Figure S4. Pathway analysis using Gene Set Enrichment Analysis (GSEA)

Gene Sets upregulated in ER+ samples

NAME	SIZE	ES	NOM p-va	FDR q-val
TACGGGT,MIR-99A,MIR-100,MIR-99B	16	0.74	0.0000	1
CHR8P11	21	0.74	0.0000	1
MODULE_288	18	0.70	0.1152	1
GCM_PPM1D	17	0.68	0.1203	1
GNF2_MAPT	20	0.67	0.0288	1
HDACI_COLON_SUL12HRS_DN	18	0.67	0.0269	1
HSA00910_NITROGEN_METABOLISM	15	0.65	0.0424	1
KIM_TH_CELLS_UP	34	0.65	0.0100	1
CHR10Q21	18	0.64	0.0393	1
CHR12Q14	21	0.63	0.0762	1
MODULE_367	15	0.62	0.1892	1
AXON_GUIDANCE	16	0.62	0.0488	1
CHR8Q13	17	0.62	0.1332	1
GTATGAT,MIR-154,MIR-487	41	0.62	0.0122	1
FRASOR_ER_UP	29	0.61	0.1089	1
ATCTTGC,MIR-31	40	0.61	0.0079	1
INOSITOL_PHOSPHATE_METABOLISM	18	0.61	0.0850	1
MMS_MOUSE_LYMPH_HIGH_24HRS_U	17	0.60	0.1286	1
CHR1P21	16	0.59	0.1106	1
CACGTTT,MIR-302A	19	0.59	0.0661	1

Gene Sets upregulated in ER- samples

NAME	SIZE	ES	NOM p-va	FDR q-val
CHEN_LUNG_SURVIVAL	16	-0.82	0.0062	0.2746
MODULE_298	16	-0.81	0.1230	0.1681
MODULE_68	16	-0.81	0.1589	0.1225
MODULE_130	15	-0.77	0.1946	0.3292
GNF2_GLTSCR2	31	-0.76	0.0557	0.2956
MODULE_29	27	-0.75	0.0873	0.3528
SMALL_NUCLEAR_RIBONUCLEOPROT	17	-0.74	0.0061	0.3232
DAC_IFN_BLADDER_UP	15	-0.73	0.0704	0.3490
GCM_TPT1	68	-0.73	0.0338	0.3753
STRUCTURAL_CONSTITUENT_OF_RIB	72	-0.73	0.0522	0.3467
LIZUKA_L0_SM_L1	17	-0.72	0.0755	0.3620
HSA03010_RIBOSOME	62	-0.71	0.0884	0.3688
INNEREAR_UP	27	-0.70	0.1527	0.4092
RIBOSOMAL_PROTEINS	83	-0.69	0.0455	0.5121
GNF2_TPT1	38	-0.68	0.1167	0.5756
ET743_SARCOMA_6HRS_UP	27	-0.68	0.0489	0.5514
MORF_TPT1	99	-0.67	0.0498	0.5572
GILDEA_BLADDER_UP	27	-0.67	0.0943	0.5801
XU_CBP_UP	17	-0.67	0.0468	0.5578
GNF2_FGR	25	-0.67	0.1222	0.5384

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