Table S9 Over-represented GO categories of significantly changed genes after heat shock in expression microarray data

Table legend

Rank	Position in the attribute list ranked by significance of association with your query
N	Number of genes in your query with this attribute
M	size of most surprising sub query
X	Number of genes overall with this attribute
LOD	The logarithm (base 10) of the odds ratio; positive and negative values indicate over- and underrepresentation, respectively
P	Single hypothesis one-sided P-value of the association between attribute and query (based on Fisher's Exact Test)
P-adj	Adjusted P-value: fraction (as a %) of 1000 null-hypothesis simulations having attributes with this single-hypothesis P value or smaller

OVERREPRESENTED ATTRIBUTES

WT downregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	228	541	434	1.27	5.00E-138	<0.001	GO:0042254:	ribosome biogenesis and assembly
2	251	642	510	1.103	3.60E-123	<0.001	GO:0022613:	ribonucleoprotein complex biogenesis and assembly
3	143	521	304	1.098	4.30E-76	<0.001	GO:0005730:	nucleolus
4	270	579	1014	0.742	6.10E-71	<0.001	GO:0043228:	non-membrane-bounded organelle
5	270	579	1014	0.742	6.10E-71	<0.001	GO:0043232:	intracellular non-membrane-bounded organelle
6	137	637	284	0.989	3.50E-62	<0.001	GO:0016072:	rRNA metabolic process
7	135	637	279	0.99	2.00E-61	<0.001	GO:0006364:	rRNA processing
8	126	1105	168	1.171	1.40E-59	<0.001	GO:0022626:	cytosolic ribosome
9	119	898	206	0.946	8.70E-48	<0.001	GO:0044445:	cytosolic part
10	153	482	575	0.752	3.90E-47	<0.001	GO:0030529:	ribonucleoprotein complex
11	53	578	64	1.682	3.30E-44	<0.001	GO:0042273:	ribosomal large subunit biogenesis and assembly
12	155	553	541	0.71	8.70E-44	<0.001	GO:0006396:	RNA processing
13	111	597	282	0.847	4.50E-42	<0.001	GO:0005840:	ribosome
14	269	536	1476	0.553	1.10E-41	<0.001	GO:0006996:	organelle organization and biogenesis
15	99	592	236	0.89	1.20E-40	<0.001	GO:0003735:	structural constituent of ribosome
16	143	455	618	0.692	3.50E-39	<0.001	GO:0031981:	nuclear lumen
17	99	632	236	0.853	5.20E-38	<0.001	GO:0033279:	ribosomal subunit

18	64	830	93	1.168	1.90E-34	<0.001	GO:0022625:	cytosolic large ribosomal subunit
19	47	577	67	1.375	2.20E-33	<0.001	GO:0042255:	ribosome assembly
20	320	610	1848	0.448	2.00E-32	<0.001	GO:0010467:	gene expression
21	44	798	51	1.613	3.80E-32	<0.001	GO:0030490:	maturation of SSU-rRNA
22	43	798	50	1.603	2.60E-31	<0.001	GO:0000462:	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
23	42	798	48	1.654	2.90E-31	<0.001	GO:0032040:	small subunit processome
24	53	1082	64	1.348	1.00E-29	<0.001	GO:0022627:	cytosolic small ribosomal subunit
25	40	577	55	1.422	1.50E-29	<0.001	GO:0042257:	ribosomal subunit assembly
26	30	529	36	1.712	1.10E-26	<0.001	GO:0000466:	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
27	32	577	41	1.533	1.70E-25	<0.001	GO:0000027:	ribosomal large subunit assembly and maintenance
28	104	592	369	0.619	2.30E-25	<0.001	GO:0005198:	structural molecule activity
29	30	529	38	1.596	2.40E-25	<0.001	GO:0000460:	maturation of 5.8S rRNA
30	60	438	182	0.853	2.80E-25	<0.001	GO:0044452:	nucleolar part
31	84	1130	149	0.775	3.60E-25	<0.001	GO:0022618:	protein-RNA complex assembly
32	114	302	880	0.594	1.30E-24	<0.001	GO:0031974:	membrane-enclosed lumen
33	114	302	880	0.594	1.30E-24	<0.001	GO:0043233:	organelle lumen
34	638	1260	2311	0.277	1.50E-23	<0.001	GO:0016043:	cellular component organization and biogenesis
35	56	592	138	0.834	3.40E-22	<0.001	GO:0015934:	large ribosomal subunit
36	430	1438	1245	0.295	4.80E-22	<0.001	GO:0016070:	RNA metabolic process
37	21	762	21	2.484	1.10E-19	<0.001	GO:0030515:	snoRNA binding
38	659	1439	2159	0.24	2.90E-19	<0.001	GO:0005634:	nucleus
39	81	1423	138	0.681	4.70E-19	<0.001	GO:0006399:	tRNA metabolic process
40	547	1438	1732	0.246	1.30E-18	<0.001	GO:0006139:	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
41	19	437	24	1.675	4.70E-18	<0.001	GO:0000469:	cleavages during rRNA processing
42	18	516	20	1.912	7.60E-18	<0.001	GO:0030684:	preribosome
43	45	696	98	0.838	8.50E-18	<0.001	GO:0015935:	small ribosomal subunit

44	17	516	19	1.887	8.20E-17	<0.001	GO:0030685:	nucleolar preribosome
45	116	302	1143	0.455	4.40E-16	<0.001	GO:0044428:	nuclear part
46	17	437	22	1.626	6.00E-16	<0.001	GO:0000447:	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-RNA, 5.8S rRNA, LSU-rRNA)
47	17	437	22	1.626	6.00E-16	<0.001	GO:0000478:	endonucleolytic cleavages during rRNA processing
48	17	437	22	1.626	6.00E-16	<0.001	GO:0000479:	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
49	41	1423	55	0.977	1.60E-15	<0.001	GO:0006400:	tRNA modification
50	1007	1294	4171	0.239	8.30E-15	<0.001	GO:0043226:	organelle
51	1007	1294	4171	0.239	8.30E-15	<0.001	GO:0043229:	intracellular organelle
52	15	437	19	1.658	1.90E-14	<0.001	GO:0000480:	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
53	57	1423	95	0.698	2.40E-14	<0.001	GO:0008033:	tRNA processing
54	132	597	711	0.377	3.10E-14	<0.001	GO:0006412:	translation
55	214	294	3119	0.413	3.90E-14	<0.001	GO:0043170:	macromolecule metabolic process
56	15	437	20	1.571	7.20E-14	<0.001	GO:0000472:	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
57	203	703	1111	0.296	3.80E-13	<0.001	GO:0044249:	cellular biosynthetic process
58	192	302	2623	0.372	5.50E-13	<0.001	GO:0044422:	organelle part
59	192	302	2623	0.372	5.50E-13	<0.001	GO:0044446:	intracellular organelle part
60	20	730	29	1.205	1.30E-12	<0.001	GO:0000054:	ribosome export from nucleus
61	20	730	29	1.205	1.30E-12	<0.001	GO:0033750:	ribosome localization
62	20	730	29	1.205	1.30E-12	<0.001	GO:0033753:	establishment of ribosome localization

63	27	1103	38	1.038	1.40E-12	<0.001	GO:0003743:	translation initiation factor activity
64	503	1374	1745	0.2	1.70E-12	<0.001	GO:0032991:	macromolecular complex
65	18	669	26	1.252	3.50E-12	<0.001	GO:0042274:	ribosomal small subunit biogenesis and assembly
66	245	294	3970	0.426	6.80E-12	<0.001	GO:0008152:	metabolic process
67	16	1029	17	1.734	6.80E-12	<0.001	GO:0005666:	DNA-directed RNA polymerase III complex
68	14	819	15	1.796	8.80E-12	<0.001	GO:0030488:	tRNA methylation
69	231	294	3643	0.394	1.10E-11	<0.001	GO:0044238:	primary metabolic process
70	13	720	14	1.829	1.20E-11	<0.001	GO:0000463:	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
71	13	720	14	1.829	1.20E-11	<0.001	GO:0000470:	maturation of LSU-rRNA
72	236	294	3777	0.398	2.00E-11	<0.001	GO:0044237:	cellular metabolic process
73	21	577	42	0.989	2.20E-11	<0.001	GO:0003724:	RNA helicase activity
74	17	577	28	1.169	3.00E-11	<0.001	GO:0004004:	ATP-dependent RNA helicase activity
75	17	577	28	1.169	3.00E-11	<0.001	GO:0008186:	RNA-dependent ATPase activity
76	22	1029	31	1.069	4.50E-11	<0.001	GO:0055029:	nuclear DNA-directed RNA polymerase complex
77	283	302	4878	0.552	8.90E-11	<0.001	GO:0009987:	cellular process
78	288	926	1369	0.225	9.00E-11	<0.001	GO:0009058:	biosynthetic process
79	140	1369	385	0.312	2.50E-10	<0.001	GO:0065003:	macromolecular complex assembly
80	22	1029	33	0.986	3.10E-10	<0.001	GO:0000428:	DNA-directed RNA polymerase complex
81	22	1029	33	0.986	3.10E-10	<0.001	GO:0030880:	RNA polymerase complex
82	150	644	883	0.285	4.20E-10	<0.001	GO:0009059:	macromolecule biosynthetic process
83	12	819	13	1.73	4.20E-10	<0.001	GO:0008175:	tRNA methyltransferase activity
84	68	234	836	0.429	5.40E-10	<0.001	GO:0003723:	RNA binding
85	22	1029	34	0.949	7.30E-10	<0.001	GO:0003899:	DNA-directed RNA polymerase activity
86	22	1029	34	0.949	7.30E-10	<0.001	GO:0034062:	RNA polymerase activity
87	112	592	659	0.32	8.40E-10	<0.001	GO:0005829:	cytosol
88	38	1066	81	0.626	1.10E-09	<0.001	GO:0016741:	transferase activity, transferring one-carbon groups
89	16	819	23	1.153	1.20E-09	<0.001	GO:0008173:	RNA methyltransferase activity

90	61	1417	128	0.484	1.40E-09	<0.001	GO:0006913:	nucleocytoplasmic transport
91	61	1417	128	0.484	1.40E-09	<0.001	GO:0051169:	nuclear transport
92	31	1103	58	0.718	1.50E-09	<0.001	GO:0008135:	translation factor activity, nucleic acid binding
93	8	482	8	2.298	1.60E-09	<0.001	GO:0030688:	nucleolar preribosome, small subunit precursor
94	37	1066	79	0.625	1.90E-09	<0.001	GO:0008168:	methyltransferase activity
95	8	516	8	2.265	2.80E-09	<0.001	GO:0030687:	nucleolar preribosome, large subunit precursor
96	25	293	143	0.653	1.60E-08	0.001	GO:0009451:	RNA modification
97	27	1103	51	0.708	2.30E-08	0.001	GO:0006413:	translational initiation
98	49	1417	101	0.497	2.90E-08	0.001	GO:0051168:	nuclear export
99	31	1103	64	0.632	3.30E-08	0.001	GO:0045182:	translation regulator activity
100	7	268	10	1.673	3.40E-08	0.001	GO:0030686:	90S preribosome
101	12	1029	14	1.39	3.80E-08	0.001	GO:0005736:	DNA-directed RNA polymerase I complex
102	27	1066	54	0.676	5.30E-08	0.001	GO:0008757:	S-adenosylmethionine-dependent methyltransferase activity
103	5	216	5	2.48	5.70E-08	0.001	GO:0030689:	Noc complex
104	23	1366	35	0.813	6.10E-08	0.001	GO:0006360:	transcription from RNA polymerase I promoter
105	14	684	25	1.001	7.00E-08	0.003	GO:0009161:	ribonucleoside monophosphate metabolic process
106	10	703	13	1.362	9.10E-08	0.003	GO:0006450:	regulation of translational fidelity
107	1296	1441	5171	0.211	9.30E-08	0.003	GO:0044424:	intracellular part
108	1309	1447	5209	0.215	1.00E-07	0.003	GO:0005622:	intracellular
109	13	1155	16	1.216	1.40E-07	0.004	GO:0042278:	purine nucleoside metabolic process
110	8	52	74	1.229	1.70E-07	0.004	GO:0008026:	ATP-dependent helicase activity
111	12	1043	15	1.236	1.90E-07	0.005	GO:0046128:	purine ribonucleoside metabolic process
112	17	1068	27	0.894	2.10E-07	0.005	GO:0009123:	nucleoside monophosphate metabolic process
113	38	1390	76	0.531	2.40E-07	0.006	GO:0006401:	RNA catabolic process
114	13	678	24	0.974	3.20E-07	0.007	GO:0009156:	ribonucleoside monophosphate biosynthetic process
115	30	1105	66	0.579	3.40E-07	0.008	GO:0006417:	regulation of translation
116	13	684	24	0.969	3.50E-07	0.008	GO:0009167:	purine ribonucleoside monophosphate metabolic process
117	9	664	12	1.346	3.70E-07	0.008	GO:0006207:	'de novo' pyrimidine base biosynthetic process
118	10	664	15	1.194	4.50E-07	0.011	GO:0019856:	pyrimidine base biosynthetic process
119	14	301	57	0.819	4.90E-07	0.012	GO:0051656:	establishment of organelle localization
120	29	1417	52	0.617	5.00E-07	0.012	GO:0006606:	protein import into nucleus
121	29	1417	52	0.617	5.00E-07	0.012	GO:0051170:	nuclear import

122	9	975	10	1.52	6.30E-07	0.014	GO:0006166:	purine ribonucleoside salvage
123	9	975	10	1.52	6.30E-07	0.014	GO:0043174:	nucleoside salvage
124	13	684	25	0.933	6.60E-07	0.015	GO:0009126:	purine nucleoside monophosphate metabolic process
125	70	925	260	0.327	6.60E-07	0.015	GO:0006519:	amino acid and derivative metabolic process
126	9	518	15	1.198	7.50E-07	0.015	GO:0016073:	snRNA metabolic process
127	16	1068	26	0.868	7.70E-07	0.015	GO:0009124:	nucleoside monophosphate biosynthetic process
128	66	925	243	0.331	1.00E-06	0.024	GO:0006520:	amino acid metabolic process
129	1333	1367	5737	0.346	1.40E-06	0.032	GO:0044464:	cell part
130	8	439	14	1.228	1.50E-06	0.033	GO:0000028:	ribosomal small subunit assembly and maintenance
131	12	678	23	0.94	1.60E-06	0.034	GO:0009168:	purine ribonucleoside monophosphate biosynthetic process
132	1333	1367	5738	0.344	1.60E-06	0.034	GO:0005623:	cell
133	45	1387	102	0.431	1.70E-06	0.036	GO:0004386:	helicase activity
134	15	610	38	0.776	1.70E-06	0.037	GO:0004812:	aminoacyl-tRNA ligase activity
135	15	610	38	0.776	1.70E-06	0.037	GO:0006418:	tRNA aminoacylation for protein translation
136	12	1043	17	1.04	1.80E-06	0.038	GO:0009119:	ribonucleoside metabolic process
137	70	925	267	0.311	1.90E-06	0.039	GO:0009308:	amine metabolic process
138	5	313	6	1.832	2.10E-06	0.045	GO:0042134:	rRNA primary transcript binding
139	12	664	24	0.914	2.30E-06	0.046	GO:0006206:	pyrimidine base metabolic process
140	16	1155	26	0.826	2.30E-06	0.048	GO:0009116:	nucleoside metabolic process

Δpbf1 downregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	230	583	434	1.223	1.10E-131	<0.001	GO:0042254:	ribosome biogenesis and assembly
2	240	610	510	1.091	2.60E-117	<0.001	GO:0022613:	ribonucleoprotein complex biogenesis and assembly
3	154	662	304	1.022	1.00E-71	<0.001	GO:0005730:	nucleolus
4	274	615	1014	0.705	1.30E-66	<0.001	GO:0043228:	non-membrane-bounded organelle
5	274	615	1014	0.705	1.30E-66	<0.001	GO:0043232:	intracellular non-membrane-bounded organelle
6	139	705	284	0.942	4.00E-58	<0.001	GO:0016072:	rRNA metabolic process
7	129	610	279	0.973	5.30E-58	<0.001	GO:0006364:	rRNA processing
8	127	1216	168	1.128	1.40E-55	<0.001	GO:0022626:	cytosolic ribosome
9	126	1063	206	0.913	6.70E-46	<0.001	GO:0044445:	cytosolic part
10	52	583	64	1.632	2.40E-42	<0.001	GO:0042273:	ribosomal large subunit biogenesis and assembly
11	148	495	575	0.708	7.50E-42	<0.001	GO:0030529:	ribonucleoprotein complex
12	162	629	541	0.662	1.10E-40	<0.001	GO:0006396:	RNA processing
13	114	664	282	0.807	9.40E-40	<0.001	GO:0005840:	ribosome
14	102	664	236	0.85	1.40E-38	<0.001	GO:0003735:	structural constituent of ribosome
15	265	545	1476	0.523	7.60E-38	<0.001	GO:0006996:	organelle organization and biogenesis
16	99	664	236	0.825	4.60E-36	<0.001	GO:0033279:	ribosomal subunit
17	175	676	618	0.588	6.30E-36	<0.001	GO:0031981:	nuclear lumen

18	46	576	67	1.345	4.60E-32	<0.001	GO:0042255:	ribosome assembly
19	64	924	93	1.11	1.40E-31	<0.001	GO:0022625:	cytosolic large ribosomal subunit
20	44	862	51	1.572	1.20E-30	<0.001	GO:0030490:	maturation of SSU-rRNA
21	43	862	50	1.562	7.20E-30	<0.001	GO:0000462:	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
22	42	862	48	1.614	7.50E-30	<0.001	GO:0032040:	small subunit processome
23	325	645	1848	0.41	1.20E-28	<0.001	GO:0010467:	gene expression
24	39	576	55	1.384	3.70E-28	<0.001	GO:0042257:	ribosomal subunit assembly
25	47	812	64	1.265	5.50E-28	<0.001	GO:0022627:	cytosolic small ribosomal subunit
26	30	598	36	1.651	4.50E-25	<0.001	GO:0000466:	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
27	31	576	41	1.476	5.30E-24	<0.001	GO:0000027:	ribosomal large subunit assembly and maintenance
28	30	598	38	1.534	9.40E-24	<0.001	GO:0000460:	maturation of 5.8S rRNA
29	105	641	369	0.58	4.70E-23	<0.001	GO:0005198:	structural molecule activity
30	87	1298	149	0.732	4.70E-23	<0.001	GO:0022618:	protein-RNA complex assembly
31	59	465	182	0.809	4.80E-23	<0.001	GO:0044452:	nucleolar part
32	675	1366	2311	0.256	2.00E-21	<0.001	GO:0016043:	cellular component organization and biogenesis
33	143	465	880	0.464	1.20E-20	<0.001	GO:0031974:	membrane-enclosed lumen
34	143	465	880	0.464	1.20E-20	<0.001	GO:0043233:	organelle lumen
35	80	1322	138	0.711	1.80E-20	<0.001	GO:0006399:	tRNA metabolic process
36	260	768	1245	0.346	3.40E-20	<0.001	GO:0016070:	RNA metabolic process
37	49	493	138	0.831	4.50E-20	<0.001	GO:0015934:	large ribosomal subunit
38	654	1428	2159	0.239	4.30E-19	<0.001	GO:0005634:	nucleus
39	21	862	21	2.421	1.50E-18	<0.001	GO:0030515:	snoRNA binding
40	43	641	98	0.844	1.70E-17	<0.001	GO:0015935:	small ribosomal subunit
41	432	1105	1732	0.252	1.40E-16	<0.001	GO:0006139:	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
42	18	615	20	1.826	1.80E-16	<0.001	GO:0030684:	preribosome
43	40	1272	55	1.002	2.40E-16	<0.001	GO:0006400:	tRNA modification

44	21	832	24	1.594	9.50E-16	<0.001	GO:0000469:	cleavages during rRNA processing
45	17	615	19	1.801	1.60E-15	<0.001	GO:0030685:	nucleolar preribosome
46	58	1410	95	0.723	3.00E-15	<0.001	GO:0008033:	tRNA processing
47	1104	1431	4171	0.225	2.60E-14	<0.001	GO:0043226:	organelle
48	1104	1431	4171	0.225	2.60E-14	<0.001	GO:0043229:	intracellular organelle
49	19	832	22	1.551	3.90E-14	<0.001	GO:0000447:	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
50	19	832	22	1.551	3.90E-14	<0.001	GO:0000478:	endonucleolytic cleavages during rRNA processing
51	19	832	22	1.551	3.90E-14	<0.001	GO:0000479:	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
52	153	466	1143	0.354	7.30E-14	<0.001	GO:0044428:	nuclear part
53	130	606	711	0.358	5.70E-13	<0.001	GO:0006412:	translation
54	17	832	20	1.503	1.60E-12	<0.001	GO:0000472:	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
55	15	598	19	1.505	2.00E-12	<0.001	GO:0000480:	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
56	18	659	26	1.259	2.70E-12	<0.001	GO:0042274:	ribosomal small subunit biogenesis and assembly
57	13	662	14	1.871	3.90E-12	<0.001	GO:0000463:	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
58	13	662	14	1.871	3.90E-12	<0.001	GO:0000470:	maturation of LSU-rRNA
59	182	626	1111	0.295	4.30E-12	<0.001	GO:0044249:	cellular biosynthetic process
60	20	780	29	1.172	4.50E-12	<0.001	GO:0000054:	ribosome export from nucleus
61	20	780	29	1.172	4.50E-12	<0.001	GO:0033750:	ribosome localization
62	20	780	29	1.172	4.50E-12	<0.001	GO:0033753:	establishment of ribosome localization

63	16	1057	17	1.72	1.00E-11	<0.001	GO:0005666:	DNA-directed RNA polymerase III complex
64	14	831	15	1.788	1.10E-11	<0.001	GO:0030488:	tRNA methylation
65	27	1241	38	0.973	2.60E-11	<0.001	GO:0003743:	translation initiation factor activity
66	22	1057	31	1.055	7.90E-11	<0.001	GO:0055029:	nuclear DNA-directed RNA polymerase complex
67	20	569	42	0.955	1.60E-10	<0.001	GO:0003724:	RNA helicase activity
68	43	1271	81	0.637	1.80E-10	<0.001	GO:0016741:	transferase activity, transferring one-carbon groups
69	509	1429	1745	0.177	2.40E-10	<0.001	GO:0032991:	macromolecular complex
70	42	1271	79	0.638	2.80E-10	<0.001	GO:0008168:	methyltransferase activity
71	168	271	2623	0.34	3.30E-10	<0.001	GO:0044422:	organelle part
72	168	271	2623	0.34	3.30E-10	<0.001	GO:0044446:	intracellular organelle part
73	16	569	28	1.113	3.40E-10	<0.001	GO:0004004:	ATP-dependent RNA helicase activity
74	16	569	28	1.113	3.40E-10	<0.001	GO:0008186:	RNA-dependent ATPase activity
75	205	622	1369	0.253	4.00E-10	<0.001	GO:0009058:	biosynthetic process
76	12	831	13	1.723	5.00E-10	<0.001	GO:0008175:	tRNA methyltransferase activity
77	22	1057	33	0.971	5.30E-10	<0.001	GO:0000428:	DNA-directed RNA polymerase complex
78	22	1057	33	0.971	5.30E-10	<0.001	GO:0030880:	RNA polymerase complex
79	22	1057	34	0.935	1.20E-09	<0.001	GO:0003899:	DNA-directed RNA polymerase activity
80	22	1057	34	0.935	1.20E-09	<0.001	GO:0034062:	RNA polymerase activity
81	16	831	23	1.146	1.40E-09	<0.001	GO:0008173:	RNA methyltransferase activity
82	177	253	3119	0.348	1.50E-09	<0.001	GO:0043170:	macromolecule metabolic process
83	143	616	883	0.281	1.50E-09	<0.001	GO:0009059:	macromolecule biosynthetic process
84	526	748	3643	0.214	1.50E-09	<0.001	GO:0044238:	primary metabolic process
85	496	653	3970	0.236	2.70E-09	<0.001	GO:0008152:	metabolic process
86	561	779	3777	0.21	3.00E-09	<0.001	GO:0044237:	cellular metabolic process
87	8	569	8	2.218	6.10E-09	<0.001	GO:0030687:	nucleolar preribosome, large subunit precursor
88	1231	1431	4878	0.202	7.40E-09	<0.001	GO:0009987:	cellular process
89	130	1303	385	0.289	8.90E-09	<0.001	GO:0065003:	macromolecular complex assembly

90	8	615	8	2.18	1.10E-08	0.001	GO:0030688:	nucleolar preribosome, small subunit precursor
91	63	286	659	0.389	2.10E-08	0.001	GO:0005829:	cytosol
92	31	1354	54	0.673	2.70E-08	0.001	GO:0008757:	S-adenosylmethionine-dependent methyltransferase activity
93	31	1241	58	0.653	3.00E-08	0.001	GO:0008135:	translation factor activity, nucleic acid binding
94	58	1424	128	0.439	4.50E-08	0.002	GO:0006913:	nucleocytoplasmic transport
95	58	1424	128	0.439	4.50E-08	0.002	GO:0051169:	nuclear transport
96	21	1102	35	0.828	4.60E-08	0.002	GO:0006360:	transcription from RNA polymerase I promoter
97	8	465	10	1.616	4.70E-08	0.002	GO:0030686:	90S preribosome
98	12	1057	14	1.376	5.20E-08	0.002	GO:0005736:	DNA-directed RNA polymerase I complex
99	64	240	836	0.375	7.00E-08	0.002	GO:0003723:	RNA binding
100	12	983	15	1.268	9.50E-08	0.002	GO:0046128:	purine ribonucleoside metabolic process
101	22	255	143	0.651	1.10E-07	0.002	GO:0009451:	RNA modification
102	14	707	25	0.984	1.10E-07	0.002	GO:0009161:	ribonucleoside monophosphate metabolic process
103	17	1023	27	0.917	1.10E-07	0.002	GO:0009123:	nucleoside monophosphate metabolic process
104	5	249	5	2.415	1.20E-07	0.002	GO:0030689:	Noc complex
105	10	740	13	1.336	1.50E-07	0.002	GO:0006450:	regulation of translational fidelity
106	10	870	12	1.4	1.90E-07	0.005	GO:0006207:	'de novo' pyrimidine base biosynthetic process
107	37	1322	76	0.537	2.10E-07	0.005	GO:0006401:	RNA catabolic process
108	1167	1296	5171	0.212	2.80E-07	0.006	GO:0044424:	intracellular part
109	12	1080	15	1.218	2.80E-07	0.006	GO:0019856:	pyrimidine base biosynthetic process
110	27	1241	51	0.643	3.00E-07	0.006	GO:0006413:	translational initiation
111	12	983	16	1.158	3.20E-07	0.006	GO:0042278:	purine nucleoside metabolic process
112	31	1180	66	0.57	4.00E-07	0.006	GO:0006417:	regulation of translation
113	16	1023	26	0.891	4.20E-07	0.006	GO:0009124:	nucleoside monophosphate biosynthetic process
114	13	698	24	0.959	4.50E-07	0.007	GO:0009156:	ribonucleoside monophosphate biosynthetic process
115	1173	1296	5209	0.212	4.80E-07	0.009	GO:0005622:	intracellular
116	13	707	24	0.953	5.20E-07	0.010	GO:0009167:	purine ribonucleoside monophosphate metabolic process
117	31	1241	64	0.567	5.50E-07	0.010	GO:0045182:	translation regulator activity
118	9	983	10	1.515	6.80E-07	0.012	GO:0006166:	purine ribonucleoside salvage
119	9	983	10	1.515	6.80E-07	0.012	GO:0043174:	nucleoside salvage
120	1225	1254	5737	0.375	7.00E-07	0.013	GO:0044464:	cell part
121	1225	1254	5738	0.373	8.10E-07	0.014	GO:0005623:	cell

122	11	937	15	1.147	9.10E-07	0.017	GO:0016073:	snRNA metabolic process
123	46	1424	101	0.441	9.30E-07	0.017	GO:0051168:	nuclear export
124	12	983	17	1.071	9.30E-07	0.017	GO:0009119:	ribonucleoside metabolic process
125	13	707	25	0.916	9.70E-07	0.020	GO:0009126:	purine nucleoside monophosphate metabolic process
126	58	719	260	0.348	1.00E-06	0.022	GO:0006519:	amino acid and derivative metabolic process
127	55	719	243	0.355	1.20E-06	0.026	GO:0006520:	amino acid metabolic process
128	15	596	38	0.787	1.30E-06	0.027	GO:0004812:	aminoacyl-tRNA ligase activity
129	15	596	38	0.787	1.30E-06	0.027	GO:0006418:	tRNA aminoacylation for protein translation
130	15	1080	24	0.878	1.50E-06	0.029	GO:0006206:	pyrimidine base metabolic process
131	15	983	26	0.845	1.80E-06	0.037	GO:0009116:	nucleoside metabolic process
132	15	596	39	0.769	1.90E-06	0.037	GO:0016875:	ligase activity, forming carbon-oxygen bonds
133	15	596	39	0.769	1.90E-06	0.037	GO:0016876:	ligase activity, forming aminoacyl-tRNA and related compounds
134	15	596	39	0.769	1.90E-06	0.037	GO:0043038:	amino acid activation
135	15	596	39	0.769	1.90E-06	0.037	GO:0043039:	tRNA aminoacylation
136	8	458	14	1.208	2.10E-06	0.044	GO:0000028:	ribosomal small subunit assembly and maintenance
137	12	698	23	0.925	2.20E-06	0.044	GO:0009168:	purine ribonucleoside monophosphate biosynthetic process
138	29	1360	57	0.557	2.50E-06	0.048	GO:0051656:	establishment of organelle localization
139	58	719	267	0.333	2.60E-06	0.049	GO:0009308:	amine metabolic process

Δpbf2 downregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	227	645	434	1.132	1.20E-116	<0.001	GO:0042254:	ribosome biogenesis and assembly
2	235	645	510	1.026	1.40E-105	<0.001	GO:0022613:	ribonucleoprotein complex biogenesis and assembly
3	152	712	304	0.964	6.90E-65	<0.001	GO:0005730:	nucleolus
4	404	1176	1014	0.56	1.40E-62	<0.001	GO:0043228:	non-membrane-bounded organelle
5	404	1176	1014	0.56	1.40E-62	<0.001	GO:0043232:	intracellular non-membrane-bounded organelle
6	136	735	284	0.897	5.80E-53	<0.001	GO:0016072:	rRNA metabolic process
7	130	1385	168	1.094	7.10E-52	<0.001	GO:0022626:	cytosolic ribosome
8	133	735	279	0.891	1.90E-51	<0.001	GO:0006364:	rRNA processing
9	121	1087	206	0.853	2.20E-40	<0.001	GO:0044445:	cytosolic part
10	491	1261	1476	0.388	2.50E-38	<0.001	GO:0006996:	organelle organization and biogenesis
11	53	754	64	1.542	5.50E-38	<0.001	GO:0042273:	ribosomal large subunit biogenesis and assembly
12	170	735	541	0.601	3.40E-36	<0.001	GO:0006396:	RNA processing
13	174	737	575	0.576	1.50E-34	<0.001	GO:0030529:	ribonucleoprotein complex
14	181	741	618	0.555	1.30E-33	<0.001	GO:0031981:	nuclear lumen
15	136	1087	282	0.671	9.50E-33	<0.001	GO:0005840:	ribosome
16	47	676	67	1.292	3.50E-30	<0.001	GO:0042255:	ribosome assembly
17	101	807	236	0.731	4.10E-30	<0.001	GO:0003735:	structural constituent of ribosome

18	101	834	236	0.713	7.00E-29	<0.001	GO:0033279:	ribosomal subunit
19	42	854	51	1.454	8.20E-28	<0.001	GO:0030490:	maturation of SSU-rRNA
20	64	1068	93	1.03	9.00E-28	<0.001	GO:0022625:	cytosolic large ribosomal subunit
21	41	854	50	1.443	5.00E-27	<0.001	GO:0000462:	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
22	40	854	48	1.48	6.30E-27	<0.001	GO:0032040:	small subunit processome
23	40	676	55	1.34	8.20E-27	<0.001	GO:0042257:	ribosomal subunit assembly
24	51	1125	64	1.239	2.80E-26	<0.001	GO:0022627:	cytosolic small ribosomal subunit
25	646	1270	2311	0.283	1.30E-24	<0.001	GO:0016043:	cellular component organization and biogenesis
26	29	554	36	1.612	2.00E-24	<0.001	GO:0000466:	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
27	349	737	1848	0.356	2.40E-24	<0.001	GO:0010467:	gene expression
28	32	676	41	1.452	2.70E-23	<0.001	GO:0000027:	ribosomal large subunit assembly and maintenance
29	29	554	38	1.509	3.30E-23	<0.001	GO:0000460:	maturation of 5.8S rRNA
30	88	1354	149	0.719	1.90E-22	<0.001	GO:0022618:	protein-RNA complex assembly
31	271	803	1245	0.347	6.90E-21	<0.001	GO:0016070:	RNA metabolic process
32	65	633	182	0.714	2.10E-20	<0.001	GO:0044452:	nucleolar part
33	80	1341	138	0.703	4.60E-20	<0.001	GO:0006399:	tRNA metabolic process
34	628	1352	2159	0.25	4.70E-20	<0.001	GO:0005634:	nucleus
35	115	827	369	0.498	2.70E-19	<0.001	GO:0005198:	structural molecule activity
36	115	362	880	0.475	8.20E-18	<0.001	GO:0031974:	membrane-enclosed lumen
37	115	362	880	0.475	8.20E-18	<0.001	GO:0043233:	organelle lumen
38	516	1352	1732	0.244	1.10E-17	<0.001	GO:0006139:	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
39	21	972	21	2.358	1.90E-17	<0.001	GO:0030515:	snoRNA binding
40	19	518	24	1.592	1.20E-16	<0.001	GO:0000469:	cleavages during rRNA processing
41	53	703	138	0.702	2.20E-16	<0.001	GO:0015934:	large ribosomal subunit
42	41	1395	55	0.989	7.50E-16	<0.001	GO:0006400:	tRNA modification
43	1003	1285	4171	0.246	2.00E-15	<0.001	GO:0043226:	organelle

44	1003	1285	4171	0.246	2.00E-15	<0.001	GO:0043229:	intracellular organelle
45	15	359	20	1.666	3.80E-15	<0.001	GO:0030684:	preribosome
46	56	1341	95	0.713	7.80E-15	<0.001	GO:0008033:	tRNA processing
47	45	834	98	0.743	9.60E-15	<0.001	GO:0015935:	small ribosomal subunit
48	17	518	22	1.543	1.10E-14	<0.001	GO:0000447:	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
49	17	518	22	1.543	1.10E-14	<0.001	GO:0000478:	endonucleolytic cleavages during rRNA processing
50	17	518	22	1.543	1.10E-14	<0.001	GO:0000479:	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
51	14	359	19	1.635	5.00E-14	<0.001	GO:0030685:	nucleolar preribosome
52	15	518	19	1.576	2.40E-13	<0.001	GO:0000480:	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
53	176	570	1143	0.317	4.30E-13	<0.001	GO:0044428:	nuclear part
54	15	518	20	1.488	8.90E-13	<0.001	GO:0000472:	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
55	21	904	29	1.165	5.30E-12	<0.001	GO:0000054:	ribosome export from nucleus
56	21	904	29	1.165	5.30E-12	<0.001	GO:0033750:	ribosome localization
57	21	904	29	1.165	5.30E-12	<0.001	GO:0033753:	establishment of ribosome localization
58	502	1385	1745	0.191	1.30E-11	<0.001	GO:0032991:	macromolecular complex
59	13	754	14	1.806	2.10E-11	<0.001	GO:0000463:	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
60	13	754	14	1.806	2.10E-11	<0.001	GO:0000470:	maturation of LSU-rRNA
61	27	1268	38	0.961	4.50E-11	<0.001	GO:0003743:	translation initiation factor activity
62	14	924	15	1.733	4.70E-11	<0.001	GO:0030488:	tRNA methylation

63	651	1262	2623	0.178	6.70E-11	<0.001	GO:0044422:	organelle part
64	651	1262	2623	0.178	6.70E-11	<0.001	GO:0044446:	intracellular organelle part
65	16	1213	17	1.645	9.30E-11	<0.001	GO:0005666:	DNA-directed RNA polymerase III complex
66	17	659	28	1.103	2.60E-10	<0.001	GO:0004004:	ATP-dependent RNA helicase activity
67	17	659	28	1.103	2.60E-10	<0.001	GO:0008186:	RNA-dependent ATPase activity
68	21	659	42	0.923	2.80E-10	<0.001	GO:0003724:	RNA helicase activity
69	17	740	26	1.128	3.00E-10	<0.001	GO:0042274:	ribosomal small subunit biogenesis and assembly
70	36	941	81	0.65	5.40E-10	<0.001	GO:0016741:	transferase activity, transferring one-carbon groups
71	35	941	79	0.647	1.00E-09	<0.001	GO:0008168:	methyltransferase activity
72	22	1213	31	0.98	1.30E-09	<0.001	GO:0055029:	nuclear DNA-directed RNA polymerase complex
73	12	924	13	1.668	1.80E-09	<0.001	GO:0008175:	tRNA methyltransferase activity
74	23	1213	34	0.916	2.30E-09	<0.001	GO:0003899:	DNA-directed RNA polymerase activity
75	23	1213	34	0.916	2.30E-09	<0.001	GO:0034062:	RNA polymerase activity
76	1189	1379	4878	0.209	4.30E-09	0.001	GO:0009987:	cellular process
77	8	570	8	2.217	6.20E-09	0.001	GO:0030687:	nucleolar preribosome, large subunit precursor
78	16	924	23	1.091	7.10E-09	0.001	GO:0008173:	RNA methyltransferase activity
79	22	1213	33	0.897	8.00E-09	0.001	GO:0000428:	DNA-directed RNA polymerase complex
80	22	1213	33	0.897	8.00E-09	0.001	GO:0030880:	RNA polymerase complex
81	127	1268	385	0.289	1.20E-08	0.001	GO:0065003:	macromolecular complex assembly
82	553	797	3643	0.195	1.40E-08	0.001	GO:0044238:	primary metabolic process
83	58	1393	128	0.452	1.90E-08	0.001	GO:0006913:	nucleocytoplasmic transport
84	58	1393	128	0.452	1.90E-08	0.001	GO:0051169:	nuclear transport
85	485	797	3119	0.184	2.10E-08	0.001	GO:0043170:	macromolecule metabolic process
86	135	737	711	0.264	2.10E-08	0.001	GO:0006412:	translation
87	7	263	10	1.682	3.00E-08	0.001	GO:0030686:	90S preribosome
88	30	1172	58	0.655	3.40E-08	0.001	GO:0008135:	translation factor activity, nucleic acid binding
89	1211	1342	5171	0.225	4.00E-08	0.001	GO:0044424:	intracellular part

90	22	1213	35	0.827	4.00E-08	0.001	GO:0006360:	transcription from RNA polymerase I promoter
91	5	216	5	2.48	5.70E-08	0.001	GO:0030689:	Noc complex
92	1188	1309	5209	0.227	7.60E-08	0.004	GO:0005622:	intracellular
93	566	797	3777	0.186	7.80E-08	0.004	GO:0044237:	cellular metabolic process
94	25	941	54	0.678	9.00E-08	0.004	GO:0008757:	S-adenosylmethionine-dependent methyltransferase activity
95	8	807	8	2.045	1.00E-07	0.004	GO:0030688:	nucleolar preribosome, small subunit precursor
96	587	794	3970	0.189	1.20E-07	0.004	GO:0008152:	metabolic process
97	189	737	1111	0.213	1.40E-07	0.005	GO:0044249:	cellular biosynthetic process
98	28	1128	57	0.631	1.70E-07	0.006	GO:0051656:	establishment of organelle localization
99	1317	1348	5737	0.383	1.90E-07	0.006	GO:0044464:	cell part
100	1317	1348	5738	0.382	2.20E-07	0.007	GO:0005623:	cell
101	10	780	13	1.31	2.50E-07	0.008	GO:0006450:	regulation of translational fidelity
102	12	1213	14	1.301	2.60E-07	0.008	GO:0005736:	DNA-directed RNA polymerase I complex
103	13	1214	16	1.188	2.60E-07	0.008	GO:0042278:	purine nucleoside metabolic process
104	26	1172	51	0.641	4.10E-07	0.011	GO:0006413:	translational initiation
105	25	346	143	0.571	4.20E-07	0.012	GO:0009451:	RNA modification
106	46	1393	101	0.454	4.70E-07	0.012	GO:0051168:	nuclear export
107	9	688	12	1.328	5.00E-07	0.014	GO:0006207:	'de novo' pyrimidine base biosynthetic process
108	233	782	1369	0.186	5.30E-07	0.014	GO:0009058:	biosynthetic process
109	36	1309	76	0.52	5.50E-07	0.014	GO:0006401:	RNA catabolic process
110	30	1172	64	0.571	5.60E-07	0.015	GO:0045182:	translation regulator activity
111	10	688	15	1.176	6.20E-07	0.015	GO:0019856:	pyrimidine base biosynthetic process
112	9	69	91	1.048	7.40E-07	0.017	GO:0009277:	fungal-type cell wall
113	163	794	883	0.21	8.90E-07	0.022	GO:0009059:	macromolecule biosynthetic process
114	10	721	15	1.153	9.70E-07	0.023	GO:0016073:	snRNA metabolic process
115	18	1349	27	0.834	1.00E-06	0.023	GO:0009123:	nucleoside monophosphate metabolic process
116	12	1214	15	1.155	1.10E-06	0.023	GO:0046128:	purine ribonucleoside metabolic process
117	30	1172	66	0.547	1.30E-06	0.024	GO:0006417:	regulation of translation
118	9	611	15	1.118	3.10E-06	0.048	GO:0006220:	pyrimidine nucleotide metabolic process

Δpbf1Δpbf2 downregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	266	1344	510	0.652	3.60E-54	<0.001	GO:0022613:	ribonucleoprotein complex biogenesis and assembly
2	240	1354	434	0.696	4.30E-54	<0.001	GO:0042254:	ribosome biogenesis and assembly
3	74	352	168	1.198	1.80E-48	<0.001	GO:0022626:	cytosolic ribosome
4	75	352	206	1.059	5.40E-42	<0.001	GO:0044445:	cytosolic part
5	74	352	236	0.958	2.90E-36	<0.001	GO:0003735:	structural constituent of ribosome
6	386	1355	1014	0.409	1.80E-35	<0.001	GO:0043228:	non-membrane-bounded organelle
7	386	1355	1014	0.409	1.80E-35	<0.001	GO:0043232:	intracellular non-membrane-bounded organelle
8	63	251	236	1.036	2.10E-35	<0.001	GO:0033279:	ribosomal subunit
9	78	352	282	0.883	5.80E-34	<0.001	GO:0005840:	ribosome
10	37	251	93	1.248	9.50E-28	<0.001	GO:0022625:	cytosolic large ribosomal subunit
11	40	531	64	1.265	5.50E-27	<0.001	GO:0022627:	cytosolic small ribosomal subunit
12	66	251	369	0.81	6.20E-26	<0.001	GO:0005198:	structural molecule activity
13	230	1355	575	0.409	1.90E-23	<0.001	GO:0030529:	ribonucleoprotein complex
14	144	1354	304	0.526	7.30E-23	<0.001	GO:0005730:	nucleolus
15	133	1320	284	0.529	1.20E-21	<0.001	GO:0016072:	rRNA metabolic process
16	468	1355	1476	0.282	1.40E-21	<0.001	GO:0006996:	organelle organization and biogenesis
17	131	1320	279	0.53	1.80E-21	<0.001	GO:0006364:	rRNA processing

18	37	251	138	0.99	8.60E-21	<0.001	GO:0015934:	large ribosomal subunit
19	38	463	98	0.915	3.10E-18	<0.001	GO:0015935:	small ribosomal subunit
20	48	1337	67	0.954	5.70E-18	<0.001	GO:0042255:	ribosome assembly
21	46	1325	64	0.964	1.60E-17	<0.001	GO:0042273:	ribosomal large subunit biogenesis and assembly
22	80	1343	149	0.626	2.80E-17	<0.001	GO:0022618:	protein-RNA complex assembly
23	41	1337	55	1.013	1.50E-16	<0.001	GO:0042257:	ribosomal subunit assembly
24	54	98	1111	0.751	2.60E-16	<0.001	GO:0044249:	cellular biosynthetic process
25	649	1355	2311	0.221	2.90E-16	<0.001	GO:0016043:	cellular component organization and biogenesis
26	37	1354	48	1.062	1.10E-15	<0.001	GO:0032040:	small subunit processome
27	60	101	1369	0.711	1.40E-15	<0.001	GO:0009058:	biosynthetic process
28	48	120	711	0.723	1.50E-15	<0.001	GO:0006412:	translation
29	193	1320	541	0.331	1.00E-14	<0.001	GO:0006396:	RNA processing
30	40	101	659	0.751	4.20E-14	<0.001	GO:0005829:	cytosol
31	46	101	883	0.707	6.30E-14	<0.001	GO:0009059:	macromolecule biosynthetic process
32	36	1354	51	0.92	2.80E-13	<0.001	GO:0030490:	maturation of SSU-rRNA
33	68	1310	138	0.56	4.90E-13	<0.001	GO:0006399:	tRNA metabolic process
34	35	1354	50	0.907	8.80E-13	<0.001	GO:0000462:	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
35	211	1354	618	0.287	1.50E-12	<0.001	GO:0031981:	nuclear lumen
36	30	1298	41	0.994	2.00E-12	<0.001	GO:0000027:	ribosomal large subunit assembly and maintenance
37	363	1320	1245	0.216	8.50E-12	<0.001	GO:0016070:	RNA metabolic process
38	27	1198	38	0.992	1.10E-11	<0.001	GO:0000460:	maturation of 5.8S rRNA
39	27	1318	36	1.022	1.40E-11	<0.001	GO:0000466:	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
40	28	1343	38	0.984	2.00E-11	<0.001	GO:0003743:	translation initiation factor activity
41	687	1340	2623	0.174	7.20E-11	<0.001	GO:0044422:	organelle part
42	687	1340	2623	0.174	7.20E-11	<0.001	GO:0044446:	intracellular organelle part
43	1032	1355	4171	0.192	1.20E-10	<0.001	GO:0043226:	organelle

44	1032	1355	4171	0.192	1.20E-10	<0.001	GO:0043229:	intracellular organelle
45	497	1320	1848	0.176	5.20E-10	<0.001	GO:0010467:	gene expression
46	33	1310	55	0.738	7.90E-10	<0.001	GO:0006400:	tRNA modification
47	20	1337	26	1.049	4.30E-09	<0.001	GO:0042274:	ribosomal small subunit biogenesis and assembly
48	47	1339	96	0.537	5.80E-09	<0.001	GO:0016757:	transferase activity, transferring glycosyl groups
49	21	1295	29	0.972	5.90E-09	<0.001	GO:0000054:	ribosome export from nucleus
50	21	1295	29	0.972	5.90E-09	<0.001	GO:0033750:	ribosome localization
51	21	1295	29	0.972	5.90E-09	<0.001	GO:0033753:	establishment of ribosome localization
52	46	1310	95	0.54	6.30E-09	<0.001	GO:0008033:	tRNA processing
53	463	1321	1732	0.164	1.00E-08	<0.001	GO:0006139:	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
54	33	1352	58	0.665	1.20E-08	<0.001	GO:0008135:	translation factor activity, nucleic acid binding
55	16	1224	20	1.163	1.60E-08	0.001	GO:0030684:	preribosome
56	16	1190	21	1.091	3.70E-08	0.001	GO:0030515:	snoRNA binding
57	18	1318	24	1.012	4.10E-08	0.001	GO:0000469:	cleavages during rRNA processing
58	472	1355	1745	0.154	5.60E-08	0.001	GO:0032991:	macromolecular complex
59	15	1224	19	1.135	6.50E-08	0.001	GO:0030685:	nucleolar preribosome
60	63	1101	182	0.391	7.20E-08	0.001	GO:0044452:	nucleolar part
61	29	1343	51	0.667	8.30E-08	0.001	GO:0006413:	translational initiation
62	33	1140	72	0.569	1.50E-07	0.001	GO:0006486:	protein amino acid glycosylation

63	344	1304	1276	0.163	2.20E-07	0.003	GO:0031224:	intrinsic to membrane
64	12	1198	14	1.308	2.20E-07	0.003	GO:0000463:	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
65	12	1198	14	1.308	2.20E-07	0.003	GO:0000470:	maturation of LSU-rRNA
66	33	1140	73	0.558	2.20E-07	0.003	GO:0043413:	biopolymer glycosylation
67	34	1140	77	0.54	2.90E-07	0.003	GO:0009101:	glycoprotein biosynthetic process
68	33	1352	64	0.573	3.00E-07	0.003	GO:0045182:	translation regulator activity
69	34	1140	78	0.53	4.30E-07	0.005	GO:0009100:	glycoprotein metabolic process
70	16	1318	22	0.962	4.90E-07	0.006	GO:0000447:	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
71	16	1318	22	0.962	4.90E-07	0.006	GO:0000478:	endonucleolytic cleavages during rRNA processing
72	16	1318	22	0.962	4.90E-07	0.006	GO:0000479:	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
73	10	753	14	1.218	5.50E-07	0.009	GO:0005736:	DNA-directed RNA polymerase I complex
74	52	1295	128	0.41	6.10E-07	0.011	GO:0006913:	nucleocytoplasmic transport
75	52	1295	128	0.41	6.10E-07	0.011	GO:0051169:	nuclear transport
76	8	252	20	1.205	6.80E-07	0.012	GO:0000079:	regulation of cyclin-dependent protein kinase activity
77	126	1344	385	0.248	7.50E-07	0.012	GO:0065003:	macromolecular complex assembly
78	33	1148	77	0.513	1.20E-06	0.020	GO:0016758:	transferase activity, transferring hexosyl groups
79	29	1333	57	0.568	1.60E-06	0.026	GO:0051656:	establishment of organelle localization
80	12	1269	15	1.13	1.80E-06	0.027	GO:0030488:	tRNA methylation
81	8	496	13	1.242	1.80E-06	0.027	GO:0006450:	regulation of translational fidelity
82	327	1304	1228	0.152	1.90E-06	0.027	GO:0016021:	integral to membrane
83	14	1318	19	0.978	2.10E-06	0.030	GO:0000480:	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
84	32	1343	66	0.523	2.20E-06	0.033	GO:0006417:	regulation of translation
85	8	252	23	1.111	2.40E-06	0.034	GO:0016538:	cyclin-dependent protein kinase regulator activity
86	131	1301	425	0.228	2.60E-06	0.038	GO:0005783:	endoplasmic reticulum

WT upregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	172	856	536	0.521	6.00E-29	<0.001	GO:0009056:	catabolic process
2	196	1134	503	0.494	1.40E-28	<0.001	GO:0044248:	cellular catabolic process
3	94	1130	179	0.71	6.10E-25	<0.001	GO:0044257:	cellular protein catabolic process
4	99	1145	195	0.673	2.80E-24	<0.001	GO:0030163:	protein catabolic process
5	898	1141	4021	0.318	8.10E-23	<0.001	GO:0005737:	cytoplasm
6	38	1081	45	1.385	3.20E-22	<0.001	GO:0000502:	proteasome complex
7	87	1130	170	0.684	3.90E-22	<0.001	GO:0051603:	proteolysis involved in cellular protein catabolic process
8	86	1130	167	0.689	3.90E-22	<0.001	GO:0006511:	ubiquitin-dependent protein catabolic process
9	86	1130	167	0.689	3.90E-22	<0.001	GO:0019941:	modification-dependent protein catabolic process
10	121	1130	287	0.534	4.50E-21	<0.001	GO:0006508:	proteolysis
11	86	1130	174	0.653	1.40E-20	<0.001	GO:0043632:	modification-dependent macromolecule catabolic process
12	61	381	287	0.662	4.10E-18	<0.001	GO:0005975:	carbohydrate metabolic process
13	132	1130	352	0.449	1.20E-17	<0.001	GO:0044265:	cellular macromolecule catabolic process
14	93	724	324	0.511	5.40E-17	<0.001	GO:0016491:	oxidoreductase activity
15	133	1053	391	0.422	2.10E-16	<0.001	GO:0009057:	macromolecule catabolic process
16	51	378	241	0.654	2.70E-15	<0.001	GO:0044262:	cellular carbohydrate metabolic process
17	107	1053	306	0.434	3.10E-14	<0.001	GO:0043285:	biopolymer catabolic process

18	53	499	211	0.608	4.90E-14	<0.001	GO:0006066:	alcohol metabolic process
19	37	489	121	0.728	3.50E-13	<0.001	GO:0005996:	monosaccharide metabolic process
20	295	1141	1108	0.242	1.80E-12	<0.001	GO:0005739:	mitochondrion
21	164	1141	532	0.314	3.10E-12	<0.001	GO:0044429:	mitochondrial part
22	72	1047	193	0.473	1.60E-11	<0.001	GO:0006091:	generation of precursor metabolites and energy
23	14	1029	14	2.154	1.70E-11	<0.001	GO:0004298:	threonine endopeptidase activity
24	14	1029	14	2.154	1.70E-11	<0.001	GO:0005839:	proteasome core complex
25	16	114	97	1.078	2.10E-11	<0.001	GO:0016052:	carbohydrate catabolic process
26	16	114	97	1.078	2.10E-11	<0.001	GO:0044275:	cellular carbohydrate catabolic process
27	390	833	2214	0.211	9.40E-11	<0.001	GO:0003824:	catalytic activity
28	18	1068	22	1.287	9.50E-11	<0.001	GO:0005838:	proteasome regulatory particle
29	18	1068	22	1.287	9.50E-11	<0.001	GO:0022624:	proteasome accessory complex
30	32	483	114	0.678	1.30E-10	<0.001	GO:0019318:	hexose metabolic process
31	11	82	61	1.273	3.60E-10	<0.001	GO:0046365:	monosaccharide catabolic process
32	27	483	88	0.73	4.20E-10	<0.001	GO:0006006:	glucose metabolic process
33	62	428	388	0.44	4.40E-10	<0.001	GO:0006082:	organic acid metabolic process
34	62	428	388	0.44	4.40E-10	<0.001	GO:0019752:	carboxylic acid metabolic process
35	107	1047	353	0.341	5.30E-10	<0.001	GO:0005740:	mitochondrial envelope
36	21	407	66	0.833	8.40E-10	<0.001	GO:0046164:	alcohol catabolic process
37	38	571	142	0.567	1.60E-09	<0.001	GO:0006732:	coenzyme metabolic process
38	9	549	10	1.807	3.80E-09	<0.001	GO:0005991:	trehalose metabolic process
39	56	1047	155	0.446	1.20E-08	<0.001	GO:0015980:	energy derivation by oxidation of organic compounds
40	18	785	33	0.91	1.50E-08	<0.001	GO:0006084:	acetyl-CoA metabolic process
41	5	38	15	1.971	2.20E-08	<0.001	GO:0006098:	pentose-phosphate shunt
42	35	513	151	0.536	2.40E-08	<0.001	GO:0032787:	monocarboxylic acid metabolic process
43	134	890	587	0.264	2.80E-08	<0.001	GO:0006950:	response to stress

44	96	1047	330	0.312	4.40E-08	<0.001	GO:0031966:	mitochondrial membrane
45	16	831	27	0.96	4.40E-08	<0.001	GO:0022900:	electron transport chain
46	16	831	27	0.96	4.40E-08	<0.001	GO:0022904:	respiratory electron transport chain
47	16	831	27	0.96	4.40E-08	<0.001	GO:0042773:	ATP synthesis coupled electron transport
48	16	831	27	0.96	4.40E-08	<0.001	GO:0042775:	organelle ATP synthesis coupled electron transport
49	16	831	27	0.96	4.40E-08	<0.001	GO:0055114:	oxidation reduction
50	187	891	893	0.222	4.50E-08	<0.001	GO:0050896:	response to stimulus
51	41	571	179	0.477	5.00E-08	<0.001	GO:0051186:	cofactor metabolic process
52	5	38	18	1.861	6.10E-08	<0.001	GO:0006740:	NADPH regeneration
53	27	633	85	0.616	6.60E-08	<0.001	GO:0016614:	oxidoreductase activity, acting on CH-OH group of donors
54	16	785	29	0.919	7.80E-08	0.001	GO:0006099:	tricarboxylic acid cycle
55	16	785	29	0.919	7.80E-08	0.001	GO:0046356:	acetyl-CoA catabolic process
56	16	1103	23	0.997	9.70E-08	0.001	GO:0016209:	antioxidant activity
57	8	65	56	1.256	1.10E-07	0.002	GO:0019320:	hexose catabolic process
58	11	381	25	1.081	1.10E-07	0.002	GO:0006081:	aldehyde metabolic process
59	5	38	21	1.774	1.40E-07	0.002	GO:0006739:	NADP metabolic process
60	43	1070	112	0.474	1.60E-07	0.002	GO:0044455:	mitochondrial membrane part
61	13	310	44	0.913	1.70E-07	0.002	GO:0009310:	amine catabolic process
62	13	310	44	0.913	1.70E-07	0.002	GO:0044270:	nitrogen compound catabolic process

63	17	785	34	0.832	2.00E-07	0.002	GO:0051187:	cofactor catabolic process
64	21	378	94	0.659	2.20E-07	0.002	GO:0016051:	carbohydrate biosynthetic process
65	10	905	12	1.38	2.80E-07	0.003	GO:0007039:	vacuolar protein catabolic process
66	6	378	7	1.817	3.90E-07	0.006	GO:0005992:	trehalose biosynthetic process
67	6	378	7	1.817	3.90E-07	0.006	GO:0046351:	disaccharide biosynthetic process
68	31	972	78	0.547	4.30E-07	0.007	GO:0016616:	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
69	9	939	10	1.539	4.50E-07	0.007	GO:0008541:	proteasome regulatory particle, lid subcomplex
70	5	82	13	1.695	4.90E-07	0.007	GO:0019321:	pentose metabolic process
71	11	1126	13	1.305	5.00E-07	0.007	GO:0008154:	actin polymerization and/or depolymerization
72	7	349	11	1.441	5.60E-07	0.008	GO:0004033:	aldo-keto reductase activity
73	39	1047	104	0.468	6.70E-07	0.01	GO:0009060:	aerobic respiration
74	7	796	7	1.997	6.90E-07	0.01	GO:0019774:	proteasome core complex, beta-subunit complex
75	25	1044	54	0.623	7.10E-07	0.01	GO:0006119:	oxidative phosphorylation
76	16	785	33	0.806	8.00E-07	0.013	GO:0009109:	coenzyme catabolic process
77	33	868	97	0.5	8.10E-07	0.013	GO:0006457:	protein folding
78	13	1103	18	1.044	8.40E-07	0.014	GO:0004601:	peroxidase activity
79	13	1103	18	1.044	8.40E-07	0.014	GO:0016684:	oxidoreductase activity, acting on peroxide as acceptor
80	15	771	30	0.84	8.60E-07	0.014	GO:0005746:	mitochondrial respiratory chain
81	7	65	51	1.231	9.80E-07	0.017	GO:0006007:	glucose catabolic process
82	29	1132	64	0.563	9.80E-07	0.017	GO:0006623:	protein targeting to vacuole
83	45	436	296	0.392	1.00E-06	0.018	GO:0006807:	nitrogen compound metabolic process
84	58	1051	182	0.36	1.10E-06	0.019	GO:0008233:	peptidase activity
85	39	1047	107	0.448	1.60E-06	0.025	GO:0045333:	cellular respiration
86	4	217	4	2.389	1.60E-06	0.028	GO:0004866:	endopeptidase inhibitor activity
87	4	217	4	2.389	1.60E-06	0.028	GO:0030414:	protease inhibitor activity
88	12	622	25	0.912	1.90E-06	0.03	GO:0004857:	enzyme inhibitor activity
89	8	415	15	1.193	2.00E-06	0.03	GO:0006536:	glutamate metabolic process

90	7	310	14	1.274	2.20E-06	0.034	GO:0042219:	amino acid derivative catabolic process
91	34	1031	91	0.473	2.70E-06	0.039	GO:0031968:	organelle outer membrane
92	10	192	50	0.915	2.90E-06	0.043	GO:0019362:	pyridine nucleotide metabolic process
93	22	1086	46	0.627	3.30E-06	0.045	GO:0006914:	autophagy
94	69	1090	228	0.309	3.60E-06	0.049	GO:0005773:	vacuole
95	4	264	4	2.299	3.60E-06	0.049	GO:0005946:	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)

Δpbf1 upregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	208	1168	536	0.476	3.40E-28	<0.001	GO:0009056:	catabolic process
2	198	1168	503	0.484	9.90E-28	<0.001	GO:0044248:	cellular catabolic process
3	117	1446	195	0.705	1.10E-27	<0.001	GO:0030163:	protein catabolic process
4	109	1446	179	0.719	1.30E-26	<0.001	GO:0044257:	cellular protein catabolic process
5	42	1315	45	1.652	7.30E-25	<0.001	GO:0000502:	proteasome complex
6	101	1446	167	0.709	2.30E-24	<0.001	GO:0006511:	ubiquitin-dependent protein catabolic process
7	101	1446	167	0.709	2.30E-24	<0.001	GO:0019941:	modification-dependent protein catabolic process
8	102	1446	170	0.701	3.20E-24	<0.001	GO:0051603:	proteolysis involved in cellular protein catabolic process
9	101	1446	174	0.665	2.00E-22	<0.001	GO:0043632:	modification-dependent macromolecule catabolic process
10	138	1408	287	0.513	5.50E-21	<0.001	GO:0006508:	proteolysis
11	68	428	287	0.668	4.70E-20	<0.001	GO:0005975:	carbohydrate metabolic process
12	1102	1450	4021	0.254	1.50E-18	<0.001	GO:0005737:	cytoplasm
13	59	428	241	0.679	3.50E-18	<0.001	GO:0044262:	cellular carbohydrate metabolic process
14	146	1315	352	0.436	9.30E-18	<0.001	GO:0044265:	cellular macromolecule catabolic process
15	155	1315	391	0.404	1.20E-16	<0.001	GO:0009057:	macromolecule catabolic process
16	98	827	324	0.472	1.50E-15	<0.001	GO:0016491:	oxidoreductase activity
17	133	1446	306	0.412	1.20E-14	<0.001	GO:0043285:	biopolymer catabolic process

18	44	645	121	0.704	3.70E-14	<0.001	GO:0005996:	monosaccharide metabolic process
19	203	1471	532	0.313	1.10E-13	<0.001	GO:0044429:	mitochondrial part
20	368	1471	1108	0.235	1.30E-13	<0.001	GO:0005739:	mitochondrion
21	49	445	211	0.619	1.40E-13	<0.001	GO:0006066:	alcohol metabolic process
22	21	1315	22	1.717	2.00E-13	<0.001	GO:0005838:	proteasome regulatory particle
23	21	1315	22	1.717	2.00E-13	<0.001	GO:0022624:	proteasome accessory complex
24	467	1003	2214	0.213	2.00E-12	<0.001	GO:0003824:	catalytic activity
25	16	107	97	1.111	7.60E-12	<0.001	GO:0016052:	carbohydrate catabolic process
26	16	107	97	1.111	7.60E-12	<0.001	GO:0044275:	cellular carbohydrate catabolic process
27	79	1203	193	0.463	9.80E-12	<0.001	GO:0006091:	generation of precursor metabolites and energy
28	31	428	114	0.719	2.80E-11	<0.001	GO:0019318:	hexose metabolic process
29	20	343	61	0.935	5.40E-11	<0.001	GO:0046365:	monosaccharide catabolic process
30	14	1161	14	2.09	9.20E-11	<0.001	GO:0004298:	threonine endopeptidase activity
31	14	1161	14	2.09	9.20E-11	<0.001	GO:0005839:	proteasome core complex
32	28	497	88	0.739	1.50E-10	<0.001	GO:0006006:	glucose metabolic process
33	22	423	66	0.845	2.50E-10	<0.001	GO:0046164:	alcohol catabolic process
34	64	1203	155	0.466	6.30E-10	<0.001	GO:0015980:	energy derivation by oxidation of organic compounds
35	129	1370	353	0.313	1.00E-09	<0.001	GO:0005740:	mitochondrial envelope
36	69	522	388	0.395	2.40E-09	<0.001	GO:0006082:	organic acid metabolic process
37	69	522	388	0.395	2.40E-09	<0.001	GO:0019752:	carboxylic acid metabolic process
38	8	387	10	1.703	1.10E-08	<0.001	GO:0005991:	trehalose metabolic process
39	51	1003	142	0.464	1.60E-08	<0.001	GO:0006732:	coenzyme metabolic process
40	68	1458	152	0.417	1.60E-08	<0.001	GO:0006512:	ubiquitin cycle
41	24	428	94	0.676	2.00E-08	<0.001	GO:0016051:	carbohydrate biosynthetic process
42	18	826	33	0.884	3.40E-08	<0.001	GO:0006084:	acetyl-CoA metabolic process
43	16	343	56	0.846	4.50E-08	<0.001	GO:0019320:	hexose catabolic process

44	166	1425	489	0.242	4.80E-08	<0.001	GO:0043687:	post-translational protein modification
45	18	1437	23	1.036	5.50E-08	<0.001	GO:0016209:	antioxidant activity
46	43	1133	104	0.496	6.90E-08	0.002	GO:0009060:	aerobic respiration
47	116	1370	330	0.284	9.20E-08	0.003	GO:0031966:	mitochondrial membrane
48	58	1003	179	0.397	1.10E-07	0.003	GO:0051186:	cofactor metabolic process
49	28	694	85	0.593	1.10E-07	0.003	GO:0016614:	oxidoreductase activity, acting on CH-OH group of donors
50	19	968	34	0.825	1.20E-07	0.003	GO:0051187:	cofactor catabolic process
51	16	826	29	0.893	1.60E-07	0.004	GO:0006099:	tricarboxylic acid cycle
52	16	826	29	0.893	1.60E-07	0.004	GO:0046356:	acetyl-CoA catabolic process
53	15	1437	18	1.154	1.70E-07	0.004	GO:0004601:	peroxidase activity
54	15	1437	18	1.154	1.70E-07	0.004	GO:0016684:	oxidoreductase activity, acting on peroxide as acceptor
55	30	428	151	0.538	1.70E-07	0.004	GO:0032787:	monocarboxylic acid metabolic process
56	5	57	15	1.774	1.80E-07	0.004	GO:0006098:	pentose-phosphate shunt
57	43	1133	107	0.475	1.80E-07	0.004	GO:0045333:	cellular respiration
58	280	1470	893	0.18	1.90E-07	0.004	GO:0050896:	response to stimulus
59	9	580	13	1.303	3.40E-07	0.01	GO:0019321:	pentose metabolic process
60	12	535	25	0.986	3.80E-07	0.011	GO:0006081:	aldehyde metabolic process
61	18	968	33	0.801	4.10E-07	0.012	GO:0009109:	coenzyme catabolic process
62	7	338	11	1.456	4.50E-07	0.012	GO:0004033:	aldo-keto reductase activity

63	6	387	7	1.806	4.50E-07	0.012	GO:0005992:	trehalose biosynthetic process
64	6	387	7	1.806	4.50E-07	0.012	GO:0046351:	disaccharide biosynthetic process
65	5	57	18	1.665	5.00E-07	0.012	GO:0006740:	NADPH regeneration
66	14	343	51	0.821	5.50E-07	0.013	GO:0006007:	glucose catabolic process
67	45	218	587	0.406	6.40E-07	0.018	GO:0006950:	response to stress
68	86	1419	228	0.308	7.40E-07	0.022	GO:0005773:	vacuole
69	79	1403	207	0.322	7.60E-07	0.022	GO:0016310:	phosphorylation
70	50	504	296	0.376	7.90E-07	0.023	GO:0006807:	nitrogen compound metabolic process
71	9	522	15	1.194	8.00E-07	0.023	GO:0006536:	glutamate metabolic process
72	25	694	78	0.575	9.90E-07	0.03	GO:0016616:	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
73	9	1315	9	1.836	1.10E-06	0.034	GO:0008540:	proteasome regulatory particle, base subcomplex
74	5	57	21	1.577	1.20E-06	0.034	GO:0006739:	NADP metabolic process
75	7	289	14	1.307	1.40E-06	0.038	GO:0042219:	amino acid derivative catabolic process
76	32	1372	64	0.537	1.60E-06	0.039	GO:0006623:	protein targeting to vacuole
77	14	803	27	0.85	1.90E-06	0.044	GO:0022900:	electron transport chain
78	14	803	27	0.85	1.90E-06	0.044	GO:0022904:	respiratory electron transport chain
79	14	803	27	0.85	1.90E-06	0.044	GO:0042773:	ATP synthesis coupled electron transport
80	14	803	27	0.85	1.90E-06	0.044	GO:0042775:	organelle ATP synthesis coupled electron transport
81	14	803	27	0.85	1.90E-06	0.044	GO:0055114:	oxidation reduction

Δpbf2 upregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	268	1696	536	0.454	2.40E-29	<0.001	GO:0009056:	catabolic process
2	121	1696	179	0.75	1.00E-28	<0.001	GO:0044257:	cellular protein catabolic process
3	254	1696	503	0.46	1.30E-28	<0.001	GO:0044248:	cellular catabolic process
4	123	1565	195	0.714	1.70E-28	<0.001	GO:0030163:	protein catabolic process
5	108	1565	167	0.741	1.90E-26	<0.001	GO:0006511:	ubiquitin-dependent protein catabolic process
6	108	1565	167	0.741	1.90E-26	<0.001	GO:0019941:	modification-dependent protein catabolic process
7	110	1591	170	0.732	2.70E-26	<0.001	GO:0051603:	proteolysis involved in cellular protein catabolic process
8	108	1565	174	0.692	2.80E-24	<0.001	GO:0043632:	modification-dependent macromolecule catabolic process
9	41	1381	45	1.504	2.10E-22	<0.001	GO:0000502:	proteasome complex
10	149	1591	287	0.507	3.70E-21	<0.001	GO:0006508:	proteolysis
11	106	828	324	0.526	1.60E-19	<0.001	GO:0016491:	oxidoreductase activity
12	77	565	287	0.597	1.20E-18	<0.001	GO:0005975:	carbohydrate metabolic process
13	172	1696	352	0.415	1.80E-17	<0.001	GO:0044265:	cellular macromolecule catabolic process
14	185	1696	391	0.389	6.60E-17	<0.001	GO:0009057:	macromolecule catabolic process
15	1248	1670	4021	0.226	9.80E-17	<0.001	GO:0005737:	cytoplasm
16	66	565	241	0.603	1.50E-16	<0.001	GO:0044262:	cellular carbohydrate metabolic process
17	233	1687	532	0.335	2.20E-16	<0.001	GO:0044429:	mitochondrial part

18	53	474	211	0.635	5.60E-15	<0.001	GO:0006066:	alcohol metabolic process
19	418	1693	1108	0.238	8.10E-15	<0.001	GO:0005739:	mitochondrion
20	147	1696	306	0.396	2.90E-14	<0.001	GO:0043285:	biopolymer catabolic process
21	37	474	121	0.744	1.30E-13	<0.001	GO:0005996:	monosaccharide metabolic process
22	70	459	388	0.474	2.20E-12	<0.001	GO:0006082:	organic acid metabolic process
23	70	459	388	0.474	2.20E-12	<0.001	GO:0019752:	carboxylic acid metabolic process
24	477	1030	2214	0.209	3.20E-12	<0.001	GO:0003824:	catalytic activity
25	20	1381	22	1.446	2.10E-11	<0.001	GO:0005838:	proteasome regulatory particle
26	20	1381	22	1.446	2.10E-11	<0.001	GO:0022624:	proteasome accessory complex
27	85	1387	193	0.438	4.30E-11	<0.001	GO:0006091:	generation of precursor metabolites and energy
28	148	1595	353	0.324	6.30E-11	<0.001	GO:0005740:	mitochondrial envelope
29	32	474	114	0.687	7.90E-11	<0.001	GO:0019318:	hexose metabolic process
30	14	89	97	1.129	8.60E-11	<0.001	GO:0016052:	carbohydrate catabolic process
31	14	89	97	1.129	8.60E-11	<0.001	GO:0044275:	cellular carbohydrate catabolic process
32	14	1173	14	2.084	1.10E-10	<0.001	GO:0004298:	threonine endopeptidase activity
33	14	1173	14	2.084	1.10E-10	<0.001	GO:0005839:	proteasome core complex
34	27	474	88	0.739	2.70E-10	<0.001	GO:0006006:	glucose metabolic process
35	23	474	66	0.819	3.40E-10	<0.001	GO:0046164:	alcohol catabolic process
36	38	508	151	0.591	3.70E-10	<0.001	GO:0032787:	monocarboxylic acid metabolic process
37	11	89	61	1.232	8.90E-10	<0.001	GO:0046365:	monosaccharide catabolic process
38	71	1439	155	0.444	1.20E-09	<0.001	GO:0015980:	energy derivation by oxidation of organic compounds
39	19	778	33	0.967	1.50E-09	<0.001	GO:0006084:	acetyl-CoA metabolic process
40	56	1105	142	0.478	2.20E-09	<0.001	GO:0006732:	coenzyme metabolic process
41	9	543	10	1.812	3.40E-09	<0.001	GO:0005991:	trehalose metabolic process
42	195	1696	489	0.251	3.70E-09	<0.001	GO:0043687:	post-translational protein modification
43	73	1575	152	0.43	3.80E-09	<0.001	GO:0006512:	ubiquitin cycle

44	321	1671	893	0.196	3.90E-09	<0.001	GO:0050896:	response to stimulus
45	29	1682	40	0.827	5.50E-09	<0.001	GO:0030479:	actin cortical patch
46	135	1611	330	0.297	6.60E-09	<0.001	GO:0031966:	mitochondrial membrane
47	5	31	15	2.073	7.50E-09	<0.001	GO:0006098:	pentose-phosphate shunt
48	17	778	29	0.983	7.50E-09	<0.001	GO:0006099:	tricarboxylic acid cycle
49	17	778	29	0.983	7.50E-09	<0.001	GO:0046356:	acetyl-CoA catabolic process
50	19	1485	23	1.127	7.90E-09	<0.001	GO:0016209:	antioxidant activity
51	226	1698	587	0.227	8.30E-09	<0.001	GO:0006950:	response to stress
52	13	497	25	1.09	1.50E-08	<0.001	GO:0006081:	aldehyde metabolic process
53	16	1485	18	1.309	1.60E-08	<0.001	GO:0004601:	peroxidase activity
54	16	1485	18	1.309	1.60E-08	<0.001	GO:0016684:	oxidoreductase activity, acting on peroxide as acceptor
55	85	1693	179	0.377	1.80E-08	<0.001	GO:0051186:	cofactor metabolic process
56	30	728	85	0.615	2.00E-08	<0.001	GO:0016614:	oxidoreductase activity, acting on CH-OH group of donors
57	5	31	18	1.963	2.10E-08	<0.001	GO:0006740:	NADPH regeneration
58	18	778	34	0.887	2.40E-08	<0.001	GO:0051187:	cofactor catabolic process
59	37	1551	64	0.602	4.80E-08	<0.001	GO:0006623:	protein targeting to vacuole
60	92	1687	202	0.346	4.90E-08	<0.001	GO:0005759:	mitochondrial matrix
61	92	1687	202	0.346	4.90E-08	<0.001	GO:0031980:	mitochondrial lumen
62	5	31	21	1.876	4.90E-08	<0.001	GO:0006739:	NADP metabolic process

63	55	1574	110	0.461	5.70E-08	<0.001	GO:0005768:	endosome
64	16	849	27	0.949	6.00E-08	<0.001	GO:0022900:	electron transport chain
65	16	849	27	0.949	6.00E-08	<0.001	GO:0022904:	respiratory electron transport chain
66	16	849	27	0.949	6.00E-08	<0.001	GO:0042773:	ATP synthesis coupled electron transport
67	16	849	27	0.949	6.00E-08	<0.001	GO:0042775:	organelle ATP synthesis coupled electron transport
68	16	849	27	0.949	6.00E-08	<0.001	GO:0055114:	oxidation reduction
69	48	1359	104	0.479	7.20E-08	<0.001	GO:0009060:	aerobic respiration
70	14	348	44	0.904	8.40E-08	<0.001	GO:0009310:	amine catabolic process
71	14	348	44	0.904	8.40E-08	<0.001	GO:0044270:	nitrogen compound catabolic process
72	60	615	296	0.377	8.90E-08	<0.001	GO:0006807:	nitrogen compound metabolic process
73	17	778	33	0.862	1.00E-07	<0.001	GO:0009109:	coenzyme catabolic process
74	56	1557	116	0.438	1.30E-07	<0.001	GO:0007034:	vacuolar transport
75	27	728	78	0.601	1.60E-07	<0.001	GO:0016616:	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
76	16	792	30	0.883	1.70E-07	<0.001	GO:0005746:	mitochondrial respiratory chain
77	6	336	7	1.872	1.90E-07	<0.001	GO:0005992:	trehalose biosynthetic process
78	6	336	7	1.872	1.90E-07	<0.001	GO:0046351:	disaccharide biosynthetic process
79	48	1359	107	0.457	2.10E-07	<0.001	GO:0045333:	cellular respiration
80	7	305	11	1.504	2.20E-07	<0.001	GO:0004033:	aldo-keto reductase activity
81	21	383	94	0.653	2.80E-07	<0.001	GO:0016051:	carbohydrate biosynthetic process
82	6	31	56	1.477	3.00E-07	<0.001	GO:0019320:	hexose catabolic process
83	46	1685	86	0.479	4.60E-07	0.001	GO:0006897:	endocytosis
84	54	1682	107	0.429	5.40E-07	0.003	GO:0030036:	actin cytoskeleton organization and biogenesis
85	43	1682	79	0.496	5.50E-07	0.004	GO:0015629:	actin cytoskeleton
86	5	89	13	1.657	7.40E-07	0.007	GO:0019321:	pentose metabolic process
87	15	839	28	0.857	8.10E-07	0.008	GO:0009084:	glutamine family amino acid biosynthetic process
88	25	1653	38	0.704	8.60E-07	0.009	GO:0003779:	actin binding
89	31	1682	51	0.604	8.70E-07	0.009	GO:0030863:	cortical cytoskeleton

90	31	1682	51	0.604	8.70E-07	0.009	GO:0030864:	cortical actin cytoskeleton
91	55	1686	111	0.411	9.90E-07	0.011	GO:0030029:	actin filament-based process
92	52	615	260	0.366	1.00E-06	0.012	GO:0006519:	amino acid and derivative metabolic process
93	53	615	267	0.362	1.00E-06	0.012	GO:0009308:	amine metabolic process
94	49	1685	96	0.437	1.20E-06	0.015	GO:0010324:	membrane invagination
95	26	1412	46	0.632	1.30E-06	0.015	GO:0006914:	autophagy
96	4	206	4	2.413	1.30E-06	0.015	GO:0004866:	endopeptidase inhibitor activity
97	4	206	4	2.413	1.30E-06	0.015	GO:0030414:	protease inhibitor activity
98	91	1557	228	0.293	1.50E-06	0.015	GO:0005773:	vacuole
99	9	1381	9	1.808	1.70E-06	0.017	GO:0008540:	proteasome regulatory particle, base subcomplex
100	12	1653	13	1.346	1.70E-06	0.017	GO:0008154:	actin polymerization and/or depolymerization
101	238	1686	664	0.179	1.80E-06	0.019	GO:0005515:	protein binding
102	54	1669	111	0.402	1.80E-06	0.019	GO:0009628:	response to abiotic stimulus
103	10	773	15	1.118	1.90E-06	0.022	GO:0006536:	glutamate metabolic process
104	81	1692	184	0.315	2.00E-06	0.023	GO:0016773:	phosphotransferase activity, alcohol group as acceptor
105	11	1022	15	1.101	2.20E-06	0.03	GO:0046395:	carboxylic acid catabolic process
106	4	236	4	2.35	2.30E-06	0.033	GO:0005946:	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
107	10	1127	12	1.265	2.30E-06	0.034	GO:0007039:	vacuolar protein catabolic process
108	64	1426	160	0.344	2.40E-06	0.035	GO:0030435:	sporulation
109	7	75	51	1.162	2.60E-06	0.038	GO:0006007:	glucose catabolic process
110	82	1522	207	0.3	2.70E-06	0.039	GO:0016310:	phosphorylation
111	42	796	156	0.401	2.90E-06	0.042	GO:0048037:	cofactor binding
112	5	31	46	1.474	3.00E-06	0.046	GO:0006769:	nicotinamide metabolic process
113	7	326	14	1.251	3.20E-06	0.048	GO:0042219:	amino acid derivative catabolic process
114	9	1485	9	1.766	3.30E-06	0.05	GO:0008379:	thioredoxin peroxidase activity
115	9	1485	9	1.766	3.30E-06	0.05	GO:0051920:	peroxiredoxin activity

Δpbf1Δpbf2 upregulated genes

Rank	N	M	X	LOD	P	P-adj	GO Attribute	
1	219	1275	536	0.462	1.20E-27	<0.001	GO:0009056:	catabolic process
2	108	1275	195	0.695	1.80E-26	<0.001	GO:0030163:	protein catabolic process
3	206	1275	503	0.461	4.20E-26	<0.001	GO:0044248:	cellular catabolic process
4	100	1275	179	0.701	6.00E-25	<0.001	GO:0044257:	cellular protein catabolic process
5	94	1300	170	0.677	2.10E-22	<0.001	GO:0051603:	proteolysis involved in cellular protein catabolic process
6	92	1300	167	0.673	8.50E-22	<0.001	GO:0006511:	ubiquitin-dependent protein catabolic process
7	92	1300	167	0.673	8.50E-22	<0.001	GO:0019941:	modification-dependent protein catabolic process
8	39	1300	45	1.357	1.40E-20	<0.001	GO:0000502:	proteasome complex
9	92	1300	174	0.634	3.90E-20	<0.001	GO:0043632:	modification-dependent macromolecule catabolic process
10	1044	1359	4021	0.273	3.90E-20	<0.001	GO:0005737:	cytoplasm
11	129	1300	287	0.503	1.00E-19	<0.001	GO:0006508:	proteolysis
12	57	351	287	0.664	3.30E-17	<0.001	GO:0005975:	carbohydrate metabolic process
13	138	1351	324	0.439	6.30E-17	<0.001	GO:0016491:	oxidoreductase activity
14	152	1275	391	0.408	1.00E-16	<0.001	GO:0009057:	macromolecule catabolic process
15	142	1300	352	0.421	1.70E-16	<0.001	GO:0044265:	cellular macromolecule catabolic process
16	122	1275	306	0.42	1.70E-14	<0.001	GO:0043285:	biopolymer catabolic process
17	40	254	241	0.717	2.40E-14	<0.001	GO:0044262:	cellular carbohydrate metabolic process

18	41	351	211	0.635	3.00E-12	<0.001	GO:0006066:	alcohol metabolic process
19	38	588	121	0.652	2.10E-11	<0.001	GO:0005996:	monosaccharide metabolic process
20	334	1359	1108	0.214	4.70E-11	<0.001	GO:0005739:	mitochondrion
21	15	103	97	1.093	5.40E-11	<0.001	GO:0016052:	carbohydrate catabolic process
22	15	103	97	1.093	5.40E-11	<0.001	GO:0044275:	cellular carbohydrate catabolic process
23	79	1250	193	0.441	7.40E-11	<0.001	GO:0006091:	generation of precursor metabolites and energy
24	181	1352	532	0.28	9.70E-11	<0.001	GO:0044429:	mitochondrial part
25	19	1300	22	1.312	1.60E-10	<0.001	GO:0005838:	proteasome regulatory particle
26	19	1300	22	1.312	1.60E-10	<0.001	GO:0022624:	proteasome accessory complex
27	12	99	61	1.229	1.80E-10	<0.001	GO:0046365:	monosaccharide catabolic process
28	14	1238	14	2.054	2.30E-10	<0.001	GO:0004298:	threonine endopeptidase activity
29	14	1238	14	2.054	2.30E-10	<0.001	GO:0005839:	proteasome core complex
30	198	382	2214	0.287	3.90E-10	<0.001	GO:0003824:	catalytic activity
31	41	150	587	0.568	4.10E-10	<0.001	GO:0006950:	response to stress
32	12	99	66	1.187	4.70E-10	<0.001	GO:0046164:	alcohol catabolic process
33	64	1342	142	0.471	9.10E-10	<0.001	GO:0006732:	coenzyme metabolic process
34	34	588	114	0.617	1.20E-09	<0.001	GO:0019318:	hexose metabolic process
35	29	588	88	0.678	1.50E-09	<0.001	GO:0006006:	glucose metabolic process
36	84	688	388	0.364	1.70E-09	<0.001	GO:0006082:	organic acid metabolic process
37	84	688	388	0.364	1.70E-09	<0.001	GO:0019752:	carboxylic acid metabolic process
38	8	313	10	1.803	2.00E-09	<0.001	GO:0005991:	trehalose metabolic process
39	52	935	151	0.474	4.90E-09	<0.001	GO:0032787:	monocarboxylic acid metabolic process
40	37	1022	85	0.59	6.80E-09	<0.001	GO:0016614:	oxidoreductase activity, acting on CH-OH group of donors
41	65	1304	155	0.432	7.00E-09	<0.001	GO:0015980:	energy derivation by oxidation of organic compounds
42	73	1342	179	0.396	1.30E-08	<0.001	GO:0051186:	cofactor metabolic process
43	115	1233	353	0.295	2.50E-08	0.001	GO:0005740:	mitochondrial envelope

44	34	1022	78	0.59	2.70E-08	0.001	GO:0016616:	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
45	14	678	25	1.005	6.30E-08	0.001	GO:0006081:	aldehyde metabolic process
46	19	678	44	0.79	6.80E-08	0.001	GO:0009310:	amine catabolic process
47	19	678	44	0.79	6.80E-08	0.001	GO:0044270:	nitrogen compound catabolic process
48	15	567	33	0.916	7.00E-08	0.001	GO:0006084:	acetyl-CoA metabolic process
49	12	727	18	1.153	8.20E-08	0.001	GO:0004601:	peroxidase activity
50	12	727	18	1.153	8.20E-08	0.001	GO:0016684:	oxidoreductase activity, acting on peroxide as acceptor
51	230	1154	893	0.199	8.90E-08	0.001	GO:0050896:	response to stimulus
52	12	1288	13	1.49	9.20E-08	0.002	GO:0019321:	pentose metabolic process
53	6	313	7	1.906	1.30E-07	0.003	GO:0005992:	trehalose biosynthetic process
54	6	313	7	1.906	1.30E-07	0.003	GO:0046351:	disaccharide biosynthetic process
55	35	929	94	0.526	1.60E-07	0.005	GO:0016051:	carbohydrate biosynthetic process
56	19	1233	29	0.864	1.70E-07	0.006	GO:0006099:	tricarboxylic acid cycle
57	19	1233	29	0.864	1.70E-07	0.006	GO:0046356:	acetyl-CoA catabolic process
58	9	99	56	1.114	2.40E-07	0.006	GO:0019320:	hexose catabolic process
59	24	1120	46	0.686	2.70E-07	0.006	GO:0006914:	autophagy
60	7	327	11	1.471	3.60E-07	0.007	GO:0004033:	aldo-keto reductase activity
61	13	727	23	0.978	3.70E-07	0.007	GO:0016209:	antioxidant activity
62	46	1233	112	0.444	4.30E-07	0.007	GO:0044455:	mitochondrial membrane part

63	45	1304	104	0.452	5.20E-07	0.009	GO:0009060:	aerobic respiration
64	45	1235	110	0.44	6.90E-07	0.011	GO:0005768:	endosome
65	4	181	4	2.472	7.90E-07	0.013	GO:0004866:	endopeptidase inhibitor activity
66	4	181	4	2.472	7.90E-07	0.013	GO:0030414:	protease inhibitor activity
67	9	1002	10	1.505	8.10E-07	0.013	GO:0008541:	proteasome regulatory particle, lid subcomplex
68	14	567	34	0.842	8.60E-07	0.015	GO:0051187:	cofactor catabolic process
69	148	1291	489	0.223	1.10E-06	0.02	GO:0043687:	post-translational protein modification
70	4	35	15	1.871	1.20E-06	0.021	GO:0006098:	pentose-phosphate shunt
71	45	1304	107	0.43	1.40E-06	0.026	GO:0045333:	cellular respiration
72	4	209	4	2.406	1.40E-06	0.028	GO:0005946:	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)
73	8	99	51	1.099	1.40E-06	0.028	GO:0006007:	glucose catabolic process
74	103	1233	330	0.264	1.50E-06	0.03	GO:0031966:	mitochondrial membrane
75	17	1233	27	0.816	1.80E-06	0.035	GO:0022900:	electron transport chain
76	17	1233	27	0.816	1.80E-06	0.035	GO:0022904:	respiratory electron transport chain
77	17	1233	27	0.816	1.80E-06	0.035	GO:0042773:	ATP synthesis coupled electron transport
78	17	1233	27	0.816	1.80E-06	0.035	GO:0042775:	organelle ATP synthesis coupled electron transport
79	17	1233	27	0.816	1.80E-06	0.035	GO:0055114:	oxidation reduction
80	6	678	6	2.014	2.00E-06	0.039	GO:0046185:	aldehyde catabolic process
81	16	1041	28	0.806	2.20E-06	0.04	GO:0009084:	glutamine family amino acid biosynthetic process
82	11	1299	13	1.227	2.30E-06	0.041	GO:0008154:	actin polymerization and/or depolymerization
83	18	1233	30	0.765	2.50E-06	0.044	GO:0005746:	mitochondrial respiratory chain
84	33	944	94	0.477	2.50E-06	0.047	GO:0019867:	outer membrane
85	16	678	40	0.733	2.60E-06	0.047	GO:0009063:	amino acid catabolic process
86	4	35	18	1.77	2.80E-06	0.049	GO:0006740:	NADPH regeneration