

S1 Table. List of fungal strains.

Species	Isolate	Host	Origin	Date isolated	Source
V.dahliae	12008	Strawberry	Kent, UK	1985	Laboratory stock
V.dahliae	12061	Strawberry	Lenham, UK	1986	Laboratory stock
V.dahliae	12062	Strawberry	Hampshire, UK	1965	Laboratory stock
V.dahliae	12064	Chrysanthemum	Bristol, UK	1968	Laboratory stock
V.dahliae	12065	Potato	Canada, USA	1969	Laboratory stock
V.dahliae	12067	Tomato	Dorset, UK	1971	Laboratory stock
V.dahliae	12068	Hops	UK	NA	Laboratory stock
V.dahliae	12072	Gerbera	Japan	1998	Laboratory stock
V.dahliae	12073	Chinese Cabbage	Japan	1998	Laboratory stock
V.dahliae	12086	Strawberry - petiole	Kent, UK	1998	Laboratory stock
V. dahliae	12158	Strawberry	Kent, UK	2000	Laboratory stock
V. dahliae	12161	Strawberry	Lincolnshire, UK	2000	Laboratory stock
V. dahliae	12251	Strawberry	Kent, UK	2012	Laboratory stock
V. dahliae	12252	Strawberry	Kent, UK	2012	Laboratory stock
V. dahliae	12253	Strawberry	Kent, UK	2012	Laboratory stock
V.dahliae	12213	Olive	NA	2002	Laboratory stock
V. albo-atrum	11001	Hop	Kent, UK	1987	Laboratory stock
V. albo-atrum	11006	Hop	Kent, UK	1995	Laboratory stock
V. nubilum	15001	NA*	NA	NA	Laboratory stock
V. tricorpus	20001	NA	NA	1998	Laboratory stock
V. dahliae	<i>Δfrq_12008</i>	-	-	-	This study
V. dahliae	<i>Δfrq_12253</i>	-	-	-	This study
V. dahliae	<i>Δwc1_12253</i>	-	-	-	This study
N. crassa	<i>30-7 bd a</i>	-	NA	NA	S. Crosthwaite

S2 Table. List of primers.

Organism	Target	Gene name	Name	Sequence (5' to 3')	Length (bp)	Sequence reference
V.dahliae	Housekeeping	Elongation factor alpha	EFA1-F	TACAACCCCAAGACTGTTCGC	104	[112]
V.dahliae	Housekeeping		EFA1-R	TCCTTCTCCCAGCCCTTGTA		
V.dahliae	Housekeeping	Tubuline Beta Chain	VdTbc-F	TTTCCAGATCACCCACTCC	111	[49, 113]
V.dahliae	Housekeeping		VdTbc-R	ACGACCGAGAAGGTAGCC		
V.dahliae	Gene of interest	frq	VdFrq-F	GTGACGGAGAAGAGCACCAA	92	This study
V.dahliae	Gene of interest		VdFrq-R	TCGCTACTGAATCGCGTACC		
V.dahliae	Gene of interest	Wc-1	VdWc1-F	CAACACCCTGACCGAGTTCA	91	This study
V.dahliae	Gene of interest		VdWc1-R	ATTGGCGTCGAGAATCTGCA		
V.dahliae	Gene of interest	cry	Vdcry_F	GAAGGGTGGTGAGGTGGATG	177	This study
V.dahliae	Gene of interest		Vdcry_R	TTCACCATCTCCTCGTGCAC		
V.dahliae	Gene of interest	ccg16	Vdccg16_F	CCCAAGGCATCACAGTCGAA	118	This study
V.dahliae	Gene of interest		Vdccg16_R	GCACCATTTGTTGTTGCCGAT		
V.dahliae	Gene of interest	vvd	Vdvvd_F	GATGTTTCATGAACGGCGAGC	135	This study
V.dahliae	Gene of interest		Vdvvd_R	GTCAGCCGATCTTCTCCTCG		
N.crassa	Housekeeping	TATA binding box protein	NcTbp-F	GGTGCCAAGTCCGAAGATGA	136	[114]
N.crassa	Housekeeping		NcTbp-R	TGGGGAACCTTGATGTCGCAA		
N.crassa	Housekeeping	Beta-tubulin	NcBtl-F	CCACTTCTTCATGGTCGGCT	103	[114]
N.crassa	Housekeeping		NcBtl-R	CTTGGGGTCGAACATCTGCT		
N.crassa	Gene of interest	Frequency	NcFrq-F	TCGACATCGCAGAGGAGAAA	66	[115]
N.crassa	Gene of interest		NcFrq-R	CAACGAAACCCCAGACGAGT		

	Primer pair	DNA Template	Overhang 5' - 3'	Sequence 5' - 3'	Length (bp)	Sequence reference
USER-Brick	B1-F	pRF-HU2	AAGGTTTAAU	TCACTGGCCGTCGTTTTA	2165	[56]
	B1-R		ATTTAAAGAU	CCGCGCGAGC		
	HygR1-F	pRF-HU2	ACGCAATACU	AGTCGGGGGATCCTCTAG	2480	[56]
	HygR1-R		ACTAGGTCAU	GGGCCCATCGATGATCAG		
	B2-F	pRF-HU2	ATCTTTAAAU	GGAGTGTCTTCTTCCCA	1658	[56]
	B2-R		AATACGACCU	TCGTGACTCCCTTAATTCT		
	HRFrq1-F	<i>V. dahliae</i>	AGGTCGTATU	GAGACTTCAGTAAATTGTGGTTGT	1600	This study
	HRFrq1-R		AGTATTGCGU	AGAGTCGTTGTCGTCGGG		
	HRFrq2-F	<i>V. dahliae</i>	ATGACCTAGU	GATCACATTTTGCATCTTTCGGG	1565	This study
	HRFrq2-R		ATTAAACCTU	GTCACCATGACTCGCTACAA		
Plasmid validation	B1.B2-F	pEcFrq-D1		TGTCATACCACTTGTCCGCC	461	This study
	B1.B2-R			CTGCCTGTTCCAAAGGTCCT		
	B1.B2.F1.H-F	pEcFrq-D1		ATGTTGCTGTCTCCCAGGTC	3600	This study
	B1.B2.F1.H-R			CCTATATCGCCGACATCACC		
	H.F2.B1-F	pEcFrq-D1		GTATGACCGGGTCGTTCACT	2190	This study
	H.F2.B1-R			CTGGCTGGTGGCAGGATA		
<i>V. dahliae</i> mutants validation	TestHygr_F	Δ frq mutants		ATTTGTGTACGCCCCGACAGT	624	This study
	TestHygr_R			AGACCTGCCTGAAACCGAAC		
	TestFrq-F	Δ frq mutants		CCATCTTCGGCGCATTTGAG	563	This study
	TestFrq-R			ACTGTGAGGAATTGCTGCGA		
	FrqUS_Hygr-F	Δ frq mutants		AGTTCCACTCGTTCGCTCTG	2182	This study
	FrqUS_Hygr-R			CGCCTATATCGCCGACATCA		

S3 Table. List of significantly enriched GO terms related to biological processes in *Δfrq_12253* versus the WT_12253 strain in light and dark.

GO.ID	Biological process term	Δfrq vs WT in D		Δfrq vs WT in L	
		UP	DOWN	UP	DOWN
GO:0006412	translation	5.40E-11		2.00E-16	
GO:0006414	translational elongation	3.40E-05			
GO:0008152	metabolic process	0.022		0.01	
GO:0045039	protein import into mitochondrial inner membrane	0.024			
GO:0009306	protein secretion	0.024		0.032	
GO:0006228	UTP biosynthetic process	0.024		0.032	
GO:0006241	CTP biosynthetic process	0.024		0.032	
GO:0046836	glycolipid transport	0.024			
GO:0006183	GTP biosynthetic process	0.024		0.032	
GO:0009116	nucleoside metabolic process	0.042			
GO:0033566	gamma-tubulin complex localization			0.032	
GO:0055114	oxidation-reduction process		2.90E-05		8.20E-05
GO:0007623	circadian rhythm		0.016		0.0221
GO:0019427	acetyl-CoA biosynthetic process from acetate		0.016		
GO:0006788	heme oxidation		0.016		0.0221
GO:0009448	gamma-aminobutyric acid metabolic processes		0.031		
GO:0006537	glutamate biosynthetic process		0.032		0.0437
GO:0001682	tRNA 5'-leader removal		0.032		
GO:0009450	gamma-aminobutyric acid catabolic processes		0.032		
GO:0072488	ammonium transmembrane transport		0.047		
GO:0006817	phosphate ion transport				0.0046
GO:0042128	nitrate assimilation				0.0046
GO:0006810	transport				0.0129
GO:0042554	superoxide anion generation				0.0221
GO:0009405	pathogenesis				0.0221
GO:0006809	nitric oxide biosynthetic process				0.0221
GO:0000160	phosphorelay signal transduction system				0.042
GO:0009395	phospholipid catabolic process				0.0437
GO:0006730	one-carbon metabolic process				0.0437

S4 Table. Expression of putative core clock genes, photoreceptor- and TF-encoding genes in WT 12253 and *Δfrq_12253* in both light and dark conditions. Transcripts displaying a Log fold change (LFC) >1 were classified as pink, dark red if the LFC > 2, light green if the LFC < -1 and dark green if the LFC < -2. Yellow boxes indicate *p*- values < 0.05.

Transcript_id	baseMean	L/D in V.d 12253		L/D in Δfrq 12253		Δfrq/WT in D		Δfrq/WT in L		Gene	Antismash	SM	Interpro
		LF C	p-value	LF C	p-value	LF C	p-value	LF C	p-value				
Clock oscillator genes													
VDAG_JR2_C	2113.8			-		-		-		fwd-1	cluster_63	cf_putative	F-box; WD40 repeat
hr6g03850	9	0.07	0.51	0.21	0.10	0.16	0.08	0.45	0.00				
VDAG_JR2_C	1748.3			-		-		-		wc-1			Zinc finger, GATA-type ATP-binding; Helicase; rRNA-processing arch, Ski2
hr2g01990	8	0.17	0.23	0.16	0.47	0.30	0.02	0.63	0.00				
VDAG_JR2_C	1474.0	-		-		-		-		frh			
hr4g00070	5	0.01	0.94	0.11	0.66	0.06	0.74	0.04	0.85				
VDAG_JR2_C	1236.8	-		-		-		-		vvd			LOV
hr3g10380	7	0.05	0.83	0.97	0.00	0.53	0.00	0.49	0.01				
VDAG_JR2_C		-		-		-		-		wc-2			Zinc finger, GATA-type
hr7g03830	698.85	0.10	0.47	0.23	0.17	0.68	0.00	0.82	0.00				
Photoreceptors genes													
VDAG_JR2_C		-		-		-		-		wc-2			Zinc finger, GATA-type
hr7g03830	698.85	0.10	0.47	0.23	0.17	0.68	0.00	0.82	0.00				
VDAG_JR2_C	1748.3			-		-		-		wc-1			Zinc finger, GATA-type
hr2g01990	8	0.17	0.23	0.16	0.47	0.30	0.02	0.63	0.00				
VDAG_JR2_C	1236.8	-		-		-		-		vvd			LOV
hr3g10380	7	0.05	0.83	0.97	0.00	0.53	0.00	0.49	0.01				
VDAG_JR2_C	1602.1			-		-		-		rgs-lov			PAS
hr1g22390	2	0.05	0.77	0.04	0.89	0.23	0.07	0.14	0.36				

VDAG_JR2_C		-				-		-			cluster_		Photolyase/cryptoc
hr6g00620	191.19	0.07	0.82	0.03	0.95	0.35	0.09	0.25	0.29	<i>cry-1</i>	60	other	hrome; FAD-
VDAG_JR2_C	1433.0					-		-					binding
hr4g09150	5	0.26	0.17	0.11	0.73	0.21	0.27	0.36	0.06	<i>phy</i>			HK; PAS;
VDAG_JR2_C	1376.5	-											Phytochrome
hr7g00170	9	0.06	0.68	0.14	0.41	0.01	0.92	0.21	0.07	<i>phr</i>			DNA-photolyase;
													FAD-binding
													G-protein glucose
VDAG_JR2_C										<i>nop-</i>			receptor;
hr1g29230	614.73	0.56	0.18	0.31	0.63	0.65	0.09	0.40	0.36	<i>l</i>			Rhodopsin
VDAG_JR2_C						-		-					
hr6g07410	386.51	0.56	0.00	0.19	0.53	0.40	0.02	0.77	0.00	<i>lov-u</i>			PAS
													Photolyase/cryptoc
VDAG_JR2_C						-		-		<i>cry-</i>	cluster_		hrome; FAD-
hr1g17210	349.67	0.99	0.00	1.11	0.00	1.16	0.00	1.05	0.00	<i>dash</i>	8	terpene	binding
Transcription factors													
VDAG_JR2_C		-		-		-		-					Zn2 Cys6;Fungal-
hr1g26850	91.41	1.03	0.00	0.19	0.72	0.93	0.00	0.09	0.81				specific TF
VDAG_JR2_C	27062.	-		-		-		-					Zinc finger, C2H2-
hr5g05720	18	1.01	0.00	0.52	0.07	0.81	0.00	0.32	0.19				type
VDAG_JR2_C	4202.9	-		-		-							Nucleic acid-
hr2g04990	2	1.05	0.00	0.67	0.06	0.35	0.20	0.03	0.93				binding proteins
VDAG_JR2_C		-		-		-							Zn2 Cys6;Fungal-
hr1g24030	47.75	1.23	0.00	0.53	0.17	0.20	0.52	0.50	0.12				specific TF
VDAG_JR2_C	1280.9					-		-					Zinc finger, C2H2-
hr5g05660	8	1.33	0.00	0.75	0.01	0.01	0.98	0.58	0.01				type
VDAG_JR2_C											cluster_	t1pks-	
hr1g23950	945.69	1.68	0.00	0.69	0.24	0.13	0.81	0.87	0.05		14	nrps	Zn2 Cys6
VDAG_JR2_C													
hr4g03300	951.19	0.51	0.01	1.09	0.00	0.35	0.06	0.93	0.00				Zn2 Cys6

VDAG_JR2_C	9249.7	-		-		-		-		cluster_ 68	cf_puta tive	Zinc finger, C2H2- type;Fungal TF
hr6g08330	7	0.76	0.00	0.45	0.01	1.27	0.00	0.95	0.00			
VDAG_JR2_C		-				-		-				
hr8g07070	412.26	0.40	0.18	0.18	0.71	1.13	0.00	0.55	0.07	cluster_ 19	cf_puta tive	Zn2 Cys6
VDAG_JR2_C	36396.	-		-		-		-				Zinc finger, C2H2- type
hr3g04200	10	0.91	0.00	0.38	0.13	1.11	0.00	0.58	0.00			
VDAG_JR2_C	3358.8											Zn2 Cys6
hr2g11050	9	0.59	0.00	0.47	0.01	1.10	0.00	0.97	0.00			
VDAG_JR2_C		-		-		-		-				
hr2g03990	18.20	0.77	0.11	0.07	0.94	1.31	0.00	0.48	0.32			Fungal-specific TF
VDAG_JR2_C		-				-		-				C2H2 and C2HC
hr8g00200	52.88	1.92	0.00	0.17	0.82	1.55	0.00	0.54	0.22			zinc fingers
VDAG_JR2_C	23846.	-		-		-		-				
hr7g07100	48	1.01	0.00	0.72	0.02	1.11	0.00	0.83	0.00	cluster_ 45	cf_puta tive	HLH
VDAG_JR2_C	1535.2	-		-		-		-				
hr5g05400	8	0.24	0.12	0.33	0.11	0.93	0.00	1.02	0.00			Zn2 Cys6
VDAG_JR2_C						-		-				Zn2/Cys6 DNA- binding domain
hr1g03770	112.66	0.86	0.00	0.28	0.60	0.88	0.00	1.47	0.00			
VDAG_JR2_C	1305.6			-		-		-				
hr1g10470	0	0.29	0.18	0.11	0.78	0.85	0.00	1.25	0.00			Zn2 Cys6
VDAG_JR2_C	2291.0			-		-		-				
hr4g09890	0	0.17	0.38	0.15	0.62	0.72	0.00	1.03	0.00			Zn2 Cys6
VDAG_JR2_C	3513.4					-		-				
hr3g08070	5	0.75	0.00	0.29	0.45	0.67	0.00	1.13	0.00			bZIP
VDAG_JR2_C		-		-		-		-				
hr1g27300	905.11	1.00	0.00	0.05	0.87	0.29	0.05	1.34	0.00			Zn2 Cys6
VDAG_JR2_C		-										Zn2 Cys6;Fungal- specific TF
hr5g00990	503.03	0.58	0.05	0.24	0.62	0.34	0.25	1.16	0.00			
VDAG_JR2_C		-										
hr7g02150	631.00	0.30	0.15	0.37	0.16	0.43	0.02	1.10	0.00			HLH
VDAG_JR2_C		-										
hr1g22480	307.59	0.20	0.36	0.30	0.25	0.56	0.00	1.06	0.00			Zn2 Cys6

[illegible]

VDAG_JR2_C		-										
hr5g10380	25.61	0.26	0.62	1.14	0.01	0.67	0.08	2.07	0.00	cluster_ 27	cf_puta tive	Zn2 Cys6
VDAG_JR2_C				-		-		-				Zn2/Cys6
hr2g13070	264.38	0.00	0.99	0.12	0.77	1.53	0.00	1.66	0.00			
VDAG_JR2_C	2339.8	-		-		-		-				C2H2
hr6g07650	4	0.12	0.56	0.20	0.47	1.13	0.00	1.21	0.00			
VDAG_JR2_C	3982.0	-		-		-		-				Homeodomain-like
hr3g07150	6	0.15	0.44	0.20	0.47	1.02	0.00	1.06	0.00			Nucleic acid- binding proteins
VDAG_JR2_C	11542.											
hr1g05850	15	0.12	0.61	0.13	0.71	1.00	0.00	1.01	0.00			
VDAG_JR2_C		-										
hr4g03340	253.43	0.02	0.94	0.18	0.54	1.08	0.00	1.29	0.00			Zn2 Cys6
VDAG_JR2_C												
hr2g10850	51.00	0.16	0.65	0.27	0.49	1.19	0.00	1.30	0.00			Zn2 Cys6
										cluster_ 17	t1pks	Winged helix
VDAG_JR2_C		-										DNA-binding
hr2g00520	69.36	0.15	0.77	0.87	0.08	1.29	0.00	2.32	0.00			domain
VDAG_JR2_C	2413.4			-								Zinc finger, C2H2- type
hr8g11340	9	0.04	0.91	0.11	0.80	1.54	0.00	1.40	0.00			
VDAG_JR2_C		-								cluster_ 17	t1pks	
hr2g00510	2.81	0.27	0.65	0.30	NA	1.79	0.00	2.35	0.00			Homeodomain-like
VDAG_JR2_C	2637.4									cluster_ 78	nrps	
hr7g10270	5	0.28	0.30	0.10	0.83	2.35	0.00	2.17	0.00			bZIP
VDAG_JR2_C						-		-				
hr3g13030	42.82	1.35	0.00	0.67	0.19	1.10	0.00	1.78	0.00			Zn2 Cys6

S5 Table. Most differentially expressed genes in *Δfrq_12253*. Transcripts displaying a Log fold change (LFC) >1 were classified as pink, dark red if the LFC > 2, light green if the LFC < -1 and dark green if the LFC < -2. Yellow boxes indicate *p*- values < 0.05.

Transcript_id	baseMean	L/D in V.d 12253		L/D in Δfrq_12 253		Δfrq/WT in D		Δfrq/WT in L		Antismash	SM	TFs	Interpro
		LF C	p-value	LF C	p-value	LF C	p-value	LF C	p-value				
Top Up-regulated genes													
VDAG_JR2_Chromosome7g10300	121.36	0.6	0.1	0.1	0.6	3.8	0.0	3.4	0.0	cluster_78	nrps		hypothetical protein
VDAG_JR2_Chromosome4g11240	55.89	0.0	0.9	1.2	0.0	1.9	0.0	3.1	0.0	cluster_47	t1pks		tubulin-tyrosine ligase
VDAG_JR2_Chromosome7g10290	151.84	0.5	0.1	0.2	0.7	3.4	0.0	3.0	0.0	cluster_78	nrps		hypothetical protein
VDAG_JR2_Chromosome7g02720	1334.29	-	0.8	0.5	0.2	2.3	0.0	2.9	0.0				Integral membrane protein
VDAG_JR2_Chromosome2g00550	10.31	0.3	0.5	1.3	0.0	1.9	0.0	2.8	0.0	cluster_17	t1pks		FAD binding domain-containing protein
VDAG_JR2_Chromosome8g11360	452.42	-	0.4	0.4	0.2	2.1	0.0	2.8	0.0				hypothetical protein
VDAG_JR2_Chromosome2g00500	5.95	0.0	0.9	0.6	0.3	2.2	0.0	2.8	0.0	cluster_17	t1pks		hypothetical protein
VDAG_JR2_Chromosome8g11370	1056.59	-	0.6	0.4	0.2	2.0	0.0	2.7	0.0				S-adenosyl-L-methionine-dependent methyltransferase
VDAG_JR2_Chromosome2g00490	58.35	0.6	0.2	0.8	0.1	2.4	0.0	2.6	0.0	cluster_17	t1pks		serine 3-dehydrogenase

VDAG_JR2_Chromosome7g10260	317.52	0.2 0	0.4 8	0.7 9	0.0 0	1.9 0	0.0 0	2.4 9	0.0 0	cluster_78	nrps		hypothetical protein
VDAG_JR2_Chromosome7g02710	2265.56	0.8 0	0.0 0	0.1 2	0.8 1	1.4 9	0.0 0	2.4 2	0.0 0				Cytochrome
VDAG_JR2_Chromosome1g24880	24.81	0.2 0	0.7 3	0.4 1	0.5 2	2.9 9	0.0 0	2.3 8	0.0 0				cerato-ulmin hydrophobin
VDAG_JR2_Chromosome2g00510	2.81	0.2 7	0.6 5	0.3 0	NA	1.7 9	0.0 0	2.3 5	0.0 0	cluster_17	t1pks	Homeodomain-like	Myb-transcription protein
VDAG_JR2_Chromosome1g23290	36.88	0.6 7	0.0 8	0.7 8	0.0 6	2.4 3	0.0 0	2.3 3	0.0 0	cluster_13	cf_putative		hypothetical protein
VDAG_JR2_Chromosome2g00520	69.36	0.1 5	0.7 7	0.8 7	0.0 8	1.2 9	0.0 0	2.3 2	0.0 0	cluster_17	t1pks	Winged helix	S-adenosyl-L-methionine-dependent methyltransferase
VDAG_JR2_Chromosome5g05550	22.44	0.7 0	0.0 6	0.6 6	0.1 0	0.9 4	0.0 0	2.3 0	0.0 0				hypothetical protein
VDAG_JR2_Chromosome8g02470	55.11	0.1 6	0.7 7	2.0 7	0.0 0	0.3 8	0.4 0	2.2 8	0.0 0				mannose-6-phosphate isomerase
VDAG_JR2_Chromosome2g02910	43.72	1.4 5	0.0 0	2.6 7	0.0 0	1.0 1	0.0 2	2.2 2	0.0 0				hypothetical protein
VDAG_JR2_Chromosome1g27430	31.46	0.7 3	0.0 5	0.3 8	0.4 0	1.1 1	0.0 0	2.2 2	0.0 0				hypothetical protein
VDAG_JR2_Chromosome8g11350	1851.53	0.1 1	0.8 0	0.0 1	0.9 9	2.0 6	0.0 0	2.1 8	0.0 0				Cytochrome
VDAG_JR2_Chromosome7g10270	2637.45	0.2 8	0.3 0	0.1 0	0.8 3	2.3 5	0.0 0	2.1 7	0.0 0	cluster_78	nrps	bZIP	bZIP transcription factor

VDAG_JR2_Chromosome8g11140	201.79	-	0.3	0.3	0.4	0.2	1.3	0.0	2.1	0.0	cluster_17	t1pks	Zn2 Cys6	hypothetical protein		
VDAG_JR2_Chromosome7g04960	100.68	-	0.7	0.1	0.4	0.4	1.9	0.0	2.1	0.0				NADP-dependent oxidoreductase domain-containing		
VDAG_JR2_Chromosome2g00540	97.06	-	0.1	0.8	1.1	0.0	0.8	0.0	2.1	0.0				Alpha/Beta hydrolase		
VDAG_JR2_Chromosome8g09650	122.03	-	0.7	0.0	0.6	0.2	2.2	0.0	2.0	0.0				Glycoside hydrolase family		
VDAG_JR2_Chromosome5g10380	25.61	-	0.2	0.6	1.1	0.0	0.6	0.0	2.0	0.0				Zn2-Cys6 transcription factor		
VDAG_JR2_Chromosome4g03070	89.63	-	2.2	0.0	1.5	0.0	2.7	0.0	1.9	0.0				Stress-induced protein, KGG		
VDAG_JR2_Chromosome6g03720	31.42	-	1.0	0.0	0.5	0.3	2.4	0.0	1.9	0.0				cluster_63	cf_putative	hypothetical protein
VDAG_JR2_Chromosome1g05450	20.37	-	0.5	0.3	0.1	0.8	2.2	0.0	1.4	0.0				cluster_3	cf_putative	Integral membrane protein
VDAG_JR2_Chromosome6g09180	468.24	-	1.6	0.0	0.2	0.7	2.0	0.0	0.5	0.2				cluster_70	cf_putative	isoamyl alcohol oxidase
VDAG_JR2_Chromosome4g10180	840.55	-	0.5	0.3	1.1	0.0	2.0	0.0	0.3	0.5						Endonuclease/Exonuclease/phosphatase
Top Down-regulated genes																
VDAG_JR2_Chromosome1g23880	410.36	-	4.2	0.0	0.4	0.5	0.3	0.5	3.4	0.0	cluster_14	t1pks-nrps		lovastatin nonaketide synthase		

VDAG_JR2_Chrlg23930	223.91	3.7 6	0.0 0	0.7 5	0.2 5	0.0 1	1.0 0	- -	3.0 2	0.0 0	cluster_ 14	t1pks- nrps	TOXD protein
VDAG_JR2_Chrlg23890	459.89	3.5 8	0.0 0	0.6 0	0.3 6	0.0 1	0.9 9	- -	2.9 9	0.0 0	cluster_ 14	t1pks- nrps	hypothetical protein
VDAG_JR2_Chrg09780	57.25	1.7 0	0.0 0	0.2 0	0.8 1	1.0 7	0.0 1	- -	2.9 7	0.0 0			hypothetical protein
VDAG_JR2_Chrlg23910	116.12	4.1 3	0.0 0	1.1 6	0.0 5	0.0 4	0.9 5	- -	2.9 3	0.0 0	cluster_ 14	t1pks- nrps	hypothetical protein
VDAG_JR2_Chrlg23920	114.15	3.4 0	0.0 0	0.4 7	0.5 0	0.0 8	0.9 1	- -	2.8 6	0.0 0	cluster_ 14	t1pks- nrps	Alpha/Beta hydrolase
VDAG_JR2_Chrlg23940	625.82	3.3 6	0.0 0	0.6 9	0.3 0	0.1 0	0.8 8	- -	2.5 8	0.0 0	cluster_ 14	t1pks- nrps	hypothetical protein
VDAG_JR2_Chrg03470	5765.1 5	0.9 8	0.0 1	0.1 9	0.7 8	1.3 7	0.0 0	- -	2.5 4	0.0 0			cytochrome P450 monooxygenase
VDAG_JR2_Chrg09260	36.24	1.0 8	0.0 2	0.2 9	0.7 1	1.6 6	0.0 0	- -	2.4 4	0.0 0			hypothetical protein
VDAG_JR2_Chrg03670	1016.6 8	- 1.9 9	- 0.0 0	- 0.1 5	- 0.8 2	- 4.2 7	- 0.0 0	- -	- 2.4 4	- 0.0 0	cluster_ 63	cf_puta tive	hypothetical protein
VDAG_JR2_Chrlg22700	4387.4 6	0.4 6	0.0 7	0.3 4	0.3 7	1.5 8	0.0 0	- -	2.3 8	0.0 0			hypothetical protein

VDAG_JR2_Chromosome4g04340	2563.03	- 1.1 9	0.0 0	0.3 7	0.5 5	- 3.8 7	0.0 0	- 2.3 2	0.0 0			hypothetical protein
VDAG_JR2_Chromosome6g04130	796.94	0.5 8	0.1 1	0.0 9	0.9 1	1.7 9	0.0 0	2.2 8	0.0 0			hypothetical protein
VDAG_JR2_Chromosome4g11840	41.01	1.1 0	0.0 0	0.0 1	0.9 9	1.1 5	0.0 0	2.2 7	0.0 0			hypothetical protein
VDAG_JR2_Chromosome5g01890	247.82	1.5 6	0.0 0	0.1 6	0.7 5	0.4 9	0.0 7	2.2 2	0.0 0	Zn2/Cys6 -Fungal TF		Zn2-Cys6 transcription factor
VDAG_JR2_Chromosome6g08940	153.16	1.2 2	0.0 1	0.4 2	0.5 6	1.3 8	0.0 0	2.1 9	0.0 0	cluster_69	cf_putative	cytochrome P450
VDAG_JR2_Chromosome8g06660	13626.04	0.0 0	0.9 9	0.6 8	0.0 6	1.4 5	0.0 0	2.1 4	0.0 0			Ammonium/urea transporter
VDAG_JR2_Chromosome8g09770	50.00	1.0 5	0.0 1	0.3 6	0.5 8	0.7 2	0.0 7	2.1 3	0.0 0			hypothetical protein
VDAG_JR2_Chromosome1g22660	1015.42	0.8 7	0.0 0	0.0 6	0.9 2	1.2 3	0.0 0	2.0 4	0.0 0			UDP-glucose 4-epimerase
VDAG_JR2_Chromosome1g01960	4976.56	- 0.0 1	- 0.9 8	- 0.7 7	- 0.0 0	- 2.8 2	- 0.0 0	- 2.0 4	- 0.0 0			Frequency clock protein
VDAG_JR2_Chromosome1g09750	2398.82	- 0.8 4	- 0.0 0	- 0.0 4	- 0.9 4	- 1.1 6	- 0.0 0	- 2.0 3	- 0.0 0			cholesterol oxidase

VDAG_JR2_Chromosome6g06730	959.89	0.3 3	0.5 9	1.6 8	0.0 0	0.0 1	0.9 9	2.0 1	0.0 0	Protein of unknown function
VDAG_JR2_Chromosome3g06750	104.25	1.2 8	0.0 1	0.3 0	0.7 1	2.7 7	0.0 0	1.2 0	0.0 1	hypothetical protein
VDAG_JR2_Chromosome5g10060	42.49	0.4 6	0.3 9	0.1 7	0.8 4	2.3 0	0.0 0	1.6 7	0.0 0	hypothetical protein
VDAG_JR2_Chromosome1g09640	1869.91	0.2 6	0.5 3	0.5 4	0.2 8	2.0 2	0.0 0	1.2 2	0.0 0	Integral membrane protein