

Supplementary Materials:

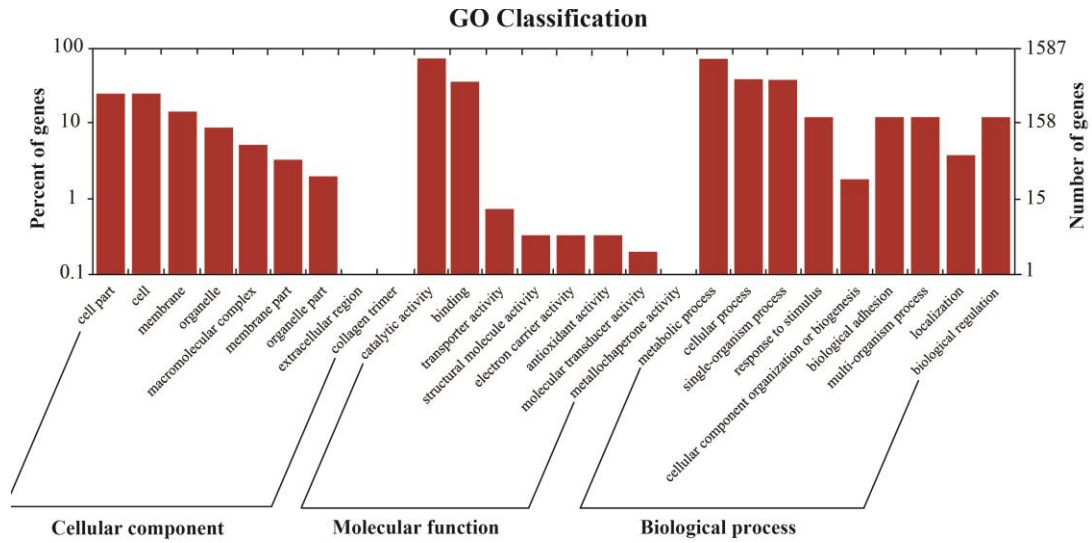


Figure S1. GO classification of predicted protein-encoding genes of *V. dahliae* strain VdLs.17.

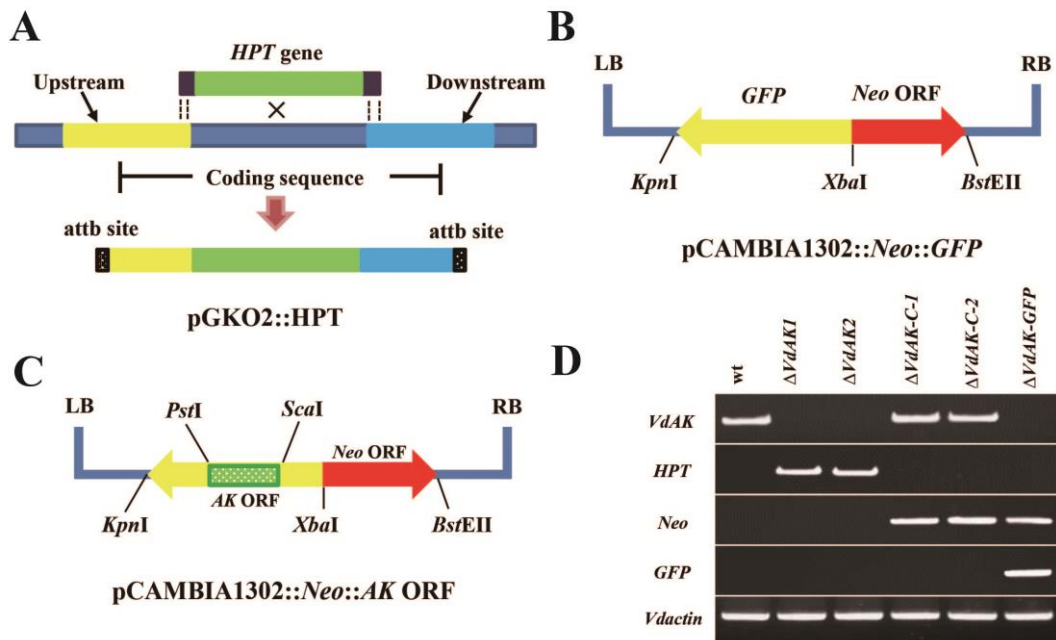


Figure S2. Generation of disruption ($\Delta VdAK$), complementation ($\Delta VdAK-C$) and $\Delta VdAK-GFP$ strains via homologous recombination. (A) Construction of *VdAK*-disrupted mutant $\Delta VdAK$. About 1.5 kb upstream and downstream of targeted gene were fused with the hygromycin resistance cassette. The whole fragment, with attb sites, was cloned using nested PCR. (B) Construction of $\Delta VdAK-GFP$. The neomycin resistance cassette, containing XbaI and BstEII restriction sites, was cloned into the pCAMBIA1302 vector. The GFP expression cassette was then cloned into the intermediate plasmid by XbaI/KpnI double-digestion (designated pCAMBIA1302::Neo::GFP). (C) Construction of $\Delta VdAK-C$. The GFP ORF of plasmid pCAMBIA1302::Neo::GFP was replaced with *VdAK* ORF via ScaI/PstI double digestion

(designated pCAMBIA1302::Neo::VdAK). (D) Expression of the targeted genes was confirmed by RT-PCR.

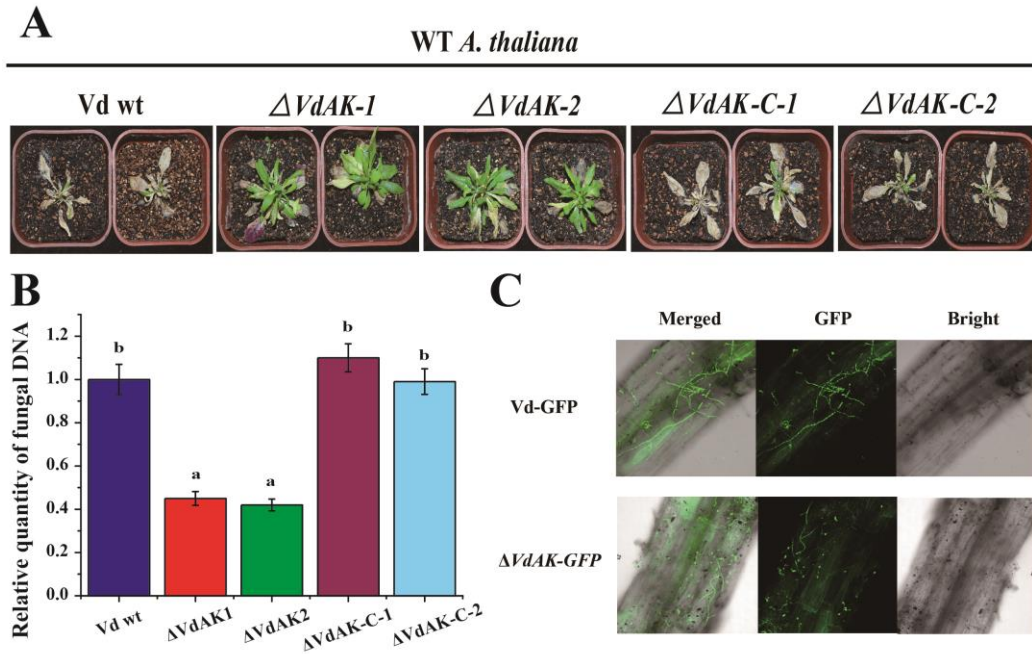


Figure S3. Virulence analysis of disruption ($\Delta VdAK$) and complementation ($\Delta VdAK-C$) mutants and wild-type *Vd* in *A. thaliana*. (A) Symptoms on seedlings at 12 days after roots were dipped in 10^6 spores/mL of $\Delta VdAK$, $\Delta VdAK-C$ or wild-type *Vd*. (B) Relative amounts of fungal DNA determined by RT-qPCR. Means (\pm SE) from three independent experiments that significantly differed among treatments in Duncan's test ($P < 0.05$) are indicated with different letters. (C) Micrographs of fluorescing fungal hyphae in *A. thaliana* root tips at 5 days post inoculation with *Vd-GFP* or $\Delta VdAK-GFP$.

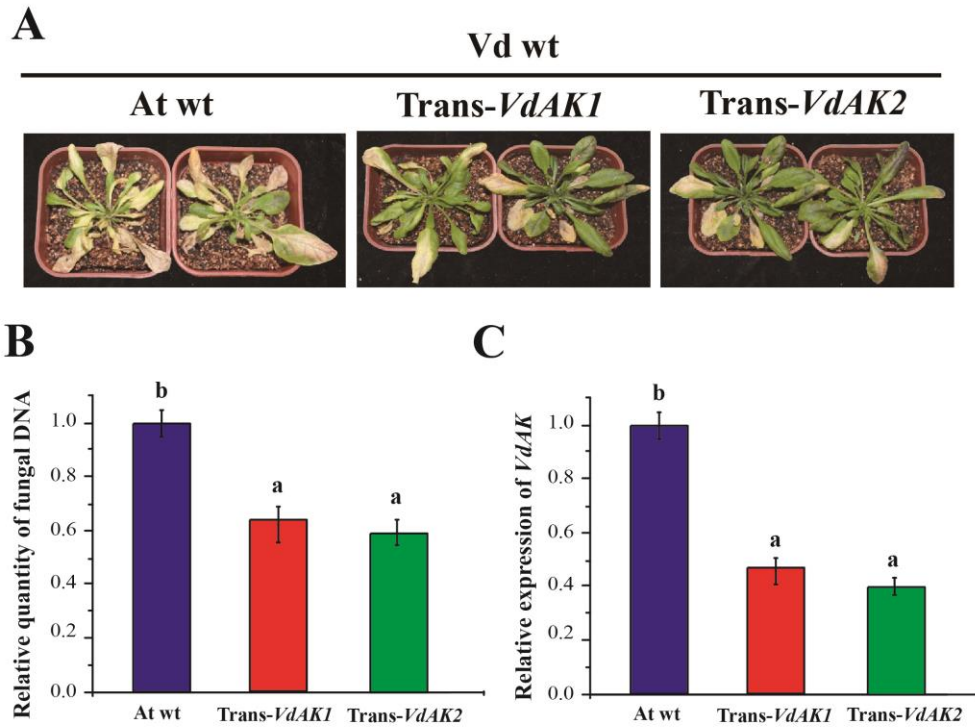


Figure S4. Expression of dsRNAs of *VdAK* in *A. thaliana* led to increased resistance against *Vd*. (A) Symptoms on transgenic and wild-type plants at 12 days after roots were dipped in 10^6 spores/mL of the respective strains. (B) Relative amounts of fungal DNA determined by RT-qPCR. (C) Transcript levels of *VdAK* in stems of transgenic and wild-type plants. Means (\pm SE) from three independent experiments were analyzed for significant differences among treatments using Duncan's test ($P < 0.05$).

Table S1. Information on RNAi constructs targeting 92 *V. dahliae* genes selected for HIGS and disease index from 10-12 days post inoculation of construct-treated plants

RNAi constr	Primer sequences (5' to 3')	Gene IDs	Annotations	Disease index		
				10 dpi	11 dpi	12 dpi
TRV:00				100	100	100
1	ATAGAATCCGTTATCCT CGTCGGTGC ATAGGATCCAGACACGG CCCGAG	VDAG_01 040.1	Adenylate kinase	15	20	25
2	ATAGAATCCCATTTCAG ACTGCCAG ATAGGATCCCTCCTCCA AAGATCC	VDAG_05 976.1	Alpha-amylase A type-1/2	15	55	65
3	ATAGAATTCATGGCGCA GAACCCC GCGTATGGAAATCCTCT CGTCCC	VDAG_07 833.1	Ankyrin repeat-containing protein	60	80	90

4	ATAGAATTCTTGTCCTCT CCAACG GGTGTAGATGAAGACAT CGTACAAG AGTGAATTCGTGCTTCAA	VDAG_07 739.1	Aquaporin-3	18	20	24
5	GCGTAC AGAGGATCCCCCTTGAA GAGAGAC AGAGAATTCATGGATTA	VDAG_07 535.1	ADP, ATP carrier protein	20	30	35
6	CCAGGGTTC TGAGGATCCCACCTTGTA GCAGATC ATAGAATTCATGTCGGA	VDAG_00 201.1	Cellular nucleic acid-binding protein	20	55	70
7	GAACCTCGC ATAGGATCCGACAGTCA AGATGCC ATAGAATTCGGTCATCG	VDAG_02 332.1	Aconitate hydratase	20	45	70
8	AGCCTGG ATATGGATCCGGAATCG TGTTCTCC AGAGAATTCTCGTCATC	VDAG_01 206.1	Pyruvate kinase	20	40	55
9	CGCAGTG ATAGGATCCCTTGTGGCT CCTCTG ATAGAATTCACCGGAGG	VDAG_09 094.1	Peroxisomal membrane protein PEX30	30	40	45
10	ACTCGGG ATAGGATCCCCTTGATC GTCCAGC AGAGAATTCTGCTAACA	VDAG_03 613.1	NADPH dehydrogenase	25	50	65
11	AGGCCGGC AGAGGATCCAGTGGATG ACCGAGG ATAGAATTCCAATCGAC	VDAG_04 294.1	60S Acidic ribosomal protein P0	40	55	75
12	GGCATCC ATAGGATCCTGCAATCG ATGCTCC AGAGAATTCCAACCTCT	VDAG_01 123.1	Hard-surface induced protein	35	50	75
13	ACGACGCC ATAGGATCCCACGGAGC TTATCGG ATAGAATTCATCAAGGC	VDAG_01 774.1	Malate synthase	60	70	80
14	GCTCAAGC AGAGGATCCAGTGAGCA TGAGACG	VDAG_03 232.1	Oligosaccharyl transferase STT3 subunit	10	25	35

15	ATAGAATTCGTGCCGAC ATCGACC ATAGGATCCGCCCACTG AATAGAGC	VDAG_08 270.1	Transport protein BOS1	75	90	100
16	ATAGAATTCGACACGGA GTACTCCG AGAGGATCCTGCTGGTG ATATGCC	VDAG_05 521.1	Vacuolar protein sorting-associated protein	50	75	90
17	ATAGAATTCATCAAGCG ACCGAGAGG ATAGGATCCATGCTCCCT GTCAGC	VDAG_01 656.1	Viral A-type inclusion protein repeat protein	25	60	75
18	ATAGAATTCGAGCCAGC CCAACAG AGAGGATCCTGGACAAG GTGTACTCG	VDAG_06 474.1	cAMP-dependent protein kinase	45	65	75
19	ATAGAATTCACCTTCCA GGACTCC ATAGGATCCTCTCTTCTG GGTACCG	VDAG_06 474.1	cAMP-dependent protein kinase	80	85	95
20	AGAGAATTCGCAGGCTA CATCAGCG ATAGGATCCGTGCTCAG CTCGTACG	VDAG_02 311.1	Solute carrier family 25 member 45	50	70	85
21	AGAGAATTCCTGGAAAG GCACCTGC ATAGGATCCAGGCATGA GAACGCC	VDAG_00 714.1	Argininosuccinate lyase	20	25	30
22	TGTGAATTCGGCCTCGA GTATAAGG ATAGGATCCGCCTTAC GTACTCG	VDAG_00 317.1	Cryptochrome DASH	65	75	85
23	AGAGAATTCGTACGTCC GCTCCTGC ATAGGATCCGAGATCTG GGTCACGG	VDAG_05 375.1	Covalently-linked cell wall protein	70	80	95
24	ATAGAATCCAACGTGA CTCCTGGC AGTGGATCCTTAACACT CGTCCGTC	VDAG_10 495.1	Endoglucanase B	65	75	85
25	ATAGAATTCAACGCTGT CTACTTCACG ATAGGATCCTGAGGTAG TAGTTGACG	VDAG_04 416.1	Chitinase A	60	70	90

26	AGAGAATTCGGAGCATA CTGACGTCC ATAGGATCCTGTGCACA GACTGATGC	VDAG_09 689.1	Guanine nucleotide-binding protein subunit beta	55	65	80
27	AGAGAATTCGCCTACCA GGAAGACC ATAGGATCCGGACTTGA TGTAGGCC	VDAG_07 192.1	1,3-Beta-glucanosylt ransferase gel4	55	65	80
28	ATAGAATTCCACGCTCA ACACGACC TTAGGATCCCTCCATGGT GTACTCG	VDAG_02 243.1	1,3-Beta-glucanosylt ransferase gel1	55	75	85
29	ATAGAATTCCTTGGCCTT AGCTGGC TTAGGATCCTCTAGGGTT GAGCCG	VDAG_02 071.1	Glucosyltransferase H	60	70	85
30	TGAGAATTCTACAGCCA GCTCTCGC ATAGGATCCCGCTGGAT ATCGAGC	VDAG_06 369.1	GTP-binding protein GTR2	40	50	65
31	AGAGAATTCCTGAGGAC TCAGCAGGC ATAGGATCCCGGATGTG CTTCAGG	VDAG_10 151.1	NADH-ubiquinone oxidoreductase 21 kDa subunit	60	70	80
32	TGAGAATTCACAGTCGA GCTCGACG ATAGGATCCGGCTGAGA GAACAGGC	VDAG_04 456.1	Nuclear pore glycoprotein p62	50	60	70
33	TTAGAATTCGACCACA GCATCACG ATAGGATCCGGATCATC TCAGTGCG	VDAG_03 673.1	Nuclear distribution protein nudeE	20	30	35
34	TGAGAATTCTTCTCCA ACGTCCG AGAGGATCCTAATGTTG GACATGCG	VDAG_09 326.1	GTP-binding protein GTR1	40	45	55
35	AGAGAATTCOAACCGTC TGGCTACC TTAGGATCCCAATGATC AGAGGGC	VDAG_09 877.1	Aspartyl/glutamyl-t RNA (Asn/Gln) amidotransferase subunit B	50	65	75
36	TTAGAATTCGAGCAGGA TTACGTGGC ATAGGATCCATACGAGC CTGCACG	VDAG_02 981.1	Methyltransferase domain-containing protein	45	55	65

37	ATAGAATTCCAAGCGGA GACTGATGG TTAGGATCCTGAATGTGC AGGTGG TGTGAATTCTCTCCTACT	VDAG_05 486.1	Atrial gland-specific antigen	31.2 5	56.2 5	62.5
38	CCGTCCG ATAGGATCCGGATATGT CGAGGTCTG AGAGAATTCCTCTTATCT	VDAG_00 647.1	Inner centromere protein	6.25	12.5	18.7 5
39	GTCGGCGG ATAGGATCCGTTGACGT GAGTCCG ATAGAATTCATCGGGCC	VDAG_00 787.1	Hypothetical protein	43.7 5	50	56.2 5
40	AAGGTGG TTAGGATCCTCACTCAGC ATGCTCG AGAGAATTCTCGCCGAG	VDAG_06 790.1	PSP1 domain-containing protein	37.5	43.7 5	56.2 5
41	ATGCTCG ATAGGATCCGGCGTCCA CATTATGG ATAGAATTCGACGAGAT	VDAG_08 982.1	Mitogen-activated protein kinase HOG1	68.7 5	81.2 5	87.5
42	TGACGAGG ATAGGATCCTCTCAAGC TCATCAGC AGAGAATTCAGCTCTGG	VDAG_03 613.1	NADPH dehydrogenase	25	31.2 5	37.5
43	GATCAAGG ATAGGATCCTTGGTCTCG TCCTCTG ATAGAATTCGCAAGATC	VDAG_04 020.1	NADPH dehydrogenase D	40	56	68
44	GCTCTGGC ATAGGATCCGAGGTAGC ACGAGC ATAGAATTCGCCTTGCTT	VDAG_08 067.1	Pectate lyase B	50	56.2 5	62.5
45	CGTTCG TAAGGATCCCTGCGAAT GTTGTACC ATAGAATTCGGACGAAG	VDAG_05 402.1	Pectate lyase	56.2 5	62.5	68.7 5
46	CAGACACG AGAGGATCCTCTCGTGA TAGGGAGG ATAGAATTCGCTTCGAG	VDAG_08 663.1	cAMP-dependent protein kinase regulatory subunit	50	55	69
47	CGTCATGG ATAGGATCCGATCCCGT CATCTCG	VDAG_08 656.1	Cell pattern formation-associate d protein stua	56.2 5	68.7 5	75

48	AGAGAATTCCAATGGCA GCAGAGC ATAGGATCCGGTTCGAGG TATAGGGC TTAGAATTCGTCAACCA	VDAG_06 649.1	Dual specificity protein kinase YAK1	20	30	35
49	GCTCGAGG ATAGGATCCCTTGATCAT GGCAGG ATAGAATTCCAGAAGCC	VDAG_07 142.1	Polysaccharide deacetylase family protein	65	75	80
50	TGTCGTGC ATAGGATCCAATCTCGTT CGTGACG ATAGAATCCGTCACCA	VDAG_08 977.1	ATP-dependent protease La	25	40	45
51	TCAACAAGGC ATAGGATCCACCTTGCTC GTGTTGG ATAGAATTCGTCAAGA	VDAG_08 977.1	ATP-dependent protease La	55	65	70
52	TACCACGGC ATAGGATCCGTAGCTCT GCGTCAGG ATAGAATTCACGTACGC	VDAG_00 279.1	Import receptor	35	45	50
53	TGCGTATCG TTAGGATCCTGATGGTGT ACTCGGC ATAGAATTCGTCAACCA	VDAG_05 060.1	Multidrug resistance protein	65	75	85
54	GGAAGTCG ATAGGATCCTACGGTAA GCCGTCG ATAGAATTCCAACGGTG	VDAG_05 084.1	ATP-dependent bile acid permease	25	30	35
55	ACCTCAAGG ATAGGATCCCTCCTCAG CCTTCTCC ATAGAATTCGGCAACCG	VDAG_04 294.1,	60S Acidic ribosomal protein P0	55	70	75
56	AGATAGCC ATAGGATCCCTGGAGTA CGGTAACC AGAGAATTCATGCTCTC	VDAG_00 335.1	Secreted protein K	60	65	70
57	CAGCCTC ATAGGATCCTCTCTCTGC AGCACG AGAGAATTCGACGACAT	VDAG_07 788.1	Microsomal signal peptidase 18 kDa subunit	60	65	70
58	GATCTCCCAG ATAGGATCCGGTGAAGG TGACCTCC	VDAG_07 546.1	Stress protein	55	65	75

59	ATAGAATTCACCTGGCC ATGAGGTC ATAGGATCCTGCGACAG CATTAC AGAGAATTCGCAAGACG	VDAG_03 187.1	General stress protein	55	65	85
60	AACGTTCC ATAGGATCCACTCGTGG AAGTGCG ATAGAATTCCTTGGGG	VDAG_01 389.1	Glycogen synthase	65	80	85
61	CTACACCC ATAGGATCCTGCTGCTGC TAGTGCC AGAGAATTCCTCGTTCAT	VDAG_01 389.1	Glycogen synthase	55	70	90
62	CTACGTCG ATAGGATCCCTCTGGTA CGTACTGCC AGAGAATTCCTGGTATCT	VDAG_01 254.1	Tryptophan synthase	50	55	65
63	CAAGGCG ATAGGATCCAGTCGTCG TGGTAGG AGAGAATTCCTGGGACT	VDAG_07 000.1	Killer toxin subunits alpha/beta	45	60	65
64	ACAAGAGCG ATAGGATCCGAGAGGCT CACAAGC AGAGAATTCTGTCAAC	VDAG_00 901.1	Killer toxin subunits alpha/beta	55	65	70
65	AGCAAGCC AGAGGATCCTGTCAAGA ATGGCAC GAGGAATTCAGAATACG	VDAG_00 825.1	Vacuolar protease A	62	72	80
66	TGGAACGGG ATAGGATCCGATGCTGC TCGTTGAC ATAGAATTCCTCCAATCC	VDAG_08 621.1	Carbon catabolite-derepress ing protein kinase	50	60	75
67	GTTGTCC ATAGGATCCAGGAGCAG CTGGTC AGAGAATTCAGTCTGGC	VDAG_04 529.1	Thioredoxin	16	23	28
68	TCATACCG ATAGGATCCAGGTTGGC AACGATG AGAGAATTCGTCGACG	VDAG_09 532.1	Serine 3-dehydrogenase	60	75	85
69	GCAAGC AGAGGATCCTTGTGCCA GCTGAGG	VDAG_05 692.1	Uricase	70	85	95

70	AGAGAATTCGCAAGCGT CCAGAAG ATAGGATCCAGACCCAG GACCCTC TATGAATTCGGTCGCAC	VDAG_09 026.1	NADH-ubiquinone oxidoreductase 29.9 kDa subunit	25	30	35
71	AGTACAACG ATAGGATCCCGACTCAA TGTCGAGG AGAGAATTCGCGAGGAG	VDAG_01 642.1	Pyruvate dehydrogenase E1 component subunit beta	70	90	95
72	ACTCTGCC ATAGGATCCGGTTGGAG CCGTACC ATAGAATTCGGTTCAAG	VDAG_03 252.1	Glycine-rich RNA-binding protein	60	70	75
73	AATATGCCG TATGGATCCACCGTGAG ACTTGAC CTAGAATTCAGGGCAT	VDAG_07 546.1	Stress protein	10	15	20
74	CCTCGTTC ATAGGATCCCCAGAAGT CTTCAGCC ATAGAATTCCTCCGGC	VDAG_06 669.1	Hypothetical protein	70	85	90
75	ATGAAGG TTAGGATCCTGAGCACC TCCATCG AGTGAATTCTGCGATTGC	VDAG_08 238.1	Glycerate kinase	80	85	90
76	GACATCC ATAGGATCCCTATCCGA CCCATGGC ATAGAATTCGTCATCTGA	VDAG_04 980.1	Thymidylate kinase	60	70	85
77	GCAGCAGC ATAGGATCCGCATTGTA GCTCATGG ATAGAATTCGGCACCA	VDAG_01 726.1	Choline kinase	70	90	95
78	CGGTCAT ATAGGATCCCGAGGACA CGAGCAC ATAGAATTCGTGTTGGTT	VDAG_02 259	Glutamate decarboxylase	65	75	95
79	GAGTCGA ATAGGATCCAACAGCCC CGTGCCGA ATAGAATTCCTCCGCTCCT	VDAG_06 992	Ferric reductase transmembrane component 4	60	70	85
80	GCGTCCC ATAGGATCCGATCTGGG TCACGGC	VDAG_04 380	Cytochrome P450 51	65	75	85

81	ATAGAATTCATTCCAAC GTGACTC ATAGGATCCCTTAACAC TCGTCCG	VDAG_10 495	Endoglucanase B	30	35	40
82	ATAGAATTCTCGAGCCA GCCCAAC ATAGGATCCCTGGACAA GGTGTA	VDAG_06 474	cAMP-dependent protein kinase	60	70	75
83	ATAGAATTCGGTCAACC AGCTCGA ATAGGATCCCCTTGATC ATGGCAGG	VDAG_07 142	Polysaccharide deacetylase family protein	40	45	60
84	ATAGAATTCGCTCAAGC CCTACGGCC ATAGGATCCAGGATCTG GCCGAAGCC	VDAG_01 845.1	Branched-chain-ami no-acid aminotransferase	65	75	95
85	ATAGAATTCGTGGTGCG CGTCTACC ATAGGATCCGATGGCCA GCTCGAGG	VDBG_07 510.1	Xylulose-5-phospha te phosphoketolase	60	70	75
86	ATAGAATTCCTGACTTC CGGCAAC ATAGGATCCGCGACAGC GTAACGA	VDAG_05 940.1,	60S Ribosomal protein L2	55	60	65
87	ATAGAATTCGTGTTGGTT GAGTCGA ATAGGATCCAACAGATC CGTGCCG	VDAG_06 992.1	Ferric reductase transmembrane component 4	60	80	100
88	ATAGAATTCOAAGTGGT ACGGCACCA ATAGGATCCCAATGGTC GAGGACAC	VDAG_01 692.1	Endoglucanase	55	65	75
89	ATAGAATTCACGGACT TCCTGAC ATAGGATCCAGAGACGG AGTGGGT	VDBG_00 534.1	1,3-Beta-glucanosylt ransferase gel1	70	80	90
90	ATAGAATTCGAGACCGA GAAGTCG ATAGGATCCACAGAGCG GGCGGGG	VDBG_07 986.1	PH domain-containing protein	65	70	80
91	ATAGAATTCGCACATTGT CGCTCTCG ATAGGATCCCAGGTAGT GGCTCAAGG	VDAG_09 595.1	Chitin synthase export chaperone	55	64	78

	ATAGAATTCGGCCTCGA					
92	GTATAAGGA	VDAG_00	Cryptochrome	50	70	85
	ATAGGATCCGCCTTAC	317.1	DASH			
	GTACTCGC					

Table S2. Primers used to produce the *VdAK* RNAi construct

Primer	Sequences (5' to 3')
trans-VdAK	<u>AAAAAAGCAGGCT</u> CGTTATCCTCGTCGGTGC <u>AAGAAAGCTGGGT</u> AGACACGGCCCGAA
BP site	GGGACAAGTTTGTACAAAAAAGCAGGCT GGGACCACTTTGTACAAGAAAGCTGGGT
Det-VdAK	ACTCGCCTAACTGTGCCTCTA GGAACCCATCCAGAATGAAGG

Table S3. Primers used to construct mutant strains of *V. dahliae*

Primer	Sequences (5' to 3')
Hygromycin resistant expression cassette	TTGAAGGAGCATTTTTGGGC TTATCTTTGCGAACCCAGGG 5F: CAGAGTACCCTGACGGCATCGGC 5R: GCCCAAAAATGCTCCTTCAAATCAAGCGCATGATAAGG TCG 3F: CCCTGGGTTTCGCAAAGATAACTTCGACGTGATCATGCAG CGC
Δ VdAK	3R: GGAAGTCTCCTGGGGTGGTGGTGG NEST-F: <u>GGGGACAAGTTTGTACAAAAAAGCAGGCTCGTCATTCC</u> ATTCCACGGACCC NEST-R: <u>GGGGACCACTTTGTACAAGAAAGCTGGGTCAAGGTACA</u> ATGTCACATACGG
Neomycin resistant expression cassette	aattctagaGTTTGC GGGCTGTCTTGACG ataggtcaccTACCTGTGCATTCTGGGTAA
gGFP expression cassette	ggctctagaCTTTCGACACTGAAATACGTCG ataggtaccGCATCAGAGCAGATTGTA CTGAGAG
Δ VdAK-com	aaaagtactATGAGACTTCGAAAGGCAG aaactgcagTCAAGCCGCAAAGCGTTT
Det-HPH	TTCGACAGCGTCTCCGACCTGA

Det-ΔVdAK	AGATGTTGGCGACCTCGTATTGGG TATAACAAGAATGGTTGGCTGCGTCCC GTGGATGGAAGGTGGTATTGTAGACACG
Det-neo	GTTGTCACTGAAGCGGGAAGGG GCGATACCGTAAAGCACGAGGAA CGACGTAAACGGCCACAAGTT
Det-GFP	TCTTTGCTCAGGGCGGACTGG

Note: Restriction sites are in bold italic font.

Table S4. Primers used for RT-qPCR

Primer	Sequences (5' to 3')
qRT-VdAK	GTGTCTACAATACCACCTTCCA CTCATCACTGCTCATAACCTC
qRT-VA	GGGTATTCAGACCCTATTGGACG CGAACTTCTTGTACTCAGCCTCC
qRT-VdATP6	CTAGACCAATTTGAAATAAGA AAAGATTCTTGGCTAATAGAT
qRT-VdAC	TCTCCATCGTCTTCACCGACATCA TCTGCACGGCGAAACACCACA
qRT-VdATP-PRT	CGACGCCAACGTGCGGTCTACAA GCCCCGAGAAGCTCGTGCCAAT
qRT-Vdactin	GGCTTCCTCAAGGTCGGCTATG GCTGCATGTCATCCCACCTTCTC
qRT-VdITS	CCGCCGGTCCATCAGTCTCTCTGTTTATAC CGCCTGCGGGACTCCGATGCGAGCTGTAAC
RT-Nbactin	GGACCTTTATGGAAACATTGTGCTCAGT CCAAGATAGAACCTCCAATCCAGACAC
RT-AtEF-1α	TGAGCACGCTCTTCTTGCTTTC GGTGGTGGCATCCATCTTGTTA

Table S5. Information on sRNAs from *V. dahliae* isolated from *Vd*-infected seedlings

Sample	Total sRNAs	Mapped sRNAs	Total mapped sRNAs
Col_1	10786798 (100.00 %)	6919974 (64.15 %)	6650 (0.10 %)
RNAi_1	4068549 (100.00 %)	3039943 (74.72 %)	5015 (0.16 %)
RNAi_2	8235986 (100.00 %)	5599526 (67.99 %)	5090 (0.09 %)
RNAi_3	9820717 (100.00 %)	6890613 (70.1 %)	9929 (0.14 %)

Table S6. Sixteen *Vd* candidate pathogenicity/virulence factor genes identified by HIGS

Gene ID	Annotation	Disease index		
		10 dpi	11 dpi	12 dpi
VDAG_01040.1	Adenylate kinase	15	20	25
VDAG_07535.1	ADP, ATP carrier protein	20	30	35
VDAG_01206.1	Pyruvate kinase	20	40	55
VDAG_09094.1	Peroxisomal membrane protein PEX30	30	40	45
VDAG_03232.1	Oligosaccharyl transferase STT3 subunit	10	25	35
VDAG_00714.1	Argininosuccinate lyase	20	25	30
VDAG_03673.1	Nuclear distribution protein nudeE	20	30	35
VDAG_00647.1	Inner centromere protein	6.25	12.5	18.75
VDAG_03613.1	NADPH dehydrogenase	25	31.25	37.5
VDAG_06649.1	Dual specificity protein kinase YAK1	20	30	35
VDAG_08977.1	ATP-dependent protease La	25	40	45
VDAG_05084.1	ATP-dependent bile acid permease	25	30	35
VDAG_04529.1	Thioredoxin	16	23	28
VDAG_09026.1	NADH ubiquinone oxidoreductase	25	30	35
VDAG_07546.1	Stress protein	10	15	20
VDAG_10495.1	Endoglucanase B	30	35	40
Control		100	100	100