

Category	Functional Category	expected genes	detected genes	significance value
KEGG	Metabolic pathways	1000	1056	7,88E-09
KEGG	Pathways in cancer	293	319	1,10E-06
KEGG	Focal adhesion	179	197	5,44E-05
KEGG	Axon guidance	115	128	1,91E-04
KEGG	Calcium signaling pathway	159	174	3,76E-04
KEGG	MAPK signaling pathway	238	257	4,60E-04
KEGG	Chemokine signaling pathway	169	184	4,60E-04
KEGG	Endocytosis	183	199	4,60E-04
KEGG	Wnt signaling pathway	135	148	6,37E-04
KEGG	Cytokine-cytokine receptor interaction	237	254	1,09E-03
KEGG	Neurotrophin signaling pathway	113	124	1,09E-03
KEGG	Chagas disease	93	103	1,31E-03
KEGG	Lysosome	108	119	1,48E-03
KEGG	Melanogenesis	91	101	1,48E-03
KEGG	Insulin signaling pathway	122	134	1,55E-03
KEGG	Peroxisome	70	78	1,55E-03
KEGG	Gastric acid secretion	66	74	2,28E-03
KEGG	Long-term potentiation	63	70	3,44E-03
KEGG	Epithelial cell signaling in Helicobacter pylori infection	61	68	3,96E-03
KEGG	T cell receptor signaling pathway	96	106	3,96E-03
KEGG	Ubiquitin mediated proteolysis	124	135	4,53E-03
KEGG	ErbB signaling pathway	78	86	4,75E-03
KEGG	Cell adhesion molecules (CAMs)	121	131	5,59E-03
KEGG	ECM-receptor interaction	75	83	5,59E-03
KEGG	Small cell lung cancer	75	83	5,59E-03
KEGG	TGF-beta signaling pathway	76	84	5,59E-03
KEGG	Tight junction	120	130	5,63E-03
KEGG	Purine metabolism	144	155	6,73E-03
KEGG	Spliceosome	114	124	8,89E-03
KEGG	Hedgehog signaling pathway	50	56	1,09E-02
KEGG	B cell receptor signaling pathway	67	74	1,18E-02
KEGG	Basal cell carcinoma	49	55	1,18E-02
KEGG	Arginine and proline metabolism	48	54	1,26E-02
KEGG	Amyotrophic lateral sclerosis (ALS)	47	53	1,30E-02
KEGG	Chronic myeloid leukemia	65	72	1,30E-02
KEGG	Regulation of actin cytoskeleton	193	205	1,30E-02
KEGG	Prostate cancer	79	87	1,42E-02
KEGG	Apoptosis	79	86	1,49E-02
KEGG	Hematopoietic cell lineage	79	86	1,49E-02
KEGG	Leukocyte transendothelial migration	105	114	1,53E-02
KEGG	Pancreatic cancer	63	69	1,53E-02
KEGG	Renal cell carcinoma	63	69	1,53E-02
KEGG	p53 signaling pathway	62	68	1,65E-02
KEGG	Vascular smooth muscle contraction	104	112	1,67E-02
KEGG	Pyrimidine metabolism	88	96	1,98E-02
KEGG	Notch signaling pathway	42	47	2,06E-02
KEGG	Glioma	58	64	2,28E-02
KEGG	Glycolysis / Gluconeogenesis	57	63	2,47E-02
KEGG	Fc gamma R-mediated phagocytosis	85	92	2,54E-02
KEGG	Vasopressin-regulated water reabsorption	39	44	2,63E-02
KEGG	NOD-like receptor signaling pathway	55	61	2,80E-02
KEGG	Phosphatidylinositol signaling system	70	76	2,83E-02
KEGG	Fatty acid metabolism	38	42	3,13E-02
KEGG	Amoebiasis	94	101	3,26E-02
KEGG	Phagosome	141	150	3,26E-02
KEGG	Gap junction	80	87	3,43E-02
KEGG	Salivary secretion	79	86	3,67E-02
KEGG	Leishmaniasis	65	71	4,02E-02
KEGG	Cell cycle	114	122	4,09E-02

Category	Functional Category	expected	detected	significance
miRNA	hsa-miR-29c	213	226	3,07E-03
miRNA	hsa-miR-30c	250	264	3,07E-03
miRNA	hsa-miR-29a	205	217	3,53E-03
miRNA	hsa-miR-103	146	156	9,43E-03
miRNA	hsa-miR-29b	209	221	1,10E-02
miRNA	hsa-miR-30a	235	248	1,10E-02
miRNA	hsa-miR-744	136	145	1,10E-02
miRNA	hsa-miR-615-5p	259	272	1,18E-02
miRNA	hsa-miR-31	125	133	1,85E-02
miRNA	hsa-miR-30d	244	256	2,14E-02
miRNA	hsa-miR-135a	115	123	2,29E-02
miRNA	hsa-miR-30e	233	244	2,29E-02
miRNA	hsa-miR-326	113	120	2,29E-02
miRNA	hsa-miR-518b	237	249	2,29E-02
miRNA	hsa-miR-886-5p	182	192	2,29E-02
miRNA	hsa-let-7i	253	265	2,53E-02
miRNA	hsa-miR-520e	277	289	2,53E-02
miRNA	hsa-miR-30b	250	262	2,58E-02
miRNA	hsa-miR-548a-3p	320	333	2,59E-02
miRNA	hsa-miR-132	136	144	2,64E-02
miRNA	hsa-miR-135b	104	111	2,64E-02
miRNA	hsa-miR-18a	137	145	2,64E-02
miRNA	hsa-miR-27a	169	178	2,64E-02
miRNA	hsa-miR-423-5p	102	109	2,64E-02
miRNA	hsa-miR-520g	267	279	2,64E-02
miRNA	hsa-miR-520h	269	281	2,64E-02
miRNA	hsa-let-7e	239	250	3,11E-02
miRNA	hsa-let-7f	236	247	3,11E-02
miRNA	hsa-let-7g	260	271	3,11E-02
miRNA	hsa-miR-139-5p	160	169	3,11E-02
miRNA	hsa-miR-886-3p	161	170	3,11E-02
miRNA	hsa-miR-133a	157	165	3,46E-02
miRNA	hsa-miR-671-3p	157	165	3,46E-02
miRNA	hsa-miR-675	91	97	4,14E-02
miRNA	hsa-miR-19a	203	212	4,30E-02
miRNA	hsa-miR-565	90	96	4,30E-02
miRNA	hsa-miR-516a-3p	201	210	4,62E-02
miRNA	hsa-miR-27b	174	183	4,77E-02
miRNA	hsa-miR-663	174	182	4,91E-02