Supplementary Figure 1: Alignment between all reported sequences PPR9-782-M, PPR9-782-I, PPR9-409, PPR9-782-(ZH). The in-del regions are highlighted in yellow.
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Supplementary Figure 2: Alignment of sequences between 10kb up and down stream of SF21 gene from *japonica* (4917224bp-4992046 bp) and *indica* (5350773 bp-5371596 bp). The sequence highlighted in yellow indicates the SF21 genomic region.
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Supplementary Figure 3: a) Amplification pattern of RMS-SF21-5 marker (targeting SF21) b) Amplification pattern of DRRMRF3-10 (Balaji et al.2012). In the above lanes L1 indicates 100 bp, L2 indicates 50bp ladder 1 indicates IR58025A, 2 indicates IR58025B, 3 indicates KMR3R and 4 indicates KRH2.
Supplementary Figure 4: Amplification pattern of RMS-PPR9-1, the candidate gene specific marker for *Rf4* in a set of public bred rice hybrids along with a known WA-CMS line (IR58025A) and a known restorer line (KMR3R)
Supplementary Figure 5: Detection of impurities in hybrid seed lot using RMS-PPR9-1 gene specific marker: DRRH3 seed lot was analyzed using gene specific marker RMS-PPR9-1 (targeting PPR9-782-M gene) specific for Rf4 loci and identified the individual plants with code number 6, 21 and 30 as off types (i.e. contaminants either as CMS line or male line are indicated with red arrow) in the hybrid seed lot of DRRH3. L indicates 50bp ladder, A indicates APMS 6A (WA-CMS line), R indicates RPHR1005 (restorer), H indicates DRRH3 (hybrid) and 1-46 samples are taken from DRRH3 hybrid seed lot.
Supplementary Figure 6: Alignment of protein sequences of putative candidate genes PPR9-782-M and PPR762.
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**Supplementary Figure 7**: Alignment between PPR9-782-M (Rf4), PPR9-409 (rf4), PPR3 and PPR762 gene sequences. The sequence highlighted in yellow represents the 105bp *in-del* present in all the putative candidate genes.
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Supplementary Figure 8: Alignment between sequenced amplicons of RMS-PPR9-1 candidate gene specific marker (for Rf4) from IR58025(WA-CMS) and KMR3R (restorer) lines shows the presence of 42 bp in-del polymorphism.