

## ПРИЛОЖЕНИЯ

к статье О.А. Подколотной, Н.Н. Твердохлеб, Н.Л. Подколотного «Выявление и анализ динамических паттернов суточной экспрессии генов млекопитающих»

### Описание таблиц S1–S19

Анализ обогащенности групп генов терминами GO выполнен с помощью системы DAVID. Представлены результаты с p-value <0.05 по критерию Бенджамини–Хохберга с поправкой на множественность выбора.

Синусоидальный паттерн суточной экспрессии	
Название таблицы	Группа / GO категория
S1 (INTERSECT_COS_CC)	intersectCos (Cellular Component)
S2 (INTERSECT_COS_BP)	intersectCos (Biological Process)
S3 (INTERSECT_COS_BP_KEGG)	intersectCos (KEGG Pathway)
S4 (LIV(only)_COS_CC)	L(only)COS (Cellular Component)
S5 (LIV(only)_COS_BP)	L(only)COS (Biological Process)
S6 (LIV(only)_COS_KEGG)	L(only)COS (KEGG Pathway)
S7 (KID(only)_COS_CC)	K(only)COS (Cellular Component)
S8 (KID(only)_COS_BP_FAT)	K(only)COS (Biological Process)
S9 (KID(only)_COS_KEGG)	K(only)COS (KEGG Pathway)
Импульсный паттерн суточной экспрессии	
S10 (INTERSECT_IMP_CC)	intersectImp (Cellular Component)
S11 (INTERSECT_IMP_BP)	intersectImp (Biological Process)
S12 (INTERSECT_IMP_KEGG)	intersectImp (KEGG Pathway)
S13 (INTERSECT_IMP_KEYWORDS)	intersectImp (KEYWORDS)
S14 (Kid(only)_Imp_CC)	K(only)IMP (Cellular Component)
S15 (Kid(only)_Imp_BP)	K(only)IMP (Biological Process)
S16 (Kid(only)_Imp_KEGG)	K(only)IMP (KEGG Pathway)
S17 (LIV(only)_IMP_CC)	L(only)IMP (Cellular Component)
S18 (LIV(only)_IMP_BP)	L(only)IMP (Biological Process)
S19 (LIV(only)_IMP_KEGG)	L(only)IMP (KEGG Pathway)

**Таблица S1**

Category	Term	Count	%	PValue	List To	Pop Hit	Pop Tot	Fold Enr	Bonferroni	Benjamini	FDR
GOTERM_C	GO:0044424~intracellular part	109	88,62	2,33E-08	121	13479	19662	1,31	7,21E-06	<b>2,40E-06</b>	3,1E-05
GOTERM_C	GO:0043226~organelle	106	86,18	1,79E-08	121	12768	19662	1,35	5,54E-06	<b>2,77E-06</b>	2,4E-05
GOTERM_C	GO:0005622~intracellular	112	91,06	9,33E-09	121	14047	19662	1,30	2,89E-06	<b>2,89E-06</b>	1,3E-05
GOTERM_C	GO:0043229~intracellular organelle	98	79,67	5,80E-07	121	11735	19662	1,36	1,80E-04	<b>4,49E-05</b>	0,00078
GOTERM_C	GO:0043227~membrane-bounded organelle	96	78,05	4,98E-06	121	11760	19662	1,33	1,54E-03	<b>3,09E-04</b>	0,00669
GOTERM_C	GO:0005634~nucleus	64	52,03	2,59E-05	121	6713	19662	1,55	8,01E-03	<b>1,15E-03</b>	0,03483
GOTERM_C	GO:0043231~intracellular membrane-bounded organ	88	71,54	2,45E-05	121	10626	19662	1,35	7,57E-03	<b>1,27E-03</b>	0,03293
GOTERM_C	GO:0031981~nuclear lumen	38	30,89	3,45E-05	121	3139	19662	1,97	1,06E-02	<b>1,33E-03</b>	0,04627
GOTERM_C	GO:0044464~cell part	118	95,93	7,03E-05	121	17135	19662	1,12	2,15E-02	<b>2,18E-03</b>	0,09432
GOTERM_C	GO:0044428~nuclear part	41	33,33	6,71E-05	121	3625	19662	1,84	2,06E-02	<b>2,31E-03</b>	0,09002
GOTERM_C	GO:0070013~intracellular organelle lumen	40	32,52	9,44E-05	121	3548	19662	1,83	2,88E-02	<b>2,44E-03</b>	0,12672
GOTERM_C	GO:0043233~organelle lumen	40	32,52	1,02E-04	121	3561	19662	1,83	3,12E-02	<b>2,44E-03</b>	0,13743
GOTERM_C	GO:0005623~cell	118	95,93	8,74E-05	121	17173	19662	1,12	2,67E-02	<b>2,46E-03</b>	0,11726
GOTERM_C	GO:0005654~nucleoplasm	30	24,39	1,21E-04	121	2325	19662	2,10	3,67E-02	<b>2,67E-03</b>	0,16193
GOTERM_C	GO:0031974~membrane-enclosed lumen	40	32,52	1,54E-04	121	3628	19662	1,79	4,67E-02	<b>3,18E-03</b>	0,20689
GOTERM_C	GO:0005737~cytoplasm	84	68,29	2,28E-04	121	10431	19662	1,31	6,83E-02	<b>4,16E-03</b>	0,30619
GOTERM_C	GO:0043232~intracellular non-membrane-bounded o	43	34,96	2,23E-04	121	4096	19662	1,71	6,68E-02	<b>4,31E-03</b>	0,29925
GOTERM_C	GO:0043228~non-membrane-bounded organelle	43	34,96	2,23E-04	121	4096	19662	1,71	6,68E-02	<b>4,31E-03</b>	0,29925
GOTERM_C	GO:0005829~cytosol	25	20,33	9,90E-04	121	2011	19662	2,02	2,64E-01	<b>1,69E-02</b>	1,32104
GOTERM_C	GO:0005856~cytoskeleton	24	19,51	2,56E-03	121	2032	19662	1,92	5,49E-01	<b>4,10E-02</b>	3,38705

**Таблица S2**

Category	Term	Count	%	PValue	List Tc	Pop Hit	Pop Tc	Fold Enri	Bonferroni	<b>Benjamini</b>	FDR
GOTERM_BP	GO:0032922~circadian regulation of gene expression	13	10,57	4,08E-15	117	61	17911	32,62	1,04E-11	<b>1,04E-11</b>	7,25E-12
GOTERM_BP	GO:0007623~circadian rhythm	17	13,82	3,56E-13	117	207	17911	12,57	8,97E-10	<b>4,49E-10</b>	6,29E-10
GOTERM_BP	GO:0048511~rhythmic process	20	16,26	3,14E-12	117	372	17911	8,23	7,92E-09	<b>2,64E-09</b>	5,55E-09
GOTERM_BP	GO:0042752~regulation of circadian rhythm	12	9,76	1,29E-10	117	110	17911	16,70	3,26E-07	<b>8,15E-08</b>	2,28E-07
GOTERM_BP	GO:0006366~transcription from RNA polymerase II promoter	29	23,58	2,85E-06	117	1700	17911	2,61	7,16E-03	<b>1,44E-03</b>	5,03E-03
GOTERM_BP	GO:0043401~steroid hormone mediated signaling pathway	9	7,32	6,88E-06	117	153	17911	9,01	1,72E-02	<b>2,47E-03</b>	1,21E-02
GOTERM_BP	GO:0006357~regulation of transcription from RNA polymerase II p	29	23,58	6,47E-06	117	1774	17911	2,50	1,62E-02	<b>2,71E-03</b>	1,14E-02
GOTERM_BP	GO:0009755~hormone-mediated signaling pathway	9	7,32	2,53E-05	117	183	17911	7,53	6,18E-02	<b>7,94E-03</b>	4,47E-02
GOTERM_BP	GO:0006351~transcription, DNA-templated	39	31,71	4,63E-05	117	3129	17911	1,91	1,10E-01	<b>1,29E-02</b>	8,17E-02
GOTERM_BP	GO:2001141~regulation of RNA biosynthetic process	40	32,52	1,84E-04	117	3458	17911	1,77	3,71E-01	<b>2,29E-02</b>	3,24E-01
GOTERM_BP	GO:0006732~coenzyme metabolic process	10	8,13	1,78E-04	117	308	17911	4,97	3,62E-01	<b>2,34E-02</b>	3,14E-01
GOTERM_BP	GO:0018130~heterocycle biosynthetic process	45	36,59	1,07E-04	117	4009	17911	1,72	2,36E-01	<b>2,42E-02</b>	1,88E-01
GOTERM_BP	GO:0019438~aromatic compound biosynthetic process	45	36,59	1,18E-04	117	4025	17911	1,71	2,57E-01	<b>2,44E-02</b>	2,07E-01
GOTERM_BP	GO:1903506~regulation of nucleic acid-templated transcription	40	32,52	1,77E-04	117	3452	17911	1,77	3,60E-01	<b>2,45E-02</b>	3,12E-01
GOTERM_BP	GO:0071383~cellular response to steroid hormone stimulus	9	7,32	9,90E-05	117	222	17911	6,21	2,21E-01	<b>2,46E-02</b>	1,75E-01
GOTERM_BP	GO:0006355~regulation of transcription, DNA-templated	40	32,52	1,74E-04	117	3449	17911	1,78	3,55E-01	<b>2,54E-02</b>	3,06E-01
GOTERM_BP	GO:0042180~cellular ketone metabolic process	8	6,50	1,34E-04	117	173	17911	7,08	2,86E-01	<b>2,56E-02</b>	2,36E-01
GOTERM_BP	GO:0048545~response to steroid hormone	11	8,94	1,47E-04	117	370	17911	4,55	3,09E-01	<b>2,61E-02</b>	2,59E-01
GOTERM_BP	GO:0051252~regulation of RNA metabolic process	41	33,33	1,73E-04	117	3575	17911	1,76	3,54E-01	<b>2,69E-02</b>	3,06E-01
GOTERM_BP	GO:0051254~positive regulation of RNA metabolic process	22	17,89	2,28E-04	117	1397	17911	2,41	4,38E-01	<b>2,70E-02</b>	4,02E-01
GOTERM_BP	GO:0034654~nucleobase-containing compound biosynthetic proces	44	35,77	1,65E-04	117	3952	17911	1,70	3,41E-01	<b>2,74E-02</b>	2,91E-01
GOTERM_BP	GO:0010629~negative regulation of gene expression	24	19,51	2,72E-04	117	1628	17911	2,26	4,97E-01	<b>3,07E-02</b>	4,80E-01
GOTERM_BP	GO:1902680~positive regulation of RNA biosynthetic process	21	17,07	3,71E-04	117	1343	17911	2,39	6,08E-01	<b>3,29E-02</b>	6,54E-01
GOTERM_BP	GO:1902679~negative regulation of RNA biosynthetic process	20	16,26	3,62E-04	117	1237	17911	2,48	5,98E-01	<b>3,32E-02</b>	6,36E-01
GOTERM_BP	GO:0043153~entrainment of circadian clock by photoperiod	4	3,25	3,23E-04	117	21	17911	29,16	5,57E-01	<b>3,34E-02</b>	5,69E-01
GOTERM_BP	GO:0045893~positive regulation of transcription, DNA-templated	21	17,07	3,57E-04	117	1339	17911	2,40	5,94E-01	<b>3,41E-02</b>	6,29E-01
GOTERM_BP	GO:1903508~positive regulation of nucleic acid-templated transcrip	21	17,07	3,57E-04	117	1339	17911	2,40	5,94E-01	<b>3,41E-02</b>	6,29E-01
GOTERM_BP	GO:0097659~nucleic acid-templated transcription	40	32,52	3,19E-04	117	3548	17911	1,73	5,52E-01	<b>3,44E-02</b>	5,62E-01
GOTERM_BP	GO:0032774~RNA biosynthetic process	40	32,52	3,53E-04	117	3565	17911	1,72	5,89E-01	<b>3,50E-02</b>	6,21E-01
GOTERM_BP	GO:0009648~photoperiodism	4	3,25	4,85E-04	117	24	17911	25,51	7,06E-01	<b>3,75E-02</b>	8,53E-01
GOTERM_BP	GO:2000112~regulation of cellular macromolecule biosynthetic pro	42	34,15	4,74E-04	117	3875	17911	1,66	6,98E-01	<b>3,78E-02</b>	8,34E-01
GOTERM_BP	GO:0006733~oxidoreduction coenzyme metabolic process	7	5,69	4,50E-04	117	151	17911	7,10	6,79E-01	<b>3,84E-02</b>	7,92E-01
GOTERM_BP	GO:0010468~regulation of gene expression	45	36,59	4,69E-04	117	4268	17911	1,61	6,93E-01	<b>3,86E-02</b>	8,24E-01
GOTERM_BP	GO:0009649~entrainment of circadian clock	4	3,25	5,49E-04	117	25	17911	24,49	7,49E-01	<b>3,99E-02</b>	9,64E-01
GOTERM_BP	GO:0051253~negative regulation of RNA metabolic process	20	16,26	5,67E-04	117	1283	17911	2,39	7,61E-01	<b>4,01E-02</b>	9,97E-01
GOTERM_BP	GO:0006082~organic acid metabolic process	16	13,01	5,42E-04	117	878	17911	2,79	7,45E-01	<b>4,06E-02</b>	9,53E-01
GOTERM_BP	GO:0010558~negative regulation of macromolecule biosynthetic pr	22	17,89	6,23E-04	117	1506	17911	2,24	7,92E-01	<b>4,16E-02</b>	1,09E+00

GOTERM_BP_GO:2000323~negative regulation of glucocorticoid receptor signalin	3	2,44	6,13E-04	117	6	17911	76,54	7,87E-01	<b>4,20E-02</b>	1,08E+00
GOTERM_BP_GO:0014070~response to organic cyclic compound	17	13,82	7,53E-04	117	1005	17911	2,59	8,50E-01	<b>4,32E-02</b>	1,32E+00
GOTERM_BP_GO:0010556~regulation of macromolecule biosynthetic process	42	34,15	7,77E-04	117	3966	17911	1,62	8,59E-01	<b>4,36E-02</b>	1,36E+00
GOTERM_BP_GO:0044283~small molecule biosynthetic process	11	8,94	7,51E-04	117	455	17911	3,70	8,49E-01	<b>4,41E-02</b>	1,32E+00
GOTERM_BP_GO:0010565~regulation of cellular ketone metabolic process	6	4,88	6,85E-04	117	108	17911	8,50	8,22E-01	<b>4,44E-02</b>	1,20E+00
GOTERM_BP_GO:0045892~negative regulation of transcription, DNA-templated	19	15,45	7,42E-04	117	1207	17911	2,41	8,46E-01	<b>4,46E-02</b>	1,30E+00
GOTERM_BP_GO:0048641~regulation of skeletal muscle tissue development	5	4,07	8,83E-04	117	66	17911	11,60	8,92E-01	<b>4,54E-02</b>	1,55E+00
GOTERM_BP_GO:0051171~regulation of nitrogen compound metabolic process	44	35,77	7,37E-04	117	4221	17911	1,60	8,44E-01	<b>4,54E-02</b>	1,29E+00
GOTERM_BP_GO:0051186~cofactor metabolic process	10	8,13	7,20E-04	117	373	17911	4,10	8,37E-01	<b>4,55E-02</b>	1,26E+00
GOTERM_BP_GO:0032870~cellular response to hormone stimulus	12	9,76	8,75E-04	117	549	17911	3,35	8,90E-01	<b>4,59E-02</b>	1,53E+00
GOTERM_BP_GO:2000113~negative regulation of cellular macromolecule biosynt	21	17,07	9,21E-04	117	1443	17911	2,23	9,02E-01	<b>4,63E-02</b>	1,61E+00
GOTERM_BP_GO:0009725~response to hormone	15	12,20	8,64E-04	117	822	17911	2,79	8,87E-01	<b>4,63E-02</b>	1,52E+00
GOTERM_BP_GO:1903507~negative regulation of nucleic acid-templated transcri	19	15,45	8,56E-04	117	1222	17911	2,38	8,85E-01	<b>4,68E-02</b>	1,50E+00
GOTERM_BP_GO:0070887~cellular response to chemical stimulus	31	25,20	9,70E-04	117	2607	17911	1,82	9,13E-01	<b>4,78E-02</b>	1,70E+00
GOTERM_BP_GO:0031327~negative regulation of cellular biosynthetic process	22	17,89	1,01E-03	117	1564	17911	2,15	9,22E-01	<b>4,89E-02</b>	1,78E+00
GOTERM_BP_GO:0019216~regulation of lipid metabolic process	9	7,32	1,05E-03	117	316	17911	4,36	9,29E-01	<b>4,96E-02</b>	1,84E+00

### Таблица S3

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Tot	Fold Enrich	Bonferroni	<b>Benjamini</b>	FDR
KEGG_PATH	mmu04710:Circadian rhythm	9	7,32	5,64E-11	61	31	7720	36,74	6,54E-09	<b>6,54E-09</b>	6,43E-08

**Таблица S4**

Category	Term	Count	%	PValue	List To Pop	Hit Pop	Tot Pop	Fold En	Bonferroni	Benjamini	FDR
GOTERM_CC_	GO:0005829~cytosol	116	18,18	4,7E-15	599	1784	19662	2,13	2,36E-12	<b>2,36E-12</b>	6,73E-12
GOTERM_CC_	GO:0005737~cytoplasm	285	44,67	1,1E-12	599	6631	19662	1,41	5,67E-10	<b>2,83E-10</b>	1,62E-09
GOTERM_CC_	GO:0070062~extracellular exosome	140	21,94	6,4E-11	599	2674	19662	1,72	3,26E-08	<b>1,09E-08</b>	9,30E-08
GOTERM_CC_	GO:0016020~membrane	285	44,67	8,7E-10	599	6998	19662	1,34	4,40E-07	<b>1,10E-07</b>	1,26E-06
GOTERM_CC_	GO:0005783~endoplasmic reticulum	82	12,85	1,1E-09	599	1323	19662	2,03	5,77E-07	<b>1,15E-07</b>	1,64E-06
GOTERM_CC_	GO:0005739~mitochondrion	96	15,05	7,6E-09	599	1721	19662	1,83	3,83E-06	<b>6,39E-07</b>	1,09E-05
GOTERM_CC_	GO:0043231~intracellular membrane-bounded organelle	54	8,46	1,2E-08	599	751	19662	2,36	5,96E-06	<b>8,51E-07</b>	1,70E-05
GOTERM_CC_	GO:0005794~Golgi apparatus	68	10,66	8,0E-07	599	1190	19662	1,88	4,03E-04	<b>5,04E-05</b>	1,15E-03
GOTERM_CC_	GO:0005789~endoplasmic reticulum membrane	47	7,37	1,3E-06	599	710	19662	2,17	6,48E-04	<b>7,20E-05</b>	1,85E-03
GOTERM_CC_	GO:0005654~nucleoplasm	91	14,26	2,8E-05	599	1935	19662	1,54	1,43E-02	<b>1,43E-03</b>	4,09E-02
GOTERM_CC_	GO:0048471~perinuclear region of cytoplasm	40	6,27	1,7E-04	599	692	19662	1,90	8,46E-02	<b>7,34E-03</b>	2,52E-01
GOTERM_CC_	GO:0045121~membrane raft	21	3,29	1,6E-04	599	262	19662	2,63	7,89E-02	<b>7,45E-03</b>	2,34E-01
GOTERM_CC_	GO:0016324~apical plasma membrane	23	3,61	4,8E-04	599	328	19662	2,30	2,14E-01	<b>1,83E-02</b>	6,84E-01
GOTERM_CC_	GO:0043234~protein complex	35	5,49	9,0E-04	599	628	19662	1,83	3,66E-01	<b>3,20E-02</b>	1,29E+00

**Таблица S5**

Category	Term	Count	%	PValue	List T	Pop Hit	Pop Tot	Fold En	Bonferroni	Benjamini	FDR
GOTERM_BP_	GO:0006082~organic acid metabolic process	86	13,48	2,8E-20	577	878	17911	3,04	1,7E-16	<b>1,7E-16</b>	5,5E-17
GOTERM_BP_	GO:0043436~oxoacid metabolic process	79	12,38	6,4E-19	577	797	17911	3,08	3,8E-15	<b>1,9E-15</b>	1,2E-15
GOTERM_BP_	GO:0019752~carboxylic acid metabolic process	78	12,23	1,5E-18	577	791	17911	3,06	8,8E-15	<b>2,9E-15</b>	2,9E-15
GOTERM_BP_	GO:0044712~single-organism catabolic process	67	10,50	9,6E-15	577	715	17911	2,91	5,7E-11	<b>1,4E-11</b>	1,9E-11
GOTERM_BP_	GO:0032787~monocarboxylic acid metabolic process	56	8,78	9,1E-14	577	553	17911	3,14	5,4E-10	<b>1,1E-10</b>	1,8E-10
GOTERM_BP_	GO:0006732~coenzyme metabolic process	37	5,80	2,2E-11	577	308	17911	3,73	1,3E-07	<b>2,2E-08</b>	4,3E-08
GOTERM_BP_	GO:0051186~cofactor metabolic process	41	6,43	2,5E-11	577	373	17911	3,41	1,5E-07	<b>2,1E-08</b>	4,9E-08
GOTERM_BP_	GO:0044248~cellular catabolic process	90	14,11	2,1E-10	577	1387	17911	2,01	1,3E-06	<b>1,6E-07</b>	4,1E-07
GOTERM_BP_	GO:0044282~small molecule catabolic process	33	5,17	2,7E-10	577	273	17911	3,75	1,6E-06	<b>1,8E-07</b>	5,3E-07
GOTERM_BP_	GO:0055114~oxidation-reduction process	68	10,66	4,7E-10	577	930	17911	2,27	2,8E-06	<b>2,8E-07</b>	9,1E-07
GOTERM_BP_	GO:0044723~single-organism carbohydrate metabolic process	51	7,99	2,0E-09	577	617	17911	2,57	1,2E-05	<b>1,0E-06</b>	3,8E-06
GOTERM_BP_	GO:0005975~carbohydrate metabolic process	55	8,62	6,0E-09	577	718	17911	2,38	3,6E-05	<b>3,0E-06</b>	1,2E-05
GOTERM_BP_	GO:0005996~monosaccharide metabolic process	28	4,39	6,1E-09	577	229	17911	3,80	3,6E-05	<b>2,8E-06</b>	1,2E-05
GOTERM_BP_	GO:0044255~cellular lipid metabolic process	63	9,87	2,2E-08	577	915	17911	2,14	1,3E-04	<b>9,5E-06</b>	4,3E-05
GOTERM_BP_	GO:0006629~lipid metabolic process	76	11,91	3,7E-08	577	1217	17911	1,94	2,2E-04	<b>1,5E-05</b>	7,2E-05
GOTERM_BP_	GO:0019318~hexose metabolic process	26	4,08	4,6E-08	577	220	17911	3,67	2,7E-04	<b>1,7E-05</b>	9,0E-05
GOTERM_BP_	GO:0044283~small molecule biosynthetic process	39	6,11	8,4E-08	577	455	17911	2,66	5,0E-04	<b>2,9E-05</b>	1,6E-04
GOTERM_BP_	GO:0019637~organophosphate metabolic process	63	9,87	1,2E-07	577	957	17911	2,04	6,8E-04	<b>3,8E-05</b>	2,2E-04
GOTERM_BP_	GO:0009108~coenzyme biosynthetic process	17	2,66	1,8E-07	577	103	17911	5,12	1,1E-03	<b>5,6E-05</b>	3,5E-04
GOTERM_BP_	GO:0006796~phosphate-containing compound metabolic process	140	21,94	2,1E-07	577	2869	17911	1,51	1,2E-03	<b>6,2E-05</b>	4,0E-04
GOTERM_BP_	GO:0006793~phosphorus metabolic process	140	21,94	2,2E-07	577	2873	17911	1,51	1,3E-03	<b>6,3E-05</b>	4,3E-04
GOTERM_BP_	GO:0042592~homeostatic process	94	14,73	2,6E-07	577	1707	17911	1,71	1,5E-03	<b>6,9E-05</b>	5,0E-04
GOTERM_BP_	GO:0007584~response to nutrient	22	3,45	3,6E-07	577	180	17911	3,79	2,1E-03	<b>9,1E-05</b>	6,9E-04
GOTERM_BP_	GO:0006091~generation of precursor metabolites and energy	31	4,86	4,3E-07	577	334	17911	2,88	2,5E-03	<b>1,1E-04</b>	8,3E-04
GOTERM_BP_	GO:0009719~response to endogenous stimulus	89	13,95	4,7E-07	577	1608	17911	1,72	2,7E-03	<b>1,1E-04</b>	9,0E-04
GOTERM_BP_	GO:1901565~organonitrogen compound catabolic process	27	4,23	4,7E-07	577	265	17911	3,16	2,8E-03	<b>1,1E-04</b>	9,2E-04
GOTERM_BP_	GO:0042180~cellular ketone metabolic process	21	3,29	7,8E-07	577	173	17911	3,77	4,6E-03	<b>1,7E-04</b>	1,5E-03
GOTERM_BP_	GO:0009725~response to hormone	54	8,46	1,2E-06	577	822	17911	2,04	6,9E-03	<b>2,5E-04</b>	2,3E-03
GOTERM_BP_	GO:0010033~response to organic substance	140	21,94	1,6E-06	577	2972	17911	1,46	9,2E-03	<b>3,2E-04</b>	3,0E-03
GOTERM_BP_	GO:0055086~nucleobase-containing small molecule metabolic process	46	7,21	1,6E-06	577	657	17911	2,17	9,4E-03	<b>3,1E-04</b>	3,1E-03
GOTERM_BP_	GO:1901605~alpha-amino acid metabolic process	21	3,29	2,3E-06	577	185	17911	3,52	1,3E-02	<b>4,3E-04</b>	4,4E-03

GOTERM_BP_]GO:0006790~sulfur compound metabolic process	27	4,23	3,2E-06	577	293	17911	2,86	1,8E-02	<b>5,8E-04</b>	6,1E-03
GOTERM_BP_]GO:0016054~organic acid catabolic process	21	3,29	3,7E-06	577	191	17911	3,41	2,2E-02	<b>6,6E-04</b>	7,1E-03
GOTERM_BP_]GO:0006631~fatty acid metabolic process	31	4,86	3,8E-06	577	371	17911	2,59	2,2E-02	<b>6,6E-04</b>	7,3E-03
GOTERM_BP_]GO:0051188~cofactor biosynthetic process	18	2,82	4,3E-06	577	145	17911	3,85	2,5E-02	<b>7,2E-04</b>	8,3E-03
GOTERM_BP_]GO:0019362~pyridine nucleotide metabolic process	17	2,66	7,1E-06	577	135	17911	3,91	4,1E-02	<b>1,2E-03</b>	1,4E-02
GOTERM_BP_]GO:0046496~nicotinamide nucleotide metabolic process	17	2,66	7,1E-06	577	135	17911	3,91	4,1E-02	<b>1,2E-03</b>	1,4E-02
GOTERM_BP_]GO:1901700~response to oxygen-containing compound	87	13,64	7,4E-06	577	1670	17911	1,62	4,3E-02	<b>1,2E-03</b>	1,4E-02
GOTERM_BP_]GO:0006733~oxidoreduction coenzyme metabolic process	18	2,82	7,5E-06	577	151	17911	3,70	4,3E-02	<b>1,2E-03</b>	1,4E-02
GOTERM_BP_]GO:0010243~response to organonitrogen compound	54	8,46	7,9E-06	577	878	17911	1,91	4,5E-02	<b>1,2E-03</b>	1,5E-02
GOTERM_BP_]GO:0016053~organic acid biosynthetic process	24	3,76	8,4E-06	577	254	17911	2,93	4,8E-02	<b>1,2E-03</b>	1,6E-02
GOTERM_BP_]GO:0072524~pyridine-containing compound metabolic process	17	2,66	8,6E-06	577	137	17911	3,85	5,0E-02	<b>1,2E-03</b>	1,7E-02
GOTERM_BP_]GO:0098586~cellular response to virus	9	1,41	9,4E-06	577	34	17911	8,22	5,4E-02	<b>1,3E-03</b>	1,8E-02
GOTERM_BP_]GO:0044419~interspecies interaction between organisms	43	6,74	9,7E-06	577	639	17911	2,09	5,6E-02	<b>1,3E-03</b>	1,9E-02
GOTERM_BP_]GO:0044403~symbiosis, encompassing mutualism through parasitism	43	6,74	9,7E-06	577	639	17911	2,09	5,6E-02	<b>1,3E-03</b>	1,9E-02
GOTERM_BP_]GO:0039528~cytoplasmic pattern recognition receptor signaling	7	1,10	9,9E-06	577	17	17911	12,78	5,6E-02	<b>1,3E-03</b>	1,9E-02
GOTERM_BP_]GO:0009117~nucleotide metabolic process	41	6,43	9,9E-06	577	596	17911	2,14	5,7E-02	<b>1,3E-03</b>	1,9E-02
GOTERM_BP_]GO:0044262~cellular carbohydrate metabolic process	24	3,76	1,3E-05	577	261	17911	2,85	7,4E-02	<b>1,7E-03</b>	2,5E-02
GOTERM_BP_]GO:0006753~nucleoside phosphate metabolic process	41	6,43	1,5E-05	577	606	17911	2,10	8,2E-02	<b>1,8E-03</b>	2,8E-02
GOTERM_BP_]GO:0043434~response to peptide hormone	30	4,70	1,5E-05	577	378	17911	2,46	8,3E-02	<b>1,8E-03</b>	2,9E-02
GOTERM_BP_]GO:0016052~carbohydrate catabolic process	16	2,51	1,6E-05	577	128	17911	3,88	8,9E-02	<b>1,9E-03</b>	3,0E-02
GOTERM_BP_]GO:0016310~phosphorylation	101	15,83	1,6E-05	577	2063	17911	1,52	9,1E-02	<b>1,9E-03</b>	3,1E-02
GOTERM_BP_]GO:0009991~response to extracellular stimulus	34	5,33	1,7E-05	577	462	17911	2,28	9,7E-02	<b>2,0E-03</b>	3,4E-02
GOTERM_BP_]GO:0033036~macromolecule localization	125	19,59	1,8E-05	577	2705	17911	1,43	1,0E-01	<b>2,1E-03</b>	3,6E-02
GOTERM_BP_]GO:0006820~anion transport	32	5,02	1,9E-05	577	423	17911	2,35	1,1E-01	<b>2,1E-03</b>	3,7E-02
GOTERM_BP_]GO:0032868~response to insulin	22	3,45	2,2E-05	577	233	17911	2,93	1,2E-01	<b>2,4E-03</b>	4,2E-02
GOTERM_BP_]GO:0031667~response to nutrient levels	32	5,02	2,6E-05	577	430	17911	2,31	1,4E-01	<b>2,8E-03</b>	5,1E-02
GOTERM_BP_]GO:0006461~protein complex assembly	69	10,82	2,7E-05	577	1277	17911	1,68	1,5E-01	<b>2,8E-03</b>	5,2E-02
GOTERM_BP_]GO:0070271~protein complex biogenesis	69	10,82	2,8E-05	577	1278	17911	1,68	1,5E-01	<b>2,8E-03</b>	5,3E-02
GOTERM_BP_]GO:0046394~carboxylic acid biosynthetic process	22	3,45	2,8E-05	577	237	17911	2,88	1,5E-01	<b>2,9E-03</b>	5,5E-02
GOTERM_BP_]GO:0009116~nucleoside metabolic process	27	4,23	3,0E-05	577	333	17911	2,52	1,6E-01	<b>3,0E-03</b>	5,9E-02
GOTERM_BP_]GO:0039530~MDA-5 signaling pathway	5	0,78	3,4E-05	577	7	17911	22,17	1,8E-01	<b>3,4E-03</b>	6,6E-02
GOTERM_BP_]GO:1901606~alpha-amino acid catabolic process	11	1,72	3,5E-05	577	64	17911	5,34	1,9E-01	<b>3,4E-03</b>	6,7E-02
GOTERM_BP_]GO:0039531~regulation of viral-induced cytoplasmic pattern	6	0,94	3,5E-05	577	13	17911	14,33	1,9E-01	<b>3,3E-03</b>	6,8E-02



GOTERM_BP_]GO:0006006~glucose metabolic process	19	2,98	3,8E-05	577	188	17911	3,14	2,0E-01	<b>3,5E-03</b>	7,3E-02
GOTERM_BP_]GO:1901652~response to peptide	31	4,86	3,8E-05	577	418	17911	2,30	2,0E-01	<b>3,5E-03</b>	7,4E-02
GOTERM_BP_]GO:0019320~hexose catabolic process	7	1,10	3,9E-05	577	21	17911	10,35	2,0E-01	<b>3,5E-03</b>	7,5E-02
GOTERM_BP_]GO:0044724~single-organism carbohydrate catabolic process	14	2,19	3,9E-05	577	107	17911	4,06	2,1E-01	<b>3,5E-03</b>	7,6E-02
GOTERM_BP_]GO:0016032~viral process	39	6,11	4,0E-05	577	589	17911	2,06	2,1E-01	<b>3,5E-03</b>	7,7E-02
GOTERM_BP_]GO:0060249~anatomical structure homeostasis	27	4,23	4,1E-05	577	339	17911	2,47	2,2E-01	<b>3,6E-03</b>	8,0E-02
GOTERM_BP_]GO:0044764~multi-organism cellular process	39	6,11	4,7E-05	577	594	17911	2,04	2,4E-01	<b>4,0E-03</b>	9,0E-02
GOTERM_BP_]GO:0048524~positive regulation of viral process	12	1,88	4,9E-05	577	80	17911	4,66	2,5E-01	<b>4,1E-03</b>	9,4E-02
GOTERM_BP_]GO:0006811~ion transport	71	11,13	5,3E-05	577	1354	17911	1,63	2,7E-01	<b>4,4E-03</b>	1,0E-01
GOTERM_BP_]GO:0071375~cellular response to peptide hormone stimulus	22	3,45	5,5E-05	577	248	17911	2,75	2,8E-01	<b>4,5E-03</b>	1,1E-01
GOTERM_BP_]GO:0034330~cell junction organization	19	2,98	8,0E-05	577	199	17911	2,96	3,7E-01	<b>6,4E-03</b>	1,5E-01
GOTERM_BP_]GO:1901698~response to nitrogen compound	56	8,78	8,0E-05	577	1004	17911	1,73	3,8E-01	<b>6,4E-03</b>	1,6E-01
GOTERM_BP_]GO:0048878~chemical homeostasis	60	9,40	8,0E-05	577	1101	17911	1,69	3,8E-01	<b>6,3E-03</b>	1,6E-01
GOTERM_BP_]GO:1901657~glycosyl compound metabolic process	27	4,23	8,1E-05	577	353	17911	2,37	3,8E-01	<b>6,2E-03</b>	1,6E-01
GOTERM_BP_]GO:0009119~ribonucleoside metabolic process	25	3,92	8,1E-05	577	313	17911	2,48	3,8E-01	<b>6,2E-03</b>	1,6E-01
GOTERM_BP_]GO:0043903~regulation of symbiosis, encompassing mutuali	26	4,08	8,5E-05	577	334	17911	2,42	4,0E-01	<b>6,4E-03</b>	1,6E-01
GOTERM_BP_]GO:0008610~lipid biosynthetic process	36	5,64	8,6E-05	577	545	17911	2,05	4,0E-01	<b>6,4E-03</b>	1,7E-01
GOTERM_BP_]GO:0051259~protein oligomerization	35	5,49	9,0E-05	577	524	17911	2,07	4,1E-01	<b>6,6E-03</b>	1,7E-01
GOTERM_BP_]GO:0005977~glycogen metabolic process	11	1,72	9,8E-05	577	72	17911	4,74	4,4E-01	<b>7,1E-03</b>	1,9E-01
GOTERM_BP_]GO:0044042~glucan metabolic process	11	1,72	9,8E-05	577	72	17911	4,74	4,4E-01	<b>7,1E-03</b>	1,9E-01
GOTERM_BP_]GO:0006073~cellular glucan metabolic process	11	1,72	9,8E-05	577	72	17911	4,74	4,4E-01	<b>7,1E-03</b>	1,9E-01
GOTERM_BP_]GO:0032870~cellular response to hormone stimulus	36	5,64	9,9E-05	577	549	17911	2,04	4,4E-01	<b>7,1E-03</b>	1,9E-01
GOTERM_BP_]GO:0006520~cellular amino acid metabolic process	19	2,98	1,0E-04	577	203	17911	2,91	4,5E-01	<b>7,3E-03</b>	2,0E-01
GOTERM_BP_]GO:0046365~monosaccharide catabolic process	7	1,10	1,1E-04	577	25	17911	8,69	4,9E-01	<b>7,9E-03</b>	2,2E-01
GOTERM_BP_]GO:0050792~regulation of viral process	24	3,76	1,4E-04	577	304	17911	2,45	5,6E-01	<b>9,5E-03</b>	2,7E-01
GOTERM_BP_]GO:1901135~carbohydrate derivative metabolic process	58	9,09	1,5E-04	577	1079	17911	1,67	5,9E-01	<b>1,0E-02</b>	2,9E-01
GOTERM_BP_]GO:0014070~response to organic cyclic compound	55	8,62	1,5E-04	577	1005	17911	1,70	6,0E-01	<b>1,0E-02</b>	3,0E-01
GOTERM_BP_]GO:1900076~regulation of cellular response to insulin stimul	11	1,72	1,5E-04	577	76	17911	4,49	6,0E-01	<b>1,0E-02</b>	3,0E-01
GOTERM_BP_]GO:0002221~pattern recognition receptor signaling pathway	13	2,04	1,7E-04	577	107	17911	3,77	6,3E-01	<b>1,1E-02</b>	3,2E-01
GOTERM_BP_]GO:1901653~cellular response to peptide	22	3,45	1,7E-04	577	269	17911	2,54	6,4E-01	<b>1,1E-02</b>	3,4E-01
GOTERM_BP_]GO:0046128~purine ribonucleoside metabolic process	23	3,61	1,8E-04	577	289	17911	2,47	6,5E-01	<b>1,1E-02</b>	3,4E-01
GOTERM_BP_]GO:0071822~protein complex subunit organization	71	11,13	1,9E-04	577	1414	17911	1,56	6,8E-01	<b>1,2E-02</b>	3,7E-01
GOTERM_BP_]GO:0010941~regulation of cell death	79	12,38	1,9E-04	577	1620	17911	1,51	6,8E-01	<b>1,2E-02</b>	3,7E-01

GOTERM_BP_]GO:0046031~ADP metabolic process	11	1,72	1,9E-04	577	78	17911	4,38	6,8E-01	<b>1,2E-02</b>	3,7E-01
GOTERM_BP_]GO:0006090~pyruvate metabolic process	12	1,88	1,9E-04	577	93	17911	4,01	6,8E-01	<b>1,2E-02</b>	3,7E-01
GOTERM_BP_]GO:0006112~energy reserve metabolic process	12	1,88	1,9E-04	577	93	17911	4,01	6,8E-01	<b>1,2E-02</b>	3,7E-01
GOTERM_BP_]GO:0032869~cellular response to insulin stimulus	17	2,66	2,1E-04	577	178	17911	2,96	7,1E-01	<b>1,3E-02</b>	4,1E-01
GOTERM_BP_]GO:0042278~purine nucleoside metabolic process	23	3,61	2,1E-04	577	293	17911	2,44	7,2E-01	<b>1,3E-02</b>	4,1E-01
GOTERM_BP_]GO:0002753~cytoplasmic pattern recognition receptor signal	7	1,10	2,2E-04	577	28	17911	7,76	7,3E-01	<b>1,3E-02</b>	4,3E-01
GOTERM_BP_]GO:0012501~programmed cell death	88	13,79	2,6E-04	577	1870	17911	1,46	7,8E-01	<b>1,5E-02</b>	4,9E-01
GOTERM_BP_]GO:0044272~sulfur compound biosynthetic process	12	1,88	2,6E-04	577	96	17911	3,88	7,8E-01	<b>1,5E-02</b>	5,0E-01
GOTERM_BP_]GO:0050790~regulation of catalytic activity	80	12,54	2,6E-04	577	1662	17911	1,49	7,8E-01	<b>1,5E-02</b>	5,0E-01
GOTERM_BP_]GO:0008219~cell death	93	14,58	2,6E-04	577	2003	17911	1,44	7,9E-01	<b>1,5E-02</b>	5,1E-01
GOTERM_BP_]GO:0030522~intracellular receptor signaling pathway	17	2,66	2,7E-04	577	182	17911	2,90	8,0E-01	<b>1,5E-02</b>	5,2E-01
GOTERM_BP_]GO:0006084~acetyl-CoA metabolic process	7	1,10	2,7E-04	577	29	17911	7,49	8,0E-01	<b>1,5E-02</b>	5,3E-01
GOTERM_BP_]GO:0039535~regulation of RIG-I signaling pathway	5	0,78	2,9E-04	577	11	17911	14,11	8,2E-01	<b>1,6E-02</b>	5,6E-01
GOTERM_BP_]GO:0061615~glycolytic process through fructose-6-phosphat	5	0,78	2,9E-04	577	11	17911	14,11	8,2E-01	<b>1,6E-02</b>	5,6E-01
GOTERM_BP_]GO:0065009~regulation of molecular function	100	15,67	3,0E-04	577	2201	17911	1,41	8,3E-01	<b>1,7E-02</b>	5,9E-01
GOTERM_BP_]GO:0009135~purine nucleoside diphosphate metabolic proces	11	1,72	3,2E-04	577	83	17911	4,11	8,5E-01	<b>1,8E-02</b>	6,2E-01
GOTERM_BP_]GO:0009179~purine ribonucleoside diphosphate metabolic pr	11	1,72	3,2E-04	577	83	17911	4,11	8,5E-01	<b>1,8E-02</b>	6,2E-01
GOTERM_BP_]GO:0065003~macromolecular complex assembly	75	11,76	3,3E-04	577	1544	17911	1,51	8,5E-01	<b>1,8E-02</b>	6,3E-01
GOTERM_BP_]GO:0071495~cellular response to endogenous stimulus	61	9,56	3,4E-04	577	1189	17911	1,59	8,6E-01	<b>1,8E-02</b>	6,5E-01
GOTERM_BP_]GO:0046686~response to cadmium ion	8	1,25	3,5E-04	577	42	17911	5,91	8,7E-01	<b>1,8E-02</b>	6,7E-01
GOTERM_BP_]GO:0009069~serine family amino acid metabolic process	8	1,25	3,5E-04	577	42	17911	5,91	8,7E-01	<b>1,8E-02</b>	6,7E-01
GOTERM_BP_]GO:0044264~cellular polysaccharide metabolic process	11	1,72	3,6E-04	577	84	17911	4,06	8,8E-01	<b>1,9E-02</b>	6,9E-01
GOTERM_BP_]GO:0002758~innate immune response-activating signal trans	13	2,04	3,6E-04	577	116	17911	3,48	8,8E-01	<b>1,9E-02</b>	6,9E-01
GOTERM_BP_]GO:0043067~regulation of programmed cell death	73	11,44	3,8E-04	577	1498	17911	1,51	8,9E-01	<b>2,0E-02</b>	7,3E-01
GOTERM_BP_]GO:0010876~lipid localization	25	3,92	4,0E-04	577	348	17911	2,23	9,0E-01	<b>2,0E-02</b>	7,7E-01
GOTERM_BP_]GO:0006000~fructose metabolic process	5	0,78	4,3E-04	577	12	17911	12,93	9,2E-01	<b>2,2E-02</b>	8,2E-01
GOTERM_BP_]GO:0043648~dicarboxylic acid metabolic process	11	1,72	4,3E-04	577	86	17911	3,97	9,2E-01	<b>2,2E-02</b>	8,3E-01
GOTERM_BP_]GO:0005976~polysaccharide metabolic process	12	1,88	4,4E-04	577	102	17911	3,65	9,2E-01	<b>2,2E-02</b>	8,4E-01
GOTERM_BP_]GO:0009968~negative regulation of signal transduction	54	8,46	4,4E-04	577	1025	17911	1,64	9,2E-01	<b>2,2E-02</b>	8,4E-01
GOTERM_BP_]GO:0010669~epithelial structure maintenance	6	0,94	4,5E-04	577	21	17911	8,87	9,3E-01	<b>2,2E-02</b>	8,6E-01
GOTERM_BP_]GO:0006081~cellular aldehyde metabolic process	9	1,41	4,5E-04	577	57	17911	4,90	9,3E-01	<b>2,2E-02</b>	8,7E-01
GOTERM_BP_]GO:0045089~positive regulation of innate immune response	16	2,51	4,5E-04	577	172	17911	2,89	9,3E-01	<b>2,2E-02</b>	8,7E-01
GOTERM_BP_]GO:0046939~nucleotide phosphorylation	11	1,72	4,7E-04	577	87	17911	3,92	9,4E-01	<b>2,3E-02</b>	9,1E-01

GOTERM_BP_]GO:0043933~macromolecular complex subunit organization	100	15,67	4,8E-04	577	2229	17911	1,39	9,4E-01	<b>2,3E-02</b>	9,2E-01
GOTERM_BP_]GO:0006109~regulation of carbohydrate metabolic process	17	2,66	4,9E-04	577	192	17911	2,75	9,5E-01	<b>2,3E-02</b>	9,5E-01
GOTERM_BP_]GO:0006915~apoptotic process	83	13,01	5,1E-04	577	1779	17911	1,45	9,5E-01	<b>2,4E-02</b>	9,9E-01
GOTERM_BP_]GO:0043900~regulation of multi-organism process	29	4,55	5,4E-04	577	442	17911	2,04	9,6E-01	<b>2,5E-02</b>	1,0E+00
GOTERM_BP_]GO:0009200~deoxyribonucleoside triphosphate metabolic pro	6	0,94	5,7E-04	577	22	17911	8,47	9,6E-01	<b>2,6E-02</b>	1,1E+00
GOTERM_BP_]GO:0009185~ribonucleoside diphosphate metabolic process	11	1,72	5,7E-04	577	89	17911	3,84	9,7E-01	<b>2,6E-02</b>	1,1E+00
GOTERM_BP_]GO:0002218~activation of innate immune response	13	2,04	6,1E-04	577	123	17911	3,28	9,7E-01	<b>2,8E-02</b>	1,2E+00
GOTERM_BP_]GO:0039532~negative regulation of viral-induced cytoplasmic	4	0,63	6,2E-04	577	6	17911	20,69	9,7E-01	<b>2,8E-02</b>	1,2E+00
GOTERM_BP_]GO:0039533~regulation of MDA-5 signaling pathway	4	0,63	6,2E-04	577	6	17911	20,69	9,7E-01	<b>2,8E-02</b>	1,2E+00
GOTERM_BP_]GO:0042493~response to drug	29	4,55	6,5E-04	577	447	17911	2,01	9,8E-01	<b>2,9E-02</b>	1,2E+00
GOTERM_BP_]GO:0009132~nucleoside diphosphate metabolic process	12	1,88	6,6E-04	577	107	17911	3,48	9,8E-01	<b>2,9E-02</b>	1,3E+00
GOTERM_BP_]GO:0007569~cell aging	11	1,72	6,8E-04	577	91	17911	3,75	9,8E-01	<b>3,0E-02</b>	1,3E+00
GOTERM_BP_]GO:0048585~negative regulation of response to stimulus	66	10,34	6,9E-04	577	1350	17911	1,52	9,8E-01	<b>3,0E-02</b>	1,3E+00
GOTERM_BP_]GO:0016042~lipid catabolic process	21	3,29	7,0E-04	577	278	17911	2,34	9,8E-01	<b>3,0E-02</b>	1,3E+00
GOTERM_BP_]GO:0045088~regulation of innate immune response	18	2,82	7,1E-04	577	218	17911	2,56	9,8E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0051260~protein homooligomerization	22	3,45	7,1E-04	577	299	17911	2,28	9,8E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0042981~regulation of apoptotic process	71	11,13	7,2E-04	577	1482	17911	1,49	9,9E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0043902~positive regulation of multi-organism process	14	2,19	7,2E-04	577	143	17911	3,04	9,9E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0009628~response to abiotic stimulus	58	9,09	7,2E-04	577	1148	17911	1,57	9,9E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0045216~cell-cell junction organization	16	2,51	7,3E-04	577	180	17911	2,76	9,9E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0008104~protein localization	104	16,30	7,5E-04	577	2367	17911	1,36	9,9E-01	<b>3,1E-02</b>	1,4E+00
GOTERM_BP_]GO:0009141~nucleoside triphosphate metabolic process	20	3,13	7,5E-04	577	259	17911	2,40	9,9E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0015980~energy derivation by oxidation of organic comp	19	2,98	7,5E-04	577	239	17911	2,47	9,9E-01	<b>3,0E-02</b>	1,4E+00
GOTERM_BP_]GO:0009215~purine deoxyribonucleoside triphosphate metab	5	0,78	8,2E-04	577	14	17911	11,09	9,9E-01	<b>3,3E-02</b>	1,6E+00
GOTERM_BP_]GO:0039529~RIG-I signaling pathway	5	0,78	8,2E-04	577	14	17911	11,09	9,9E-01	<b>3,3E-02</b>	1,6E+00
GOTERM_BP_]GO:0044085~cellular component biogenesis	114	17,87	8,6E-04	577	2654	17911	1,33	9,9E-01	<b>3,4E-02</b>	1,7E+00
GOTERM_BP_]GO:0010648~negative regulation of cell communication	58	9,09	9,3E-04	577	1160	17911	1,55	1,0E+00	<b>3,7E-02</b>	1,8E+00
GOTERM_BP_]GO:0009057~macromolecule catabolic process	52	8,15	9,8E-04	577	1010	17911	1,60	1,0E+00	<b>3,8E-02</b>	1,9E+00
GOTERM_BP_]GO:0023057~negative regulation of signaling	58	9,09	9,9E-04	577	1164	17911	1,55	1,0E+00	<b>3,9E-02</b>	1,9E+00
GOTERM_BP_]GO:0070887~cellular response to chemical stimulus	112	17,55	9,9E-04	577	2607	17911	1,33	1,0E+00	<b>3,8E-02</b>	1,9E+00
GOTERM_BP_]GO:0044270~cellular nitrogen compound catabolic process	21	3,29	1,0E-03	577	287	17911	2,27	1,0E+00	<b>4,0E-02</b>	2,0E+00
GOTERM_BP_]GO:0042772~DNA damage response, signal transduction res	5	0,78	1,1E-03	577	15	17911	10,35	1,0E+00	<b>4,1E-02</b>	2,1E+00
GOTERM_BP_]GO:0009151~purine deoxyribonucleotide metabolic process	5	0,78	1,1E-03	577	15	17911	10,35	1,0E+00	<b>4,1E-02</b>	2,1E+00

GOTERM_BP_]GO:0008285~negative regulation of cell proliferation	37	5,80	1,1E-03	577	649	17911	1,77	1,0E+00	<b>4,2E-02</b>	2,1E+00
GOTERM_BP_]GO:0035383~thioester metabolic process	10	1,57	1,1E-03	577	81	17911	3,83	1,0E+00	<b>4,3E-02</b>	2,2E+00
GOTERM_BP_]GO:0006637~acyl-CoA metabolic process	10	1,57	1,1E-03	577	81	17911	3,83	1,0E+00	<b>4,3E-02</b>	2,2E+00
GOTERM_BP_]GO:0051128~regulation of cellular component organization	104	16,30	1,2E-03	577	2399	17911	1,35	1,0E+00	<b>4,4E-02</b>	2,2E+00
GOTERM_BP_]GO:0098602~single organism cell adhesion	43	6,74	1,2E-03	577	796	17911	1,68	1,0E+00	<b>4,4E-02</b>	2,3E+00
GOTERM_BP_]GO:0046942~carboxylic acid transport	19	2,98	1,3E-03	577	250	17911	2,36	1,0E+00	<b>4,6E-02</b>	2,4E+00
GOTERM_BP_]GO:0035384~thioester biosynthetic process	6	0,94	1,3E-03	577	26	17911	7,16	1,0E+00	<b>4,6E-02</b>	2,4E+00
GOTERM_BP_]GO:0006760~folic acid-containing compound metabolic proc	6	0,94	1,3E-03	577	26	17911	7,16	1,0E+00	<b>4,6E-02</b>	2,4E+00
GOTERM_BP_]GO:0071616~acyl-CoA biosynthetic process	6	0,94	1,3E-03	577	26	17911	7,16	1,0E+00	<b>4,6E-02</b>	2,4E+00
GOTERM_BP_]GO:0009394~2'-deoxyribonucleotide metabolic process	6	0,94	1,3E-03	577	26	17911	7,16	1,0E+00	<b>4,6E-02</b>	2,4E+00
GOTERM_BP_]GO:0048525~negative regulation of viral process	11	1,72	1,3E-03	577	99	17911	3,45	1,0E+00	<b>4,7E-02</b>	2,5E+00
GOTERM_BP_]GO:0098609~cell-cell adhesion	55	8,62	1,3E-03	577	1101	17911	1,55	1,0E+00	<b>4,8E-02</b>	2,5E+00
GOTERM_BP_]GO:0051291~protein heterooligomerization	14	2,19	1,4E-03	577	153	17911	2,84	1,0E+00	<b>4,8E-02</b>	2,6E+00

## Таблица S6

Category	Term	Count	%	PValue	List To	Pop Hit:	Pop Tot:	Fold Enri	Bonferroni	Benjamini	FDR
KEGG_PATH\	mmu01100:Metabolic pathways	98	15,36	2,1E-10	319	1278	7720	1,8558	5,659E-08	<b>5,659E-08</b>	2,79E-07
KEGG_PATH\	mmu01200:Carbon metabolism	15	2,35	0,00027	319	116	7720	3,1294	0,0704497	<b>0,0358681</b>	0,359617

## Таблица S7

Category	Term	Count	%	PValue	List Tot	Pop Hits	Pop Tot	Fold Enri	Bonferroni	Benjamini	FDR
GOTERM_CC_	GO:0005737~cytoplasm	178	46,23	4,91E-09	368	6631	19662	1,4342	1,8E-06	1,838E-06	6,8E-06
GOTERM_CC_	GO:0070062~extracellular exosome	89	23,12	4,67E-08	368	2674	19662	1,7783	1,7E-05	8,725E-06	6,4E-05
GOTERM_CC_	GO:0005783~endoplasmic reticulum	53	13,77	2,72E-07	368	1323	19662	2,1404	0,0001	3,391E-05	0,00038
GOTERM_CC_	GO:0005925~focal adhesion	24	6,234	1,39E-06	368	391	19662	3,2796	0,00052	0,00013	0,00192
GOTERM_CC_	GO:0005790~smooth endoplasmic reticulum	7	1,818	1,34E-05	368	29	19662	12,897	0,005	0,0010026	0,01852
GOTERM_CC_	GO:0016020~membrane	168	43,64	5,02E-05	368	6998	19662	1,2827	0,01861	0,0026804	0,06936
GOTERM_CC_	GO:0016323~basolateral plasma membrane	14	3,636	1,20E-04	368	203	19662	3,6848	0,04379	0,0055819	0,16523
GOTERM_CC_	GO:0030054~cell junction	29	7,532	2,09E-04	368	718	19662	2,158	0,07503	0,0086282	0,2876
GOTERM_CC_	GO:0030027~lamellipodium	12	3,117	2,66E-04	368	164	19662	3,9095	0,09471	0,0099012	0,36679
GOTERM_CC_	GO:0001726~ruffle	9	2,338	4,04E-04	368	95	19662	5,0617	0,14033	0,0136516	0,55682
GOTERM_CC_	GO:0030426~growth cone	11	2,857	8,28E-04	368	159	19662	3,6964	0,26635	0,0235437	1,13729
GOTERM_CC_	GO:0048471~perinuclear region of cytoplasm	26	6,753	0,001357	368	692	19662	2,0075	0,39827	0,0278245	1,85831
GOTERM_CC_	GO:0005829~cytosol	52	13,51	0,001477	368	1784	19662	1,5574	0,42476	0,0286846	2,0214
GOTERM_CC_	GO:0016324~apical plasma membrane	16	4,156	0,001349	368	328	19662	2,6063	0,39641	0,0292612	1,84716
GOTERM_CC_	GO:0005739~mitochondrion	51	13,25	0,001139	368	1721	19662	1,5833	0,34703	0,0299862	1,56171

## Таблица S8

Category	Term	Count	%	PValue	List Tc	Pop Hit	Pop Tot	Fold Enric	Bonferron	Benjamini	FDR
GOTERM_BP_GO:0044085	cellular component biogenesis	91	24	2,71E-08	346	2654	17911	1,77494	0,00013	0,00013	5E-05
GOTERM_BP_GO:0030334	regulation of cell migration	37	9,6	3,62E-07	346	742	17911	2,58132	0,00176	0,00059	7E-04
GOTERM_BP_GO:0022607	cellular component assembly	82	21	2,89E-07	346	2418	17911	1,7555	0,0014	0,0007	5E-04
GOTERM_BP_GO:0051128	regulation of cellular component organization	80	21	8,5E-07	346	2399	17911	1,72625	0,00411	0,00103	0,002
GOTERM_BP_GO:0040012	regulation of locomotion	38	9,9	1,38E-06	346	819	17911	2,40184	0,00665	0,00111	0,003
GOTERM_BP_GO:0022610	biological adhesion	59	15	1,7E-06	346	1595	17911	1,91485	0,00822	0,00118	0,003
GOTERM_BP_GO:2000145	regulation of cell motility	37	9,6	1,25E-06	346	782	17911	2,44928	0,00606	0,00121	0,002
GOTERM_BP_GO:0051270	regulation of cellular component movement	38	9,9	2,95E-06	346	846	17911	2,32518	0,01422	0,00143	0,006
GOTERM_BP_GO:0007155	cell adhesion	58	15	2,87E-06	346	1583	17911	1,89667	0,01384	0,00155	0,005
GOTERM_BP_GO:0051674	localization of cell	52	14	2,57E-06	346	1348	17911	1,9969	0,01239	0,00156	0,005
GOTERM_BP_GO:0048870	cell motility	52	14	2,57E-06	346	1348	17911	1,9969	0,01239	0,00156	0,005
GOTERM_BP_GO:0040011	locomotion	56	15	4,53E-06	346	1529	17911	1,89594	0,02175	0,00169	0,009
GOTERM_BP_GO:0022603	regulation of anatomical structure morphogenesis	43	11	3,86E-06	346	1033	17911	2,15482	0,01853	0,0017	0,007
GOTERM_BP_GO:0006928	movement of cell or subcellular component	61	16	4,44E-06	346	1724	17911	1,83162	0,02128	0,00179	0,008
GOTERM_BP_GO:0016477	cell migration	47	12	5,95E-06	346	1199	17911	2,02919	0,02843	0,00206	0,011
GOTERM_BP_GO:0010810	regulation of cell-substrate adhesion	15	3,9	1E-05	346	179	17911	4,33792	0,04741	0,00323	0,019
GOTERM_BP_GO:0007010	cytoskeleton organization	44	11	1,21E-05	346	1120	17911	2,03366	0,05702	0,00366	0,023
GOTERM_BP_GO:0051094	positive regulation of developmental process	47	12	1,83E-05	346	1252	17911	1,94329	0,08498	0,00492	0,035
GOTERM_BP_GO:0072358	cardiovascular system development	42	11	1,73E-05	346	1062	17911	2,04724	0,08056	0,00493	0,033
GOTERM_BP_GO:0072359	circulatory system development	42	11	1,73E-05	346	1062	17911	2,04724	0,08056	0,00493	0,033
GOTERM_BP_GO:0030335	positive regulation of cell migration	24	6,2	1,95E-05	346	446	17911	2,78561	0,09022	0,00496	0,037

## Таблица S9

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	<b>Benjamini</b>	FDR
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## Таблица S10

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini FDR
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## Таблица S11

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	<b>Benjamini</b>	FDR
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## Таблица S12

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
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### Таблица S13

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_KEYW	Chaperone	5	45,5	9,84E-07	11	191	22680	53,9743	4,72E-05	4,722E-05	0,00094

## Таблица S14

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	<b>Benjamini</b>	FDR
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## Таблица S15

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	<b>Benjamini</b>	FDR
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## Таблица S16

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	<b>Benjamini</b>	FDR
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## Таблица S17

Category	Term	Count	%	PValue	List Tot	Pop Hit	Pop To	Fold Enri	Bonferroni	Benjamini	FDR
GOTERM_CC_	GO:0072562~blood microparticle	16	9,14	6,1E-13	171	133	19662	13,832	1,177E-10	<b>1,177E-10</b>	7,56E-10
GOTERM_CC_	GO:0005615~extracellular space	44	25,1	1,5E-12	171	1504	19662	3,3638	2,97E-10	<b>1,485E-10</b>	1,91E-09
GOTERM_CC_	GO:0070062~extracellular exosome	55	31,4	7,9E-10	171	2674	19662	2,365	1,528E-07	<b>5,094E-08</b>	9,82E-07
GOTERM_CC_	GO:0005576~extracellular region	42	24	2,7E-09	171	1753	19662	2,7549	5,185E-07	<b>1,296E-07</b>	3,33E-06
GOTERM_CC_	GO:0070469~respiratory chain	8	4,57	6,6E-07	171	58	19662	15,86	0,0001284	<b>2,569E-05</b>	0,000826
GOTERM_CC_	GO:0045277~respiratory chain complex IV	3	1,71	0,00073	171	5	19662	68,989	0,1321905	<b>0,0233535</b>	0,907321



## Таблица S18

Category	Term	Count	%	PValue	List To	Pop Hi	Pop Tot	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_BP_GO:0002526	acute inflammatory response	15	8,57	1,3E-11	164	130	17911	12,60155	4,2E-08	<b>4,204E-08</b>	2E-08
GOTERM_BP_GO:0006953	acute-phase response	10	5,71	3,5E-10	164	47	17911	23,2369	1,1E-06	<b>5,466E-07</b>	6E-07
GOTERM_BP_GO:0010466	negative regulation of peptidase activity	15	8,57	1,1E-08	164	216	17911	7,584265	3,5E-05	<b>8,806E-06</b>	2E-05
GOTERM_BP_GO:0045861	negative regulation of proteolysis	17	9,71	9,2E-09	164	289	17911	6,424319	2,9E-05	<b>9,662E-06</b>	2E-05
GOTERM_BP_GO:0006954	inflammatory response	21	12	7,9E-07	164	613	17911	3,741406	0,00248	<b>0,0004971</b>	0,001
GOTERM_BP_GO:0051346	negative regulation of hydrolase activity	16	9,14	1,1E-06	164	362	17911	4,827112	0,0036	<b>0,0006015</b>	0,002
GOTERM_BP_GO:0052547	regulation of peptidase activity	15	8,57	4,5E-06	164	354	17911	4,627687	0,0142	<b>0,0020415</b>	0,008
GOTERM_BP_GO:0030449	regulation of complement activation	5	2,86	6,2E-06	164	14	17911	39,00479	0,0192	<b>0,0024201</b>	0,011
GOTERM_BP_GO:2000257	regulation of protein activation cascade	5	2,86	8,3E-06	164	15	17911	36,40447	0,0259	<b>0,0026211</b>	0,015
GOTERM_BP_GO:0006952	defense response	32	18,3	9,5E-06	164	1481	17911	2,359777	0,02955	<b>0,002723</b>	0,017
GOTERM_BP_GO:0002682	regulation of immune system process	29	16,6	7,9E-06	164	1249	17911	2,53578	0,02452	<b>0,0027543</b>	0,014
GOTERM_BP_GO:0030162	regulation of proteolysis	19	10,9	1,3E-05	164	615	17911	3,374073	0,04002	<b>0,0033978</b>	0,024
GOTERM_BP_GO:0002920	regulation of humoral immune response	6	3,43	1,5E-05	164	35	17911	18,7223	0,04692	<b>0,0036901</b>	0,028
GOTERM_BP_GO:0070613	regulation of protein processing	7	4	3,3E-05	164	67	17911	11,41036	0,09768	<b>0,0073146</b>	0,059
GOTERM_BP_GO:1903317	regulation of protein maturation	7	4	3,6E-05	164	68	17911	11,24256	0,10585	<b>0,0074313</b>	0,064
GOTERM_BP_GO:0007596	blood coagulation	10	5,71	4,1E-05	164	180	17911	6,067412	0,11994	<b>0,0079533</b>	0,074
GOTERM_BP_GO:0006956	complement activation	7	4	4,9E-05	164	72	17911	10,61797	0,14359	<b>0,0090762</b>	0,089
GOTERM_BP_GO:1900047	negative regulation of hemostasis	6	3,43	5,3E-05	164	45	17911	14,56179	0,15471	<b>0,0092944</b>	0,097
GOTERM_BP_GO:0030195	negative regulation of blood coagulation	6	3,43	5,3E-05	164	45	17911	14,56179	0,15471	<b>0,0092944</b>	0,097
GOTERM_BP_GO:0022900	electron transport chain	7	4	7,2E-05	164	77	17911	9,928492	0,20274	<b>0,0107314</b>	0,13
GOTERM_BP_GO:0050819	negative regulation of coagulation	6	3,43	6,6E-05	164	47	17911	13,94214	0,18776	<b>0,0108855</b>	0,12
GOTERM_BP_GO:0007599	hemostasis	10	5,71	7E-05	164	193	17911	5,658726	0,19696	<b>0,0109075</b>	0,126
GOTERM_BP_GO:0045333	cellular respiration	9	5,14	8,4E-05	164	154	17911	6,382602	0,23199	<b>0,0114106</b>	0,152
GOTERM_BP_GO:0050817	coagulation	10	5,71	8,2E-05	164	197	17911	5,543828	0,22639	<b>0,0116</b>	0,148
GOTERM_BP_GO:0042060	wound healing	14	8	9E-05	164	406	17911	3,76598	0,24632	<b>0,0117137</b>	0,163
GOTERM_BP_GO:0043086	negative regulation of catalytic activity	18	10,3	0,00011	164	659	17911	2,983067	0,29088	<b>0,0136554</b>	0,198
GOTERM_BP_GO:0072376	protein activation cascade	7	4	0,00013	164	85	17911	8,994046	0,32544	<b>0,0150282</b>	0,226
GOTERM_BP_GO:0034105	positive regulation of tissue remodeling	5	2,86	0,00013	164	29	17911	18,8299	0,33867	<b>0,0151985</b>	0,238
GOTERM_BP_GO:0009605	response to external stimulus	39	22,3	0,00016	164	2301	17911	1,851075	0,40273	<b>0,0182383</b>	0,296
GOTERM_BP_GO:0061045	negative regulation of wound healing	6	3,43	0,00018	164	58	17911	11,29794	0,43627	<b>0,0195708</b>	0,329
GOTERM_BP_GO:0010955	negative regulation of protein processing	5	2,86	0,00022	164	33	17911	16,54749	0,49971	<b>0,022093</b>	0,398

GOTERM_BP_GO:1903318~negative regulation of protein maturation	5	2,86	0,00022	164	33	17911	16,54749	0,49971	<b>0,022093</b>	0,398
GOTERM_BP_GO:1990267~response to transition metal nanoparticle	8	4,57	0,00022	164	133	17911	6,569228	0,49383	<b>0,0224407</b>	0,391
GOTERM_BP_GO:0006091~generation of precursor metabolites and ener	12	6,86	0,00025	164	334	17911	3,923835	0,54199	<b>0,0241066</b>	0,448
GOTERM_BP_GO:0002684~positive regulation of immune system process	19	10,9	0,00028	164	782	17911	2,653523	0,5853	<b>0,0263205</b>	0,505
GOTERM_BP_GO:0006508~proteolysis	29	16,6	0,00037	164	1556	17911	2,035469	0,68416	<b>0,0315072</b>	0,661
GOTERM_BP_GO:0015980~energy derivation by oxidation of organic com	10	5,71	0,00035	164	239	17911	4,569599	0,66569	<b>0,0317121</b>	0,629
GOTERM_BP_GO:0050878~regulation of body fluid levels	12	6,86	0,00036	164	349	17911	3,755189	0,67856	<b>0,0319068</b>	0,651
GOTERM_BP_GO:0006119~oxidative phosphorylation	6	3,43	0,00041	164	69	17911	9,496819	0,72677	<b>0,034458</b>	0,744
GOTERM_BP_GO:1903035~negative regulation of response to wounding	6	3,43	0,00041	164	69	17911	9,496819	0,72677	<b>0,034458</b>	0,744
GOTERM_BP_GO:0002455~humoral immune response mediated by circul	6	3,43	0,00044	164	70	17911	9,36115	0,7502	<b>0,0358442</b>	0,795
GOTERM_BP_GO:0022904~respiratory electron transport chain	6	3,43	0,00047	164	71	17911	9,229303	0,77267	<b>0,037271</b>	0,849
GOTERM_BP_GO:0015672~monovalent inorganic cation transport	13	7,43	0,00049	164	422	17911	3,364394	0,78886	<b>0,0381344</b>	0,891
GOTERM_BP_GO:0010035~response to inorganic substance	15	8,57	0,00059	164	558	17911	2,935844	0,84514	<b>0,0444737</b>	1,068
GOTERM_BP_GO:0032101~regulation of response to external stimulus	18	10,3	0,00066	164	769	17911	2,556361	0,87296	<b>0,04581</b>	1,181
GOTERM_BP_GO:0034103~regulation of tissue remodeling	6	3,43	0,00064	164	76	17911	8,622112	0,86826	<b>0,0460438</b>	1,16
GOTERM_BP_GO:0046034~ATP metabolic process	9	5,14	0,00064	164	208	17911	4,72558	0,86814	<b>0,0470933</b>	1,159
GOTERM_BP_GO:0042730~fibrinolysis	4	2,29	0,00075	164	20	17911	21,84268	0,90637	<b>0,0491428</b>	1,354
GOTERM_BP_GO:0044092~negative regulation of molecular function	20	11,4	0,00074	164	922	17911	2,369055	0,90176	<b>0,0491917</b>	1,327

## Таблица S19

Category	Term	Count	%	PValue	List Tot	Pop Hits	Pop To Fold Enr	Bonferroni	Benjamini	FDR	
KEGG_PATHV	mmu04610:Complement and coagulation cascades	9	5,14	1,2E-06	83	76	7720	11,01	0,0001697	<b>0,00016972</b>	0,0014
KEGG_PATHV	mmu00190:Oxidative phosphorylation	11	6,29	1,84E-06	83	139	7720	7,361	0,0002589	<b>0,00012944</b>	0,0022
KEGG_PATHV	mmu01100:Metabolic pathways	30	17,1	2,61E-05	83	1278	7720	2,183	0,0036692	<b>0,00091857</b>	0,0308