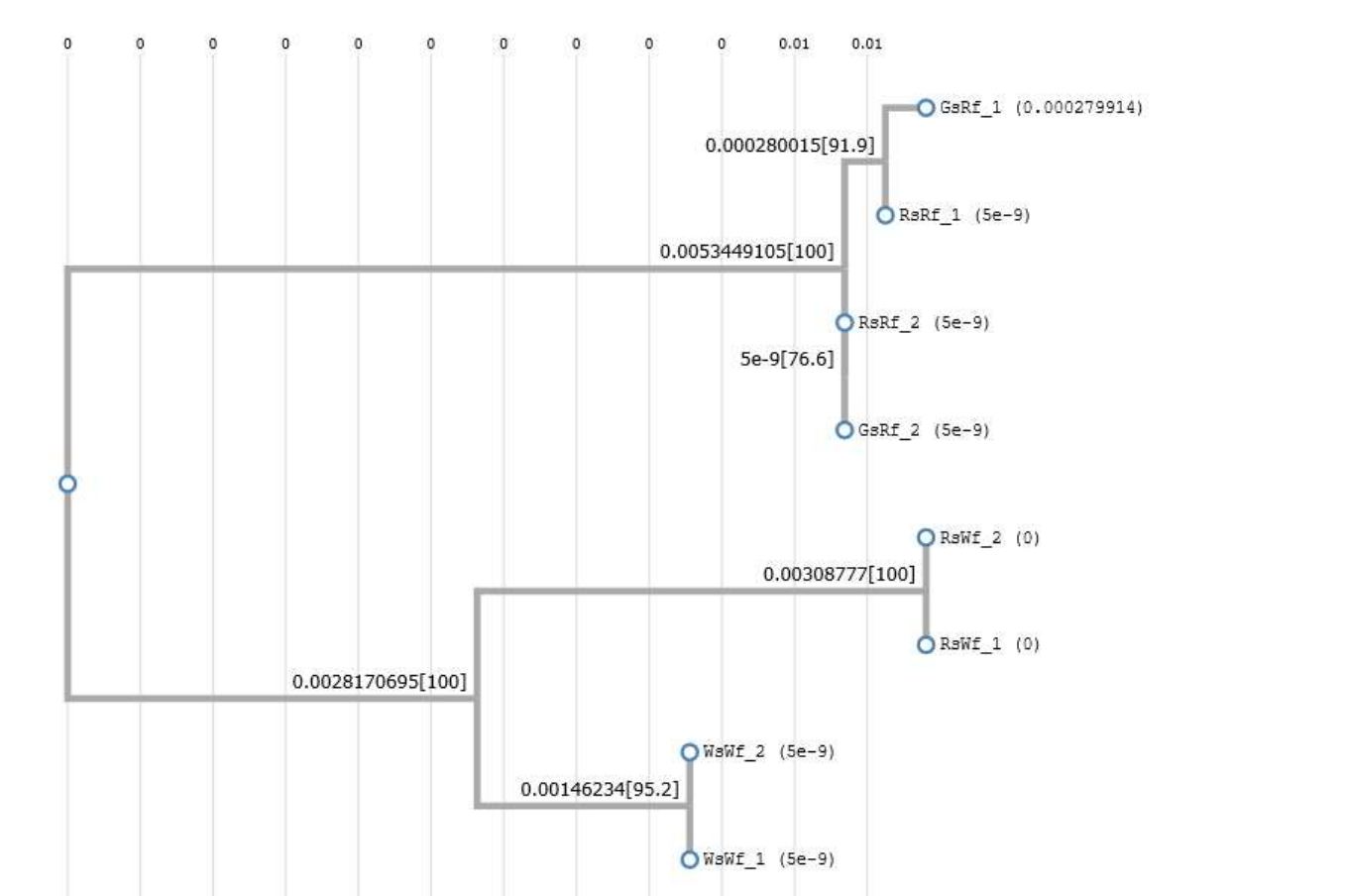


*RsTT8* genomic DNA



| Region   | Between Rf and Wf |       |     | WsWf specific |       |     | RsWf specific |       |     |
|----------|-------------------|-------|-----|---------------|-------|-----|---------------|-------|-----|
|          | SNP               | InDel | SSR | SNP           | InDel | SSR | SNP           | InDel | SSR |
| Promoter | 16                | 2     | 1   | 2             | 4     | 1   | 2             | -     | -   |
| Exon     | 2                 | -     | -   | 1             | -     | -   | 3             | 1     | -   |
| Intron   | 10                | 1     | 2   | 3             | 3     | 2   | 4             | -     | 1   |
| Total    | 28                | 3     | 3   | 6             | 7     | 3   | 9             | 1     | 1   |

# Nucleotide sequences

>RsWf\_1

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>RsWf\_2

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>GsRf\_1

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[illegible]

# Sequence comparison

CLUSTAL 2.1 Multiple Sequence Alignments

Sequence type explicitly set to DNA  
Sequence format is Pearson  
Sequence 1: RsWf\_1 3934 bp  
Sequence 2: RsWf\_2 3934 bp  
Sequence 3: GsRf\_1 3965 bp  
Sequence 4: GsRf\_2 3961 bp  
Sequence 5: RsRf\_1 3961 bp  
Sequence 6: RsRf\_2 3967 bp  
Sequence 7: WsWf\_1 4041 bp  
Sequence 8: WsWf\_2 4039 bp  
Start of Pairwise alignments

```

                                                    -1233
                                                    GsRf_1  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    RsRf_2  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    RsRf_1  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    GsRf_2  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    RsWf_1  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    RsWf_2  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    WsWf_1  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    WsWf_2  CACAGCTAGCCGCATCAATATGTTAGCAACTGA
                                                    *****

-1200
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*****

                                                    Rf-PF: 5'-TTGGTCGACAAAAAAGGCCAAGA
GsRf_1  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
RsRf_2  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
RsRf_1  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
GsRf_2  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
RsWf_1  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
RsWf_2  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
WsWf_1  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
WsWf_2  CATCGTCCACACATGGACAGAAATTTGGACGCACCCAGTCAATCCAAGTGGCCGTTAGTATAAAACATAATCCTGAAGCACAAGCCAAATAAATCTTATTTATTTGTTCGACAAAAAAGGCC
*****
                                                    Wf-PF: 5'-GGTCGACAAAAACGCCAAGAA

-960
GsRf_1  AAGAACGTTTAAATGTTGCTTTTGTCTAAACCAGGATACATCTCACATACCACATACCCAACCTGTATAAACTATGTGTACGTAACGTATCTATGTGTCTATCAAAATTTTATATGTTT
RsRf_2  AAGAACGTTTAAATGTTGCTTTTGTCTAAACCAGGATACATCTCACATACCACATACCCAACCTGTATAAACTATGTGTACGTAACGTATCTATGTGTCTATCAAAATTTTATATGTTT
RsRf_1  AAGAACGTTTAAATGTTGCTTTTGTCTAAACCAGGATACATCTCACATACCACATACCCAACCTGTATAAACTATGTGTACGTAACGTATCTATGTGTCTATCAAAATTTTATATGTTT
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WsWf_1  AAGAACGTTTAAATGTTGCTTTTGTCTAAACCAGGATACATCTCACATACCACATACCCAACCTGTATAAACTATGTGTACGTAACGTATCTATGTGTCTATCAAAATTTTATATGTTT
WsWf_2  AAGAACGTTTAAATGTTGCTTTTGTCTAAACCAGGATACATCTCACATACCACATACCCAACCTGTATAAACTATGTGTACGTAACGTATCTATGTGTCTATCAAAATTTTATATGTTT
*****

Rf-PR: 5'-CCAGTTAGATATAGCTGACCCGA
-840
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RsRf_2  CTCGGGTACAGTATATCTAACTTTATTGAGTTTTTCCAAGACATTACAAGGGAACAGATGGTGGCTACTTGGCTAGCAATTCACATCAATTA---TTAAAAACTTGAATTGTGAAACATC
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GsRf_2  CTCGGGTACAGTATATCTAACTTTATTGAGTTTTTCCAAGACATTACAAGGGAACAGATGGTGGCTACTTGGCTAGCAATTCACATCAATTA---TTAAAAACTTGAATTGTGAAACATC
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RsWf_2  CTCGGGTACAGTATATCTAACTTTATTGAGTTTTTCCAAGACATTACAAGGGAACAGATGGTGGCTACTTGGCTAGCAATTCACATCAATTA---TTAAAAACTTGAATTGTGAAACATC
WsWf_1  CTCGGGTACAGTATATCTAACTTTATTGAGTTTTTCCAAGACATTACAAGGGAACAGATGGTGGCTACTTGGCTAGCAATTCACATCAATTA---TTAAAAACTTGAATTGTGAAACATC
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*****

Wf-PR: 5'-CCAGTTAGACATAGCTGACCCGA

-720
Weak MRE
GsRf_1  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
RsRf_2  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
RsRf_1  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
GsRf_2  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
RsWf_1  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
RsWf_2  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
WsWf_1  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
WsWf_2  TCATTCTCCTCCTTTATTACACAAACTACTTTCTTTCTCTACTTACCGGTACAGGTCAACAGTCTACCAATCCCTTCTCTTTTACTCTTTTGTGTTAAATAAAACTAAAGATGCT
*****

-600
BRE
GsRf_1  ACTCTTTTATTATGGTTGATAAAACACTGGAATATTGCAAATTTCCAAATAAGAGAAAAAGAGAGAGATATAAAACCGAAATCATAGTAACACAAGTCAAAGCAACGCTGTGTTTCTCTT
RsRf_2  ACTCTTTTATTATGGTTGATAAAACACTGGAATATTGCAAATTTCCAAATAAGAGAAAAAGAGAGAGATATAAAACCGAAATCATAGTAACACAAGTCAAAGCAACGCTGTGTTTCTCTT
RsRf_1  ACTCTTTTATTATGGTTGATAAAACACTGGAATATTGCAAATTTCCAAATAAGAGAAAAAGAGAGAGATATAAAACCGAAATCATAGTAACACAAGTCAAAGCAACGCTGTGTTTCTCTT
GsRf_2  ACTCTTTTATTATGGTTGATAAAACACTGGAATATTGCAAATTTCCAAATAAGAGAAAAAGAGAGAGATATAAAACCGAAATCATAGTAACACAAGTCAAAGCAACGCTGTGTTTCTCTT
```

RsWf\_1 ACTCTTTTATTATGGTTGATAAACACCTGGAATATTGCAAAATTTCCAAATAAGAGAAAAGAAAGAGAGATGTAAACCAGAAATCATAGTAAACACAAGTCAAAGCAACGCTGTTTCTCTT  
RsWf\_2 ACTCTTTTATTATGGTTGATAAACACCTGGAATATTGCAAAATTTCCAAATAAGAGAAAAGAAAGAGAGATGTAAACCAGAAATCATAGTAAACACAAGTCAAAGCAACGCTGTTTCTCTT  
Wsf\_1 ACTCTTTTATTATGGTTGATAAACACCTGGAATATTGCAAAATTTCCAAATAAGAGAAAAGAAAGAGAGATGTAAACCAGAAATCATAGTAAACACAAGTCAAAGCAACGCTGTTTCTCTT  
Wsf\_2 ACTCTTTTATTATGGTTGATAAACACCTGGAATATTGCAAAATTTCCAAATAAGAGAAAAGAAAGAGAGATGTAAACCAGAAATCATAGTAAACACAAGTCAAAGCAACGCTGTTTCTCTT

----- MYB-core ----- BRE

GsRf\_1 GGTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG  
RsRf\_2 GTTTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG  
RsRf\_1 GGTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG  
GsRf\_2 GTTTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG  
RsWf\_1 GTTTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG  
Wsf\_1 GTTTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG  
Wsf\_2 GTTTGTGCACTTACGCTATTTTCTCTACTGAAATATGTTATGCTTTTTTCCAAATAATATATTATAACATATTAATAAATATGCAATTCGGCATTTTTTGGTCTCCAATCAGTGGGGGAACAG

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----- MRE (ACII MYB) -----

GsRf\_1 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
RsRf\_2 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
RsRf\_1 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
GsRf\_2 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
RsWf\_1 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
RsWf\_2 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
Wsf\_1 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT  
Wsf\_2 ATTACAAGACAATTACATCTTTTATTTCTGATCTGATTCTACTCTCTCATCCACGCTCTGGTTTACCAACAGTCAAGACGCATAAAAGTCAACTTTTACTAAATCTTGAGTTTTTGGT

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GsRf\_1 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA  
RsRf\_2 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA  
GsRf\_2 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA  
RsWf\_1 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA  
RsWf\_2 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA  
Wsf\_1 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA  
Wsf\_2 CATGCATTATACACATACATAGAATAATCTAGATTACTTTACTTATGTGACGATGTTACGAAAACACTAAAATGGTATATATATACATACATATTGAATTAAACCGTGGTCCCAACCA

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GsRf\_1 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
RsRf\_2 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
RsRf\_1 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
GsRf\_2 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
RsWf\_1 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
RsWf\_2 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
Wsf\_1 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA  
Wsf\_2 ATTAAATCAGCATAAAGAATATCTTCCCTTTTCATATCAAAACCCCTTCAGAGTTGCAAGATCTTACTCTCAGAGAGCTAATCATGTTTTCATCTCGGGGAAAA

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----- Wf-F -----

GsRf\_1 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
RsRf\_2 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
RsRf\_1 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
GsRf\_2 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
RsWf\_1 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
RsWf\_2 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
Wsf\_1 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA  
Wsf\_2 ATGATGAATCAAGTATTATACCGGTATGGAAGTATCGGAGCTGAGGAAAAGAGATTCAGGGCTACTTAAGGCGGTGGTGAATCTGTGGGGTGGACTTATAGTCTCTCTTGCGCA

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GsRf\_1 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG 240  
RsRf\_2 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG  
RsRf\_1 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG  
GsRf\_2 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG  
RsWf\_1 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG  
RsWf\_2 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG  
Wsf\_1 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG  
Wsf\_2 CTTTGTCCTCAACGAAGTTCTCTTTTCATTTCATCCATCTCTCACAATATATAAAGCAATATATTAATTATCCTTATTAATTATAAC-----AAGTAGAAGTACTAA-TG

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----- Exon 2 -----

GsRf\_1 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC 360  
RsRf\_2 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC  
RsRf\_1 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC  
GsRf\_2 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC  
RsWf\_1 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC  
RsWf\_2 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC  
Wsf\_1 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC  
Wsf\_2 TTAATCGATTAGAAATTTGGTGTGGAGTAGTGGATTCTACAACGCTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGGGAATAACGCGCTGAAGAGGCTGCGTTGGAGAGAAGCCAAC

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----- SSR-F -----

GsRf\_1 AGCTCATGGAGCTTTTACCAGACGCTTTTGGCGGAGAATCATCGATGGAAGCGAGGGCTTGACACGACCTGCGCTGAGGATTTGACGACACTGAATGGTTTTATGTGCTGTGCTCA 480  
RsRf\_2 AG

[illegible]



|                                                                                                                                                                                                                                                        |                                                                                                                          |      |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------|------|
| *****                                                                                                                                                                                                                                                  |                                                                                                                          |      |
| GsRf_1                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  | 2520 |
| RsRf_2                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| RsRf_1                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| GsRf_2                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| RsWf_1                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| RsWf_2                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| WsWf_1                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| WsWf_2                                                                                                                                                                                                                                                 | CTTAACGAGAGATTATAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTA AACCATCTTTGTAAGAGGATCCATGAG  |      |
| *****                                                                                                                                                                                                                                                  |                                                                                                                          |      |
| GsRf_1                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  | 2640 |
| RsRf_2                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| RsRf_1                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| GsRf_2                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| RsWf_1                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| RsWf_2                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| WsWf_1                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| WsWf_2                                                                                                                                                                                                                                                 | CTGGAATCTACTCATCACGAGCCAAACCAAAAGCGGATGCGTATCGGTAAAGGGAAGAACGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTAGAGATGAGATGCGAG  |      |
| *****                                                                                                                                                                                                                                                  |                                                                                                                          |      |
| GsRf_1                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG | 2760 |
| RsRf_2                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| RsRf_1                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| GsRf_2                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| RsWf_1                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| RsWf_2                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| WsWf_1                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| WsWf_2                                                                                                                                                                                                                                                 | TACCGAGATGGTTTATTGCTCAACATTCTTCAGGTACTTAAGGAGCTGGGTATAGAGACCACTGCAGTTACACCCGCCGTGAACGACCATGATTTTGAGGCAGAGATAAGGGCGAAAGTG |      |
| *****                                                                                                                                                                                                                                                  |                                                                                                                          |      |
| GsRf_1                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 3965 |
| RsRf_2                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 3967 |
| RsRf_1                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 3961 |
| GsRf_2                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 3961 |
| RsWf_1                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 3934 |
| RsWf_2                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 3934 |
| WsWf_1                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 4041 |
| WsWf_2                                                                                                                                                                                                                                                 | AGAGGGAAGAAACCAACCATTTGCTGAGGTTAAAAATAGCCATCCATCAAATCATATCTCAAAATAAACTCTAG                                               | 4039 |
| *****                                                                                                                                                                                                                                                  |                                                                                                                          |      |
| Yellow: cis-acting sequence                                                                                                                                                                                                                            |                                                                                                                          |      |
| Red: SNP or InDel between Rf and Wf                                                                                                                                                                                                                    |                                                                                                                          |      |
| Blue: WsWf specific SNP or InDel                                                                                                                                                                                                                       |                                                                                                                          |      |
| Green: RsWF specific SNP or InDel                                                                                                                                                                                                                      |                                                                                                                          |      |
| Brown: primer sequences                                                                                                                                                                                                                                |                                                                                                                          |      |
| Red letter: key nucleotide for domain                                                                                                                                                                                                                  |                                                                                                                          |      |
| Numbers: given from ATG start codon                                                                                                                                                                                                                    |                                                                                                                          |      |
| MRE: MYB-recognition motif, BRE: bHLH-recognition motif                                                                                                                                                                                                |                                                                                                                          |      |
| Cis-elements on promoter were not different from each other. Therefore, we should examine expression of transcription factors that might form different MBW complex to regulate the TT8 expression, such as MYB5, GL3, EGL3, TTG1, TTG2, TT1 and TT16. |                                                                                                                          |      |

ATGGATGAATCAAGTATTATACCGGTATGGAHAGTGATCGGAGCTGAGGGAAAAAGAGATTAGAGGGCTACTTAAGCCGGTGGTGCAATCTGTGGGGTGGACTTATAGTCTCTTCTGGCAACTTT  
GTCTTCAACGAGGAAAACTGGTTGTGGGATAGTGGATTTCTACAAACGGTGCAATTAAGAGCTAGAAGACAGCTCAGCCGCGCGGAAATACCGCTGAAGAGGCTCGCTGTGGAGAGAACCCACAGCT  
CATGGAGCGTTTACAGACGGTTTGTTCGGCGAGAGATCATCGATGGAAGCGAGGGCTCCACAGCACTGTGCGCTGAGGATTTGTACGGGACCATGAATGGTTTTATGTGCTGTCTCACTACTCT  
TTTGAACCTCCTTCTGGGATGCCAGGAAAGGCGTATGCGAGGAGGAAGCAAGTATGGATGAGTGGTGTAAATGAGGTTGCACAGTAAAAATCTTCTCTAGGGCTATTCTCTGCAAGAGTGCACAAA  
TTCAGACAGTGGTTTGTCAATCCCGTCTGTATGGGCTTTGTGAAATAGGCAACAGCAAGGTCAAGAGAAATGAAGAGTTTGTGAACACATAAAGAGTTTCTTCCAAACCCACCGGAGT  
AAACCAAGGACCTGCTCTTTTGAACACTCCATCAACGAAGATCATGAAGAGACAGGAAGAAGTATGAAGAAATGACAATGTTCAGAGGAGATTAAGACTTGGTCTCTGTATGACGATGAGCTC  
TCCAATCAAAATCTACTCTGTGATTTCCATATAGAAGCACCCAAATAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAATATTCTCAGACAGTATCAACACTTCTCA  
TGTCACAACTCCCCAATCTCTTTCAGATTCAGTTTCCCACTCTTCTACGTCTCAATCATCGTTGTGCTCGTGGAGGGTGTGAAGATGTCAAGAGACCATGACCAATATCAACGAGGAGGAAGAC  
GTGCTGCTATCTCGTGCAGATGGATGCTCAAAACATCATGATCTTGAGAGTTCTCTTACTCTGAAGAACATAAAACAAAGAGGGTGTCCGCGGGAAGAGCTCAACCTATGTGGTGGCCGACGA  
CGCAGAAGAGAGAAGCTTAACGAGAGATTCTAACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATCCTTGGAGACACCATTGATTACGTAAACCATCTTTGTGAAGA  
GGATCCATGAGCTGGAATTTACTCATCAGGAGCCATCAACAAAGCGGATCGCATTCGGTAGGGGAGAGCTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTGTAGAGATGAG  
ATCGSAGTAGGAGATGTTTATTGGTCTCAACATCTTACCGTACTTAAGGAGCTGGGTATAGAGACCATGCGATCTCACCCGCGTGAACGACCATTGATTTTGAGGCAGAGATAAGGGCGAAA  
GTGAGAGGGAAGAAACCAACCATTTGCTGAGGTTTAAATAGCCATCCATCAATCATATCTCAAAATAAACTCTAG

ATGGATGAATCAAGTATTATACCGGATATGGAGAGTGATCGGAGCTTGAAGGAAAAAGAGATTCAAGGGCTACTTAAGGCGGTGGTGCAATCTGTGGGGTGGACTTATAGTCTCTTCTTGCCAACCTTT  
GTCTTCAACCGAAGGAAATTTGGTGTGGGAGTAGTGGATTCTTACAAACGGTGCAATAAAGACTAGAAAGACAACCTCAGCCGCGCGGAAATACCGCTGTAAGAGCGCTCGCTGTGGAGAGAGCCCAACAGCT  
CATGGAGCTTTTCCACAGACGCTTTTTCGGCAGAGATCATCGATGGAGAGCGAGGGCTTCCACAGACATCTGCCTCGAGGATTTGTACGGCAGCATGAATGGTTTATGTGCTGTGTCTTACTACTCT  
TTTGAACCTCCTTCTGGGATGCCAGGAAAGGCGTATGCGAGGAGGAAGCAAGTATGGATGAGTGGTGTAAATGAGGTTGCACAGTAAAAATCTTCTCTAGGGCTATTCTCTGCAAGAGTGCCAAAA  
TTCAGACAGTGTTTGTCAATCCCGTCTGTATGGGCTTTTGGAAATAGGCACAACGAAAGCTCAAGAAAGATGAAGAGTTTGTGAACACATAAAGAGTTTCTTCCAAACCAACCCGGAAGTC  
AAACCAAGCAAGCTGCTCTTTTGAACACTCCATCAACGAAGATCATGAAGAGACAGGAAGAAAGTATGAAGAAATGACAATGTTCAGAGGAGATTAAGACTTGGTCTCTCTGATGACGATGAGCTC  
TCCAATCAAAATCTACTCTGTGATTTCCATATAGAAGCACCCAAATAGTTTAGATACACAATGGACATGATGAATCTAATGGAGGAAGGCGGAAATATTCTCAGACAGTATCAACACTTCTCA  
TGTCACAACCTCCCCAATCTCTTTTCAGATTCAGTTTCCCACTCTTCTTACGTTCAATCATCTGTTGTCTCGTGGAGGGTGTGAGAAATGTCAAAAGAGCTCAGCAATATCAACGAGAGGAGAAAGC  
GCTGCTGATCTCTGTCGCAATGGATGCTCAACACATGATCTTGAGAGTTCTTTTACTCTCAAAAACTAAAAACAAGAGGGTGCBCGGGAAAGAGCTCAACACTGTGGTGGCCGAGCGCA  
CGCAGAAGAGGAAGGCTTAAACGAGAGGATTCAACGTTGAGATCATGGTTCCATTCTGTACCAAGATGGATTAAGGCTCTGATCCTTGGAGACACCATTGATTACGTGAACCATCTTTGTAAAGA  
GGATCCATACCTCGGAATCTACTCATCAACGCAACCAAAAGCGGATTCGCTATTCGTAAGGGAAGAACCTGTGGGAAGAGGTGGAGGTTTCCATTATAGAGAGCGATGTTTGTGTAGAGATGAG  
ATGCGAGTAGCCGAGATGGTTTATTGTCTCAACACTTCTTCAAGTACTTAAAGGACTTGGGATATAGAGACCATGCAGTCTACACCGCGGTGAACGACCATTGATTTTGAAGGCAGAGATAAGGGCGAAA  
TGAGAGGGAAGAAACCAACCATTCGTGAGGTTTAAATAGGCATCCATCAATCATATCTCAAAATAAACTCTAG

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RsWf\_2 GGTTCCTCTGATGACGATGACGTCTCCAATCAAATCTACTCTCTGATTTCATATAGAA  
\*\*\*\*\*

RsRf\_1 GCACCCAGTAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
RsRf\_2 GCACCCAGTAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
GsRf\_2 GCACCCAGTAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
GsRf\_1 GCACCCAGTAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
WsWf\_1 GCACCCAAATAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
WsWf\_2 GCACCCAAATAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
RsWf\_1 GCACCCAAATAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
RsWf\_2 GCACCCAAATAGTTTAGATACACAAATGGACATGATGAATCTAATGGAGGAAGGCGGAAAT  
\*\*\*\*\*

RsRf\_1 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
RsRf\_2 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
GsRf\_2 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
GsRf\_1 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
WsWf\_1 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
WsWf\_2 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
RsWf\_1 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
RsWf\_2 TATTCTCAGACAGTATCAACACTTCTCATGTGCACAACTCCCCAATCTTCTTCAGATTCA  
\*\*\*\*\*

RsRf\_1 GTTTCACATCTCTTACGTTCAATCATCGTTTGTCTCGTGGAGGGTTGAGAAATGTCAAA  
RsRf\_2 GTTTCACATCTCTTACGTTCAATCATCGTTTGTCTCGTGGAGGGTTGAGAAATGTCAAA  
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WsWf\_1 GTTTCACATCTTCTTACGTTCAATCATCGTTTGTCTCGTGGAGGGTTGAGAAATGTCAA  
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RsWf\_1 GTTTCACATCTTCTTACGTTCAATCATCGTTTGTCTCGTGGAGGGTTGAGAAATGTCAA  
RsWf\_2 GTTTCACATCTTCTTACGTTCAATCATCGTTTGTCTCGTGGAGGGTTGAGAAATGTCAA  
\*\*\*\*\*

RsRf\_1 GAGCATCAGCAATATCAACGAGAGGAGAAAGCGTCGTCATCCTCGTCGCAATGGATG  
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RsWf\_2 GAGCATCAGCAATATCAACGAGAGGAGAAAGCGTCGTCATCCTCGTCGCAATGGATG  
\*\*\*\*\*

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RsWf\_2 CTCAAACACATGATCTTGAGAGTTCCTTTACTCCATGAAAACACTAAAAACAAGAGGGTG  
\*\*\*\*\*

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GsRf\_1 CCGCGGGAAGAGCTCAACCATGTGGTGGCCGAGCGACGAGAAGAGAGAAGCTTAACGAG  
WsWf\_1 CCGCGGGAAGAGCTCAACCATGTGGTGGCCGAGCGACGAGAAGAGAGAAGCTTAACGAG  
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RsWf\_1 CCGCGGGAAGAGCTCAACCATGTGGTGGCCGAGCGACGAGAAGAGAGAAGCTTAACGAG  
RsWf\_2 CCGCGGGAAGAGCTCAACCATGTGGTGGCCGAGCGACGAGAAGAGAGAAGCTTAACGAG  
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RsWf\_2 AGATTCAATACGTTGAGATCATTGGTTCCATTGTGACCAAGATGGATAAAGTCTCGATC  
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RsRf\_1 CTTGGAGACACCATTGATTACGTAACCATCTTTGTAAGAGGATCCATGAGCTGGAATCT  
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RsWf\_2 GTGGAGGTTTCCATTATAGAGAGCGATGTTTTGTTAGAGATGAGATGCGAGTACCGAGAT  
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\*\*\*\*\*

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\*\*\*\*\*

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\*\*\*\*\*

RsRf\_1 TAG 1560  
RsRf\_2 TAG 1560  
GsRf\_2 TAG 1560  
GsRf\_1 TAG 1560  
WsWf\_1 TAG 1560  
WsWf\_2 TAG 1560  
RsWf\_1 TAG 1563  
RsWf\_2 TAG 1563  
\*\*\*

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FEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSR AISAKSAKIQT VVCIPVLDGVLEIGTTNKVKENEEFVEHMKSFQNHPSNTK PALFEHSINEEHEEDEEEVEEEMTMSEEIRLGSPDDDDVS  
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MIR

GsRf\_2 ACTALSPEDLTDTEWFFVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF 200  
RsRf\_1 ACTALSPEDLTDTEWFFVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
RsRf\_2 ACTALSPEDLTDTEWFFVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
GsRf\_1 ACTALSPEDLTDTEWFFVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
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RsWf\_2 ACTALSPEDLTDTEWFFVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
\* \*\*\*\*\*

WD/AD

GsRf\_2 FQNHPKSNTPALFEHSINEEHEEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLLSDS 300  
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RsWf\_2 FQNHPKSNTPALFEHSINEEHEEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPNSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLLSDS  
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basic Helix 1 Loop

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RsRf\_2 VSTSSVQSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFVTMKDKVSI  
GsRf\_1 VSTSSVQSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFVTMKDKVSI  
WsWf\_1 VSTSSVQSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFVTMKDKVSI  
WsWf\_2 VSTSSVQSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFVTMKDKVSI  
RsWf\_1 VSTSSVQSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFVTMKDKVSI  
RsWf\_2 VSTSSVQSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFVTMKDKVSI  
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bHLH region

Helix 2

GsRf\_2 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK 500  
RsRf\_1 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
RsRf\_2 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
GsRf\_1 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
WsWf\_1 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
WsWf\_2 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
RsWf\_1 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
RsWf\_2 LGDTIDYVNHLCRKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
\*\*\*\*\*

ACT-like domain: dimerization

GsRf\_2 KPTIAEVKIAIHQII SQNKL 519  
RsRf\_1 KPTIAEVKIAIHQII SQNKL 519  
RsRf\_2 KPTIAEVKIAIHQII SQNKL 519  
GsRf\_1 KPTIAEVKIAIHQII SQNKL 519  
WsWf\_1 KPTIAEVKIAIHQII SQNKL 519  
WsWf\_2 KPTIAEVKIAIHQII SQNKL 519  
RsWf\_1 KPTIAEVKIAIHQII SQNKL 520  
RsWf\_2 KPTIAEVKIAIHQII SQNKL 520  
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GsRf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR 100  
RsRf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
RsRf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
GsRf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
WsWf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
WsWf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
RsWf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
RsWf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEAR  
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GsRf\_2 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF 200  
RsRf\_1 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
RsRf\_2 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
GsRf\_1 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
WsWf\_1 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
WsWf\_2 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
RsWf\_1 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
RsWf\_2 ACTALSPEDLTDTEWFYVLCITYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEFEVHMKSF  
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GsRf\_2 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS 300  
RsRf\_1 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
RsRf\_2 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
GsRf\_1 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
WsWf\_1 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
WsWf\_2 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
RsWf\_1 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
RsWf\_2 FQNHPKSNTPALFEHSINEEHEDEE-VEEMTMSEIIRLGSPPDDDDVSNQNLSDFHIEAPSSLDTQMDMMNLMEEGGNYSTVSTLLMSQLPNLLSDS  
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GsRf\_2 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI 400  
RsRf\_1 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
RsRf\_2 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
GsRf\_1 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
WsWf\_1 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
WsWf\_2 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
RsWf\_1 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
RsWf\_2 VSTSSVQSSSFVSRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRRREKLNERFITLRSVPFFVTMKDKVSI  
\*\*\*\*\*

GsRf\_2 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK 500  
RsRf\_1 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
RsRf\_2 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
GsRf\_1 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
WsWf\_1 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
WsWf\_2 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
RsWf\_1 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
RsWf\_2 LGDTIDYVNLCKRIHELESTHHEPNQKRMRIKGRTWEEVEVSIIESDVLEMRCEYRDGLLLNQLVQLKELGIETTAVHTAVNDHDFEAEIRAKVRGK  
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GsRf\_2 KPTIAEVKIAIHQIISQNL 519  
RsRf\_1 KPTIAEVKIAIHQIISQNL 519  
RsRf\_2 KPTIAEVKIAIHQIISQNL 519  
GsRf\_1 KPTIAEVKIAIHQIISQNL 519  
WsWf\_1 KPTIAEVKIAIHQIISQNL 519  
WsWf\_2 KPTIAEVKIAIHQIISQNL 519  
RsWf\_1 KPTIAEVKIAIHQIISQNL 520  
RsWf\_2 KPTIAEVKIAIHQIISQNL 520  
\*\*\*\*\*

RsRf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
RsRf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
GsRf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
GsRf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
WsWf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
WsWf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
RsWf\_1 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
RsWf\_2 MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYISLFWQLCPQRRKLWSSGFYNGAIK  
AtT8 MDESSIIPAQKVAGAEKKELQGLLKAVQSVWDVTSVFWQFCPQQRVLVWNGNYNGAIK  
\*\*\*\*\* \*\* \*\* \*\* \*\*:\*\*\*\*\*: \*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*

RsRf\_1 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
RsRf\_2 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
GsRf\_2 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
RsRf\_1 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
WsWf\_1 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
WsWf\_2 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
RsWf\_1 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
RsWf\_2 TRKTTQPAEITAEAAALERSQQLMELVQTLFAGESSMEARACTALSPEDLTDTEWFYVLC  
AtT8 TRKTTQPAEITAEAAALERSQQLRELJETLLAGESTSEARACTALSPEDLTETEFYVLMC  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*

RsRf\_1 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
RsRf\_2 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
GsRf\_2 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
GsRf\_1 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
WsWf\_1 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
WsWf\_2 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
RsWf\_1 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
RsWf\_2 LTYSFEPPSGMPGKAYARRKQVWMSGVNEVDSKIFSRSAISAKSAKIQTVVCIPLVDGVLE  
AtTT8 VVSFPPPPSGMPGKAYARRKHVWLSGANEVDSKTFSRILAKSAKIQTVVCIPLMDGVVE  
: : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \*

RsRf\_1 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
RsRf\_2 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
GsRf\_2 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
GsRf\_1 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
WsWf\_1 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
WsWf\_2 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
RsWf\_1 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
RsWf\_2 IGTNNKVENEEFVEHMKSFQNHPSNTKPALEHNSINEEHEEED---VEEMTMSEE  
AtTT8 LGTTKKVREDVEFVELTKSFFYDHCKTNPALSEHSTYEVHEEADEEEVEEMTMSEE  
: \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \*

RsRf\_1 IRLGSPDDDDVSNQNLSDFI EAPSSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLL  
RsRf\_2 IRLGSPDDDDVSNQNLSDFI EAPSSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLL  
GsRf\_2 IRLGSPDDDDVSNQNLSDFI EAPSSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLL  
GsRf\_1 IRLGSPDDDDVSNQNLSDFI EAPSSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLL  
WsWf\_1 IRLGSPDDDDVSNQNLSDFI EAPNSLDTQMDMMNLMEEGGSYSQTVSTLLMSQLPNLL  
WsWf\_2 IRLGSPDDDDVSNQNLSDFI EAPNSLDTQMDMMNLMEEGGSYSQTVSTLLMSQLPNLL  
RsWf\_1 IRLGSPDDDDVSNQNLSDFI EAPNSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLL  
RsWf\_2 IRLGSPDDDDVSNQNLSDFI EAPNSLDTQMDMMNLMEEGGNYSQTVSTLLMSQLPNLL  
AtTT8 MRLGSPDDEDVSNQNLHSDLHI ESTHTLDTMDMMNLMEEGGNYSQTVSTLLMSHPTSL  
: \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \* : \* \* \* \* \*

RsRf\_1 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
RsRf\_2 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
GsRf\_2 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
GsRf\_1 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
WsWf\_1 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
WsWf\_2 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
RsWf\_1 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
RsWf\_2 SDSVSTSSYVQSSFVSWRVENVKEHQYQREEKASSSSSQWMLKHMILRVPLHENTKN  
AtTT8 SDSVSTSSYIQSSFATWRVENGKEHQVKTAP-----SSQWVLKQMFVRVPLHDNTKD  
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RsRf\_1 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
RsRf\_2 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
GsRf\_2 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
GsRf\_1 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
WsWf\_1 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
WsWf\_2 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
RsWf\_1 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
RsWf\_2 KRVPREELNHVVAERRRREKLNERFITLRSLVPFVTKMDKVSILGDTIDYVNLCKRIHE  
AtTT8 KRLPREDLSHVVAERRRREKLNEKFITLRSMVPFVTKMDKVSILGDTIAYVNLKRVRVHE  
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RsRf\_1 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
RsRf\_2 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
GsRf\_2 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
GsRf\_1 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
WsWf\_1 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
WsWf\_2 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
RsWf\_1 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
RsWf\_2 LESTHHEPNQKMRIGKGRTWEEVEVSIIESDVLLEMRCEYRDGLLLNILQVLKELGIET  
AtTT8 LENTHHEQQHKRTRTCKRKTSEEVEVSIENDVLEMRCEYRDGLLLDILQVLHELGIET  
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RsRf\_1 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
RsRf\_2 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
GsRf\_2 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
GsRf\_1 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
WsWf\_1 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
WsWf\_2 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
RsWf\_1 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
RsWf\_2 TAVHTAVNDHDFEAEIRAKVRGKKPTIAEVKIAIHQII SQNKL-  
AtTT8 TAVHTSVNDHDFEAEIRAKVRGKKASIAEVKRAIHQVIIHDTNL  
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>AtTT8  
MDESSIIPAEKVAGAEKKEIQGLLKTAVQSVGWYTSVFWQFCPQRRVLVWNGGYNGAIKTRKTTQPAEITAEEAALERSQQLMELYQTLLFAGESSMEARACTALSPEDLTETEFYLMCVSFS  
FPPSGMPGKAYARRKHVWLSGANEVDSKTFRAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEEFVEHIKSFFQNHPSNTKPALEHSHSTYEVHEEAEDEEEVEEMTMSEEMRLGSPDD  
EDVSNQNLHSDLHIESTHTLDTHMDMMNLMEEGGNYSTVTLLMSHPTSLLSDSVSTSSYIQSSFATWRVENVKEHQYQREKASSSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERRR  
EKLNEKFITLRSMPVPVTKMDKVSILGDTIAYVNLHKKRVHELENTHEQQHKRTRTCKRKTSEEVEVSIIESDVLLEMRCEYRDGLLLDILQVLHELGIETTAVHTSVNDHDFEAEIRAKVRG  
KKASIAEVKRAIHQVIIHDNTL

>RsWf\_1  
MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYTSVFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEEAALERSQQLMELYQTLLFAGESSMEARACTALSPEDLTDTEFWYVLCITYS  
FPPSGMPGKAYARRKQVWMSGVNEVDSKIFRAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEEFVEHIKSFFQNHPSNTKPALEHSHSTYEVHEEAEDEEEVEEMTMSEEMRLGSPDDDDV  
SNQNLSDFHIEAPNSLDTQMDMMNLMEEGGNYSTVTLLMSQLPNLLSDSVSTSSYVQSSFVSWRVENVKEHQYQREKASSSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERR  
RREKLNERFITLRSVLPVFTKMDKVSILGDTIDYVNLHCKRIHELESTHHEPNQKMRIGKRTWEEVEVSIIESDVLLEMRCEYRDGLLLNQLQVLHELGIETTAVHTAVNDHDFEAEIRAK  
VRGKKPTIAEVKIAIHQIISQNL

>RsWf\_2  
MDESSIIPVWKVIGAEKEIQGLLKAVVQSVGWYTSVFWQLCPQRRKLWSSGFYNGAIKTRKTTQPAEITAEEAALERSQQLMELYQTLLFAGESSMEARACTALSPEDLTDTEFWYVLCITYS  
FPPSGMPGKAYARRKQVWMSGVNEVDSKIFRAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEEFVEHIKSFFQNHPSNTKPALEHSHSTYEVHEEAEDEEEVEEMTMSEEMRLGSPDDDDV  
SNQNLSDFHIEAPNSLDTQMDMMNLMEEGGNYSTVTLLMSQLPNLLSDSVSTSSYVQSSFVSWRVENVKEHQYQREKASSSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERR  
RREKLNERFITLRSVLPVFTKMDKVSILGDTIDYVNLHCKRIHELESTHHEPNQKMRIGKRTWEEVEVSIIESDVLLEMRCEYRDGLLLNQLQVLHELGIETTAVHTAVNDHDFEAEIRAK  
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>GsRf\_1  
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RREKLNERFITLRSVLPVFTKMDKVSILGDTIDYVNLHCKRIHELESTHHEPNQKMRIGKRTWEEVEVSIIESDVLLEMRCEYRDGLLLNQLQVLHELGIETTAVHTAVNDHDFEAEIRAK  
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>GsRf\_2  
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>RsRf\_1  
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>RsRf\_2  
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FPPSGMPGKAYARRKQVWMSGVNEVDSKIFRAISAKSAKIQTVCIPVLDGVLEIGTTNKVKENEEFVEHIKSFFQNHPSNTKPALEHSHSTYEVHEEAEDEEEVEEMTMSEEMRLGSPDDDDV  
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RGKKPTIAEVKIAIHQIISQNL

>WsWf\_1  
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RGKKPTIAEVKIAIHQIISQNL

>WsWf\_2  
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SNQNLSDFHIEAPNSLDTQMDMMNLMEEGGNYSTVTLLMSQLPNLLSDSVSTSSYVQSSFVSWRVENVKEHQYQREKASSSSSSQWMLKHMILRVPLHENTKNKRVPREELNHVVAERR  
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RGKKPTIAEVKIAIHQIISQNL

**Figure S1.** Nucleotide sequence of the *RsTT8* gene isolated from four radish inbred lines. Shaded regions indicate exons. Yellow: cis-acting sequence; red: SNP or InDel between red-fleshed and white-fleshed genotypes; blue: white skin/white flesh (WsWf)-specific SNP or InDel; green: red skin/white flesh (RsWf)-specific SNP or InDel; brown: primer sequences; red letter: key nucleotide for domain; numbers: relative to the transcription start site (TSS).