GW_243

Global Summary

%DE = 0.15

genes with fdr < 0.2 = 1936 (1069 + / 867 −)

genes with fdr < 0.1 = 1548 (864 + / 684 −)

genes with fdr < 0.05 = 1298 (727 + / 571 −)

genes with fdr < 0.01 = 939 (533 + / 406 −)

genes in genesets = 16332

<FC> = 0

<shrinkage−t> = 0

<p−value> = 0.09

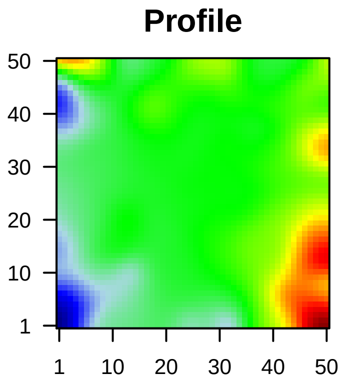
<fdr> = 0.85

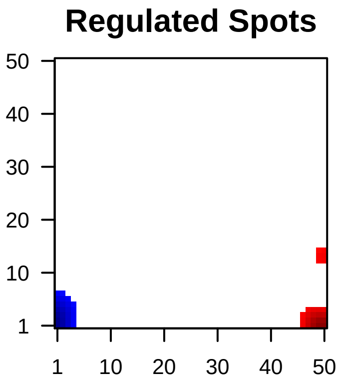
Global Genelist

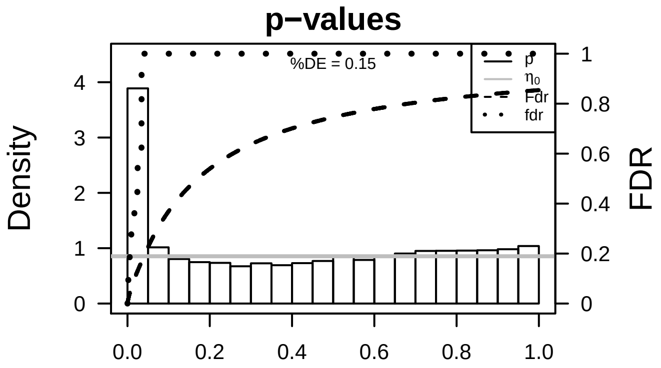
Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	124	2.02	2e−16	3e−14	50 x 11	alcohol dehydrogenase 1A (class I), alpha polypeptide [Sourc
2	126	1.86	2e−16	3e−14	50 x 12	alcohol dehydrogenase 1C (class I), gamma polypeptide [Sou
3	131	2.1	2e−16	3e−14	1 x 50	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
4	218	1.87	2e−16	3e−14	1 x 50	aldehyde dehydrogenase 3 family, member A1 [Source:HGN
5	55107	−1.4	2e−16	3e−14	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HG
6	445	1.55	2e−16	3e−14	50 x 47	argininosuccinate synthase 1 [Source:HGNC Symbol;Acc:75
7	640	1.38	2e−16	3e−14	46 x 4	B lymphoid tyrosine kinase [Source:HGNC Symbol;Acc:1057]
8	655	1.23	2e−16	3e−14	50 x 50	bone morphogenetic protein 7 [Source:HGNC Symbol;Acc:1
9	339512	1.23	2e−16	3e−14	50 x 50	chromosome 1 open reading frame 110 [Source:HGNC Sym
10	730	1.31	2e−16	3e−14	49 x 7	complement component 7 [Source:HGNC Symbol;Acc:1346]
11	375791	1.4	2e−16	3e−14	1 x 50	chromosome 9 open reading frame 169 [Source:HGNC Sym
12	57172	1.61	2e−16	3e−14	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
13	6363	2.54	2e−16	3e−14	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
14	6366	2.44	2e−16	3e−14	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
15	414062	−1.72	2e−16	3e−14	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symb
16	9560	−1.35	2e−16	3e−14	32 x 1	chemokine (C−C motif) ligand 4−like 1 [Source:HGNC Symb
17	1236	2.06	2e−16	3e−14	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
18	930	2.22	2e−16	3e−14	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
19	919	1.65	2e−16	3e−14	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
20	939	1.57	2e−16	3e−14	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]

Global Geneset Analysis

Rank	GSZ	p−value	#all	Geneset	
Overexpressed					
1	17.47	NULL	417	H.Tiss	WIRTH_Immune system
2	12.55	NULL	135	H.Tiss	WIRTH_Mucosa
3	9.03	NULL	28	BP	B cell receptor signaling pathway
4	8.83	NULL	9	GSEA C2	REACTOME_ETHANOL_OXIDATION
5	8.7	NULL	9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
6	8.07	NULL	119	BP	xenobiotic metabolic process
7	7.71	NULL	81	BP	viral transcription
8	7.57	NULL	87	BP	translational termination
9	7.52	NULL	16	GSEA C2	SU_THYMUS
10	7.45	NULL	92	BP	translational elongation
11	7.39	NULL	12	BP	dendritic cell chemotaxis
12	7.29	NULL	115	BP	nuclear−transcribed mRNA catabolic process, nonsense−mediated
13	7.16	NULL	92	BP	viral life cycle
14	7.06	NULL	28	BP	B cell activation
15	7.04	NULL	109	BP	SRP−dependent cotranslational protein targeting to membrane
16	6.9	NULL	128	BP	translational initiation
17	6.65	NULL	15	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_E
18	6.44	NULL	18	MF	aromatase activity
19	6.34	NULL	11	GSEA C2	BIOCARTA_THELPER_PATHWAY
20	6.32	NULL	327	Lymphoma	SPANG_CD40 6hrs UP
Underexpressed					
1	−11.53	NULL	242	BP	extracellular matrix organization
2	−10.3	NULL	190	CC	extracellular matrix
3	−9.9	NULL	15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	−9.87	NULL	69	BP	extracellular matrix disassembly
5	−9.82	NULL	64	BP	collagen catabolic process
6	−9.23	NULL	1182	CC	extracellular region
7	−9.17	NULL	250	Lymphoma	LENZ_Stromal signature 1
8	−9.11	NULL	683	CC	extracellular space
9	−8.43	NULL	9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
10	−8.22	NULL	117	Glio	GIEZELT_GBM_WT_up_VS_mut
11	−8.12	NULL	16	GSEA C2	MAHADEVAN_RESPONSE_TO_MP470_UP
12	−8.08	NULL	68	Glio	cultured astroglia vs. in vivo astrocytes
13	−7.57	NULL	183	CC	proteinaceous extracellular matrix
14	−7.52	NULL	6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
15	−7.5	NULL	572	Disease	GUDJ_psoriasis up
16	−7.3	NULL	12	GSEA C2	ZHU_CMV_8_HR_UP
17	−7.28	NULL	11	GSEA C2	BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
18	−7.22	NULL	13	GSEA C2	FRIDMAN_SENESCENCE_UP
19	−7.19	NULL	16	GSEA C2	XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR
20	−7.17	NULL	16	GSEA C2	UROSEVIC_RESPONSE_TO_IMIQUIMOD







GW_243

Local Summary

%DE = 0.85

metagenes = 19

genes = 295

genes in genesets = 293

genes with fdr < 0.1 = 224 (212 + / 12 −)

genes with fdr < 0.05 = 207 (198 + / 9 −)

genes with fdr < 0.01 = 189 (184 + / 5 −)

<r> metagenes = 0.99

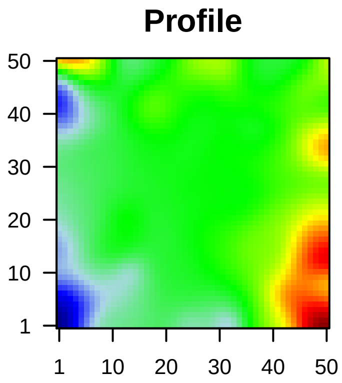
<r> genes = 0.59

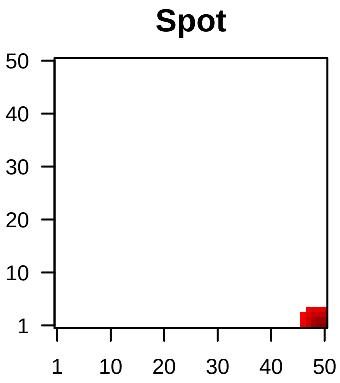
<FC> = 0.6

<shrinkage−t> = 21.06

<p−value> = 0

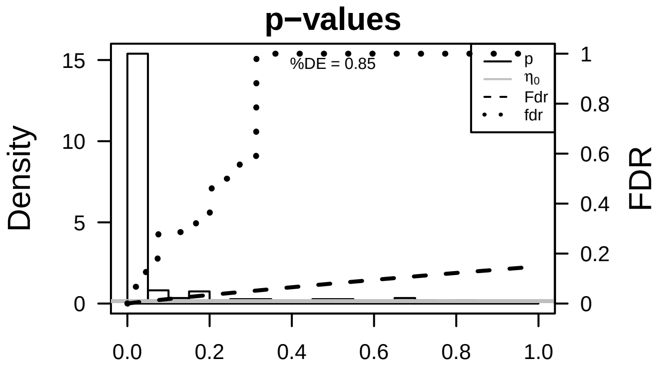
<fdr> = 0.3





Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	57172	1.61	2e−16	3e−16	49 x 1	calcium/calmodulin−dependent protein kinase IG [Source:HG
2	6363	2.54	2e−16	3e−16	50 x 1	chemokine (C−C motif) ligand 19 [Source:HGNC Symbol;Acc
3	6366	2.44	2e−16	3e−16	50 x 2	chemokine (C−C motif) ligand 21 [Source:HGNC Symbol;Acc
4	1236	2.06	2e−16	3e−16	50 x 1	chemokine (C−C motif) receptor 7 [Source:HGNC Symbol;Ac
5	930	2.22	2e−16	3e−16	49 x 1	CD19 molecule [Source:HGNC Symbol;Acc:1633]
6	919	1.65	2e−16	3e−16	50 x 1	CD247 molecule [Source:HGNC Symbol;Acc:1677]
7	939	1.57	2e−16	3e−16	49 x 1	CD27 molecule [Source:HGNC Symbol;Acc:11922]
8	962	1.59	2e−16	3e−16	50 x 1	CD48 molecule [Source:HGNC Symbol;Acc:1683]
9	1043	1.31	2e−16	3e−16	50 x 1	CD52 molecule [Source:HGNC Symbol;Acc:1804]
10	974	1.4	2e−16	3e−16	48 x 1	CD79b molecule, immunoglobulin−associated beta [Source:H
11	51755	1.55	2e−16	3e−16	49 x 1	cyclin−dependent kinase 12 [Source:HGNC Symbol;Acc:242
12	1545	2.25	2e−16	3e−16	50 x 4	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
13	55619	1.33	2e−16	3e−16	50 x 1	dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:2347
14	9214	1.8	2e−16	3e−16	49 x 1	Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;A
15	84824	1.9	2e−16	3e−16	49 x 1	Fc receptor−like A [Source:HGNC Symbol;Acc:18504]
16	221472	1.25	2e−16	3e−16	49 x 1	FYVE, RhoGEF and PH domain containing 2 [Source:HGNC
17	3119	1.23	2e−16	3e−16	49 x 1	major histocompatibility complex, class II, DQ beta 1 [Source:
18	3512	2.65	2e−16	3e−16	50 x 1	immunoglobulin J polypeptide, linker protein for immunoglobu
19	3394	1.64	2e−16	3e−16	50 x 1	interferon regulatory factor 8 [Source:HGNC Symbol;Acc:535
20	3820	1.5	2e−16	3e−16	50 x 1	killer cell lectin−like receptor subfamily B, member 1 [Source:



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	30.16	NULL	99 / 417	H.Tiss	WIRTH_Immune system
2	25.7	NULL	105 / 553	Cancer	Lembcke_Colonic Inflammation
3	22.76	NULL	12 / 15	CC	MHC class II protein complex
4	21.17	NULL	9 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_1
5	19.45	NULL	5 / 12	BP	dendritic cell chemotaxis
6	19.2	NULL	5 / 17	BP	positive regulation of neutrophil chemotaxis
7	18.39	NULL	11 / 28	BP	B cell receptor signaling pathway
8	17.93	NULL	7 / 11	GSEA C2	BIOCARTA_THELPER_PATHWAY
9	17.69	NULL	3 / 9	GSEA C2	MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
10	17.49	NULL	6 / 8	Glio	Donson−migration tethering and rolling−associated with LTS in HG
11	17.41	NULL	7 / 15	GSEA C2	FINAK_BREAST_CANCER_SDPP_SIGNATURE
12	16.95	NULL	7 / 11	GSEA C2	BIOCARTA_TCYTOTOXIC_PATHWAY
13	16.42	NULL	18 / 60	BP	T cell costimulation
14	16.25	NULL	3 / 7	GSEA C2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN
15	15.84	NULL	8 / 16	GSEA C2	SU_THYMUS
16	15.47	NULL	55 / 312	BP	immune response
17	15.12	NULL	2 / 10	BP	positive regulation of chemotaxis
18	14.79	NULL	4 / 22	BP	positive regulation of phosphatidylinositol 3−kinase activity
19	14.4	NULL	4 / 27	BP	release of sequestered calcium ion into cytosol
20	14.38	NULL	2 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
21	13.63	NULL	2 / 12	BP	positive regulation of receptor−mediated endocytosis
22	13.62	NULL	6 / 12	GSEA C2	BIOCARTA_CTL_PATHWAY
23	13.6	NULL	3 / 5	GSEA C2	WONG_ENDOMETRIAL_CANCER_LATE
24	13.43	NULL	8 / 13	Cancer	GENTLES_modul18
25	13.07	NULL	3 / 11	BP	activation of Rho GTPase activity
26	13.01	NULL	18 / 74	BP	regulation of immune response
27	12.77	NULL	5 / 10	GSEA C2	LEE_DIFFERENTIATING_T_LYMPHOCYTE
28	12.75	NULL	27 / 162	CC	external side of plasma membrane
29	12.74	NULL	5 / 8	GSEA C2	BIOCARTA_TCRA_PATHWAY
30	12.73	NULL	15 / 47	BP	antigen processing and presentation
31	12.44	NULL	4 / 14	BP	ruffle organization
32	12.43	NULL	6 / 14	GSEA C2	BIOCARTA_NO2IL12_PATHWAY
33	12.33	NULL	4 / 10	GSEA C2	LEE_EARLY_T_LYMPHOCYTE_DN
34	12.32	NULL	1 / 2	GSEA C2	GUTIERREZ_MULTIPLE_MYELOMA_UP
35	12.16	NULL	3 / 10	BP	negative thymic T cell selection
36	12	NULL	5 / 11	BP	positive regulation of B cell differentiation
37	11.96	NULL	3 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_D
38	11.81	NULL	4 / 8	GSEA C2	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN
39	11.74	NULL	4 / 8	GSEA C2	BIOCARTA_TCAPOPTOSIS_PATHWAY
40	11.52	NULL	6 / 13	GSEA C2	BIOCARTA_IL17_PATHWAY

GW_243

Local Summary

%DE = 0.91

metagenes = 6

genes = 67

genes in genesets = 67

genes with fdr < 0.1 = 54 (53 + / 1 −)

genes with fdr < 0.05 = 53 (52 + / 1 −)

genes with fdr < 0.01 = 43 (42 + / 1 −)

<r> metagenes = 0.98

<r> genes = 0.35

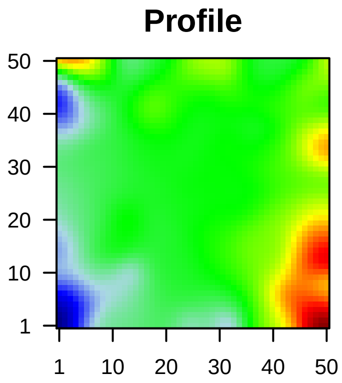
<FC> = 0.56

<shrinkage−t> = 19.56

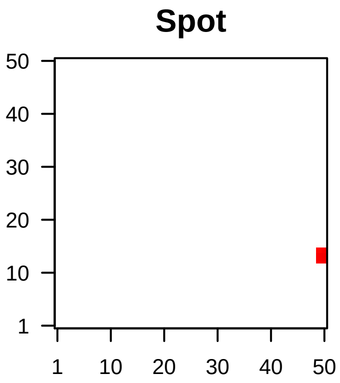
<p−value> = 0

<fdr> = 0.26

Profile



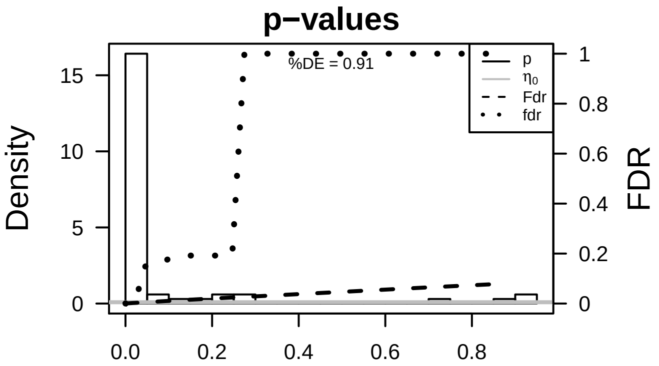
Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	2568	1.75	2e−16	4e−16	50 x 13	gamma−aminobutyric acid (GABA) A receptor, pi [Source:HG
2	51316	1.49	2e−16	4e−16	50 x 13	placenta−specific 8 [Source:HGNC Symbol;Acc:19254]
3	169166	1.26	2e−16	4e−16	50 x 13	sorting nexin 31 [Source:HGNC Symbol;Acc:28605]
4	3248	1.08	6e−13	6e−12	50 x 13	hydroxyprostaglandin dehydrogenase 15−(NAD) [Source:HG
5	66002	1.05	2e−12	3e−11	50 x 13	cytochrome P450, family 4, subfamily F, polypeptide 12 [Sour
6	2053	1.02	7e−12	3e−10	50 x 14	epoxide hydrolase 2, cytoplasmic [Source:HGNC Symbol;Acc
7	55268	0.98	7e−11	7e−10	50 x 14	enoyl CoA hydratase domain containing 2 [Source:HGNC Sy
8	3131	0.95	2e−10	9e−10	50 x 14	hepatic leukemia factor [Source:HGNC Symbol;Acc:4977]
9	260293	0.94	4e−10	3e−09	50 x 14	cytochrome P450, family 4, subfamily X, polypeptide 1 [Sourc
10	29997	0.83	1e−09	3e−09	50 x 15	glioma tumor suppressor candidate region gene 2 [Source:H
11	6228	0.9	2e−09	3e−09	50 x 14	ribosomal protein S23 [Source:HGNC Symbol;Acc:10410]
12	8543	0.9	2e−09	5e−09	50 x 15	LIM domain only 4 [Source:HGNC Symbol;Acc:6644]
13	2205	0.89	3e−09	6e−09	50 x 13	Fc fragment of IgE, high affinity I, receptor for; alpha polypept
14	391267	0.88	4e−09	6e−09	50 x 13	ankyrin repeat domain 20 family, member A11, pseudogene [
15	399948	0.87	5e−09	6e−09	50 x 15	colorectal cancer associated 1 [Source:HGNC Symbol;Acc:3
16	57189	0.87	6e−09	7e−08	50 x 15	KIAA1147 [Source:HGNC Symbol;Acc:29472]
17	7155	0.84	2e−08	1e−07	50 x 15	topoisomerase (DNA) II beta 180kDa [Source:HGNC Symbol
18	155066	0.82	4e−08	5e−07	50 x 15	ATPase, H+ transporting V0 subunit e2 [Source:HGNC Symb
19	1153	0.79	1e−07	5e−07	50 x 15	cold inducible RNA binding protein [Source:HGNC Symbol;A
20	8857	−0.77	2e−07	1e−06	50 x 13	Fc fragment of IgG binding protein [Source:HGNC Symbol;A

p−values



Local Geneset Analysis

Overexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	26.93	NULL	2 / 7	GSEA C2	HUPER_BREAST_BASAL_VS_LUMINAL_DN
2	23.95	NULL	1 / 5	GSEA C2	SMID_BREAST_CANCER_ERBB2_DN
3	18.06	NULL	2 / 10	BP	epoxygenase P450 pathway
4	17.47	NULL	1 / 8	GSEA C2	HEIDENBLAD_AMPLICON_12P11_12_UP
5	15.65	NULL	1 / 4	GSEA C2	NICK_RESPONSE_TO_PROC_TREATMENT_UP
6	15.26	NULL	1 / 4	GSEA C2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_5
7	15.16	NULL	1 / 10	MF	GABA−A receptor activity
8	15.07	NULL	3 / 15	GSEA C2	DOANE_BREAST_CANCER_CLASSES_UP
9	14.28	NULL	1 / 11	GSEA C2	JAZAERI_BREAST_CANCER_BRCA1_VS_BRCA2_DN
10	13.65	NULL	2 / 16	GSEA C2	TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_
11	13.31	NULL	2 / 15	GSEA C2	NAKAJIMA_MAST_CELL
12	12.72	NULL	2 / 12	MF	NAD+ binding
13	12.32	NULL	1 / 14	GSEA C2	SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_
14	12.32	NULL	1 / 14	GSEA C2	TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP
15	12.32	NULL	1 / 14	GSEA C2	RIZKI_TUMOR_INVASIVENESS_2D_DN
16	12.3	NULL	1 / 6	GSEA C2	KAPOSI_LIVER_CANCER_POOR_SURVIVAL_DN
17	12.15	NULL	1 / 11	BP	negative regulation of multicellular organism growth
18	12.09	NULL	2 / 18	MF	aromatase activity
19	11.96	NULL	1 / 3	miRNA target	miR−223
20	11.9	NULL	2 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
21	11.9	NULL	2 / 15	Cancer	SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
22	11.81	NULL	1 / 15	GSEA C2	SABATES_COLORECTAL_ADENOMA_UP
23	11.81	NULL	1 / 15	GSEA C2	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
24	11.53	NULL	2 / 21	BP	drug metabolic process
25	11.36	NULL	1 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_
26	11.36	NULL	1 / 16	GSEA C2	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR
27	11.36	NULL	1 / 16	GSEA C2	DOANE_BREAST_CANCER_ESR1_DN
28	11.36	NULL	1 / 16	GSEA C2	ROY_WOUND_BLOOD_VESSEL_DN
29	11.36	NULL	1 / 16	GSEA C2	YANG_BREAST_CANCER_ESR1_DN
30	11.36	NULL	1 / 16	GSEA C2	RICKMAN_HEAD_AND_NECK_CANCER_A
31	10.81	NULL	3 / 49	BP	arachidonic acid metabolic process
32	10.26	NULL	2 / 30	BP	response to cold
33	10.08	NULL	2 / 10	GSEA C2	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM
34	10.08	NULL	2 / 10	GSEA C2	KEGG_LIMONENE_AND_PINENE_DEGRADATION
35	9.74	NULL	2 / 14	GSEA C2	VANTVEER_BREAST_CANCER_METASTASIS_UP
36	9.66	NULL	2 / 15	GSEA C2	ZHAN_MULTIPLE_MYELOMA_CD1_DN
37	9.6	NULL	1 / 7	GSEA C2	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINE
38	9.5	NULL	2 / 11	BP	neurotransmitter biosynthetic process
39	9.26	NULL	1 / 4	miRNA target	miR−204
40	9.25	NULL	1 / 10	BP	lipoxygenase pathway

GW_243

Local Summary

%DE = 0.93

metagenes = 25

genes = 367

genes in genesets = 364

genes with fdr < 0.1 = 320 (4 + / 316 −)

genes with fdr < 0.05 = 311 (3 + / 308 −)

genes with fdr < 0.01 = 256 (2 + / 254 −)

<r> metagenes = 0.93

<r> genes = 0.33

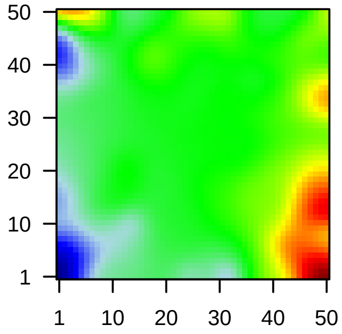
<FC> = −0.56

<shrinkage−t> = −19.46

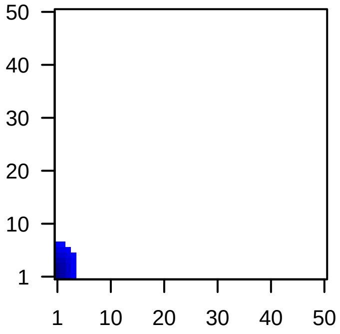
<p−value> = 0

<fdr> = 0.29

Profile

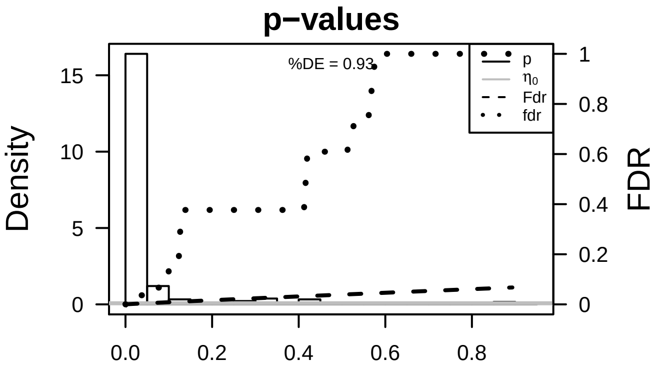


Spot



Local Genelist

Rank	ID	log(FC)	p−value	fdr	Metagene	Description
1	55107	−1.4	2e−16	3e−16	1 x 5	anoctamin 1, calcium activated chloride channel [Source:HGN
2	414062	−1.72	2e−16	3e−16	1 x 1	chemokine (C−C motif) ligand 3−like 3 [Source:HGNC Symbo
3	1277	−1.28	2e−16	3e−16	2 x 1	collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:2197]
4	1289	−1.23	2e−16	3e−16	2 x 1	collagen, type V, alpha 1 [Source:HGNC Symbol;Acc:2209]
5	2919	−1.49	2e−16	3e−16	1 x 1	chemokine (C−X−C motif) ligand 1 (melanoma growth stimula
6	285761	−1.4	2e−16	3e−16	1 x 4	discoidin, CUB and LCCL domain containing 1 [Source:HGN
7	3040	−1.54	2e−16	3e−16	4 x 1	hemoglobin, alpha 2 [Source:HGNC Symbol;Acc:4824]
8	10644	−1.27	2e−16	3e−16	1 x 6	insulin−like growth factor 2 mRNA binding protein 2 [Source:H
9	3553	−1.52	2e−16	3e−16	1 x 1	interleukin 1, beta [Source:HGNC Symbol;Acc:5992]
10	3569	−1.27	2e−16	3e−16	1 x 1	interleukin 6 (interferon, beta 2) [Source:HGNC Symbol;Acc:6
11	3576	−2.75	2e−16	3e−16	1 x 1	interleukin 8 [Source:HGNC Symbol;Acc:6025]
12	4312	−2.06	2e−16	3e−16	1 x 1	matrix metallopeptidase 1 (interstitial collagenase) [Source:H
13	4314	−2.44	2e−16	3e−16	1 x 1	matrix metallopeptidase 3 (stromelysin 1, progelatinase) [Sou
14	5743	−1.51	2e−16	3e−16	1 x 1	prostaglandin−endoperoxide synthase 2 (prostaglandin G/H s
15	12	−1.54	2e−16	3e−16	1 x 1	
16	5054	−1.46	2e−16	3e−16	1 x 2	serpin peptidase inhibitor, clade E (nexin, plasminogen activa
17	7130	−1.34	2e−16	3e−16	1 x 1	tumor necrosis factor, alpha−induced protein 6 [Source:HGN
18	51330	−1.3	2e−16	3e−16	1 x 4	tumor necrosis factor receptor superfamily, member 12A [Sou
19	10381	−1.34	2e−16	3e−16	1 x 4	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772]
20	4502	−1.19	2e−15	3e−14	1 x 3	metallothionein 2A [Source:HGNC Symbol;Acc:7406]



Local Geneset Analysis

Underexpression

Rank	GSZ	p−value	#in/all	Geneset	
1	−28.9	NULL	75 / 242	BP	extracellular matrix organization
2	−25.65	NULL	33 / 69	BP	extracellular matrix disassembly
3	−24.87	NULL	12 / 15	GSEA C2	CROMER_TUMORIGENESIS_UP
4	−24.84	NULL	73 / 250	Lymphoma	LENZ_Stromal signature 1
5	−24.64	NULL	29 / 64	BP	collagen catabolic process
6	−24.64	NULL	60 / 190	CC	extracellular matrix
7	−22.52	NULL	15 / 16	MMML CGS	MACIEJ_MMML 1
8	−21.35	NULL	4 / 9	GSEA C2	ZERBINI_RESPONSE_TO_SULINDAC_UP
9	−19.99	NULL	45 / 265	Glio	willscher_GBM_Verhaak−CL_expression_B_up
10	−19.99	NULL	45 / 265	Glio	willscher_GBM_Verhaak−MES_expression_B_up
11	−19.99	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNwt_expression_B_down
12	−19.99	NULL	45 / 265	Glio	willscher_GBM_Verhaak−PNmut_expression_B_down
13	−19.14	NULL	122 / 1182	CC	extracellular region
14	−19.11	NULL	85 / 683	CC	extracellular space
15	−19.06	NULL	2 / 6	GSEA C2	SEIKE_LUNG_CANCER_POOR_SURVIVAL
16	−18.95	NULL	7 / 11	MF	platelet−derived growth factor binding
17	−18.25	NULL	70 / 553	Cancer	Lembcke_Colonic Inflammation
18	−18.23	NULL	1 / 3	GSEA C2	REN_MIF_TARGETS_DN
19	−17.73	NULL	8 / 15	GSEA C2	LEE_LIVER_CANCER_HEPATOBLAST
20	−17.69	NULL	7 / 11	Glio	Phillips MES up vs Prolif & PN
21	−17.18	NULL	12 / 16	GSEA C2	FARMER_BREAST_CANCER_CLUSTER_5
22	−17.03	NULL	9 / 13	GSEA C2	MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH
23	−16.9	NULL	6 / 10	GSEA C2	VERRECCHIA_RESPONSE_TO_TGFB1_C4
24	−16.83	NULL	21 / 57	MF	extracellular matrix structural constituent
25	−16.73	NULL	9 / 15	GSEA C2	ONDER_CDH1_SIGNALING_VIA_CTNNB1
26	−16.61	NULL	11 / 40	BP	cellular response to amino acid stimulus
27	−16.53	NULL	38 / 183	CC	proteinaceous extracellular matrix
28	−16.52	NULL	3 / 6	Glio	Martinez_Glio_hypometh
29	−16.29	NULL	16 / 68	Glio	cultured astroglia vs. in vivo astrocytes
30	−16.13	NULL	4 / 11	GSEA C2	BIOCARTA_STEM_PATHWAY
31	−15.88	NULL	6 / 13	GSEA C2	FRIDMAN_SENESCENCE_UP
32	−15.79	NULL	16 / 37	BP	collagen fibril organization
33	−15.74	NULL	8 / 12	miRNA target	miR−29c
34	−15.7	NULL	8 / 15	GSEA C2	ONDER_CDH1_TARGETS_2_UP
35	−15.52	NULL	13 / 35	Glio	Colman_survival_associated
36	−15.5	NULL	4 / 10	GSEA C2	IYENGAR_RESPONSE_TO_ADIPOCYTE_FACTORS
37	−14.9	NULL	8 / 16	GSEA C2	ROZANOV_MMP14_TARGETS_SUBSET
38	−14.76	NULL	7 / 16	GSEA C2	AMIT_EGF_RESPONSE_60_HELA
39	−14.74	NULL	5 / 12	GSEA C2	LY_AGING_MIDDLE_UP
40	−14.59	NULL	3 / 5	GSEA C2	VERNELL_RETINOBLASTOMA_PATHWAY_DN