0.779637	2.226986	0	0.002074	0.096

Figure S1D

DAVID – siBRD4 and JQ1 regulated genes

Annotation Cluster 1	Enrichment Score: 9.38	Count	P_Value	FDR
SP_PIR_KEYWORDS	glycoprotein	225	1.9E-13	2.7E-10
SP_PIR_KEYWORDS	signal	180	1.0E-12	1.5E-9
UP_SEQ_FEATURE	signal peptide	180	1.8E-12	3.1E-9
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	213	6.7E-12	1.2E-8
SP_PIR_KEYWORDS	Secreted	101	9.9E-9	1.4E-5
GOTERM_CC_FAT	extracellular region	120	4.1E-8	5.6E-5
SP_PIR_KEYWORDS	disulfide bond	144	8.7E-7	1.3E-3
UP_SEQ_FEATURE	disulfide bond	140	1.2E-6	2.1E-3
Annotation Cluster 2	Enrichment Score: 7.59	Count	P_Value	FDR
GOTERM_CC_FAT	extracellular region part	76	3.2E-10	4.3E-7
GOTERM_CC_FAT	extracellular region	120	4.1E-8	5.6E-5
GOTERM_CC_FAT	extracellular space	52	1.3E-6	1.8E-3
Annotation Cluster 3	Enrichment Score: 6.16	Count	P_Value	FDR
GOTERM_BP_FAT	response to wounding	48	1.3E-8	2.3E-5
GOTERM_BP_FAT	defense response	48	1.1E-6	2.0E-3
GOTERM_BP_FAT	inflammatory response	29	2.2E-5	3.8E-2
Annotation Cluster 4	Enrichment Score: 5.85	Count	P_Value	FDR
SP_PIR_KEYWORDS	nucleosome core	17	1.6E-12	2.4E-9
GOTERM_CC_FAT	nucleosome	19	6.6E-12	9.0E-9
GOTERM_BP_FAT	nucleosome assembly	20	1.2E-10	2.1E-7
GOTERM_BP_FAT	chromatin assembly	20	2.3E-10	3.9E-7
GOTERM_CC_FAT	protein-DNA complex	20	2.3E-10	3.2E-7
GOTERM_BP_FAT	protein-DNA complex assembly	20	5.1E-10	8.9E-7
GOTERM_BP_FAT	nucleosome organization	20	7.6E-10	1.3E-6
KEGG_PATHWAY	Systemic lupus erythematosus	20	2.6E-9	3.1E-6
SP_PIR_KEYWORDS	citruination	10	1.6E-8	2.4E-5
GOTERM_BP_FAT	DNA packaging	20	4.1E-8	7.1E-5
SP_PIR_KEYWORDS	chromosomal protein	21	7.8E-8	1.1E-4
GOTERM_BP_FAT	chromatin assembly or disassembly	20	1.6E-7	2.7E-4
SP_PIR_KEYWORDS	methylation	25	2.1E-6	3.0E-3
GOTERM_CC_FAT	chromatin	23	4.7E-6	6.4E-3
SP_PIR_KEYWORDS	isopeptide bond	27	2.8E-5	4.0E-2
Annotation Cluster 5	Enrichment Score: 4.82	Count	P_Value	FDR
GOTERM_BP_FAT	epidermis development	34	2.0E-14	3.6E-11
GOTERM_BP_FAT	ectoderm development	34	2.1E-13	3.6E-10
GOTERM_CC_FAT	cornified envelope	10	3.8E-8	5.2E-5
GOTERM_BP_FAT	epidermal cell differentiation	15	2.5E-7	4.4E-4
GOTERM_BP_FAT	keratinocyte differentiation	13	3.9E-6	6.7E-3
GOTERM_BP_FAT	epithelium development	24	9.0E-6	1.6E-2
Annotation Cluster 6	Enrichment Score: 3.86	Count	P_Value	FDR
SP_PIR_KEYWORDS	glycoprotein	225	1.9E-13	2.7E-10
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	213	6.7E-12	1.2E-8
Annotation Cluster 7	Enrichment Score: 3.76	Count	P_Value	FDR
GOTERM_CC_FAT	extracellular matrix	30	3.2E-5	4.3E-2
Annotation Cluster 8	Enrichment Score: 3.55	Count	P_Value	FDR
SP_PIR_KEYWORDS	cell adhesion	35	2.2E-6	3.1E-3
GOTERM_BP_FAT	cell adhesion	50	8.0E-6	1.4E-2
GOTERM_BP_FAT	biological adhesion	50	8.1E-6	1.4E-2
GOTERM_BP_FAT	cell-cell adhesion	26	2.6E-5	4.5E-2

Figure S1E

MCF12A

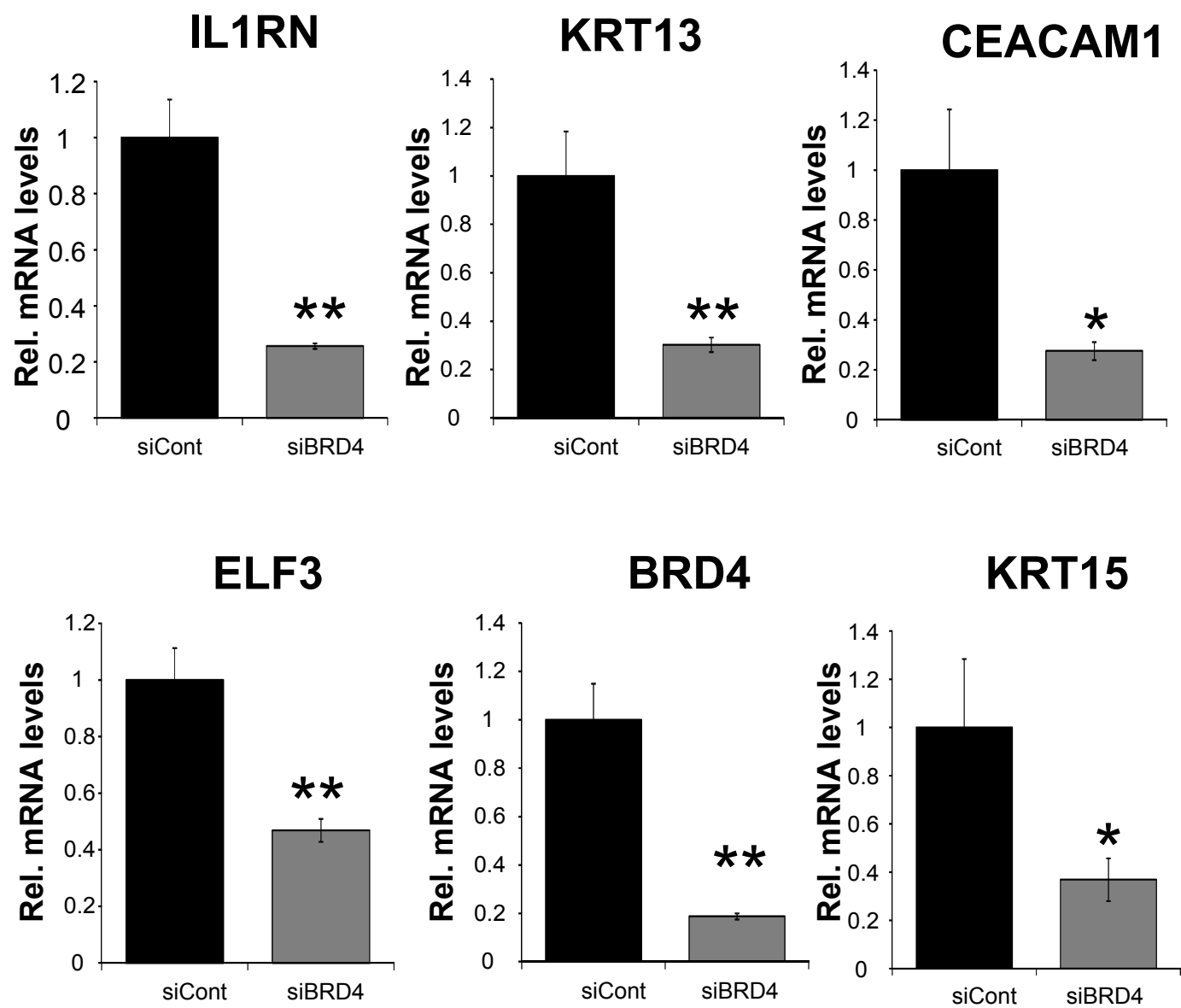


Figure S1F

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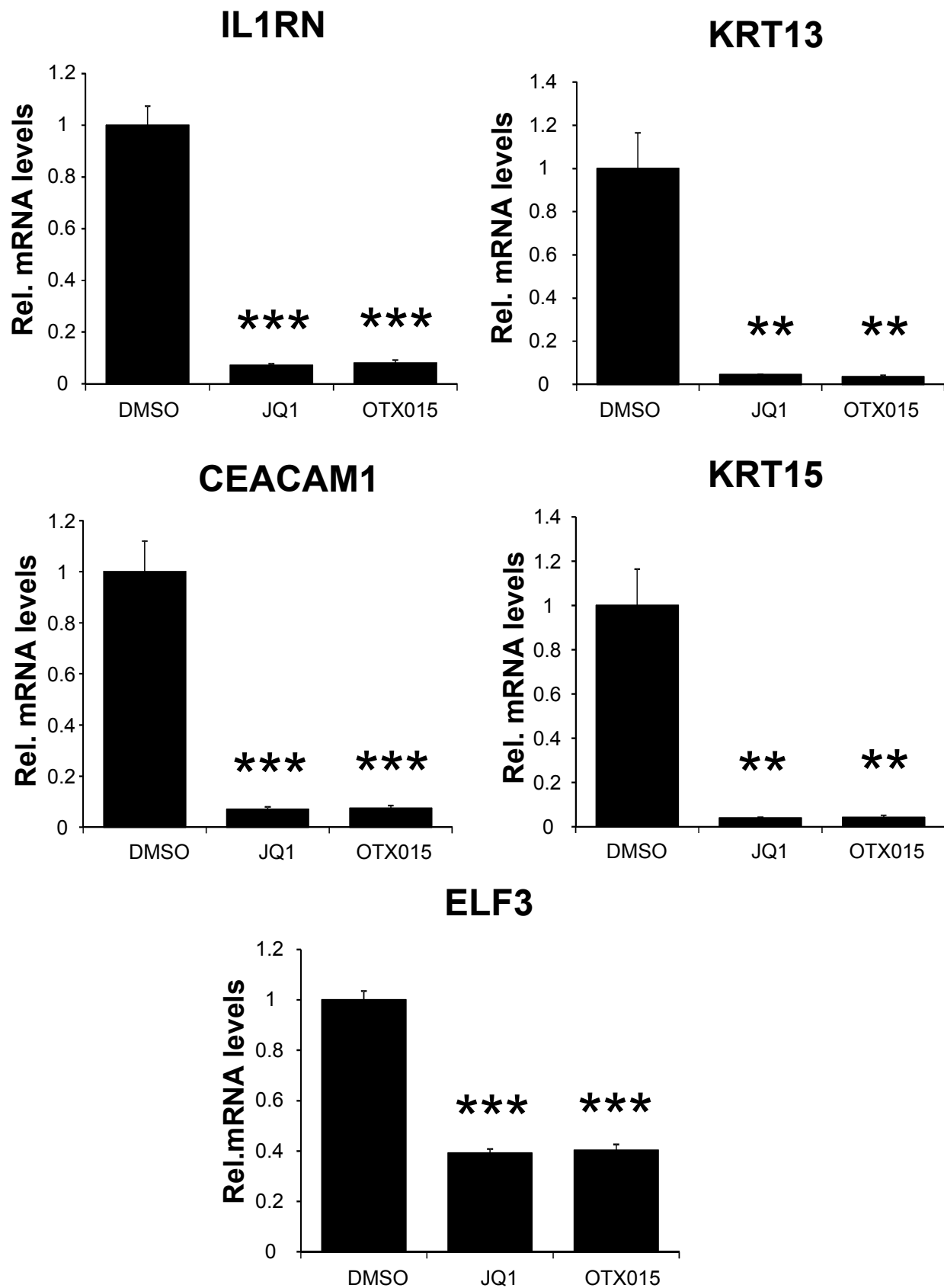


Figure S1

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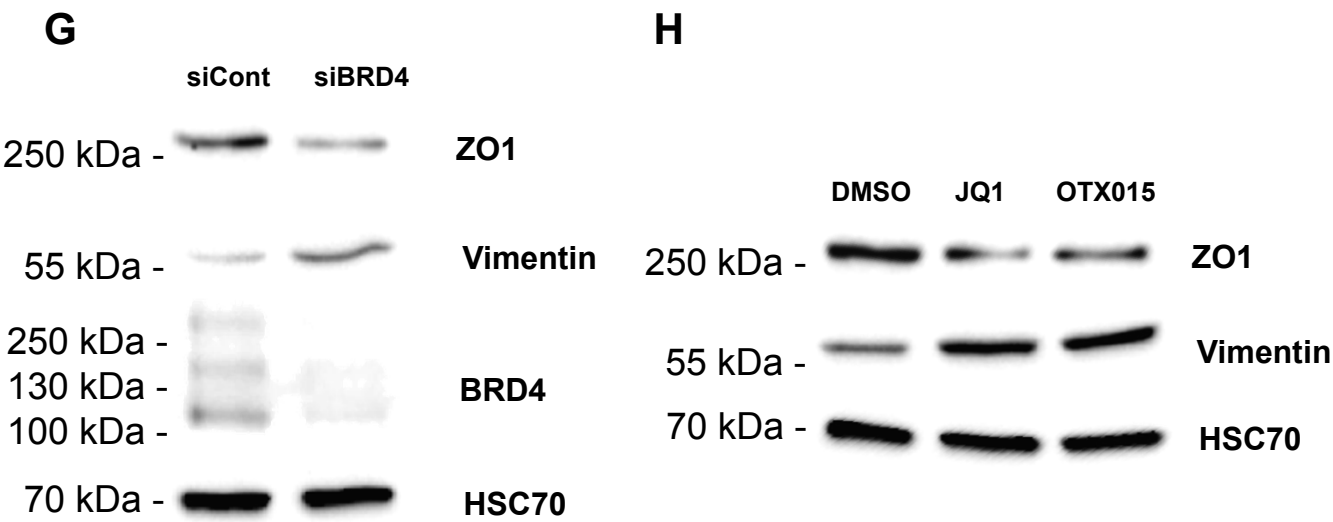


Figure S1

MCF12A

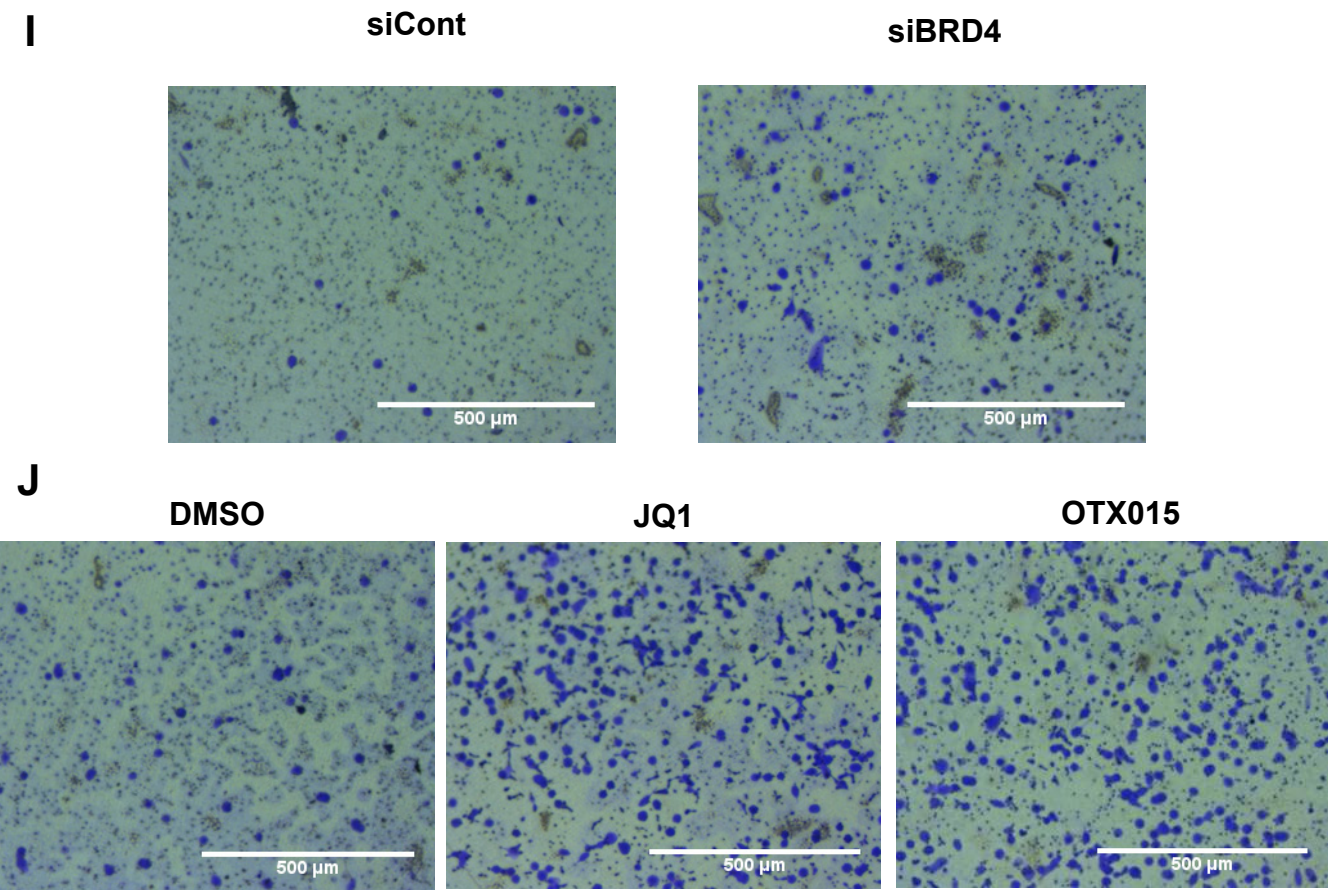


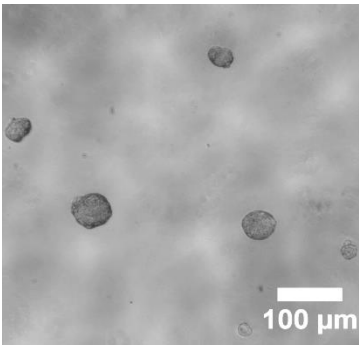
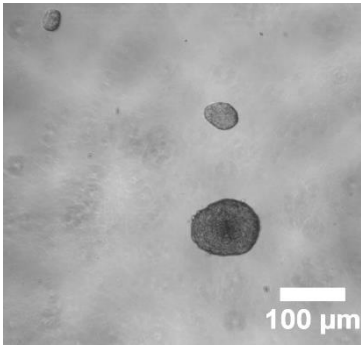
Figure S1

MCF10A

K

siCont

siBRD4



L

DMSO

JQ1

OTX015

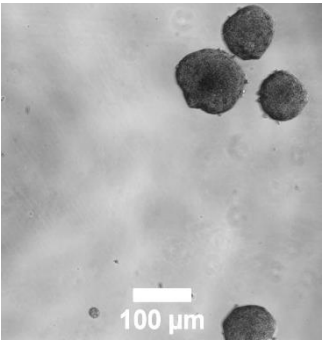
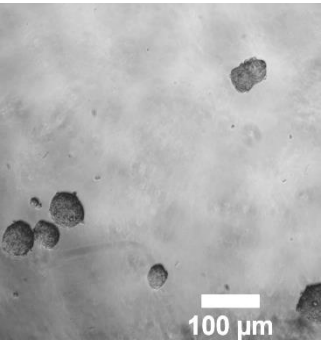
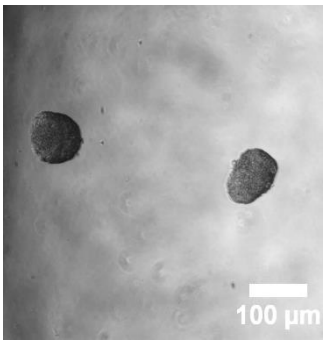


Figure S2

MCF12A

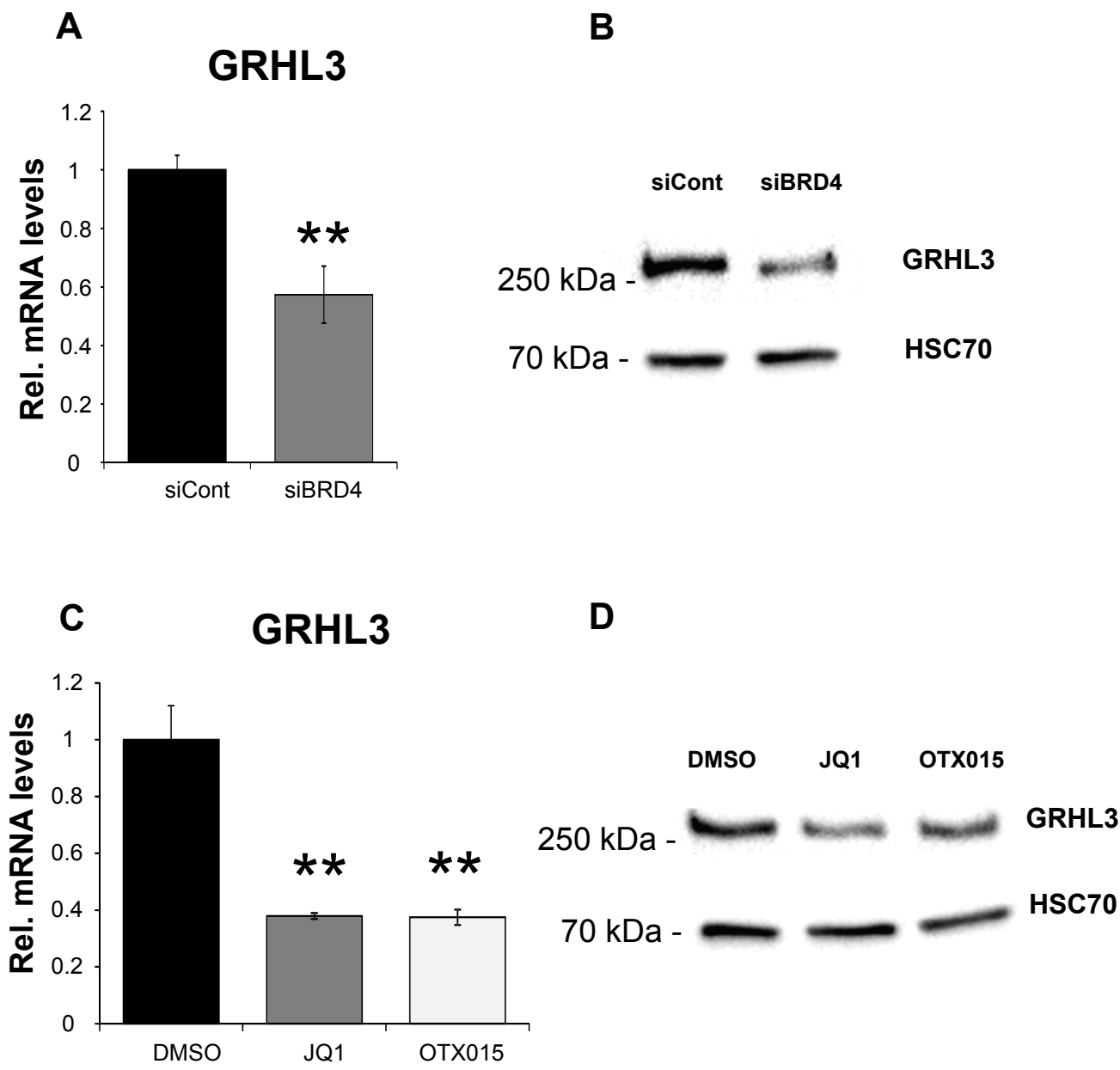


Figure S2

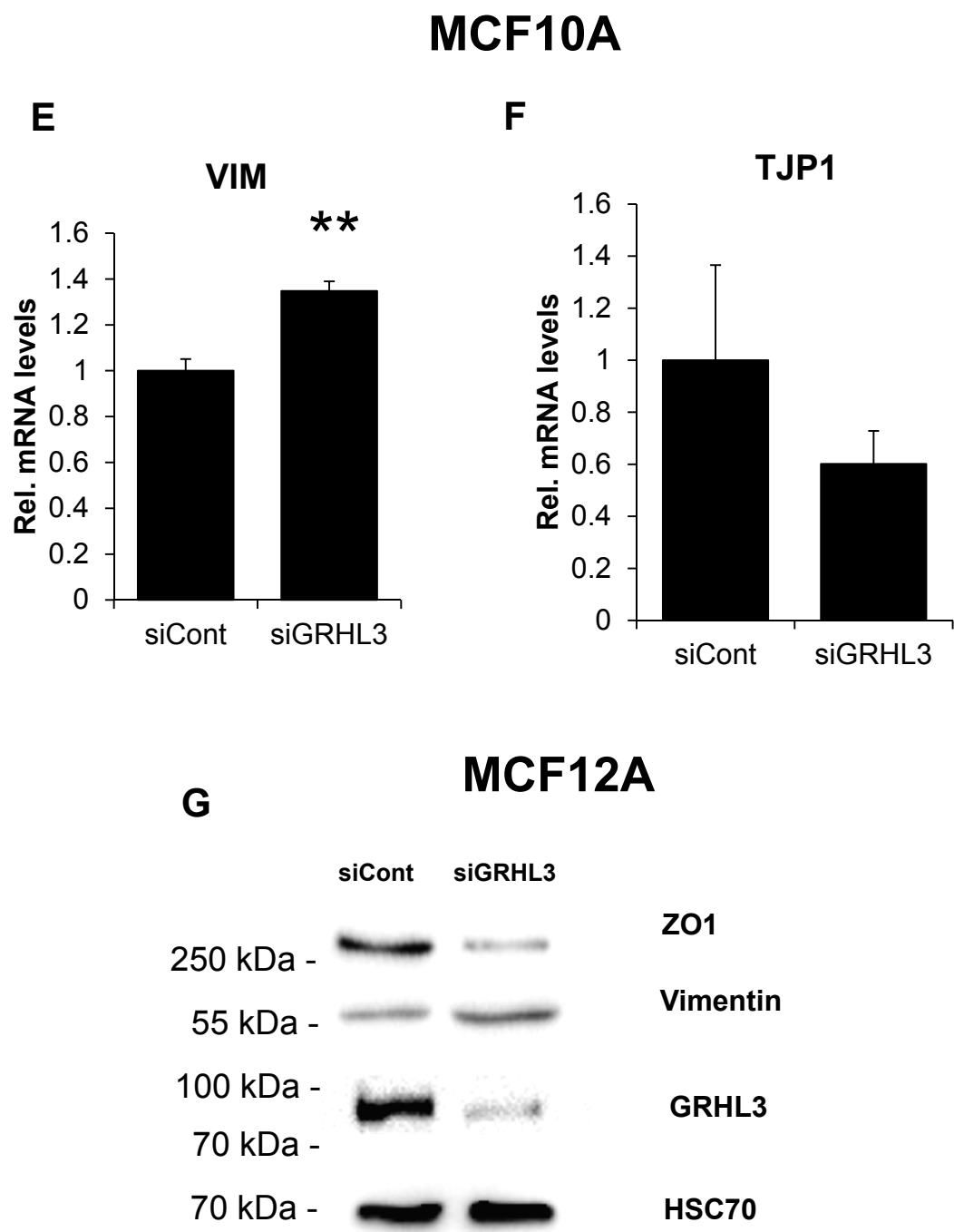


Figure S2

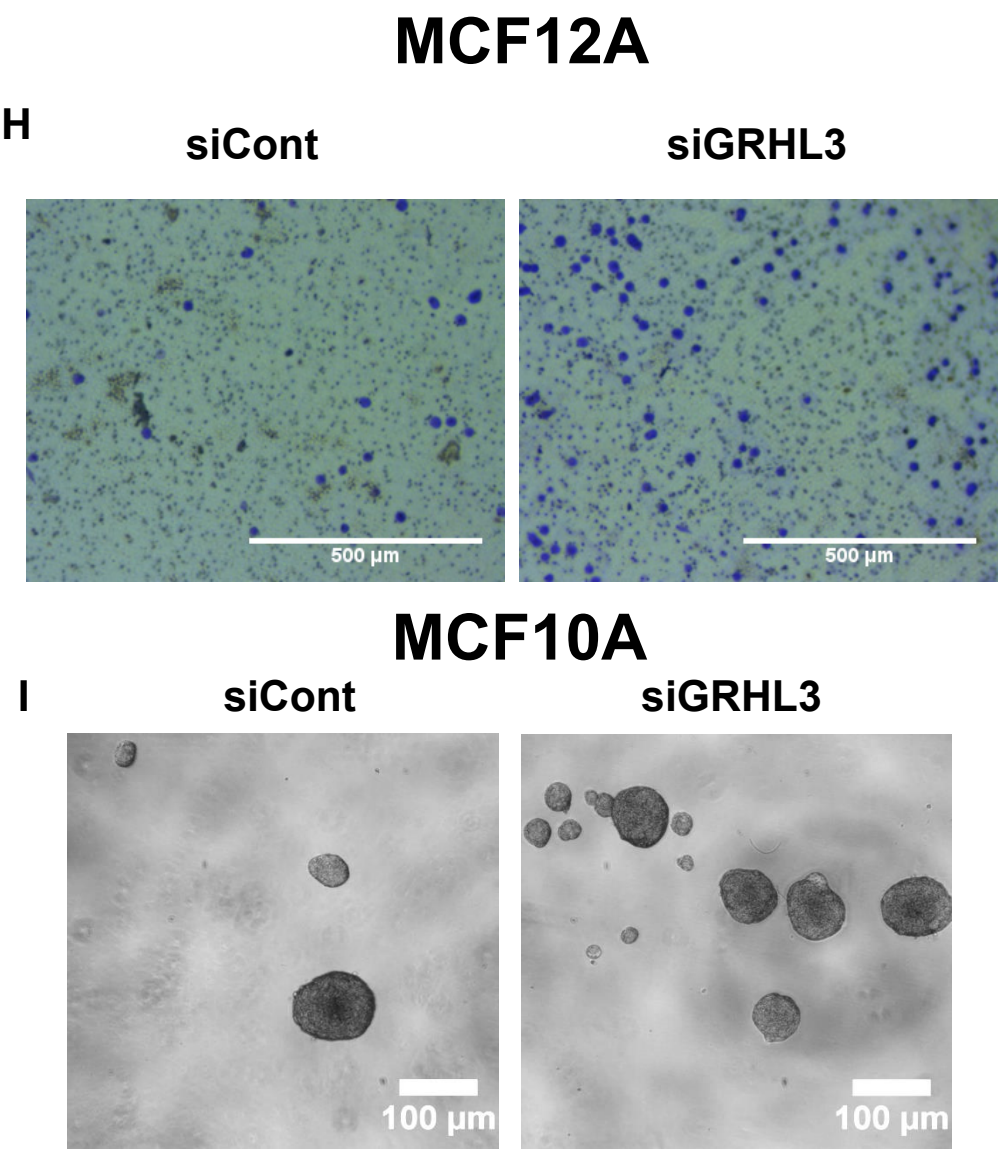


Figure S2J

MCF12A

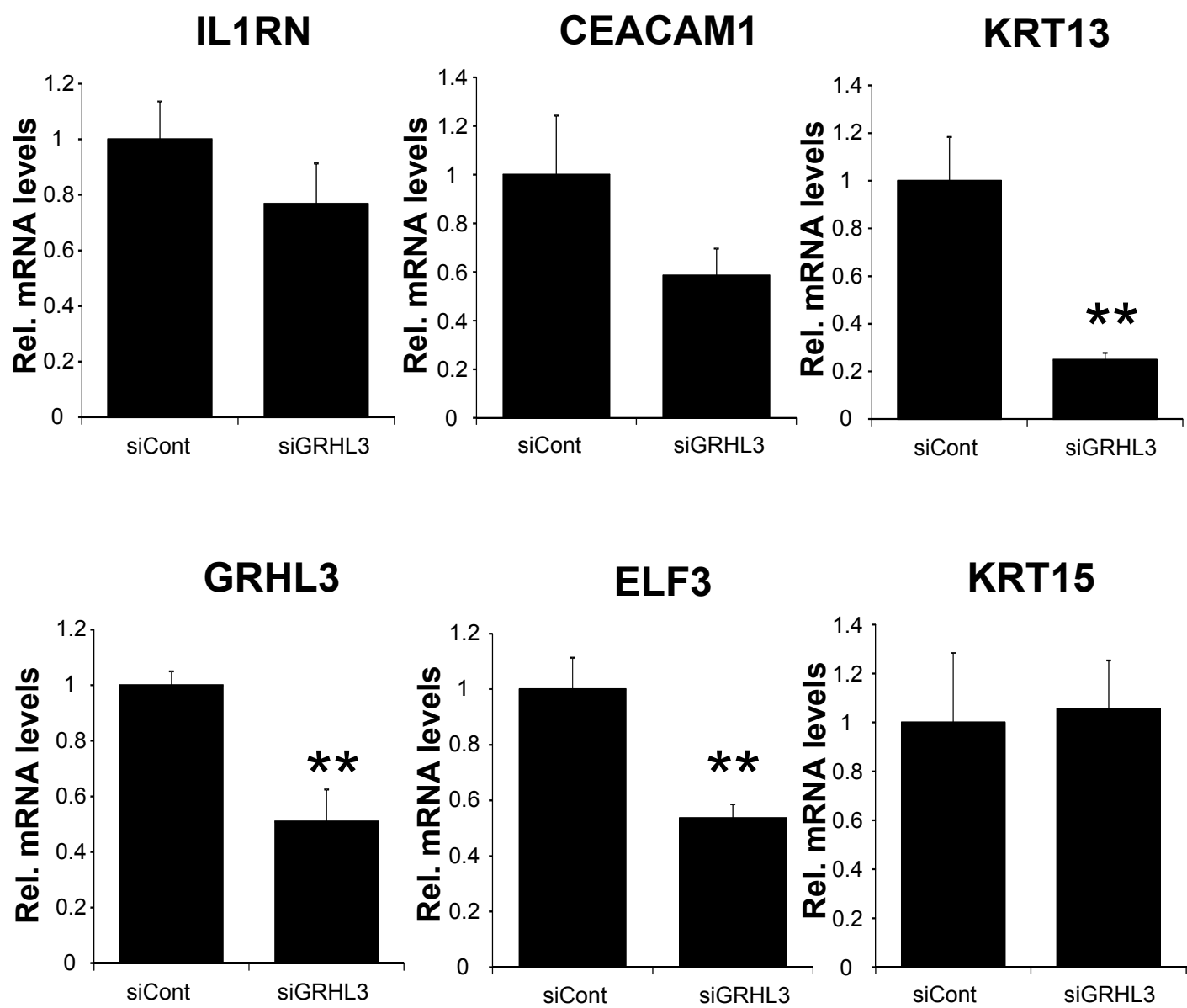
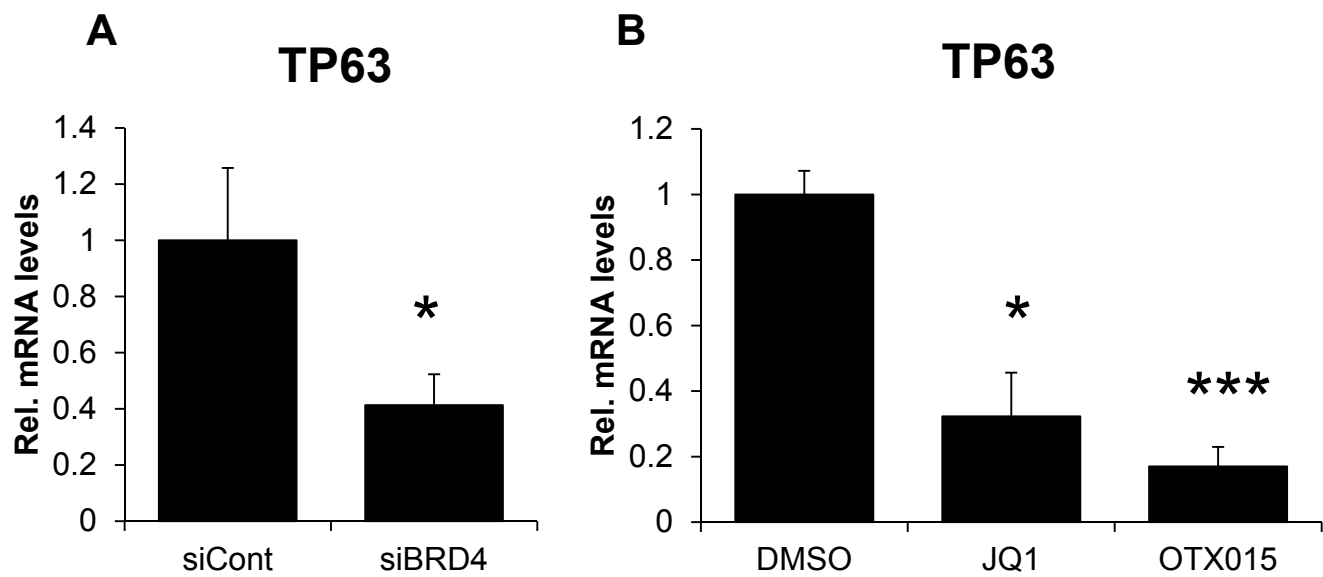


Figure S3

MCF10A



MCF12A

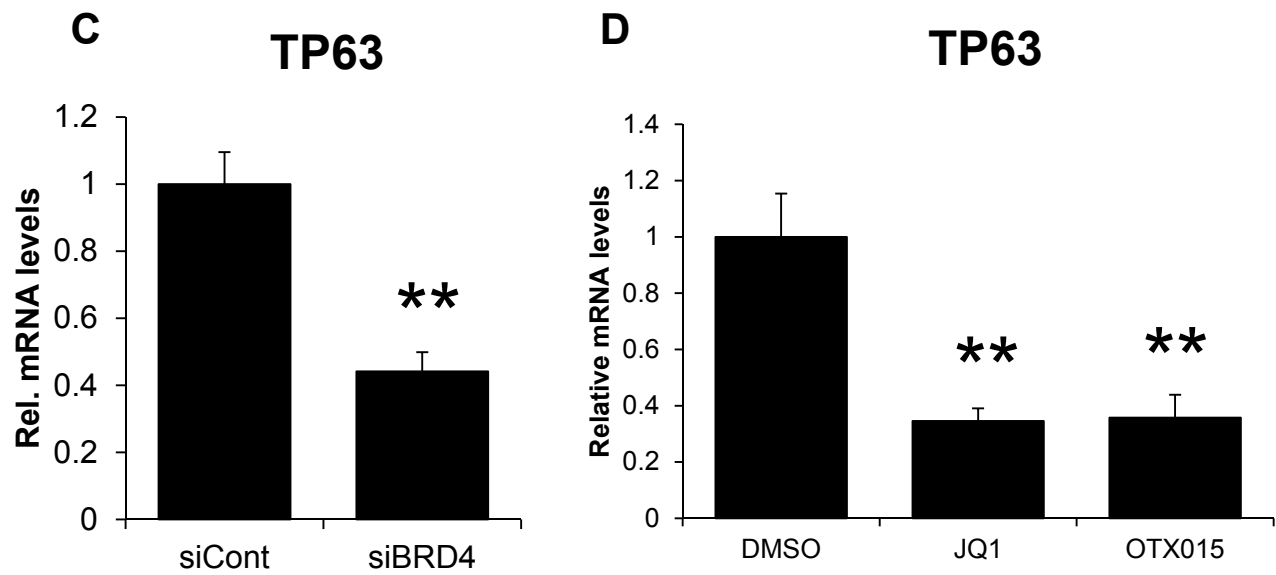


Figure S3E

MDA MB 231

DMSO JQ1 (nM)

2500 250 25

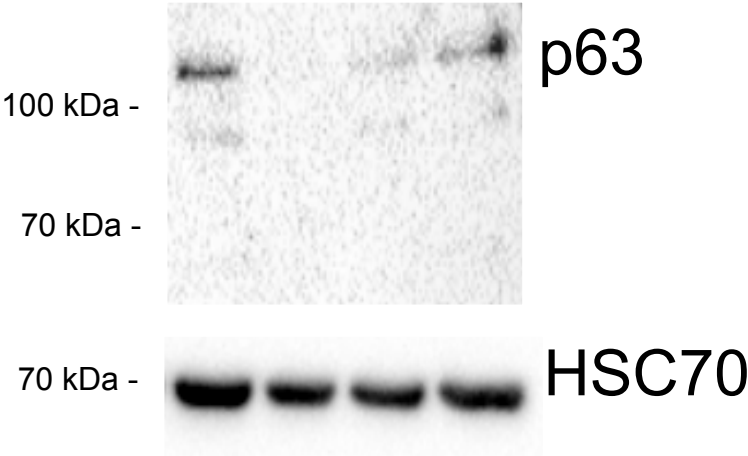


Figure S4

GREAT analysis of BRD4 ChIP-seq data

A

GREAT analysis MSigDB ID	Rank	Enrichment	HyperP-value	HyperFdrQ-value	No. of genes
GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN	1	2.888598	1.69E-08	6.79E-07	307
RICKMAN_METASTASIS_DN	2	2.334234	5.17E-03	3.97E-02	252
ENK_UV_RESPONSE_KERATINOCYTE_UP	3	1.811303	7.05E-07	1.99E-05	559
LOPEZ_MBD_TARGETS	4	1.561421	1.89E-14	2.63E-12	864
MILI_PSEUDOPODIA_HAPTOTAXIS_DN	5	1.606377	3.16E-13	3.27E-11	625
PEREZ_TP53_TARGETS	8	1.36504	1.09E-14	1.73E-12	1074
GRADE_COLON_CANCER_UP	9	1.596171	1.30E-10	7.36E-09	733
DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_DN	11	1.963506	1.59E-07	5.17E-06	230
NIKOLSKY_BREAST_CANCER_11Q12_Q14_AMPLICON	12	3.087131	3.10E-03	2.65E-02	146
MULLIGHAN_MLL_SIGNATURE_2_UP	13	1.767729	4.02E-06	9.19E-05	410
ACEVEDO_METHYLATED_IN_LIVER_CANCER_UP	15	1.256599	6.86E-05	1.08E-03	2166
MULLIGHAN_MLL_SIGNATURE_1_UP	16	1.804335	2.31E-04	3.13E-03	374
ACEVEDO_LIVER_CANCER_DN	19	1.540871	3.92E-05	6.95E-04	534
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_UP	21	1.604129	1.36E-10	7.53E-09	502
NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON	22	2.033119	5.61E-05	9.25E-04	315
BLALOCK_ALZHEIMERS_DISEASE_UP	23	1.228076	4.46E-16	1.06E-13	1709
WELCSH_BRCA1_TARGETS_1_DN	24	2.297363	1.09E-05	2.21E-04	124
DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	26	1.849647	3.49E-08	1.34E-06	321
PEREZ_TP63_TARGETS	27	1.46908	2.60E-06	6.25E-05	344
ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_TUMOR_DN	29	1.614371	7.56E-04	8.28E-03	367
AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP	31	1.807004	6.98E-03	4.97E-02	291
AMIT_EGF_RESPONSE_480_HELA	32	1.796868	4.88E-05	8.33E-04	161
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_UP	33	1.488997	1.21E-04	1.80E-03	418
MILI_PSEUDOPODIA_CHEMOTAXIS_DN	34	1.457013	1.73E-10	9.13E-09	434
LAHO_COLORECTAL_CANCER_SERRATED_DN	36	2.120581	1.91E-03	1.82E-02	93
KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN	38	1.315731	4.98E-14	5.63E-12	869
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_UP	40	1.437858	1.85E-06	4.68E-05	349
DAIRKEE_TERT_TARGETS_UP	41	1.6026	3.19E-06	7.42E-05	322
DOUGLAS_BMI1_TARGETS_UP	42	1.344078	1.87E-07	5.84E-06	512
LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN	43	1.342718	3.89E-14	4.62E-12	736
BENPORATH_MYC_TARGETS_WITH_EBOX	49	1.695023	9.16E-05	1.39E-03	235
LINDGREN_BLADDER_CANCER_CLUSTER_1_DN	53	1.433087	4.04E-05	7.10E-04	372
HSIAO_HOUSEKEEPING_GENES	54	1.48888	5.31E-05	8.87E-04	417
GARY_CD5_TARGETS_UP	55	1.373439	6.23E-04	7.24E-03	462
GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN	56	1.707374	3.00E-05	5.52E-04	167
LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP	60	1.798463	3.62E-04	4.54E-03	177
PEREZ_TP53_AND_TP63_TARGETS	64	1.418166	1.98E-06	4.89E-05	200
PENG_GLUTAMINE_DEPRIVATION_DN	70	2.207145	3.99E-04	4.91E-03	85
HELLER_HDAC_TARGETS_UP	73	1.44039	3.81E-04	4.76E-03	300
ONDER_CDH1_TARGETS_1_UP	76	1.644275	1.70E-03	1.66E-02	136
KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN	81	1.208951	3.02E-16	7.98E-14	961
DANG_BOUND_BY_MYC	87	1.21116	1.28E-17	5.08E-15	1063
DODD_NASOPHARYNGEAL_CARINOMA_UP	88	1.149949	1.23E-04	1.82E-03	1524
KIM_GASTRIC_CANCER_CHEMOSENSITIVITY	89	1.771583	4.56E-03	3.63E-02	103
OSMAN_BLADDER_CANCER_DN	90	1.345075	9.62E-05	1.45E-03	390
GAZDA_DIAMOND_BLACKFAN_ANEMIA_ERYTHROID_DN	99	1.291734	3.23E-04	4.10E-03	491
SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1	102	1.280633	3.40E-03	2.87E-02	438
PENG_RAPAMYCIN_RESPONSE_DN	103	2.093438	1.75E-03	1.68E-02	69
STEIN_ESRRA_TARGETS_UP	110	1.307094	3.59E-08	1.35E-06	385

Figure S4B

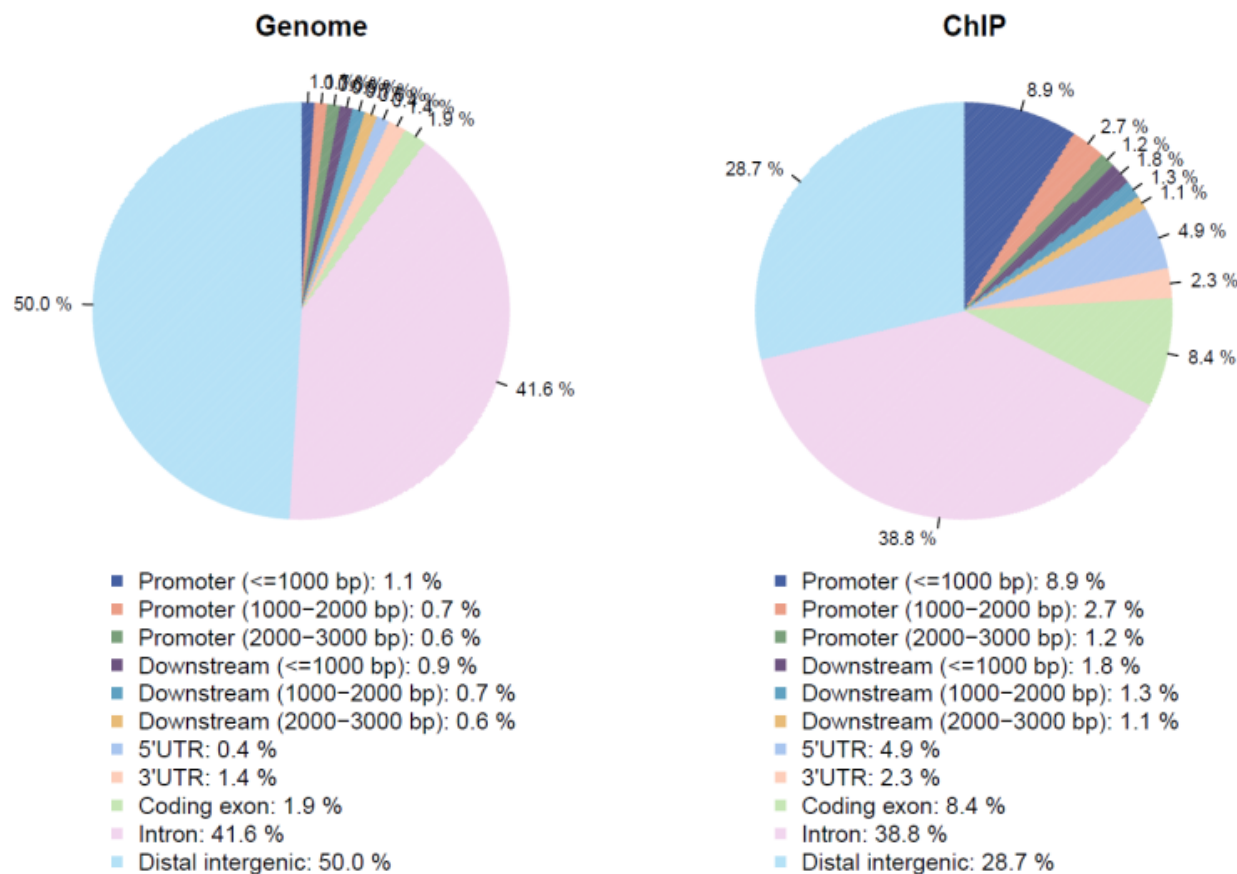
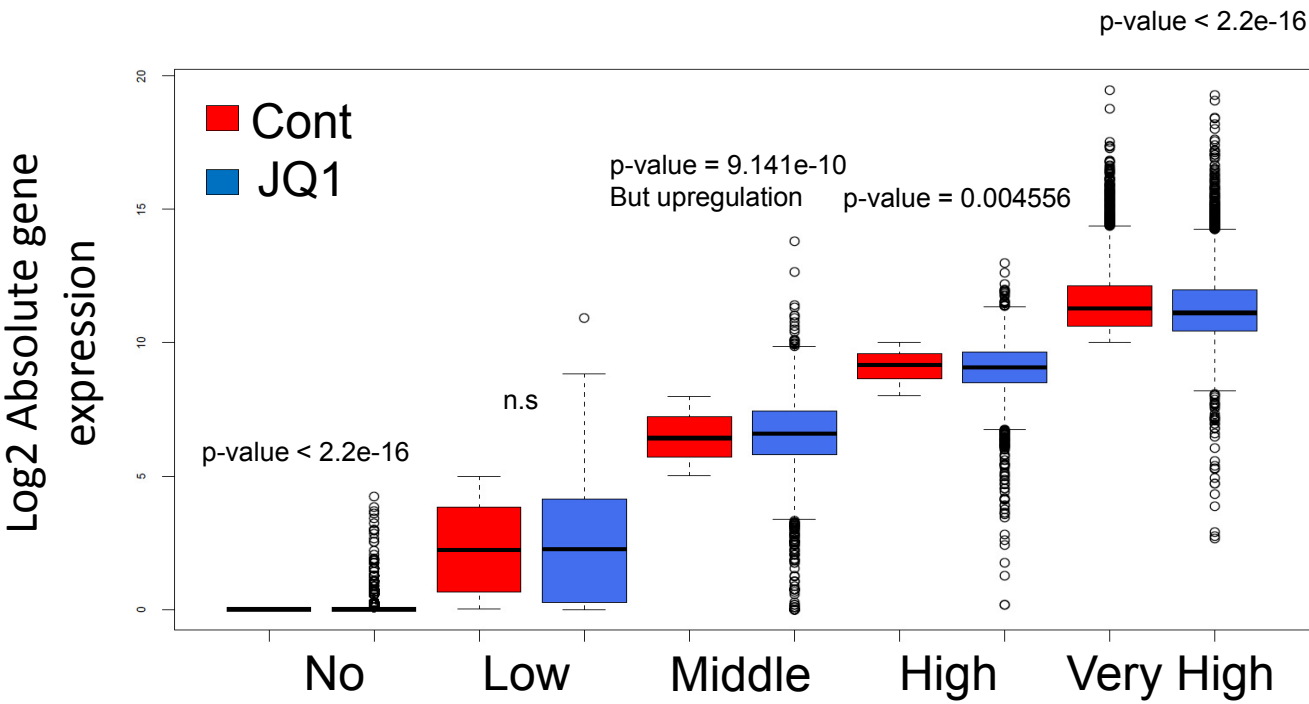


Figure S4

C



D

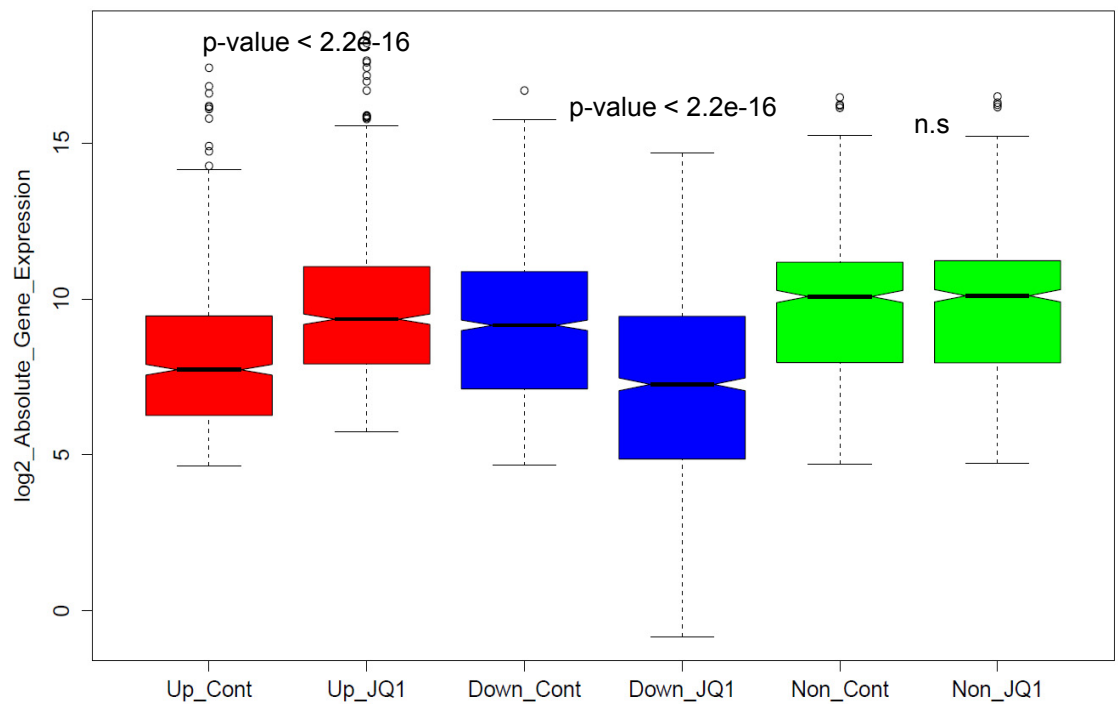


Figure S4E

Heatmap analysis on BRD4⁺ H3K4me3⁻

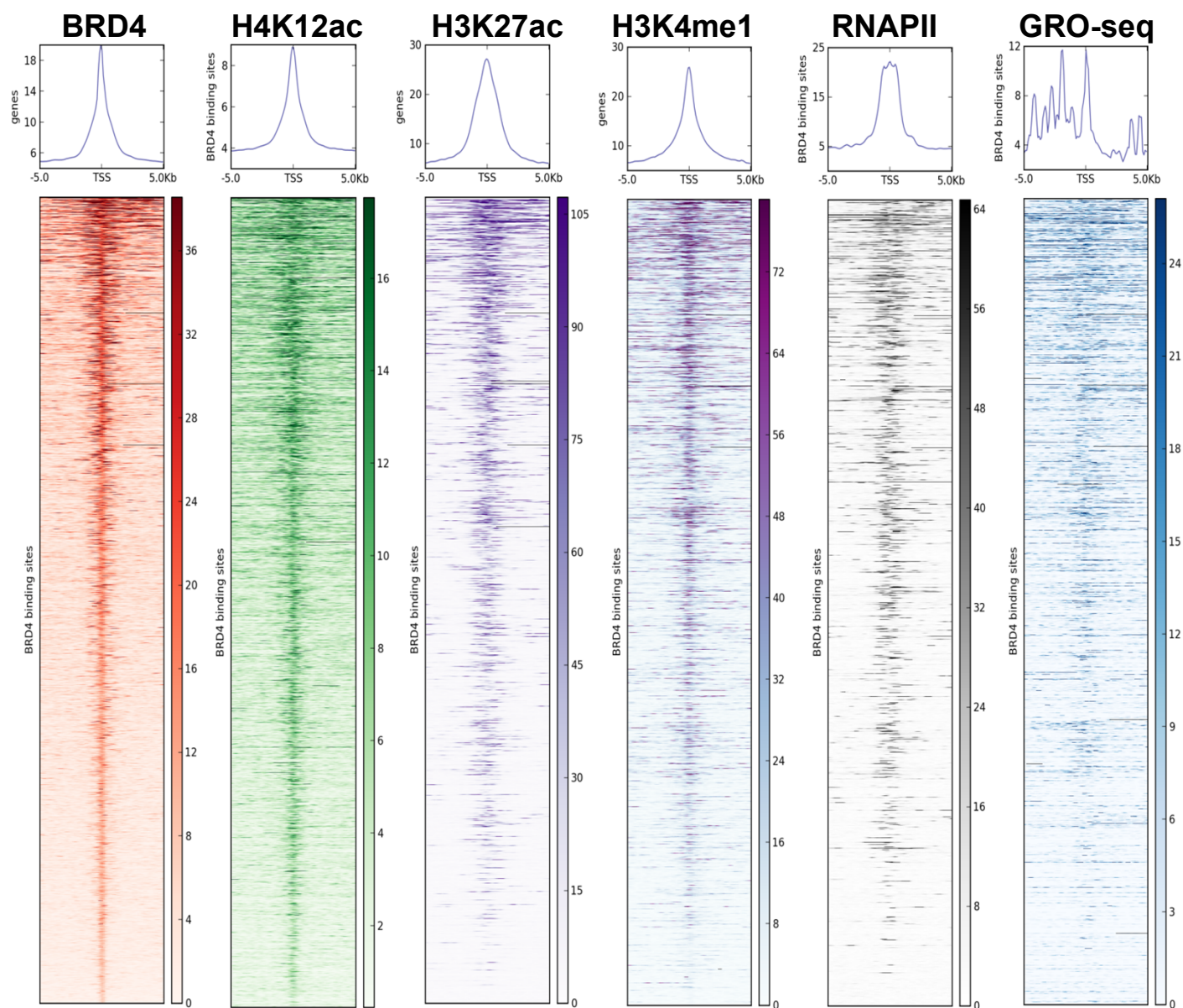


Figure S4F

Correlation analysis on BRD4⁺ H3K4me3⁻

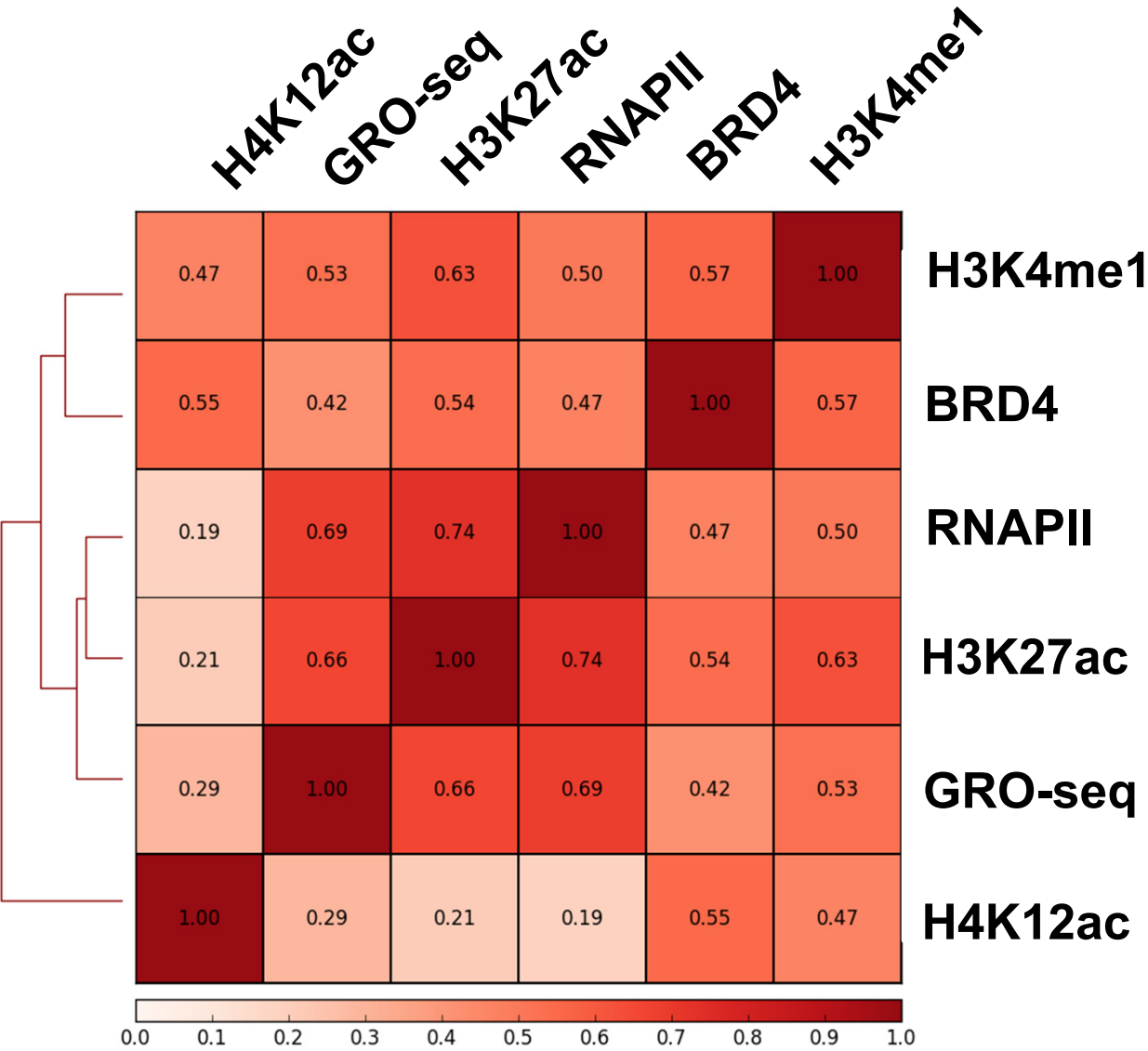


Figure S4

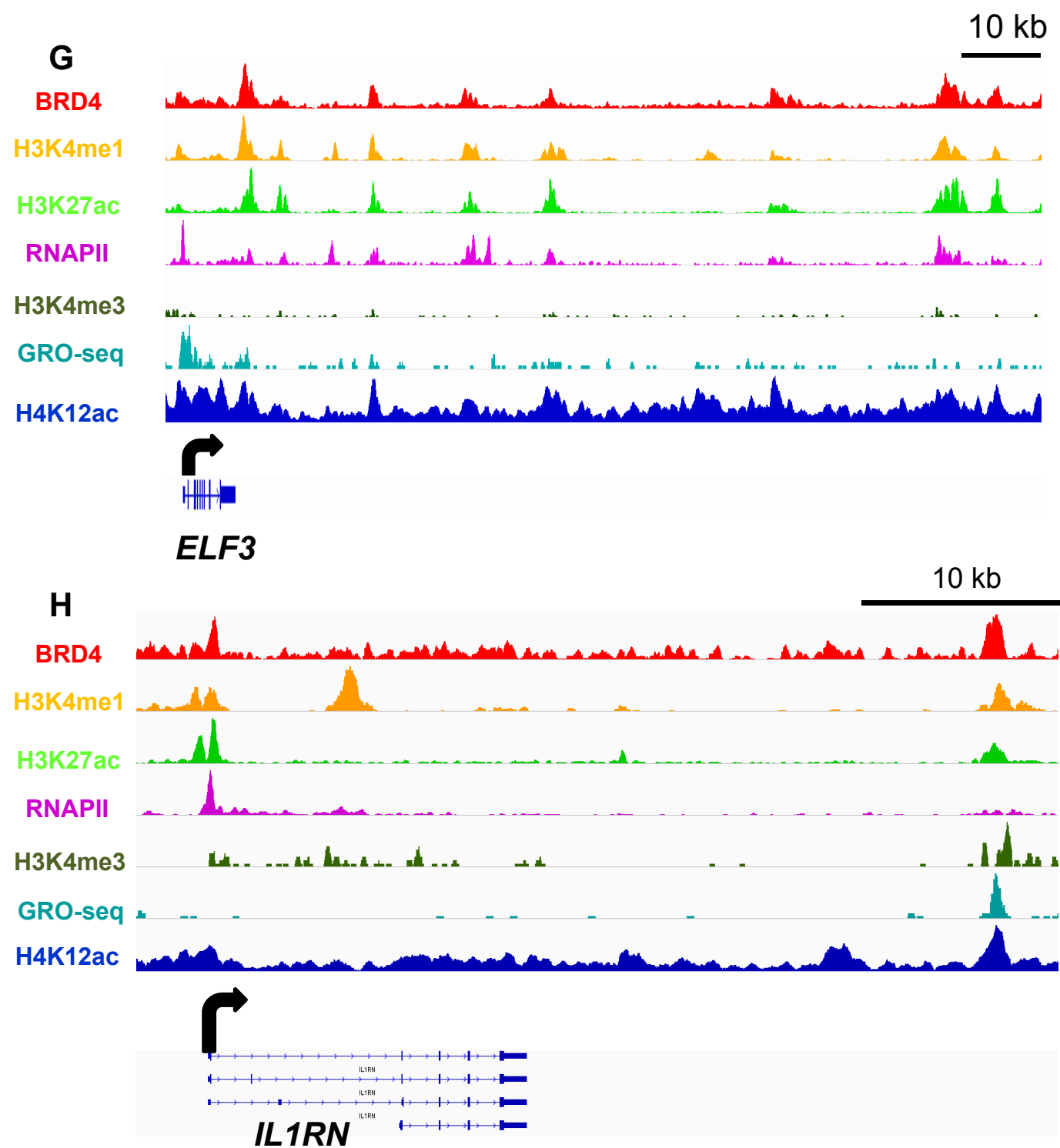


Figure S4I

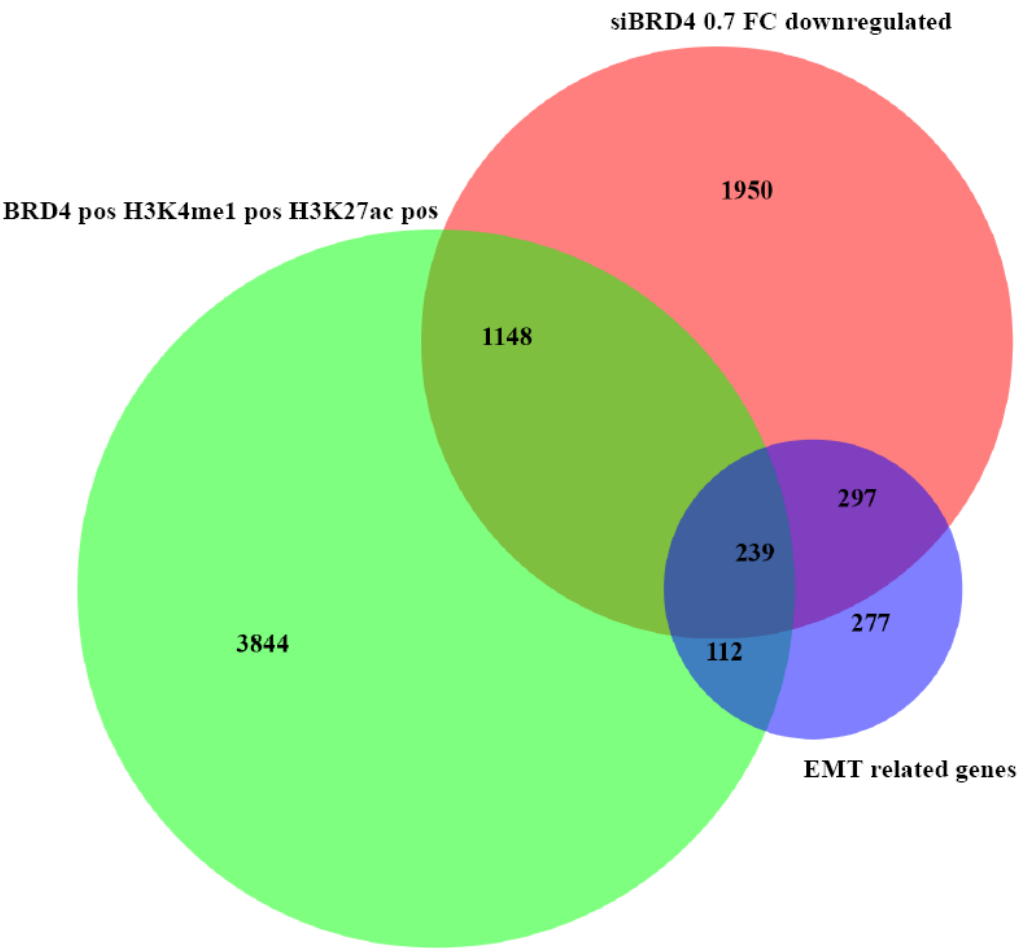
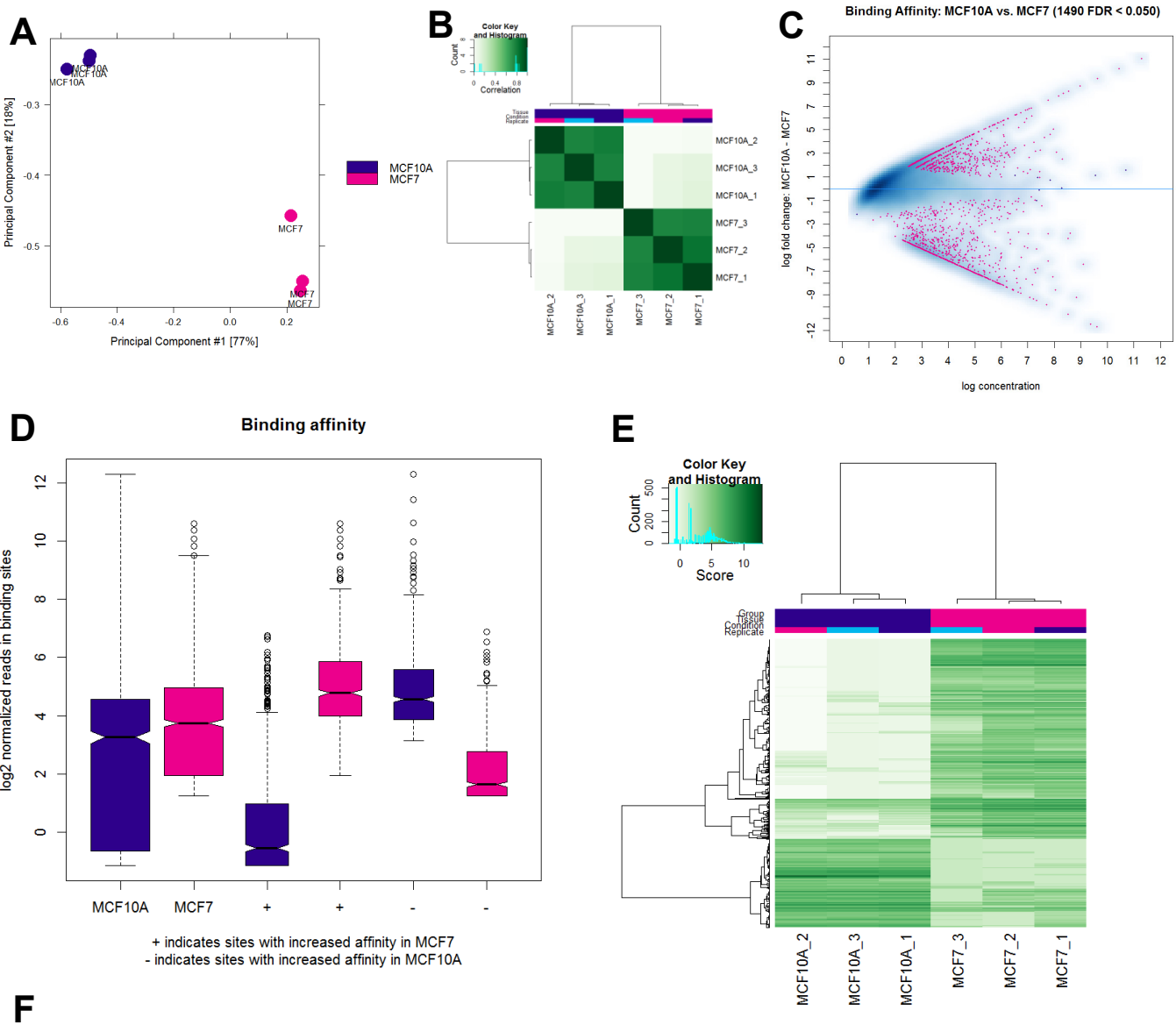


Figure S4J

Pathway analysis on BRD4⁺ H3K4me1⁺ H3K27ac⁺ H3K4me3⁻ sites

ID	Region Fold Enrichment	HyperP	HyperFdrQ	Total Genes
PID_DELTANP63PATHWAY	3.56E+00	1.22E-06	8.06E-04	47
PID_LKB1_PATHWAY	3.84E+00	1.63E-03	3.64E-02	47
PID_A6B1_A6B4_INTEGRIN_PATHWAY	3.40E+00	1.05E-05	1.55E-03	46
PID_P73PATHWAY	3.01E+00	3.47E-06	9.16E-04	79
PID_MYC_REPRESSPATHWAY	2.61E+00	4.52E-05	3.31E-03	63
PID_MTOR_4PATHWAY	2.78E+00	5.51E-06	1.04E-03	68
PID_P53DOWNSTREAMPATHWAY	2.06E+00	3.57E-05	3.14E-03	137
PID_FOXOPATHWAY	2.63E+00	4.32E-06	9.50E-04	49
KEGG_INSULIN_SIGNALING_PATHWAY	2.05E+00	1.24E-03	3.08E-02	138
PID_RXR_VDR_PATHWAY	3.83E+00	7.21E-04	2.16E-02	26
PID_TAP63PATHWAY	2.80E+00	3.19E-06	1.05E-03	53
PID_AP1_PATHWAY	2.29E+00	1.45E-06	6.40E-04	70
PID_PI3KCIPATHWAY	2.77E+00	1.92E-03	3.96E-02	50
PID_CMYB_PATHWAY	1.97E+00	3.72E-04	1.49E-02	84
REACTOME_PLATELET_ACTIVATION_SIGNALIN G_AND_AGGREGATION	1.71E+00	2.50E-04	1.10E-02	198

Figure S5



p-values for median values	MCF10A.DB	MCF7.DB	MCF10A.DB+	MCF7.DB+	MCF10A.DB-	MCF7.DB-
MCF10A.DB	1.00E+00	4.22E-41	2.29E-64	6.46E-103	3.67E-78	1.54E-01
MCF7.DB	4.22E-41	1.00E+00	2.18E-233	9.94E-62	5.47E-43	1.94E-77
MCF10A.DB+	2.29E-64	2.18E-233	1.00E+00	1.46E-133	7.18E-209	1.53E-120
MCF7.DB+	6.46E-103	9.94E-62	1.46E-133	1.00E+00	3.31E-03	1.67E-203
MCF10A.DB-	3.67E-78	5.47E-43	7.18E-209	3.31E-03	1.00E+00	1.17E-113
MCF7.DB-	1.54E-01	1.94E-77	1.53E-120	1.67E-203	1.17E-113	1.00E+00

Figure S5G

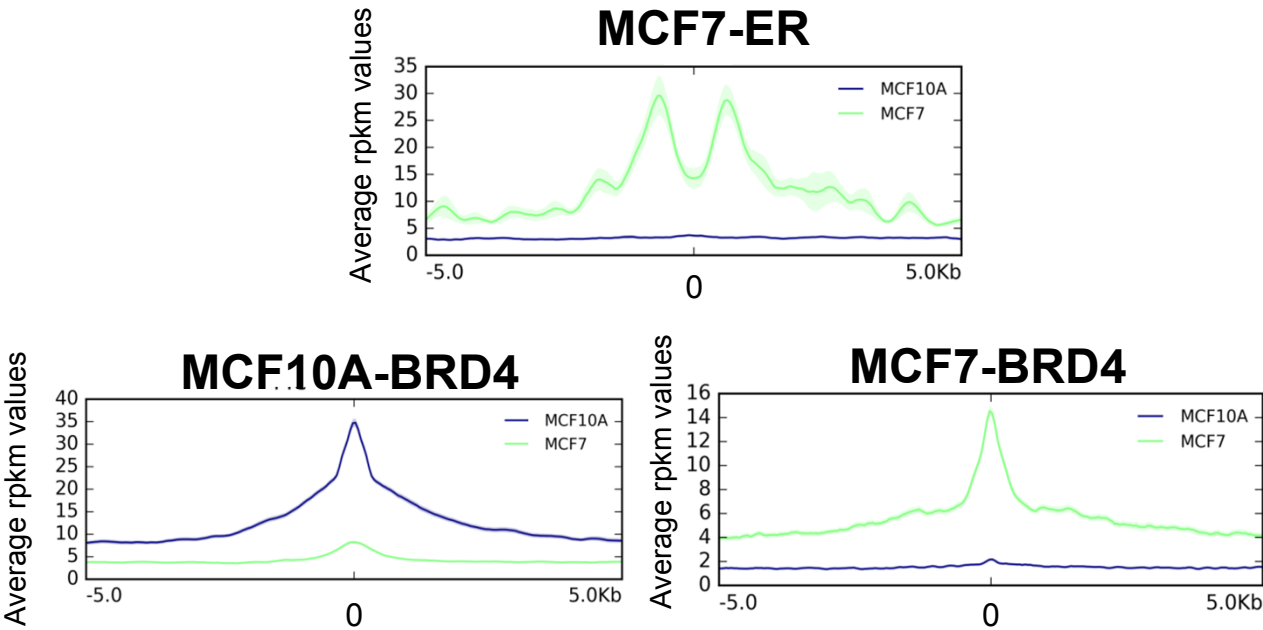


Figure S5H

MSigDB perturbation

ID	Desc	Bino mRank	RegionFold Enrich	HyperP	HyperFdrQ	GeneFold Enrich	Total Gene s
NAGASHIMA_EGF_SIGNALING_UP	Genes up-regulated in MCF7 cells (breast cancer) after stimulation with EGF [GeneID=1950].	1	1.17E+01	6.73E-07	1.89E-04	6.57E+00	56
NAGASHIMA_NRG1_SIGNALING_UP	Genes up-regulated in MCF7 cells (breast cancer) after stimulation with NRG1 [GeneID=3084].	2	6.19E+00	1.51E-07	7.27E-05	3.98E+00	168
AMIT_SERUM_RESPONSE_120_MCF10A	Genes whose expression peaked at 120 min after stimulation of MCF10A cells with serum.	3	8.70E+00	2.31E-06	4.85E-04	5.84E+00	63
LEONARD_HYPOXIA	Genes up-regulated in HK-2 cells (kidney tubular epithelium) under hypoxia and down-regulated on re-oxygenation.	4	1.38E+01	4.56E-04	2.32E-02	4.99E+00	47
BURTON_ADIPOGENESIS_1	Strongly up-regulated at 2 h during differentiation of 3T3-L1 cells (fibroblast) into adipocytes.	5	1.23E+01	4.33E-06	7.28E-04	8.11E+00	33
JAEGER_METASTASIS_DN	Genes down-regulated in metastases from malignant melanoma compared to the primary tumors.	6	4.32E+00	7.01E-07	1.82E-04	3.16E+00	254
SMID_BREAST_CANCER_BASAL_UP	Genes up-regulated in basal subtype of breast cancer samples.	7	2.72E+00	1.52E-04	1.07E-02	1.92E+00	628
MARTENS_BOUND_BY_PML_RARA_FUSION	Genes with promoters occupied by PML-RARA fusion [GeneID=5371,5914] protein in acute promyelocytic leukemia (APL) cells NB4 and two APL primary blasts, based on ChIP-seq data.	10	3.52E+00	7.81E-05	6.41E-03	2.22E+00	423
RICKMAN_METASTASIS_DN	Genes down-regulated in metastatic vs non-metastatic HNSCC (head and neck squamous cell carcinoma) samples.	11	5.34E+00	4.73E-04	2.37E-02	2.44E+00	247
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	Genes up-regulated in T24 (bladder cancer) cells in response to the photodynamic therapy (PDT) stress.	12	2.42E+00	2.46E-06	4.88E-04	2.04E+00	789
ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF	Class I of genes transiently induced by EGF [GeneID=1950] in 184A1 cells (mammary epithelium).	13	2.61E+00	9.56E-13	3.22E-09	3.26E+00	482
MANALO_HYPOXIA_UP	Genes up-regulated in response to both hypoxia and overexpression of an active form of HIF1A [GeneID=3091].	18	3.50E+00	1.64E-07	6.89E-05	3.66E+00	201
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	Genes up-regulated in macrophages by aerolysin-related cytotoxic enterotoxin (Act) from <i>Aeromonas hydrophila</i> .	20	7.12E+00	9.73E-04	3.52E-02	3.54E+00	85
KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3	Genes with promoters occupied by SMAD2 or SMAD3 [GeneID=4087, 4088] in HaCaT cells (keratinocyte) according to a ChIP-chip analysis.	21	2.25E+00	4.22E-09	7.09E-06	2.32E+00	809
CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	Up-regulated genes in the left ventricle myocardium of patients with heart failure following implantation of LVAD (left ventricular assist device).	23	5.30E+00	4.03E-07	1.51E-04	4.87E+00	103
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_RED_UP	Genes from the red module which are up-regulated in HAEC cells (primary aortic endothelium) after exposure to the oxidized 1-palmitoyl-2-arachidonoyl-sn-3-glycerophosphorylcholine (oxPAPC).	24	1.72E+01	1.38E-03	4.28E-02	7.88E+00	17
ZWANG_EGF_INTERVAL_DN	Genes repressed in the time interval between two pulses of EGF [GeneID=1950] in 184A1 cells (mammary epithelium).	26	3.85E+00	2.12E-08	2.37E-05	3.95E+00	195
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN	Down-regulated genes in angioimmunoblastic lymphoma (AILT) compared to normal T lymphocytes.	29	4.15E+00	7.24E-06	1.16E-03	3.89E+00	129
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1	Genes co-regulated in uterus during a time course response to progesterone [PubChem=5994]: SOM cluster 1.	32	5.54E+00	6.01E-07	1.84E-04	5.99E+00	67
SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN	Genes down-regulated in bone relapse of breast cancer.	33	2.98E+00	6.73E-04	2.94E-02	2.25E+00	298
RHEIN_ALL_GLUCCORTICOID_THERAPY_UP	Genes up-regulated in ALL (acute lymphoblastic leukemia) blasts after 1 week of treatment with glucocorticoids.	34	6.11E+00	7.55E-05	6.35E-03	4.46E+00	75
DAZARD_RESPONSE_TO_UV_SCC_DN	Genes down-regulated in SCC12B2 cells (squamous cell carcinoma) by UV-B irradiation.	36	3.90E+00	1.08E-03	3.74E-02	3.02E+00	122
ONDER_CDH1_TARGETS_2_DN	Genes down-regulated in HMLE cells (immortalized nontransformed mammary epithelium) after E-cadherin (CDH1) [GeneID=999] knockdown by RNAi.	38	2.40E+00	1.36E-07	7.64E-05	2.63E+00	458
VARELA_ZMPSTE24_TARGETS_UP	Top genes up-regulated in liver tissue from mice with knockout of ZMPSTE24 [GeneID=10269].	39	9.64E+00	1.15E-04	9.02E-03	6.17E+00	38

Figure S5

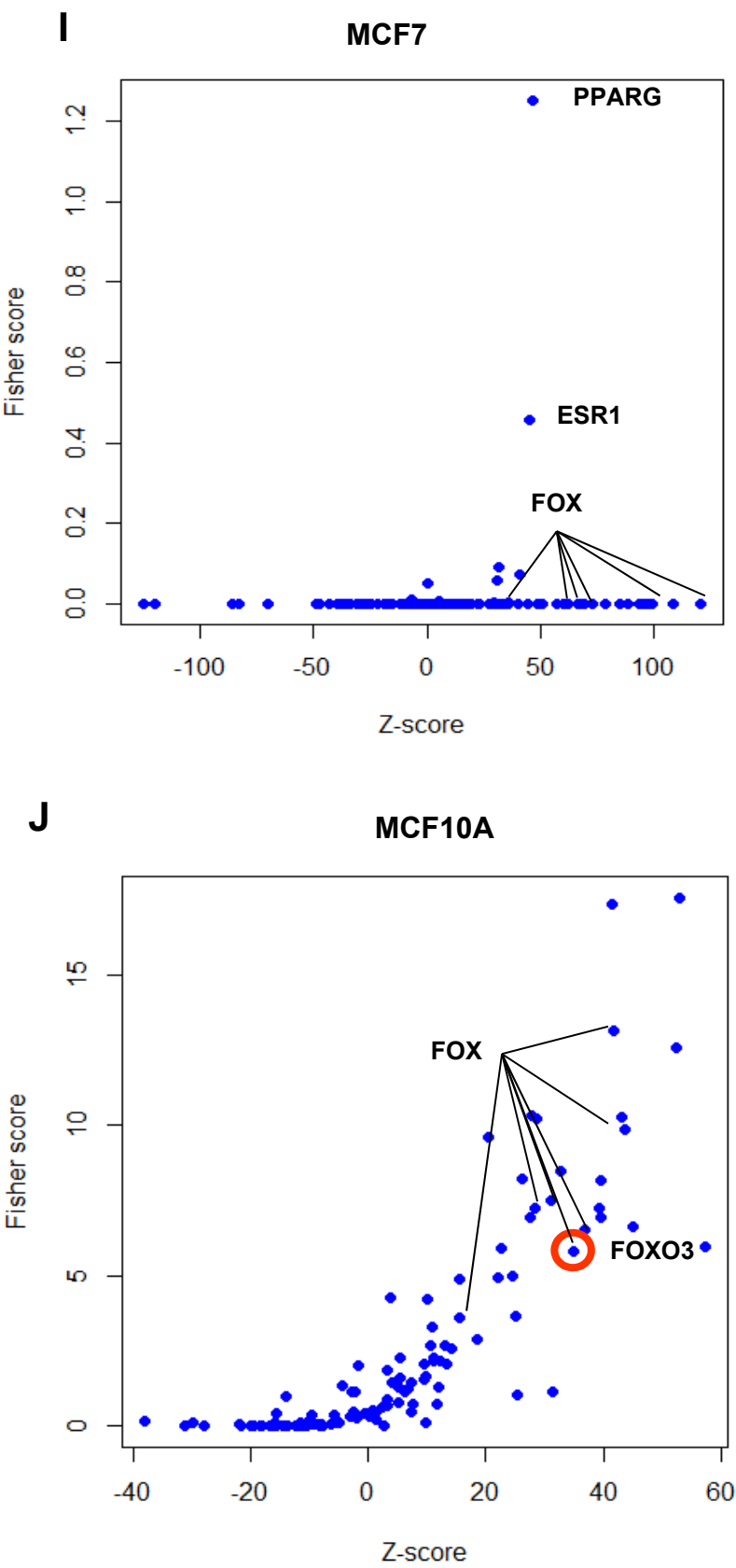


Figure S5

MCF10A specific RNAPII peaks surrounding BRD4
bound distal regions

K

PANTHER	Description	Enrichment	P-value	FDR q-value	Total Genes
P00048	PI3 kinase pathway	1.18E+01	7.94E-04	4.02E-02	48
P00005	Angiogenesis	4.33E+00	2.06E-04	3.14E-02	151
P00047	PDGF signaling pathway	2.89E+00	6.13E-04	4.66E-02	124

L

MSigDB_pathway_ID	P-value	Enrichment	FDR q-value	Total Genes
a6b1 and a6b4 Integrin signaling	4.65e-31	12.0795	1.2154e-2	46

Figure S5M

MCF10A specific RNAPII peaks surrounding BRD4 bound distal regions

MSigDB_Perturbation_ID	Enrichment	P-value	FDR q-value	Total Genes
BURTON_ADIPOGENESIS_1	2.38E+01	8.52E-06	1.59E-03	33
NAGASHIMA_NRG1_SIGNALING_UP	9.44E+00	3.75E-07	3.16E-04	168
NAGASHIMA_EGF_SIGNALING_UP	1.63E+01	5.38E-07	3.62E-04	56
AMIT_SERUM_RESPONSE_120_MCF10A	1.28E+01	1.67E-06	5.63E-04	63
CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	1.03E+01	1.06E-07	1.19E-04	103
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN	7.22E+00	1.74E-06	5.33E-04	129
NAKAMURA_ADIPOGENESIS_EARLY_UP	9.08E+00	1.54E-05	2.47E-03	64
ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF	3.39E+00	1.72E-10	5.80E-07	482
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1	9.30E+00	2.99E-06	7.74E-04	67
LEONARD_HYPOXIA	1.45E+01	7.08E-04	3.45E-02	47
NAKAMURA_ADIPOGENESIS_LATE_UP	7.00E+00	2.17E-05	3.04E-03	101
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	9.82E+00	1.51E-04	1.15E-02	85
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	2.80E+00	1.15E-06	4.30E-04	789
MANALO_HYPOXIA_UP	4.11E+00	1.85E-05	2.71E-03	201
VARELA_ZMPSTE24_TARGETS_UP	1.43E+01	2.28E-05	3.06E-03	38
ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	3.83E+00	1.22E-04	1.08E-02	211
YAGI_AML_FAB_MARKERS	4.33E+00	4.92E-04	2.85E-02	190
KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3	2.52E+00	6.07E-09	1.02E-05	809
ZWANG_EGF_INTERVAL_DN	4.56E+00	6.72E-07	3.77E-04	195
JAEGER_METASTASIS_DN	3.87E+00	7.64E-06	1.51E-03	254

Figure S6

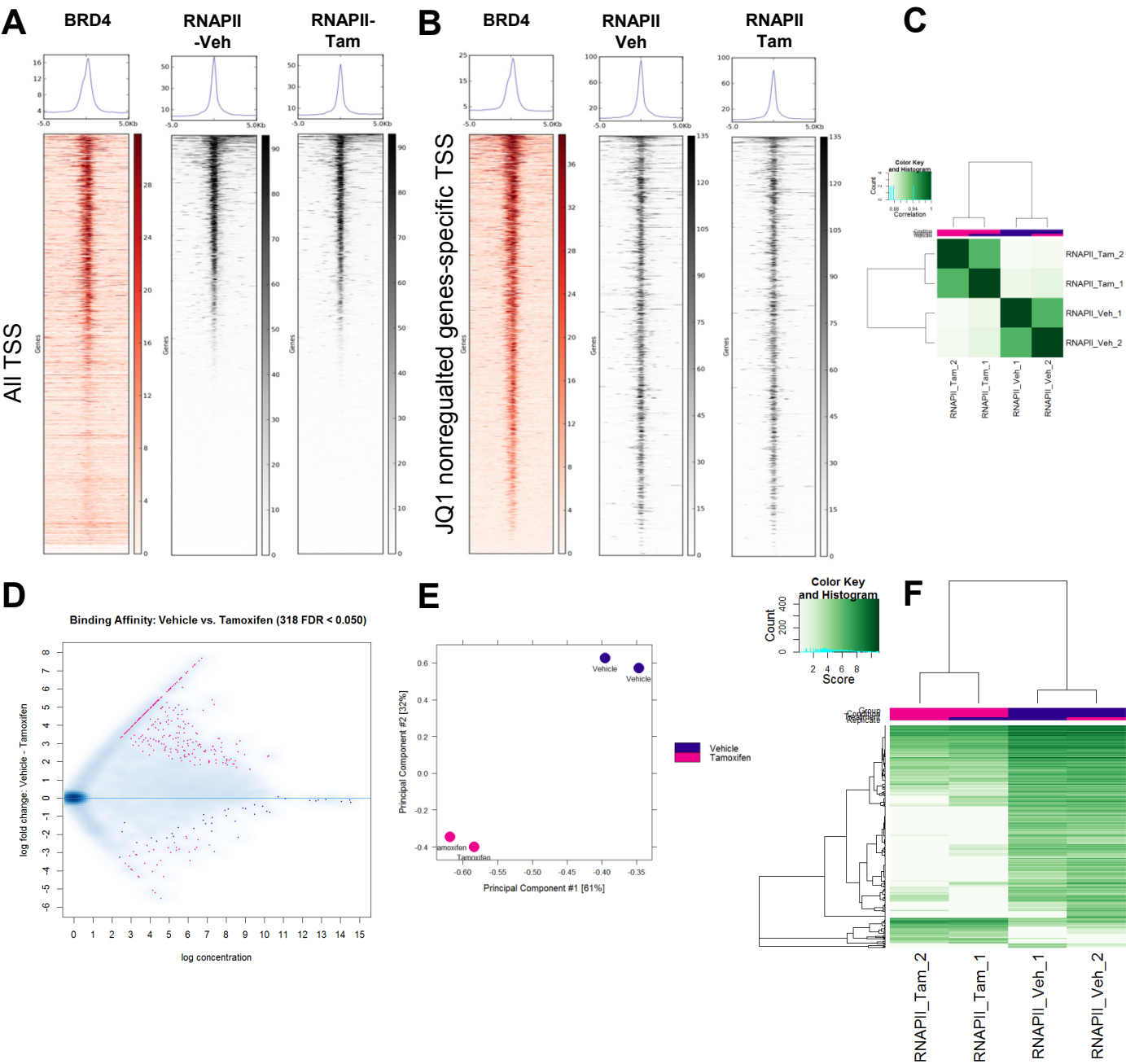


Figure S6

G

MSigDB_perturbation-ID	Region Fold Enrichment	HyperP	HyperFdr Q	TotalGene s
AMIT_SERUM_RESPONSE_120_MCF10A	1.18E+01	6.25E-07	1.24E-04	63
ONDER_CDH1_TARGETS_2_DN	3.95E+00	9.97E-17	3.35E-13	458
SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN	7.74E+00	2.44E-11	4.10E-08	146
BASSO_CD40_SIGNALING_UP	1.04E+01	4.68E-05	3.50E-03	101
KOINUMA_TARGETS_OF_SMAD2_OR_SMAD3	2.96E+00	5.04E-11	5.65E-08	809
CROMER_METASTASIS_DN	1.17E+01	7.64E-07	1.29E-04	80
LEONARD_HYPOXIA	1.50E+01	3.99E-04	1.48E-02	47
BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP	2.99E+00	4.75E-05	3.48E-03	789
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_DN	6.16E+00	7.44E-08	2.50E-05	129
BILD_HRAS_ONCOGENIC_SIGNATURE	4.47E+00	7.38E-11	6.20E-08	248
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	1.01E+01	6.60E-05	4.19E-03	85
BURTON_ADIPOGENESIS_1	1.29E+01	5.49E-04	1.69E-02	33
NAGASHIMA_NRG1_SIGNALING_UP	5.55E+00	1.11E-05	1.04E-03	168
DAZARD_RESPONSE_TO_UV_SCC_DN	5.59E+00	2.39E-07	5.75E-05	122
ZHAN_MULTIPLE_MYELOMA_CD1_DN	1.23E+01	2.13E-04	9.55E-03	42
TSAI_RESPONSE_TO_IONIZING_RADIATION	5.93E+00	1.40E-05	1.24E-03	149
ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	4.02E+00	3.17E-09	2.13E-06	211
CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_UP	8.27E+00	8.11E-08	2.48E-05	112
NAGASHIMA_EGF_SIGNALING_UP	9.21E+00	1.51E-04	7.34E-03	56
JAEGER_METASTASIS_DN	4.19E+00	1.58E-06	2.21E-04	254
GESERICK_TERT_TARGETS_DN	1.58E+01	5.77E-05	4.04E-03	21
BURTON_ADIPOGENESIS_PEAK_AT_2HR	9.55E+00	7.94E-06	8.62E-04	50
MCBRYAN_PUBERTAL_BREAST_4_5WK_UP	3.88E+00	3.52E-08	1.31E-05	264
ZWANG_CLASS_2_TRANSIENTLY_INDUCED_BY_EGF	8.89E+00	4.49E-04	1.54E-02	48
BRUECKNER_TARGETS_OF_MIRLET7A3_UP	5.47E+00	4.73E-04	1.59E-02	110

H

MSigDB_Oncogenic_signatures-ID	RegionFoldEnrich	HyperP	HyperFdrQ	TotalGenes
ATF2_UP.V1_DN	3.64E+00	1.43E-03	3.82E-02	181
P53_DN.V1_UP	3.15E+00	6.58E-04	3.08E-02	191
MYC_UP.V1_DN	4.10E+00	1.35E-03	4.22E-02	153
KRAS.DF.V1_DN	2.79E+00	2.01E-03	4.19E-02	189
CSR_EARLY_UP.V1_UP	2.96E+00	5.18E-04	3.23E-02	160
MEK_UP.V1_UP	2.47E+00	1.82E-04	1.71E-02	191
LTE2_UP.V1_UP	1.90E+00	1.49E-03	3.49E-02	182
RAF_UP.V1_UP	1.82E+00	2.47E-03	4.62E-02	194
STK33_NOMO_UP	1.60E+00	6.80E-05	1.27E-02	276
STK33_UP	1.55E+00	8.16E-04	3.05E-02	281

Figure S7A

HepG2

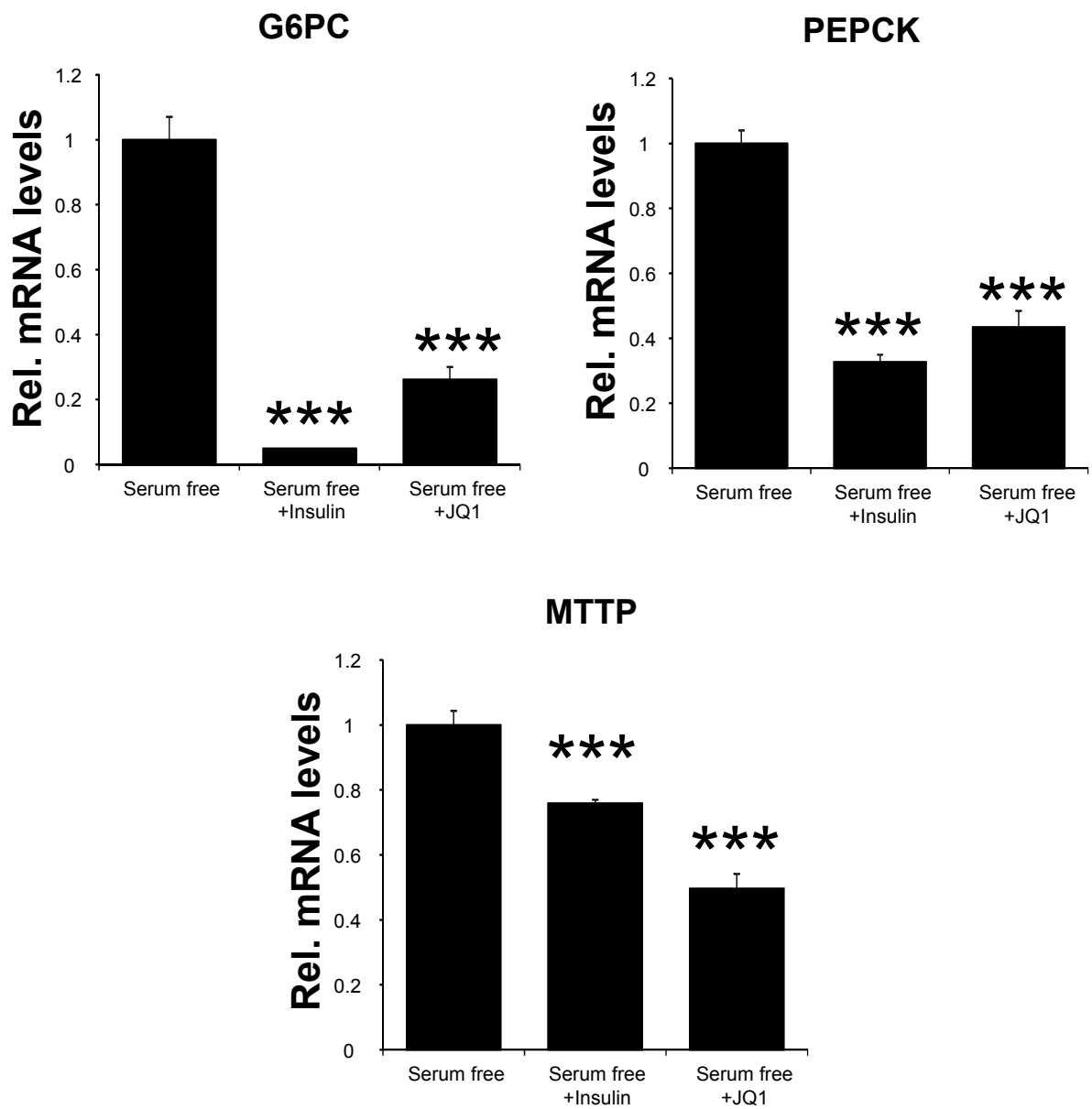


Figure S7B

