

**Table W1.** Suppressed Gene Sets That Overlap with the Genes That Suppressed with ET-743 Treatment in ESFT Cells.

Name	Size	NOM, <i>P</i>	FDR, <i>q</i>
UVC_XPCS_ALL_DN	478	<.001	0.0000
UVC_XPCS_8HR_DN	408	<.001	0.0000
DIAB_NEPH_DN	374	<.001	0.0155
UVC_TTD_ALL_DN	358	<.001	0.0000
HSC_MATURE_ADULT	331	<.001	0.0238
UVC_TTD_4HR_DN	297	<.001	0.0000
UVB_NHEK1_DN	270	<.001	0.0000
ET743_SARCOMA_DN	269	<.001	0.0271
UVC_XPCS_4HR_DN	242	<.001	0.0000
BAF57_BT549_UP	238	<.001	0.0002
HDACL_COLON_SUL_DN	215	<.001	0.0202
VENTRICLES_UP	205	<.001	0.0258
HSA04810_REGULATION_OF_ACTIN_CYTOSKELETON	198	<.001	0.0315
HSA04510_FOCAL_ADHESION	194	<.001	0.0100
GH_GHRHR_KO_24HRS_DN	172	<.001	0.0050
UVC_TTD_8HR_DN	165	<.001	0.0000
OLD_FIBRO_DN	158	<.001	0.0202
BRCA_BRCA1_NEG	154	<.001	0.0218
UVC_TTD_XPCS_COMMON_DN	144	<.001	0.0000
BRENTANI_PROTEIN_MODIFICATION	143	<.001	0.0104
GH_GHRHR_KO_24HRS_UP	142	<.001	0.0199
CALCIUM_REGULATION_IN_CARDIAC_CELLS	140	<.001	0.0318
HSA04530_TIGHT_JUNCTION	132	<.001	0.0063
UVB_NHEK1_C6	130	<.001	0.0000
HSA04360_AXON_GUIDANCE	128	<.001	0.0038
GH_AUTOCRINE_DN	122	<.001	0.0039
HSA01030_GLYCAN_STRUCTURES_BIOSYNTHESIS_1	111	<.001	0.0362
G_PROTEIN_SIGNALING	90	<.001	0.0070
PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	88	<.001	0.0002
BRCA1KO_MEF_DN	79	<.001	0.0209
ST_INTEGRIN_SIGNALING_PATHWAY	78	<.001	0.0054
CREB_BRAIN_8WKS_UP	75	<.001	0.0042
HSA04520_ADHERENS_JUNCTION	75	<.001	0.0157
HSA04664_FC_EPSILON_RI_SIGNALING_PATHWAY	74	<.001	0.0283
CARIES_PULP_DN	70	<.001	0.0299
HSA04720_LONG_TERM_POTENTIATION	69	<.001	0.0052
UVB_NHEK3_C8	66	<.001	0.0002
UVC_LOW_ALL_DN	58	<.001	0.0000
OLDONLY_FIBRO_DN	53	<.001	0.0092
NFATPATHWAY	52	<.001	0.0006
HDACL_COLON_CUR_DN	49	<.001	0.0002
ET743PT650_COLONCA_DN	44	<.001	0.0000
NOVA2_KO_SPLICING	42	<.001	0.0019
CMV_HCMV_TIMECOURSE_14HRS_DN	41	<.001	0.0089
BIOPEPTIDSPATHWAY	38	<.001	0.0002
DFOSB_BRAIN_2WKS_UP	38	<.001	0.0010
UVB_NHEK3_C5	35	<.001	0.0000
AT1RPATHWAY	34	<.001	0.0068
GLYCOGEN_METABOLISM	34	<.001	0.0159
HSA00970_AMINOACYL_TRNA_BIOSYNTHESIS	31	<.001	0.0071
HDACPATHWAY	30	<.001	0.0002
CREBPATHWAY	27	<.001	0.0007
HDACL_COLON_CUR24HRS_DN	25	<.001	0.0069

The microarray data generated by treating TC32 and TC71 with ET-743 was compared with more than 1892 curated gene sets using GSEA [36]. All had  $P < .001$  and  $FDR < 0.05$ .

The source of the data can be found on the Web site (<http://www.broad.mit.edu/gsea/>) and is referenced in the text where appropriate.

Shaded data indicate data sets discussed in the text.

Size indicates the number of genes in the gene set that shows overlap with the ones in the expression data set.

**Table W2.** Induced Gene Sets That Showed Significant Overlap.

Name	Size	NOM, <i>P</i>	FDR, <i>q</i>
CMV_HCMV_TIMECOURSE_ALL_UP	464	<.001	0.0393
REOVIRUS_HEK293_UP	236	<.001	0.0053
CARIES_PULP_UP	205	<.001	0.0085
UVB_NHEK1_UP	173	<.001	0.0006
CMV_UV_HCMV_6HRS_UP	120	<.001	0.0054
BLEO_HUMAN_LYMPH_HIGH_24HRS_UP	92	<.001	0.0008
LVAD_HEARTFAILURE_UP	89	<.001	0.0025
UVB_NHEK3_C0	82	<.001	0.0017
HYPOXIA_REVIEW	81	<.001	0.0125
UVC_TTD_ALL_UP	76	<.001	0.0000
DNMT1_KO_UP	72	<.001	0.0045
APOPTOSIS	67	<.001	0.0248
BRENTANI_TRANSCRIPTION_FACTORS	64	<.001	0.0236
UVC_XPCS_ALL_UP	61	<.001	0.0000
UVC_XPCS_8HR_UP	58	<.001	0.0000
UVC_TTD_4HR_UP	58	<.001	0.0020
ET743_HELA_UP	56	<.001	0.0007
CMV_HCMV_6HRS_DN	55	<.001	0.0000
CMV_HCMV_TIMECOURSE_6HRS_DN	52	<.001	0.0007
TPA_SENS_LATE_UP	52	<.001	0.0394
CMV_HCMV_TIMECOURSE_14HRS_UP	45	<.001	0.0000
ZUCCHI_EPITHELIAL_DN	43	<.001	0.0008
TNFALPHA_30MIN_UP	42	<.001	0.0065
EGF_HDMEC_UP	42	<.001	0.0066
ADIP_DIFF_CLUSTER2	40	<.001	0.0002
HYPOXIA_REG_UP	38	<.001	0.0000
DSRNA_UP	38	<.001	0.0002
IFN_GAMMA_UP	38	<.001	0.0014
STRESS_GENOTOXIC_SPECIFIC_UP	34	<.001	0.0045
ST_TUMOR_NECROSIS_FACTOR_PATHWAY	29	<.001	0.0065
OXSTRESS_BREASTCA_UP	29	<.001	0.0071
DAC_BLADDER_UP	28	<.001	0.0046
CMV_UV-CMV_COMMON_HCMV_6HRS_DN	27	<.001	0.0064
IFNALPHA_NL_UP	27	<.001	0.0084
CMV_HCMV_6HRS_UP	25	<.001	0.0010
AD12_ANY_DN	25	<.001	0.0034
IDX_TSA_UP_CLUSTER1	25	<.001	0.0048

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Size indicates the number of genes in the gene set that shows overlap with the ones in the expression data set.