Table S7. List of SNPs associated with environmental factors in wild and cultivated rice subgroups

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chr. | Position (bp) | Gene ID a | Ref b | Alt c | The Freq. of Ref Allele | | | | Protein | Annotation |
| *AUS* | *IND* | *TEJ* | *TRJ* |
| 1 | 29642503 | [LOC\_Os01g51610](http://rice.plantbiology.msu.edu/cgi-bin/ORF_infopage.cgi?orf=LOC_Os01g51610) | T | C | 0.95 | 1.00 | 1.00 | 0.07 | Met→Thr | *OsLFL* |
| 1 | 31586773 | LOC\_Os01g54920 | T | A | 1.00 | 1.00 | 0.97 | 0.00 | Leu→stop codon | Heat- And Acid-Stable Phosphoprotein |
| 1 | 36075576 | LOC\_Os01g62330 | G | T | 1.00 | 0.25 | 0.99 | 0.99 | Arg→stop codon | Retrotransposon Protein |
| 2 | 28916153 | LOC\_Os02g47350 | T | C | 0.98 | 0.22 | 0.98 | 0.99 | Cys→Ser | Oxidoreductase, Short Chain Dehydrogenase/Reductase Family |
| 2 | 35349952 | LOC\_Os02g57720 | T | C | 0.61 | 0.02 | 0.90 | 0.70 | Val→Ala | *RWC3* |
| 3 | 3740218 | LOC\_Os03g07360 | C | T | 0.57 | 0.35 | 0.99 | 1.00 | Nonsynonymous | *OsDof12* |
| 4 | 28574775 | LOC\_Os04g48030 | C | T | 0.75 | 0.08 | 0.98 | 0.99 | Ser →Phe | Heat Stress Transcription Factor B-1 |
| 4 | 28602569 | LOC\_Os04g48070 | G | A | 1.00 | 1.00 | 0.00 | 1.00 | Gly→Ser | *ROC4* |
| 4 | 28809638 | LOC\_Os04g48320 | G | A | 1.00 | 0.27 | 1.00 | 1.00 | Gly→Ser | Retrotransposon Protein |
| 4 | 30313367 | LOC\_Os04g51180 | C | A | 1.00 | 0.99 | 1.00 | 0.37 | Cys→stop codon | *COLD1* |
| 4 | 30314011 | LOC\_Os04g51180 | C | T | 0.88 | 0.29 | 0.98 | 0.85 | Intron | *COLD1* |
| 5 | 2247939 | LOC\_Os05g04740 | A | C | 0.59 | 0.76 | 1.00 | 0.92 | Arg→Pro | *APG* |
| 6 | 2927171 | LOC\_Os06g06300 | T | C | 0.01 | 0.26 | 0.99 | 0.99 | Val→Ala | *RFT1* |

Table S7 continued

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chr. | Position (bp) | Gene ID a | Ref b | Alt c | The Freq. of Ref Allele | | | | Protein | Annotation |
| *AUS* | *IND* | *TEJ* | *TRJ* |
| 6 | 9336938 | LOC\_Os06g16370 | A | G | 0.17 | 0.88 | 0.26 | 0.05 | Asp→Gly | *Hd1* |
| 6 | 9337148 | LOC\_Os06g16370 | G | A | 0.00 | 0.00 | 0.73 | 0.04 | Nonsynonymous | *Hd1* |
| 6 | 9338330 | LOC\_Os06g16370 | G | A | 0.17 | 0.89 | 0.76 | 0.04 | Nonsynonymous | *Hd1* |
| 6 | 28103980 | LOC\_Os06g46340 | C | T | 0.99 | 1.00 | 0.99 | 0.31 | His→Tyr | Glycosyl Hydrolase |
| 6 | 28375654 | LOC\_Os06g46710 | C | A | 0.98 | 0.22 | 0.94 | 0.99 | Leu→Met | Retrotransposon Protein |
| 7 | 538827 | LOC\_Os07g01900 | G | A | 0.82 | 0.17 | 0.98 | 0.99 | Arg→Lys | Predicted Protein |
| 7 | 9152479 | LOC\_Os07g15770 | G | C | 0.88 | 0.30 | 0.97 | 0.99 | Arg→Ser | *Ghd7* |
| 7 | 9153799 | LOC\_Os07g15770 | T | C | 0.65 | 0.06 | 0.97 | 0.99 | Intron | *Ghd7* |
| 8 | 22689418 | LOC\_Os08g36000 | C | A | 0.01 | 0.00 | 0.96 | 0.97 | Ala→Asp | F-box Family (*COLDF*) |
| 8 | 22755828 | LOC\_Os08g36110 | C | T | 0.01 | 0.01 | 0.96 | 0.97 | Thr→Met | Zos8-06 - C2H2 Zinc Finger Protein |
| 8 | 22780583 | LOC\_Os08g36150 | T | A | 1.00 | 1.00 | 0.26 | 1.00 | Ala→Ala | Activator Of 90 Kda Heat Shock Protein Atpase Homolog |
| 8 | 22919119 | LOC\_Os08g36360 | T | G | 0.01 | 0.01 | 0.96 | 0.97 | Nonsynonymous | Retrotransposon Protein |

a: Gene ID of the MSU rice genome annotation project (http://rice.plantbiology.msu.edu/). b: Reference genome (Nipponbare) allele. c: Alternative allele.