GW_014

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1892 (1046 + / 846 −)

genes with fdr < 0.1 = 1579 (894 + / 685 −)

genes with fdr < 0.05 = 1216 (725 + / 491 −)

genes with fdr < 0.01 = 813 (521 + / 292 −)

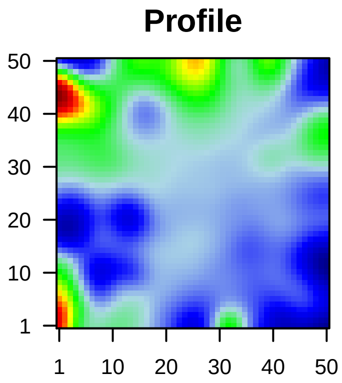
genes in genesets = 16332

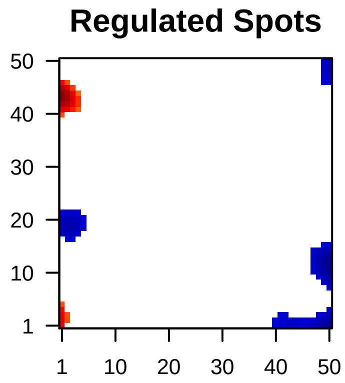
<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.1

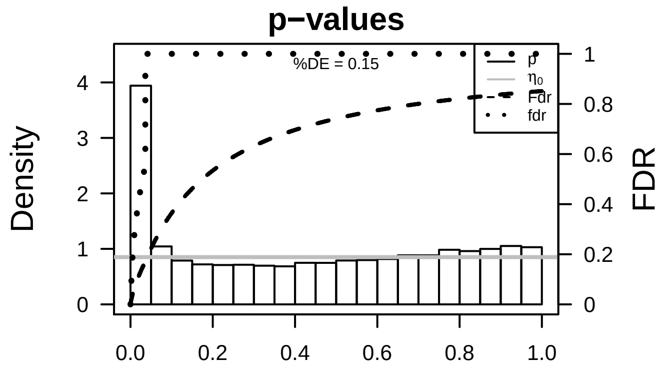
<fdr> = 0.85





Global Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	214	−1.34	2e−16	3e−14	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
2	401138	1.73	2e−16	3e−14	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
3	25805	1.25	2e−16	3e−14	8 x 1	BMP and activin membrane−bound inhibitor [Source:HGNC S
4	10409	1.62	2e−16	3e−14	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
5	633	1.22	2e−16	3e−14	3 x 1	biglycan [Source:HGNC Symbol;Acc:1044]
6	684	1.29	2e−16	3e−14	32 x 1	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;A
7	440712	1.35	2e−16	3e−14	1 x 39	chromosome 1 open reading frame 186 [Source:HGNC Symb
8	760	1.35	2e−16	3e−14	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
9	51806	−1.49	2e−16	3e−14	4 x 50	calmodulin−like 5 [Source:HGNC Symbol;Acc:18180]
10	908	1.45	2e−16	3e−14	40 x 50	chaperonin containing TCP1, subunit 6A (zeta 1) [Source:HG
11	978	1.26	2e−16	3e−14	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
12	9635	1.3	2e−16	3e−14	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
13	1366	−1.43	2e−16	3e−14	6 x 50	claudin 7 [Source:HGNC Symbol;Acc:2049]
14	1258	1.72	2e−16	3e−14	1 x 7	cyclic nucleotide gated channel beta 1 [Source:HGNC Symbo
15	1308	1.88	2e−16	3e−14	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
16	1288	1.74	2e−16	3e−14	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
17	1289	1.37	2e−16	3e−14	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
18	1290	1.51	2e−16	3e−14	2 x 1	collagen, type V, alpha 2 [Source:HGNC Symbol;Acc:2210]
19	51200	1.42	2e−16	3e−14	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
20	83716	1.38	2e−16	3e−14	2 x 1	cysteine−rich secretory protein LCCL domain containing 2 [S



Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	11.44	NULL	8	GSEA C2	ROETH_TERT_TARGETS_UP
2	11.14	NULL	16	GSEA C2	EINAV_INTERFERON_SIGNATURE_IN_CANCER
3	10.94	NULL	16	GSEA C2	MOSERLE_IFNA_RESPONSE
4	10.62	NULL	51	BP	type I interferon signaling pathway
5	10.57	NULL	64	BP	collagen catabolic process
6	10.42	NULL	69	BP	extracellular matrix disassembly
7	10.18	NULL	572	Disease	GUDJ_psoriasis up
8	10.06	NULL	242	BP	extracellular matrix organization
9	9.87	NULL	13	GSEA C2	BOWIE_RESPONSE_TO_TAMOXIFEN
10	9.67	NULL	717	Chr	Chr 16
11	9.33	NULL	10	GSEA C2	BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX
12	9.23	NULL	4	MMML CGS	MACIEJ_MMML 47
13	9.09	NULL	16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
14	9	NULL	1720	Chr	Chr 1
15	8.93	NULL	16	GSEA C2	ZHANG_INTERFERON_RESPONSE
16	8.62	NULL	14	GSEA C2	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP
17	8.61	NULL	123	BP	defense response to virus
18	8.15	NULL	31	BP	negative regulation of viral genome replication
19	8.04	NULL	190	CC	extracellular matrix
20	8.03	NULL	12	BP	hemidesmosome assembly
Underexpressed					
1	−8.23	NULL	918	Chr	Chr 17
2	−7.53	NULL	914	Chr	Chr 3
3	−7.2	NULL	1135	Chr	Chr 19
4	−5.89	NULL	52	Chr	Chr HSCHR6_MHC_QBL
5	−5.75	NULL	714	Chr	Chr 6
6	−5.68	NULL	15	CC	MHC class II protein complex
7	−5.54	NULL	16	GSEA C2	CROMER_TUMORIGENESIS_DN
8	−5.35	NULL	44	MF	structural constituent of muscle
9	−5.28	NULL	11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
10	−5.05	NULL	633	Chr	Chr 9
11	−5.01	NULL	16	GSEA C2	KORKOLA_TERATOMA_UP
12	−4.91	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
13	−4.9	NULL	87	BP	translational termination
14	−4.9	NULL	81	BP	viral transcription
15	−4.87	NULL	386	Chr	Chr 22
16	−4.86	NULL	128	BP	translational initiation
17	−4.84	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
18	−4.8	NULL	375	Disease	GUDJ_psoriasis down
19	−4.67	NULL	6	GSEA C2	KORKOLA_CHORIOCARCINOMA_UP
20	−4.67	NULL	23	Chr	Chr HSCHR6_MHC_DBB

GW_014

Local Summary

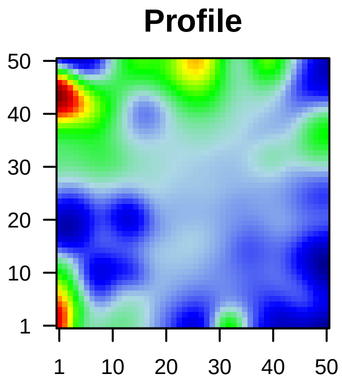
%DE = 0.88
metagenes = 7
genes = 135
genes in genesets = 133

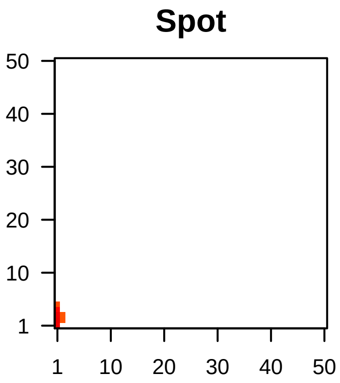
genes with fdr < 0.1 = 98 (90 + / 8 −)
genes with fdr < 0.05 = 96 (89 + / 7 −)
genes with fdr < 0.01 = 89 (82 + / 7 −)

<r> metagenes = 0.98
<r> genes = 0.38

<FC> = 0.55
<shrinkage−t> = 19.3
<p−value> = 0

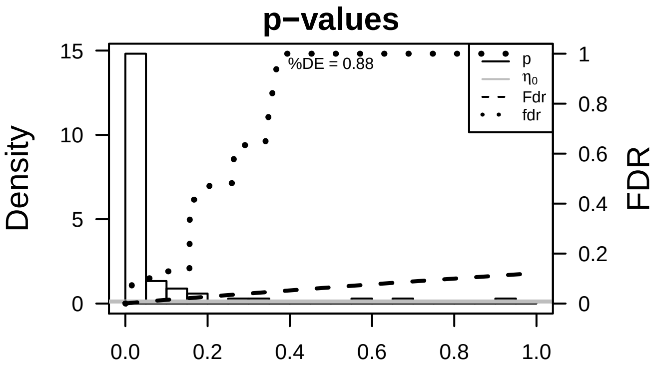
<fdr> = 0.3





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	401138	1.73	2e−16	3e−16	1 x 5	amelotin [Source:HGNC Symbol;Acc:33188]
2	10409	1.62	2e−16	3e−16	1 x 2	brain abundant, membrane attached signal protein 1 [Source:
3	6372	1.98	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 6 [Source:HGNC Symbol;Ac
4	56603	1.43	2e−16	3e−16	1 x 4	cytochrome P450, family 26, subfamily B, polypeptide 1 [Sour
5	8988	2	2e−16	3e−16	1 x 4	heat shock 27kDa protein 3 [Source:HGNC Symbol;Acc:5248
6	153572	1.55	2e−16	3e−16	1 x 5	iroquois homeobox 2 [Source:HGNC Symbol;Acc:14359]
7	4312	1.53	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
8	4319	1.92	2e−16	3e−16	1 x 3	matrix metallopeptidase 10 (stromelysin 2) [Source:HGNC Sy
9	4322	2.94	2e−16	3e−16	1 x 2	matrix metallopeptidase 13 (collagenase 3) [Source:HGNC S
10	4314	2.5	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
11	10630	1.24	2e−16	3e−16	1 x 2	podoplanin [Source:HGNC Symbol;Acc:29602]
12	6999	1.32	2e−16	3e−16	1 x 2	tryptophan 2,3−dioxygenase [Source:HGNC Symbol;Acc:117
13	7045	1.26	2e−16	3e−16	1 x 2	transforming growth factor, beta−induced, 68kDa [Source:HG
14	10381	1.31	2e−16	3e−16	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
15	2919	1.22	4e−16	1e−14	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
16	2195	1.22	4e−16	1e−14	1 x 5	FAT atypical cadherin 1 [Source:HGNC Symbol;Acc:3595]
17	163782	1.21	1e−15	2e−13	1 x 2	KN motif and ankyrin repeat domains 4 [Source:HGNC Symb
18	51050	1.16	1e−14	2e−13	1 x 2	peptidase inhibitor 15 [Source:HGNC Symbol;Acc:8946]
19	6447	1.15	2e−14	1e−11	1 x 1	secretogranin V (7B2 protein) [Source:HGNC Symbol;Acc:10
20	10512	1.08	7e−13	2e−11	1 x 4	sema domain, immunoglobulin domain (Ig), short basic doma



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	24.57	NULL	8 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
2	20.66	NULL	9 / 64	BP	collagen catabolic process
3	19.82	NULL	9 / 69	BP	extracellular matrix disassembly
4	16.79	NULL	28 / 242	BP	extracellular matrix organization
5	16.32	NULL	2 / 16	GSEA C2	MURATA_VIRULENCE_OF_H_PILORI
6	16.05	NULL	1 / 8	miRNA target	miR−9
7	15.2	NULL	6 / 81	MF	metalloendopeptidase activity
8	14.99	NULL	5 / 73	MF	metallopeptidase activity
9	14.16	NULL	13 / 183	CC	proteinaceous extracellular matrix
10	14.1	NULL	3 / 15	GSEA C2	TRAYNOR_RETT_SYNDROM_UP
11	14.01	NULL	2 / 15	GSEA C2	MUELLER_METHYLATED_IN_GLIOBLASTOMA
12	13.96	NULL	39 / 683	CC	extracellular space
13	13.45	NULL	4 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
14	13.37	NULL	14 / 190	CC	extracellular matrix
15	13.05	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
16	12.89	NULL	2 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
17	12.8	NULL	2 / 12	GSEA C2	LY_AGING_MIDDLE_UP
18	12.69	NULL	2 / 14	GSEA C2	DAZARD_UV_RESPONSE_CLUSTER_G4
19	12.61	NULL	6 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
20	12.59	NULL	51 / 1182	CC	extracellular region
21	12.1	NULL	3 / 16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
22	12.1	NULL	4 / 51	BP	regulation of cell migration
23	12.03	NULL	1 / 13	GSEA C2	CHIBA_RESPONSE_TO_TSA_UP
24	12.01	NULL	4 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
25	11.63	NULL	1 / 2	TF	MYC_ECM cell adhesion DOWN
26	11.41	NULL	3 / 15	GSEA C2	WU_HBX_TARGETS_1_UP
27	11.4	NULL	4 / 37	Glio	Christensen_hypomethylated_in_ependymoma
28	11.16	NULL	2 / 12	GSEA C2	SHI_SPARC_TARGETS_UP
29	11.07	NULL	1 / 5	GSEA C2	OXFORD_RALA_AND_RALB_TARGETS_UP
30	11.06	NULL	1 / 15	GSEA C2	CHANG_POU5F1_TARGETS_UP
31	10.83	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
32	10.6	NULL	2 / 6	Glio	Martinez_Glio_hypometh
33	10.39	NULL	1 / 5	GSEA C2	STAEGE_EWING_FAMILY_TUMOR
34	10.05	NULL	2 / 15	GSEA C2	SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_
35	10.01	NULL	1 / 6	GSEA C2	SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
36	10	NULL	4 / 16	GSEA C2	GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN
37	9.98	NULL	2 / 10	GSEA C2	VETTER_TARGETS_OF_PRKCA_AND_ETS1_DN
38	9.95	NULL	3 / 16	CC	lamellipodium membrane
39	9.89	NULL	3 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
40	9.76	NULL	3 / 12	BP	hemidesmosome assembly

GW_014

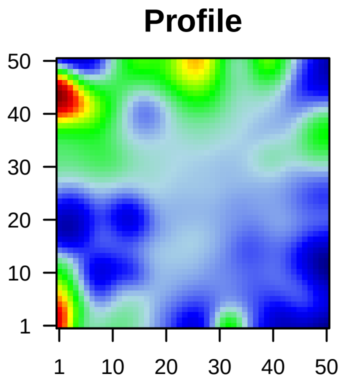
Local Summary

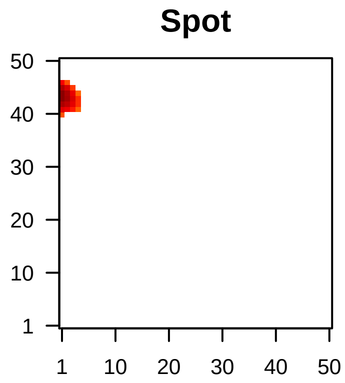
%DE = 0.81
metagenes = 22
genes = 268
genes in genesets = 263

genes with fdr < 0.1 = 180 (174 + / 6 −)
genes with fdr < 0.05 = 164 (159 + / 5 −)
genes with fdr < 0.01 = 137 (133 + / 4 −)

<r> metagenes = 0.96
<r> genes = 0.36

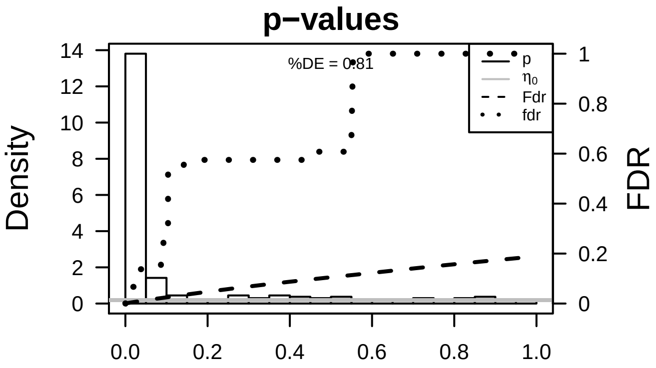
<FC> = 0.52
<shrinkage−t> = 18.21
<p−value> = 0
<fdr> = 0.37





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	760	1.35	2e−16	5e−16	1 x 44	carbonic anhydrase II [Source:HGNC Symbol;Acc:1373]
2	978	1.26	2e−16	5e−16	1 x 46	cytidine deaminase [Source:HGNC Symbol;Acc:1712]
3	9635	1.3	2e−16	5e−16	1 x 46	chloride channel accessory 2 [Source:HGNC Symbol;Acc:20
4	1308	1.88	2e−16	5e−16	1 x 43	collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:2194
5	1288	1.74	2e−16	5e−16	1 x 43	collagen, type IV, alpha 6 [Source:HGNC Symbol;Acc:2208]
6	51200	1.42	2e−16	5e−16	1 x 44	carboxypeptidase A4 [Source:HGNC Symbol;Acc:15740]
7	9547	1.96	2e−16	5e−16	1 x 46	chemokine (C−X−C motif) ligand 14 [Source:HGNC Symbol;
8	1823	1.53	2e−16	5e−16	1 x 45	desmocollin 1 [Source:HGNC Symbol;Acc:3035]
9	11072	1.37	2e−16	5e−16	1 x 44	dual specificity phosphatase 14 [Source:HGNC Symbol;Acc:1
10	2167	2.53	2e−16	5e−16	1 x 44	fatty acid binding protein 4, adipocyte [Source:HGNC Symbol
11	2352	1.67	2e−16	5e−16	1 x 42	folate receptor 3 (gamma) [Source:HGNC Symbol;Acc:3795]
12	2697	1.63	2e−16	5e−16	1 x 44	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;
13	8111	1.27	2e−16	5e−16	1 x 42	G protein−coupled receptor 68 [Source:HGNC Symbol;Acc:4
14	3429	1.36	2e−16	5e−16	1 x 42	interferon, alpha−inducible protein 27 [Source:HGNC Symbol
15	374918	2.58	2e−16	5e−16	1 x 45	IGF−like family member 1 [Source:HGNC Symbol;Acc:24093
16	3861	1.16	2e−16	5e−16	1 x 45	keratin 14 [Source:HGNC Symbol;Acc:6416]
17	9119	1.83	2e−16	5e−16	1 x 44	keratin 75 [Source:HGNC Symbol;Acc:24431]
18	387882	1.83	2e−16	5e−16	2 x 41	chromosome 12 open reading frame 75 [Source:HGNC Symb
19	9935	1.38	2e−16	5e−16	1 x 45	v−maf avian musculoaponeurotic fibrosarcoma oncogene hor
20	9788	1.31	2e−16	5e−16	2 x 43	metastasis suppressor 1 [Source:HGNC Symbol;Acc:20443]



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	19.41	NULL	3 / 6	GSEA C2	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
2	14.39	NULL	7 / 16	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_UP
3	14.15	NULL	5 / 12	BP	hemidesmosome assembly
4	11.96	NULL	3 / 15	GSEA C2	SENESE_HDAC1_AND_HDAC2_TARGETS_DN
5	11.08	NULL	57 / 572	Disease	GUDJ_psoriasis up
6	11.06	NULL	2 / 10	GSEA C2	KIM_MYCL1_AMPLIFICATION_TARGETS_UP
7	10.72	NULL	2 / 6	GSEA C2	WALLACE_PROSTATE_CANCER_DN
8	10.5	NULL	2 / 12	MF	fatty acid binding
9	10.42	NULL	5 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
10	10.36	NULL	15 / 82	CC	intermediate filament
11	9.55	NULL	14 / 76	BP	epidermis development
12	9.54	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_TARGETS_DN
13	9.52	NULL	3 / 16	GSEA C2	BECKER_TAMOXIFEN_RESISTANCE_DN
14	9.19	NULL	8 / 21	CC	desmosome
15	8.91	NULL	3 / 21	CC	gap junction
16	8.89	NULL	4 / 16	GSEA C2	ELVIDGE_HIF1A_AND_HIF2A_TARGETS_DN
17	8.86	NULL	1 / 10	BP	white fat cell differentiation
18	8.8	NULL	1 / 4	MMML CGS	MACIEJ_MMML 47
19	8.75	NULL	3 / 11	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_G_UP
20	8.38	NULL	1 / 11	GSEA C2	REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED_
21	8.34	NULL	4 / 25	BP	brown fat cell differentiation
22	8.29	NULL	4 / 13	BP	intermediate filament cytoskeleton organization
23	8.1	NULL	2 / 10	MF	gap junction channel activity
24	8.02	NULL	3 / 25	BP	response to zinc ion
25	7.79	NULL	3 / 15	GSEA C2	FRIDMAN_IMMORTALIZATION_DN
26	7.76	NULL	5 / 44	CC	keratin filament
27	7.61	NULL	2 / 11	GSEA C2	BIOCARTA_VITCB_PATHWAY
28	7.6	NULL	1 / 13	BP	cellular response to lithium ion
29	7.38	NULL	14 / 186	MF	structural molecule activity
30	7.24	NULL	2 / 15	GSEA C2	KARAKAS_TGFB1_SIGNALING
31	7.11	NULL	2 / 15	GSEA C2	KEGG_P53_SIGNALING_PATHWAY
32	6.98	NULL	1 / 15	BP	triglyceride catabolic process
33	6.97	NULL	2 / 8	GSEA C2	DORN_ADENOVIRUS_INFECTION_24HR_UP
34	6.82	NULL	2 / 10	BP	skeletal muscle tissue regeneration
35	6.73	NULL	4 / 20	MF	scaffold protein binding
36	6.66	NULL	3 / 15	GSEA C2	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN
37	6.62	NULL	2 / 2	miRNA target	miR−199a*
38	6.46	NULL	6 / 70	BP	cell junction assembly
39	6.45	NULL	2 / 16	GSEA C2	KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_UP
40	6.45	NULL	2 / 16	GSEA C2	KOKKINAKIS_METHIONINE_DEPRIVATION_96HR_UP

GW_014

Local Summary

%DE = 0.69

metagenes = 28

genes = 449

genes in genesets = 436

genes with fdr < 0.1 = 218 (25 + / 193 −)

genes with fdr < 0.05 = 177 (21 + / 156 −)

genes with fdr < 0.01 = 105 (13 + / 92 −)

<r> metagenes = 0.87

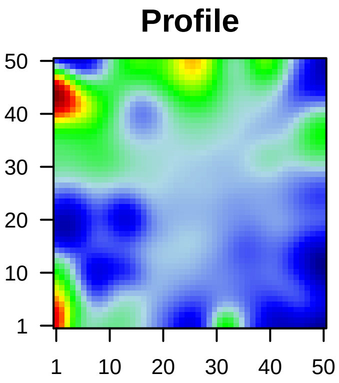
<r> genes = 0.44

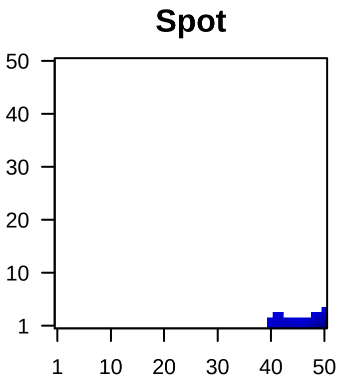
<FC> = −0.23

<shrinkage−t> = −7.95

<p−value> = 0.01

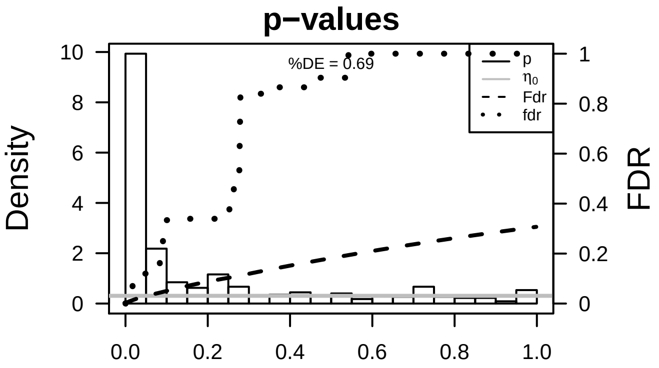
<fdr> = 0.61





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	3127	1.32	2e−16	3e−14	43 x 1	major histocompatibility complex, class II, DR beta 5 [Source:
2	3108	−1.11	2e−13	2e−10	50 x 1	major histocompatibility complex, class II, DM alpha [Source:
3	6366	1.07	1e−12	5e−09	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
4	3122	−0.93	4e−11	5e−09	50 x 1	major histocompatibility complex, class II, DR alpha [Source:
5	1545	0.98	7e−11	1e−08	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
6	255231	0.96	2e−10	1e−08	49 x 1	mucolipin 2 [Source:HGNC Symbol;Acc:13357]
7	3126	−0.96	2e−10	4e−08	50 x 1	major histocompatibility complex, class II, DR beta 4 [Source:
8	169044	0.94	5e−10	6e−08	45 x 1	collagen, type XXII, alpha 1 [Source:HGNC Symbol;Acc:2298
9	6376	−0.92	1e−09	6e−08	44 x 1	chemokine (C−X3−C motif) ligand 1 [Source:HGNC Symbol;
10	260436	0.91	1e−09	8e−08	50 x 1	follicular dendritic cell secreted protein [Source:HGNC Symb
11	3543	0.83	2e−09	1e−07	49 x 1	immunoglobulin lambda−like polypeptide 1 [Source:HGNC S
12	3002	−0.89	4e−09	1e−07	49 x 1	granzyme B (granzyme 2, cytotoxic T−lymphocyte−associate
13	152007	−0.89	4e−09	3e−07	50 x 3	GLI pathogenesis−related 2 [Source:HGNC Symbol;Acc:180
14	3109	−0.88	6e−09	4e−07	50 x 1	major histocompatibility complex, class II, DM beta [Source:H
15	26580	−0.86	1e−08	4e−07	43 x 1	Berardinelli−Seip congenital lipodystrophy 2 (seipin) [Source:
16	9181	−0.86	1e−08	4e−07	44 x 1	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Sourc
17	5996	0.85	1e−08	4e−07	50 x 1	regulator of G−protein signaling 1 [Source:HGNC Symbol;Ac
18	972	−0.85	2e−08	6e−07	50 x 1	CD74 molecule, major histocompatibility complex, class II inv
19	3001	−0.84	2e−08	3e−06	48 x 1	granzyme A (granzyme 1, cytotoxic T−lymphocyte−associate
20	3620	−0.82	5e−08	1e−05	48 x 1	indoleamine 2,3−dioxygenase 1 [Source:HGNC Symbol;Acc:



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−25.2	NULL	14 / 15	CC	MHC class II protein complex
2	−17.05	NULL	98 / 417	H.Tiss	WIRTH_Immune system
3	−16.42	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
4	−16.3	NULL	2 / 3	GSEA C2	KEGG_VIRAL_MYOCARDITIS
5	−16.12	NULL	4 / 7	Glio	Donson−cytotoxic effectors−associated with LTS in HGA
6	−15.73	NULL	17 / 47	BP	antigen processing and presentation
7	−14.71	NULL	5 / 12	BP	immunoglobulin mediated immune response
8	−14.64	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
9	−13.93	NULL	2 / 4	GSEA C2	KEGG_LEISHMANIA_INFECTION
10	−13.76	NULL	6 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
11	−13	NULL	1 / 2	GSEA C2	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUC
12	−13	NULL	1 / 2	GSEA C2	KEGG_AUTOIMMUNE_THYROID_DISEASE
13	−13	NULL	1 / 2	GSEA C2	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS
14	−12.83	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
15	−12.48	NULL	3 / 8	GSEA C2	LINDSTEDT_DENDRITIC_CELL_MATURATION_D
16	−12.44	NULL	3 / 6	GSEA C2	SANA_RESPONSE_TO_IFNG_UP
17	−12.11	NULL	19 / 74	BP	regulation of immune response
18	−12.02	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
19	−11.38	NULL	5 / 16	GSEA C2	FERRANDO_TAL1_NEIGHBORS
20	−11.26	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
21	−11.05	NULL	3 / 10	GSEA C2	HOSHIDA_LIVER_CANCER_SUBCLASS_S1
22	−11.04	NULL	61 / 312	BP	immune response
23	−10.63	NULL	5 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY
24	−10.53	NULL	9 / 52	Chr	Chr HSCHR6_MHC_QBL
25	−10.43	NULL	9 / 21	CC	clathrin−coated endocytic vesicle membrane
26	−10.4	NULL	5 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
27	−10.37	NULL	1 / 3	GSEA C2	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
28	−10.25	NULL	6 / 13	Cancer	GENTLES_modul18
29	−10.11	NULL	4 / 8	GSEA C2	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWE
30	−10.1	NULL	2 / 5	GSEA C2	WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN
31	−9.91	NULL	9 / 23	CC	integral to lumenal side of endoplasmic reticulum membrane
32	−9.83	NULL	4 / 16	BP	cytolysis
33	−9.69	NULL	43 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
34	−9.69	NULL	43 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
35	−9.69	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
36	−9.69	NULL	43 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
37	−9.66	NULL	10 / 28	CC	transport vesicle membrane
38	−9.65	NULL	2 / 4	GSEA C2	REACTOME_CLASSICAL_ANTIBODY_MEDIATED_COMPLEME
39	−9.59	NULL	2 / 6	GSEA C2	LUI_THYROID_CANCER_CLUSTER_4
40	−9.53	NULL	2 / 8	GSEA C2	KEGG_CELL_ADHESION_MOLECULES_CAMS

GW_014

Local Summary

%DE = 0.77

metagenes = 28

genes = 304

genes in genesets = 300

genes with fdr < 0.1 = 148 (15 + / 133 −)

genes with fdr < 0.05 = 123 (13 + / 110 −)

genes with fdr < 0.01 = 69 (8 + / 61 −)

<r> metagenes = 0.9

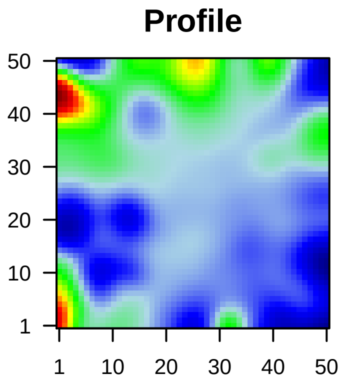
<r> genes = 0.25

<FC> = −0.25

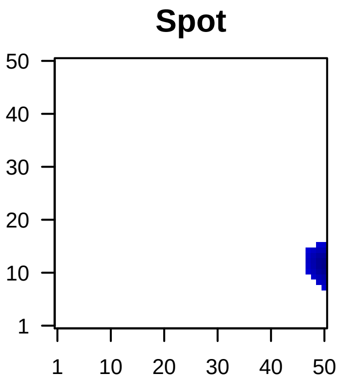
<shrinkage−t> = −8.9

<p−value> = 0.01

<fdr> = 0.63



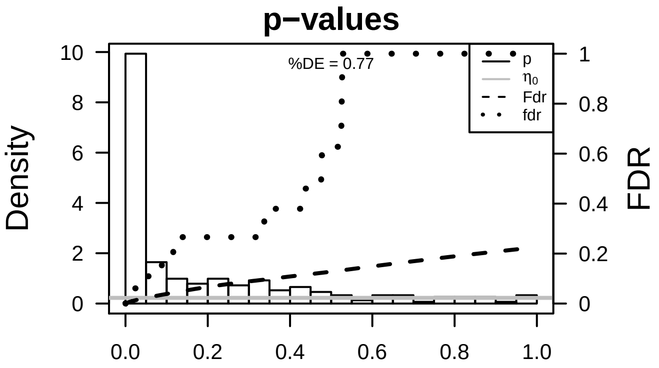
Profile



Spot

Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2878	−1.51	2e−16	2e−14	50 x 9	glutathione peroxidase 3 (plasma) [Source:HGNC Symbol;Ac
2	9249	−1.11	2e−13	9e−12	50 x 13	dehydrogenase/reductase (SDR family) member 3 [Source:H
3	6192	1.1	3e−13	2e−09	50 x 9	ribosomal protein S4, Y−linked 1 [Source:HGNC Symbol;Acc
4	57153	−1.01	2e−11	2e−08	49 x 14	solute carrier family 44 (choline transporter), member 2 [Sour
5	3169	−0.95	3e−10	7e−07	50 x 12	forkhead box A1 [Source:HGNC Symbol;Acc:5021]
6	8857	−0.86	1e−08	2e−06	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;Ac
7	8543	−0.83	4e−08	2e−06	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
8	7033	−0.82	5e−08	3e−06	50 x 10	trefoil factor 3 (intestinal) [Source:HGNC Symbol;Acc:11757]
9	92304	−0.8	1e−07	3e−06	50 x 10	secretoglobin, family 3A, member 1 [Source:HGNC Symbol;A
10	92747	−0.78	2e−07	3e−06	50 x 10	BPI fold containing family B, member 1 [Source:HGNC Symb
11	8495	−0.78	2e−07	3e−06	50 x 14	PTPRF interacting protein, binding protein 2 (liprin beta 2) [Sc
12	53335	−0.78	2e−07	2e−05	50 x 16	B−cell CLL/lymphoma 11A (zinc finger protein) [Source:HGN
13	148170	−0.76	6e−07	2e−05	50 x 9	CDC42 effector protein (Rho GTPase binding) 5 [Source:HGN
14	11272	−0.74	9e−07	7e−05	50 x 10	proline rich 4 (lacrimal) [Source:HGNC Symbol;Acc:18020]
15	256691	0.72	2e−06	1e−04	50 x 9	MAM domain containing 2 [Source:HGNC Symbol;Acc:23673
16	4602	−0.7	4e−06	1e−04	50 x 16	v−myb avian myeloblastosis viral oncogene homolog [Source
17	4781	−0.68	7e−06	1e−04	50 x 8	nuclear factor I/B [Source:HGNC Symbol;Acc:7785]
18	2934	−0.68	7e−06	1e−04	50 x 9	gelsolin [Source:HGNC Symbol;Acc:4620]
19	27134	−0.67	1e−05	1e−04	50 x 12	tight junction protein 3 [Source:HGNC Symbol;Acc:11829]
20	6124	−0.66	1e−05	2e−04	47 x 15	ribosomal protein L4 [Source:HGNC Symbol;Acc:10353]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset
1	−16.7	NULL	11 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_D
2	−11.5	NULL	3 / 13	GSEA C2 WONG_ENDMETRIUM_CANCER_UP
3	−10.45	NULL	4 / 14	MF selenium binding
4	−10.25	NULL	3 / 7	GSEA C2 HUPER_BREAST_BASAL_VS_LUMINAL_DN
5	−9.8	NULL	6 / 15	GSEA C2 POOLA_INVASIVE_BREAST_CANCER_DN
6	−9.7	NULL	3 / 7	TF Tissue VAQUERIZAS_Appendix
7	−9.09	NULL	3 / 14	GSEA C2 SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_D
8	−8.95	NULL	4 / 16	TF Tissue VAQUERIZAS_Salivary gland
9	−8.86	NULL	3 / 10	BP epoxygenase P450 pathway
10	−8.02	NULL	3 / 12	GSEA C2 PROVENZANI_METASTASIS_UP
11	−7.88	NULL	2 / 11	CC photoreceptor outer segment membrane
12	−7.7	NULL	1 / 14	MF glutathione peroxidase activity
13	−7.55	NULL	3 / 16	GSEA C2 YANG_BREAST_CANCER_ESR1_BULK_UP
14	−7.52	NULL	4 / 14	GSEA C2 SMID_BREAST_CANCER_LUMINAL_A_UP
15	−7.42	NULL	4 / 21	BP drug metabolic process
16	−7.28	NULL	1 / 5	GSEA C2 FERRARI_RESPONSE_TO_FENRETINIDE_DN
17	−7.22	NULL	2 / 16	GSEA C2 RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
18	−7.17	NULL	2 / 8	GSEA C2 LEE_SP4_THYMOCYTE
19	−7.12	NULL	4 / 24	TF Tissue VAQUERIZAS_Trachea
20	−7.1	NULL	5 / 16	GSEA C2 TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
21	−7.06	NULL	3 / 16	GSEA C2 RICKMAN_HEAD_AND_NECK_CANCER_A
22	−7.05	NULL	1 / 7	GSEA C2 NEBEN_AML_WITH_FLT3_OR_NRAS_UP
23	−7	NULL	4 / 16	GSEA C2 TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
24	−6.99	NULL	3 / 18	MF aromatase activity
25	−6.94	NULL	6 / 16	GSEA C2 CROMER_TUMORIGENESIS_DN
26	−6.66	NULL	2 / 20	BP phosphatidylcholine biosynthetic process
27	−6.48	NULL	1 / 9	GSEA C2 REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS
28	−6.48	NULL	1 / 19	BP hydrogen peroxide catabolic process
29	−6.44	NULL	2 / 20	Lymphoma DAVE_Immune response 2
30	−6.38	NULL	3 / 10	GSEA C2 YAMASHITA_LIVER_CANCER_WITH_EPCAM_DN
31	−6.33	NULL	2 / 5	GSEA C2 SMID_BREAST_CANCER_ERBB2_DN
32	−6.3	NULL	2 / 10	Glio willscher_ GBM_LTSwt_proteomics−G_UP
33	−6.28	NULL	2 / 12	BP negative regulation of axon extension
34	−6.27	NULL	3 / 16	GSEA C2 DOANE_BREAST_CANCER_ESR1_DN
35	−6.22	NULL	4 / 13	GSEA C2 HUANG_DASATINIB_RESISTANCE_DN
36	−6.16	NULL	2 / 14	GSEA C2 VANTVEER_BREAST_CANCER_ESR1_UP
37	−6.1	NULL	3 / 12	GSEA C2 PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP
38	−6.09	NULL	1 / 4	GSEA C2 NICK_RESPONSE_TO_PROC_TREATMENT_UP
39	−5.98	NULL	3 / 16	GSEA C2 BOYAULT_LIVER_CANCER_SUBCLASS_G1_UP
40	−5.96	NULL	4 / 7	GSEA C2 LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN

GW_014

Local Summary

%DE = 0.72

metagenes = 25

genes = 250

genes in genesets = 248

genes with fdr < 0.1 = 65 (1 + / 64 −)

genes with fdr < 0.05 = 58 (1 + / 57 −)

genes with fdr < 0.01 = 38 (1 + / 37 −)

<r> metagenes = 0.97

<r> genes = 0.3

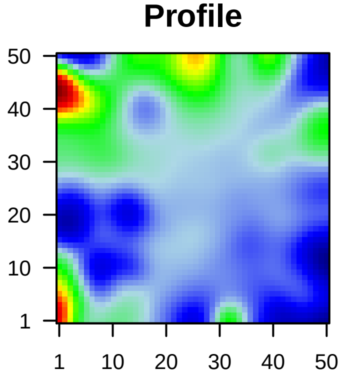
<FC> = −0.23

<shrinkage−t> = −8.09

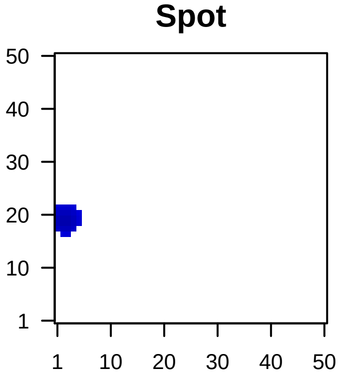
<p−value> = 0.04

<fdr> = 0.75

Profile



Spot



Local Genelist

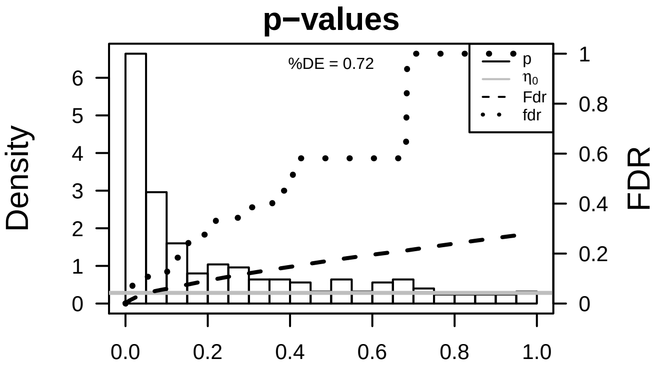
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	284085	−1.41	2e−16	2e−14	3 x 18	keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874
2	2288	−0.85	2e−08	5e−06	1 x 19	FK506 binding protein 4, 59kDa [Source:HGNC Symbol;Acc:
3	389541	−0.8	1e−07	2e−05	3 x 19	late endosomal/lysosomal adaptor, MAPK and MTOR activat
4	79897	−0.76	4e−07	7e−05	3 x 19	ribonuclease P/MRP 21kDa subunit [Source:HGNC Symbol;
5	11331	−0.73	1e−06	3e−04	4 x 18	prohibitin 2 [Source:HGNC Symbol;Acc:30306]
6	2597	−0.63	5e−06	4e−04	2 x 17	glyceraldehyde−3−phosphate dehydrogenase [Source:HGNC
7	51702	−0.65	2e−05	4e−04	1 x 21	peptidyl arginine deiminase, type III [Source:HGNC Symbol;A
8	55168	−0.64	2e−05	4e−04	2 x 20	mitochondrial ribosomal protein S18A [Source:HGNC Symbo
9	84300	−0.63	3e−05	4e−04	2 x 18	ubiquinol−cytochrome c reductase complex assembly factor
10	8079	−0.63	3e−05	4e−04	3 x 18	myeloid leukemia factor 2 [Source:HGNC Symbol;Acc:7126]
11	4704	−0.63	3e−05	6e−04	3 x 19	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9,
12	58477	−0.62	4e−05	8e−04	2 x 21	signal recognition particle receptor, B subunit [Source:HGNC
13	30968	−0.61	6e−05	8e−04	2 x 20	stomatin (EPB72)−like 2 [Source:HGNC Symbol;Acc:14559]
14	64951	−0.6	6e−05	8e−04	2 x 18	mitochondrial ribosomal protein S24 [Source:HGNC Symbol;
15	430	0.6	7e−05	2e−03	2 x 20	achaete−scute family bHLH transcription factor 2 [Source:HG
16	1460	−0.58	1e−04	2e−03	1 x 20	casein kinase 2, beta polypeptide [Source:HGNC Symbol;Ac
17	9328	−0.58	1e−04	2e−03	4 x 20	general transcription factor IIIC, polypeptide 5, 63kDa [Source
18	5435	−0.57	2e−04	2e−03	3 x 17	polymerase (RNA) II (DNA directed) polypeptide F [Source:H
19	10939	−0.56	2e−04	2e−03	5 x 19	AFG3−like AAA ATPase 2 [Source:HGNC Symbol;Acc:315]
20	9533	−0.56	2e−04	4e−03	3 x 17	polymerase (RNA) I polypeptide C, 30kDa [Source:HGNC Sy

Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−14.68	NULL	2 / 6	GSEA C2	KORKOLA_CHORIOCARCINOMA_UP
2	−14.5	NULL	4 / 10	MF	NADH dehydrogenase activity
3	−12.75	NULL	3 / 9	GSEA C2	MOREIRA_RESPONSE_TO_TSA_UP
4	−12.67	NULL	3 / 16	GSEA C2	KORKOLA_EMBRYONAL_CARCINOMA_UP
5	−11.62	NULL	5 / 19	CC	mitochondrial small ribosomal subunit
6	−11.3	NULL	77 / 1318	CC	mitochondrion
7	−10.86	NULL	20 / 153	MF	structural constituent of ribosome
8	−10.33	NULL	25 / 304	CC	mitochondrial inner membrane
9	−10.17	NULL	4 / 13	GSEA C2	MOOTHA_VOXPHOS
10	−9.96	NULL	3 / 15	GSEA C2	KORKOLA_YOLK_SAC_TUMOR_UP
11	−9.69	NULL	2 / 4	TF	MYC_Cell growth and proliferation UP
12	−9.62	NULL	4 / 15	CC	mitochondrial large ribosomal subunit
13	−8.97	NULL	10 / 83	BP	respiratory electron transport chain
14	−8.9	NULL	21 / 253	BP	translation
15	−8.87	NULL	2 / 10	CC	DNA−directed RNA polymerase I complex
16	−8.83	NULL	3 / 15	CC	DNA−directed RNA polymerase III complex
17	−8.75	NULL	1 / 4	GSEA C2	DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_D
18	−8.58	NULL	3 / 14	BP	mitochondrial ATP synthesis coupled proton transport
19	−8.38	NULL	5 / 34	MF	NADH dehydrogenase (ubiquinone) activity
20	−8.34	NULL	16 / 167	CC	ribosome
21	−8.11	NULL	5 / 36	CC	mitochondrial respiratory chain complex I
22	−8.03	NULL	2 / 16	GSEA C2	KORKOLA_SEMINOMA_UP
23	−7.99	NULL	3 / 18	BP	termination of RNA polymerase III transcription
24	−7.99	NULL	3 / 18	BP	transcription elongation from RNA polymerase III promoter
25	−7.57	NULL	1 / 3	TF	MYC_Tumor supressor genes UP
26	−7.44	NULL	1 / 8	miRNA target	miR−155
27	−7.34	NULL	4 / 40	BP	transcription from RNA polymerase III promoter
28	−7.19	NULL	4 / 16	GSEA C2	WONG_MITOCHONDRIA_GENE_MODULE
29	−7.02	NULL	6 / 62	Glio	Stuehler_Proteins_up_in_STS
30	−6.83	NULL	1 / 4	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G5_UP
31	−6.78	NULL	4 / 16	GSEA C2	MOOTHA_HUMAN_MITODB_6_2002
32	−6.78	NULL	4 / 16	GSEA C2	MOOTHA_MITOCHONDRIA
33	−6.63	NULL	1 / 2	miRNA 3UTR	GTGCG−371
34	−6.58	NULL	1 / 10	BP	chaperone−mediated protein folding
35	−6.48	NULL	2 / 23	Chr	Chr HSCHR6_MHC_DBB
36	−6.48	NULL	1 / 4	miRNA target	miR−27a
37	−6.47	NULL	1 / 5	GSEA C2	GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
38	−6.47	NULL	3 / 14	Pathw Act	BENTINK_myc.1
39	−6.46	NULL	11 / 152	BP	cellular metabolic process
40	−6.45	NULL	4 / 35	BP	mitochondrial electron transport, NADH to ubiquinone

p−values



GW_014

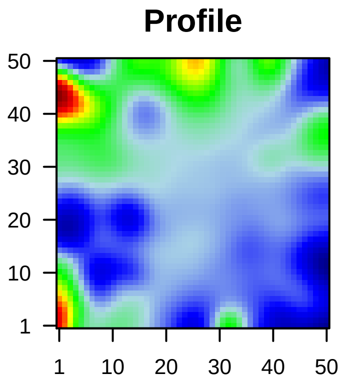
Local Summary

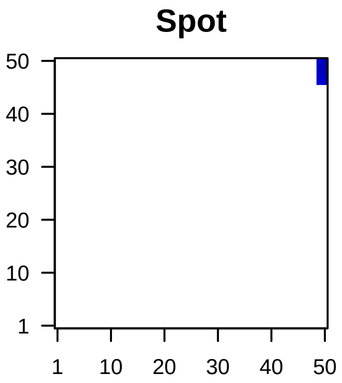
%DE = 0.78
metagenes = 10
genes = 160
genes in genesets = 159

genes with fdr < 0.1 = 77 (8 + / 69 −)
genes with fdr < 0.05 = 72 (7 + / 65 −)
genes with fdr < 0.01 = 44 (4 + / 40 −)

<r> metagenes = 0.97
<r> genes = 0.28

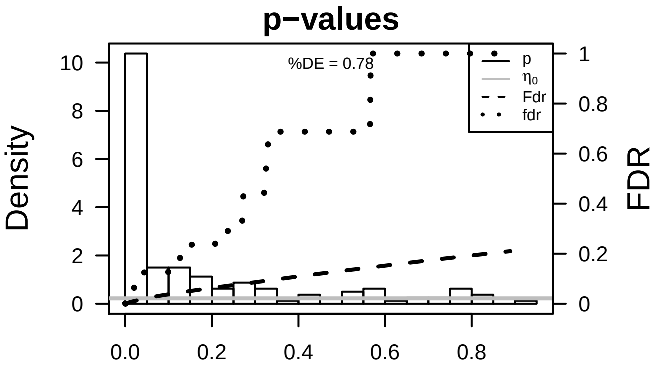
<FC> = −0.28
<shrinkage−t> = −9.77
<p−value> = 0
<fdr> = 0.57





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	214	−1.34	2e−16	2e−15	50 x 50	activated leukocyte cell adhesion molecule [Source:HGNC Sy
2	3880	−1.69	2e−16	2e−15	50 x 49	keratin 19 [Source:HGNC Symbol;Acc:6436]
3	3856	−1.99	2e−16	2e−15	50 x 48	keratin 8 pseudogene 3 [Source:HGNC Symbol;Acc:31056]
4	80896	1.32	2e−16	2e−15	50 x 50	N−acetylneuraminate pyruvate lyase (dihydrodipicolinate synt
5	4922	−1.13	8e−14	2e−10	50 x 50	neurotensin [Source:HGNC Symbol;Acc:8038]
6	216	−1.04	5e−12	1e−09	50 x 50	aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
7	57216	0.99	5e−11	1e−09	50 x 48	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;A
8	26227	−0.98	7e−11	1e−07	50 x 46	phosphoglycerate dehydrogenase [Source:HGNC Symbol;Ac
9	3866	−0.88	5e−09	1e−07	50 x 50	keratin 15 [Source:HGNC Symbol;Acc:6421]
10	51804	−0.87	7e−09	1e−07	50 x 46	SIX homeobox 4 [Source:HGNC Symbol;Acc:10890]
11	875	−0.87	1e−08	7e−07	49 x 47	cystathionine−beta−synthase [Source:HGNC Symbol;Acc:15
12	339512	−0.83	3e−08	7e−07	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Symb
13	59271	−0.82	5e−08	8e−06	50 x 48	eva−1 homolog C (C. elegans) [Source:HGNC Symbol;Acc:1
14	56256	−0.78	3e−07	3e−05	50 x 50	SERTA domain containing 4 [Source:HGNC Symbol;Acc:252
15	8544	−0.74	1e−06	3e−05	50 x 50	pirin (iron−binding nuclear protein) [Source:HGNC Symbol;Ac
16	89894	−0.72	2e−06	3e−05	50 x 50	transmembrane protein 116 [Source:HGNC Symbol;Acc:250
17	139728	−0.71	3e−06	3e−05	49 x 49	pregnancy up−regulated nonubiquitous CaM kinase [Source:
18	1056	−0.7	3e−06	4e−05	50 x 50	carboxyl ester lipase [Source:HGNC Symbol;Acc:1848]
19	57549	−0.69	4e−06	4e−05	49 x 47	immunoglobulin superfamily, member 9 [Source:HGNC Symb
20	8702	−0.69	6e−06	6e−05	50 x 50	UDP−Gal:betaGlcNAc beta 1,4− galactosyltransferase, polyp



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−24.48	NULL	3 / 8	GSEA C2	LIU_CDX2_TARGETS_DN
2	−14.54	NULL	4 / 13	BP	regulation of blood vessel size
3	−14.02	NULL	3 / 11	GSEA C2	ITO_PTTG1_TARGETS_UP
4	−13.75	NULL	2 / 7	GSEA C2	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
5	−13.14	NULL	2 / 6	GSEA C2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN
6	−13.09	NULL	4 / 15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
7	−11.33	NULL	1 / 11	GSEA C2	WHITESIDE_CISPLATIN_RESISTANCE_DN
8	−10.87	NULL	2 / 14	GSEA C2	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM
9	−10.85	NULL	3 / 12	GSEA C2	HELLER_SILENCED_BY_METHYLATION_DN
10	−10.32	NULL	1 / 13	GSEA C2	CHEN_LUNG_CANCER_SURVIVAL
11	−10.05	NULL	3 / 16	GSEA C2	KAN_RESPONSE_TO_ARSENIC_TRIOXIDE
12	−10.04	NULL	2 / 12	BP	cellular aldehyde metabolic process
13	−9.95	NULL	3 / 19	BP	cellular amino acid biosynthetic process
14	−9.9	NULL	1 / 14	GSEA C2	LIANG_SILENCED_BY_METHYLATION_UP
15	−9.82	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
16	−9.52	NULL	1 / 15	GSEA C2	LE_SKI_TARGETS_UP
17	−9.52	NULL	1 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
18	−9.18	NULL	1 / 16	CC	dystrophin−associated glycoprotein complex
19	−9.18	NULL	1 / 16	GSEA C2	DORN_ADENOVIRUS_INFECTION_12HR_UP
20	−8.98	NULL	1 / 7	GSEA C2	FREDERICK_PRKCI_TARGETS
21	−8.93	NULL	1 / 11	Glio	willscher_GBM_Verhaak−CL_expression_M_down
22	−8.93	NULL	1 / 11	Glio	willscher_GBM_Verhaak−MES_expression_M_down
23	−8.93	NULL	1 / 11	Glio	willscher_GBM_Verhaak−PNmut_expression_M_up
24	−8.83	NULL	2 / 12	GSEA C2	KAYO_AGING_MUSCLE_UP
25	−8.59	NULL	1 / 18	CC	costamere
26	−8.44	NULL	2 / 13	GSEA C2	BLUM_RESPONSE_TO_SALIRASIB_UP
27	−8.27	NULL	3 / 16	GSEA C2	BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN
28	−8.19	NULL	3 / 9	GSEA C2	REACTOME_METABOLISM_OF_AMINO_ACIDS
29	−8.15	NULL	2 / 16	GSEA C2	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP
30	−8.15	NULL	2 / 16	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP
31	−8.13	NULL	1 / 6	GSEA C2	SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN
32	−7.98	NULL	2 / 18	MF	acyl−CoA dehydrogenase activity
33	−7.87	NULL	1 / 21	BP	sarcomere organization
34	−7.78	NULL	2 / 15	GSEA C2	UDAYAKUMAR_MED1_TARGETS_UP
35	−7.78	NULL	2 / 15	GSEA C2	KRIGE_AMINO_ACID_DEPRIVATION
36	−7.76	NULL	1 / 9	GSEA C2	ABDULRAHMAN_KIDNEY_CANCER_VHL_DN
37	−7.76	NULL	1 / 9	GSEA C2	REACTOME_ETHANOL_OXIDATION
38	−7.7	NULL	2 / 10	GSEA C2	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
39	−7.66	NULL	2 / 10	BP	biotin metabolic process
40	−7.63	NULL	2 / 18	BP	glutamine metabolic process