### The transcription factor *StWRKY1* regulates secondary cell wall thickening metabolites in potato resistant to late blight

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Fig. S1. Phytophthora infestans infected potato stems with susceptible (Shepody) and resistant (F06025) genotypes, at 9 dpi.



Fig. S2. (A) The number of resistance related metabolites identified in stem of resistant potato genotype inoculated with water or *Phytophthora infestans*. Acronyms: RRC, resistance related constitutive; RRI, resistance related induced metabolites; (B) Resistance related (RR) metabolites identified in the resistant potato genotype, inoculated with mock-solution or *P. infestans* and their classification according to chemical groups.





















Fig. S3. In silico fragmentation of resistance related metabolites



Fig. S4. Laser scanning confocal micrographs of stem sections, exhibiting secondary cell wall thickening, due to hydroxycinnamic acid amides (HCAAs- blue fluorescence). RP is resistant genotype with *P. infestans* inoculation, RM is resistant genotype with mock inoculation, SP is susceptible genotype with *P. infestans* inoculation, SM is susceptible genotype with mock inoculation. Epi is epidermis, CP is cortical parenchyma.

|   | 1  | 10   | 20   | 30   | 40   | 50  | 60  | 70  | 80   | 90   | 100  | 110   | 120   | 130   |
|---|--|--|--|--|--|---|---|---|--|--|--|---|---|---|
| E06025-HRKY1  | CTTGG  | 6C68T-666  | 000000000000000000000000000000000000000  | CATECTCCCE   | CCGCCATGG  | CCGCGGGGATTO  | TEGETCARE   | гсөттөсөөт  | AGACACACTTI  | TAAGGTTTGA   | баватссава   | бтбааатбтб  | ттастатстт  | асалат  |
| Shepody-WRKY1   | CTTGG  | GCGATTGGG  | CCGACGTCG  | CATGCTCCCGG  | CCGCCATGG  | CCGCGGGATTO   | TGGGTCAAG   | FCATTACAAT  | AGACACACTT   | FAAGGTTTGA   | GAAATCCAAA   | GTGAAATGTG  | TTAGTATGTT  | GAGAAAT   |
| Consensus   | CTTGG  | GCGAT.GGG  | CCGACGTCG  | CATECTCCCGG  | ICCGCCATGG   | CCGCGGGATTO   | TGGGTCAAG   | ГСАТТАСААТ  | AGACACACTT   | FAAGGTTTGA   | GAAATCCAAAA  | GTGAAATGTG  | TTAGTATGTT  | GAGAAAT   |
|   | 131  | 140  | 150  | 160  | 170  | 180   | 190   | 200   | 210  | 220  | 230  | 240   | 250   | 260   |
| E06025-URKY1  | тесаа  | аттетостт  | антсанты   | татесатове   | aatttee  | TGTTAAGCAAA   | тестетвае   | сааттасат   | ассаттвасс   | ттастатса  | атесстара  | ттетевттат  | TECCETTTEE  | ATTTCA  |
| Shepody-WRKY1   | TGCAA  | ATTCTGCTT  | GAATCAATG  | CTATCCATGGC  | AATTTCAGG  | TGTTAAGCAAF   | TCCTCTGAC   | CCAATTGCAT  | ACCATTGACCO  | СТТАСТАТСА   | CATCCCTAGG   | TTCTCGTTAT  | TGCCATTTAA  | ATTTCCA   |
| Consensus   | TGCAAI   | ATTCTGCTT  | GAATCAATGO   | CTATCCATGGC  | AATTTCAGG  | TGTTAAGCAAA   | тсстстбас   | CCAATTGCAT  | ACCATTGACCO  | сттастатса   | CATCCCTAGG   | TTCTCGTTAT  | TGCCATTTAAI   | ATTTCaA   |
|   | 261  | 270  | 280  | 290  | 300  | 310   | 320   | 330   | 340  | 350  | 360  | 370   | 380   | 390   |
| E00096_00/V4  | тотот  | TTCOOCCOO  | тоотсоост  | тотогосооо   | оттосотос  | 0001000011  | оттессоте   | POOTCCCOCT  | ссоостстто   | осттосссто   |  | отессотесс  | TOCOCOTCOO  |   |
| Shepody-WRKY1   | TATAT  | r <mark>g</mark> caa <mark>a</mark> caa  | ATAATGAACI   | FATACACGAAA  | ATTAGA <mark>C</mark> AG   | AAGTCACATTI   | ATTCCCATG   | RAATCGGACT  | CCAACTCTTA   | AGTTAGGCTA   | AAATATTACI   | ATCCGATCCC  | TATACATCAA  | TTTCAA  |
| Consensus   | TATAT  | T <mark>g</mark> CAAaCAAI  | ATAATGAACI   | FATACACGAAA  | iattaga <mark>c</mark> ag  | AAGTCACATTI   | ATTCCCATG   | AAATC <mark>C</mark> GACT   | CCAACTCTTA   | AGTTAGGCTA   | A <mark>a</mark> ATATTACI  | ATCCGATCCC  | TA <mark>c</mark> acatcaa   | etttCaA   |
|   | 391  | 400  | 410  | 420  | 430  | 440   | 450   | 460   | 470  | 480  | 490  | 500   | 510   | 520   |
|   |  | CTTCOCTC:  | +  | CTOTCTOCCO   | +  |   |   | COTCOTCCT   | CICCOCTITI   |  | TOCCTOODT  |   |   |   |
| Shepody-WRKY1   | AGTGT  | CGTTGAGTG  | TATCATGA   | AGTATGTAGCA  | ACTGTAAAT  | GAGAAAGCTCC   | ATCGAGATC   | IGATGATGGT  | GTGGAGTTTT   | ATTTA <mark>G</mark> ATTGI   | STA <mark>A</mark> GTAAATI   | ACATGTCTAT  | AATTACCTTT  | ICTATAT   |
| Consensus   | AGTGT  | CGTTGAGTG  | TATCATGA   | AGTATGTAGCA  | AC <mark>a</mark> gtaaat   | GAGAAAaCTCC   | ATCGAGATC   | FGATGATGGT  | GTGGAGTTTT   | ATTTA <mark>g</mark> ATTG(   | GTA <mark>a</mark> GTAAATI   | ACATGTCTAT  | AATTACCTTT  | ICTATAT   |
|   |  |  |  |  |  |   |   |   |  |  |  |   |   |   |
|   | 521  | 530  | 540  | 550  | 560  | 570   | 580   | 590   | 600  | 610  | 620  | 630   | 640   | 650   |
| F06025-URKY1  | 521<br>  | 530<br><br>INTCTNTGT   | 540<br>+<br>IGCTC68861   | 550<br>+   | 560<br><br>ATCATCATG   | 570<br>+<br>TGTTGTGTCC1   | 580<br>+  | 590<br>   |  | 610<br>+   | 620<br>+<br>SACATCATTT   | 630<br>+<br>TTATAAGATA  | 640<br>   | 650<br> <br>ATTCTAT   |
| F06025-WRKY1<br>Shepody-WRKY1   | 521<br> <br>TATGA<br>TATGA   | 530<br>FATCTATGT<br>FATATATGT  | 540<br>FGCTCGAAGT<br>FGCTCGAAGT  | 550<br>FTTTAAAAGAT<br>FTTTAAAAGAT  | 560<br>ATCATCATG<br>ATCATCATG  | 570<br>TGTTGTATCC1<br>TGTTGTATCC1   | 580<br>TTAAAATCT<br>TTAAAATCT   | 590<br>+<br>ATGCATTTTT<br>ATGCATTTTT  | 600<br>TAGATCCGTCI<br>TAGATCCGTCI  | 610<br>ACATGACCGCI<br>ACATGACCGCI  | 620<br>GACATCATTT<br>GACATCATTT  | 630<br>TTATAAGATA<br>TTATAAGATA   | 640<br>CGAGCAATATI<br>CGAGCAATATI   | 650<br>I<br>ATTCTAT<br>ATTCTAT  |
| F06025-NRKY1<br>Shepody-NRKY1<br>Consensus  | 521<br> <br>TATGA<br>TATGA<br>TATGA  | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>TATATATGT  | 540<br>FGCTCGAAGT<br>FGCTCGAAGT<br>FGCTCGAAGT  | 550<br>FTTTAAAAGAT<br>FTTTAAAAGAT<br>FTTTAAAAAGAT  | ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG   | 570<br>TGTTGTATCC1<br>TGTTGTATCC1<br>TGTTGTATCC1  | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT  | 590<br>TGCATTTTT<br>TGCATTTTT<br>TGCATTTTT  | 600<br>TAGATCCGTCI<br>TAGATCCGTCI<br>TAGATCCGTCI   | 610<br>ACATGACCGCI<br>ACATGACCGCI<br>ACATGACCGCI   | 620<br>ACATCATTT<br>ACATCATTT<br>GACATCATTT  | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA   | 640<br>CGAGCAATATA<br>CGAGCAATATA<br>CGAGCAATATA  | 650<br>I<br>ATTCTAT<br>ATTCTAT<br>ATTCTAT   |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus  | 521<br> <br>TATGA<br>TATGA<br>TATGA<br>651   | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>G60  | 540<br>FGCTCGAAGT<br>FGCTCGAAGT<br>FGCTCGAAGT<br>670   | 550<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>680   | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690   | 570<br>TGTTGTATCCI<br>TGTTGTATCCI<br>TGTTGTATCCI<br>700   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710  | 590<br>TGCATTTT<br>TGCATTTTT<br>TGCATTTTT<br>TGCATTTTT<br>720   | 600<br>TAGATCCGTC<br>TAGATCCGTC<br>TAGATCCGTC<br>TAGATCCGTC<br>730   | 610<br>ACATGACCGCI<br>ACATGACCGCI<br>ACATGACCGCI<br>ACATGACCGCI<br>740   | 620<br>SACATCATTT<br>SACATCATTT<br>SACATCATTT<br>SACATCATTT<br>750   | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760  | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770  | 650<br>1<br>ATTCTAT<br>ATTCTAT<br>ATTCTAT<br>ATTCTAT<br>780   |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1  | 521<br>I<br>TATGA<br>TATGA<br>TATGA<br>651<br>I  | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>HAGTTCTAC   | 540<br>IGCTCGAAGT<br>IGCTCGAAGT<br>IGCTCGAAGT<br>670<br>GTGTGGAGT  | 550<br>ITTTAAAAGAT<br>ITTTAAAAAGAT<br>ITTTAAAAAGAT<br>680<br>IACTCCTTTAT   | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC   |   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>710<br>710<br>710  | 590<br>ATGCATTTTT<br>ATGCATTTTT<br>ATGCATTTTT<br>ATGCATTTTT<br>720<br>CAGTGCGGCC  | 600<br>TAGATCCGTCI<br>TAGATCCGTCI<br>TAGATCCGTCI<br>730<br>GCCTGCAGGTI   | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATGC   | 620<br>SACATCATTT<br>SACATCATTT<br>SACATCATTT<br>750<br>GGAGAGCTCCI  | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG  | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>GATGCATAGCI  | 650<br> <br>ATTCTAT<br>ATTCTAT<br>ATTCTAT<br>ATTCTAT<br>780<br>   |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1<br>Shepody-WRKY1   | 521<br> <br>TATGA<br>TATGA<br>TATGA<br>651<br> <br>GATACI<br>GATACI  | 530<br>FATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>AAGTTCTACI<br>AAGTTCTACI  | 540<br>IGCTCGAAGT<br>IGCTCGAAGT<br>IGCTCGAAGT<br>670<br>670<br>670<br>670<br>670<br>670<br>670<br>670<br>670<br>670  | 550<br>ITTTAAAAGAT<br>ITTTAAAAAGAT<br>ITTTAAAAAGAT<br>680<br>IACTCCTTTAT<br>IACTCCTTTAT  | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC  | 570<br>TGTTGTATCCT<br>TGTTGTATCCT<br>TGTTGTATCCT<br>700<br>700<br>TATAGTGCCCC<br>TATAGTGCCC   | 580<br>TTTAAAATCT<br>TTTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>  | 590<br>ATGCATTTTT<br>ATGCATTTTT<br>ATGCATTTTT<br>720<br>CAGTGCGGCC<br>CAGTGCGGCC  | 600<br>TAGATCCGTC<br>TAGATCCGTC<br>TAGATCCGTCI<br>730<br>GCCTGCAGGTI<br>GCCTGCAGGTI  | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATGA<br>CGACCATATGA   | 620<br>GACATCATTTT<br>GACATCATTTT<br>GACATCATTTT<br>GACATCATTTT<br>750<br>GAGAGAGCTCCI<br>GAGAGAGCTCCI   | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG<br>CAACGCGTTG                                    | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>GATGCATAGC<br>GATGCATAGC  | 650<br> <br>ATTCTAT<br>ATTCTAT<br>ATTCTAT<br> <br>TTGAGTA<br>ITGAGTA  |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1<br>Shepody-WRKY1<br>Consensus  | 521<br> <br>TATGA<br>TATGA<br>TATGA<br>651<br> <br>GATACI<br>GATACI<br>GATACI  | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>AAGTTCTAC<br>AAGTTCTAC  | 540<br>FGCTCGAAGT<br>FGCTCGAAGT<br>FGCTCGAAGT<br>670<br>GTGTGGAGT<br>GTGTGGAGT<br>GTGTGGAGT  | 550<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>680<br>FACTCCTTTAT<br>FACTCCTTTAT<br>FACTCCTTTAT  | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC  |   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>ATGCATTTTT<br>ATGCATTTTT<br>ATGCATTTTT<br>720<br>CAGTGCGGCC<br>CAGTGCGGCC<br>CAGTGCGGCC<br>CAGTGCGGCC                      | 600<br>TAGATCCGTCI<br>TAGATCCGTCI<br>TAGATCCGTCI<br>730<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>GCCTGCAGGTI   | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATGA<br>CGACCATATGG<br>CGACCATATGG<br>CGACCATATGG                                      | 620<br>SACATCATTT<br>SACATCATTT<br>SACATCATTT<br>SACATCATTT<br>750<br>SGAGAGCTCCI<br>SGAGAGCTCCI<br>SGAGAGCTCCI  | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG<br>CAACGCGTTG<br>CAACGCGTTG                                    | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>GATGCATAGC<br>GATGCATAGC<br>GATGCATAGC  | 650<br><br>ATTCTAT<br>ATTCTAT<br>ATTCTAT<br>TTCTAT<br>780<br><br>ITGAGTA<br>ITGAGTA<br>ITGAGTA  |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1<br>Shepody-WRKY1<br>Consensus  | 521<br>I<br>TATGA<br>TATGA<br>TATGA<br>651<br>I<br>GATACI<br>GATACI<br>781   | 530<br>IATCTATGT<br>IATATATGT<br>IATATATGT<br>660<br>ARGTTCTACI<br>ARGTTCTACI<br>790   | 540<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGGAG<br>800   | 550<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>680<br>680<br>TACTCCTTTAT<br>TACTCCTTTAT<br>TACTCCTTTAT<br>810  | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC<br>820  | 570<br>TGTTGTATCCT<br>TGTTGTATCCT<br>TGTTGTATCCT<br>700<br>700<br>TATAGTGCCC<br>TATAGTGCCC<br>830   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>TIGCATTTTT<br>TIGCATTTTT<br>TIGCATTTTT<br>TIGCATTTTT<br>720<br>CAGTGCGGCC<br>CAGTGCGGCC<br>CAGTGCGGCC<br>850               | 600<br>TAGATCCGTCI<br>TAGATCCGTCI<br>TAGATCCGTCI<br>730<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>860                               | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>740<br>CGACCATATG<br>CGACCATATG<br>CGACCATATG<br>CGACCATATG<br>870                            | 620<br>GACATCATTT<br>GACATCATTT<br>GACATCATTT<br>GACATCATTT<br>GAGAGAGCTCC<br>GAGAGAGCTCCI<br>GAGAGCTCCI<br>880  | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>TATAAGATA<br>760<br>760<br>CAACGCGTTG<br>CAACGCGTTG<br>CAACGCGTTG<br>890         | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>770<br>GATGCATAGC<br>GATGCATAGC<br>GATGCATAGC<br>900                              | 650<br><br>1<br>1TCTAT<br>1TCTAT<br>1TCTAT<br>780<br><br>780<br><br>1<br>TGAGTA<br>1TGAGTA<br>1TGAGTA<br>910  |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1  | 521<br>I<br>TATGAT<br>TATGAT<br>TATGA<br>651<br>I<br>GATACI<br>GATACI<br>GATACI<br>GATACI<br>781<br>I<br>TICTA   | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>ARGTTCTACI<br>ARGTTCTACI<br>790<br>TRGTGTCACI   | 540<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGGAG<br>FGCTGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FG | 550<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>680<br>FACTCCTTTAT<br>FACTCCTTTAT<br>FACTCCTTTAT<br>810<br>TTGGGGTAATC  | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC<br>820<br>ATGGTCATA   |   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>TIGCATTTTT<br>TIGCATTTTT<br>TIGCATTTTT<br>TIGCATTTTT<br>720<br>CAGTGCGGCC<br>CAGTGCGGCC<br>850<br>511A1CCGCT               | 600<br>TAGATCCGTCI<br>TAGATCCGTCI<br>730<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>860<br>CACABTTCCCC  | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATG<br>CGACCATATG<br>CGACCATATG<br>870<br>ACACATACGA                                   | 620<br>GACATCATTT<br>GACATCATTT<br>GACATCATTT<br>GACATCATTT<br>GAGAGAGCTCCI<br>GAGAGAGCTCCI<br>880<br>CCCGGAAGCCA                                      | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG<br>CAACGCGTTG<br>890<br>TAAGGTGTAAA                            | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>  | 650<br>   |
| F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1<br>Shepody-WRKY1<br>Consensus<br>F06025-WRKY1<br>Shepody-WRKY1                                   | 521<br>I<br>TATGA'<br>TATGA'<br>651<br>I<br>GATACI<br>GATACI<br>GATACI<br>781<br>I<br>TICTA<br>TTCTA   | 530<br>TRATCATGT<br>TATATATGT<br>TATATATGT<br>660<br>ARGTTCTACI<br>ARGTTCTACI<br>790<br>TRACTGTCACI<br>TAGTGTCACI  | 540<br>+   | 550<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>G80<br>FACTCCTTTAT<br>FACTCCTTTAT<br>FACTCCTTTAT<br>810<br>TTGGCGTAATC<br>TTGGCGTAATC   | 550<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC<br>820<br>ATGGTCATA<br>ATGGTCATA                                  |   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>TGCATTTTT<br>TGCATTTTT<br>TGCATTTTT<br>TGCATTTTT<br>720<br>CAGTGCGGCC<br>CAGTGCGGCC<br>850<br>GTTATCCGCT<br>STTATCCGCT     | 600<br>TAGATCCGTCI<br>TAGATCCGTCI<br>730<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>GCCTGCAGGTI<br>860<br>CACAATTCCCI  | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATG<br>CGACCATATG<br>CGACCATATG<br>870<br>ACACATACGAC                                  | 620<br>ACATCATTT<br>ACATCATTT<br>ACATCATTT<br>ACATCATTT<br>750<br>56AGAGCTCCI<br>56AGAGCTCCI<br>880<br>56CCGGAAGCA                                     | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG<br>CAACGCGTTG<br>CAACGCGTTG<br>890<br>TAAGTGTAAA<br>TAAGTGTAAA | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>  | 650<br>4TTCTAT<br>4TTCTAT<br>4TTCTAT<br>4TTCTAT<br>780<br>1<br>1TGAGTA<br>1TGAGTA<br>1TGAGTA<br>910<br>1<br>CCTAATG<br>CCTAATG  |
| F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus                      | 521<br>I<br>TATGA<br>TATGA<br>TATGA<br>TATGA<br>651<br>I<br>GATACI<br>GATACI<br>GATACI<br>GATACI<br>TICTA<br>TICTA   | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>ARGTTCTACI<br>ARGTTCTACI<br>790<br>TAGTGTCACI<br>TAGTGTCACI<br>TAGTGTCACI   | 540<br>+<br>TGCTCGAAG<br>TGCTCGAAG<br>TGCTCGAAG<br>TGCTCGAAG<br>570<br>570<br>570<br>570<br>570<br>570<br>570<br>570   | 550<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>680<br>FACTCCTTTAT<br>FACTCCTTTAT<br>RACTCCTTTAT<br>810<br>TTGGCGTAATC<br>TTGGCGTAATC<br>TTGGCGTAATC                      | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC<br>820<br>820<br>ATGGTCATA<br>ATGGTCATA                           |   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>720<br>740<br>740<br>740<br>740<br>740<br>740<br>740<br>74 | 590<br>   | 600<br>TAGATCCGTC/<br>TAGATCCGTC/<br>TAGATCCGTC/<br>730<br>GCCTGCAGGT/<br>GCCTGCAGGT/<br>GCCTGCAGGT/<br>860<br>CACAATTCCC/<br>CACAATTCCC/<br>CACAATTCCC/ | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATG<br>CGACCATATG<br>CGACCATATG<br>870<br>ACACATACGAC<br>ACACATACGAC                   | 620<br>ACATCATTT<br>ACATCATTT<br>ACATCATTT<br>ACATCATTT<br>560<br>560<br>560<br>560<br>560<br>560<br>560<br>560  |   | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>4<br>6<br>ATGCATAGCT<br>GATGCATAGCT<br>900<br>GCCTGGGGTGG<br>GCCTGGGGTGG<br>GCCTGGGGTGG          | 650<br>650<br>117<br>117<br>117<br>117<br>117<br>117<br>117<br>11   |
| F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus                      | 521<br>I<br>TATGA<br>TATGA<br>TATGA<br>TATGA<br>651<br>I<br>GATACI<br>GATACI<br>GATACI<br>GATACI<br>TATCA<br>TICTA<br>TICTA<br>TICTA<br>911                                    | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>ARGTTCTACI<br>ARGTTCTACI<br>790<br>TAGTGTCACI<br>TAGTGTCACI<br>790<br>TAGTGTCACI<br>920                                   | 540<br>+   | 550<br>TTTTAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>G80<br>TACTCCTTTAT<br>FACTCCTTTAT<br>RACTCCTTTAT<br>810<br>TTGGCGTAATC<br>TTGGCGTAATC<br>TTGGCGTAATC<br>TTGGCGTAATC<br>940 | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>TAGGTTATC<br>820<br>ATGGTCATA<br>ATGGTCATA<br>ATGGTCATA<br>ATGGTCATA<br>949 |   | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>   | 600<br>TAGATCCGTC/<br>TAGATCCGTC/<br>730<br>GCCTGCAGGT(<br>GCCTGCAGGT(<br>GCCTGCAGGT(<br>860<br>CACAATTCCC/<br>CACAATTCCC/<br>CACAATTCCC/                | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATGA<br>CGACCATATGA<br>CGACCATATGA<br>870<br>ACACATACGAA<br>ACACATACGAA<br>ACACATACGAA | 620<br>GACATCATTT<br>GACATCATTTT<br>GACATCATTTT<br>GACATCATTTT<br>750<br>GAGAGAGCTCCC<br>GAGAGCTCCC<br>880<br>500000000000000000000000000000000        |   | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATAGC<br>770<br>GATGCATAGCC<br>GATGCATAGCC<br>900<br>GCCTGGGGGTGG<br>GCCTGGGGGTGG<br>GCCTGGGGGTGG | 650<br>650<br>11777<br>17777<br>17777<br>17777<br>17777<br>17780<br>17680<br>17680<br>17680<br>17680<br>17680<br>17680<br>17680<br>17680<br>17680<br>17690<br>17690<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>177777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>177777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>17777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>177777<br>1777777<br>1777777<br>177777777 |
| F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus                      | 521<br>I<br>TATGA<br>TATGA<br>TATGA<br>TATGA<br>651<br>I<br>GATACI<br>GATACI<br>GATACI<br>781<br>I<br>TICTA<br>TICTA<br>TICTA<br>911<br>I                                      | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>AAGTTCTACI<br>AAGTTCTACI<br>790<br>TAGTGTCACI<br>TAGTGTCACI<br>1920   | 540<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGTGGAGAG<br>FGTGGAGAG<br>STGTGGAGAG<br>S00<br>CTAAATAGC<br>CTAAATAGC<br>CTAAATAGC<br>G30   | 550<br>TTTTAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>680<br>TACTCCTTTAT<br>ACTCCTTTAT<br>810<br>TTGGCGTAATC<br>TTGGCGTAATC<br>TTGGCGTAATC<br>940                                | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>820<br>ATGGTCATA<br>ATGGTCATA<br>ATGGTCATA<br>ATGGTCATA<br>949<br>949       | 570<br>TGTTGTATCCT<br>TGTTGTATCCT<br>TGTTGTATCCT<br>TGTTGTATCCT<br>700<br>TATAGTGCCCCT<br>TATAGTGCCC<br>830<br>GCTGTTTCCTC<br>GCTGTTTCCTC | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>TIGCATTTTT<br>TIGCATTTTT<br>TIGCATTTTT<br>720<br>CAGTGCGGCC<br>CAGTGCGGCC<br>850<br>GTTATCCGCT<br>GTTATCCGCT<br>GTTATCCGCT | 600<br>TAGATCCGTC/<br>TAGATCCGTC/<br>730<br>GCCTGCAGGT(<br>GCCTGCAGGT(<br>GCCTGCAGGT(<br>860<br>CACAATTCCC/<br>CACAATTCCC/<br>CACAATTCCC/                | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATGA<br>CGACCATATGA<br>CGACCATATGA<br>870<br>ACACATACGAA<br>ACACATACGAA<br>ACACATACGAA | 620<br>GACATCATTTT<br>GACATCATTTT<br>GACATCATTTT<br>GACAACATTTT<br>750<br>GAGAGAGCTCCC<br>GAGAGCTCCCC<br>880<br>GCCGGAAGCA<br>GCCGGAAGCA<br>GCCGGAAGCA | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG<br>CAACGCGTTG<br>890<br>TAAGTGTAAA<br>TAAGTGTAAA<br>TAAGTGTAAA | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>GATGCATAGCT<br>GATGCATAGCT<br>GATGCATAGCT<br>900<br>GCCTGGGGTGG<br>GCCTGGGGTGG<br>GCCTGGGGTGG    | 650<br>650<br>117777<br>117777<br>117777<br>117777<br>117777<br>117777<br>1176878<br>1168678<br>1168678<br>910<br>1<br>2078876<br>910<br>1<br>2078876<br>2078876<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>2078776<br>207877777<br>2078776<br>2078777777<br>20787777777777<br>207877777777777777777777777777777777777  |
| F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Consensus<br>F06025-HRKY1<br>Shepody-HRKY1<br>Shepody-HRKY1<br>Shepody-HRKY1 | 521<br>I<br>TATGA<br>TATGA<br>TATGA<br>TATGA<br>651<br>I<br>GATACI<br>GATACI<br>GATACI<br>GATACI<br>GATACI<br>TTCTA<br>TTCTA<br>TTCTA<br>TTCTA<br>911<br>I<br>AGTGAU<br>AGTGAU | 530<br>TATCTATGT<br>TATATATGT<br>TATATATGT<br>660<br>AAGTTCTACI<br>AAGTTCTACI<br>790<br>TAGTGTCACI<br>TAGTGTCACI<br>1920<br>500<br>500<br>500<br>500<br>500<br>500<br>500<br>5 | 540<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGCTCGAAG<br>FGTGGAGAG<br>FGTGGAGAG<br>TGTGGAGAG<br>800<br>CTAAATAGC<br>CTAAATAGC<br>930<br>CATTAATTGC   | 550<br>TTTTAAAAGAT<br>TTTTAAAAAGAT<br>TTTTAAAAAGAT<br>G80<br>TACTCCTTTAT<br>ACTCCTTTAT<br>810<br>TTGGCGTAATC<br>TTGGCGTAATC<br>TTGGCGTAATC<br>940<br>CGTTGCGCTCC                 | 560<br>ATCATCATG<br>ATCATCATG<br>ATCATCATG<br>690<br>TAGGTTATC<br>TAGGTTATC<br>820<br>ATGGTCATA<br>ATGGTCATA<br>ATGGTCATA<br>ATGGTCATA<br>949<br>          | 570<br>TGTTGTATCCT<br>TGTTGTATCCT<br>TGTTGTATCCT<br>700<br>TATAGTGCCCCC<br>TATAGTGCCC<br>830<br>GCTGTTTCCTC<br>GCTGTTTCCTC                | 580<br>TTAAAATCT<br>TTAAAATCT<br>TTAAAATCT<br>710<br>   | 590<br>   | 600<br>TAGATCCGTC/<br>TAGATCCGTC/<br>730<br>GCCTGCAGGT(<br>GCCTGCAGGT(<br>GCCTGCAGGT(<br>860<br>CACAATTCCC/<br>CACAATTCCC/<br>CACAATTCCC/                | 610<br>ACATGACCGCC<br>ACATGACCGCC<br>ACATGACCGCC<br>740<br>CGACCATATGA<br>CGACCATATGA<br>CGACCATATGA<br>870<br>ACACATACGAA<br>ACACATACGAA<br>ACACATACGAA | 620<br>GACATCATTT<br>GACATCATTTT<br>GACATCATTTT<br>750<br>GAGAGAGCTCCC<br>GAGAGCTCCC<br>880<br>GCCGGAAGCA<br>GCCGGAAGCA<br>GCCGGAAGCA                  | 630<br>TTATAAGATA<br>TTATAAGATA<br>TTATAAGATA<br>760<br>CAACGCGTTG<br>CAACGCGTTG<br>890<br>TAAGTGTAAA<br>TAAGTGTAAA<br>TAAGTGTAAA | 640<br>CGAGCAATATI<br>CGAGCAATATI<br>CGAGCAATATI<br>770<br>GATGCATAGCT<br>GATGCATAGCT<br>GATGCATAGCT<br>900<br>GCCTGGGGTGG<br>GCCTGGGGTGG<br>GCCTGGGGTGG    | 650<br>650<br>11TCTAT<br>1TCTAT<br>1TCTAT<br>780<br>780<br>780<br>11GAGTA<br>11GAGTA<br>11GAGTA<br>910<br>910<br>0<br>1<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0<br>0   |





Fig. S6. (A) Analysis of purified recombinant StWRKY1 protein on 12% Sodium dodecyl sulphate-Polyacrylamide gel electrophoresis. StWRKY1 was cloned in pTrc HisB vector (Invitrogen, USA), overexpressed in *Escherichia coli* BL21 cells and was purified by affinity chromatography using nickel NTA as matrix. Different protein fraction were loaded and electrophoresed in 12% SDS-polyacrylamide gel and were stained with Sigma EZBlue<sup>TM</sup> Gel Staining Reagent (Sigma, USA). M, Precision plus Protein<sup>TM</sup> Prestained Marker (Biorad, Canada); E1 to E7 represent various eluted protein fractions. (B) Electrophoretic mobility gel shift assay (EMSA) showing DNA-protein interaction of THT promoter with StWRKY1. The position of the specifically retarded DNA/protein complex (THT-WRKY1) and that of the free probe (U) is also shown on the right side of the panel with an arrow mark.



Fig. S7. (A) Schematic representation of tobacco rattle virus (TRV) based virus induced gene silencing (VIGS) vectors. TRV cDNA clones were placed in between the duplicated cauliflower mosaic virus (CaMV) 35S promoter (2 X 35S) and the nopaline synthase terminator (NOS) in a T-DNA vector. LB and RB refer to left and right borders of T-DNA. Rz, self-cleaving ribozyme. (b) Silencing of the phytoene desaturase (PDS) gene. Infection of recombinant TRV carrying the PDS sequence silences endogenous PDS in potato plants and causes inhibition of carotenoid biosynthesis resulting in the photobleaching phenotype.

## Table S1. Primer sequences used for quantifying resistance related gene expression in potato genotypes

| Genbank name                      | Gene<br>name        | Forward primer (5'-3')         | Reverse primer (5'-3')            |
|-----------------------------------|---------------------|--------------------------------|-----------------------------------|
| A. Biomass quantification         |                     |                                |                                   |
| GQ371195.1                        | O-8                 | GAAAGGCATAGAAGGTAGA            | TAACCGACCAAGTAGTAAA               |
| AB061263.1                        | StEf1-α             | ATTGGAAACGGATATGCTCCA          | TCCTTACCTGAACGCCTGTCA             |
| Z33382.1                          | b-tubulin           | ATGTTCAGGCGCAAGGCTT            | TCTGCAACCGGGTCATTCAT              |
| B. qRT-PCR primers                |                     |                                |                                   |
| AF150686.1                        | St4CL               | ATCCTGAGGCCACAGCTAGA           | TTACGGGACAACAGCAGCAT              |
| JX896425.1                        | StTHT               | TGTTGTTGTCAGCTGTGGCT           | TTTGCAAAGGCTTGAAGGGC              |
| PGSC0003DMT400038501 <sup>a</sup> | SpTyDC              | AGTGGTGGTGGAGGTGTACT           | AGGTCCCAGATAGGGTCGTT              |
| AJ278507.1                        | StWRKY1             | GAGGAAATATGGACAAAAGGCTG        | TTTGTCAATGGGATGTGAATGC            |
| AB061263.1                        | StEf1-α             | ATTGGAAACGGATATGCTCCA          | TCCTTACCTGAACGCCTGTCA             |
| Z33382.1                          | b-tubulin           | ATGTTCAGGCGCAAGGCTT            | TCTGCAACCGGGTCATTCAT              |
| C. Primers for sequencing         | g                   |                                |                                   |
| AJ278507.1                        | StWRKY1             | TCTAAAATGGAGAATTATGCAACAA      | TTAAAAGGAAGTATAGATTTGCATCTGA      |
| PGSC0003DMT400069966 <sup>a</sup> | StWRKY1<br>promoter | CTGGGTCAAGTCATTACAATAGA        | TTTCTTCATGGGGCACTATAGA            |
| D. Primers for BiFC assag         | y                   |                                |                                   |
| AJ278507.1                        | StWRKY              | GTCGACATGGAGAATTATGCAACAAT     | GAATTCAAAGGAAGTATAGATTTGCA        |
| AB091780.1                        | StMEK1              |                                |                                   |
| E. Primers for LUC assay          |                     |                                |                                   |
| AF150686.1                        | St4CL               | CTCGAGGAGTGTCAATTTTGACCAATTTTT | GGATCCATCTGGGCATCTTGAGAGCTAA      |
| JX896425.1                        | StTHT               | CTCGAGTCATCGCCCACAAGTTATGA     | GGATCCGGGAAAGTATTTAGTTAAATTTGGAGA |
| PGSC0003DMT400038501 <sup>a</sup> | SpTyDC              | CTCGAG CCCACCCCTATCGCCTAT      | GGATCCTTTCAATTTGTGTGTGTATGTTGTCTT |

<sup>a</sup> Solanaceae Genomics Resource, Michigan State University, USA.

| Observe<br>d mass<br>(Da) | Exact<br>mass (Da) | RT<br>(Min) | AME<br>(ppm) | Metabolite names                                | Observed<br>fragmentation                        | Database<br>fragmentation                              | Database ID               |
|---------------------------|--------------------|-------------|--------------|---|--|--|---------------------------|
| A. Ph                     | enylpropano        | ids         |              |   |  |  |                           |
| 148.0530                  | 148.0524           | 2.83        | 1.60         | trans-Cinnamic acid                             | <b>148.20,</b> 104.05, <b>103.30</b> , 91.48     | <b>147.0, 103.05</b> , 101.04, 77.04                   | C00423                    |
| 162.0320                  | 162.0316           | 2.50        | 2.14         | 4-hydroxycoumarin                               | <b>161.02,</b> 131.06, <b>116.54</b>             | <b>161.02, 117.03</b> , 41.00                          | CPD-12111                 |
| 165.0793                  | 165.0790           | 1.62        | 2.15         | L-Phenylalanine                                 | 163.90,149.05,147.12,<br>120.22, 72.05           | <b>163.9, 148.8, 147.2</b> , 146.5, <b>120.1, 71.9</b> | PHE                       |
| 166.0622                  | 166.0620           | 1 909       | 0.95         | Dihydro-3-coumaric                              | <b>150.14, 149.01,</b> 123.14,                   | <b>149.00</b> , 121.06, 119.05,                        | CPD-12218                 |
| 100.0033                  | 100.0030           | 1.898       | 9.85         |   | 95.14  | 100.04   | 000402                    |
| 1/4.0533                  | 174.0528           | 18.61       | 2.90         | Shikimate                                       | 175.32, <b>157.11</b> ,132.94,<br>131.05         | 157.05,17.00   | C00493<br>In silico       |
| 181.0742                  | 181.0739           | 0.72        | 1.88         | α-amino oxy-<br>β-phenyl<br>propionate          | 163.19, 136.16, 119.16,<br>93.09                 | 162.05, 135.04, 120.04,<br>119.04, 93.03               | CPD-7021                  |
| 192.0273                  | 192.0270           | 0.44        | 1.48         | Citrate   | 155.15, 148.12, 129.20,<br>111.00                | 154.60, 148.20, 129.20,<br>111.10                      | CIT                       |
| 192.0637                  | 192.0634           | 5.83        | 1.50         | Quinate   | 191.07,173.07,171.08,12<br>6.98, 111.03,92.99    | 191.3, 173.4, 170.8,<br>127.0, 111.4, 93.0             | C00296                    |
| 194.0585                  | 194.0579           | 4.40        | 2.89         | Ferulic acid                                    | 193.22, <b>178.34</b> ,175.10,<br>173.13,        | <b>178.02</b> ,134.03,133.02                           | METLIN                    |
| 208.0552                  | 208.0558           | 23.47       | 2.71         | Methyl 5-(1-Propynyl)-<br>2-thiophenepropanoate | 179.14, <b>149.30</b>                            | 177.03, <b>149.04</b>                                  | 90185-Metlin<br>In silico |
| 264.1472                  | 264.1474           | 10.54       | 0.73         | Feruloylputrescine                              | 249.19, 248.28, 247.42                           | 249.12, 248.12, 247.14                                 | In silico                 |
| 300.0844                  | 300.0845           | 1.21        | 0.43         | Salicylate β-D-<br>glucose ester                | 217.05, 201.30, 161.33,<br><b>137.11</b> , 93.08 | 179.26, <b>137.15</b>                                  | CPD-12629                 |

## Table S2. Resistance related detected in resistant potato genotype following *P. infestans* or mock-solution inoculation

|          |             | 12.35 | 0.64 | Feruloylagmatine         | 100 12 162 15 140 10            | 280 14 262 13 177 05                    | CPD-12236         |
|----------|-------------|-------|------|--------------------------|---------------------------------|---|-------------------|
|          |             |       |      |                          | 200.23, <b>203.25</b> , 240.20, | 289.14, <b>203.13</b> , 177.03,         | (Gunnaiah et al., |
| 306.1690 | 306.1692    |       |      |                          | 149.12, 154.15                  | 149.00                                  | 2012)             |
| 313.1317 | 313.1314    | 17.25 | 0.86 | N-Feruloyltyramine       | <b>178.13,</b> 177.12, 166.15,  | <b>178.0</b> ,122,138                   | C02717            |
|          |             |       |      |                          | 148.24,                         |   | (Yogendra et al., |
|          |             |       |      |                          |                                 |   | 2015)             |
| 329.1271 | 329.1263    | 15.18 | 2.45 | N-Feruloyloctopamine     | 328.37, <b>313.76,312.43</b> ,  | 314.10, 312.12                          | METLIN            |
|          |             |       |      |                          | 269.20,                         |   | (Yogendra et al., |
|          |             |       |      |                          |                                 |   | 2015)             |
| 342.0946 | 342.0951    | 8.26  | 1.45 | Caffeic acid 3-glucoside | 323.30, 273.19, 177.20,         | 325.09, 271.08, 179.03,                 | C10431            |
|          |             |       |      |                          | 163.35                          | 163.06                                  | In silico         |
| 354.0958 | 354.0951    | 6.76  | 1.86 | Scopolin                 | 330.99,192.05, <b>191.08</b> ,  | 339.07, <b>191.03</b> , 163.06          | C01527            |
|          |             |       |      |                          | 178.96,                         |   | (Yogendra et al., |
|          |             |       |      |                          |                                 |   | 2015)             |
| 368.1115 | 368.1107    | 8.58  | 2.11 | 5-O-Feruloylquinic acid  | 351.90, <b>193.13</b> ,191.05   | 353.08, 351.10, <b>193.05</b> ,         | C02572            |
|          |             |       |      |                          |                                 | 175.06                                  |                   |
| 386.1215 | 386.1213    | 3.23  | 0.50 | 1-O-Sinapoyl-beta-D-     | 247.23, 223.04, 205.19          | 247.06, 223.06, 205.04                  | C01175            |
|          |             |       |      | glucose                  |                                 |   |                   |
| 582.1941 | 582.1949    | 14.24 | 1.32 | 10-Acetoxyligustroside   | 566.58, 401.35                  | 565.19, 403.12, 179.07                  | 90532-Metlin      |
|          |             |       |      |                          |                                 |   | In silico         |
| 592.1790 | 592.1792    | 13.90 | 0.32 | 1,2-di-O-sinapoyl-       | 429.23, <b>385.18</b> , 367.15, | <b>385.11</b> , 369.11, <b>223.06</b> , | 12-BIS-O-         |
|          |             |       |      | β-D-glucose              | 323.07, <b>223.16</b> , 205.15  | 207.06                                  | SINAPOYL-         |
|          |             |       |      |                          |                                 |   | BETA-D-           |
|          |             |       |      |                          |                                 |   | GLUCOSIDE         |
| B. Sp    | hingolipids |       |      |                          |                                 |   |                   |
| 479.4357 | 479.4338    | 30.83 | 3.87 | Cer(d14:2(4E,6E)/16:0)   | <b>448.38, 253.14,</b> 252.13,  | 448.41, 254.24, 225.18                  | LMSP02010051      |
|          |             |       |      |                          | 224.10                          |   | In silico         |
| 537.5138 | 537.5121    | 23.48 | 3.10 | Cer(d18:1/16:0)          | <b>521.97, 507.34,</b> 388.72,  | <b>520.50, 506.49,</b> 283.26,          | LMSP02010004      |
|          |             |       |      |                          | 253.01                          | 254.24                                  | In silico         |

| 595.5880 | 595.5903    | 36.05   | 3.86 | Cer(d18:0/20:0)          | <b>580.16,</b> 578.49, <b>564.21,</b> | <b>580.56, 564.57,</b> 310.31,  | LMSP02020009 |
|----------|-------------|---------|------|--------------------------|---------------------------------------|---------------------------------|--------------|
|          |             |         |      |                          | 285.06                                | 285.27                          | In silico    |
|          |             | 30.81   | 0.79 | GlcCer(d15:2(4E,6E)/1    | 682.61, 489.90, 400.55,               | 682.52, 490.46, 401.25,         | LMSP0501AA58 |
| 683.5331 | 683.5336    |         |      | 8:0)                     | 286.15                                | 282.27                          | In silico    |
| 711.5643 | 711.5649    | 30.11   | 0.89 | GlcCer(d15:2(4E,6E)/2    | 354.64, 353.01, <b>310.94</b>         | 401.25, <b>310.31</b>           | LMSP0501AA59 |
|          |             |         |      | 0:0)                     |                                       |                                 |              |
| 851.5776 | 851.5793    | 23.52   | 2.04 | (3'-sulfo)Galbeta-       | 704.41, 522.05, <b>325.41</b>         | 525.27, <b>326.30</b>           | LMSP06020005 |
|          |             |         |      | Cer(d18:0/20:0(2OH))     |                                       |                                 | In silico    |
|          |             |         |      |                          |                                       |                                 |              |
|          |             |         |      |                          |                                       |                                 |              |
| C. Gl    | ycerophosph | olipids |      |                          |                                       |                                 |              |
|          |             | 23.46   | 4.37 | 1-(9Z-nonadecenoyl)-     | 536.21, 520.84,                       | 536.29, 522.28, 339.28,         | LMGP03050019 |
| 537.3090 | 537.3067    |         |      | glycero-3-phosphoserine  | 339.37, 197.29                        | 198.01                          |              |
| 537.3790 | 537.3794    | 23.48   | 0.82 | 1-hexadecyl-2-propionyl- | 455.12, <b>354.30</b> ,               | 522.35, 464.35, <b>355.32</b> , | LMGP01020068 |
|          |             |         |      | sn-glycero-3-            | 182.98                                | 182.05                          |              |
|          |             |         |      | phosphocholine           |                                       |                                 |              |
| 537.4151 | 537.4158    | 23.48   | 1.36 | 1-octadecyl-2-ethyl-sn-  | <b>493.57,</b> 455.12                 | 492.38                          | LMGP01040053 |
|          |             |         |      | glycero-3-phosphocholine | e                                     |                                 |              |

AME: Accurate Mass Error= ((Observed mass - expected mass) / expected mass) X 10<sup>6</sup>, RT: Retention time

**Database ID examples**: Number-METLIN, LMP-LIPIDMAPS, KEGG-C05610, KNAPSACK- C00002775, HMDB-HMDB33026, and PMN-Plant Metabolic Network, *In silico*: In silico fragmentation

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## Table S3. Promoter analysis of resistance related gene in resistant potato genotype

| 4-CL promoter                | THT promoter                          | TYDC promoter                 | HCT promoter                 |
|------------------------------|---------------------------------------|-------------------------------|------------------------------|
| 4cl-CMA2a: light             | 3-AF1 binding site: light responsive  | ABRE: cis-acting element      | 3-AF3 binding site: light    |
| responsive element           | element                               | involved in the abscisic acid | responsive element           |
|                              |                                       | responsiveness                |                              |
| 4cl-CMA2b: light             | ACE: cis-acting element involved in   | ARE: cis-acting regulatory    | AACA_motif: involved in      |
| responsive element           | light responsiveness                  | element essential for the     | endosperm-specific negative  |
|                              |                                       | anaerobic induction           | expression                   |
| AC-I: negative regulation of | AE-box: part of a module for light    | Box I: light responsive       | AC-I: negative regulation of |
| phloem expression            | response                              | element                       | phloem expression            |
| AC-II: enhanced xylem        | ARE: cis-acting regulatory element    | Box 4: light responsive       | ACE: cis-acting element      |
| expression and repressed     | essential for the anaerobic induction | element                       | involved in light            |
| phloem                       |                                       |                               | responsiveness               |
| Box-W1: WRKY1 protein        | Box-W1: WRKY1 protein                 | Box-W1: WRKY1 protein         | ARE: cis-acting regulatory   |
| binding site                 | binding site                          | binding site                  | element essential for the    |
|                              |                                       |                               | anaerobic induction          |
| CAAT-box: common cis-        | Box I: light responsive element       | CAAT-box: common cis-         | Box I: light responsive      |
| acting element in promoter   |                                       | acting element in promoter    | element                      |
| and enhancer regions         |                                       | and enhancer regions          |                              |
| GA-motif: part of a light    | CAAT-box: common cis-acting           | CGTCA-motif: cis-acting       | CAAT-box: common cis-        |
| responsive element           | element in promoter and enhancer      | regulatory element involved   | acting element in promoter   |
|                              | regions                               | in the MeJA-responsiveness    | and enhancer regions         |
| L-box: part of a light       | CGTCA-motif: cis-acting regulatory    | ERE: ethylene-responsive      | ERE: ethylene-responsive     |
| responsive element           | element involved in the MeJA-         | element                       | element                      |
|                              | responsiveness                        |                               |                              |

| OBP-1 site: cis-acting      | ELI-box3: elicitor-responsive       | G-Box: cis-acting regulatory | G-Box: cis-acting regulatory  |
|-----------------------------|-------------------------------------|------------------------------|-------------------------------|
| regulatory element          | element                             | element involved in light    | element involved in light     |
|                             |                                     | responsiveness               | responsiveness                |
| TATA-box: core promoter     | GCN4_motif: cis-regulatory          | GARE-motif: gibberellin-     | GARE-motif: gibberellin-      |
| element around -30 of       | element involved in endosperm       | responsive element           | responsive element            |
| transcription start         | expression                          |                              |                               |
| TC-rich repeats: cis-acting | HSE: cis-acting element involved    | HSE: cis-acting element      | HSE: cis-acting element       |
| element involved in defense | in heat stress responsiveness       | involved in heat stress      | involved in heat stress       |
| and stress responsiveness   |                                     | responsiveness               | responsiveness                |
| TCA-element: cis-acting     | MBS: MYB binding site involved in   | Skn-1_motif: cis-acting      | MBS: MYB binding site         |
| element involved in SA      | drought-inducibility                | regulatory element required  | involved in drought-          |
| responsiveness              |                                     | for endosperm expression     | inducibility                  |
| TCT-motif: part of a light  | Skn-1_motif: cis-acting regulatory  | TATA-box: core promoter      | Skn-1_motif: cis-acting       |
| responsive element          | element required for endosperm      | element around -30 of        | regulatory element required   |
|                             | expression                          | transcription start          | for endosperm expression      |
| Unnamed4                    | TATA-box: core promoter element     | TCA-element: cis-acting      | TATA-box: core promoter       |
|                             | around -30 of transcription start   | element involved in SA       | element around -30 of         |
|                             |                                     | responsiveness               | transcription start           |
| W box: Binds WRKY type      | W box: Binds WRKY type              | W box: Binds WRKY type       | TC-rich repeats: cis-acting   |
| transcription factors       | transcription factors               | transcription factors        | element involved in defense   |
|                             |                                     |                              | and stress responsiveness     |
| chs-Unit 1 m1: part of a    | TC-rich repeats: cis-acting element | chs-CMA1a: part of a light   | as-2-box: involved in shoot-  |
| light responsive element    | involved in defense and stress      | responsive element           | specific expression and light |
|                             | responsiveness                      |                              | responsiveness                |
| Circadian: cis-acting       | Circadian: cis-acting regulatory    | Circadian: cis-acting        | Circadian: cis-acting         |
| regulatory element involved | element involved in circadian       | regulatory element involved  | regulatory element involved   |
| in circadian control        | control                             | in circadian control         | in circadian control          |

# Table S4. Promoter analysis of *StWRKY1* gene in resistant and susceptible potato genotypes

| F06025 WRKY1 promoter                        | Shepody WRKY1 promoter                       |
|--|--|
| ABRE: involved in the abscisic acid          | ABRE: involved in the abscisic acid          |
| responsiveness                               | responsiveness                               |
| ATC-motif: conserved DNA module involved     | ATC-motif: conserved DNA module involved     |
| in light responsiveness                      | in light responsiveness                      |
| Box 4: conserved DNA module involved in      | Box 4: conserved DNA module involved in      |
| light responsiveness                         | light responsiveness                         |
| -  | Box I (TTTCAAA): light responsive element    |
| Box II: part of a light responsive element   | Box II: part of a light responsive element   |
| -  | Box III (CATTTACACT ): protein binding       |
|  | site   |
| Box-W1: WRKY1 protein binding site           | Box-W1: WRKY1 protein binding site           |
| CAAT-box: cis-acting element in promoter     | CAAT-box: cis-acting element in promoter     |
| and enhancer regions                         | and enhancer regions                         |
| CGTCA-motif: cis-acting regulatory element   | CGTCA-motif: cis-acting regulatory element   |
| involved in the MeJA-responsiveness          | involved in the MeJA-responsiveness          |
| G-Box: cis-acting regulatory element         | G-Box: cis-acting regulatory element         |
| involved in light responsiveness             | involved in light responsiveness             |
| G-Box: cis-acting regulatory element         | G-Box: cis-acting regulatory element         |
| involved in light responsiveness             | involved in light responsiveness             |
| GA-motif: part of a light responsive element | GA-motif: part of a light responsive element |
| HSE (AGAAAATTCG): cis-acting element         | -  |
| involved in heat stress responsiveness       |  |
| I-box: part of a light responsive element    | I-box: part of a light responsive element    |
| MBS: MYB Binding Site                        | MBS: MYB Binding Site                        |
| MNF1: light responsive element               | MNF1: light responsive element               |
| MRE: MYB binding site involved in light      | MRE: MYB binding site involved in light      |
| responsiveness                               | responsiveness                               |
| O2-site: cis-acting regulatory element       | O2-site: cis-acting regulatory element       |
| involved in zein metabolism regulation       | involved in zein metabolism regulation       |
| Skn-1_motif: cis-acting regulatory element   | Skn-1_motif: cis-acting regulatory element   |
| required for endosperm expression            | required for endosperm expression            |
| TATA-box                                     | TATA-box                                     |
| TATCCAT/C-motif:                             | TATCCAT/C-motif:                             |
| TC-rich repeats: cis-acting element involved | TC-rich repeats: cis-acting element involved |
| in defense and stress responsiveness         | in defense and stress responsiveness         |
| TGA-element: auxin-responsive element        | TGA-element: auxin-responsive element        |

| TGACG-motif: cis-acting regulatory element | TGACG-motif: cis-acting regulatory element |
|--|--|
| involved in the MeJA-responsiveness        | involved in the MeJA-responsiveness        |
| Unnamed4                                   | Unnamed4                                   |
| Unnamed5                                   | Unnamed5                                   |
| W box: WRKY binding site                   | W box: WRKY binding site                   |
| Circadian: is-acting regulatory element    | Circadian: is-acting regulatory element    |
| involved in circadian control              | involved in circadian control              |

Table S5. The differentially expressed heat shock proteins (HSPs) detected in potato following *P. infestans* inoculation using RNA-seq analysis

|                         |                      |            | FPKM    | FPKM<br>Russet | log2          |                      |                     |
|-------------------------|----------------------|------------|---------|----------------|---------------|----------------------|---------------------|
| Gene name               | PGSC ID <sup>a</sup> | Chromosome | F06025  | Burbank        | (fold change) | P value              | Q value             |
| Prefoldin chaperone     |                      |            |         |                |               |                      |                     |
| subunit family protein  | PGSC0003DMG400001646 | 1          | 13.6312 | 3.48311        | 1.96847       | 0.000932             | 0.032868            |
| Heat shock protein 17.8 | PGSC0003DMG400019137 | 10         | 17.8939 | 0.235663       | 6.2466        | 4.88E <sup>-12</sup> | 2.7E <sup>-09</sup> |
| HSP26.5                 |                      |            |         |                |               |                      |                     |
| (26.5 kDa heat shock    |                      |            |         |                |               |                      |                     |
| protein, mitochondrial) | PGSC0003DMG400028624 | 12         | 2.16571 | 0.245899       | 3.1387        | 0.000958             | 0.033606            |

<sup>a</sup> Solanaceae Genomics Resource, Michigan State University, USA.

FPKM, Fragments per kilo base of exon per million fragments mapped; Q value, the false discovery rate (FDR)-adjusted p-value of the test statistic.

F06025- Resistant potato genotype, Russet Burbank- Susceptible potato genotype.

Cufflinks-2.0.1 program was used to find significant changes in transcript expression.