Dissecting the genome-wide genetic variants of milling and appearance quality traits in rice

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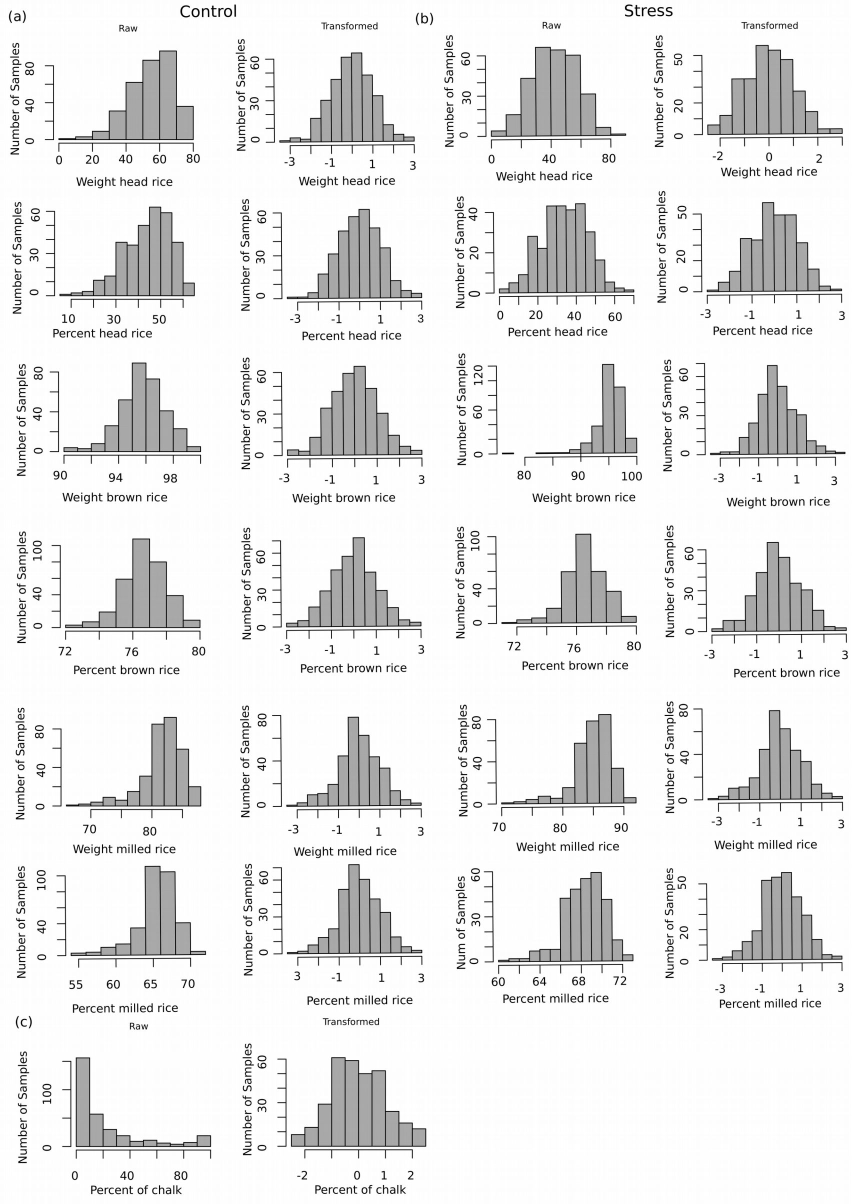


Figure S1: Phenotypic variation for milling quality traits and chalkiness in 320 indica panel. Raw and transformed phenotypic values for weight head rice, head rice yield, weight brown rice, percent brown rice, weight milled rice and percent milled rice, in controlled condition (a) and moister stressed condition (b); (c) Raw and transformed phenotypic value for percent grain chalkiness. X-axis represents respective absolute (in raw) or transformed trait values and y-axis represents the number of samples. All of the traits matched with the normal distribution pattern after getting transformed.

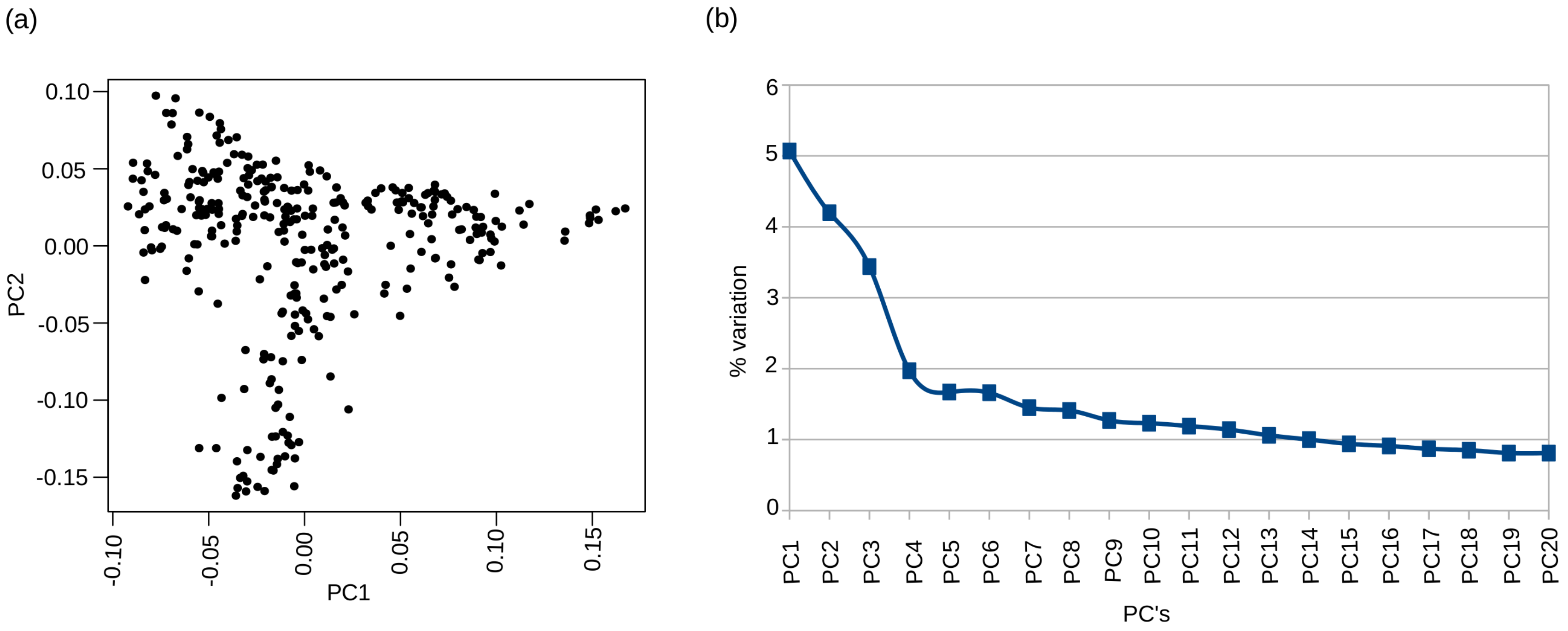


Figure S2: Principal component analysis (PCA) of 320 resequenced lines. (a) Biplot of the first two components, principal component (PC) 1, and PC2 based on 2.26 million high-dense SNPs. (b) Representation of percent variation explained in each PC as scree plot. First 4 PC's were detected to explain major proportion (14%) of the total variations.

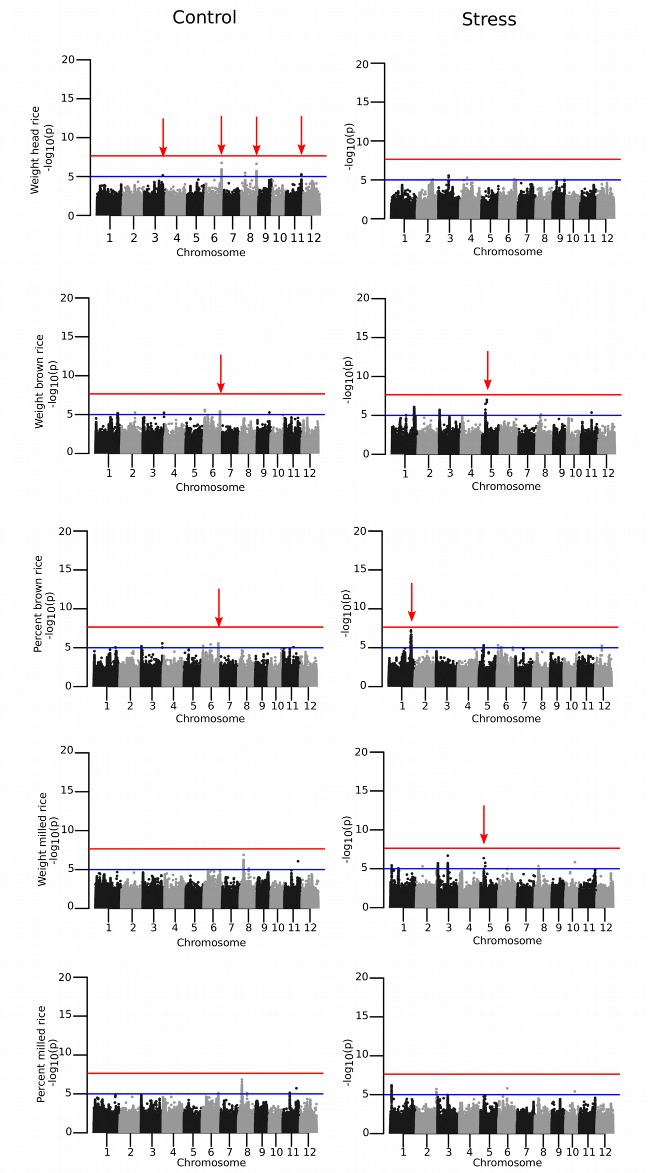


Figure S3: Manhattan-plots generated in GWAS for milling quality traits within *indica* germplasm. Manhattan plots generated for the output of single-locus GWAS for control and moister stress conditions were further validated using the multi-locus GWAS, and marked by red vertical arrow; Head rice yield (HRY) (a); weight head rice (WHR) (b); percent milled rice (PMR) (c); weight milled rice (WMR) (d); percent brown rice (PBR) (e) and weight brown rice (WBR) (f). Horizontal red and blue line in Manhattan plots represents the genome-wide significant threshold -$\log_{10}(P)$ value of 7.5 and 5, respectively.

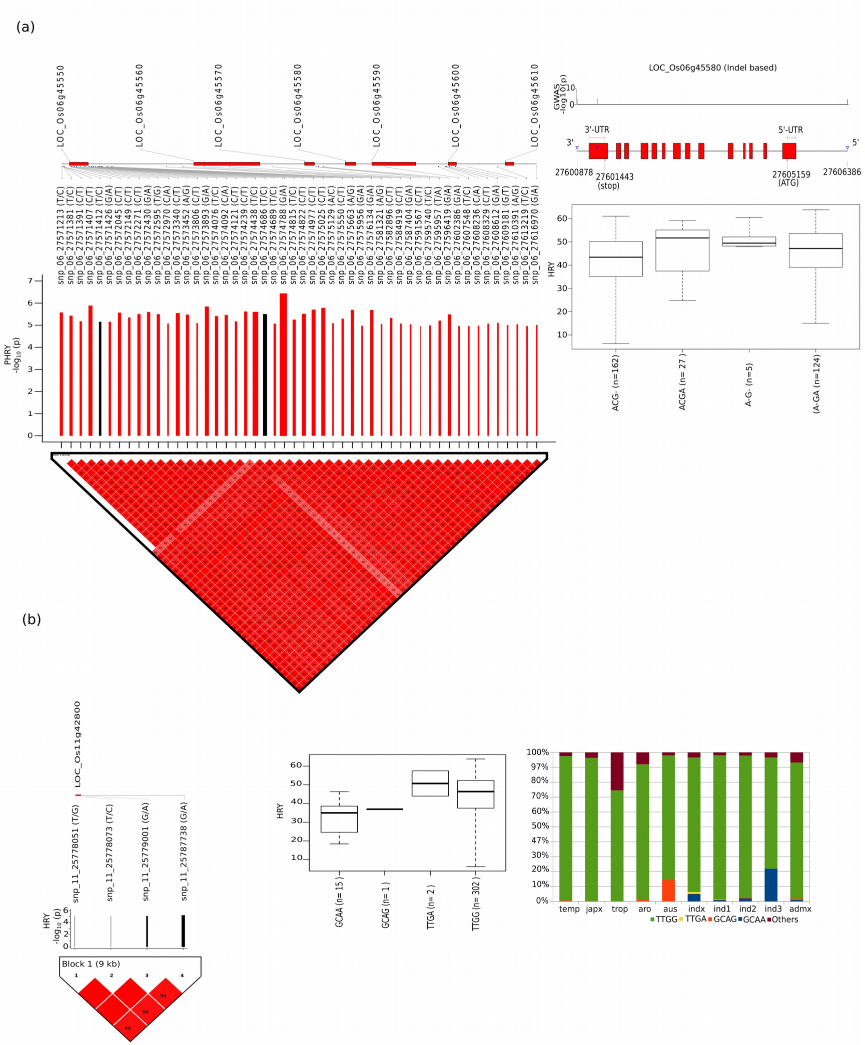


Figure S4: Single-locus GWAS for head rice yield (HRY) revealed the association of chromosome 6 and 11 genomic regions. (a) Linkage disequilibrium (LD) plot of the tag SNPs on chromosome 6 significantly associated with HRY. A scaled and highly dense LD-based plot within the hotspot genomic region on the chromosome is represented. Haplotypes constructed based on presence of Indels within neighboring region of LOC_Os06g45590, and their respective HRY phenotypic values were represented as boxplot. Deletion is mentioned as a dash (-) in haplotypes; (b) the linkage disequilibrium (LD) plot of 4 tagged SNP on chromosome 11 significantly associated with HRY. The positions of the tagged SNPs marked with the log $_{10}$-scaled P-values ($\log_{10}(P)$) and black/red bars reflecting their relative positive/negative effect sizes, respectively. Haplotypes with phenotypic values for HRY are represented as boxplot; the distribution of these haplotypes was further examined with data from the 3000 Rice Genomes Project (2014).

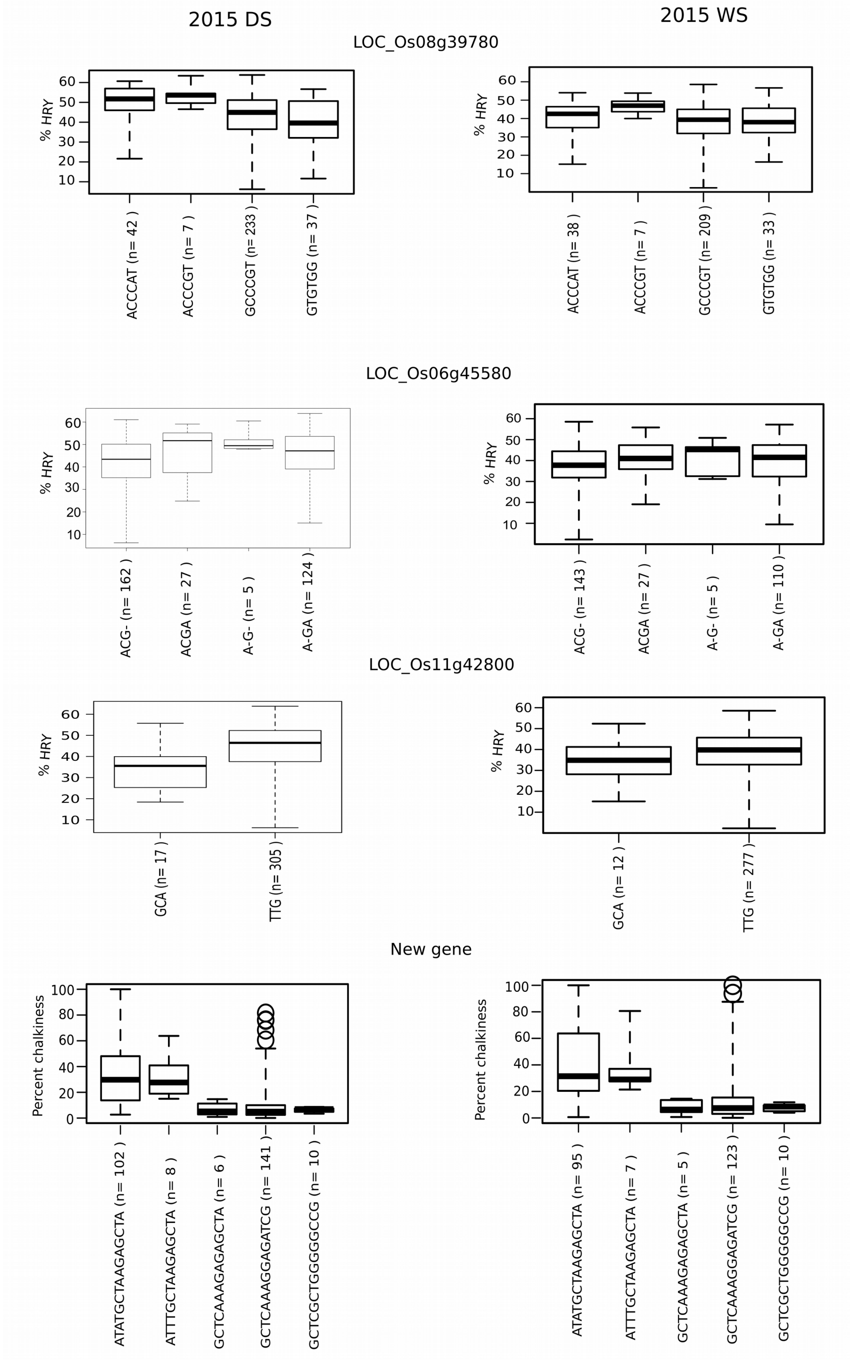


Figure S5: Variation in the phenotypic values of percent HRY and chalkiness observed for different haplotypes across dry and wet seasons. The phenotypic variations for % HRY in 2015DS and 2015WS were reflected by haplotypes identified in the candidates LOC_Os08g39780, LOC_Os06g45580 and LOC_Os11g42800 on chromosome 8, 6 and 11, respectively. Similarly, for percent chalkiness, haplotypes identified within a new gene (Chalk5.1) also depicted the consistency in the phenotype across the seasons.

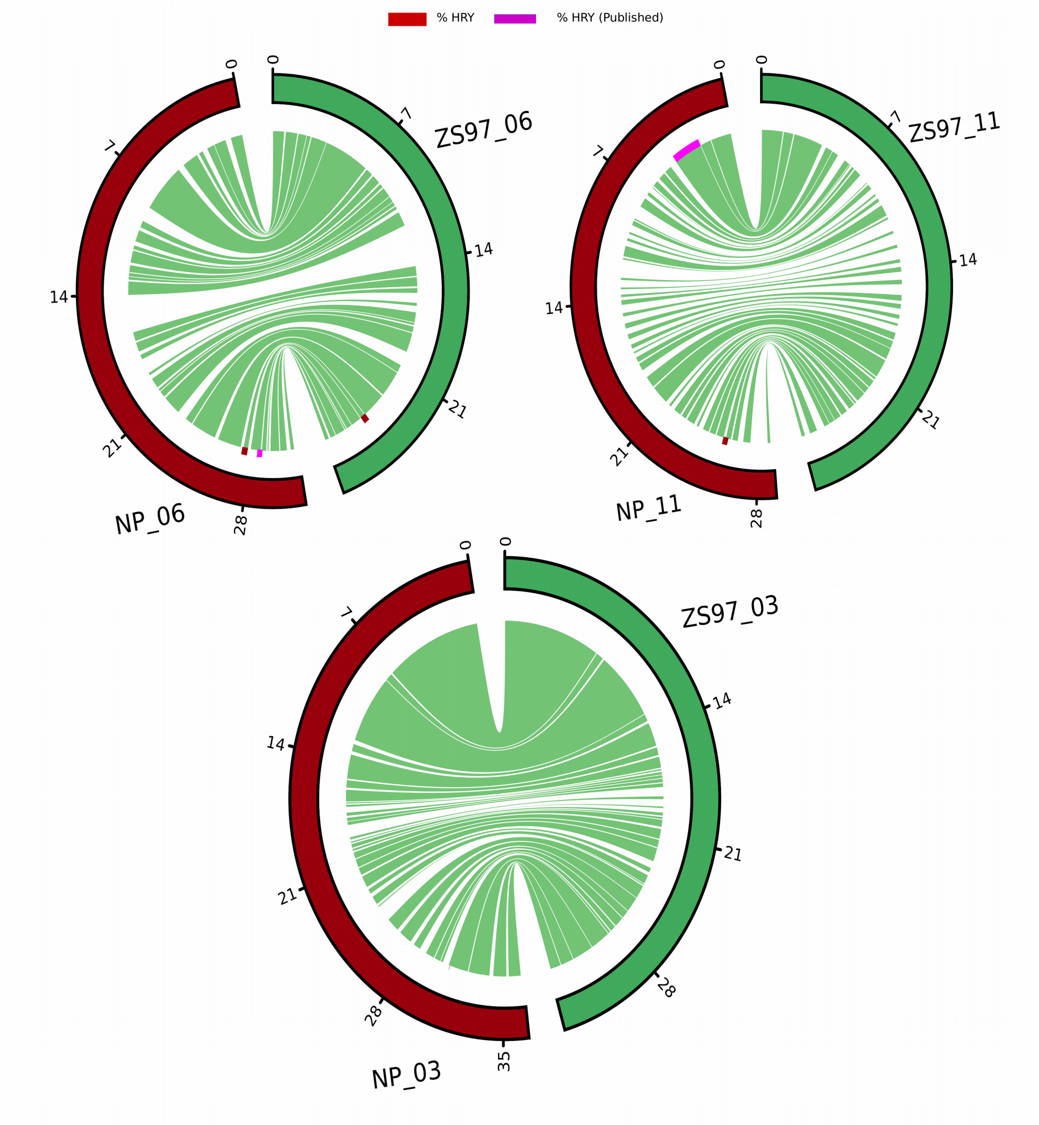


Figure S6: Comprehensive representation of structural variation and collinearity between *japonica* cultivar Nipponbare and *indica* cultivar ZS97. Circos plots depicted collinearity in chromosomes 3, 6 and 11(physical size shown in Mb), within *both* subspecies based on protein sequence alignment. The significant hotspot regions for HRY detected in our study (red colour) and previous studies (pink colour) were mapped on respective genomic positions. Likewise, the genomic region regulating chalk is represented in blue colour in the synteny map (circos). The conserved regions were represented in green lines, while, white gap in the region signifies the collinearity break in the region.

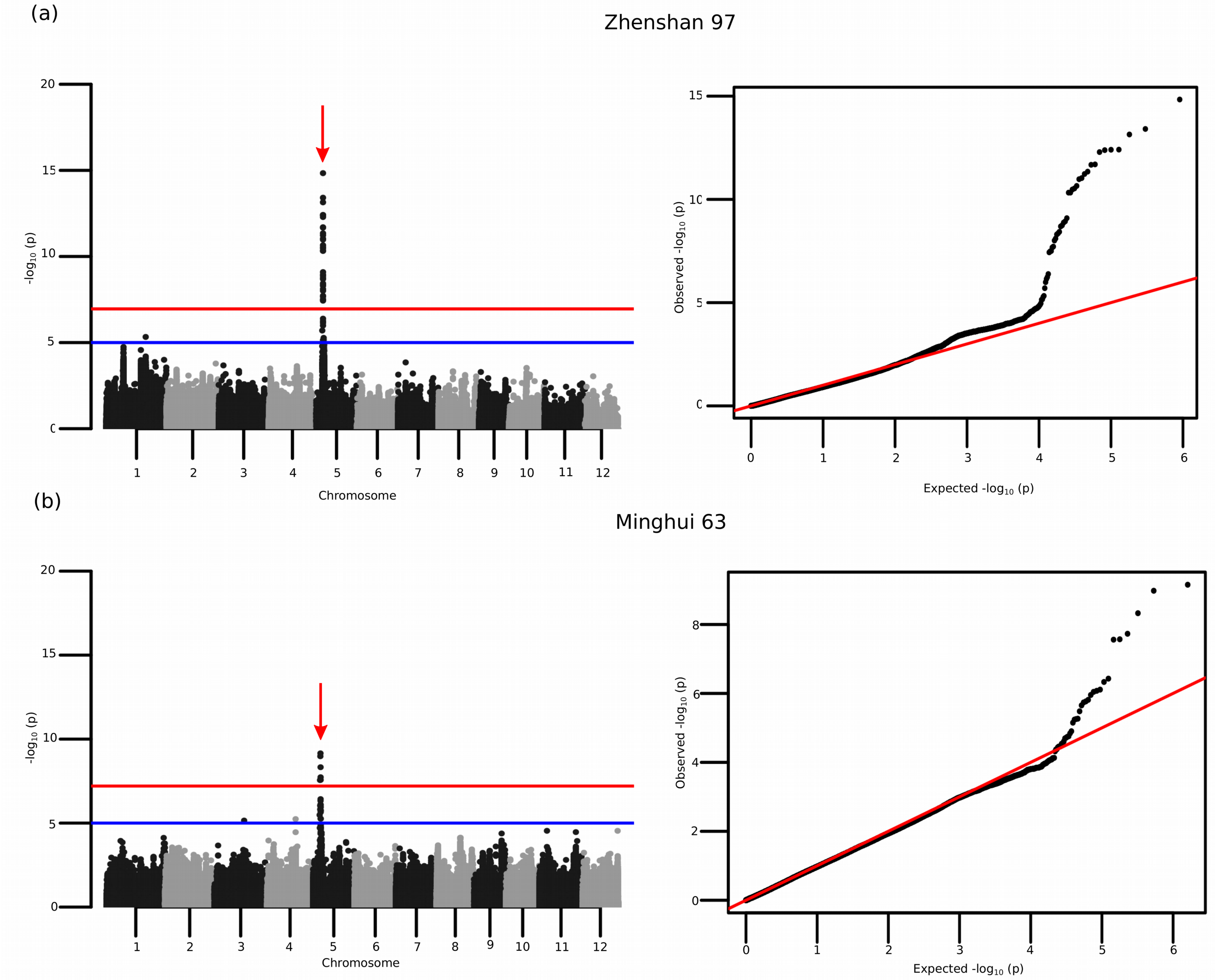


Figure S7: Single-locus GWAS for grain chalkiness identified prominent candidate loci on chromosomes 5 using *indica* reference genomes Zhanshan 97 (ZS97) and Minghui 63 (MH63). Manhattan and QQ- plots of the GWAS conducted on percent grain with chalkiness (PGC) in *indica* germplasm panel using ZS97 (a) and MH63 (b) reference genomes, respectively. A association peak on chromosome 5 was identified using both references and further validated using the multi-locus GWAS, and marked by red vertical arrow; Horizontal red and blue line in Manhattan plots represents the genome-wide significant threshold -log$_{10}$(*P*) value of 7 and 5, respectively.

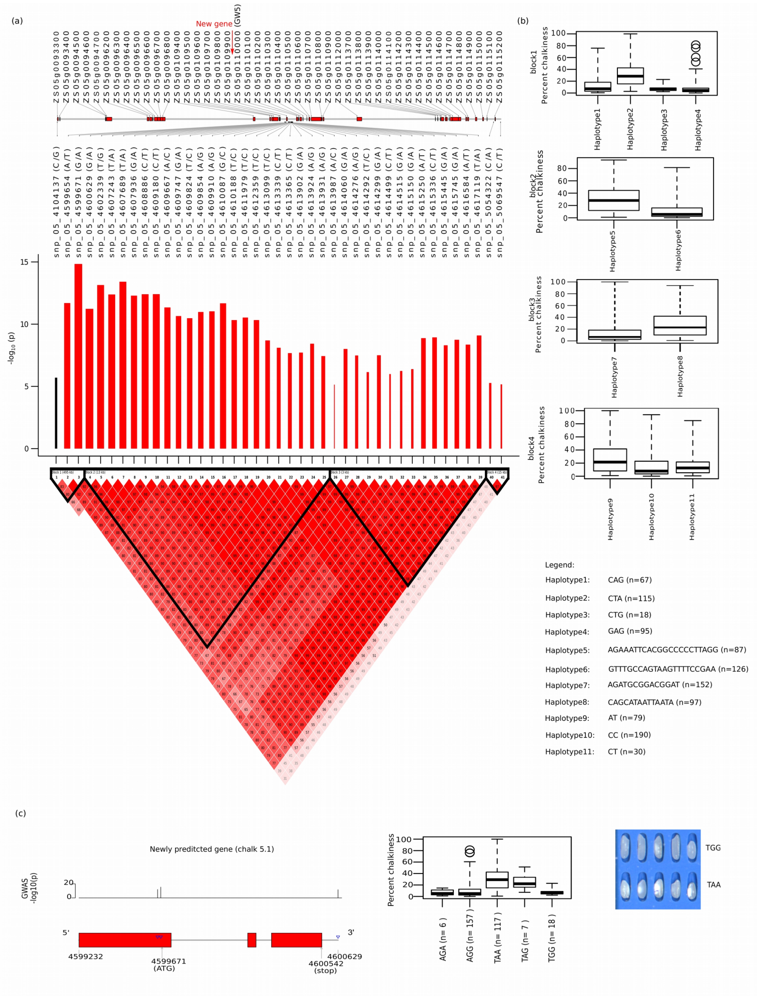
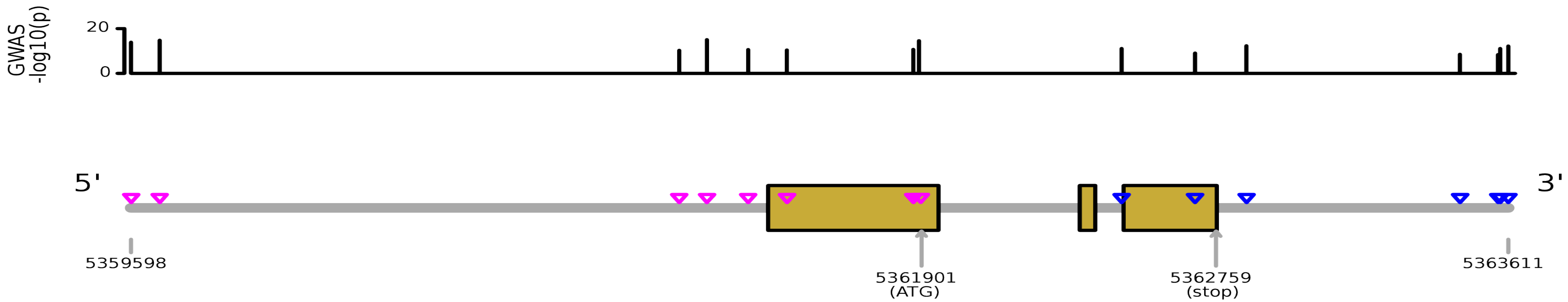


Figure S8: Single-locus GWAS for PGC revealed the significant association on chromosome 5 hotspot region to PGC using Zhenshan97 (*indica*) as a reference genome. (a) Scaled linkage disequilibrium (LD) plot of the 41 tagged-SNPs in the hotspot genomic region significantly associated with PGC and the position of newly predicted gene is highlighted in red arrow. The 41 tagged-SNPs were indicated with the log10-scaled P values (log10(P)) and black/red bars reflecting their relative positive/negative effect sizes, respectively, (b) 11 haplotypes constructed within 4 LD-blocks and their respective phenotypic values for PGC are represented as boxplots with haplotype allelic combination underneath. (c) TGAS of newly predicted gene (termed as chalk 5.1) identified the significant low chalk haplotype TGG, which is represented in boxplots with rest haplotype combinations, leftmost is the predicted gene modal with identified key SNPs while rightmost section depicted the image of 5 lines from each of two selected haplotypes showing grain phenotype.



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Nipponbare        GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCGTGTCACCCCCCACACCCCCACATAGACA
MH63              GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCGTGTCACCCCCCACACCCCCACATAGACA
10294_low         GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCGTGTCACCCCCCACACCCCCACATAGACA
10400_low         GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCGTGTCACCCCCCACACCCCCACATAGACA
10191_low         GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCATGTCACCCCCCACACCCCCACATAGACA
ZS97              GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCATGTCACCCCCCACACCCCCACATAGACA
10103_high        GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCATGTCACCCCCCACACCCCCACATAGACA
9617_high         GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCATGTCACCCCCCACACCCCCACATAGACA
10226_high        GACAAGGTGGGTCGATCGACCCAGCTATAGCCCCATGTCACCCCCCACACCCCCACATAGACA
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                                                                 snp_05_5359681(bHLH)
Nipponbare        CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAACTGC
MH63              CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAACTGC
10294_low         CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAACTGC
10400_low         CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAACTGC
10191_low         CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAACTGC
ZS97              CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAATTGC
10103_high        CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAATTGC
9617_high         CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAATTGC
10226_high        CCTCTAGCCCTCCTAGCAGCATATCCTGTCAACCCCACCAGCCTGATAAGTCAACAATTGC
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                         snp_05_5361195
Nipponbare        TATATGTAGAAAAAGTTTTTTTTTTAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
MH63              TATATGTAGAAAAAGTTTTTTTTTTAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
10294_low         TATATGTAGAAAAAGTTTTTTTTTTAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
10400_low         TATATGTAGAAAAAGTTTTTTTTTTAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
10191_low         TATATGTAGAAAAAGTTTTTTTTTTAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
ZS97              TATATGTAGAAAAAGTTTTTTTTTAAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
10103_high        TATATGTAGAAAAAGTTTTTTTTTAAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
9617_high         TATATGTAGAAAAAGTTTTTTTTTAAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
10226_high        TATATGTAGAAAAAGTTTTTTTTTAAAAAAAAATAAACATAGTTTAACAGTTTAGAAAAACGTAC
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                                                     snp_05_5361276 (Trihelix)
Nipponbare        TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAACTCCATAGACTCATATGA
MH63              TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAACTCCATAGACTCATATGA
10294_low         TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAACTCCATAGACTCATATGA
10400_low         TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAACTCCATAGACTCATATGA
10191_low         TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAACTCCATAGACTCATATGA
ZS97              TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAATTCCATAGACTCATATGA
10103_high        TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAATTCCATAGACTCATATGA
9617_high         TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAATTCCATAGACTCATATGA
10226_high        TAACAGAAAAATGAGAAAGTTACCGCTCAGATCTTAGACTTAATTCCATAGACTCATATGA
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                                                    snp_05_5361396(Myb)
Nipponbare        TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCATCTTTCGTGTATAACGT
MH63              TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCATCTTTCGTGTATAACGT
10294_low         TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCATCTTTCGTGTATAACGT
10400_low         TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCATCTTTCGTGTATAACGT
10191_low         TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCATCTTTCGTGTATAACGT
ZS97              TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCGTCTTTCGTGTATAATGT
10103_high        TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCGTCTTTCGTGTATAATGT
9617_high         TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCGTCTTTCGTGTATAATGT
10226_high        TCAACCGATGAGGTTGTACTTTGGATACATGTGTGCGAGTGCGTCTTTCGTGTATAACGT
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                                              Newly predicted genes Exon1
Nipponbare        GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
MH63              GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
10294_low         GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
10400_low         GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
10191_low         GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
ZS97              GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
10103_high        GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
9617_high         GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
10226_high        GGCCCTGTTCTTCCCCTCCCCACACACACATGAATGTGTGTGTATTTAAACGGCTTTTGGGG
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                                                snp_05_5361509 (AT-Hook)
Nipponbare        GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGAAAAAAATTGCAAGGCCGGGGCTTAG
MH63              GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGAAAAAAATTGCAAGGCCGGGGCTTAG
10294_low         GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGAAAAAAATTGCAAGGCCGGGGCTTAG
10400_low         GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGAAAAAAATTGCAAGGCCGGGGCTTAG
10191_low         GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGAAAAAAATTGCAAGGCCGGGGCTTAG
ZS97              GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGCAAAAAATTGCAAGGCCGGGGCTTAG
10103_high        GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGCAAAAAATTGCAAGGCCGGGGCTTAG
9617_high         GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGCAAAAAATTGCAAGGCCGGGGCTTAG
10226_high        GGTCACCTTTCGCAGGTACTATACCCCAAGAGCTGCAAAAAATTGCAAGGCCGGGGCTTAG
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                               snp_05_5361877/snp_05_4599654(TBP)
Nipponbare        TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTATGGATGAGTCATCAGT
MH63              TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTATGGATGAGTCATCAGT
10294_low         TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTATGGATGAGTCATCAGT
10400_low         TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTATGGATGAGTCATCAGT
10191_low         TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTATGGATGAGTCATCAGT
ZS97              TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTTTGGATGAGTCATCAGT
10103_high        TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTTTGGATGAGTCATCAGT
9617_high         TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTTTGGATGAGTCATCAGT
10226_high        TCGTTAGCAACAGTGGCCACGAGTCAAGATGCTGTATATATATGTTTGGATGAGTCATCAGT
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      snp_05_5361894/snp_05_4599671(C2H2)
Nipponbare        GTGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
MH63              GTGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
10294_low         GTGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
10400_low         GTGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
10191_low         GTGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
ZS97              ATGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
10103_low         ATGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
9617_low          ATGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
10226_low         ATGATGCATGATCTCACATCTCGTCACTGATGATCTCCAGCTTGAGCTTGCGCTGAGGTG
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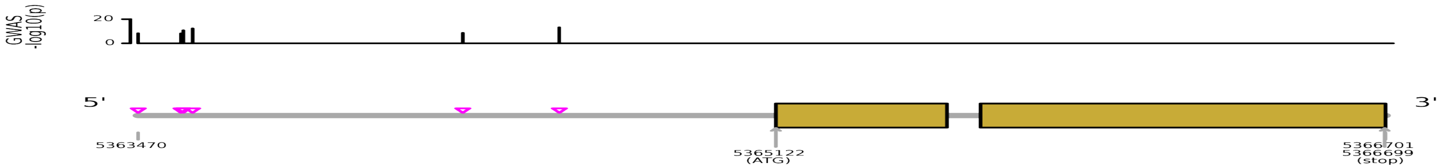

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MH63             GGGGTAGATCGACTCCCAGAAATCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
10294_low        GGGGTAGATCGACTCCCAGAAATCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
10400_low        GGGGTAGATCGACTCCCAGAAATCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
10191_low        GGGGTAGATCGACTCCCAGAAATCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
ZS97             GGGGTAGATCGACTCCCAGAAGTCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
10103_high       GGGGTAGATCGACTCCCAGAAGTCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
9617_high        GGGGTAGATCGACTCCCAGAAGTCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
10226_high       GGGGTAGATCGACTCCCAGAAGTCGGCGGCGGCCGGACCTGGACCGGCTACGGGAAGGGC
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                 snp_05_5363581(AP2)  snp_05_5363587(AP2)   snp_05_5363611(Tify)
Nipponbare       CGAGATTGGCTGTGCCGCCGCCAGGGACGACGGAAGGGGATCGGGAAGAGACAGATTACC
MH63             CGAGATTGGCTGTGCCGCCGCCAGGGACGACGGAAGGGGATCGGGAAGAGACAGATTACC
10294_low        CGAGATTGGCTGTGCCGCCGCTAGGGATGACGGAAGGGGATCGGGAAGAGACAGATTACC
10400_low        CGAGATTGGCTGTGCCGCCGCTAGGGATGACGGAAGGGGATCGGGAAGAGACAGATTACC
10191_low        CGAGATTGGCTGTGCCGCCGCCAGGGACGACGGAAGGGGATCGGGAAGAGACAGATTACC
ZS97             CGAGATTGGCTGCGCCGCTGCCAGGGACGACGGAAGGGGATCAGGAAGAGACAGATTACC
10103_high       CGAGATTGGCTGCGCCGCTGCCAGGGACGACGGAAGGGGATCAGGAAGAGACAGATTACC
9617_high        CGAGATTGGCTGCGCCGCTGCCAGGGACGACGGAAGGGGATCAGGAAGAGACAGATTACC
10226_high       CGAGATTGGCTGCGCCGCTGCCAGGGACGACGGAAGGGGATCAGGAAGAGACAGATTACC
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                                 snp_05_5364311(Tify)
Nipponbare       TGGGCTTACACTGTCCCTTTTTTATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
MH63             TGGGCTTACACTGTCCCTTTTTTATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
10294_low        TGGGCTTACACTGTCCCTTTTTTATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
10400_low        TGGGCTTACACTGTCCCTTTTTTATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
8674_low         TGGGCTTACACTGTCCCTTTTTTATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
10191_low        TGGGCTTACACTGTCCCTTTTTTATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
ZS97             TGGGCTTACACTGTCCCTTTTTGATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
10103_high       TGGGCTTACACTGTCCCTTTTTGATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
9617_high        TGGGCTTACACTGTCCCTTTTTGATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
10226_high       TGGGCTTACACTGTCCCTTTTTGATCGCTGCGTCCAATCCTAATCCACTATTTATGCCTA
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                                     snp_05_5364561 (MADF)
Nipponbare       AATGGTCTGAATTGTTCGTTATTAAGGGTAAATTATAAATTTACTAATATAATGATTACG
MH63             AATGGTCTGAATTGTTCGTTATTAAGGGTAAATTATAAATTTACTAATATAATGATTACG
10294_low        AATGGTCTGAATTGTTCGTTATTAAGGGTAAATTATAAATTTACTAATATAATGATTACG
10400_low        AATGGTCTGAATTGTTCGTTATTAAGGGTAAATTATAAATTTACTAATATAATGATTACG
10191_low        AATGGTCTGAATTGTTCGTTATTAAGGGTAAATTATAAATTTACTAATATAATGATTACG
ZS97             AATGGTCTGAATTGTTCGTTATTAAGGGTAAAGTATAAATTTACTAATATAATGATTACG
10103_high       AATGGTCTGAATTGTTCGTTATTAAGGGTAAAGTATAAATTTACTAATATAATGATTACG
9617_high        AATGGTCTGAATTGTTCGTTATTAAGGGTAAAGTATAAATTTACTAATATAATGATTACG
10226_high       AATGGTCTGAATTGTTCGTTATTAAGGGTAAAGTATAAATTTACTAATATAATGATTACG
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Figure S9: Nucleotide sequence alignment in the prominent chromosome 5 hotspot regions within cultivars with extreme chalk phenotypes. (a) Highly significant SNPs identified using TGAS in the newly predicted gene (*chalk5.1*) especially in the upstream region were represented in the gene model. Below, genome sequence of newly predicted gene region (*chalk5.1*) within three lines, possessing low (10294, 10400, 10191) and high chalky phenotypes (10103, 9617, 10226) were aligned with the three cultivars, Nipponbare (Intermediate chalk), ZS97 (high chalk) and MH63 (Low chalk), which were also used as reference genomes in present study. Highly significant allelic variations identified using the Nipponbare reference, in the promotor and 5'-UTR region, were observed consistent with their chalk phenotype; Significant SNPs observed in promotor region were predicted within the binding site of bHLH protein (snp_05_5359598, snp_05_5359681), tri-helix protein (topmost associated SNP; snp_05_5361276) and Myb-factor binding site (snp_05_5361396), whereas SNPs lying in 5'-UTR region were predicted within binding site of AT-hook (snp_05_5361509), TATA-binding protein (same SNP detected against Nipponbare references, snp_05_5361877; and ZS97 reference, snp_05_4599654) and C2H2-binding site (same SNP detected against Nipponbare references, snp_05_5361894; and ZS97 reference, snp_05_4599671). (b) Significant SNPs identified using TGAS in the upstream region of *GW5* (LOC_OS05g09520) gene, which harbour the binding site for transcription factor including AP2, TIFY, C2H2 and MADF. Blue highlighted region corresponds to 5'-UTR region and nucleotides highlighted in green signifies the corresponding transcription factor binding site.

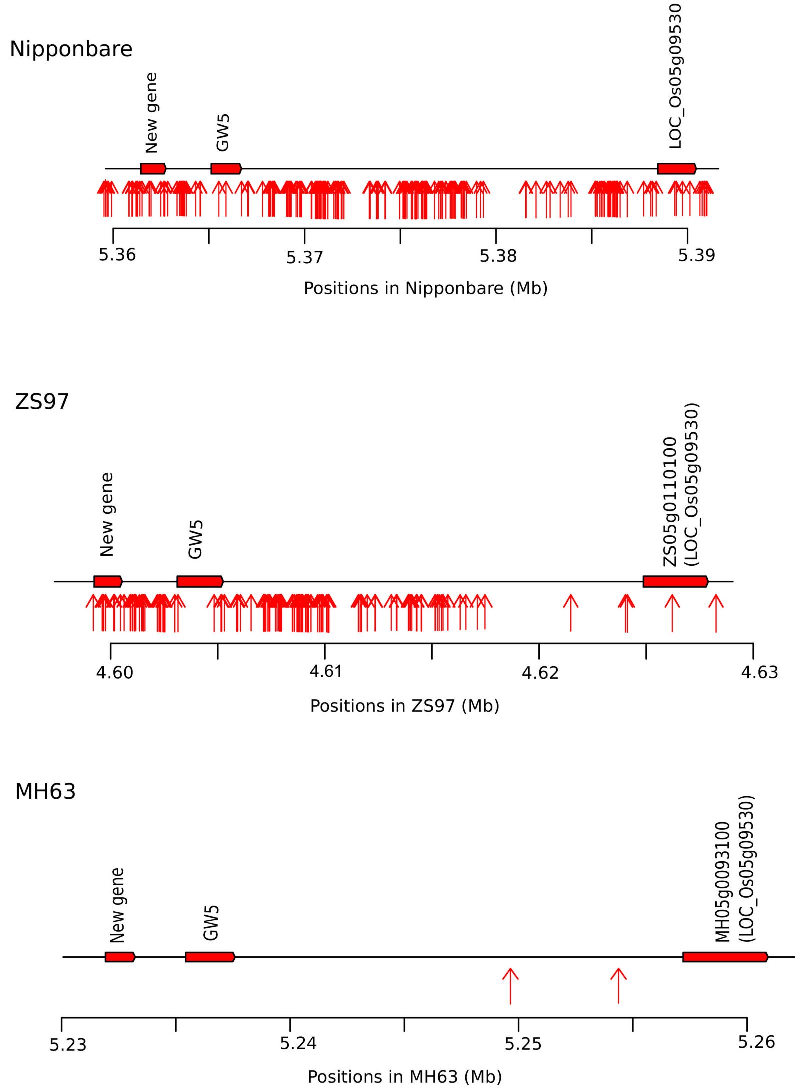

Figure S10: SNPs in the genomic sequence of chromosome 5 hotspot region regulating PGC, in the three cultivars (Nipponbare, ZS97, and MH63), used as reference genomes in the present study. In the genomic sequence of MH63, the very few SNPs are detected in the key genomic region, whereas, unlike MH63, in case of other ZS97 and Nippponbare, hotspot region possess sufficient SNPs, enabling the detection of three candidate genes regulating PGC. In the case of ZS97 and MH63, the gene ID in parenthesis showed the corresponding gene ID from the Nipponbare reference genome.

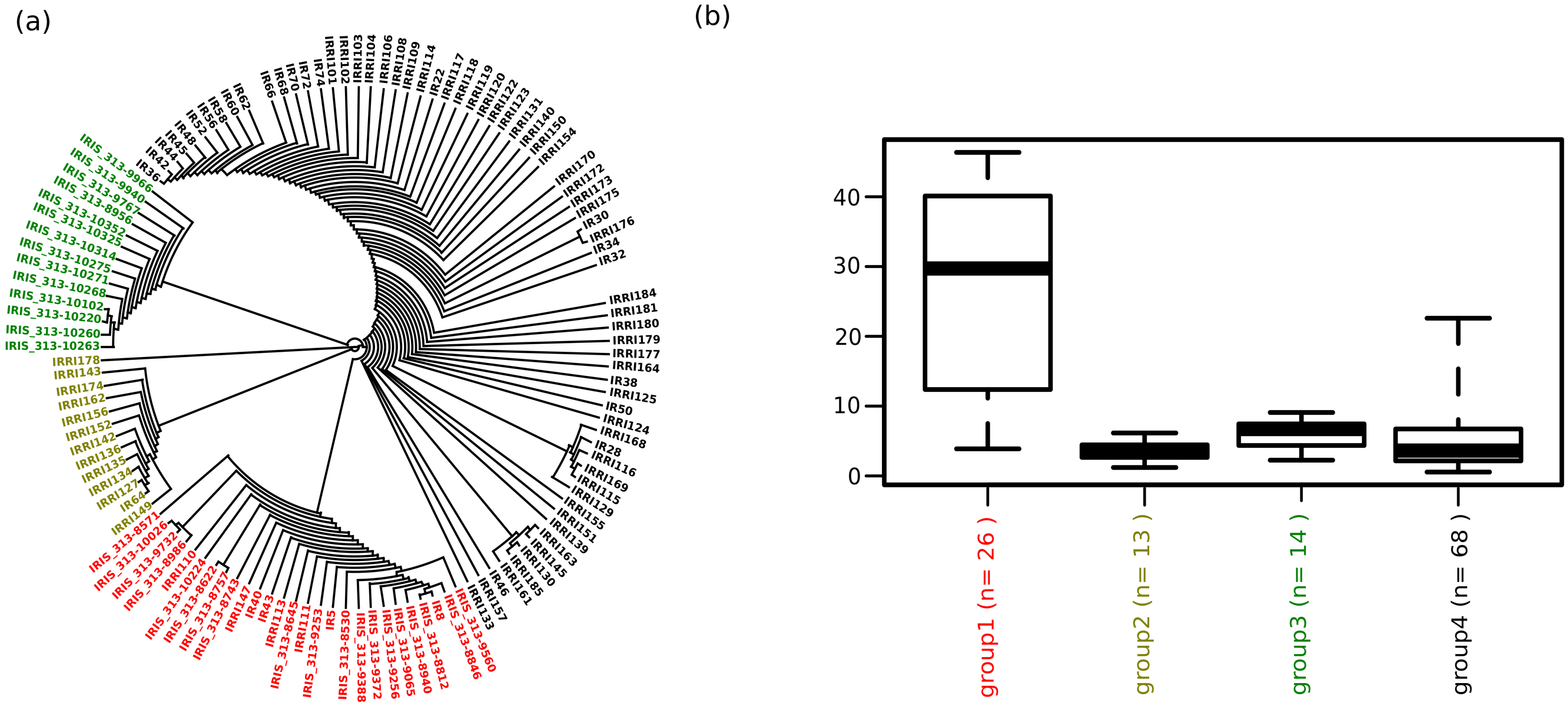

Figure S11: Allelic variations exist in chromosome 5 hotspot region and their distribution in IRRI breeding lines and selected core-collection cultivars. Unrooted dendrogram (a) and boxplot (b) for haplotypes of chromosome 5 hotspot region associated with percent grain chalkiness (PGC), group-1 (in red colour) clustered lines identified as high chalky (median 29.7%) consist of cultivars with high-chalk haplotype from core collection and IRRI breeding lines with high chalk phenotype, group-2 (yellowish green color) showed the low chalk lines (median 3.6%) including mega-varieties like IR-64, group-3 (green colour) depicted low chalkiness (median 6.7%) grouped the cultivars possessing low chalk haplotype lines from core collection and group-4 was represented in low chalk lines (median 3.6%) showing relatively high variance for PGC.