GW_080

Global Summary

%DE = 0.13

genes with fdr < 0.2 = 1745 (1084 + / 661 −)

genes with fdr < 0.1 = 1321 (887 + / 434 −)

genes with fdr < 0.05 = 1084 (768 + / 316 −)

genes with fdr < 0.01 = 837 (624 + / 213 −)

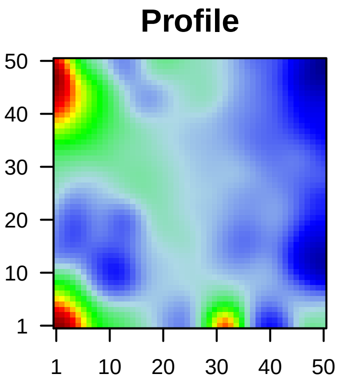
genes in genesets = 16332

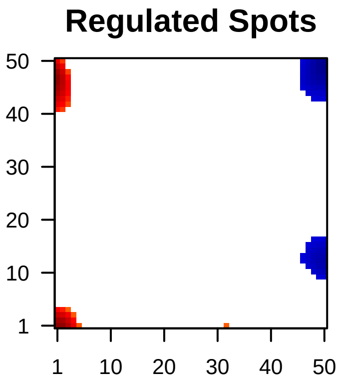
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

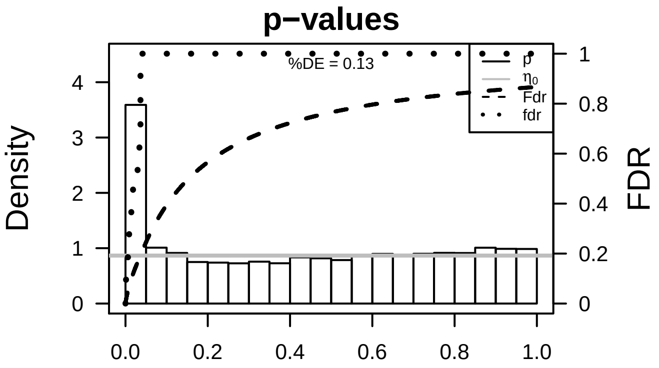
<fdr> = 0.87





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	154	1.28	2e−16	2e−14	1 x 40	adrenoceptor beta 2, surface [Source:HGNC Symbol;Acc:286
2	57016	1.24	2e−16	2e−14	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
3	216	−1.6	2e−16	2e−14	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
4	115701	1.4	2e−16	2e−14	50 x 3	alpha−kinase 2 [Source:HGNC Symbol;Acc:20565]
5	401138	2.42	2e−16	2e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
6	200315	1.49	2e−16	2e−14	1 x 40	apolipoprotein B mRNA editing enzyme, catalytic polypeptide
7	9070	1.4	2e−16	2e−14	47 x 46	ash2 (absent, small, or homeotic)−like (Drosophila) [Source:H
8	633	1.09	2e−16	2e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
9	684	1.39	2e−16	2e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
10	387695	1.99	2e−16	2e−14	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
11	24141	1.16	2e−16	2e−14	7 x 1	lysosomal−associated membrane protein family, member 5 [S
12	760	1.31	2e−16	2e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
13	1041	1.88	2e−16	2e−14	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
14	163732	1.24	2e−16	2e−14	1 x 43	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
15	84518	1.42	2e−16	2e−14	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
16	1308	1.16	2e−16	2e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
17	1277	1.69	2e−16	2e−14	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
18	1278	1.18	2e−16	2e−14	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
19	1281	1.21	2e−16	2e−14	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
20	1289	1.2	2e−16	2e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	26.47	NULL	572	Disease	GUDJ_psoriasis up
2	17.99	NULL	21	CC	cornified envelope
3	17.97	NULL	250	Lymphoma	LENZ_Stromal signature 1
4	16.87	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
5	16.66	NULL	1182	CC	extracellular region
6	16.25	NULL	553	Cancer	Lembcke_Colonic Inflammation
7	16.09	NULL	190	CC	extracellular matrix
8	16.03	NULL	135	H.Tiss	WIRTH_Mucosa
9	14.97	NULL	51	BP	type I interferon signaling pathway
10	14.15	NULL	242	BP	extracellular matrix organization
11	14.05	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
12	14.04	NULL	76	BP	epidermis development
13	13.88	NULL	31	BP	negative regulation of viral genome replication
14	13.51	NULL	123	BP	defense response to virus
15	13.44	NULL	53	BP	keratinocyte differentiation
16	13.06	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
17	12.72	NULL	69	BP	extracellular matrix disassembly
18	12.67	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
19	12.62	NULL	683	CC	extracellular space
20	12.58	NULL	64	BP	collagen catabolic process
Underexpressed					
1	−7.09	NULL	280	Chr	Chr 13
2	−6.39	NULL	1318	CC	mitochondrion
3	−5.56	NULL	370	BP	mitotic cell cycle
4	−5.21	NULL	152	BP	cellular metabolic process
5	−5.19	NULL	6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
6	−5.1	NULL	4640	CC	nucleus
7	−5	NULL	630	Chr	Chr X
8	−4.94	NULL	1253	BP	small molecule metabolic process
9	−4.93	NULL	949	CC	nucleoplasm
10	−4.85	NULL	149	BP	DNA replication
11	−4.85	NULL	92	BP	translational elongation
12	−4.8	NULL	649	BP	gene expression
13	−4.68	NULL	298	BP	DNA repair
14	−4.58	NULL	220	CC	mitochondrial matrix
15	−4.58	NULL	519	Chr	Chr 14
16	−4.58	NULL	717	Chr	Chr 16
17	−4.5	NULL	153	MF	structural constituent of ribosome
18	−4.49	NULL	253	BP	translation
19	−4.48	NULL	1233	TF	KIM_MYC targets
20	−4.33	NULL	755	Lymphoma	SPANG_BCR UP

GW_080

Local Summary

%DE = 0.88

metagenes = 16

genes = 259

genes in genesets = 258

genes with fdr < 0.1 = 203 (201 + / 2 −)

genes with fdr < 0.05 = 203 (201 + / 2 −)

genes with fdr < 0.01 = 181 (180 + / 1 −)

<r> metagenes = 0.96

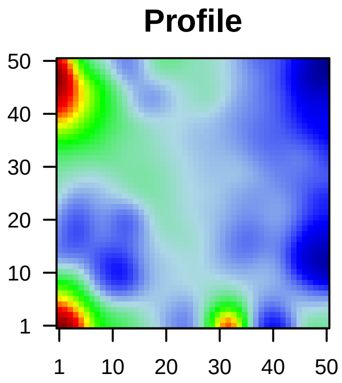
<r> genes = 0.4

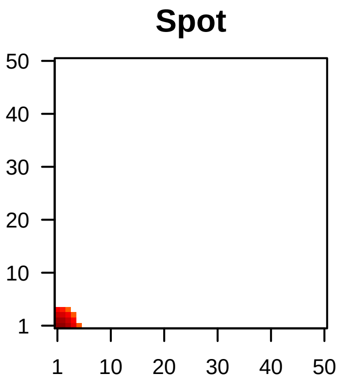
<FC> = 0.58

<shrinkage−t> = 20.34

<p−value> = 0

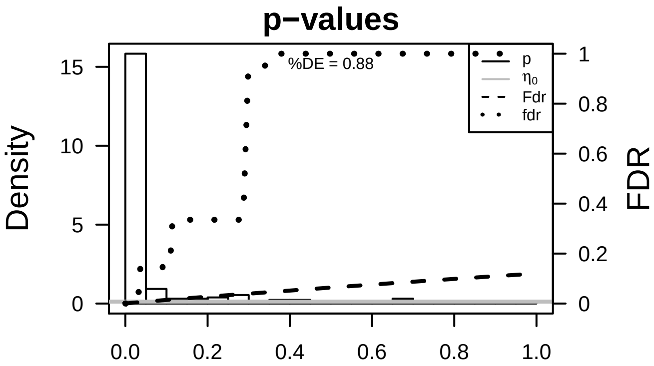
<fdr> = 0.27





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	633	1.09	2e−16	3e−16	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
2	1277	1.69	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
3	1278	1.18	2e−16	3e−16	2 x 1	collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:2198]
4	1281	1.21	2e−16	3e−16	2 x 1	collagen, type III, alpha 1 [Source:HGNC Symbol;Acc:2201]
5	1289	1.2	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
6	1464	1.17	2e−16	3e−16	1 x 3	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Ac
7	3039	1.57	2e−16	3e−16	5 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
8	3040	2.16	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
9	3043	2.07	2e−16	3e−16	5 x 1	hemoglobin, beta [Source:HGNC Symbol;Acc:4827]
10	3576	1.18	2e−16	3e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
11	4060	1.91	2e−16	3e−16	2 x 1	lumican [Source:HGNC Symbol;Acc:6724]
12	4312	1.4	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
13	4319	1.62	2e−16	3e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
14	4320	1.91	2e−16	3e−16	3 x 1	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Sy
15	4322	1.79	2e−16	3e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
16	4314	1.96	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
17	4316	1.21	2e−16	3e−16	2 x 1	matrix metallopeptidase 7 (matrilysin, uterine) [Source:HGNC
18	10631	1.31	2e−16	3e−16	2 x 1	periostin, osteoblast specific factor [Source:HGNC Symbol;Ac
19	6423	1.15	2e−16	3e−16	3 x 1	secreted frizzled−related protein 2 [Source:HGNC Symbol;Ac
20	23213	1.22	2e−16	3e−16	2 x 1	sulfatase 1 [Source:HGNC Symbol;Acc:20391]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	40.13	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
2	39.04	NULL	62 / 190	CC	extracellular matrix
3	37.67	NULL	28 / 64	BP	collagen catabolic process
4	37.39	NULL	31 / 69	BP	extracellular matrix disassembly
5	33.48	NULL	67 / 242	BP	extracellular matrix organization
6	33.06	NULL	71 / 250	Lymphoma	LENZ_Stromal signature 1
7	32	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
8	31.19	NULL	8 / 11	MF	platelet−derived growth factor binding
9	28.25	NULL	15 / 37	BP	collagen fibril organization
10	25.56	NULL	2 / 4	MMML CGS	MACIEJ_MMML 23
11	25.07	NULL	8 / 12	miRNA target	miR−29c
12	24.99	NULL	20 / 57	MF	extracellular matrix structural constituent
13	23.19	NULL	11 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
14	23.08	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
15	22.01	NULL	101 / 1182	CC	extracellular region
16	21.77	NULL	37 / 183	CC	proteinaceous extracellular matrix
17	21.28	NULL	11 / 19	MF	extracellular matrix binding
18	20.28	NULL	75 / 683	CC	extracellular space
19	19.85	NULL	12 / 40	BP	cellular response to amino acid stimulus
20	19.36	NULL	6 / 13	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
21	19.13	NULL	62 / 553	Cancer	Lembcke_Colonic Inflammation
22	18.95	NULL	23 / 119	Lymphoma	ROSOLOWSKI_green total
23	18.86	NULL	7 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
24	18.45	NULL	5 / 10	GSEA C2	KEGG_ECM_RECEPTOR_INTERACTION
25	18.35	NULL	10 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
26	17.94	NULL	5 / 11	BP	dermatan sulfate biosynthetic process
27	17.55	NULL	18 / 68	CC	collagen
28	17.19	NULL	5 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
29	17.07	NULL	4 / 8	GSEA C2	HAEGERSTRAND_RESPONSE_TO_IMATINIB
30	17.04	NULL	7 / 15	GSEA C2	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP
31	16.87	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
32	16.8	NULL	4 / 5	GSEA C2	COLLER_MYC_TARGETS_DN
33	16.61	NULL	7 / 16	GSEA C2	CROONQUIST_STROMAL_STIMULATION_UP
34	16	NULL	6 / 10	GSEA C2	JEON_SMAD6_TARGETS_UP
35	15.82	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
36	15.55	NULL	5 / 13	GSEA C2	PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
37	15.54	NULL	4 / 10	BP	protein heterotrimerization
38	15.46	NULL	6 / 11	MMML CGS	MACIEJ_MMML 31
39	15.39	NULL	8 / 25	BP	chondroitin sulfate biosynthetic process
40	15.37	NULL	5 / 15	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_N

GW_080

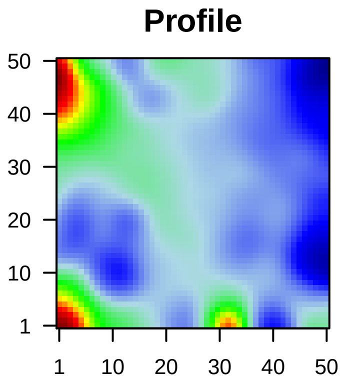
Local Summary

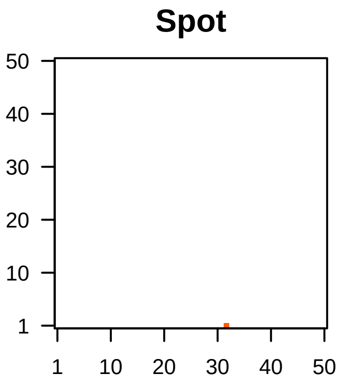
%DE = 0.92
metagenes = 1
genes = 96
genes in genesets = 94

genes with fdr < 0.1 = 87 (87 + / 0 −)
genes with fdr < 0.05 = 87 (87 + / 0 −)
genes with fdr < 0.01 = 82 (82 + / 0 −)

<r> metagenes = NA
<r> genes = 0.52

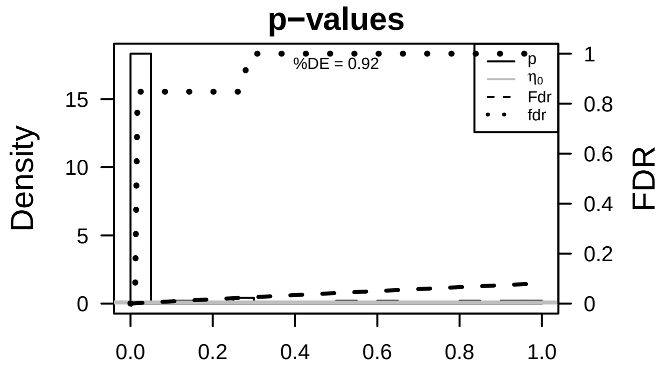
<FC> = 0.84
<shrinkage−t> = 29.57
<p−value> = 0
<fdr> = 0.1





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	684	1.39	2e−16	8e−17	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
2	3627	1.85	2e−16	8e−17	32 x 1	chemokine (C−X−C motif) ligand 10 [Source:HGNC Symbol;A
3	6373	1.69	2e−16	8e−17	32 x 1	chemokine (C−X−C motif) ligand 11 [Source:HGNC Symbol;A
4	94240	1.25	2e−16	8e−17	32 x 1	epithelial stromal interaction 1 (breast) [Source:HGNC Symbo
5	2633	1.46	2e−16	8e−17	32 x 1	guanylate binding protein 1, interferon−inducible [Source:HGN
6	10866	1.19	2e−16	8e−17	32 x 1	HLA complex P5 (non−protein coding) [Source:HGNC Symbo
7	51191	1.22	2e−16	8e−17	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
8	55008	1.54	2e−16	8e−17	32 x 1	HECT and RLD domain containing E3 ubiquitin protein ligase
9	10561	1.33	2e−16	8e−17	32 x 1	interferon−induced protein 44 [Source:HGNC Symbol;Acc:16
10	10964	2.04	2e−16	8e−17	32 x 1	interferon−induced protein 44−like [Source:HGNC Symbol;Ac
11	2537	1.58	2e−16	8e−17	32 x 1	interferon, alpha−inducible protein 6 [Source:HGNC Symbol;A
12	3434	1.28	2e−16	8e−17	32 x 1	interferon−induced protein with tetratricopeptide repeats 1 [So
13	3433	1.42	2e−16	8e−17	32 x 1	interferon−induced protein with tetratricopeptide repeats 2 [So
14	9636	2.15	2e−16	8e−17	32 x 1	ISG15 ubiquitin−like modifier [Source:HGNC Symbol;Acc:405
15	27074	1.26	2e−16	8e−17	32 x 1	lysosomal−associated membrane protein 3 [Source:HGNC Sy
16	4061	1.18	2e−16	8e−17	32 x 1	lymphocyte antigen 6 complex, locus E [Source:HGNC Symb
17	4599	1.38	2e−16	8e−17	32 x 1	myxovirus (influenza virus) resistance 1, interferon−inducible
18	4600	1.78	2e−16	8e−17	32 x 1	myxovirus (influenza virus) resistance 2 (mouse) [Source:HG
19	85441	1.23	2e−16	8e−17	32 x 1	helicase with zinc finger 2, transcriptional coactivator [Source
20	91543	1.44	2e−16	8e−17	32 x 1	radical S−adenosyl methionine domain containing 2 [Source:I



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	62.16	NULL	12 / 16	GSEA C2	MOSERLE_IFNA_RESPONSE
2	55.76	NULL	28 / 51	BP	type I interferon signaling pathway
3	55.64	NULL	9 / 10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
4	51.45	NULL	10 / 16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
5	50.4	NULL	10 / 13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
6	49.54	NULL	6 / 8	GSEA C2	ROETH_TERT_TARGETS_UP
7	49.26	NULL	11 / 16	GSEA C2	ZHANG_INTERFERON_RESPONSE
8	46.12	NULL	8 / 11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
9	42.11	NULL	10 / 16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD
10	41.64	NULL	30 / 123	BP	defense response to virus
11	40.58	NULL	13 / 31	BP	negative regulation of viral genome replication
12	38.19	NULL	7 / 10	GSEA C2	GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
13	38.04	NULL	7 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
14	37.45	NULL	6 / 14	GSEA C2	RADAEVA_RESPONSE_TO_IFNA1_UP
15	36.98	NULL	3 / 4	GSEA C2	KRASNOSELSKAYA_ILF3_TARGETS_UP
16	35.74	NULL	26 / 109	BP	response to virus
17	34.88	NULL	3 / 5	GSEA C2	KIM_LRRC3B_TARGETS
18	34.44	NULL	6 / 12	GSEA C2	TSAI_DNAJB4_TARGETS_UP
19	33.83	NULL	3 / 4	MMML CGS	MACIEJ_MMML 47
20	32.32	NULL	6 / 16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
21	30.68	NULL	5 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
22	30.2	NULL	33 / 204	BP	cytokine−mediated signaling pathway
23	29.55	NULL	4 / 10	GSEA C2	DAUER_STAT3_TARGETS_DN
24	29.38	NULL	6 / 14	GSEA C2	XU_AKT1_TARGETS_6HR
25	27.89	NULL	2 / 2	MMML CGS	MACIEJ_MMML 27
26	27.54	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
27	27.14	NULL	4 / 16	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
28	26.91	NULL	5 / 6	Lymphoma	DAVE_MHCCII BL DN
29	26.11	NULL	30 / 274	Lymphoma	SPANG_IL21 DN
30	25.16	NULL	4 / 12	GSEA C2	ZHU_CMV_8_HR_UP
31	24.77	NULL	4 / 15	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_UP
32	24.48	NULL	3 / 9	GSEA C2	DER_IFN_ALPHA_RESPONSE_UP
33	24.48	NULL	3 / 9	GSEA C2	DER_IFN_GAMMA_RESPONSE_UP
34	24.29	NULL	45 / 572	Disease	GUDJ_psoriasis up
35	23.8	NULL	4 / 14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP
36	23.54	NULL	16 / 60	BP	interferon−gamma−mediated signaling pathway
37	23.21	NULL	6 / 14	Glio	Donson−immune cell intra signaling−associated with LTS in HGA
38	22.59	NULL	4 / 14	GSEA C2	SANA_TNF_SIGNALING_UP
39	22.46	NULL	4 / 10	GSEA C2	GRANDVAUX_IRF3_TARGETS_UP
40	21.45	NULL	6 / 10	CC	MHC class I protein complex

GW_080

Local Summary

%DE = 0.85

metagenes = 27

genes = 363

genes in genesets = 356

genes with fdr < 0.1 = 264 (243 + / 21 −)

genes with fdr < 0.05 = 264 (243 + / 21 −)

genes with fdr < 0.01 = 238 (220 + / 18 −)

<r> metagenes = 0.87

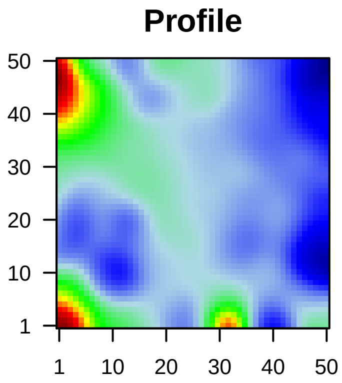
<r> genes = 0.35

<FC> = 0.57

<shrinkage−t> = 20.03

<p−value> = 0

<fdr> = 0.29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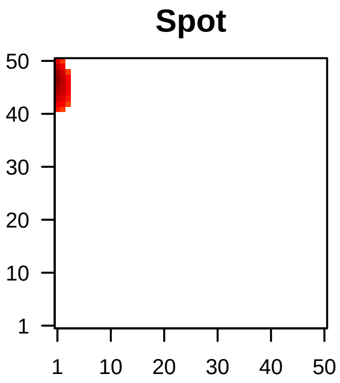
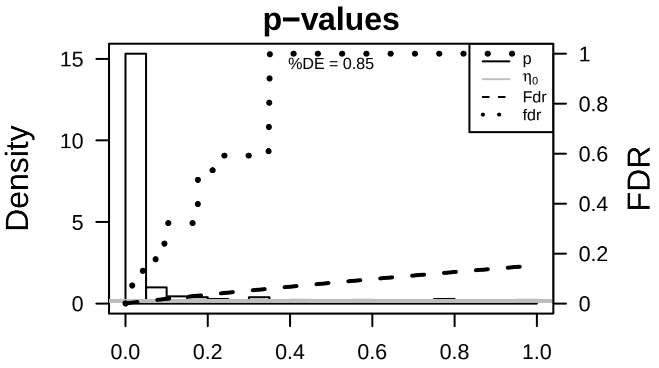

Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57016	1.24	2e−16	2e−16	1 x 50	aldo−keto reductase family 1, member B10 (aldose reductase
2	387695	1.99	2e−16	2e−16	1 x 49	chromosome 10 open reading frame 99 [Source:HGNC Symb
3	760	1.31	2e−16	2e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
4	1041	1.88	2e−16	2e−16	1 x 46	corneodesmosin [Source:HGNC Symbol;Acc:1802]
5	163732	1.24	2e−16	2e−16	1 x 43	Cbp/p300−interacting transactivator, with Glu/Asp−rich carbo
6	84518	1.42	2e−16	2e−16	1 x 50	cornifelin [Source:HGNC Symbol;Acc:30183]
7	1308	1.16	2e−16	2e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
8	54544	1.38	2e−16	2e−16	1 x 50	cysteine−rich C−terminal 1 [Source:HGNC Symbol;Acc:2987
9	49860	−1.68	2e−16	2e−16	1 x 50	cornulin [Source:HGNC Symbol;Acc:1230]
10	1475	1.4	2e−16	2e−16	1 x 50	cystatin A (stefin A) [Source:HGNC Symbol;Acc:2481]
11	9547	1.37	2e−16	2e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
12	55894	1.43	2e−16	2e−16	1 x 47	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
13	414325	1.87	2e−16	2e−16	1 x 48	defensin, beta 103B [Source:HGNC Symbol;Acc:31702]
14	1673	1.54	2e−16	2e−16	1 x 49	defensin, beta 4B [Source:HGNC Symbol;Acc:30193]
15	1823	1.23	2e−16	2e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
16	1824	1.27	2e−16	2e−16	1 x 48	desmocollin 2 [Source:HGNC Symbol;Acc:3036]
17	1828	1.69	2e−16	2e−16	1 x 48	desmoglein 1 [Source:HGNC Symbol;Acc:3048]
18	1830	1.22	2e−16	2e−16	1 x 48	desmoglein 3 [Source:HGNC Symbol;Acc:3050]
19	2152	1.66	2e−16	2e−16	1 x 43	coagulation factor III (thromboplastin, tissue factor) [Source:H
20	2171	1.22	2e−16	2e−16	1 x 46	fatty acid binding protein 5 (psoriasis−associated) [Source:H


p−values

Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all		Geneset
1	39.39	NULL	18 / 21	CC	cornified envelope
2	31.5	NULL	85 / 135	H.Tiss	WIRTH_Mucosa
3	27.61	NULL	28 / 76	BP	epidermis development
4	27.5	NULL	122 / 572	Disease	GUDJ_psoriasis up
5	26.11	NULL	25 / 53	BP	keratinocyte differentiation
6	25.51	NULL	20 / 42	BP	keratinization
7	16.87	NULL	10 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
8	16.81	NULL	12 / 21	CC	desmosome
9	14.72	NULL	15 / 79	MF	serine−type endopeptidase inhibitor activity
10	13.03	NULL	10 / 19	BP	peptide cross−linking
11	12.39	NULL	8 / 16	GSEA C2	ONDER_CDH1_TARGETS_3_DN
12	11.7	NULL	4 / 16	GSEA C2	AMIT_SERUM_RESPONSE_480_MCF10A
13	11.12	NULL	10 / 52	BP	negative regulation of endopeptidase activity
14	11.01	NULL	4 / 15	GSEA C2	CHANG_IMMORTALIZED_BY_HPV31_DN
15	10.82	NULL	7 / 29	BP	regulation of proteolysis
16	10.62	NULL	71 / 1182	CC	extracellular region
17	10.59	NULL	3 / 10	GSEA C2	AUJLA_IL22_AND_IL17A_SIGNALING
18	10.56	NULL	5 / 13	BP	negative regulation of peptidase activity
19	10.4	NULL	5 / 16	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN
20	10.12	NULL	4 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_DN
21	9.98	NULL	4 / 10	GSEA C2	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_P
22	9.66	NULL	6 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
23	9.51	NULL	3 / 10	GSEA C2	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON
24	9.46	NULL	4 / 10	GSEA C2	FOURNIER_ACINAR_DEVELOPMENT_LATE_UP
25	9.1	NULL	5 / 16	GSEA C2	JAEGER_METASTASIS_DN
26	9.09	NULL	4 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
27	8.92	NULL	31 / 186	MF	structural molecule activity
28	8.89	NULL	3 / 15	MF	interleukin−1 receptor binding
29	8.82	NULL	2 / 7	GSEA C2	YE_METASTATIC_LIVER_CANCER
30	8.78	NULL	2 / 8	GSEA C2	MCLACHLAN_DENTAL_CARIES_UP
31	8.62	NULL	23 / 82	CC	intermediate filament
32	8.54	NULL	5 / 10	MF	RAGE receptor binding
33	8.51	NULL	3 / 15	GSEA C2	PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN
34	8.41	NULL	6 / 15	GSEA C2	AIGNER_ZEB1_TARGETS
35	8.26	NULL	7 / 15	GSEA C2	HINATA_NFKB_TARGETS_KERATINOCYTE_DN
36	8.22	NULL	3 / 13	GSEA C2	CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN
37	8.2	NULL	2 / 9	GSEA C2	MCLACHLAN_DENTAL_CARIES_DN
38	8.19	NULL	3 / 11	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN
39	8.13	NULL	4 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
40	7.73	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP

GW_080

Local Summary

%DE = 0.79

metagenes = 30

genes = 329

genes in genesets = 324

genes with fdr < 0.1 = 171 (17 + / 154 −)

genes with fdr < 0.05 = 171 (17 + / 154 −)

genes with fdr < 0.01 = 99 (11 + / 88 −)

<r> metagenes = 0.91

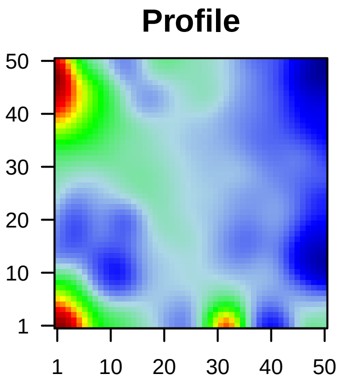
<r> genes = 0.25

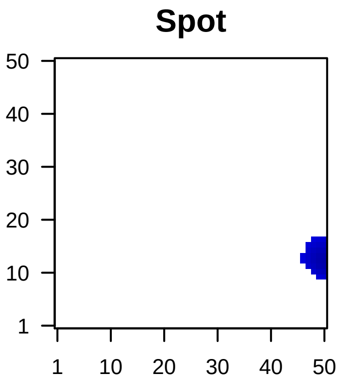
<FC> = −0.26

<shrinkage−t> = −9.06

<p−value> = 0.01

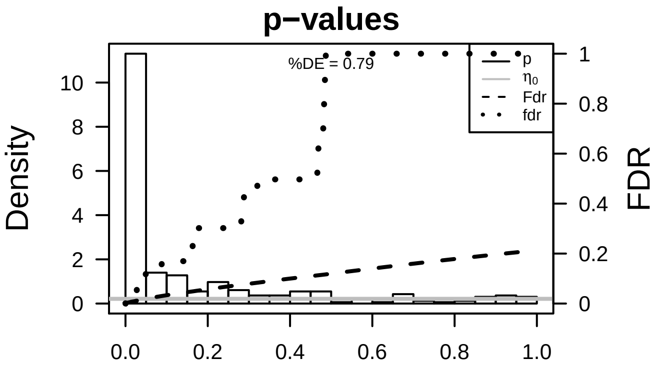
<fdr> = 0.56





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	10232	−1.16	2e−16	8e−15	50 x 11	mesothelin [Source:HGNC Symbol;Acc:7371]
2	7033	−1.61	2e−16	8e−15	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
3	8857	1.12	1e−15	2e−13	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
4	2568	−1.1	3e−15	2e−12	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
5	909	1.06	3e−14	3e−10	50 x 16	CD1a molecule [Source:HGNC Symbol;Acc:1634]
6	3169	−0.97	5e−12	1e−09	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
7	92747	−0.94	2e−11	1e−08	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
8	8470	0.89	2e−10	1e−07	50 x 10	sorbin and SH3 domain containing 2 [Source:HGNC Symbol;
9	55930	−0.83	3e−09	1e−07	50 x 13	myosin VC [Source:HGNC Symbol;Acc:7604]
10	26751	−0.83	4e−09	2e−07	49 x 13	SH3 and SYLF domain containing 1 [Source:HGNC Symbol;
11	92304	−0.81	6e−09	1e−06	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
12	7018	−0.77	4e−08	1e−06	50 x 10	transferrin [Source:HGNC Symbol;Acc:11740]
13	6138	−0.77	4e−08	1e−06	48 x 13	ribosomal protein L15 [Source:HGNC Symbol;Acc:10306]
14	2053	−0.76	6e−08	4e−06	50 x 14	epoxide hydrolase 2, cytoplasmic [Source:HGNC Symbol;Acc
15	11272	−0.73	2e−07	4e−06	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
16	56994	−0.73	2e−07	7e−06	50 x 16	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:17
17	27134	−0.72	3e−07	7e−06	50 x 12	tight junction protein 3 [Source:HGNC Symbol;Acc:11829]
18	113246	−0.71	4e−07	1e−05	49 x 16	chromosome 12 open reading frame 57 [Source:HGNC Symb
19	84188	−0.69	8e−07	1e−05	48 x 15	fatty acyl CoA reductase 1 [Source:HGNC Symbol;Acc:26222
20	9071	−0.69	8e−07	1e−05	50 x 12	claudin 10 [Source:HGNC Symbol;Acc:2033]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−16.84	NULL	11 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
2	−16.04	NULL	3 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
3	−14.42	NULL	3 / 13	GSEA C2	WONG_ENDMETRIUM_CANCER_UP
4	−13.83	NULL	4 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
5	−13.31	NULL	1 / 5	GSEA C2	FERRARI_RESPONSE_TO_FENRETINIDE_DN
6	−12.56	NULL	2 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
7	−11.87	NULL	3 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
8	−10.24	NULL	4 / 21	BP	drug metabolic process
9	−10.1	NULL	4 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
10	−9.96	NULL	2 / 10	GSEA C2	LUI_THYROID_CANCER_CLUSTER_5
11	−9.71	NULL	2 / 13	GSEA C2	YANG_BREAST_CANCER_ESR1_UP
12	−9.61	NULL	1 / 9	GSEA C2	GOUYER_TATI_TARGETS_UP
13	−9.22	NULL	2 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
14	−8.82	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_N
15	−7.84	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_BULK_UP
16	−7.75	NULL	3 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
17	−7.74	NULL	2 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
18	−7.7	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_N
19	−7.7	NULL	3 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
20	−7.61	NULL	3 / 14	GSEA C2	LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_DN
21	−7.24	NULL	3 / 13	GSEA C2	HUANG_DASATINIB_RESISTANCE_DN
22	−7.07	NULL	3 / 12	GSEA C2	PROVENZANI_METASTASIS_UP
23	−7.05	NULL	1 / 3	miRNA 3UTR	ACGC−210
24	−6.97	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
25	−6.76	NULL	2 / 14	GSEA C2	VANTVEER_BREAST_CANCER_ESR1_UP
26	−6.72	NULL	1 / 3	GSEA C2	RUNNE_GENDER_EFFECT_DN
27	−6.65	NULL	2 / 14	GSEA C2	KIM_RESPONSE_TO_TSA_AND_DECITABINE_UP
28	−6.6	NULL	4 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP
29	−6.58	NULL	2 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
30	−6.57	NULL	1 / 7	GSEA C2	NEBEN_AML_WITH_FLT3_OR_NRAS_UP
31	−6.42	NULL	2 / 14	GSEA C2	HEDENFALK_BREAST_CANCER_BRACX_UP
32	−6.33	NULL	2 / 11	CC	photoreceptor outer segment membrane
33	−6.13	NULL	1 / 10	MF	GABA−A receptor activity
34	−6.07	NULL	3 / 15	GSEA C2	HORIUCHI_WTAP_TARGETS_UP
35	−5.95	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
36	−5.93	NULL	6 / 15	GSEA C2	POOLA_INVASIVE_BREAST_CANCER_DN
37	−5.8	NULL	1 / 11	GSEA C2	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
38	−5.8	NULL	2 / 10	BP	negative regulation of blood coagulation
39	−5.66	NULL	2 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
40	−5.65	NULL	4 / 61	CC	secretory granule

GW_080

Local Summary

%DE = 0.75

metagenes = 37

genes = 414

genes in genesets = 411

genes with fdr < 0.1 = 215 (16 + / 199 −)

genes with fdr < 0.05 = 178 (13 + / 165 −)

genes with fdr < 0.01 = 98 (13 + / 85 −)

<r> metagenes = 0.91

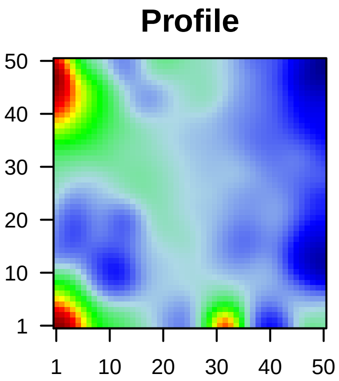
<r> genes = 0.24

<FC> = −0.26

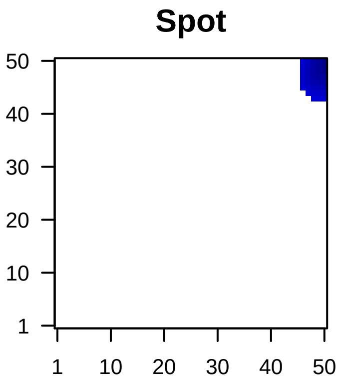
<shrinkage−t> = −9.11

<p−value> = 0.01

<fdr> = 0.62



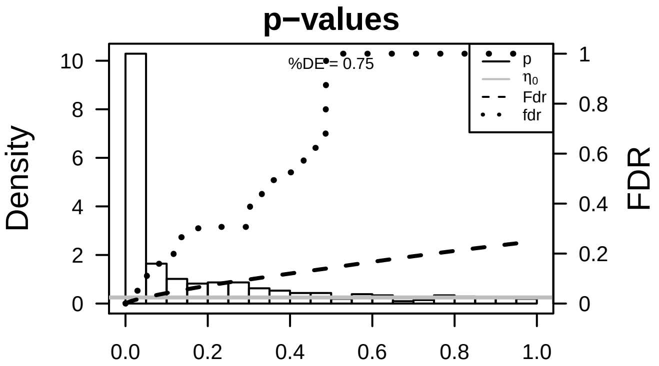
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	216	−1.6	2e−16	5e−15	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGN
2	9070	1.4	2e−16	5e−15	47 x 46	ash2 (absent, small, or homeotic)−like (Drosophila) [Source:
3	3880	−3.56	2e−16	5e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
4	4922	−1.55	2e−16	5e−15	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
5	26227	−1.18	2e−16	5e−15	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
6	9076	1.12	2e−15	4e−13	49 x 50	claudin 1 [Source:HGNC Symbol;Acc:2032]
7	3866	−1.1	6e−15	1e−10	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
8	139728	−0.99	1e−12	6e−10	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
9	4072	−0.96	7e−12	1e−09	50 x 50	epithelial cell adhesion molecule [Source:HGNC Symbol;Acc:
10	2944	−0.93	3e−11	1e−09	50 x 50	glutathione S−transferase mu 1 [Source:HGNC Symbol;Acc:
11	84223	−0.93	4e−11	1e−09	47 x 46	IQ motif containing G [Source:HGNC Symbol;Acc:25251]
12	928	−0.92	5e−11	1e−09	50 x 50	CD9 molecule [Source:HGNC Symbol;Acc:1709]
13	116028	−0.92	5e−11	3e−08	46 x 47	RecQ mediated genome instability 2 [Source:HGNC Symbol;
14	2946	−0.87	6e−10	3e−08	50 x 50	glutathione S−transferase mu 2 (muscle) [Source:HGNC Sym
15	25975	0.86	7e−10	6e−08	48 x 50	EGF−like−domain, multiple 6 [Source:HGNC Symbol;Acc:32
16	339512	−0.85	2e−09	6e−08	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
17	2222	−0.84	2e−09	1e−07	50 x 50	farnesyl−diphosphate farnesyltransferase 1 [Source:HGNC S
18	84707	−0.83	3e−09	2e−06	50 x 48	brain expressed X−linked 2 [Source:HGNC Symbol;Acc:3093
19	2304	0.77	4e−08	2e−06	50 x 50	forkhead box E1 (thyroid transcription factor 2) [Source:HGN
20	10966	−0.76	7e−08	2e−06	50 x 50	RAB40B, member RAS oncogene family [Source:HGNC Sym



p−values

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−26.66	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−16.22	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
3	−14.81	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
4	−14.22	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
5	−13.69	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
6	−13.69	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
7	−13.22	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
8	−13.22	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
9	−12.72	NULL	2 / 18	CC	costamere
10	−11.37	NULL	1 / 21	BP	sarcomere organization
11	−11.16	NULL	5 / 15	GSEA C2	KEGG_GLUTATHIONE_METABOLISM
12	−10.72	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
13	−10.58	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
14	−10.34	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
15	−9.98	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
16	−9.62	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
17	−9.18	NULL	3 / 11	MF	glutathione binding
18	−9.18	NULL	3 / 11	GSEA C2	KEGG_DRUG_METABOLISM_CYTOCHROME_P450
19	−9.12	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
20	−8.51	NULL	1 / 35	CC	cell periphery
21	−8.44	NULL	2 / 12	BP	cellular aldehyde metabolic process
22	−8.39	NULL	8 / 30	BP	DNA strand elongation involved in DNA replication
23	−8.35	NULL	2 / 14	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
24	−8.32	NULL	5 / 20	MF	glutathione transferase activity
25	−8.31	NULL	9 / 34	BP	glutathione metabolic process
26	−8.02	NULL	4 / 13	BP	regulation of blood vessel size
27	−7.95	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
28	−7.95	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
29	−7.94	NULL	6 / 25	BP	glutathione derivative biosynthetic process
30	−7.73	NULL	5 / 82	MF	structural constituent of cytoskeleton
31	−7.57	NULL	4 / 13	GSEA C2	SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
32	−7.53	NULL	4 / 11	GSEA C2	KALMA_E2F1_TARGETS
33	−7.53	NULL	4 / 13	GSEA C2	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_
34	−7.49	NULL	1 / 10	GSEA C2	MAINA_VHL_TARGETS_UP
35	−7.49	NULL	1 / 10	GSEA C2	FRIDMAN_SENESCENCE_DN
36	−7.42	NULL	4 / 29	MF	cofactor binding
37	−7.35	NULL	5 / 19	BP	cellular amino acid biosynthetic process
38	−7.09	NULL	3 / 82	CC	intermediate filament
39	−7.02	NULL	4 / 11	GSEA C2	REACTOME_UNWINDING_OF_DNA
40	−6.96	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN