

1 **Supplementary Materials**

2

3 **Article title:** Genome-wide characterization of *Stb6* ortholog genes and identification of  
4 *MdStb6-13* as a gene conferring resistance to *Botrytis cinerea* in *Malus domestica*

5 Authors: Peiran Qi, Xiuxia Liu, Siying Yang, Mengya Zhou, Min Li, Fukun Luan, Weiwei  
6 Zhang, Xinkai Zhou, Xianpu Wang, Xuesen Chen, Shujing Wu

7

8 The following supplementary materials are available for this article:

9 Table S1. The identity between the genes in MdStb6 homologs in apple genome.

10 Table S2. Accession numbers of genes used in the phylogenetic analysis.

11 Table S3. Primers used in this study.

12 **Supplementary file**

13

14 Table S1 The identity between the genes in MdStb6 homologs in apple genome

15

16

	MdStb 6-1	MdStb 6-2	MdStb 6-3	MdStb 6-4	MdStb 6-5	MdStb 6-6	MdStb 6-7	MdStb 6-8	MdStb 6-9	MdStb 6-10	MdStb 6-11	MdStb 6-12	MdStb 6-13	MdStb 6-14	MdStb 6-15
MdStb6-1	100%	81.54%	77.37%	28.11%	35.85%	35.44%	34.21%	29.20%	30.02%	29.03%	26.43%	89.69%	41.95%	40.62%	72.62%
MdStb6-2	81.54%	100%	69.53%	26.30%	33.66%	32.85%	32.70%	26.81%	28.59%	26.97%	23.94%	73.64%	38.27%	37.09%	67.57%
MdStb6-3	77.37%	69.53%	100%	29.89%	35.92%	34.19%	34.05%	29.16%	31.06%	29.89%	25.94%	69.81%	41.35%	40.62%	58.83%
MdStb6-4	28.11%	26.30%	29.89%	100%	31.87%	30.95%	46.91%	42.54%	40.81%	38.46%	39.84%	26.92%	29.59%	28.44%	26.48%
MdStb6-5	35.85%	33.66%	35.92%	31.87%	100%	92.23%	35.60%	29.82%	32.03%	31.13%	31.11%	33.33%	31.47%	33.14%	32.35%
MdStb6-6	35.44%	32.85%	34.19%	30.95%	92.23%	100%	35.31%	29.43%	31.24%	32.48%	29.74%	33.82%	31.78%	31.85%	31.59%
MdStb6-7	34.21%	32.70%	34.05%	46.91%	35.60%	35.31%	100%	40.05%	42.94%	39.79%	42.39%	32.59%	32.77%	30.16%	31.19%
MdStb6-8	29.20%	26.81%	29.16%	42.54%	29.82%	29.43%	40.05%	100%	43.12%	33.02%	31.07%	28.81%	27.95%	26.53%	25.88%
MdStb6-9	30.02%	28.59%	31.06%	40.81%	32.03%	31.24%	42.94%	43.12%	100%	33.87%	38.20%	28.68%	29.37%	28.76%	26.79%
MdStb6-10	29.03%	26.97%	29.89%	38.46%	31.13%	32.48%	39.79%	33.02%	33.87%	100%	36.64%	28.27%	27.97%	28.16%	25.08%
MdStb6-11	26.43%	23.94%	25.94%	39.84%	31.11%	29.74%	42.39%	31.07%	38.20%	36.64%	100%	25.42%	26.72%	25.85%	23.42%
MdStb6-12	89.69%	73.64%	69.81%	26.92%	33.33%	33.82%	32.59%	28.81%	28.68%	28.27%	25.42%	100%	39.69%	39.79%	77.46%
MdStb6-13	41.95%	38.27%	41.35%	29.59%	31.47%	31.78%	32.77%	27.95%	29.37%	27.97%	26.72%	39.69%	100%	41.84%	37.58%
MdStb6-14	40.62%	37.09%	40.62%	28.44%	33.14%	31.85%	30.16%	26.53%	28.76%	28.16%	25.85%	39.79%	41.84%	100%	38.17%
MdStb6-15	72.62%	67.57%	58.83%	26.48%	32.35%	31.59%	31.19%	25.88%	26.79%	25.08%	23.42%	77.46%	37.58%	38.17%	100%

17 Table S2 Accession numbers of genes used in the phylogenetic analysis

<b>Accession number</b>	<b>Gene</b>	<b>Accession number</b>	<b>Gene</b>
FvH4_2g35060.1	FvWAK1	FvH4_3g09860.1	FvWAK2
FvH4_3g10350.1	FvWAK3	FvH4_3g10360.1	FvWAK4
FvH4_3g10510.1	FvWAK5	FvH4_3g10610.1	FvWAK6
FvH4_3g10620.1	FvWAK7	FvH4_3g10690.1	FvWAK8
FvH4_3g11730.1	FvWAK9	FvH4_5g06860.1	FvWAK10
FvH4_5g06940.1	FvWAK11	FvH4_6g53140.1	FvWAK12
FvH4_7g31880.1	FvWAK13	FvH4_7g31920.1	FvWAK14
FvH4_1g03330.1	FvWAKL1	FvH4_1g07120.1	FvWAKL2
FvH4_2g12540.1	FvWAKL3	FvH4_3g24040.1	FvWAKL4
FvH4_3g35290.1	FvWAKL5	FvH4_4g34420.1	FvWAKL6
FvH4_5g11780.1	FvWAKL7	FvH4_6g23830.1	FvWAKL9
FvH4_6g37660.1	FvWAKL10	FvH4_6g37670.1	FvWAKL11
FvH4_6g38990.1	FvWAKL12	FvH4_6g39000.1	FvWAKL13
FvH4_6g39020.1	FvWAKL14	FvH4_7g04160.1	FvWAKL15
FvH4_7g05990.1	FvWAKL16	FvH4_7g06010.1	FvWAKL17
FvH4_7g06020.1	FvWAKL18	FvH4_7g06040.1	FvWAKL19
FvH4_7g17870.1	FvWAKL20	FvH4_7g20630.1	FvWAKL21
FvH4_7g23160.1	FvWAKL22	Prupe.1G442500.1	PpWAK1
Prupe.4G091900.1	PpWAK2	Prupe.4G092700.1	PpWAK3
Prupe.4G092900.1	PpWAK4	Prupe.4G093100.1	PpWAK5
Prupe.4G093100.2	PpWAK6	Prupe.4G093200.1	PpWAK7
Prupe.4G093300.1	PpWAK8	Prupe.4G093400.1	PpWAK9
Prupe.4G093500.1	PpWAK10	Prupe.4G094100.1	PpWAK11
Prupe.4G094500.1	PpWAK12	Prupe.1G315000.1	PpWAKL1
Prupe.1G315000.2	PpWAKL2	Prupe.1G315900.1	PpWAKL3
Prupe.1G315900.2	PpWAKL4	Prupe.1G318900.1	PpWAKL5
Prupe.2G047400.1	PpWAKL6	Prupe.2G047400.2	PpWAKL7
Prupe.2G047500.1	PpWAKL8	Prupe.2G087100.1	PpWAKL9
Prupe.2G087800.1	PpWAKL10	Prupe.2G088100.1	PpWAKL11
Prupe.2G088900.1	PpWAKL12	Prupe.2G089000.2	PpWAKL13
Prupe.2G093400.1	PpWAKL14	Prupe.2G103300.1	PpWAKL15
Prupe.2G200600.1	PpWAKL16	Prupe.2G240400.1	PpWAKL17
Prupe.3G145600.1	PpWAKL18	Prupe.3G145700.1	PpWAKL19

Prupe.3G145800.1	PpWAKL20	Prupe.3G146200.1	PpWAKL21	18
Prupe.3G146500.1	PpWAKL22	Prupe.3G180500.1	PpWAKL23	19
Prupe.3G180600.1	PpWAKL24	Prupe.3G181100.1	PpWAKL25	20
Prupe.3G181100.2	PpWAKL26	Prupe.3G181200.1	PpWAKL27	21
Prupe.3G181200.2	PpWAKL28	Prupe.3G181400.1	PpWAKL29	22
Prupe.3G181800.1	PpWAKL30	Prupe.3G181900.1	PpWAKL31	23
Prupe.3G182400.1	PpWAKL32	Prupe.3G182700.1	PpWAKL33	24
Prupe.4G093000.1	PpWAKL34	Prupe.4G094000.1	PpWAKL35	25
Prupe.5G051200.1	PpWAKL36	Prupe.5G051600.1	PpWAKL37	26
Prupe.5G223900.2	PpWAKL38	Prupe.5G223900.3	PpWAKL39	27
Prupe.6G137900.1	PpWAKL40	Prupe.6G138000.1	PpWAKL41	28
Prupe.6G142200.1	PpWAKL42	Prupe.6G142300.1	PpWAKL43	29
Prupe.6G142300.2	PpWAKL44	Prupe.6G261100.1	PpWAKL45	30
Prupe.6G352900.1	PpWAKL46	Prupe.6G352900.2	PpWAKL47	31
Prupe.6G358300.1	PpWAKL48	LOC112187187	RcWAK4	32
LOC112164997	RcWAK8	MDP0000304127	MdStb6-1	33
MDP0000635134	MdStb6-2	MDP0000198217	MdStb6-3	34
MDP0000319460	MdStb6-4	MDP0000148991	MdStb6-5	35
MDP0000258582	MdStb6-6	MDP0000198624	MdStb6-7	36
MDP0000277334	MdStb6-8	MDP0000282292	MdStb6-9	37
MDP0000272246	MdStb6-10	MDP0000169760	MdStb6-11	38
MDP0000193657	MdStb6-12	MDP0000152330	MdStb6-13	39
MDP0000147988	MdStb6-14	MDP0000190181	MdStb6-15	40
Zm00001d008458	ZmWAKL	Os09g38850	OsWAK91	41
Os09g38910	OsWAK92	Os10g10130	OsWAK112	42
Os02g42150	OsWAK14	Gh_A02G0727	GhWAK7A	43
OsXa4	KU761305	AT1G21250	AtWAK1	44
AT1G21270	AtWAK2	AT1G21240	AtWAK3	45
AT1G21210	AtWAK4	AT1G21230	AtWAK5	46
KY485204	TaStb6-17	MG256390.1	TaWAK6	47
Solyc02g068660.2.1	SIWAK1	Solyc07g007020.3.1	SIWAK2	48
Solyc09g014710.3.1	SIWAK3	Solyc09g014720.2.1	SIWAK4	49
Solyc09g014730.3.1	SIWAK5			50
				51
				52
				53
				54
				55
				56
				57
				58
				59
				60
				61
				62
				63
				64
				65
				66
				67
				68
				69
				70
				71

74 Table S3 Primers used in this study

75

76

77

78

79

80

81

82

83

84

85

86

87

88

89

90

91

92

93

94

95

96

97

98

99

100

101

102

103

104

105

106

107

108

109

Primer name	Primer sequence (5' - 3')
<b>Primers used for plasmid construct</b>	
MdStb6-5-GFP-F	gagaacacgggggactctagaATGACAATCTCTTTCTTCATCCTGTT
MdStb6-5-GFP-R	gcccttgctcaccatggatccTTCTAATTCGGAGATGACTGGTAACT
MdStb6-13-GFP-F	gagaacacgggggactctagaATGCCTAATCACCTATTCCTAACACTAC
MdStb6-13-GFP-R	gcccttgctcaccatggatccATCCAGAAAAGAACATGTAATTGATAACG
MdStb6-13-Flag-F	acgggggactctagaggatccATGCCTAATCACCTATTCCTAACACTAC
MdStb6-13-Flag-R	gtccttgtagtcagaaggcctATCCAGAAAAGAACATGTAATTGATAACG
<b>Primers used for quantitative real-time PCR</b>	
MdStb6-1-F	CTTCATCAGAAACCCAGCA
MdStb6-1-R	TTGGATGTAGAACGGGTGGC
MdStb6-2-F	CCTAAGCATCAGCTATCCG
MdStb6-2-R	TGGGTAGGCTTCTTCGTCGT
MdStb6-3-F	ACTTCGGTTCTTGCTGTGCC
MdStb6-3-R	AGAGGCACCCTCTCCCAA
MdStb6-4-F	CAAGCCTAGTGACCGTCCTG
MdStb6-4-R	GCGATGGTAAGCCAGCCTAT
MdStb6-5-F	TCCCTTGCCTTAGTGGGACT
MdStb6-5-R	CGGTACCGTTTTGCTTGCTT
MdStb6-6-F	GGGACGACATACGCATCCAT
MdStb6-6-R	CCTTACTGAACCAGCGGGG
MdStb6-7-F	GTGCTCTTGGCGTGTACTCT
MdStb6-7-R	GTGAAGGCCAGGATCGACAA
MdStb6-8-F	TCTGGCAACAATGTCAGCGT
MdStb6-8-R	TTTCCTCCTGCCTTGTGCAT
MdStb6-9-F	CCAGGCTTGTAGCACCTCAA
MdStb6-9-R	TGAGCTGGTTTATTCTCAACTCG
MdStb6-10-F	CAGCTGCCAAGATCACTGGA
MdStb6-10-R	CAAAGCCTCCTTGACCGAGT
MdStb6-11-F	ATTGGAGGGCCAAGTGATCG
MdStb6-11-R	CAGATCATGCCTGCTGACCA
MdStb6-12-F	CGTCCCCACAACCTGTTACGA
MdStb6-12-R	TCTTGGTTTGGACCCAGCTC
MdStb6-13-F	CTGACACGCCGGATAAGCTC
MdStb6-13-R	GATCACGAGGTCCATCACCG
MdActin-F	CGAAGCCATCATCAACTGCG
MdActin-R	GAACACGGGAACGCTGTCTA