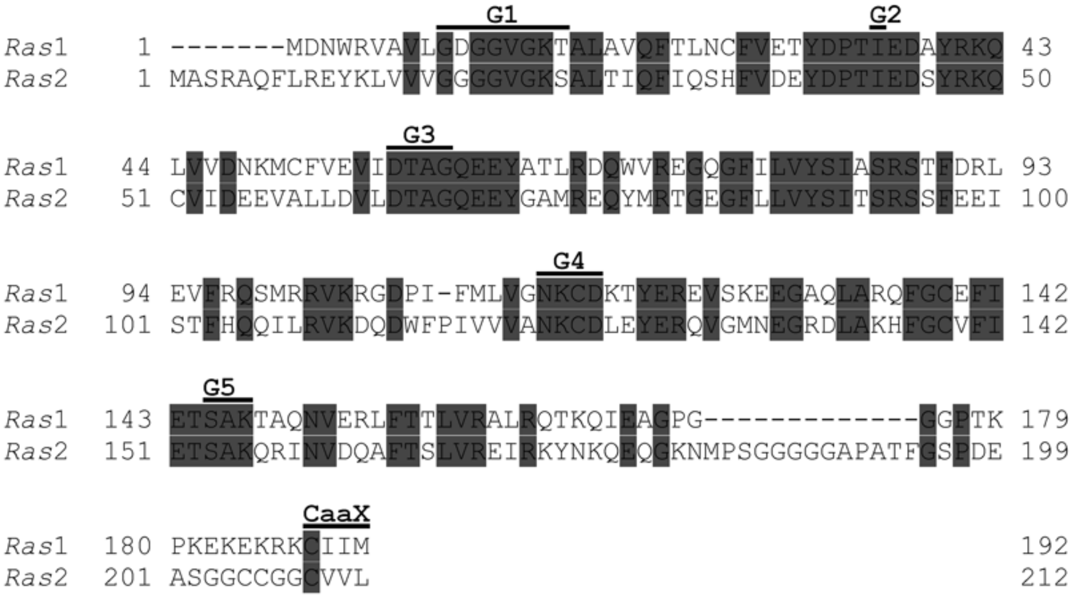
Table S1: Primer sequences used in this study. All the primers are presented in 5′–3′ direction.

Name	**Sequence**
Rasdown1	GACCGCAGCCCCCTCCTTCTC
Rasup2	CTGAAGCAAGACAGCGACGGCAGA
RasPromdown	GGTGTGCAATGATTTCCTTCGTGATG
ras-1	GCATCCCGCTCCACATTC
ras-2	ACACTTCCCGCTCGTAGGTC
G12V-1	GCAGTACTAGGCGATGTTGGGGTGGGCAAAACCGC
G12V-2	GCGGTTTTGCCCACCCCAACATCGCCTAGTACTGC
Q61L-1	TCATAGACACTGCCGGACTGGGTGCGTGCTTGCAC
Q61L-2	GTGCAAGCACGCACCCAGTCCGGCAGTGTCTATGA
G15N-1	CGATGGTGGGGTGAACAAAACCGCTCTCGCAGTC
G15N-2	GACTGCGAGAGCGGTTTTGTTCACCCCACCATCG
tef-1	AGCTTGGCAAGGGTTCCTTCA
tef-2	AACTTCCAGAGGGCGATATCA



```
Ras1    1 -------MDNWRVAVLGDGGVGKTALAVQFTLNCFVETYDPTIEDAYRKQ 43
Ras2    1 MASRAQFLREYKLVVVGGGGVGKSALTIQFIQSHFVDEYDPTIEDSYRKQ 50

Ras1   44 LVVDNKMCFVEVIDTAGQEEYATLRDQWVREGQGFILVYSIASRSTFDRL 93
Ras2   51 CVIDEEVALLDVLDTAGQEEYGAMREQYMRTGEGFLLVYSITSRSSFEEI 100

Ras1   94 EVFRQSMRRVKRGDPI-FMLVGNKCDKTYEREVSKEEGAQLARQFGCEFI 142
Ras2  101 STFHQQILRVKDQDWFPIVVVANKCDLEYERQVGMNEGRDLAKHFGCVFI 142

Ras1  143 ETSAKTAQNVERLFTTLVRALRQTKQIEAGPG-------------GGPTK 179
Ras2  151 ETSAKQRINVDQAFTSLVREIRKYNKQEQGKNMPSGGGGGAPATFGSPDE 199

Ras1  180 PKEKEKRKCIIM                                      192
Ras2  201 ASGGCCGGCVVL                                      212
```

Figure S2: Sequence alignment of Ras1 (protein ID 45883) and Ras2 (protein ID 67931) of *Schizophyllum commune*. Position of five domains involved in GTP binding/hydrolysis (G1-G5) and the CaaX prenylation motif at the C-terminus are indicated. The sequences were aligned with CLUSTALX.

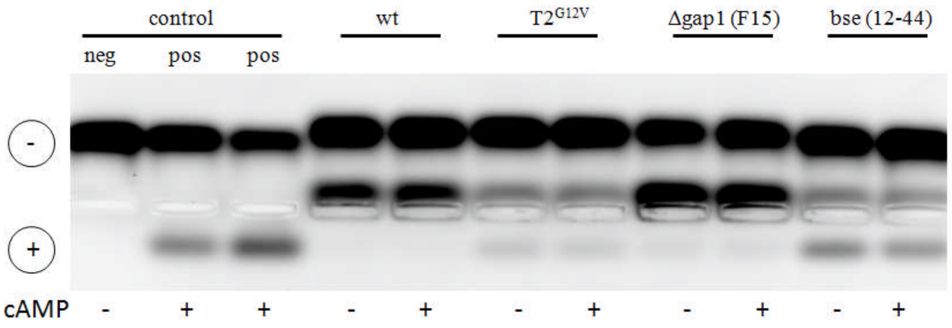


Figure S3: Examination of the cAMP dependent PKA activity using protein extracts of different Ras mutant strains. The original mutant *bse* strain with a reported increase of intracellular cAMP concentration showed the highest PKA activation compared to constitutive active Ras1 and Δgap1 strains.

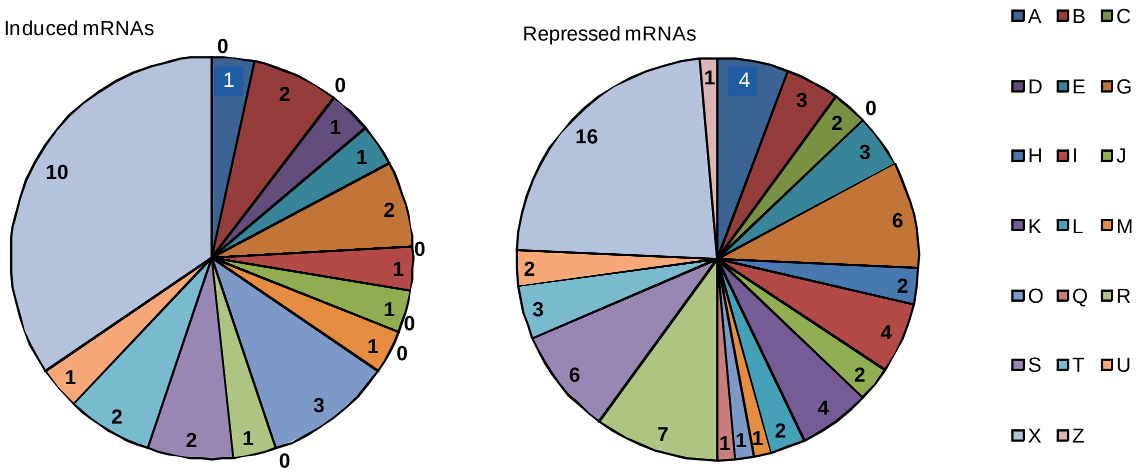


Figure S4: Detailed KOG classification of transcriptional regulated mRNAs in *S. commune* Ras^{G12V} mutant. Numbers indicate the number of regulated mRNA in this functional group ($P \leq 0.05$, fold change ≥ 3 / ≤ -3). Detailed KOG classification: A, RNA processing and modification; B, chromatin structure and dynamics; C, energy production and conversion; D, cell cycle control, cell division, chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination, and repair; M, cell all/membrane/envelope biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction only; S, function unknown; T, signal transduction; U, intracellular trafficking, secretion, and vesicular transport; V, defense mechanisms; W, extracellular structures; Y, nuclear structure; Z, cytoskeleton.

Table S5: Differentially regulated genes in Ras1 mutant T2^{G12V}. Fold = fold change. Putative function written in bold letters indicates annotation of genome, written in normal letters are Blastp results. The effected genes are not regulated in the other mutant strains.

12-43 *vs.* 4-39		**Ras1 *vs.* 12-43**		**Ras1 *vs.* 4-39**		**protein ID**	**putative function**
Fold	**pValue**	**Fold**	**pValue**	**Fold**	**pValue**		
							INDUCED GENES
1.32	2.81E-01	1844	3.04E-16	2425.5	1.68E-16	82266	**Transketolase. Pentose phosphate pathway**
-1.5	3.70E-01	260.9	6.51E-10	172.54	2.11E-09	13593	**Nucleolar protein NOP52/RRP1**
-1.4	6.29E-01	36.25	7.03E-05	25.84	1.96E-04	234329	**Glycoside hydrolase. chitinase active site**
1.19	7.75E-01	30.61	3.06E-05	36.51	1.71E-05	77889	**Histone deacetylase complex. catalytic component RPD3**
1.28	7.21E-01	16.76	6.17E-04	21.4	2.84E-04	48206	**Meiotic cell division protein Pelota/DOM34. eRF1 domain 1. Probable translation factor pelota**
1.2	6.05E-01	16.57	2.56E-07	19.84	1.08E-07	111002	**Putative RNA binding protein**
1.76	3.69E-01	15.35	3.48E-04	27	5.04E-05	236254	**FOG: Low-complexity**
-1.6	3.69E-01	15.14	5.32E-05	9.48	3.68E-04	53495	**SWI-SNF chromatin remodeling complex. Snf5 subunit**
1.62	5.15E-01	13.79	2.10E-03	22.31	5.00E-04	105160	**Cyclin-like F-box**
-1.4	6.34E-01	11.74	1.64E-03	8.53	4.69E-03	83710	**C-type lectin**
1.22	8.51E-01	9.29	4.54E-02	11.31	3.11E-02	235404	**Aldehyde dehydrogenase**
-2	2.48E-01	8.68	1.52E-03	4.38	1.96E-02	238773	**SPRT-like metalloprotease**
1.15	8.56E-01	6.71	2.45E-02	7.74	1.68E-02	111240	**Gluconate transport-inducing protein**
1.09	8.67E-01	6.35	1.36E-03	6.9	9.39E-04	106922	**Polo-like serine/threonine protein kinase**
-1.1	8.78E-01	5.46	2.20E-02	4.92	3.02E-02	106206	**Thioredoxin-related. cell redox homeostasis**
1.07	7.41E-01	4.16	3.27E-06	4.47	1.76E-06	15188	**Predicted pilin-like transcription factor. peptide-methionine-(S)-S-oxide reductase activity**
-1.1	8.26E-01	4.13	8.21E-05	3.88	1.31E-04	77899	**ER-Golgi vesicle-tethering protein p115**
1.51	3.64E-01	4.02	6.12E-03	6.09	8.16E-04	232651	**Molecular chaperone (small heat-shock protein Hsp26/Hsp42)**
-1.1	5.27E-01	3.91	2.31E-06	3.45	7.76E-06	65863	**Lipid phosphate phosphatase and related enzymes of the PAP2 family**
-1.1	7.14E-01	3.67	1.05E-04	3.34	2.29E-04	76560	**Pyruvate decarboxylase. Thiamine pyrophosphate-requiring enzyme**
1.06	8.79E-01	3.55	6.04E-03	3.78	4.33E-03	107249	**Cyclin-dependent kinase inhibitor**
-1.3	4.43E-01	37.97	1.76E-09	29.68	5.04E-09	106884	merzoite surface protein 1 [*Plasmodium reichenowi*]
1.18	7.75E-01	27.36	2.53E-05	32.36	1.42E-05	107796	F-box domain containing protein [*Metarhizium acridum* CQMa 102]
-1.1	8.99E-01	15.15	1.41E-03	13.82	1.87E-03	258882	hypothetical protein
1.26	8.15E-01	9.29	3.65E-02	11.74	2.26E-02	237713	zinc finger. C2H2 type family protein [*Zea mays*]
-1.5	5.79E-01	9.23	6.52E-03	6.16	2.14E-02	113651	RNA polymerase sigma-54 factor [*Serratia odorifera* 4Rx13]
-1.1	8.70E-01	8.47	4.25E-06	8.03	5.82E-06	112805	other/FunK1 protein kinase [*Coprinopsis cinerea okayama* 7#130]
-1.6	4.10E-01	7.73	1.56E-03	4.88	9.61E-03	54123	Ribonuclease P 40kDa (Rpp40) subunit superfamily [pfam08584]
1	1.00E+00	5.94	2.84E-05	5.94	2.84E-05	109821	alpha/beta hydrolase. putative [*Neosartorya fischeri* NRRL 181]
							REPRESSED GENES
1.47	8.10E-02	-603	2.28E-16	-411.4	6.36E-16	255314	**Bifunctional leukotriene A4 hydrolase/aminopeptidase LTA4H. Peptidase M1. membrane alanine aminopeptidase**
1.17	6.04E-01	-503	1.30E-13	-430.3	1.97E-13	84513	**Mitochondrial inner membrane protein (mitofilin)**
-1.4	2.90E-01	-379	2.44E-12	-546.6	9.27E-13	84546	**Asparagine synthase (glutamine-hydrolyzing)**
-1.3	5.54E-01	-330	3.97E-10	-433.6	1.94E-10	84467	**Galactose-1-phosphate uridylyltransferase**
1.16	7.44E-01	-204	1.56E-09	-175.6	2.41E-09	80706	**Predicted carbohydrate kinase. contains PfkB domain**
1.53	4.01E-01	-106	3.35E-08	-69.4	1.29E-07	81279	**Nucleoside diphosphate-sugar hydrolase of the MutT (NUDIX) family**

-1.4	2.53E-01	-88.9	2.60E-11	-126	7.91E-12	233954	**KEKE-like motif-containing transcription regulator (Rlr1)/suppressor of sin4**
-1.3	8.20E-01	-52.4	1.50E-03	-66.78	9.12E-04	256033	**Cyclin**
1.18	7.18E-01	-51.9	1.36E-07	-43.85	2.48E-07	109113	**Histone acetyltransferase SAGA/ADA. catalytic subunit PCAF/GCN5 and related proteins. Zn-finger-like. PHD finger**
1.6	9.12E-02	-49.4	3.50E-11	-30.94	2.58E-10	63938	**Nucleosome remodeling factor. subunit CAF1/NURF55/MSI1. G-protein beta WD-40 repeat**
1.29	5.84E-01	-47.3	2.00E-07	-36.55	5.12E-07	103679	**Glucan 1.4-alpha-glucosidase**
-1.1	8.76E-01	-36.5	5.04E-04	-41.65	3.59E-04	51157	**Nuclear exosomal RNA helicase MTR4. DEAD-box superfamily**
1.02	9.80E-01	-34.7	1.88E-03	-33.9	1.99E-03	34765	**RNA polymerase II transcriptional regulation mediator. MED6 mediator**
-1.1	6.98E-01	-31.7	4.25E-09	-35.96	2.50E-09	103636	**Tuftelin-interacting protein TIP39. contains G-patch domain. Zn-finger. C2H2 type**
-1.1	8.70E-01	-31.3	9.29E-09	-33.06	7.35E-09	50648	**Isoamyl acetate-hydrolyzing esterase. Lipolytic enzyme. G-D-S-L**
1.42	4.41E-01	-28.9	8.43E-07	-20.31	3.52E-06	70633	**RNA helicase. DEAD/DEAH box helicase. N-terminal**
1.07	7.88E-01	-18	5.76E-10	-16.9	8.09E-10	65761	**Glucosidase I**
1.39	1.62E-01	-16.8	5.05E-10	-12.09	3.29E-09	64183	**Biotin synthase. Radical SAM**
-1.2	8.22E-01	-14.9	5.28E-04	-17.22	3.24E-04	16640	**Alcohol dehydrogenase. class V**
1.23	7.55E-01	-10.3	2.20E-03	-8.4	4.36E-03	47592	**Vigilin. KH. type 1. RNA binding**
1.31	2.76E-01	-8.57	9.21E-08	-6.52	5.97E-07	110853	**Glucan endo-1.3-alpha-glucosidase**
-1	9.19E-01	-7.95	2.02E-07	-8.16	1.70E-07	50254	**Metalloexopeptidases. G-protein beta WD-40 repeat**
1.08	7.12E-01	-7.54	1.32E-08	-6.99	2.29E-08	47747	**Inositol monophosphatase**
-1.5	6.00E-01	-7.45	1.40E-02	-11.02	4.49E-03	14418	**Phospholipid/glycerol acyltransferase**
1.18	7.06E-01	-7.25	2.72E-04	-6.14	6.18E-04	81374	**FUN14**
-1	9.28E-01	-7.13	7.32E-04	-7.44	6.01E-04	13226	**6-phosphogluconate dehydrogenase**
1.21	7.88E-01	-6.79	1.29E-02	-5.63	2.28E-02	38732	**mRNA capping enzyme. guanylyltransferase (alpha) subunit**
-1	9.00E-01	-6.75	1.54E-05	-7.03	1.20E-05	256186	**DHHC-type Zn-finger proteins**
1.9	1.95E-01	-6.66	9.71E-04	-3.5	1.75E-02	85448	**Cellular protein (glioma tumor suppressor candidate region gene 2)**
1.15	6.50E-01	-5.98	1.42E-05	-5.21	3.56E-05	47635	**Serine/threonine protein phosphatase**
-1.7	1.84E-01	-5.53	2.62E-04	-9.26	1.53E-05	81303	**Proteins containing regions of low-complexity**
1.18	6.05E-01	-5.32	4.68E-05	-4.52	1.39E-04	62043	**RNA polymerase II holoenzyme and mediator subcomplex. subunit SURB7/SRB7**
1.24	4.20E-01	-5.22	6.72E-06	-4.22	3.42E-05	13366	**Succinyl-CoA synthetase. alpha subunit. Citrate cycle**
1.2	3.71E-01	-5.11	2.91E-07	-4.25	1.44E-06	65904	**Serine carboxypeptidases**
1.1	8.76E-01	-4.9	1.82E-02	-4.45	2.51E-02	51977	**Translation initiation factor 2B. beta subunit (eIF-2Bbeta/GCD7)**
-1.1	6.10E-01	-4.67	4.33E-06	-5.27	1.66E-06	64009	**Dopey and related predicted leucine zipper transcription factors**
1.19	6.02E-01	-4.61	2.24E-04	-3.87	7.01E-04	108333	**Ran-binding protein RANBP1 and related RanBD domain proteins**
1.15	5.93E-01	-4.5	2.57E-05	-3.9	7.80E-05	81380	**Phosphatidylinositol synthase**
1.34	2.45E-01	-4.24	1.43E-05	-3.17	1.66E-04	256079	**Regulator of chromosome condensation. RCC1**
-1.1	6.68E-01	-4.22	2.08E-04	-4.82	8.33E-05	60330	**Alpha-mannosidase**
-1.3	6.70E-01	-4.13	2.36E-02	-5.3	9.57E-03	16984	**Mitochondrial tryptophanyl-tRNA synthetase**
-1	8.68E-01	-4.09	2.70E-07	-4.21	2.04E-07	84499	**beta-1.6-N-acetylglucosaminyltransferase. contains WSC domain**
-1.3	4.17E-01	-4.01	3.66E-04	-5.2	6.36E-05	255409	**Phosphoglucomutase/phosphomannomutase**
-1	9.16E-01	-3.91	1.25E-04	-4.02	1.00E-04	50708	**Very-long-chain acyl-CoA dehydrogenase. Cytochrome b5**
1	9.93E-01	-3.85	2.52E-07	-3.85	2.56E-07	74357	**Folylpolyglutamate synthase. Folate biosynthesis**
-1.1	9.01E-01	-3.73	1.09E-02	-3.95	8.34E-03	109000	**Zn-finger. C2H2 type**
-1.2	7.27E-01	-3.7	4.60E-03	-4.27	2.13E-03	232775	**WASP-interacting protein VRP1/WIP. contains WH2 domain. DNA-binding SAP**
-1.1	8.82E-01	-3.64	3.94E-02	-3.97	2.91E-02	84485	**DNA polymerase delta. regulatory subunit 55**
-1	8.83E-01	-3.58	1.69E-05	-3.7	1.26E-05	14523	**Leptin receptor gene-related protein. Vacuolar protein sorting 55**
-1.2	3.80E-01	-3.38	1.99E-05	-4.08	3.51E-06	84101	**Antifreeze protein. type I. C-type lectin**
-1.2	5.26E-01	-3.04	1.13E-04	-3.52	3.01E-05	72933	**Mitochondrial import inner membrane translocase. subunit TIM22**
-1	9.30E-01	-44.4	8.05E-11	-45.51	7.30E-11	13289	PcbC . Isopenicillin N synthase and related dioxygenases [COG3491]

1.58	1.35E-01	-32.3	1.19E-09	-20.42	9.92E-09	105675	predicted: collagen alpha-1(XXVII) chain-like [*Monodelphis domestica*]
-1.3	5.95E-01	-24.3	7.13E-06	-31.85	2.57E-06	48548	integral inner nuclear membrane protein Ima1 [*Schizosaccharomyces pombe* 972h-]
1	9.94E-01	-23.6	1.74E-08	-23.5	1.76E-08	86060	replicase [Potato virus X]
-1.4	6.36E-01	-21.2	1.96E-04	-28.96	7.14E-05	110865	oxidoreductase [*Lactococcus garvieae* ATCC 49156]
-1.3	6.69E-01	-20.6	4.86E-05	-26.31	2.02E-05	84126	hypothetical protein
1.82	2.81E-01	-20.3	3.17E-05	-11.18	3.21E-04	103131	succinate-CoA ligase (GDP-forming) [*Dictyostelium purpureum*]
-1.5	2.08E-01	-14.8	1.05E-07	-22.1	1.43E-08	81356	hamartin [*Schizosaccharomyces japonicus* yFS275]
1.63	2.94E-01	-13	2.76E-05	-7.98	2.60E-04	10509	erythronolide synthase [*Shewanella sediminis* HAW-EB3]
1.52	5.97E-02	-12.7	7.68E-10	-8.33	1.15E-08	81382	ExoD [*Cellvibrio japonicus* Ueda107]
1.53	5.89E-01	-10	8.09E-03	-6.56	2.56E-02	231110	putative long-chain-fatty-acid--CoA ligase [*Sinorhizobium fredii* NGR234]
1.16	5.16E-01	-9.28	2.40E-08	-7.97	6.61E-08	105839	F-box-like [pfam12937]
1.07	8.34E-01	-5.82	3.03E-05	-5.45	4.67E-05	103413	oligopeptide ABC transporter permease [*Methanosarcina barkeri str.* Fusaro]
-1.1	8.01E-01	-5.67	3.76E-04	-6.26	2.18E-04	13288	DUF2413 domain. Pc16g07860 [*Penicillium chrysogenum Wisconsin* 54-1255]
-1.3	6.41E-01	-5.59	1.07E-02	-7.43	3.86E-03	103965	predicted: GRAM domain-containing protein 4-like [*Oreochromis niloticus*]
1.16	6.34E-01	-4.9	6.52E-05	-4.23	1.79E-04	105630	hypothetical protein
1.43	2.80E-01	-4.38	2.70E-04	-3.06	3.00E-03	110215	hypothetical protein
-1	9.50E-01	-3.97	7.49E-03	-4.09	6.53E-03	16995	LETM1 [pfam07766]. LETM1-like protein; inner mitochondrial membrane proteins
-1.6	5.02E-02	-3.39	7.37E-05	-5.57	1.26E-06	72748	DUF2404 [pfam10296]. putative integral membrane protein conserved region

Table S6: Blastp results of "unknown function" of exclusively regulated genes in Ras1 mutant. n.a. – not available

Protein ID	**putative function**	**Accession No**	**Coverage / EValue**
	INDUCED GENES		
106884	merzoite surface protein 1 [*Plasmodium reichenowi*]	CAH10285.1	33% / 0.011
107796	F-box domain containing protein [*Metarhizium acridum* CQMa 102]	EFY85273.1	82% / 0.001
258882	hypothetical protein		
237713	zinc finger. C2H2 type family protein [*Zea mays*]	NP_001152939.1	7% / 8.5
113651	RNA polymerase sigma-54 factor [*Serratia odorifera* 4Rx13]	ZP_06191518.1	10% / 3.5
112805	other/FunK1 protein kinase [*Coprinopsis cinerea okayama*7#130]	XP_001835156.2	78% / 1e-15
54123	Ribonuclease P 40kDa (Rpp40) subunit superfamily [pfam08584]		2.66e-15
109821	alpha/beta hydrolase. putative [*Neosartorya fischeri* NRRL 181]	XP_001258274.1	66% / 3e-12
	REPRESSED GENES		
13289	PcbC . Isopenicillin N synthase and related dioxygenases [COG3491]	n.a.	1.33e-12
105675	predicted: collagen alpha-1(XXVII) chain-like [*Monodelphis domestica*]	XP_003339678.1	40% / 3.7
48548	integral inner nuclear membrane protein Ima1 [*Schizosaccharomyces pombe* 972h-]	NP_588365.1	58% / 4e-19
86060	replicase [*Potato virus X*]	CAD33246.1	78% / 0.36
110865	oxidoreductase [*Lactococcus garvieae* ATCC 49156]	YP_004779881.1	51% / 7.3
84126	hypothetical protein		
103131	succinate-CoA ligase (GDP-forming) [*Dictyostelium purpureum*]	XP_003291936.1	80% / 6.8
81356	hamartin [*Schizosaccharomyces japonicus* yFS275]	XP_002172257.1	79% / 6e-23
10509	erythronolide synthase [*Shewanella sediminis* HAW-EB3]	YP_001474934.1	64% / 0.33
81382	ExoD [*Cellvibrio japonicus* Ueda107]	YP_001983993.1	43% / 0.49
231110	putative long-chain-fatty-acid--CoA ligase [*Sinorhizobium fredii* NGR234]	YP_002825453.1	31% / 1.8
105839	F-box-like [pfam12937]	n.a.	7.31e-03

103413	oligopeptide ABC transporter permease [*Methanosarcina barkeri* str. Fusaro]	YP_307118.1	72% / 0.42
13288	DUF2413 domain. Pc16g07860 [*Penicillium chrysogenum* Wisconsin 54-1255]	XP_002561108.1	84% / 1e-25
103965	predicted: GRAM domain-containing protein 4-like [*Oreochromis niloticus*]	XP_003445122.1	19% / 1e-04
105630	hypothetical protein	n.a.	n.a.
110215	hypothetical protein	n.a.	n.a.
16995	LETM1 [pfam07766]. LETM1-like protein; inner mitochondrial membrane proteins	n.a.	9.35e-11
72748	DUF2404 [pfam10296]. putative integral membrane protein conserved region	n.a.	3.72e-33

Table S7: Differentially expressed genes in ΔGap1 mutant. Fold = fold change. Putative function indicates annotation of genome. Genes with unknown function are written as last genes. The effected genes are not regulated in the other mutant strains. Febit-ID includes protein ID in the middle.

12-43 *vs.* 4-39		**ΔGap1 x ΔGap1 *vs.* W22 x 12-43**		**febit-ID**	**putative function**
Fold	**pValue**	**Fold**	**pValue**		
INDUCED GENES					
-1.3	0.785	15.89	0.00485	295-102318-PM	Aminoacyl-tRNA synthetase. class I
-1.3	0.753	13.07	0.00908	124-256320-PM	Transcription regulator XNP/ATRX. DEAD-box superfamily. Shugoshin. N terminal
-1.1	0.883	12.67	0.00716	171-42694-PM	Pseudouridylate synthase
1.21	0.822	11.54	0.0083	196-45628-PM	HMG-box transcription factor. Helix-turn-helix. Fis-type
-1.2	0.805	10.98	0.0125	115-80616-PM	Spindle pole body protein - Sad1p. Peptidase C19. ubiquitin carboxyl-terminal hydrolase 2
-1	0.976	10.6	0.00893	126-235815-PM	Predicted steroid reductase
-1.6	0.629	9.5	0.0384	170-109412-PM	AAA+-type ATPase
1.23	0.801	8.65	0.0181	56-51001-PM	Nucleolar GTPase/ATPase p130
-1.2	0.834	8.58	0.047	85-69766-PM	3-phosphoinositide-dependent protein kinase (PDK1). Protein kinase
-1	0.981	8.38	0.0232	107-108327-PM	Rab GTPase activator activity
-1.2	0.798	8.34	0.00658	55-257431-PM	Chitinase. N-Glycan degradation. Sphingoglycolipid metabolism. Exo-alpha-sialidase
-1.1	0.897	7.9	0.0191	129-84176-PM	Myosin assembly protein/sexual cycle protein and related proteins
-1.2	0.85	7.35	0.02	69-53882-PM	Flavonol reductase/cinnamoyl-CoA reductase. Cinnamyl-alcohol dehydrogenase
1.31	0.721	7.24	0.0158	153-61334-PM	Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)
-1.6	0.489	7.15	0.0053	224-114530-PM	Zn-finger. C2H2 type
-1.4	0.53	6.99	0.00093	63-61055-PM	Tannase and feruloyl esterase
1.54	0.591	6.35	0.0313	171-58751-PM	Nuclear AAA ATPase (VCP subfamily). Peptidase S16. lon protease
-1.1	0.865	5.83	0.0195	93-15362-PM	G-protein beta WD40 repeat-containing protein. 2-acetyl-1-alkylglycerophosphocholine esterase
1.03	0.967	5.26	0.0433	57-113856-PM	Serine/threonine protein kinase
-1.3	0.302	5.23	1.1E-06	58-109925-PM	protein kinase activity
-1	0.96	5.12	0.0316	235-231200-PM	Zn-finger. MYND type
-1.3	0.262	4.98	5.6E-06	54-112724-PM	Cyclin-like F-box
-1.8	0.386	4.96	0.0207	283-57845-PM	Short-chain dehydrogenase/reductase SDR. Predicted integral membrane protein
-1	0.938	4.72	0.00708	105-84518-PM	Histone H1
1.27	0.535	4.7	0.00085	68-110288-PM	R-Golgi vesicle-tethering protein p115

-1.2	0.808	4.64	0.0393	57-256713-PM	GATA-4/5/6 transcription factors
-1.6	0.301	4.41	0.00434	102-49013-PM	Ornithine aminotransferase
-1	0.917	4.35	4.8E-06	78-231712-PM	Cyclin-dependent kinase WEE1. protein kinase activity
-1.3	0.644	4.29	0.0133	99-65844-PM	Molecular chaperones HSP70/HSC70. HSP70 superfamily
-2	0.0394	4.13	0.00023	316-59130-PM	Amidohydrolase-like
1.53	0.4	4.08	0.0109	107-232771-PM	Transcription regulator XNP/ATRX. DEAD-box superfamily. Cytochrome c heme-binding site
-1.1	0.884	4.05	0.0101	75-106125-PM	Cyclin-like F-box
-1.2	0.524	3.9	0.00028	62-76871-PM	Cytochrome P450. Unspecific monooxygenase
-1.5	0.512	3.7	0.0317	62-50580-PM	Signal recognition particle receptor. beta subunit (small G protein superfamily). GTP1/OBG
-1.2	0.719	3.61	0.0139	356-107962-PM	Bestrophin
-1.4	0.248	3.58	0.0004	67-71133-PM	Meltrins. fertilins and related Zn-dependent metalloproteinases of the ADAMs family. Disintegrin. Peptidase M12B. ADAM/reprolysin
1.93	0.0663	3.5	0.00163	129-238097-PM	hydrolase activity. hydrolyzing O-glycosyl compounds. carbohydrate metabolic process. Glycoside hydrolase. family 10
-1.1	0.737	3.46	0.00028	348-55177-PM	Predicted transporter (major facilitator superfamily)
1.29	0.445	3.43	0.0016	57-82890-PM	hydrolase activity. hydrolyzing O-glycosyl compounds. carbohydrate metabolic process. Glycoside hydrolase. family 7
1.19	0.66	3.39	0.00554	288-103992-PM	Myosin class II heavy chain
1.55	0.402	3.34	0.0312	67-77659-PM	DNA repair protein RAD50. ABC-type ATPase/SMC superfamily
-1	0.984	3.25	0.00735	56-77406-PM	TFIIF-interacting CTD phosphatase. including NLI-interacting factor (involved in RNA polymerase II regulation)
-1.3	0.42	3.06	0.00312	58-256692-PM	Myosin class II heavy chain. Lipocalin-related protein and Bos/Can/Equ allergen
1.25	0.42	3.06	0.00079	55-84301-PM	PPR repeat
1.28	0.552	3	0.0154	128-58593-PM	Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins
1.52	0.751	121.5	0.0018	219-61757-PM	*unknown*
-1.5	0.668	49.12	0.00048	146-79246-PM	*unknown*
-1.1	0.875	35.6	0.00021	53-57001-PM	*unknown*
1.38	0.777	25.93	0.0101	293-113076-PM	*unknown*
-1.7	0.407	23.09	7.4E-05	111-42141-PM	*unknown*
-1.2	0.865	20.2	0.00505	118-106931-PM	*unknown*
1.64	0.624	20.02	0.00741	154-235734-PM	*unknown*
1.17	0.865	17.61	0.00635	122-230333-PM	*unknown*
-1.3	0.771	12.73	0.00493	102-69462-PM	*Protein of unknown function DUF663*
-1.1	0.913	12.49	0.0036	104-231961-PM	*unknown*
-1.1	0.872	12.44	0.0066	178-43113-PM	*unknown*
1.18	0.787	11.5	0.00082	236-106104-PM	*unknown*
-1.4	0.655	10.65	0.00521	155-112763-PM	*unknown*
-1.4	0.729	10.34	0.0287	121-57287-PM	*unknown*
-1.5	0.701	8.85	0.0367	314-106297-PM	*unknown*
-1	0.998	8.71	0.00746	135-112849-PM	*unknown*
-1.9	0.464	7.73	0.026	215-237461-PM	*unknown*
-1.3	0.32	7.51	6.2E-07	63-85715-PM	*Uncharacterized conserved protein (tumor-rejection antigen MAGE in humans)*
1.03	0.966	7.45	0.00311	78-236440-PM	*unknown*
-1.4	0.687	6.93	0.0234	357-112020-PM	*Uncharacterized conserved protein BCNT*
1.1	0.897	6.63	0.0199	402-108687-PM	*Uncharacterized conserved coiled-coil protein*
-1.1	0.929	6.45	0.00151	61-61583-PM	*unknown*
-1.3	0.576	6.22	0.00058	65-107045-PM	*unknown*
-1.7	0.507	5.16	0.0393	203-236276-PM	*unknown*
1.06	0.894	4.81	0.00316	130-78007-PM	*unknown*
1.41	0.243	4.24	8.6E-05	74-78760-PM	*unknown*
1.22	0.711	4.12	0.0175	85-59277-PM	*Protein of unknown function DUF1253*

-1.5	0.125	4.07	6.9E-05	67-258043-PM	*unknown*
1.46	0.408	3.91	0.00692	79-12191-PM	*unknown*
-1.3	0.597	3.86	0.0228	53-234757-PM	*unknown*
-1.1	0.807	3.65	5.3E-05	61-85535-PM	*unknown*
1.07	0.91	3.59	0.0366	65-111352-PM	*unknown*
-1.7	0.238	3.39	0.00931	148-71969-PM	*unknown*
-1.4	0.392	3.12	0.00904	339-32474-PM	*unknown*
1.43	0.337	3.11	0.00622	74-85346-PM	*unknown*
REPRESSED GENES					
1.28	0.713	-165.93	5.1E-07	103-79176-PM	Vesicle coat complex COPII. subunit SEC23. Gelsolin regio
-1.31	0.296	-124.48	6.1E-13	113-86056-PM	Ubiquitin and ubiquitin-like proteins
-1.09	0.877	-55.81	2.1E-06	153-17256-PM	Transferrin receptor and related proteins containing the protease-associated (PA) domain. Peptidase M28
1.86	0.466	-55.18	0.00017	149-39575-PM	dUTPase
1.1	0.88	-45.02	1.9E-05	123-15875-PM	Predicted gamma-butyrobetaine.2-oxoglutarate dioxygenase. Trimethyllysine dioxygenase.
-1.59	0.622	-41.14	0.00086	105-14451-PM	Glia maturation factor beta. Actin-binding. cofilin/tropomyosin type
-1.55	0.47	-18.01	0.00016	59-109225-PM	NADH-ubiquinone oxidoreductase. subunit NDUFB10/PDSW
-1.43	0.637	-12.29	0.00381	141-60009-PM	Protein of unknown function UPF0203
-1.16	0.814	-11.58	0.00092	70-46796-PM	Myosin regulatory light chain. EF-Hand protein superfamily. Calcium-binding EF-hand
1.31	0.701	-10.68	0.00317	63-48018-PM	Histidinol-phosphatase
1.89	0.0261	-7.43	6.5E-07	175-231351-PM	beta-1.6-N-acetylglucosaminyltransferase. contains WSC domain
1.16	0.715	-7.18	0.00016	53-109359-PM	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes. AMP-dependent synthetase and ligase
-1.2	0.84	-6.93	0.0465	150-17184-PM	Lipase. class 3
-1.05	0.943	-6.19	0.0119	69-77743-PM	Permease of the major facilitator superfamily
1.29	0.542	-6.14	0.00033	178-71465-PM	Sexual differentiation process protein ISP4. Oligopeptide transporter OPT superfamily
-1.26	0.671	-5.5	0.00585	68-14103-PM	Transport protein particle (TRAPP) complex subunit
1.13	0.812	-5.45	0.00416	120-31488-PM	SLT
-1.5	0.183	-5.14	2.9E-05	60-68724-PM	60s ribosomal protein L34
1.23	0.437	-4.72	1.3E-05	57-105121-PM	Fungal hydrophobin. beta-1.6-N-acetylglucosaminyltransferase. contains WSC domain
1.02	0.929	-4.3	1.5E-06	127-61170-PM	oxidoreductase activity. FAD linked oxidase. N-terminal
-1.23	0.7	-4.24	0.0146	100-79125-PM	Short-chain dehydrogenase/reductase SDR. 3-oxoacyl-[acyl-carrier protein] reductase.
1.7	0.214	-4.23	0.00261	80-113652-PM	conserved protein. DSS1/SEM1
-1.1	0.55	-4.05	9.8E-08	106-64360-PM	Ribosome biogenesis protein NIP7
-1.62	0.109	-3.47	0.00044	96-80323-PM	Tripeptidyl-peptidase I. Peptidase S8 and S53. subtilisin. kexin. sedolisin
1.15	0.531	-3.46	2.7E-05	123-104099-PM	Glycine cleavage system H protein (lipoate-binding)
1.17	0.547	-3.42	0.00013	92-57671-PM	60s ribosomal protein L39
1.26	0.5	-3.42	0.00214	182-235154-PM	Splicing coactivator SRm160/300. subunit SRm160 (contains PWI domain)
-1.12	0.654	-3.39	0.00012	71-231179-PM	Pleiotropic drug resistance proteins (PDR1-15). ABC superfamily. ABC transporter
-1.03	0.943	-3.33	0.00653	108-257346-PM	beta-1.6-N-acetylglucosaminyltransferase. contains WSC domain
-1.3	0.543	-3.3	0.0115	209-52896-PM	Cobyrinic acid a.c-diamide synthase
-1.16	0.696	-3.29	0.00536	95-235908-PM	RNA-binding protein LARP/SRO9 and related La domain proteins
-1.01	0.978	-3.2	0.00586	68-9862-PM	DNA-directed RNA polymerase. subunit RPB7.0
-1.19	0.737	-3.11	0.0436	399-85953-PM	Molecular chaperone Prefoldin. subunit 3
-1.35	0.219	-3.09	0.00016	92-16727-PM	Predicted haloacid-halidohydrolase and related hydrolases. Riboflavin kinase
1.14	0.674	-3.04	0.00248	55-84848-PM	Haloacid dehalogenase/epoxide hydrolase
-1.1	0.884	-111.71	2.1E-06	147-17490-PM	*unknown*

-1.46	0.316	-14.74	1.1E-06	94-76730-PM	*unknown*
-1.08	0.943	-12.7	0.0339	101-107338-PM	*unknown*
1.09	0.766	-11.24	2.7E-07	53-104909-PM	*unknown*
1.47	0.73	-11.19	0.0401	113-104625-PM	*unknown*
-1.2	0.464	-10.94	2.4E-08	102-85227-PM	*unknown*
-1.04	0.974	-10.43	0.0459	101-54808-PM	*Uncharacterized conserved protein*
1.08	0.783	-5.96	7.6E-06	53-255808-PM	*unknown*
-1.39	0.611	-4.9	0.0242	65-56668-PM	*unknown*
1.58	0.135	-4.71	5.5E-05	83-109873-PM	*unknown*
1.6	0.144	-4.7	0.0001	84-72462-PM	*unknown*
-1.17	0.717	-4.61	0.00254	119-102877-PM	*unknown*
1.09	0.668	-4.11	1.9E-06	73-85818-PM	*unknown*
-1.12	0.643	-3.64	5.4E-05	56-113207-PM	*unknown*
1.33	0.152	-3.54	4.6E-06	84-103827-PM	*unknown*
-1.57	0.141	-3.54	0.00046	217-234366-PM	*unknown*

Table S8: Differentially expressed genes in Cdc42 mutant. Fold = fold change. Putative function indicates annotation of genome, genes with unknown function are written as last genes. The effected genes are not regulated in the other mutant strains. Febit-ID includes protein ID in the middle.

12-43 *vs.* 4-39		**Cdc42 *vs.* 12-43**		**Cdc42 *vs.* 4-39**		**febit-ID**	**putative function**
Fold	**pValue**	**Fold**	**pValue**	**Fold**	**pValue**		
INDUCED GENES							
-1.19	8.49E-01	102.6	9.50E-05	86.08	1.42E-04	131-13754-PM	Riboflavin kinase
1.53	5.46E-01	29.62	1.30E-04	45.26	3.67E-05	437-257367-PM	Transcription regulator dachshund. contains SKI/SNO domain. microtubule-based process. N-Glycan degradation
-1.49	5.46E-01	15.58	5.78E-04	10.43	2.19E-03	331-47163-PM	Tyrosyl-DNA phosphodiesterase
1.8	1.93E-01	9.75	6.59E-05	17.54	4.55E-06	63-232539-PM	C-type lectin
1.35	6.19E-01	9.75	1.31E-03	13.16	4.39E-04	69-233965-PM	SPRT-like metalloprotease
-1.29	7.62E-01	9.49	1.56E-02	7.33	2.94E-02	429-108668-PM	Galactokinase
-1.7	2.53E-01	9.47	1.05E-04	5.58	1.31E-03	68-256685-PM	Heme oxygenase (decyclizing)
-1.29	7.83E-01	9.23	2.61E-02	7.15	4.55E-02	57-232699-PM	Phytanoyl-CoA dioxygenase
1.01	9.93E-01	8.55	3.10E-02	8.62	3.05E-02	254-235639-PM	von Willebrand factor and related coagulation proteins
1.05	9.57E-01	8.48	4.26E-02	8.94	3.83E-02	58-111021-PM	Zn-finger. MYND type
-1.09	8.74E-01	7.42	1.23E-03	6.83	1.75E-03	61-36077-PM	Predicted tubulin-tyrosine ligase
-1.59	2.59E-01	6.88	1.41E-04	4.34	1.73E-03	131-29538-PM	Ricin B lectin
-1.64	2.34E-01	6.82	1.75E-04	4.16	2.48E-03	69-59166-PM	Zinc-binding oxidoreductase
-1.21	7.98E-01	6.8	1.67E-02	5.64	2.85E-02	168-52935-PM	Two-component phosphorelay intermediate involved in MAP kinase cascade regulation. Hpt
1.58	4.81E-01	5.95	1.23E-02	9.41	2.63E-03	54-37594-PM	Intradiol ring-cleavage dioxygenase
-1.34	4.47E-01	5.74	2.34E-04	4.28	1.24E-03	146-108473-PM	Permease of the major facilitator superfamily
-1.04	8.95E-01	5.73	4.60E-05	5.49	6.05E-05	55-238491-PM	Alpha/beta hydrolase fold
1.3	6.70E-01	5.57	1.21E-02	7.26	4.79E-03	236-40476-PM	GTP-binding protein. HSR1-related. GTPase
-1.61	2.07E-01	5.39	2.26E-04	3.36	3.81E-03	60-113557-PM	Cyclin-like F-box
1.11	6.29E-01	5.28	7.56E-07	5.88	3.25E-07	78-255668-PM	DNA-directed DNA polymerase
-1.63	1.29E-01	5.01	6.53E-05	3.07	1.95E-03	58-47838-PM	Glycine dehydrogenase (decarboxylating)
-1.17	7.68E-01	3.9	1.92E-02	3.33	3.53E-02	99-113614-PM	Tetrahydrobiopterin biosynthesis enzymes-like
1	1.00E+00	3.71	3.57E-02	3.71	3.57E-02	106-106587-PM	PHD Zn-finger protein
-1.16	7.40E-01	3.71	8.93E-03	3.19	1.81E-02	81-71339-PM	Squalene monooxygenase
-1.1	7.44E-01	3.62	3.05E-04	3.29	6.23E-04	120-67376-PM	Coproporphyrinogen III oxidase CPO/HEM13
1.04	9.00E-01	3.6	2.23E-04	3.73	1.70E-04	218-231299-PM	Transcription initiation factor TFIID. subunit BDF1

							and related bromodomain proteins
1.05	8.80E-01	3.3	1.60E-03	3.47	1.15E-03	111-236180-PM	Cytochrome P450 CYP2 subfamily
1.37	5.67E-01	3.25	4.12E-02	4.44	1.25E-02	87-60997-PM	Chromosome condensation complex Condensin. subunit G
1.17	6.79E-01	3.23	5.28E-03	3.77	2.13E-03	261-231975-PM	Splicing coactivator SRm160/300. subunit SRm300. Peptidase M. neutral zinc metallopeptidases. zinc-binding site
1.2	7.33E-01	3.2	3.71E-02	3.82	1.84E-02	69-37220-PM	Notchless-like WD40 repeat-containing protein. G-protein
1.23	4.79E-01	3.06	1.21E-03	3.77	2.55E-04	103-83427-PM	H+/oligopeptide symporter. TGF-beta receptor. type I/II extracellular region
-1.14	9.08E-01	30.38	7.94E-03	26.61	1.02E-02	108-113864-PM	*unknown*
-1.72	4.79E-01	20.39	8.56E-04	11.89	4.10E-03	243-241485-PM	*unknown*
-1.62	4.43E-01	19.27	1.70E-04	11.87	9.13E-04	113-233311-PM	*unknown*
-1.87	3.17E-01	17.15	2.20E-04	9.16	2.03E-03	249-238674-PM	*unknown*
1.11	8.73E-01	16.41	4.14E-04	18.2	2.93E-04	96-231761-PM	*unknown*
1.24	6.65E-01	14.31	3.93E-05	17.71	1.63E-05	95-236353-PM	*unknown*
-1.5	3.57E-01	13.26	1.28E-05	8.86	8.66E-05	165-113776-PM	*unknown*
1.01	9.86E-01	12.62	1.17E-03	12.77	1.12E-03	370-38937-PM	*unknown*
-1.13	8.71E-01	11.23	5.49E-03	9.9	7.82E-03	75-230599-PM	*unknown*
1.47	3.18E-01	11.04	6.01E-06	16.19	9.12E-07	264-48837-PM	*unknown*
1.34	7.40E-01	10.51	1.52E-02	14.11	7.47E-03	207-233156-PM	*unknown*
1.68	3.93E-01	10.24	1.09E-03	17.21	1.66E-04	74-107062-PM	*unknown*
-1.26	7.12E-01	8.85	2.64E-03	7.01	5.93E-03	56-112604-PM	*unknown*
1.23	6.86E-01	8.41	5.76E-04	10.35	2.39E-04	56-114493-PM	*unknown*
1.44	6.98E-01	7.91	4.00E-02	11.42	1.80E-02	152-84654-PM	*unknown*
1.03	9.57E-01	7.46	7.17E-04	7.66	6.38E-04	99-58098-PM	*unknown*
-1.87	4.00E-02	7.18	2.19E-06	3.84	1.78E-04	233-241488-PM	*unknown*
1.03	9.71E-01	7.12	1.11E-02	7.3	1.03E-02	120-257269-PM	*unknown*
-1.83	3.45E-02	6.85	1.20E-06	3.75	1.03E-04	57-232483-PM	*unknown*
1.21	7.44E-01	6	6.28E-03	7.25	3.07E-03	63-16019-PM	*unknown*
1.79	3.97E-01	5.28	2.40E-02	9.46	3.84E-03	54-106345-PM	*unknown*
1.32	4.48E-01	5.25	2.68E-04	6.96	5.29E-05	187-105384-PM	*unknown*
-1.16	6.44E-01	4.95	7.66E-05	4.28	2.05E-04	56-53807-PM	*unknown*
-1.36	3.10E-01	4.66	6.70E-05	3.42	6.12E-04	55-85639-PM	*unknown*
1.49	4.82E-01	4.46	1.56E-02	6.66	3.38E-03	191-102263-PM	*unknown*
1.16	7.74E-01	4.18	1.38E-02	4.86	7.45E-03	576-113450-PM	*unknown*
1.7	2.45E-01	4.09	5.31E-03	6.95	3.94E-04	273-108673-PM	*unknown*
1.27	7.07E-01	3.79	4.79E-02	4.81	2.23E-02	59-114329-PM	*Uncharacterized conserved protein*
1.58	4.33E-01	3.77	3.31E-02	5.96	6.22E-03	92-234309-PM	*unknown*
-1.04	9.31E-01	3.62	1.61E-02	3.47	1.93E-02	296-11856-PM	*unknown*
1.52	4.42E-01	3.45	3.32E-02	5.25	6.44E-03	67-231760-PM	*unknown*
1.25	6.14E-01	3.1	1.85E-02	3.88	6.27E-03	138-51005-PM	*unknown*
1.26	6.61E-01	3.01	4.62E-02	3.78	1.88E-02	70-82151-PM	*unknown*
REPRESSED GENES							
1.17	8.30E-01	-56.8	4.08E-05	-48.38	6.37E-05	106-111246-PM	Cyclin-like F-box
-1.1	7.94E-01	-45.3	8.75E-09	-49.94	6.03E-09	54-75404-PM	Fumarate reductase. flavoprotein subunit. Succinate dehydrogenase
-1.2	7.95E-01	-32.5	2.80E-05	-38.15	1.66E-05	183-256250-PM	Zn-finger. C2H2 type
-1.1	9.14E-01	-29.5	1.79E-05	-31.44	1.44E-05	65-233429-PM	Predicted transporter (major facilitator superfamily). Tetracycline resistance protein TetB
-1.1	9.26E-01	-26.6	6.44E-05	-28.23	5.31E-05	54-112999-PM	peroxidase activity. Haem peroxidase. plant/fungal/bacterial
1.3	7.68E-01	-26.4	1.63E-03	-20.3	3.12E-03	159-102651-PM	WD40 repeat protein G-protein
1.31	6.40E-01	-22.6	3.97E-05	-17.23	1.06E-04	189-52965-PM	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily). Epoxide hydrolase

1.03	9.74E-01	-20.8	8.96E-04	-20.3	9.63E-04	78-70937-PM	Dynactin subunit p27/WS-3. involved in transport of organelles along microtubules
1.29	6.65E-01	-20.7	7.41E-05	-16.01	1.86E-04	118-105103-PM	Phosphoglycerate mutase
-1.1	9.29E-01	-17.9	1.23E-02	-19.63	1.02E-02	132-49025-PM	Protein involved in vacuolar protein sorting
-1.6	5.76E-01	-16.5	3.24E-03	-26.32	9.42E-04	61-16399-PM	Cytochrome P450 CYP3/CYP5/CYP6/CYP9 subfamilies
1.1	9.03E-01	-15.2	2.32E-03	-13.82	3.03E-03	105-255629-PM	Esterase D
1.75	3.39E-01	-14.5	2.07E-04	-8.3	1.71E-03	66-12537-PM	Glucose-6-phosphate 1-dehydrogenase
1.45	4.72E-01	-14.4	6.40E-05	-9.89	2.99E-04	68-61335-PM	RNA polymerase III subunit C11
1.33	2.26E-01	-14.2	1.40E-09	-10.67	7.62E-09	66-52108-PM	Peptidase M35. deuterolysin
1.19	7.71E-01	-13.5	4.42E-04	-11.33	8.35E-04	134-81735-PM	Protein required for meiosis
1.65	1.57E-01	-13.2	7.38E-07	-7.99	1.14E-05	60-56910-PM	Ubiquitin-like protein
1.46	5.58E-01	-12.9	8.47E-04	-8.83	3.09E-03	97-73874-PM	26S proteasome regulatory complex. subunit RPN6/PSMD11
1.3	4.88E-01	-12.1	3.94E-06	-9.31	1.54E-05	143-67567-PM	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies
1.98	1.54E-01	-11.9	4.92E-05	-5.98	1.15E-03	84-77964-PM	Glycoside hydrolase. family 61
1.2	6.48E-01	-10.9	1.44E-05	-9.08	3.64E-05	161-254867-PM	Multicopper oxidases. Laccase
1.67	5.46E-01	-10.8	1.07E-02	-6.46	3.80E-02	480-231100-PM	NADH-cytochrome b-5 reductase. KOG0534: NADH-cytochrome b-5 reductase
-1.2	2.49E-01	-10.3	1.05E-11	-12.28	3.34E-12	53-11367-PM	Fungal hydrophobin
1.77	3.52E-01	-8.98	1.88E-03	-5.07	1.46E-02	423-108300-PM	Immunoglobin and related proteins. Cytochrome c heme-binding site
1.02	9.84E-01	-7.96	2.13E-02	-7.83	2.23E-02	60-255897-PM	G-protein beta WD-40 repeat
1.84	2.83E-01	-7.55	1.94E-03	-4.09	2.06E-02	200-106879-PM	UbiA prenyltransferase
-1.5	6.67E-01	-7.5	4.52E-02	-11.27	1.87E-02	70-238569-PM	Microtubule-associated protein TAU
1.93	5.16E-02	-7.4	7.16E-06	-3.83	5.19E-04	153-111169-PM	Zn-finger. RING
1.49	3.90E-01	-6.8	5.94E-04	-4.55	4.01E-03	152-49983-PM	TIP41-like protein
1.56	2.46E-01	-6.76	7.32E-05	-4.35	9.39E-04	103-76066-PM	26S proteasome regulatory complex. ATPase RPT4
-1.4	5.43E-01	-6.71	2.86E-03	-9.42	7.46E-04	61-82928-PM	3-hydroxyisobutyrate dehydrogenase
1.42	5.66E-01	-6.71	5.41E-03	-4.73	1.87E-02	73-75752-PM	Mannosyl-oligosaccharide alpha-1.2-mannosidase and related glycosyl hydrolases
-1.2	7.85E-01	-6.62	2.53E-02	-8.19	1.43E-02	94-235928-PM	Glycoside hydrolase. family 43
-1.4	6.74E-01	-6.6	1.48E-02	-8.88	5.99E-03	62-105151-PM	Zn-finger. MYND type
1.28	1.70E-01	-6.58	3.59E-09	-5.16	2.77E-08	54-67642-PM	Putative translation initiation inhibitor UK114/IBM1
-1.1	8.75E-01	-6.47	1.31E-03	-7	9.27E-04	157-112062-PM	P-II protein urydylation site
1.89	4.29E-02	-6.44	6.63E-06	-3.41	5.83E-04	97-82703-PM	Gluconate kinase
1.88	2.87E-02	-6.38	2.11E-06	-3.39	2.42E-04	206-103905-PM	Splicing coactivator SRm160/300. subunit SRm300
1.23	4.16E-01	-6.2	1.28E-06	-5.04	5.94E-06	95-58166-PM	Predicted panthothenate kinase/uridine kinase-related protein
-1.1	7.83E-01	-6.16	2.43E-04	-6.88	1.34E-04	308-46655-PM	Hypoxia induced protein conserved region
1.04	9.04E-01	-6.04	4.29E-05	-5.8	5.52E-05	108-56010-PM	Acyl-coA-binding protein. ACBP
-1.1	7.79E-01	-5.99	6.54E-05	-6.6	3.65E-05	111-255875-PM	Kynurenine aminotransferase. glutamine transaminase K
1.63	2.25E-02	-5.92	5.55E-08	-3.64	4.05E-06	78-83883-PM	20S proteasome. regulatory subunit beta type PSMB2/PRE1
1.14	6.94E-01	-5.88	3.81E-05	-5.17	8.65E-05	110-65238-PM	GTPase Rab2. small G protein superfamily
1.17	4.74E-01	-5.75	3.53E-07	-4.91	1.26E-06	143-72421-PM	Alcohol dehydrogenase. class III
-1.1	8.77E-01	-5.65	3.76E-02	-6.37	2.75E-02	54-81364-PM	MADS box transcription factor
1.35	3.67E-01	-5.56	6.77E-05	-4.1	4.77E-04	53-47866-PM	Predicted dioxygenase
1.34	2.54E-01	-5.43	3.17E-06	-4.05	3.12E-05	248-232365-PM	20S proteasome. regulatory subunit alpha type PSMA7/PRE6
1.43	5.66E-01	-5.36	1.39E-02	-3.74	4.56E-02	56-62348-PM	Ca2+-binding protein (centrin/caltractin). EF-Hand superfamily protein
1.66	7.06E-02	-5.34	7.14E-06	-3.21	3.63E-04	74-57285-PM	Dosage compensation regulatory complex/histone acetyltransferase complex. subunit MSL-3/MRG15/EAF3. and related CHROMO domain-containing proteins

1.04	9.19E-01	-5.33	2.29E-04	-5.14	2.85E-04	53-231008-PM	Von Willebrand factor and related coagulation proteins
1.24	5.33E-01	-5.18	1.46E-04	-4.18	5.67E-04	102-14057-PM	Branched chain alpha-keto acid dehydrogenase E1. beta subunit
-1	8.98E-01	-4.96	5.18E-07	-5.09	4.14E-07	88-77161-PM	Zn-finger. C2H2 type
1.17	6.55E-01	-4.92	3.10E-04	-4.19	8.23E-04	96-81268-PM	Sorbitol dehydrogenase
-1.1	8.98E-01	-4.65	2.52E-02	-5.05	1.93E-02	401-46068-PM	RNA polymerase III. subunit C34
1.25	4.45E-01	-4.64	5.62E-05	-3.7	2.88E-04	53-114479-PM	Cyclin-like F-box
-1.3	6.89E-01	-4.61	4.13E-02	-6.11	1.82E-02	58-105955-PM	von Willebrand factor and related coagulation proteins
1	9.96E-01	-4.59	4.47E-04	-4.58	4.52E-04	96-48271-PM	PP-loop. Uncharacterized conserved protein with similarity to predicted ATPase of the PP-loop superfamily
1.43	3.84E-01	-4.56	1.46E-03	-3.19	1.00E-02	170-46550-PM	Replication factor C. subunit RFC1 (large subunit). BRCT
1.41	1.24E-01	-4.55	1.76E-06	-3.23	3.94E-05	170-113902-PM	Multidrug/pheromone exporter. ABC superfamily
1.3	4.24E-01	-4.54	1.82E-04	-3.5	1.05E-03	142-13020-PM	20S proteasome. regulatory subunit alpha type PSMA1/PRE5
1.15	6.90E-01	-4.54	4.84E-04	-3.94	1.16E-03	143-255062-PM	Permease of the major facilitator superfamily
1.06	8.66E-01	-4.39	4.19E-04	-4.14	6.05E-04	329-69673-PM	UDP-glucose pyrophosphorylase
1.33	5.27E-01	-4.37	4.09E-03	-3.28	1.61E-02	60-61466-PM	Predicted molecular chaperone (DnaJ superfamily)
1.24	5.91E-01	-4.22	2.00E-03	-3.4	6.51E-03	154-114488-PM	DNA polymerase sigma. PAP/25A-associated
1.25	6.17E-01	-4.04	5.33E-03	-3.24	1.57E-02	62-48129-PM	Transcription initiation factor TFIID. subunit TAF5 (also component of histone acetyltransferase SAGA)
1.21	6.68E-01	-3.95	6.38E-03	-3.26	1.60E-02	73-69593-PM	Alcohol dehydrogenase. class IV
1.28	5.10E-01	-3.95	1.44E-03	-3.1	6.18E-03	96-71602-PM	Ricin B lectin
1.2	4.89E-01	-3.88	5.93E-05	-3.24	2.60E-04	111-106337-PM	Zn-finger. MYND type
1.06	7.99E-01	-3.82	8.36E-06	-3.62	1.38E-05	87-83849-PM	Aldehyde dehydrogenase
1.13	7.26E-01	-3.8	1.21E-03	-3.36	2.61E-03	82-258522-PM	Mandelate racemase/muconate lactonizing enzyme. Galactonate dehydratase
-1.6	1.38E-01	-3.75	5.33E-04	-6.07	2.11E-05	304-13426-PM	TatD-related DNase
1.12	7.64E-01	-3.72	2.76E-03	-3.32	5.33E-03	185-37734-PM	Anaphase-promoting complex (APC). subunit 10
1.19	6.62E-01	-3.59	4.02E-03	-3.02	1.04E-02	233-82620-PM	Predicted MutS-related protein involved in mismatch repair
-1.1	7.50E-01	-3.56	1.72E-04	-3.88	8.72E-05	171-235829-PM	Cyclin-like F-box
1.03	9.42E-01	-3.54	1.30E-02	-3.42	1.52E-02	67-71876-PM	Translation initiation factor 2C (eIF-2C) and related proteins. Argonaute and Dicer protein. PAZ
1.14	5.00E-01	-3.5	6.52E-06	-3.06	2.51E-05	53-14572-PM	MOT2 transcription factor. RNA-binding region RNP-1 (RNA recognition motif)
-1.2	5.63E-01	-3.49	3.17E-03	-4.32	8.84E-04	78-84564-PM	Lipase. active site
-1.1	8.48E-01	-3.45	9.31E-03	-3.74	6.15E-03	67-111476-PM	Acinus (induces apoptotic chromatin condensation)
-1.4	3.24E-01	-3.41	3.26E-03	-4.9	3.63E-04	112-68620-PM	Beta subunit of farnesyltransferase
-1.5	2.12E-01	-3.37	8.48E-04	-4.98	5.48E-05	275-69750-PM	Carbohydrate-binding domain. family V/XII
-1.5	1.94E-01	-3.36	1.04E-03	-5.09	5.93E-05	58-256647-PM	Protein involved in Snf1 protein kinase complex assembly
-1	9.90E-01	-3.32	1.89E-03	-3.34	1.84E-03	148-109979-PM	Protein kinase containing WD40 repeats
-1.1	4.68E-01	-3.29	5.17E-06	-3.76	1.32E-06	106-255161-PM	Heat shock transcription factor
-1.1	7.65E-01	-3.25	3.74E-03	-3.62	1.94E-03	238-51868-PM	Cytosine deaminase FCY1 and related enzymes
-1.1	7.03E-01	-3.19	1.66E-03	-3.6	7.18E-04	169-257326-PM	Splicing coactivator SRm160/300. subunit SRm300. Glucan 1.4-alpha-glucosidase
-1.3	5.86E-01	-3.16	1.07E-02	-3.95	3.25E-03	130-102431-PM	Cyclin-like F-box
-1.9	1.63E-01	-3.03	1.95E-02	-5.66	8.61E-04	61-33094-PM	Transcription initiation factor TFIID. subunit TAF11
-1.2	4.21E-01	-3.01	5.29E-04	-3.72	9.23E-05	106-103430-PM	Predicted signal transduction protein. Protein-tyrosine-phosphatase
-1.1	8.85E-01	-132	3.69E-07	-144.8	2.88E-07	55-103113-PM	*unknown*
-1.4	6.44E-01	-76.8	7.21E-06	-105.9	2.97E-06	87-112677-PM	*unknown*
-1	9.95E-01	-50.5	1.10E-04	-50.71	1.08E-04	119-111173-PM	*unknown*

-1.4	7.05E-01	-27.3	1.41E-03	-38.09	6.14E-04	88-84888-PM	*unknown*
1.05	9.61E-01	-20	1.13E-02	-18.95	1.25E-02	131-61214-PM	*unknown*
1.43	7.07E-01	-19.1	6.16E-03	-13.31	1.38E-02	64-85084-PM	*unknown*
-1.9	4.73E-01	-15.7	6.85E-03	-30.3	1.41E-03	588-14082-PM	*unknown*
-1.8	3.30E-01	-15.5	3.01E-04	-28.4	3.73E-05	88-257049-PM	*unknown*
1.08	9.01E-01	-14.5	5.64E-04	-13.42	7.41E-04	87-12684-PM	*unknown*
-1.8	4.70E-01	-11.4	9.26E-03	-20.92	1.89E-03	59-106970-PM	*unknown*
1.16	7.44E-01	-11	4.57E-05	-9.5	9.03E-05	84-63789-PM	*unknown*
-1.2	7.84E-01	-9.43	2.69E-03	-11.27	1.47E-03	82-255226-PM	*unknown*
-1.4	7.09E-01	-9.23	1.81E-02	-12.74	8.16E-03	93-230979-PM	*unknown*
1.44	5.93E-01	-8.57	5.26E-03	-5.94	1.67E-02	237-103277-PM	*unknown*
-1.8	1.05E-01	-8.41	5.50E-06	-14.73	2.60E-07	90-110679-PM	*unknown*
1.58	6.79E-02	-7.83	1.05E-07	-4.96	3.02E-06	53-74722-PM	*Uncharacterized conserved protein*
1.06	8.43E-01	-6.83	1.70E-06	-6.47	2.46E-06	209-103063-PM	*unknown*
1.19	7.86E-01	-6.62	9.30E-03	-5.55	1.66E-02	287-232649-PM	*unknown*
-1.4	4.13E-01	-6.4	1.31E-04	-8.78	2.35E-05	191-235337-PM	*unknown*
-1	9.77E-01	-5.99	1.22E-03	-6.07	1.14E-03	61-86084-PM	*unknown*
1.32	6.55E-01	-5.69	1.19E-02	-4.3	3.05E-02	111-106390-PM	*unknown*
1.13	7.00E-01	-5.67	2.99E-05	-5.03	6.63E-05	180-85576-PM	*unknown*
1.27	7.19E-01	-5.5	1.90E-02	-4.32	3.98E-02	383-102818-PM	*unknown*
1.31	6.41E-01	-5.2	1.05E-02	-3.96	2.80E-02	112-11429-PM	*unknown*
1.35	3.71E-01	-4.94	1.39E-04	-3.66	9.85E-04	58-84836-PM	*unknown*
-1.3	2.84E-01	-4.86	1.15E-05	-6.47	1.44E-06	64-104205-PM	*unknown*
1.3	5.14E-01	-4.5	1.26E-03	-3.47	5.34E-03	288-114974-PM	*unknown*
-1.9	1.37E-01	-4.43	1.51E-03	-8.2	5.51E-05	94-103477-PM	*unknown*
1.14	5.88E-01	-4.31	9.98E-06	-3.78	2.97E-05	68-109462-PM	*unknown*
-1.1	8.59E-01	-4.13	2.36E-03	-4.44	1.60E-03	53-104546-PM	*unknown*
-1.1	7.10E-01	-4.07	1.24E-04	-4.53	5.68E-05	53-83841-PM	*unknown*
1.23	5.16E-01	-3.82	5.35E-04	-3.1	2.25E-03	83-69452-PM	*unknown*
1.21	6.39E-01	-3.82	3.35E-03	-3.17	9.32E-03	90-109477-PM	*unknown*
1.04	9.49E-01	-3.78	2.51E-02	-3.65	2.86E-02	90-235433-PM	*unknown*
-1.5	3.01E-01	-3.76	2.61E-03	-5.61	2.62E-04	93-84110-PM	*unknown*
1.06	8.56E-01	-3.66	8.46E-04	-3.45	1.26E-03	69-105669-PM	*unknown*
-1.3	3.81E-01	-3.61	6.98E-05	-4.5	1.15E-05	57-84920-PM	*unknown*
-1.1	8.79E-01	-3.54	3.76E-02	-3.86	2.76E-02	131-53144-PM	*unknown*
1.06	9.04E-01	-3.33	2.34E-02	-3.14	3.00E-02	71-66966-PM	*Unknown*

Table S9: Differentially regulated genes in the pathways of Ras1/Gap1/Cdc42. Bold letters in putative function column indicate annotation of genome homepage (genome.jgi-psf.org/Schco1), normal letters indicate Blastp (blast.ncbi.nlm.nih.gov) annotated gene functions (details see Table S7). Fold = fold change, if between +2 and -2 = no regulation. Positive value = increased expression, negative value = decreased expression compared to mono- or dikaryon. Protein ID refers to numbers for proteins on genome homepage.

putative function	**Comparisons** **Ras1/Gap1/Cdc42 pathway - induced genes**										**Protein ID**
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22x12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
***aay4*. Homeodomain transcription factor activity**	11.1	2.14E-3	14.2	9.55E-4	9.89	3.07E-3	7.21	8.55E-3	9.23	3.85E-3	231556
Zn-finger. CCHC type. nucleic acid binding	12.9	2.08E-3	15	1.31E-3	16.85	9.09E-4	5.37	2.89E-2	6.23	1.88E-2	237097

general substrate transporter	4.88	5.68E-3	3.05	4.00E-2	7.98	6.80E-4	15	4.80E-5	9.36	3.44E-4	66123
***aax4*; protein of unknown function**	39.6	5.69E-7	37.7	6.77E-7	8.52	3.05E-4	15	2.58E-5	14.3	3.15E-5	64664
vomeronasal 1 receptor monDomV1R1217 [*Monodelphis domestica*]	19.5	2.92E-6	10.1	5.70E-5	39.02	1.81E-7	36.8	2.25E-7	19	3.26E-6	237981
secreted protein [*Melampsora larici-populina* 98AG31]	4.95	1.70E-3	6.88	3.26E-4	4.14	4.18E-3	8.68	1.04E-4	12.1	2.18E-5	27681
F-Box containing protein	4.01	2.16E-2	6.76	2.86E-3	6.16	4.12E-3	4.71	1.17E-2	7.94	1.52E-3	105141
Ras1/Gap1/Cdc42 pathway - repressed genes											
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22 x 12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
serine/threonine-protein kinase involved in autophagy. kinase activity. transmembrane receptor protein kinase activity	-21.5	1.00E-5	-13.62	6.32E-5	-3.88	1.40E-2	-17.3	2.37E-5	-11	1.57E-4	235720
FMN-dependent alpha-hydroxy acid dehydrogenase. electron transport. Glycolate oxidase	-18	7.52E-3	-15.37	1.07E-2	-11.6	1.97E-2	-44.7	9.59E-4	-38	1.37E-3	48810
complement regulator acquiring protein 1 [*Borrelia burgdorferi*]	-192	4.11E-11	-240.4	2.14E-11	-327	8.99E-12	-3.75	1.73E-3	-4.7	4.52E-4	85939
colicin I receptor [*Stenotrophomonas sp.* SKA14]	-7.7	1.38E-6	-9.09	4.86E-7	-7.41	1.75E-6	-3.39	4.46E-4	-4	1.27E-4	81398
ubiquitin ligase protein MIB2. putative [*Pediculus humanus corporis*]	-7.69	1.02E-3	-12.04	1.58E-4	-118	4.88E-8	-10.8	2.43E-4	-17	3.99E-5	50388
integral membrane protein [*Mycoplasma penetrans* HF-2]	-9.46	8.72E-3	-7.18	1.87E-2	-20.6	9.49E-4	-28.1	3.92E-4	-21	8.59E-4	231319
Nnf1 superfamily. polyamine-modulated factor 1 [*Xenopus tropicalis*]	-5.06	3.71E-3	-3.09	3.17E-2	-3.13	3.03E-2	-41.5	5.99E-7	-25	3.76E-6	107950
Ras1/Gap1 pathway - induced genes											
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22 x 12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
3-hydroxy-anthranilate oxygenase HAAO. tryptophan metabolism	268.7	2.16E-12	365.3	9.11E-13	425.9	6.01E-13	1.1	6.85E-1	1.6	1.82E-1	86160
multidrug/pheromone exporter. ABC superfamily	25.8	1.21E-3	14.35	5.52E-3	21.55	1.93E-3	1.3	7.88E-1	-1.43	6.75E-1	60306
SNF2 family DNA-	3.63	3.35E-3	4.4	1.11E-3	3.15	7.41E-3	1.1	8.94E-1	1.3	5.26E-1	50771

dependent ATPase domain-containing protein. Helicase. C-terminal											
DUF544 superfamily. protein of unknown function	22.04	3.08E-6	19.86	4.73E-6	5.71	1.32E-3	-1.55	3.48E-1	-1.7	2.48E-1	50742
nuclear transport factor 2 (NTF2) family protein [*Arabidopsis thaliana*]	6.33	1.20E-2	6.72	9.85E-3	4.59	3.28E-2	-1.61	4.78E-1	-1.5	5.35E-1	231457
DUF89 domain-containing protein [*Coprinopsis cinerea okayama*7#130]	3.56	3.91E-2	4.65	1.49E-2	10.59	6.63E-4	-1.67	3.81E-1	-1.3	6.76E-1	80832
Ras1/Gap1 pathway - repressed genes											
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22 x 12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
mitochondrial carnitine-acylcarnitine carrier protein	-173	7.19 E-10	-226	3.31 E-10	-3.46	8.71E-3	1.5	3.63E-1	1.1	7.70E-1	72928
5' nucleotidase. Metallophosphoesterase	-132	5.25E-6	-189.8	2.15E-6	-14.5	2.35E-3	1.2	8.52E-1	-1.2	7.74E-1	69253
histidine acid phosphatase	-26.9	3.65E-8	-37.53	9.02E-9	-4.15	7.75E-4	1.3	4.68E-1	-1.1	8.38E-1	65802
cyclophilin-type peptidyl-prolyl cis-trans isomerase. RNA-binding region RNP-1	-44.3	3.84E-5	-33.11	9.17E-5	-11.6	2.37E-3	1.3	7.23E-1	1.7	4.44E-1	50077
cyclophilin type peptidyl-prolyl cis-trans isomerase	-3.35	1.47E-3	-5.33	6.64E-5	-4.39	2.37E-4	1.3	4.73E-1	-1.26	4.79E-1	78835
glycosyl transferase. family 2 [*Crocosphaera watsonii* WH 8501]	-18.9	8.65E-4	-10	5.74E-3	-22.4	5.28E-4	-1.54	5.61E-1	1.2	7.81E-1	256679
hypothetical protein	-10	6.42E-3	-9.78	6.88E-3	-14.7	2.10E-3	-1.51	5.83E-1	-1.5	6.05E-1	109956
Ras1/Cdc42 pathway - induced genes											
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22 x 12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
Cyclin-dependent protein kinase activity	3.57	3.44E-2	3.24	4.87E-2	1.84	2.84E-1	9.57	7.75E-4	8.68	1.13E-3	230362
Cyclin-like F-box. Cyclic nucleotide-binding	9.22	9.20E-4	12.1	3.17E-4	-1.3	6.71E-1	5.74	5.83E-3	7.56	2.00E-3	256849
SWI-SNF chromatin-remodeling complex protein	3.06	1.35E-2	4.21	2.50E-3	1.74	1.89E-1	4.9	1.11E-3	6.75	2.05E-4	255941
Ankyrin	6.01	1.87E-3	4.99	4.23E-3	-1.3	5.54E-1	4.82	4.96E-3	4.01	1.11E-2	107207
cytochrome P450 . Unspecific monooxygenase	4.07	1.57E-3	4.03	1.66E-3	-1.1	7.91E-1	3.57	3.39E-3	3.53	3.59E-3	55523
RTA1 domain protein [*Aspergillus oryzae* RIB40]	22.6	1.49E-3	34.9	4.77E-4	-1.2	8.02E-1	38.7	3.66E-4	59.7	1.20E-4	46742
spore wall assembly -related protein	10.2	8.06E-5	6.55	6.33E-4	-1.1	8.18E-1	8.87	1.51E-4	5.72	1.21E-3	53069

[*Cryptococcus gattii* WM276]											
gamma-glutamyltranspeptidase [*Alteromonas macleodii* str. 'Deep ecotype']	4.5	1.01E-3	5.64	2.82E-4	1.43	3.63E-1	7.72	5.00E-5	9.66	1.52E-5	236328
Ras1/Cdc42 pathway - repressed genes											
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22 x 12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
carbon-nitrogen hydrolase. Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	-522	1.94 E-10	-478.9	2.40 E-10	-1.09	8.53E-1	-3.29	2.08E-2	-3	3.03E-2	81287
predicted hydrolase (HIT family). Zn-finger. C2H2 type	-38.1	2.00E-5	-59.02	5.10E-6	-1.48	5.34E-1	-6.9	6.52E-3	-11	1.42E-3	27513
D-aspartate oxidase	-36.8	2.44E-4	-32.84	3.33E-4	-1.39	6.79E-1	-11.2	6.62E-3	-9.9	9.04E-3	55341
polynucleotide kinase 3' phosphatase	-36.1	3.31E-3	-25.53	6.74E-3	1.36	7.76E-1	-17.6	1.42E-2	-13	2.81E-2	81277
GCN5-related N-acetyltransferase	-22.2	2.96E-6	-13.08	2.80E-5	-1.63	2.96E-1	-19	5.67E-6	-11.	5.67E-5	80737
dihydrodipicolinate synthetase	-13.6	1.54E-3	-26.32	1.96E-4	-1.94	3.53E-1	-12.8	1.85E-3	-25	2.36E-4	82277
esterase/lipase/thioesterase	-12.5	1.03E-5	-8.91	5.35E-5	1.13	7.61E-1	-4.92	1.16E-3	-3.5	6.91E-3	69185
dimeric dihydrodiol dehydrogenase. Oxidoreductase. N-terminal	-9.33	1.42E-2	-13.81	5.11E-3	-1.68	5.32E-1	-8.37	1.87E-2	-12.	6.80E-3	54187
serine/threonine protein kinase. HMG-I and HMG-Y. DNA-binding	-6.6	6.33E-4	-3.32	1.66E-2	-1.36	5.00E-1	-9.19	1.33E-4	-4.6	3.50E-3	112167
methylcrotonyl-CoA carboxylase. alpha chain/Acetyl-CoA carboxylase. biotin carboxylase subunit	-6.22	8.93E-3	-5.65	1.24E-2	1.24	7.30E-1	-5.11	1.74E-2	-4.6	2.39E-2	72682
mercaptopyruvate sulfurtransferase/thiosulfate sulfurtransferase. Rhodanese-like	-5.16	1.18E-3	-4.87	1.60E-3	-1.16	7.34E-1	-7.41	1.88E-4	-7	2.51E-4	255362
predicted histone tail methylase containing SET domain	-5.1	3.94E-8	-4.51	1.20E-7	1.35	1.02E-1	-5.79	1.34E-8	-5.1	3.86E-8	84901
AAA+-type ATPase. Chaperonin clpA/B	-4.65	9.23E-3	-3.45	3.02E-2	-1.18	7.55E-1	-8.7	6.98E-4	-6.5	2.41E-3	48854
predicted hydrolase (HIT family). Zn-finger. C2H2 type	-3.53	2.37E-3	-3.74	1.66E-3	1.36	3.93E-1	-23	8.83E-8	-24	6.81E-8	84558
telomeric DNA binding	-18.9	3.58E-5	-10.09	4.32E-4	-1.12	8.38E-1	-6.09	3.38E-3	-3.2	4.08E-2	256094

protein [*Coprinopsis cinerea okayama*7#130]											
hypothetical protein	-96.5	4.87E-4	-115.4	3.40E-4	-1.26	8.30E-1	-63	1.17E-3	-75	8.15E-4	233957
nucleoside H$^+$ symporter (3-phenylpropionic acid transporter). membrane protein [*Pseudomonas brassicacearum subsp. brassicacearum* NFM421]	-43.9	6.33E-5	-50.22	4.30E-5	-1.36	6.74E-1	-10.1	5.01E-3	-11	3.33E-3	84078
hypothetical protein	-17.8	2.70E-5	-24.01	8.34E-6	-1.98	1.94E-1	-38.8	1.43E-6	-52	5.00E-7	255445
GG21300 [*Drosophila erecta*] DAAF1_DROER Dynein assembly factor 1. axonemal homolog. Defective transmitter-recycling protein.Leucine-rich repeat-containing protein 50 homolog	-11.6	1.79E-4	-9.42	4.25E-4	-1.27	6.43E-1	-22	1.30E-5	-18	2.91E-5	103746
phosphoribosylglycinamide synthetase [*Schizophyllum commune* H4-8]	-6.97	1.27E-2	-4.51	4.53E-2	1.91	3.65E-1	-11	3.11E-3	-7.2	1.18E-2	108947
hypothetical protein CC1G_13966 [*Coprinopsis cinerea okayama*7#130]. LabA_like protein	-5.06	1.52E-2	-8.45	2.44E-3	1.75	3.62E-1	-6.8	5.31E-3	-11	8.36E-4	105541
Gap1/Cdc42 pathway - selected repressed genes											
	Ras1 *vs.* 12-43		Ras1 *vs.* 4-39		ΔGap1 x ΔGap1 *vs.* W22 x 12-43		Cdc42 *vs.* 12-43		Cdc42 *vs.* 4-39		
	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	Fold	pValue	
hydrophobin SC1	-1.18	7.79E-1	-1.01	9.83E-1	-32.7	1.6E-4	-16.8	1.62E-3	-20	9.35E-5	49129
hydrophobin SC3	-1.17	2.83E-1	1.01	9.33E-1	1.01	9.4E-1	-10	1.05E-11	-12	3.34E-12	11367
hydrophobin SC4	-1.15	8.97E-1	-1.12	9.19E-1	-4	2.21E-1	-126	3.62E-5	-130	3.41E-5	73533
hydrophobin SC6	-1.66	1.47E-1	-2.11	3.75E-2	-6.96	1.93E-5	-1.19	6.09E-1	1.07	8.32E-1	13059
hydrophobin SC15	-1.93	4.25E-1	-1.69	5.21E-1	-9.34	1.28E-2	-50	1.45E-5	-57	1.04E-5	82353
hydrophobin Hyd2	1.23	5.11E-1	2.12	2.83E-2	-8.88	2.39E-6	-2.4	1.28E-2	-4.1	3.13E-5	56457
hydrophobin Hyd4	1.29	6.03E-1	1.51	3.98E-1	-16.6	1.73E-5	-5.49	2.29E-4	-6.4	1.1E-4	51576
hydrophobin Hyd8	-1.3	3.24E-1	-1.59	8.77E-3	-4.72	1.29E-5	-1.88	2.48E-3	-1.5	1.14E-1	105121

Table S10: Blastp results**.** Function show the first results, which are not “hypothetical” or “predicted” or “expressed” protein (protein IDs from Tab. S6).

Protein IDs	Putative function	Accession #	Query coverage and Evalue
64664	*aax4*; protein of unknown function		
27681	secreted protein [*Melampsora larici-populina* 98AG31]	EGG07858.1	Coverage 92% EValue 1e-48
237981	vomeronasal 1 receptor monDomV1R1217 [*Monodelphis domestica*]	NP_001160971.1	Coverage 32% EValue 0.32
105141	F-Box containing protein. similar ones found in several Agaricomycetes		
85939	complement regulator acquiring protein 1 [*Borrelia*	AAU08838.1	Coverage 18% EValue 3.1

	burgdorferi]		
81398	colicin I receptor [*Stenotrophomonas sp*. SKA14]	ZP_05136417.1	Coverage 70% EValue 3.3
50388	ubiquitin ligase protein MIB2. putative [*Pediculus humanus corporis*]	XP_002431228.1	Coverage 91% EValue 2.1
231319	integral membrane protein [*Mycoplasma penetrans* HF-2]	NP_757710.1	Coverage 37% EValue 4.2
107950	Nnf1 superfamily. polyamine-modulated factor 1 [*Xenopus (Silurana) tropicalis*]	NP_001107702.1	Coverage 81% EValue 5e-06
50742	DUF544 superfamily. protein of unknown function		
231457	Nuclear transport factor 2 (NTF2) family protein [*Arabidopsis thaliana*]	NP_568142.1	Coverage 67% EValue 8e-10
80832	DUF89 domain-containing protein [*Coprinopsis cinerea okayama*7#130]	XP_001829216.1	Coverage 98% EValue 0.0
256679	Glycosyl transferase. family 2 [*Crocosphaera watsonii* WH 8501]	ZP_00517983.1	Coverage 30% EValue 2.3
109956	hypothetical protein		
46742	RTA1 domain protein [*Aspergillus oryzae* RIB40]	XP_001727792.1	Coverage 94% EValue 2e-121
53069	spore wall assembly-related protein [*Cryptococcus gattii* WM276]	XP_003193763.1	Coverage 98% EValue 9e-97
236328	gamma-glutamyltranspeptidase [*Alteromonas macleodii* str. 'Deep ecotype']	YP_004427352.1	Coverage 65% EValue 0.86
256094	telomeric DNA binding protein [*Coprinopsis cinerea okayama* 7#130]	XP_001833597.1	Coverage 98% EValue 0.0
233957	hypothetical protein		
84078	nucleoside H+ symporter (3-phenylpropionic acid transporter). membrane protein [*Pseudomonas brassicacearum subsp. brassicacearum* NFM421]	YP_004354876.1	Coverage 36% EValue 3.5
255445	hypothetical protein		
103746	GG21300 [*Drosophila erecta*] DAAF1_DROER Dynein assembly factor 1. axonemal homolog. Defective transmitter-recycling proteinLeucine-rich repeat-containing protein 50 homolog	XP_001974037.1	Coverage 32% EValue 9.0
108947	phosphoribosylglycinamide synthetase [*Schizophyllum commune* H4-8]	XP_003029395.1	Coverage 49% EValue 1e-77
105541	hypothetical protein CC1G_13966 [*Coprinopsis cinerea okayama*7#130]. LabA_like protein	XP_002911926.1	Coverage 69% EValue 6e-17