

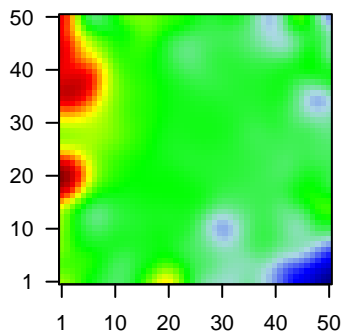
# A2\_mel

## Global Summary

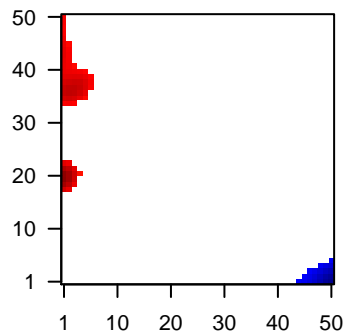
%DE = 0.21  
 # genes with  $fdr < 0.2 = 2610$  ( 1583 + / 1027 -)  
 # genes with  $fdr < 0.1 = 2267$  ( 1402 + / 865 -)  
 # genes with  $fdr < 0.05 = 1732$  ( 1084 + / 648 -)  
 # genes with  $fdr < 0.01 = 1128$  ( 714 + / 414 -)  
 # genes in genesets = 14839

<FC> = 0  
 <shrinkage-t> = 0.05  
 <p-value> = 0.08  
 <fdr> = 0.79

Profile



Regulated Spots



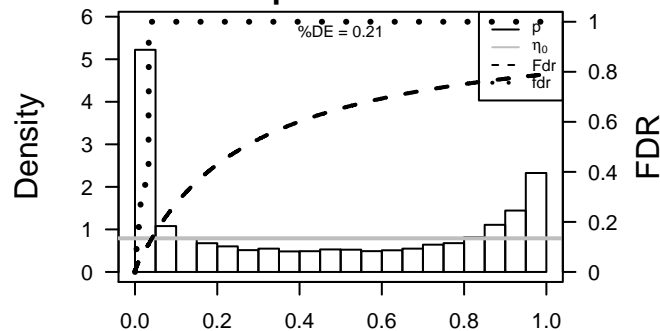
## Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANKRD28	-1.67	2e-16	1e-13	50 x 5 ankryrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC]
2	BCAP29	-1.46	2e-16	1e-13	41 x 47 B-cell receptor-associated protein 29 [Source:HGNC Symbol;Acc:HGNC]
3	CDKN3	-1.65	2e-16	1e-13	6 x 50 cyclin-dependent kinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC]
4	CNIH1	-1.08	2e-16	1e-13	29 x 46 cornichon family AMPA receptor auxiliary protein 1 [Source:HGNC Symbol;Acc:HGNC]
5	CRYAB	-1.82	2e-16	1e-13	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
6	DCN	1.95	2e-16	1e-13	43 x 13 decorin [Source:HGNC Symbol;Acc:HGNC:2705]
7	DHX36	-1.32	2e-16	1e-13	30 x 12 DEAH (Asp-Glu-Ala-His) box polypeptide 36 [Source:HGNC Symbol;Acc:HGNC]
8	DNAJA1	-1.6	2e-16	1e-13	41 x 47 DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:HGNC Symbol;Acc:HGNC]
9	GGH	-1.18	2e-16	1e-13	4 x 47 gamma-glutamyl hydrolase (conjugase, folic polyglutamate hydrolase) [Source:HGNC Symbol;Acc:HGNC]
10	HSD17B4	-1.63	2e-16	1e-13	11 x 50 hydroxysteroid (17-beta) dehydrogenase 4 [Source:HGNC Symbol;Acc:HGNC]
11	LGALS1	-1.68	2e-16	1e-13	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol;Acc:HGNC]
12	M6PR	-0.85	2e-16	1e-13	3 x 41 mannose-6-phosphate receptor (cation dependent) [Source:HGNC Symbol;Acc:HGNC]
13	MORN2	-1.33	2e-16	1e-13	47 x 37 MORN repeat containing 2 [Source:HGNC Symbol;Acc:HGNC]
14	MSC	-1.62	2e-16	1e-13	32 x 1 myosin, cardiac, isoform 1 [Source:HGNC Symbol;Acc:HGNC:7321]
15	PMP22	-1.42	2e-16	1e-13	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC]
16	PSMD10	-1.53	2e-16	1e-13	40 x 49 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC Symbol;Acc:HGNC]
17	PSMF1	-1.42	2e-16	1e-13	45 x 50 proteasome (prosome, macropain) inhibitor subunit 1 (PI31) [Source:HGNC Symbol;Acc:HGNC]
18	SDAD1	-1.75	2e-16	1e-13	50 x 44 SDA1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC]
19	SETD5	-1.6	2e-16	1e-13	36 x 50 SET domain containing 5 [Source:HGNC Symbol;Acc:HGNC]
20	TK1	-1.55	2e-16	1e-13	4 x 50 thymidine kinase 1, soluble [Source:HGNC Symbol;Acc:HGNC]

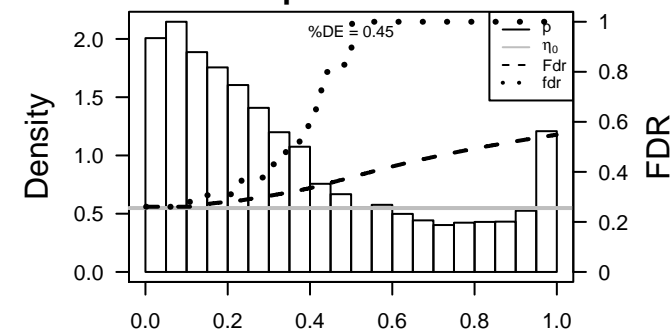
## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	6.33	0.002	421	GSEA C2MOOTHA_MITOCHONDRIA
2	6.16	0.002	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
3	5.98	0.002	401	CC mitochondrial inner membrane
4	5.87	0.002	27	GSEA C2REACTOME_DNA_STRAND_ELONGATION
5	5.68	0.002	1468	CC mitochondrion
6	5.49	0.003	29	BP DNA strand elongation involved in DNA replication
7	5.41	0.003	405	GSEA C2MOOTHA_HUMAN_MITODB_6_2002
8	5.23	0.003	278	GSEA C2MANALO_HYPOXIA_DN
9	5.21	0.003	32	GSEA C2REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLI
10	5.04	0.003	63	Glio Stuehler_Proteins_up_in_STS
11	5.03	0.003	11	GSEA C2REACTOME_UNWINDING_OF_DNA
12	4.92	0.004	233	GSEA C2PENG_RAPAMYCIN_RESPONSE_DN
13	4.88	0.004	83	GSEA C2I_DCP2_BOUND_MRNA
14	4.87	0.004	277	BP translation
15	4.79	0.004	338	GSEA C2DAIRKEE_TERT_TARGETS_UP
16	4.76	0.004	32	GSEA C2KEGG_DNA_REPLICATION
17	4.75	0.004	188	HM HALLMARK_MYC_TARGETS_V1
18	4.69	0.004	62	GSEA C2RAMASWAMY_METASTASIS_UP
19	4.69	0.004	139	BP DNA replication
20	4.69	0.004	10	BP biotin metabolic process
<i>Underexpressed</i>				
1	-5.45	0.003	286	GSEA C2PASINI_SUZ12_TARGETS_DN
2	-5.09	0.003	784	GSEA C2BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_UP
3	-4.93	0.004	145	GSEA C2BROWNE_HCMV_INFECTION_6HR_DN
4	-4.5	0.005	15	MF L-ascorbic acid binding
5	-4.39	0.006	302	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_DN
6	-4.35	0.006	221	GSEA C2DANG_REGULATED_BY_MYC_DN
7	-4.35	0.006	57	GSEA C2GARCIA_TARGETS_OF_FLU1_AND_DAX1_UP
8	-4.26	0.006	472	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_DN
9	-4.19	0.006	37	GSEA C2TAVOR_CEBPA_TARGETS_UP
10	-4.13	0.007	163	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
11	-4.08	0.007	101	GSEA C2ZHANG_TLX_TARGETS_DN
12	-4.01	0.007	71	GSEA C2RODRIGUES_THYROID_CARCINOMA_DN
13	-3.99	0.008	171	miRNA target-miR-607
14	-3.98	0.008	317	GSEA C2PHONG_TNF_RESPONSE_NOT_VIA_P38
15	-3.97	0.008	930	GSEA C2NUYTEN_EZH2_TARGETS_UP
16	-3.97	0.008	12	GSEA C2GERHOLD_RESPONSE_TO_TZD_DN
17	-3.94	0.008	10	BP negative regulation of JUN kinase activity
18	-3.89	0.008	457	GSEA C2SENESE_HDAC3_TARGETS_UP
19	-3.87	0.008	16	GSEA C2Y_AGING_MIDDLE_DN
20	-3.87	0.008	618	GSEA C2GOZIGT_ESR1_TARGETS_DN

p-values



p-values



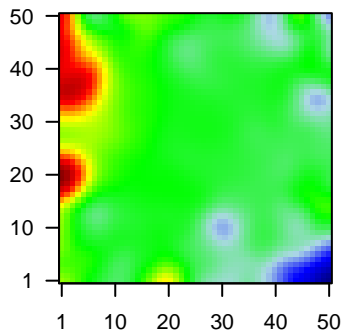
# A2\_mel

## Local Summary

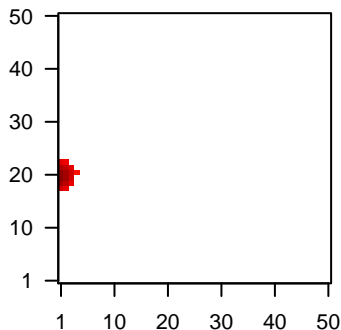
%DE = 0.87  
 # metagenes = 17  
 # genes = 247  
 # genes in genesets = 246  
  
 # genes with  $fdr < 0.1$  = 177 ( 155 + / 22 - )  
 # genes with  $fdr < 0.05$  = 147 ( 131 + / 16 - )  
 # genes with  $fdr < 0.01$  = 116 ( 104 + / 12 - )

$\langle r \rangle$  metagenes = 0.97  
 $\langle r \rangle$  genes = 0.15  
  
 $\langle FC \rangle$  = 0.35  
 $\langle \text{shrinkage-t} \rangle$  = 6.09  
 $\langle p\text{-value} \rangle$  = 0  
 $\langle fdr \rangle$  = 0.46

Profile



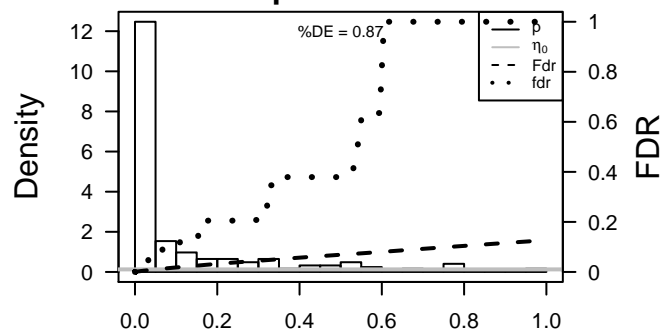
Spot



## Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	PIGY	0.7	2e-11	6e-10	1 x 20 phosphatidylinositol glycan anchor biosynthesis, class Y [Sou
2	PTP4A1	1.2	3e-11	6e-09	1 x 21 protein tyrosine phosphatase type IVA, member 1 [Source:HC
3	FAM131A	1.45	2e-10	3e-08	1 x 22 family with sequence similarity 131, member A [Source:HGNC
4	GET4	1.39	1e-09	2e-07	1 x 19 golgi to ER traffic protein 4 homolog (S. cerevisiae) [Source:HC
5	NRSN2	-1.23	1e-08	2e-07	1 x 19 neurensin 2 [Source:HGNC Symbol;Acc:HGNC:16229]
6	DNAJC4	1.3	1e-08	2e-07	1 x 19 DnaJ (Hsp40) homolog, subfamily C, member 4 [Source:HGNC
7	RFK	1.29	2e-08	6e-06	1 x 23 riboflavin kinase [Source:HGNC Symbol;Acc:HGNC:30324]
8	P4HB	0.48	2e-07	6e-06	1 x 20 prolyl 4-hydroxylase, beta polypeptide [Source:HGNC Symb
9	PDIA3	0.68	4e-07	9e-06	1 x 20 protein disulfide isomerase family A, member 3 [Source:HGNC
10	TRAP1	-1.11	9e-07	9e-06	1 x 18 TNF receptor-associated protein 1 [Source:HGNC Symbol;Acc:HGNC:10808]
11	E2F4	1.11	1e-06	9e-06	1 x 20 E2F transcription factor 4, p107/p130-binding [Source:HGNC
12	AP000295.9	1.1	1e-06	9e-06	3 x 21
13	UBQLN1	1	2e-06	2e-05	1 x 21 ubiquilin 1 [Source:HGNC Symbol;Acc:HGNC:12508]
14	ATR	1.08	2e-06	2e-05	1 x 22 ATR serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:10808]
15	IFNAR2	1.07	3e-06	5e-05	1 x 20 interferon (alpha, beta and omega) receptor 2 [Source:HGNC
16	YIPF4	1.03	6e-06	5e-05	1 x 21 Yip1 domain family, member 4 [Source:HGNC Symbol;Acc:HGNC:10808]
17	RCN1	0.5	1e-05	5e-05	1 x 23 reticulocalbin 1, EF-hand calcium binding domain [Source:HGNC
18	TMEM123	0.41	1e-05	5e-05	1 x 21 transmembrane protein 123 [Source:HGNC Symbol;Acc:HGNC:10808]
19	CAMKK2	1	1e-05	5e-05	4 x 21 calcium/calmodulin-dependent protein kinase kinase 2, beta
20	TOR2A	1	1e-05	5e-05	1 x 21 torsin family 2, member A [Source:HGNC Symbol;Acc:HGNC:10808]

p-values



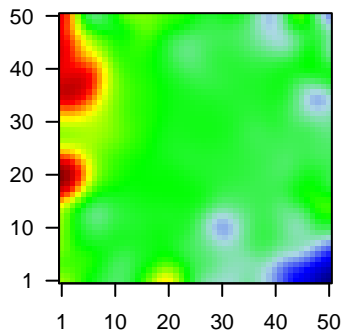
# A2\_mel

## Local Summary

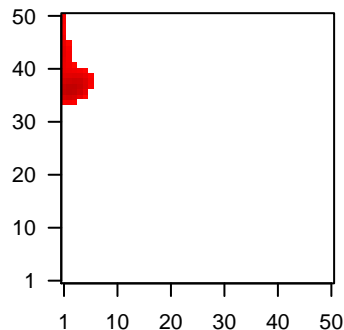
%DE = 0.74  
 # metagenes = 52  
 # genes = 666  
 # genes in genesets = 663  
  
 # genes with  $fdr < 0.1$  = 363 ( 310 + / 53 - )  
 # genes with  $fdr < 0.05$  = 302 ( 261 + / 41 - )  
 # genes with  $fdr < 0.01$  = 197 ( 171 + / 26 - )

$\langle r \rangle$  metagenes = 0.85  
 $\langle r \rangle$  genes = 0.12  
  
 $\langle FC \rangle$  = 0.29  
 $\langle \text{shrinkage-t} \rangle$  = 5.02  
 $\langle p\text{-value} \rangle$  = 0.01  
 $\langle fdr \rangle$  = 0.55

Profile



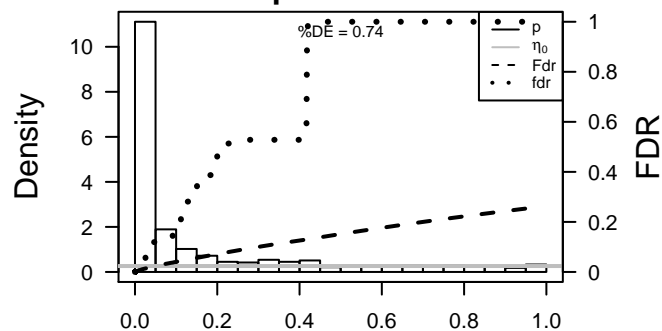
Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	M6PR	-0.85	2e-16	4e-14	3 x 41 mannose-6-phosphate receptor (cation dependent) [Source:
2	RARRES1	1.77	1e-14	2e-10	5 x 36 retinoic acid receptor responder (tazarotene induced) 1 [Sour
3	EIF4A3	0.69	1e-12	8e-10	4 x 40 eukaryotic translation initiation factor 4A3 [Source:HGNC Syn
4	ZNF30	1.57	6e-12	5e-09	4 x 37 zinc finger protein 30 [Source:HGNC Symbol;Acc:HGNC:130
5	SMPD2	1.51	3e-11	2e-08	3 x 34 sphingomyelin phosphodiesterase 2, neutral membrane (neut
6	ZFYVE19	1.46	1e-10	6e-08	1 x 47 zinc finger, FYVE domain containing 19 [Source:HGNC Synt
7	FAM71E1	1.42	5e-10	6e-08	5 x 37 family with sequence similarity 71, member E1 [Source:HGNC
8	ST6GALNAC1	1.09	9e-10	6e-08	1 x 44 ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-
9	TREX1	1.39	1e-09	3e-07	1 x 47 three prime repair exonuclease 1 [Source:HGNC Symbol;Acc
10	TOM1L1	-1.25	3e-09	5e-07	1 x 38 target of myb1 (chicken)-like 1 [Source:HGNC Symbol;Acc:H
11	CDCA7	1.33	6e-09	8e-07	1 x 49 cell division cycle associated 7 [Source:HGNC Symbol;Acc:H
12	ZDHHC20	1.3	1e-08	8e-07	4 x 37 zinc finger, DHHC-type containing 20 [Source:HGNC Symbo
13	KNTC1	1.25	3e-08	8e-07	1 x 50 kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:
14	REEP6	1.27	3e-08	8e-07	1 x 43 receptor accessory protein 6 [Source:HGNC Symbol;Acc:HGNC:
15	HDAC2	0.69	3e-08	8e-07	1 x 45 histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:48
16	MCM6	1.27	3e-08	2e-06	1 x 50 minichromosome maintenance complex component 6 [Source:
17	NCAPH2	1.25	5e-08	2e-06	1 x 50 non-SMC condensin II complex, subunit H2 [Source:HGNC S
18	NUDT5	-1.14	5e-08	4e-06	1 x 39 nudix (nucleoside diphosphate linked moiety X)-type motif 5 [
19	RAD51	1.23	8e-08	4e-06	1 x 50 RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:981
20	CD58	-1.1	1e-07	4e-06	1 x 43 CD58 molecule [Source:HGNC Symbol;Acc:HGNC:1688]

p-values



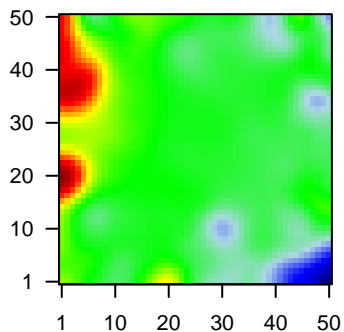
# A2\_mel

## Local Summary

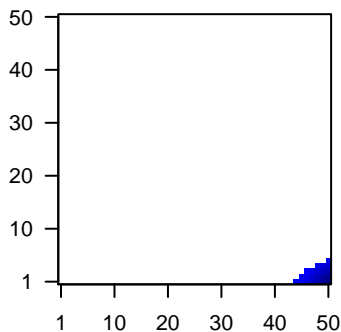
%DE = 0.82  
 # metagenes = 22  
 # genes = 366  
 # genes in genesets = 366  
  
 # genes with  $fdr < 0.1$  = 217 ( 43 + / 174 - )  
 # genes with  $fdr < 0.05$  = 155 ( 33 + / 122 - )  
 # genes with  $fdr < 0.01$  = 80 ( 18 + / 62 - )

$\langle r \rangle$  metagenes = 0.96  
 $\langle r \rangle$  genes = 0.18  
  
 $\langle FC \rangle = -0.28$   
 $\langle \text{shrinkage-t} \rangle = -4.72$   
 $\langle p\text{-value} \rangle = 0.01$   
 $\langle fdr \rangle = 0.61$

Profile



Spot



## Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ANKRD28	-1.67	2e-16	4e-15	50 x 5 ankyrin repeat domain 28 [Source:HGNC Symbol;Acc:HGNC
2	CRYAB	-1.82	2e-16	4e-15	50 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:HGNC:2389]
3	LGALS1	-1.68	2e-16	4e-15	50 x 1 lectin, galactoside-binding, soluble, 1 [Source:HGNC Symbol
4	PMP22	-1.42	2e-16	4e-15	48 x 1 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC
5	CNN3	-0.71	1e-14	2e-12	47 x 1 calponin 3, acidic [Source:HGNC Symbol;Acc:HGNC:2157]
6	MARCKS	-0.81	6e-14	2e-12	46 x 1 myristoylated alanine-rich protein kinase C substrate [Source
7	TGIF1	-1.46	7e-14	9e-12	50 x 1 TGFB-induced factor homeobox 1 [Source:HGNC Symbol;Ac
8	FABP3	-1.44	2e-13	4e-10	50 x 1 fatty acid binding protein 3, muscle and heart [Source:HGNC
9	RAI14	-1.18	6e-12	1e-09	44 x 1 retinoic acid induced 14 [Source:HGNC Symbol;Acc:HGNC:1
10	PLOD2	-1.36	2e-11	4e-09	49 x 3 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 [Source
11	ITGB5	1.47	1e-10	4e-09	49 x 3 integrin, beta 5 [Source:HGNC Symbol;Acc:HGNC:6160]
12	STAM	-1.32	1e-10	2e-07	50 x 3 signal transducing adaptor molecule (SH3 domain and ITAM)
13	SYNE1	-0.88	6e-09	2e-07	49 x 1 spectrin repeat containing, nuclear envelope 1 [Source:HGNC
14	ARMCS9	-1.16	7e-09	2e-07	50 x 3 armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HG
15	PRNP	-1.23	9e-09	1e-06	47 x 2 prion protein [Source:HGNC Symbol;Acc:HGNC:9449]
16	SLAIN2	1.25	5e-08	1e-06	50 x 4 SLAIN motif family, member 2 [Source:HGNC Symbol;Acc:HC
17	TAGLN2	-1.03	5e-08	1e-06	50 x 2 transgelin 2 [Source:HGNC Symbol;Acc:HGNC:11554]
18	PTPRZ1	1.23	7e-08	1e-05	50 x 1 protein tyrosine phosphatase, receptor-type, Z polypeptide 1
19	DCBLD2	-1.09	2e-07	1e-05	47 x 1 discoidin, CUB and LCCL domain containing 2 [Source:HGNC
20	NOV	-1.08	6e-07	1e-05	50 x 1 nephroblastoma overexpressed [Source:HGNC Symbol;Acc:t

p-values

