

Supplement 1

Sensitive group

term	es	nes	p	q	geneNo	pct	leadFC
GO_CHEMOKINE_ACTIVITY	0.657652	2.012104	0	0.0031	47	0.489	24.933
LEE_LIVER_CANCER_MYC_TGFA_DN	0.626162	2.255945	0	6.12E-05	64	0.562	5.764
GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	0.71324	2.045248	0	0.00218	24	0.625	15.692
LEE_LIVER_CANCER_SURVIVAL_UP	0.470228	2.025048	0	0.00278	184	0.429	7.992
LEE_LIVER_CANCER_ACOX1_DN	0.542582	1.97407	0	0.00483	65	0.554	5.672
HOSHIDA_LIVER_CANCER_SUBCLASS_S3	0.414317	1.893403	0	0.00972	265	0.442	7.698
LEE_LIVER_CANCER_DENA_DN	0.519861	1.862994	0	0.013	74	0.446	5.891
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING	0.551953	1.830191	0	0.01693	39	0.538	27.732
WOO_LIVER_CANCER_RECURRENCE_DN	0.472666	1.803018	0	0.0207	78	0.436	7.503
SERVITJA_ISLET_HNF1A_TARGETS_DN	0.562453	2.21848	0	0.00023	107	0.523	12.886
GO_FATTY_ACID_BINDING	0.580397	1.879041	0	0.01137	39	0.513	25.997
GO_REGULATION_OF_DNA_REPLICATION	0.461263	1.928151	0	0.00718	111	0.333	2.349

Resistant group

term	es	nes	p	q	geneNo	pct	leadFC
MEBARKI_HCC_PROGENITOR_WNT_UP_CTNNB1_INDEPENDENT	-0.735497	-2.175221	0	0.0011	24	0.625	31.494
STEGER_ADIPOGENESIS_DN	-0.700805	-2.07138	0	0.004	24	0.542	73.491
REACTOME_SIGNALING_BY_PDGF	-0.457052	-1.674236	0	0.06875	58	0.414	18.379
GO_COLLAGEN_FIBRIL_ORGANIZATION	-0.61874	-2.25321	0	0.0005	55	0.564	29.182
JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP	-0.581989	-2.244427	0	0.00048	67	0.507	28.517
GO_BASEMENT_MEMBRANE	-0.521862	-2.117274	0	0.00229	103	0.495	11.984
KEGG_ECM_RECEPTOR_INTERACTION	-0.523889	-2.03403	0	0.00619	84	0.512	26.899
KIM_HYPOXIA	-0.644429	-1.829555	0	0.03151	17	0.412	3.269
WOO_LIVER_CANCER_RECURRENCE_UP	-0.414063	-1.750644	0	0.04948	104	0.404	8.012
HUANG_DASATINIB_RESISTANCE_UP	-0.655525	-2.584306	0	0	78	0.628	10.14

Supplement 2

Sensitive group

term	es	nes	p	q	geneNo	pct	leadFC
GNF2_LCAT	0.672858	2.763401	0	0	124	0.613	19.935
GNF2_HPX	0.664673	2.723419	0	0	135	0.615	22.588
GNF2_HPNI	0.660768	2.689661	0	0	134	0.619	17.679
AIZARANI_LIVER_C17_HEPATOCYTES_3	0.66812	2.687396	0	0	102	0.618	51.091
MANALO_HYPOXIA_DN	0.564186	2.681867	0	0	286	0.339	2.132
HALLMARK_E2F_TARGETS	0.580632	2.659341	0	0	198	0.359	2.102
HSIAO_LIVER_SPECIFIC_GENES	0.587281	2.656614	0	0	249	0.586	24.912
AIZARANI_LIVER_C14_HEPATOCYTES_2	0.577865	2.588725	0	0	225	0.551	20.858
MODULE_8	0.521455	2.555847	0	0	416	0.377	2.731
GNF2_GSTM1	0.64054	2.52192	0	0	109	0.578	19.313
DUTERTRE ESTRADIOL_RESPONSE_24HR_UP	0.524509	2.509006	0	0	319	0.398	2.262
SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP	0.568746	2.508156	0	0	150	0.387	2.074
GNF2_TST	0.630887	2.484063	0	0	104	0.606	20.578
CAR_HPX	0.697248	2.482988	0	0	73	0.685	32.593
GAO_SMALL_INTESTINE_24W_C4_ENTEROCYTE_PROGENITOR_SUBTYPE_2	0.639577	2.475842	0	0	97	0.588	13.136
MUELLER_PLURINET	0.51749	2.447742	0	0	297	0.3	2.22
AIZARANI_LIVER_C11_HEPATOCYTES_1	0.520308	2.44747	0	0	296	0.541	16.651
FAN_EMBRYONIC_CTX_MICROGLIA_1	0.55725	2.428236	0	0	149	0.315	2.046
ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR	0.611882	2.424119	0	0	82	0.39	2.127
REACTOME_G2_M_CHECKPOINTS	0.565066	2.423994	0	0	134	0.351	2.139
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER	0.562917	2.41686	0	0	138	0.42	2.191
GO_DNA_DEPENDENT_DNA_REPLICATION	0.547692	2.414437	0	0	151	0.377	2.099
GNF2_CEBPA	0.665523	2.404393	0	0	64	0.625	19.935
BENPORATH_PROLIFERATION	0.555239	2.401085	0	0	142	0.338	2.171
GNF2_PCNA	0.628484	2.384347	0	0	67	0.373	2.107
GSE22886_UNSTIM_VS_IL15_STIM_NKCELL_DN	0.528274	2.377719	0	0	195	0.374	2.21

term	es	nes	p	q	geneNo	pct	leadFC
GNF2_CCNA2	0.625324	2.369808	0	0	67	0.403	2.102
KANG_DOXORUBICIN_RESISTANCE_UP	0.643258	2.367318	0	0	54	0.389	2.384
GNF2_RRM1	0.60107	2.360866	0	0	87	0.368	2.218
WP_DNA_REPLICATION	0.685941	2.360731	0	0	42	0.548	2.091
GSE5679_CTRL_VS_PPARG_LIGAND_ROSIGLITAZONE_TREATED_DC_UP	0.52668	2.356942	0	0	193	0.352	2.198
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	0.703146	2.353807	0	0	37	0.568	2.102
REACTOME_DNA_REPLICATION	0.55284	2.350811	0	0	128	0.359	2.121
GNF2_RFC4	0.629305	2.345567	0	2.2E-05	59	0.356	2.102
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_INFLUENZA_A_DEL_NS1_INFECTION_DN	0.527842	2.338127	0	2.1E-05	185	0.411	2.188
REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE	0.683849	2.326631	0	2E-05	42	0.381	2.212
GNF2_CDC2	0.606886	2.315728	0	1.9E-05	61	0.344	2.064
REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	0.719646	2.315663	0	1.9E-05	33	0.576	2.064
CAR_IGFBP1	0.675217	2.314688	0	1.8E-05	57	0.702	25.29
GNF2_SMC4L1	0.590487	2.31408	0	1.8E-05	83	0.325	2.217
HP_SIDEROBLASTIC_ANEMIA	0.699939	2.310126	0	1.7E-05	33	0.333	2.017
REACTOME_DNA_REPLICATION_PRE_INITIATION	0.584221	2.29905	0	5.1E-05	85	0.412	2.064
BLANCO_MELO_HUMAN_PARAINFLUENZA_VIRUS_3_INFECTION_A594_CELLS_DN	0.543355	2.29435	0	4.9E-05	118	0.559	9.535
GAO_LARGE_INTESTINE_ADULT_CH_MKI67HIGH_CELLS	0.561546	2.289986	0	4.7E-05	104	0.375	2.27
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	0.803019	2.289408	0	4.6E-05	25	0.56	42.408
REACTOME_CHROMOSOME_MAINTENANCE	0.557177	2.287756	0	4.5E-05	92	0.348	2.21
REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR	0.604019	2.279671	0	4.3E-05	67	0.313	2.193
GNF2_CENPF	0.614892	2.274119	0	4.3E-05	61	0.361	2.031

term	es	nes	p	q	geneNo	pct	leadFC
SONG_TARGETS_OF_IE86_CMV_PROTEIN	0.62071	2.271684	0	4.2E-05	54	0.426	1.999
CROONQUIST_IL6_DEPRIVATION_DN	0.565881	2.270153	0	5.5E-05	94	0.426	2.158

Resistant group

term	es	nes	p	q	geneNo	pct	leadFC
WANG_SMARCE1_TARGETS_UP	-0.611851	-2.940414	0	0	287	0.537	9.072
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	-0.632545	-2.929763	0	0	198	0.631	25.387
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	-0.593547	-2.898839	0	0	346	0.587	11.333
ANASTASSIOU_MULTICANCER_INVASIVENESS_SIGNATURE	-0.752657	-2.840556	0	0	64	0.656	46.94
CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_DN	-0.56247	-2.832176	0	0	459	0.481	11.984
GAO_LARGE_INTESTINE_ADULT_CJ_IMMUNE_CELLS	-0.557267	-2.798794	0	0	502	0.514	10.346
ONDER_CDH1_TARGETS_2_UP	-0.568392	-2.742936	0	0	250	0.556	11.604
AIZARANI_LIVER_C21_STELLATE_CELLS_1	-0.584216	-2.640184	0	0	192	0.589	6.411
LIM_MAMMARY_STEM_CELL_UP	-0.520996	-2.597996	0	0	472	0.475	7.534
HUANG_DASATINIB_RESISTANCE_UP	-0.655525	-2.584306	0	0	78	0.628	10.14
BOQUEST_STEM_CELL_UP	-0.548448	-2.580178	0	0	258	0.547	11.604
SENESE_HDAC1_AND_HDAC2_TARGETS_DN	-0.557633	-2.574752	0	0	228	0.522	7.062
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	-0.561846	-2.518914	0	0	171	0.602	10.211
MODULE_47	-0.539342	-2.518081	0	0	224	0.603	12.755
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	-0.496942	-2.510299	0	0	448	0.433	10.598
BLANCO_MELO_HUMAN_PARAINFLUENZA_VIRUS_3_INFECTION_A594_CELLS_UP	-0.547322	-2.507976	0	0	199	0.487	9.202
GAO_LARGE_INTESTINE_24W_C1_DCLK1POS_PROGENITOR	-0.621453	-2.502035	0	0	99	0.586	23.666
MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_DN	-0.533108	-2.496406	0	0	231	0.472	12.536

term	es	nes	p	q	geneNo	pct	leadFC
PETROVA_ENDOTHELIUM_LYMPHATIC_VS_BLOOD_DN	-0.559423	-2.493275	0	0	162	0.543	11.551
RIGGI_EWING_SARCOMA_PROGENITOR_DN	-0.547994	-2.475181	0	0	192	0.484	8.07
AIZARANI_LIVER_C10_MVECS_1	-0.520332	-2.460186	0	0	265	0.464	6.444
VERRECCHIA_EARLY_RESPONSE_TO_TGFB1	-0.659045	-2.449676	0	0	54	0.537	29.334
AIZARANI_LIVER_C29_MVECS_2	-0.507592	-2.434855	0	0	308	0.468	6.833
MODULE_1	-0.499383	-2.432406	0	0	362	0.453	6.068
BROWNE_HCMV_INFECTION_24HR_DN	-0.553498	-2.421337	0	0	142	0.451	7.658
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	-0.570939	-2.419084	0	4.77E-05	168	0.518	14.34
FAN_EMBRYONIC_CTX_BRAIN_ENDOTHELIAL_2	-0.502957	-2.416368	0	4.59E-05	299	0.458	6.05
MEBARKI_HCC_PROGENITOR_WNT_UP	-0.536932	-2.408009	0	4.43E-05	196	0.556	13.168
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_TENSILE_STRENGTH	-0.719148	-2.407189	0	4.28E-05	41	0.634	47.951
HU_FETAL_RETINA_FIBROBLAST	-0.486971	-2.402831	0	4.13E-05	381	0.459	6.69
CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN	-0.707825	-2.393484	0	4.00E-05	35	0.657	33.128
CSR_LATE_UP.V1_DN	-0.542933	-2.392405	0	3.88E-05	144	0.465	7.574
KINSEY_TARGETS_OF_EWSR1_FLI1_FUSION_DN	-0.492972	-2.392308	0	3.76E-05	324	0.42	3.879
HENDRICKS_SMARCA4_TARGETS_UP	-0.648039	-2.386856	0	3.65E-05	54	0.704	5.921
REN_ALVEOLAR_RHABDOMYOSARCOMA_DN	-0.474534	-2.38374	0	3.54E-05	405	0.375	5.939
WP_MIRNA_TARGETS_IN_ECM_AND_MEMBRANE_RECEPTORS	-0.710965	-2.383408	0	3.45E-05	42	0.476	79.976
REACTOME_ECM_PROTEOGLYCANS	-0.6357	-2.382562	0	3.35E-05	76	0.566	26.899
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	-0.525448	-2.381114	0	6.52E-05	208	0.495	7.349
REACTOME_COLLAGEN_CHAIN_TRIMERIZATION	-0.697647	-2.3789	0	6.35E-05	44	0.636	35.989
DURANTE_ADULT_OLFACTORY_NEUROEPITHELIUM_FIBROBLASTS_STROMAL_CELLS	-0.603592	-2.377641	0	6.19E-05	81	0.568	11.503
NABA_COLLAGENS	-0.697647	-2.375186	0	6.04E-05	44	0.636	35.989

term	es	nes	p	q	geneNo	pct	leadFC
CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_DN	-0.643101	-2.374664	0	5.90E-05	51	0.667	7.19
GO_COLLAGEN_TRIMER	-0.622579	-2.369353	0	5.76E-05	87	0.494	14.708
GNF2_CDH11	-0.750493	-2.364806	0	5.63E-05	25	0.84	29.182
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_DN	-0.519086	-2.354986	0	8.20E-05	170	0.459	8.346
HALLMARK_UV_RESPONSE_DN	-0.53719	-2.354751	0	8.02E-05	142	0.43	6.577
WILCOX_RESPONSE_TO_PROGESTERONE_DN	-0.621176	-2.339614	0	0.0001	62	0.597	10.422
SWEET_KRAS_TARGETS_UP	-0.590008	-2.330094	0	0.00013	81	0.605	6.177
BROWNE_HCMV_INFECTION_20HR_DN	-0.563798	-2.327204	0	0.00015	96	0.406	10.091
GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	-0.689805	-2.315119	0	0.0002	40	0.475	20.189

Supplement 3

gene_id	gene_name	gene_type
ENSG00000042980.11	ADAM28	protein_coding
ENSG00000129038.14	LOXL1	protein_coding
ENSG00000136235.14	GPNMB	protein_coding
ENSG00000133636.9	NTS	protein_coding
ENSG00000198019.11	FCGR1B	protein_coding
ENSG00000164692.16	COL1A2	protein_coding
ENSG00000123095.5	BHLHE41	protein_coding
ENSG00000078098.12	FAP	protein_coding
ENSG00000108821.12	COL1A1	protein_coding
ENSG00000197956.8	S100A6	protein_coding
ENSG00000168542.11	COL3A1	protein_coding
ENSG00000026751.15	SLAMF7	protein_coding
ENSG00000090104.10	RGS1	protein_coding
ENSG00000106624.7	AEBP1	protein_coding
ENSG00000134028.13	ADAMDEC1	protein_coding
ENSG00000100979.13	PLTP	protein_coding
ENSG00000124225.14	PMEPA1	protein_coding
ENSG00000100985.7	MMP9	protein_coding
ENSG00000077274.8	CAPN6	protein_coding
ENSG00000164694.15	FNDC1	protein_coding