

Mapping of *Rf20(t)*, a minor fertility restorer gene for rice wild abortive

cytoplasmic male sterility in the maintainer line ‘Zhenshan97B’

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Supplementary Materials

Supplemental Table 1. Primer Sequences utilized in the Study

Primer	Forward Primer (5'-3')	Reverse Primer (5'-3')
RM25292	TGTCCCTTTCTCCAATTCTCTCG	TGTCTTCATCTTTGGCTCGATGG
RM25384	GGTGACCTGTGATGATGATATGC	CCAGACAGAGATTGAGAGATAACAAGC
RM24883	AGCTAGCTAACCAGTGGAGTAACC	GACTGAAGTTTGAAGCCAATGC
RM24919	TTATGAGCAGGATCTGACCAACG	CACAACTTCTCCGCTCAATTTCC
RM24957	CAGTAAGAACTTGGATCTCCTTCTCG	CACCTGCAATAGCCGATAACAACC
RM24963	ACCTCTCCTCCTCCTCTGATCC	GGCATATCCCACACGAAACC
ID10M00344	AGAGTGTTTAGCTGGGATCA	TGTGATCTTTGTCATCTTGG
STS10-122	TCACTTCACCGAATCAGCCT	CCGATGAGGACAAATTGTGGG
STS10-125	AGGGAAAAAAGATTTAGGGATCT	GGTAACTTGCACAAAAGAAA
STS10-126	GTTTGGTTCATGCATCTCACG	ACAAGGTGAGATGCAAGGGA
RM413	CCAATCTTGCTTCCGGATCTTGC	AGATAGCCATGGGCGATTCTTGG
RM3683	TGAGAATGGATACCTCCGACTCC	AACAGGAAACCCAATTCGATCC
RM18405	GATCGAACCAGCGCCTTTATCC	GGTGGAGGAGGAAGCAACACC
RM21953	TTGGCAAAGAAGCTCACAACAGG	GAAGAGATGGTGGACGATGATGAGG
RM27933	AACGAACGTGAACGAGCTAGGG	CAGGCTTGACGGACGACTCC
RM28651	ATGCTTCCTGGCTTCAACTCTGG	ATGCTTCCTGGCTTCAACTCTGG
qRT-10g02650 CDS-1	TGGACGATGGAGTGAGGCTGAC	TCCTGAAGCATCCTGAGTTCTGTCT
10g02650CX1-1	AAGCACAAGTGGTGAACATATCC	AGTGAAGACAGAGTTCTCATCCA
10g02650CX1-2	TGAGCAAACCTGAACAGCCTTA	AGTGAAGACAGAGTTCTCATCCA
10g02650CX2-1	CATCACACGCATACTTAGGACAT	GGAGTTCTTCAAGGTTTCAGGAA
10g02650CX2-2	CATCACACGCATACTTAGGACAT	ATGCCAAAGTGATTACCAAAGC
10g02650CX3-1	TCGCCTTCCTGAAACCTTGA	ATAGTGTGCTTGTGTAGAATGAGG
10g02650CX4-1	ATGAGATCAGGTGCAACATTGG	CGCTTACACGACGATGATATGG
<i>OsActin</i>	GGAAGTACAGTGTCTGGATTGGAG	TCTTGGCTTAGCATTCTTGGGT

Supplemental Table 2: Sequencing Data Summary for Each Sample

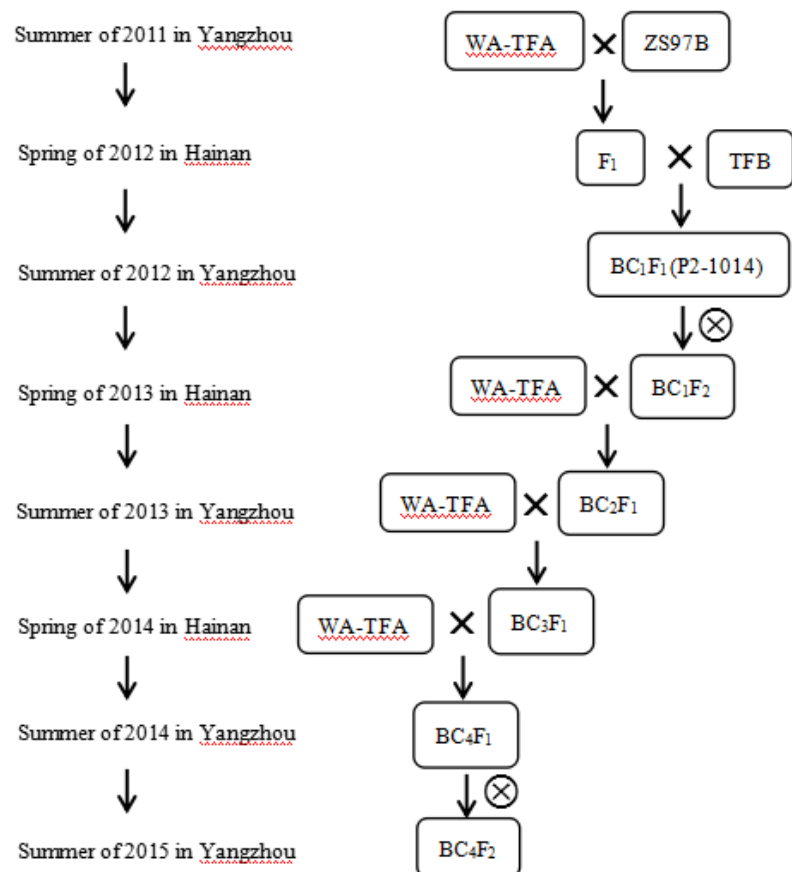
Sample	Total reads	Q30 percentage (%)	GC percentage (%)	SLAF number	Total depth	Average depth
Fertile pool	7,092,642	94.55	47.58	58,668	3,550,091	60.51
Sterile pool	7,514,607	92.98	47.80	58,383	3,717,785	63.68
TianfengB	3,316,879	94.36	47.26	56,138	1,718,411	30.61
Zhenshan 97B	3,087,650	93.92	47.04	56,132	1,536,702	27.38

Supplemental Table 3: Distribution of SLAF Markers on Each Chromosome

Chromosome ID	SLAF number	Polymorphic marker number	Selected for mapping
Chr 1	6846	403	88
Chr 2	5699	378	63
Chr 3	6257	616	310
Chr 4	5850	451	35
Chr 5	5585	483	240
Chr 6	4752	465	13
Chr7	4412	268	37
Chr 8	4311	272	41
Chr 9	3984	572	83
Chr 10	3572	564	112
Chr 11	3847	347	26
Chr 12	3783	487	114
Others	252	21	0
Total	59150	5327	1162

Supplemental Table 4: Predicted Genes in the 245-kb Target Region

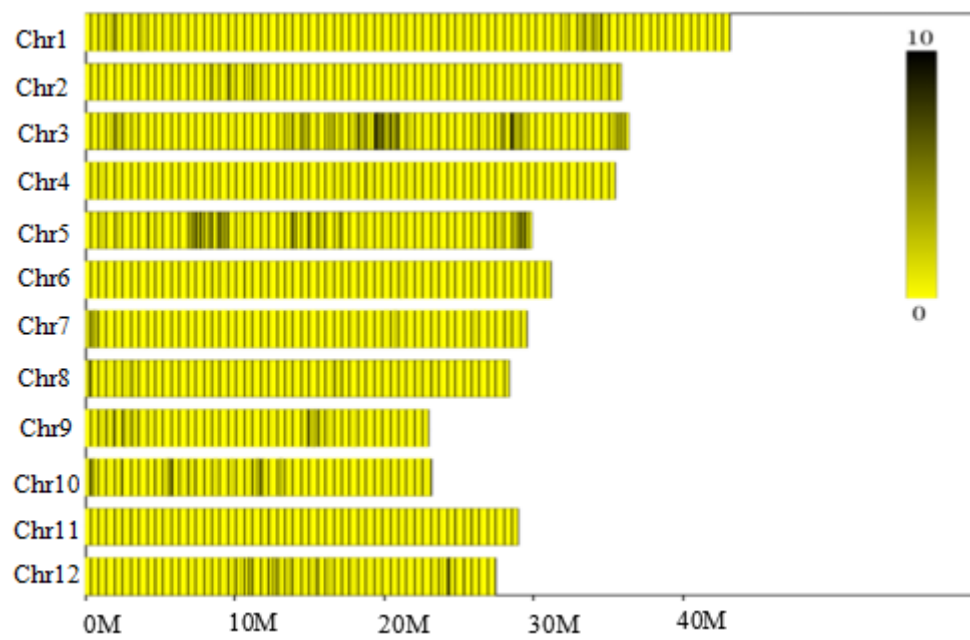
Locus Name	Gene Product Name
LOC_Os10g02380	oxidoreductase, aldo/keto reductase family protein, putative, expressed
LOC_Os10g02400	transposon protein, putative, unclassified, expressed
LOC_Os10g02410	expressed protein
LOC_Os10g02420	retrotransposon protein, putative, unclassified, expressed
LOC_Os10g02430	retrotransposon protein, putative, unclassified, expressed
LOC_Os10g02440	retrotransposon protein, putative, unclassified, expressed
LOC_Os10g02450	retrotransposon, putative, centromere-specific
LOC_Os10g02470	deoxymugineic acid synthase1, putative
LOC_Os10g02480	oxidoreductase, aldo/keto reductase family protein, putative, expressed
LOC_Os10g02490	oxidoreductase, aldo/keto reductase family protein, putative, expressed
LOC_Os10g02500	serine/threonine-protein kinase BRI1-like 2 precursor, putative, expressed
LOC_Os10g02509	GAGA-binding protein, putative, expressed
LOC_Os10g02520	transposon protein, putative, unclassified, expressed
LOC_Os10g02530	retrotransposon protein, putative, Ty3-gypsy subclass
LOC_Os10g02544	retrotransposon protein, putative, Ty3-gypsy subclass, expressed
LOC_Os10g02560	retrotransposon protein, putative, Ty3-gypsy subclass, expressed
LOC_Os10g02570	retrotransposon protein, putative, unclassified
LOC_Os10g02584	GAGA-binding protein, putative, expressed
LOC_Os10g02600	retrotransposon protein, putative, unclassified, expressed
LOC_Os10g02610	expressed protein
LOC_Os10g02620	GAGA-binding protein, putative, expressed
LOC_Os10g02625	gibberellin regulated protein, putative, expressed
LOC_Os10g02630	transposon protein, putative, CACTA, En/Spm sub-class, expressed
LOC_Os10g02640	expressed protein
LOC_Os10g02644	hypothetical protein
LOC_Os10g02650	PPR repeat containing protein, expressed
LOC_Os10g02660	transposon protein, putative, unclassified, expressed
LOC_Os10g02670	expressed protein
LOC_Os10g02680	EF hand family protein, putative, expressed
LOC_Os10g02690	expressed protein
LOC_Os10g02700	retrotransposon protein, putative, unclassified, expressed



Supplemental Fig. 1: Schematic Representation of the Experimental Design



Supplemental Fig. 2: Isolation treatment and Experimental Setup (TFA/ZS97B//TFB population, TFA/ZS97B F₁, and WA-TFA plants were surrounded by a sheet of 2-meter high polythene and natural).



Supplemental Fig. 3: Distribution of Polymorphic Tags on Chromosomes