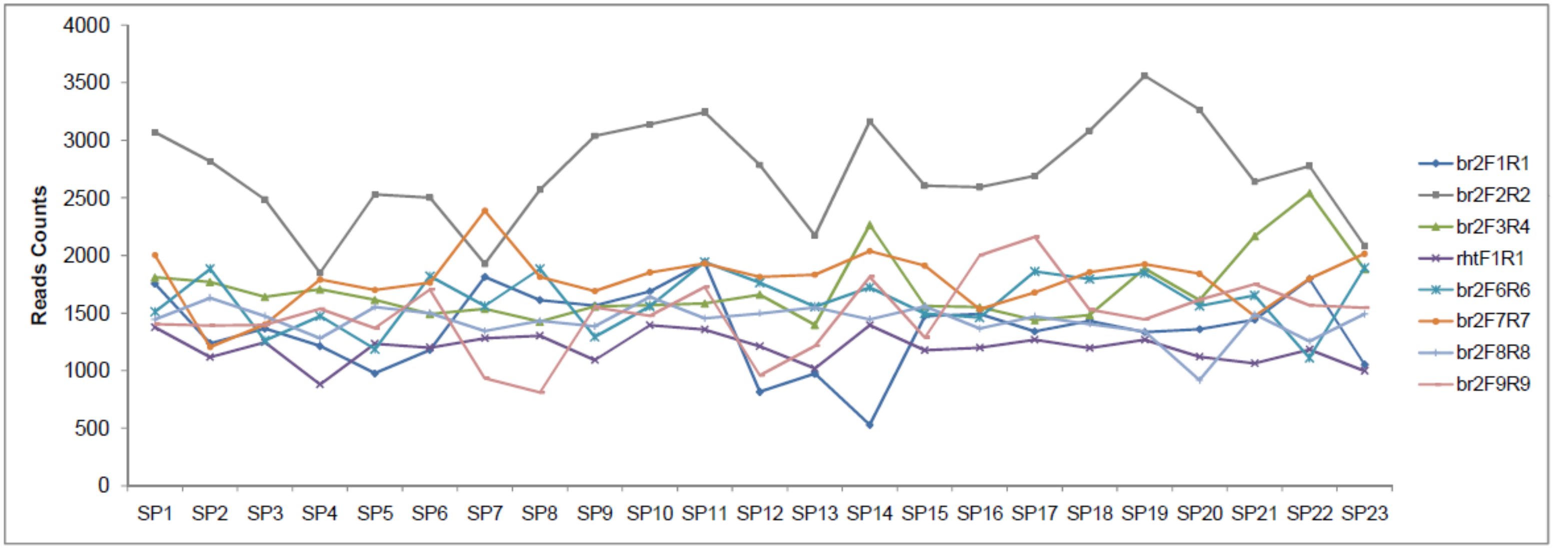
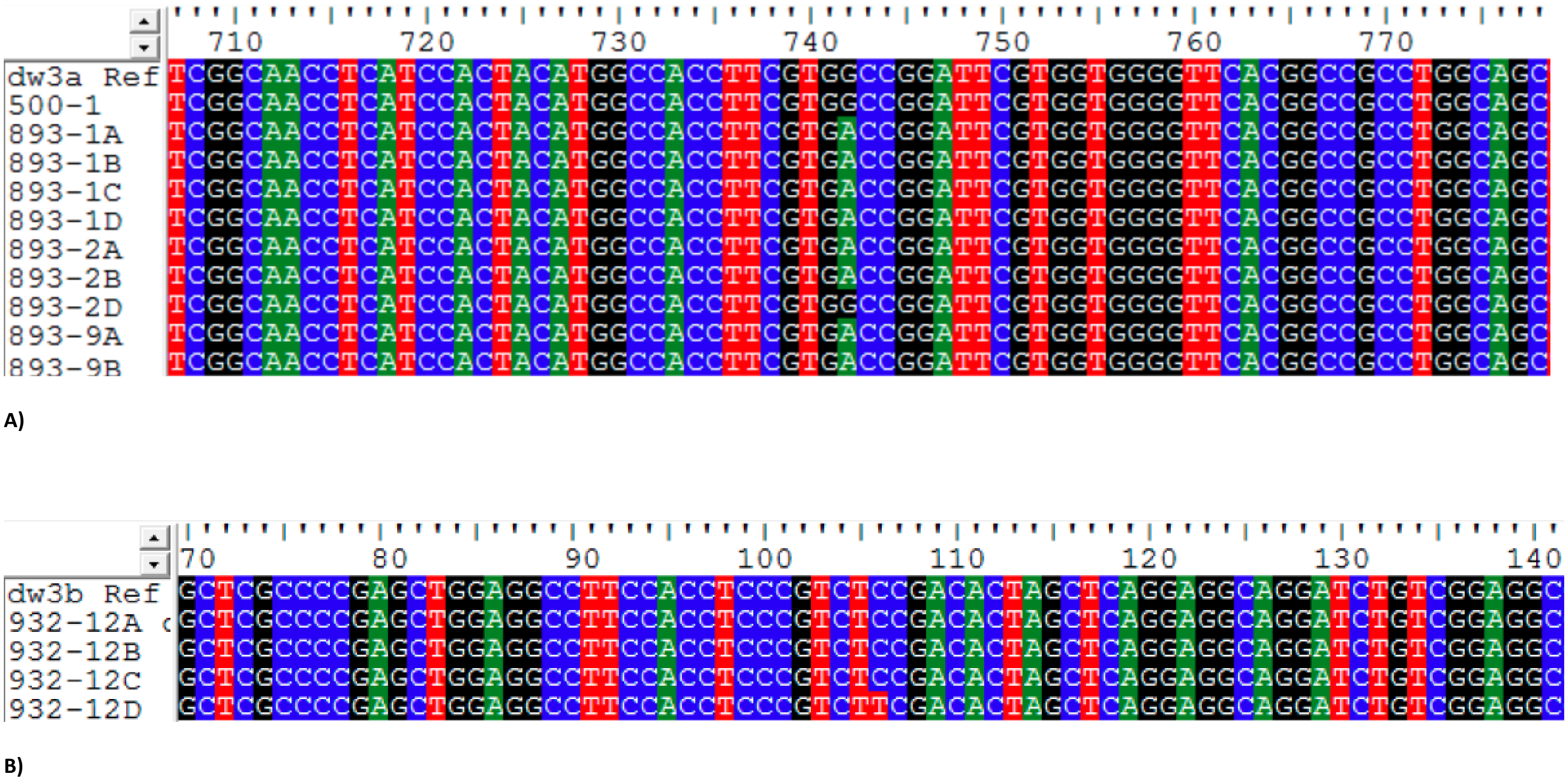


Figure S1 454 read distribution of 8 amplicons in the 23 superpools. X axis represents 23 superpools from the 21,210 EMS mutagenized tef lines. Y axis represents the number of reads in the superpools. 8 different signs represent 8 amplicons. Among them, rhtF1R1 was amplified from *rht*1 genes and the other 7 were amplified from *dw*3 genes



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           710       720       730       740       750       760       770
dw3a Ref  TCGGCAACCTCATCCACTACATGGCCACCTTCGTGGCCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
500-1     TCGGCAACCTCATCCACTACATGGCCACCTTCGTGGCCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-1A    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-1B    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-1C    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-1D    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-2A    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-2B    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-2D    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGGCCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-9A    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
893-9B    TCGGCAACCTCATCCACTACATGGCCACCTTCGTGACCGGATTCGTGGTGGGGTTCACGGCCGCCTGGCAGC
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A)

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          70        80        90        100       110       120       130       140
dw3b Ref  GCTCGCCCCGAGCTGGAGGCCTTCCACCTCCCGTCTCCGACACTAGCTCAGGAGGCAGGATCTGTCGGAGGC
932-12A   GCTCGCCCCGAGCTGGAGGCCTTCCACCTCCCGTCTCCGACACTAGCTCAGGAGGCAGGATCTGTCGGAGGC
932-12B   GCTCGCCCCGAGCTGGAGGCCTTCCACCTCCCGTCTCCGACACTAGCTCAGGAGGCAGGATCTGTCGGAGGC
932-12C   GCTCGCCCCGAGCTGGAGGCCTTCCACCTCCCGTCTCCGACACTAGCTCAGGAGGCAGGATCTGTCGGAGGC
932-12D   GCTCGCCCCGAGCTGGAGGCCTTCCACCTCCCGTCTTCGACACTAGCTCAGGAGGCAGGATCTGTCGGAGGC
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B)

Figure S2 Sanger sequencing validation on M3 generation plants segregating for mutations in a candidate tef dwarfing gene. A) p893 mutant alignment with reference sequence of dw3a gene. The G742A mutation is validated by seven p893 M3 lines; B) p932 mutant alignment with reference sequence of the dw3b gene. The C106T mutation is validated by one p932 M3 line, 932-12D

Figure S3 Phenotypes of *dw3* homologue mutants in M3 lines of tef (500-1: control; 893-1 and 893-9: G742A mutants; 932-12: C106T mutant)

Table S1 Summary of tef genomic fosmid library

Accession number	PI 524434
Source of genomic DNA	1-month-old seedlings
Total number of colony forming units	102,191
Number of superpools	25
Number of pools	1,187
Average insert size	35 kb – 45kb
Haploid genome size	714Mbp
Library coverage	5.0X – 6.4X

Table S2 Primers for 454 sequencing

Primer name	Fusion primer (5'-3')	MID_Tag	PCR primer (5'-3')
dw3E1F1_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCAC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGT	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTG	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGT	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAG	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGAT	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGT	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTAC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP10_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTAGACT	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTA	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP12_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACTCTCG	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP13_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGAGACG	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP14_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACTGTACA	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP15_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ATAGAGTA	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP16_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CACGCTAC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP17_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGTAGAC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP18_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGACGTGA	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP19_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGATCAC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP20_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGCACTA	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP21_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGAGA	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP22_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGCAGTAC	CTAGYAGCGACCCGGAGGAGAT
dw3E1F1_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAG	CTAGYAGCGACCCGGAGGAGAT
dw3E1R1a_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		ACYTGGCCACCAGCCGCACCA
dw3E1R2a_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGCGT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCACTC	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGTAG	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTGTC	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGTCT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAGTG	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGATAC	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGTAC	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTACTC	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP10_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTAGACTAG	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTATG	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP12_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACTCTCGTG	TGGCTCCGCGACGACAGCTT

dw3E1R2a_SP13_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGAGACGAG	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP14_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACTGTACAGT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP15_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ATAGAGTACT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP16_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CACGCTACGT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP17_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGTAGACGT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP18_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGACGTGACT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP19_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGATCACGT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP20_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGCACTAGT	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP21_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGAGAGA	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP22_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGCAGTACGA	TGGCTCCGCGACGACAGCTT
dw3E1R2a_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAGTA	TGGCTCCGCGACGACAGCTT
dw3E1F2a_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		ATGGTGCGGCTGGTGGCCARG
dw3E1R4_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGC	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCAC	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGT	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTG	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGT	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAG	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGAT	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGT	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTAC	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP10_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTAGACT	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTA	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP12_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACTCTCG	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP13_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGAGACG	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP14_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACTGTACA	GTGACGGGTAGGCGAAGTCAAC
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dw3E1R4_SP16_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CACGCTAC	GTGACGGGTAGGCGAAGTCAAC
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dw3E1R4_SP18_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGACGTGA	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP19_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGATCAC	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP20_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGCACTA	GTGACGGGTAGGCGAAGTCAAC
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dw3E1R4_SP22_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGCAGTAC	GTGACGGGTAGGCGAAGTCAAC
dw3E1R4_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAG	GTGACGGGTAGGCGAAGTCAAC
dw3E1F3a_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		AAGCTGTCGTCGCGGAGCCA
rht1F1_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGCGT	AAGGACAAGATGATGGTGGC
rht1F1_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCACTC	AAGGACAAGATGATGGTGGC
rht1F1_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGTAG	AAGGACAAGATGATGGTGGC

rht1F1_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTGTC	AAGGACAAGATGATGGTGGC
rht1F1_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGTCT	AAGGACAAGATGATGGTGGC
rht1F1_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAGTG	AAGGACAAGATGATGGTGGC
rht1F1_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGATAC	AAGGACAAGATGATGGTGGC
rht1F1_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGTAC	AAGGACAAGATGATGGTGGC
rht1F1_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTACTC	AAGGACAAGATGATGGTGGC
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rht1F1_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAGTA	AAGGACAAGATGATGGTGGC
rht1R1_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		GAAGACGAGGACGAGGAAGA
dw3E2R1_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGC	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCAC	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGT	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTG	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGT	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAG	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGAT	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGT	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTAC	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP10_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTAGACT	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTA	GCAGCTTGATGATGAATGAGTG
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dw3E2R1_SP17_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGTAGAC	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP18_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGACGTGA	GCAGCTTGATGATGAATGAGTG

dw3E2R1_SP19_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGATCAC	GCAGCTTGATGATGAATGAGTG
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dw3E2R1_SP21_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGAGA	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP22_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGCAGTAC	GCAGCTTGATGATGAATGAGTG
dw3E2R1_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAG	GCAGCTTGATGATGAATGAGTG
dw3E1F6_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		GTTGACTTCGCCTACCCGTC
dw3E3F9_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGCGT	TGAGCGCGGTCTGCAGCTGT
dw3E3F9_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCACTC	TGAGCGCGGTCTGCAGCTGT
dw3E3F9_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGTAG	TGAGCGCGGTCTGCAGCTGT
dw3E3F9_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTGTC	TGAGCGCGGTCTGCAGCTGT
dw3E3F9_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGTCT	TGAGCGCGGTCTGCAGCTGT
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dw3E3F9_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTATG	TGAGCGCGGTCTGCAGCTGT
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dw3E3F9_SP13_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGAGACGAG	TGAGCGCGGTCTGCAGCTGT
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dw3E3F9_SP17_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGTAGACGT	TGAGCGCGGTCTGCAGCTGT
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dw3E3F10_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTG	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGT	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAG	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGAT	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGT	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTAC	TCCGACTTCTCCAACGCCGACT

dw3E3F10_SP10_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTAGACT	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTA	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP12_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACTCTCG	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP13_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGAGACG	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP14_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACTGTACA	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP15_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ATAGAGTA	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP16_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CACGCTAC	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP17_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGTAGAC	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP18_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGACGTGA	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP19_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGATCAC	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP20_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGCACTA	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP21_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGAGA	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP22_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGCAGTAC	TCCGACTTCTCCAACGCCGACT
dw3E3F10_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAG	TCCGACTTCTCCAACGCCGACT
dw3E3R10_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		GATGGCGGARCGCACGTTCT
dw3E3F11_SP1_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACGAGTGCGT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP2_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGACGCACTC	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP3_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGCACTGTAG	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP4_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CTCGCGTGTC	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP5_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGATACGTCT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP6_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CATAGTAGTG	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP7_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGAGAGATAC	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP8_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTCTAGTAC	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP9_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TGTACTACTC	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP10_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGTAGACTAG	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP11_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACGAGTATG	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP12_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TACTCTCGTG	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP13_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TAGAGACGAG	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP14_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ACTGTACAGT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP15_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	ATAGAGTACT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP16_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CACGCTACGT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP17_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CAGTAGACGT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP18_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGACGTGACT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP19_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGATCACGT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP20_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TCGCACTAGT	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP21_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	AGTCGAGAGA	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP22_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	CGCAGTACGA	GCATCTCGGTGATCGTGCAG
dw3E3F11_SP23_FA	CCATCTCATCCCTGCGTGTCTCCGACTCAG	TATGCTAGTA	GCATCTCGGTGATCGTGCAG
dw3E3R11_FB	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG		GGAGACCATGAGCACCATGAAG

Table S3 Comparison of two *dw3* homoeologous genes

	Identity
Gene level	0.916
Coding region	0.948
Noncoding region	0.667
Protein level	0.941
dN (nonsynonymous substitution rate)	0.033
dS (synonymous substitution rate)	0.125

Table S4 Summary of 454 reads

Region	PCR length (bp)	Ave length of reads(bp)	Number of reads
dw3E1F1/R1	468	399	31,309
dw3E1F2/R2	416	354	61,602
dw3E1F3/R4	488	413	37,817
dw3E1F6/E2R1	471	347	37,119
dw3E3F9/E3R1	428	359	41,259
dw3E3F10/E3R11	513	371	32,929
dw3E3F11/E3R11	458	380	34,237
rhtF1/R1	521	398	35,954
others			14,910

Table S5 Spectrum of mutations identified in the dwarfing candidate genes

Gene	Freq[a]	Position	WT_Nu[b]	Mu_Nu[c]	WT_AA[d]	Mu_AA[e]	Function[f]	SIFT[f]	Superpool	EMS[g]	Validation[h]
dw3a	5	89	A	G	E	G	missense	0	sp2	1.5%	
dw3a	7	104	C	T	P	L	missense	0	sp19	1.5%	
dw3a	3	200	A	G	N	S	missense	0	sp11	1.5%	
dw3a	17	238	A	G	S	G	missense	0.4	sp6	1.0%	
dw3a	19	503	C	T	A	V	missense	1	sp19	1.5%	YES
dw3a	11	582	C	T	R	R	silent	1	sp14	1.5%	
dw3a	6	628	A	T	T	S	missense	0	sp9	1.0%	
dw3a	3	677	T	A	V	D	missense	0	sp17	1.5%	
dw3a	3	730	G	A	A	T	missense	0.2	sp2	1.5%	
dw3a	10	742	G	A	A	T	missense	0	sp19	1.5%	YES
dw3a	3	838	G	A	A	T	missense	0.2	sp3	1.0%	
dw3a	6	840	G	A	A	A	silent	1	sp19	1.5%	
dw3a	9	863	G	A	R	Q	missense	0.1	sp11	1.5%	
dw3a	3	1023	G	A	G	G	silent	1	sp17	1.5%	
dw3a	6	1105	C	T	R	C	missense	0.1	sp14	1.5%	YES
dw3a	11	1124	G	A	G	D	missense	0	sp7	1.0%	
dw3a	4	1139	C	T	T	I	missense	0.1	sp7	1.0%	YES
dw3a	3	1177	C	T	Q	*	Stop codon	0	sp14	1.5%	NO
dw3a	9	1185	G	A	P	P	silent	1	sp9	1.0%	
dw3a	13	1189	A	T	S	C	missense	0.2	sp1	1.0%	
dw3a	5	1200	C	T	F	F	silent	1	sp14	1.5%	
dw3a	3	1228	A	G	K	E	missense	0	sp19	1.5%	
dw3a	4	1270	G	A	D	N	missense	0.5	sp16	1.5%	
dw3a	3	1294	A	G	T	A	missense	0.8	sp22	1.5%	
dw3a	8	1295	C	T	T	M	missense	0.1	sp14	1.5%	
dw3a	5	1315	G	A	G	S	missense	0.1	sp22	1.5%	
dw3a	10	1526	T	A	L	H	missense	0	sp17	1.5%	
dw3a	5	1564	C	T	L	L	silent	1	sp21	1.5%	
dw3a	9	1594	C	T	L	L	silent	1	sp21	1.5%	
dw3a	4	1606	G	A	D	N	missense	0.2	sp15	1.5%	
dw3a	7	1642	G	A	A	T	missense	0	sp23	1.5%	
dw3a	8	1811	G	A	S	N	missense	0	sp9	1.0%	
dw3a	3	1814	C	A	A	E	missense	0	sp15	1.5%	
dw3a	11	1840	G	A	V	M	missense	0	sp16	1.5%	
dw3a	3	1849	G	A	A	T	missense	0	sp2	1.5%	
dw3a	3	1960	A	T	I	F	missense	0.6	sp7	1.0%	
dw3a	4	1964	G	A	G	E	missense	0	sp23	1.5%	

dw3a	3	1999	G	A	G	S	missense	0.1	sp5	1.0%	
dw3a	3	2288	G	A	R	K	missense	0.2	sp17	1.5%	
dw3a	3	2451	G	A	Y	Y	silent	1	sp12	1.0%	
dw3a	6	2593	G	A	A	T	missense	0	sp14	1.5%	
dw3a	5	2855	C	T	A	V	missense	0	sp14	1.5%	
dw3a	3	2863	C	T	R	C	missense	0	sp6	1.0%	
dw3a	5	2867	C	T	A	V	missense	0	sp23	1.5%	
dw3a	3	2922	C	A	A	A	silent	1	sp10	1.0%	
dw3b	14	48	C	T	G	G	silent	1	sp18	1.5%	
dw3b	4	76	C	T	P	S	missense	0	sp18	1.5%	
dw3b	6	95	A	T	H	L	missense	0	sp15	1.5%	
dw3b	4	106	C	T	P	S	missense	0	sp20	1.5%	YES
dw3b	3	118	C	T	Q	*	Stop codon	0	sp19	1.5%	NO
dw3b	6	127	G	A	G	R	missense	0.2	sp21	1.5%	
dw3b	6	230	C	T	S	F	missense	0.1	sp18	1.5%	
dw3b	4	266	A	G	Q	R	missense	0	sp9	1.0%	
dw3b	9	377	C	T	A	V	missense	0	sp11	1.5%	
dw3b	4	427	C	T	L	F	missense	0	sp7	1.0%	NO
dw3b	3	478	C	T	L	L	silent	1	sp11	1.5%	
dw3b	3	495	G	A	L	L	silent	1	sp2	1.5%	
dw3b	3	499	T	G	Y	D	missense	0.9	sp2	1.5%	
dw3b	11	513	G	A	G	G	silent	1	sp19	1.5%	
dw3b	4	517	G	A	A	T	missense	0.1	sp20	1.5%	NO
dw3b	3	530	C	T	A	V	missense	1	sp16	1.5%	
dw3b	4	642	C	T	T	T	silent	1	sp16	1.5%	
dw3b	19	689	C	T	A	V	missense	0.1	sp20	1.5%	
dw3b	8	746	C	T	A	V	missense	0.2	sp22	1.5%	
dw3b	4	764	T	A	F	Y	missense	0.1	sp21	1.5%	
dw3b	5	813	C	T	V	V	silent	1	sp14	1.5%	
dw3b	4	829	G	A	A	T	missense	0	sp22	1.5%	
dw3b	3	843	C	T	L	L	silent	1	sp10	1.0%	
dw3b	8	850	G	A	A	T	missense	0.3	sp19	1.5%	
dw3b	10	855	G	A	A	A	silent	1	sp19	1.5%	
dw3b	8	920	A	T	Q	L	missense	0	sp23	1.5%	
dw3b	6	929	C	T	A	V	missense	0.1	sp1	1.0%	
dw3b	5	1041	C	T	L	L	silent	1	sp18	1.5%	
dw3b	4	1051	G	A	G	S	missense	0	sp21	1.5%	
dw3b	3	1143	C	T	A	A	silent	1	sp13	1.5%	
dw3b	3	1146	C	T	I	I	silent	1	sp20	1.5%	

dw3b	3	1163	C	T	S	F	missense	0	sp14	1.5%	
dw3b	6	1273	C	T	L	F	missense	0.1	sp20	1.5%	
dw3b	3	1318	G	A	V	M	missense	0	sp10	1.0%	
dw3b	3	1322	C	T	T	M	missense	0.1	sp17	1.5%	
dw3b	3	1354	G	A	A	T	missense	0.2	sp21	1.5%	
dw3b	7	1460	C	T	T	M	missense	0	sp19	1.5%	
dw3b	11	1481	G	A	R	K	missense	0	sp17	1.5%	
dw3b	3	1604	G	A	S	N	missense	0	sp8	1.0%	
dw3b	4	1621	C	T	L	L	silent	1	sp2	1.5%	
dw3b	6	1683	C	T	N	N	silent	1	sp14	1.5%	
dw3b	6	1738	G	T	E	*	Stop codon	0	sp14	1.5%	
dw3b	5	1739	A	G	E	G	missense	0	sp14	1.5%	
dw3b	4	1760	G	A	G	D	missense	0	sp18	1.5%	
dw3b	5	1831	G	A	A	T	missense	0	sp18	1.5%	
dw3b	5	1841	C	T	A	V	missense	0	sp11	1.5%	
dw3b	8	1867	G	A	V	M	missense	0	sp2	1.5%	
dw3b	3	1884	C	T	R	R	silent	1	sp16	1.5%	
dw3b	5	1899	G	A	R	R	silent	1	sp11	1.5%	
dw3b	3	1941	C	T	K	K	silent	1	sp6	1.0%	
dw3b	6	1984	G	A	E	K	missense	0	sp18	1.5%	
dw3b	3	2077	G	A	A	T	missense	0.7	sp19	1.5%	
dw3b	3	2210	T	C	F	S	missense	0.3	sp3	1.0%	
dw3b	14	2238	G	A	E	E	silent	1	sp19	1.5%	
dw3b	10	2257	A	T	M	L	missense	0.7	sp2	1.5%	
dw3b	3	2284	G	A	A	T	missense	0.6	sp17	1.5%	
dw3b	5	2287	G	A	G	R	missense	0.6	sp3	1.0%	
dw3b	11	2289	G	A	A	A	silent	1	sp15	1.5%	
dw3b	3	2387	C	G	A	G	missense	0	sp1	1.0%	
dw3b	7	2440	C	T	P	S	missense	0.5	sp5	1.0%	
dw3b	5	2772	G	A	R	R	silent	1	sp14	1.5%	
dw3b	10	2784	G	A	V	V	silent	1	sp18	1.5%	
dw3b	3	2797	G	A	V	M	missense	0	sp4	1.0%	
dw3b	5	2803	C	T	P	S	missense	0	sp23	1.5%	
dw3b	3	2892	G	A	I	I	silent	1	sp16	1.5%	
dw3b	8	2925	C	T	V	V	silent	1	sp20	1.5%	
dw3b	5	3035	G	A	G	E	missense	0	sp20	1.5%	
dw3b	3	3059	C	T	A	V	missense	0	sp6	1.0%	
dw3b	4	3133	C	T	R	C	missense	0	sp21	1.5%	
rht1a	4	358	C	T	P	S	missense	0	sp18	1.5%	YES

rht1a	3	408	C	T	G	G	silent	1	sp2	1.5%
rht1b	5	108	G	A	V	V	silent	1	sp21	1.5%
rht1b	3	160	G	A	A	T	missense	0.1	sp13	1.5%
rht1b	3	184	C	T	Q	*	Stop codon	0	sp23	1.5%
rht1b	4	219	C	A	A	A	silent	1	sp5	1.0%

[a] The mutation frequency in the total dataset

[b] The wild type nucleotide

[c] The mutated nucleotide

[d] The wild type amino acid

[e] The mutated amino acid

[f] Function and SIFT represent predicted protein function effect and the scores, respectively. A score value < 0.05 is usually predicted as damaging effect

[g] The EMS concentration used to treat the seeds

[h] PCR validation of selected mutations. YES indicates that a mutation was validated by Sanger sequencing. NO indicates that a mutation was found to be a false positive by Sanger sequencing

Table S6 Comparison of expected and observed types of mutations

	dw3		*rht1*	
	Expected	Observed	Expected	Observed
Missense	50.36%	70.18%	57.14%	50.00%
Silent	46.59%	27.19%	41.35%	50.00%
Stop codon	3.05%	2.63%	1.50%	