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The mitogen-activated protein kinase CgHog1 is required for iron homeostasis, adherence and virulence in *Candida glabrata*

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Supplementary tables 1-2

Table S1: Functional categories of differentially expressed genes using the FungiFun webserver (https://sbi.hki-jena.de/FungiFun/FungiFun.cgi)

Response of *C. glabrata* wild-type cells to iron starvation

Up processes			**Down processes**		
FunCat ID	**Category**	**p-value**	**FunCat ID**	**Category**	**p-value**
12.01.01	**ribosomal proteins**	**4.75E-03**	**02.13.03**	**aerobic respiration**	**6.11E-17**
20.09.13	**vacuolar/lysosomal transport**	**6.10E-03**	**11.02.03**	**mRNA synthesis**	**2.44E-10**
20.09.16	**cellular export and secretion**	**1.17E-02**	**20.01.15**	**electron transport**	**2.84E-10**
01.07.07	**regulation of the metabolism of vitamins, cofactors, and prosthetic groups**	**1.18E-02**	**02.11.05**	**accessory proteins of electron transport and membrane-associated energy conservation**	**4.73E-09**
20.09.04	**mitochondrial transport**	**1.57E-02**	**10.03.01**	**mitotic cell cycle and cell cycle control**	**8.47E-09**
20.01.03	**C-compound and carbohydrate transport**	**1.71E-02**	**20.09.04**	**mitochondrial transport**	**1.41E-08**
02.45.11	**conversion to kinetic energy (e.g. movement)**	**2.52E-02**	**12.01.01**	**ribosomal proteins**	**5.72E-08**
02.01.03	**regulation of glycolysis and gluconeogenesis**	**2.55E-02**	**16.21.08**	**Fe/S binding**	**6.71E-08**
01.05.06	**C-2 compound and organic acid metabolism**	**2.55E-02**	**10.01.09**	**DNA restriction or modification**	**3.06E-06**
32.01.01	**oxidative stress response**	**2.78E-02**	**10.01.05**	**DNA recombination and DNA repair**	**7.65E-06**
02.13.03	**aerobic respiration**	**2.82E-02**	**34.11.03**	**chemoperception and response**	**2.53E-05**
02.16.01	**alcohol fermentation**	**3.42E-02**	**16.03.03**	**RNA binding**	**5.55E-05**
42.04.05	**microtubule cytoskeleton**	**3.44E-02**	**14.13.01**	**cytoplasmic and nuclear protein degradation**	**5.73E-05**
			16.17.09	**heavy metal binding (Cu, Fe, Zn)**	**6.38E-05**
			01.20.19	**metabolism of secondary products derived from glycine, L-serine and L-alanine**	**8.62E-05**
			43.01.03	**fungal and other eukaryotic cell type differentiation**	**1.43E-04**
			01.02.03	**sulfur metabolism**	**2.40E-04**
			16.21.01	**heme binding**	**4.51E-04**

01.01.06	**metabolism of the aspartate family**	**4.55E-04**
16.03.01	**DNA binding**	**7.33E-04**
01.01.05	**metabolism of urea cycle, creatine and polyamines**	**8.62E-04**
02.45.15	**energy generation (e.g. ATP synthase)**	**1.16E-03**
20.01.07	**amino acid/amino acid derivatives transport**	**1.34E-03**
01.05.05	**C-1 compound metabolism**	**1.90E-03**
30.01.05	**enzyme mediated signal transduction**	**2.13E-03**
01.01.03	**assimilation of ammonia, metabolism of the glutamate group**	**2.69E-03**
20.09.16	**cellular export and secretion**	**3.86E-03**
01.03.04	**pyrimidine nucleotide/nucleoside/nucleobase metabolism**	**4.20E-03**
10.01.03	**DNA synthesis and replication**	**4.25E-03**
20.01.13	**lipid/fatty acid transport**	**5.48E-03**
01.07.01	**biosynthesis of vitamins, cofactors, and prosthetic groups**	**5.80E-03**
01.03.01	**purin nucleotide/nucleoside/nucleobase metabolism**	**7.72E-03**
42.10.03	**organization of chromosome structure**	**7.95E-03**
01.01.09	**metabolism of the cysteine - aromatic group**	**8.87E-03**
42.04.03	**actin cytoskeleton**	**9.02E-03**
10.03.04	**nuclear and chromosomal cycle**	**1.11E-02**
14.07.03	**modification by phosphorylation, dephosphorylation, autophosphorylation**	**1.24E-02**
16.13.03	**fatty acid binding (e.g. acyl-carrier protein)**	**1.64E-02**
11.04.03	**mRNA processing (splicing, 5'-, 3'-end processing)**	**1.67E-02**

			10.03.02	meiosis	1.69E-02
			01.05.02	sugar, glucoside, polyol and carboxylate metabolism	2.23E-02
			01.06.05	fatty acid metabolism	2.65E-02
			32.01.03	osmotic and salt stress response	2.94E-02
			16.19.03	ATP binding	3.18E-02
			18.02.01	enzymatic activity regulation / enzyme regulator	3.26E-02
			20.09.18	cellular import	4.55E-02

Response of *C. glabrata* wild-type cells to iron surplus

Up processes			Down processes		
FunCat ID	Category	p-value	FunCat ID	Category	p-value
02.13.03	aerobic respiration	2.72E-03	34.01.01	homeostasis of cations	7.26E-08
01.06.06	isoprenoid metabolism	6.36E-03	20.09.18	cellular import	7.13E-07
			20.01.03	C-compound and carbohydrate transport	3.98E-06
			20.01.01	ion transport	2.19E-05
			20.01.27	drug/toxin transport	1.21E-04
			20.01.11	amine / polyamine transport	1.44E-04
			32.07.05	detoxification by export	2.53E-04
			32.05.01	resistance proteins	1.23E-03
			20.09.16	cellular export and secretion	1.46E-03
			01.05.25	regulation of C-compound and carbohydrate metabolism	2.20E-03
			34.11.12	perception of nutrients and nutritional adaptation	9.54E-03
			20.01.23	allantoin and allantoate transport	1.09E-02
			02.01.03	regulation of glycolysis and gluconeogenesis	1.11E-02
			01.06.05	fatty acid metabolism	1.65E-02
			01.20.37	metabolism of peptide derived compounds	2.05E-02
			01.03.16	polynucleotide degradation	2.86E-02

			20.01.13	**lipid/fatty acid transport**	**3.61E-02**
			40.02.03	**activity of intercellular mediators**	**4.09E-02**
			02.16.13	**acetate fermentation**	**4.09E-02**
			16.19.03	**ATP binding**	**4.36E-02**

Response of *C. glabrata* cells to *CgHOG1* disruption

Up processes			**Down processes**		
FunCat ID	**Category**	**p-value**	**FunCat ID**	**Category**	**p-value**
11.04.01	**rRNA processing**	**1.63E-30**	**01.05.02**	**sugar, glucoside, polyol and carboxylate metabolism**	**8.21E-17**
16.03.01	**DNA binding**	**3.58E-10**	**20.01.15**	**electron transport**	**1.60E-09**
20.09.18	**cellular import**	**1.10E-08**	**20.01.01**	**ion transport**	**3.05E-08**
34.01.01	**homeostasis of cations**	**1.37E-07**	**11.02.03**	**mRNA synthesis**	**8.79E-07**
10.01.03	**DNA synthesis and replication**	**1.97E-07**	**01.05.03**	**polysaccharide metabolism**	**2.10E-06**
01.05.02	**sugar, glucoside, polyol and carboxylate metabolism**	**2.17E-07**	**10.01.09**	**DNA restriction or modification**	**3.17E-06**
14.07.11	**protein processing (proteolytic)**	**2.49E-07**	**20.03.02**	**carrier (electrochemical potential-driven transport)**	**3.74E-06**
11.02.01	**rRNA synthesis**	**3.84E-07**	**32.01.01**	**oxidative stress response**	**4.30E-06**
10.01.05	**DNA recombination and DNA repair**	**5.62E-07**	**16.03.03**	**RNA binding**	**5.22E-06**
10.01.09	**DNA restriction or modification**	**9.80E-07**	**01.06.05**	**fatty acid metabolism**	**7.79E-06**
16.03.03	**RNA binding**	**1.09E-06**	**12.01.01**	**ribosomal proteins**	**1.56E-05**
11.04.03	**mRNA processing (splicing, 5'-, 3'-end processing)**	**5.89E-06**	**34.01.01**	**homeostasis of cations**	**1.89E-05**
20.01.15	**electron transport**	**1.19E-05**	**01.20.17**	**metabolism of secondary products derived from primary amino acids**	**2.26E-05**
42.10.03	**organization of chromosome structure**	**1.55E-05**	**11.04.03**	**mRNA processing (splicing, 5'-, 3'-end processing)**	**2.35E-05**
20.01.10	**protein transport**	**1.65E-05**	**02.45.15**	**energy generation (e.g. ATP synthase)**	**2.51E-05**
10.03.04	**nuclear and chromosomal cycle**	**2.79E-05**	**16.21.07**	**NAD/NADP binding**	**2.88E-05**
20.09.07	**vesicular transport (Golgi network, etc.)**	**3.61E-05**	**20.09.03**	**peroxisomal transport**	**3.10E-05**

11.06.02	tRNA modification	4.09E-05	10.01.05	DNA recombination and DNA repair	4.65E-05
10.01.02	DNA topology	5.23E-05	20.01.03	C-compound and carbohydrate transport	8.09E-05
20.01.01	ion transport	5.75E-05	10.03.01	mitotic cell cycle and cell cycle control	1.12E-04
18.02.01	enzymatic activity regulation / enzyme regulator	9.78E-05	10.01.03	DNA synthesis and replication	1.19E-04
14.13.01	cytoplasmic and nuclear protein degradation	1.11E-04	20.09.07	vesicular transport (Golgi network, etc.)	1.36E-04
11.04.02	tRNA processing	2.06E-04	01.05.11	aromate metabolism	7.96E-04
11.02.03	mRNA synthesis	4.61E-04	01.01.03	assimilation of ammonia, metabolism of the glutamate group	8.87E-04
11.02.02	tRNA synthesis	7.35E-04	01.05.07	C-3 compound metabolism	9.82E-04
30.01.05	enzyme mediated signal transduction	7.37E-04	02.16.01	alcohol fermentation	1.15E-03
20.09.13	vacuolar/lysosomal transport	7.40E-04	01.05.06	C-2 compound and organic acid metabolism	1.21E-03
16.17.09	heavy metal binding (Cu, Fe, Zn)	9.11E-04	34.01.03	homeostasis of anions	1.29E-03
01.06.02	membrane lipid metabolism	1.00E-03	32.07.03	detoxification by modification	1.29E-03
01.03.01	purin nucleotide/nucleoside/nucleobase metabolism	1.23E-03	20.09.04	mitochondrial transport	1.35E-03
02.13.03	aerobic respiration	1.50E-03	20.01.11	amine / polyamine transport	2.87E-03
01.05.25	regulation of C-compound and carbohydrate metabolism	1.56E-03	16.19.03	ATP binding	3.74E-03
16.21.07	NAD/NADP binding	2.55E-03	02.07.01	pentose-phosphate pathway oxidative branch	3.96E-03
01.06.05	fatty acid metabolism	2.85E-03	20.01.10	protein transport	4.63E-03
10.03.01	mitotic cell cycle and cell cycle control	3.01E-03	20.01.07	amino acid/amino acid derivatives transport	5.20E-03
20.09.16	cellular export and secretion	3.86E-03	02.13.03	aerobic respiration	7.05E-03
11.06.01	rRNA modification	4.69E-03	32.07.09	detoxification by degradation	7.48E-03
18.01.01	regulation by modification	5.55E-03	32.01.03	osmotic and salt stress response	8.58E-03
32.01.01	oxidative stress response	6.23E-03	32.01.09	DNA damage response	1.32E-02
20.09.04	mitochondrial transport	7.98E-03	01.20.29	metabolism of secondary products derived from L-glutamic acid, L-proline and L-ornithine	1.67E-02

40.01.03	**directional cell growth (morphogenesis)**	**9.04E-03**	**01.20.05**	**metabolism of acetic acid derivatives**	**1.87E-02**
12.01.01	**ribosomal proteins**	**1.20E-02**	**20.09.01**	**nuclear transport**	**1.93E-02**
01.06.06	**isoprenoid metabolism**	**1.28E-02**	**20.01.27**	**drug/toxin transport**	**2.64E-02**
12.04.01	**translation initiation**	**1.72E-02**	**02.01.03**	**regulation of glycolysis and gluconeogenesis**	**2.73E-02**
16.17.07	**magnesium binding**	**2.50E-02**	**32.07.05**	**detoxification by export**	**2.94E-02**
43.01.03	**fungal and other eukaryotic cell type differentiation**	**2.74E-02**	**02.16.05**	**butyrate and butanol-acetoine fermentation**	**3.17E-02**
01.07.01	**biosynthesis of vitamins, cofactors, and prosthetic groups**	**2.75E-02**	**02.01.01**	**glycolysis methylglyoxal bypass**	**3.17E-02**
14.07.09	**posttranslational modification of amino acids (e.g. hydroxylation, methylation)**	**3.04E-02**	**01.06.06**	**isoprenoid metabolism**	**4.24E-02**
14.07.02	**modification with sugar residues (e.g. glycosylation, deglycosylation)**	**3.09E-02**	**20.01.13**	**lipid/fatty acid transport**	**4.81E-02**
01.01.13	**regulation of amino acid metabolism**	**3.12E-02**			
20.09.14	**cytoskeleton-dependent transport**	**3.47E-02**			
01.03.16	**polynucleotide degradation**	**3.66E-02**			
32.01.05	**heat shock response**	**3.74E-02**			
01.01.11	**metabolism of the pyruvate family (alanine, isoleucine, leucine, valine) and D-alanine**	**4.89E-02**			
40.10.02	**apoptosis (type I programmed cell death)**	**4.93E-02**			
30.01.09	**second messenger mediated signal transduction**	**4.93E-02**			

Response of *Cghog1*Δ cells to iron starvation

Up processes			**Down processes**		
FunCat ID	**Category**	**p-value**	**FunCat ID**	**Category**	**p-value**
32.01.01	**oxidative stress response**	**3.25E-07**	**12.01.01**	**ribosomal proteins**	**8.62E-20**
01.05.02	**sugar, glucoside, polyol and carboxylate metabolism**	**1.18E-06**	**02.13.03**	**aerobic respiration**	**2.72E-17**
34.01.01	**homeostasis of cations**	**4.79E-06**	**16.21.08**	**Fe/S binding**	**6.49E-14**
14.13.04	**lysosomal and vacuolar protein**	**5.63E-06**	**43.01.03**	**fungal and other eukaryotic cell**	**2.65E-09**

	degradation			**type differentiation**	
16.03.03	**RNA binding**	**1.08E-05**	**02.11.05**	**accessory proteins of electron transport and membrane-associated energy conservation**	**6.23E-09**
01.05.03	**polysaccharide metabolism**	**1.05E-04**	**20.01.15**	**electron transport**	**1.04E-08**
11.04.01	**rRNA processing**	**1.26E-04**	**11.02.03**	**mRNA synthesis**	**1.33E-08**
16.21.07	**NAD/NADP binding**	**3.11E-04**	**16.17.09**	**heavy metal binding (Cu, Fe, Zn)**	**4.97E-08**
10.01.05	**DNA recombination and DNA repair**	**5.80E-04**	**10.03.01**	**mitotic cell cycle and cell cycle control**	**8.85E-08**
10.01.03	**DNA synthesis and replication**	**9.18E-04**	**20.09.07**	**vesicular transport (Golgi network, etc.)**	**2.10E-06**
20.01.01	**ion transport**	**1.30E-03**	**14.13.01**	**cytoplasmic and nuclear protein degradation**	**7.20E-06**
20.01.13	**lipid/fatty acid transport**	**1.38E-03**	**16.21.01**	**heme binding**	**7.64E-06**
20.01.03	**C-compound and carbohydrate transport**	**1.42E-03**	**01.20.19**	**metabolism of secondary products derived from glycine, L-serine and L-alanine**	**9.58E-06**
16.19.03	**ATP binding**	**1.58E-03**	**34.11.03**	**chemoperception and response**	**2.72E-05**
01.05.11	**aromate metabolism**	**2.48E-03**	**10.01.09**	**DNA restriction or modification**	**7.09E-05**
20.09.18	**cellular import**	**4.82E-03**	**20.09.13**	**vacuolar/lysosomal transport**	**7.11E-05**
32.01.11	**nutrient starvation response**	**5.64E-03**	**01.05.25**	**regulation of C-compound and carbohydrate metabolism**	**1.19E-04**
16.21.05	**FAD/FMN binding**	**6.04E-03**	**10.03.04**	**nuclear and chromosomal cycle**	**1.65E-04**
20.01.15	**electron transport**	**1.08E-02**	**20.09.04**	**mitochondrial transport**	**2.39E-04**
02.01.03	**regulation of glycolysis and gluconeogenesis**	**1.32E-02**	**11.04.01**	**rRNA processing**	**4.51E-04**
01.05.06	**C-2 compound and organic acid metabolism**	**1.32E-02**	**10.01.03**	**DNA synthesis and replication**	**1.09E-03**
20.09.07	**vesicular transport (Golgi network, etc.)**	**1.58E-02**	**10.01.05**	**DNA recombination and DNA repair**	**1.10E-03**
32.07.07	**oxygen and radical detoxification**	**1.59E-02**	**11.06.02**	**tRNA modification**	**1.81E-03**
16.03.01	**DNA binding**	**1.76E-02**	**14.07.05**	**modification by ubiquitination, deubiquitination**	**2.61E-03**
10.03.01	**mitotic cell cycle and cell cycle control**	**1.88E-02**	**10.03.03**	**cytokinesis (cell division) /septum formation and hydrolysis**	**2.83E-03**
20.01.07	**amino acid/amino acid derivatives transport**	**1.99E-02**	**18.02.01**	**enzymatic activity regulation / enzyme regulator**	**3.37E-03**
02.16.01	**alcohol fermentation**	**1.99E-02**	**12.04.02**	**translation elongation**	**3.82E-03**

02.01.01	**glycolysis methylglyoxal bypass**	**2.24E-02**	**20.09.16**	**cellular export and secretion**	**4.31E-03**
42.10.03	**organization of chromosome structure**	**2.28E-02**	**10.03.02**	**meiosis**	**4.41E-03**
01.20.17	**metabolism of secondary products derived from primary amino acids**	**2.99E-02**	**11.02.01**	**rRNA synthesis**	**5.00E-03**
20.01.10	**protein transport**	**3.07E-02**	**20.01.21**	**RNA transport**	**5.87E-03**
20.01.27	**drug/toxin transport**	**3.52E-02**	**20.09.18**	**cellular import**	**7.41E-03**
02.07.01	**pentose-phosphate pathway oxidative branch**	**3.57E-02**	**20.01.17**	**nucleotide/nucleoside/nucleobase transport**	**1.30E-02**
32.07.03	**detoxification by modification**	**3.68E-02**	**14.07.03**	**modification by phosphorylation, dephosphorylation, autophosphorylation**	**1.32E-02**
14.07.11	**protein processing (proteolytic)**	**3.95E-02**	**30.01.05**	**enzyme mediated signal transduction**	**1.44E-02**
11.02.03	**mRNA synthesis**	**4.29E-02**	**16.19.03**	**ATP binding**	**1.67E-02**
			14.07.02	**modification with sugar residues (e.g. glycosylation, deglycosylation)**	**2.11E-02**
			32.01.03	**osmotic and salt stress response**	**2.12E-02**
			11.06.01	**rRNA modification**	**2.58E-02**
			16.13.03	**fatty acid binding (e.g. acyl-carrier protein)**	**2.69E-02**
			01.05.13	**transfer of activated C-1 groups**	**2.81E-02**
			42.10.03	**organization of chromosome structure**	**2.91E-02**
			01.20.31	**metabolism of secondary products derived from L-lysine, L-arginine and L-histidine**	**3.18E-02**
			01.07.01	**biosynthesis of vitamins, cofactors, and prosthetic groups**	**3.53E-02**
			42.04.05	**microtubule cytoskeleton**	**3.92E-02**
			01.06.06	**isoprenoid metabolism**	**4.22E-02**
			11.04.03	**mRNA processing (splicing, 5'-, 3'-end processing)**	**4.64E-02**

Response of *Cghog1*Δ cells to iron surplus

Up processes			**Down processes**		
FunCat ID	**Category**	**p-value**	**FunCat ID**	**Category**	**p-value**
20.01.03	**C-compound and carbohydrate transport**	**1.01E-04**	**11.04.01**	**rRNA processing**	**1.71E-10**

11.02.03	**mRNA synthesis**	**1.29E-04**	**20.09.18**	**cellular import**	**4.50E-06**
01.06.02	**membrane lipid metabolism**	**3.41E-04**	**16.03.03**	**RNA binding**	**7.68E-05**
20.01.07	**amino acid/amino acid derivatives transport**	**5.57E-04**	**11.04.03**	**mRNA processing (splicing, 5'-, 3'-end processing)**	**3.40E-04**
12.01.01	**ribosomal proteins**	**6.19E-04**	**20.09.16**	**cellular export and secretion**	**4.02E-04**
10.01.05	**DNA recombination and DNA repair**	**7.28E-04**	**20.01.01**	**ion transport**	**1.21E-03**
16.03.03	**RNA binding**	**2.15E-03**	**12.01.01**	**ribosomal proteins**	**1.34E-03**
14.07.01	**modification with fatty acids (e.g. myristylation, palmitylation, farnesylation)**	**2.65E-03**	**11.02.03**	**mRNA synthesis**	**2.11E-03**
14.07.02	**modification with sugar residues (e.g. glycosylation, deglycosylation)**	**3.90E-03**	**18.02.01**	**enzymatic activity regulation / enzyme regulator**	**4.20E-03**
20.03.01	**channel / pore class transport**	**4.99E-03**	**10.01.09**	**DNA restriction or modification**	**4.23E-03**
01.06.06	**isoprenoid metabolism**	**1.54E-02**	**01.05.02**	**sugar, glucoside, polyol and carboxylate metabolism**	**5.29E-03**
16.03.01	**DNA binding**	**1.79E-02**	**01.03.01**	**purin nucleotide/nucleoside/nucleobase metabolism**	**1.57E-02**
20.01.27	**drug/toxin transport**	**1.94E-02**	**43.01.03**	**fungal and other eukaryotic cell type differentiation**	**1.86E-02**
01.05.03	**polysaccharide metabolism**	**2.04E-02**	**01.06.02**	**membrane lipid metabolism**	**1.92E-02**
11.04.03	**mRNA processing (splicing, 5'-, 3'-end processing)**	**2.43E-02**	**20.01.03**	**C-compound and carbohydrate transport**	**1.92E-02**
16.19.03	**ATP binding**	**2.51E-02**	**34.01.01**	**homeostasis of cations**	**2.23E-02**
			20.09.07	**vesicular transport (Golgi network, etc.)**	**2.83E-02**
			01.07.01	**biosynthesis of vitamins, cofactors, and prosthetic groups**	**3.23E-02**
			32.01.07	**unfolded protein response (e.g. ER quality control)**	**3.56E-02**

Table S2: List of strains, plasmids and primers used in the study

Yeast strain	**Relevant genotype**	**Reference**
YRK19	*ura3Δ::Tn903* G418^R	Cormack & Falkow, 1999
YRK20	*URA3*	De Las Peñas *et al*., 2003
YRK603	*URA3 Cgslt2Δ::nat1*	Borah *et al*., 2011
YRK599	*ura3Δ::Tn903* G418^R *Cgslt2Δ::nat1*	Borah *et al*., 2011
YRK637	*ura3Δ::Tn903* G418^R *Cgslt2Δ::nat1*/pRK846	Borah *et al*., 2011
YRK964	*URA3 Cghog1Δ::nat1*	This study
YRK975	*URA3 Cghog1Δ::nat1Cgslt2::Tn7*	This study
YRK1024	*ura3Δ::Tn903* G418^R *Cghog1Δ::nat1*	This study
YRK1047	*ura3Δ::Tn903* G418^R *Cghog1Δ::nat1*/pRK1027	This study

Plasmid	**Description**	**Reference**
pRK74	A CEN-ARS plasmid (pGRB2.2) of *C. glabrata* carrying *S. cerevisiae URA3* as a selection marker. MCS sites are flanked by *S. cerevisiae PGK1* promoter at one end and by 3' UTR of HIS3 at the other end.	Frieman *et al*., 2002
pRK625	pCR2.1 plasmid containing the *nat1* gene	Cormack laboratory
pRK846	*CgSLT2* ORF (1.4 kb) cloned in pRK74	Borah *et al*., 2011
pRK1027	*CgHOG1* ORF (1.3 kb) cloned in BamH*I*-Xma*I* sites in pRK74	This study

Primer name	**Sequence (5'-3')**	**Target Gene**
For generation and confirmation of *C. glabrata* deletion strains		
OgRK1451	ATTACTTGATGCCAGAACGTTCC	*CgHOG1*
OgRK1452	GCGTCGACCTGCAGCGTACGCTGTTGTCGCTATTATCTTTGGGT	*CgHOG1*
OgRK1453	GATGTTCAAAGGATAAACGCGTTC	*CgHOG1*
OgRK1454	CGACGGTGTCGGTCTCGTAGCATTAATACCACATTTTTGTTACC	*CgHOG1*
OgRK1455	GAAATCTGCATTTATGAGAAAATTG	*CgHOG1*
OgRK1456	ATGTAGAAGAAGTTGCAGACCATG	*CgHOG1*
OgRK1457	TTAACTTGGCAGAAATACGACGTC	*CgHOG1*
OgRK1458	ATAACTCTCCATGTGTCTACTGGT	*CgHOG1*
OgRK1475	CGTGTTCTGATCGGAGTTAGTAAA	*CgHOG1*
OgRK1476	TGGAAAAGAGCCTCAAAAGATATGG	*CgHOG1*
OgRK340	CGTACGCTGCAGGTCGACGCCTTCCGCTGCTAGGCGCGCCGTG	*nat1*
OgRK341	CTACGAGACCGACACCGTCGGGCCGCTGACGAAGT	*nat1*
OgRK342	GTCTACTACTTTGGATGATAC	*nat1*

OgRK343	TCTGTTCCAACCAGAATAAG	*nat1*
OgRK344	TGCGCACGTCAAGACTGTCAAGG	*nat1*
OgRK345	TGTGAATGCTGGTCGCTATACTGC	*nat1*
For qPCR		
OgRK680	TTAGGTTTGATGATGCACGAAG	*CgFTR1*
OgRK681	TGTTGTCCATACGGTTTAGCAG	*CgFTR1*
OgRK688	TGTAAAGGTCCCAACTCAAGGT	*CgFET3*
OgRK689	GCGATCATAGTGATACCCAACA	*CgFET3*
OgRK682	TATTTCCCCTGCATCCTCTAAA	*CgAFT1*
OgRK683	CAAGAATTCATCTCCAACGTCA	*CgAFT1*
OgRK89	CTCCACCACTGCTGAAAGAG	*CgACT1*
OgRK90	GGTCAATACCAGCAGATTCTAG	*CgACT1*
OgRK734	GATGTCAATAAGATTAGCGACCAGT	*CgYFH1*
OgRK735	GCGTCATGTAGCTCTTTGTCTAGTA	*CgYFH1*
OgRK1091	TGGGTATCACACAGGTTCCA	*CgGRX4*
OgRK1092	GGGAGTCTTCGTCAAGGTCA	*CgGRX4*
OgRK1572	CTCAGGCAGACGTAGATCTTCT	*CgMSN2*
OgRK1573	TGACGAGTTAGGGCTTATACTTG	*CgMSN2*
OgRK69	GTACGCTATGTTCTCTGAAGA	*CgYPS5*
OgRK70	AACTGCTCTCCTGAGAAACAC	*CgYPS5*
OgRK1183	ACTATGTTACTTTATGGTTA	*CgEPA1*
OgRK1184	TGAGCCCCAGATGGCGTAGG	*CgEPA1*
For cloning		
OgRK1579	CATAGGATCCATGGCTACTAATGAAGAGTTC	*CgHOG1*
OgRK1580	CATACCCGGGTTATTGTTGGAATTCATTTG	*CgHOG1*

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