**Table S1.** Distribution of SNPs across the 12 rice chromosomes used in GWAS analysis in this study.

| Chromosome | Length (bp, IRGSP-1.0) | SNP position (bp, start-end) | No. of SNPs | SNPs/Mb |
|---|---|---|---|---|
| 1 | 43,270,923 | 1,695-43,269,728 | 37,852 | 860.27 |
| 2 | 35,937,250 | 1,933-35,935,363 | 33,110 | 919.72 |
| 3 | 36,413,819 | 2,137-36,402,891 | 33,400 | 902.70 |
| 4 | 35,502,694 | 5,098-35,499,193 | 22,160 | 615.56 |
| 5 | 29,958,434 | 28,278-29,766,349 | 21,579 | 719.30 |
| 6 | 31,248,787 | 40,333-31,236,749 | 24,680 | 771.25 |
| 7 | 29,697,621 | 4,996-29,682,463 | 21,120 | 704.00 |
| 8 | 28,443,022 | 10,132-28,439,244 | 20,976 | 723.31 |
| 9 | 23,012,720 | 38,929-22,938,953 | 18,284 | 794.96 |
| 10 | 23,207,287 | 4,426-23,205,938 | 18,890 | 787.08 |
| 11 | 29,021,106 | 25,385-29,011,352 | 20,967 | 698.90 |
| 12 | 27,531,856 | 51,004-27,529,256 | 16,551 | 591.11 |
| Total (aver.) | 373,245,519 | - | 289,569 (24,131) | (757.35) |

**Table S2.** Evaluation of SPAD values with respect to epistasis of QTLs.

| Group | No. genetic resources | SPAD value | | | |
|---|---|---|---|---|---|
| | | Range | | Mean ± SD | |
| A | 9 | 47.6 ~ 55.3 | | 50.7 ± 2.7 | |
| B | 32 | 40.2 ~ 53.8 | | 45.6 ± 2.9 | |
| C | 60 | 34.1 ~ 44.3 | | 38.7 ± 2.1 | |
| | | | (32.4 ~ 55.4) | | (41.1 ± 4.3) |
| D | 5 | 38.0 ~ 45.0 | | 40.8 ± 2.9 | |
| E | 16 | 32.4 ~ 42.3 | | 37.9 ± 3.0 | |
| F | 38 | 33.7 ~ 44.5 | | 39.9 ± 2.8 | |

( ): Values in parentheses indicate the total range and total mean ± SD across genetic resources, A: *qSV3-1* + *qSV3-2* + *qSV6* + *qSV7*; B: *qSV3-1* + *qSV6* + *qSV7*; C: *qSV3-1* + *qSV7*; D: *qSV6* + *qSV7*; E: *qSV6*; F: None.

**Table S3.** Identification of candidate genes associated with SPAD values within a 200 kb flanking region of lead SNPs.

| MSU ID / RAP ID | Gene | Chromosome | Position (IRGSP – 1.0) (bp) | Function |
|---|---|---|---|---|
| *LOC_Os03g49870 / -* | - | 3 | - | transposon protein, putative, Mariner sub-class, expressed |
| *LOC_Os03g49880 / Os03g0706500* | *OsTB1/FC1* | 3 | 28428504 - 28430438 | TCP family transcription factor, putative, expressed |
| *LOC_Os03g49890 / -* | - | 3 | - | hypothetical protein |
| *LOC_Os03g49900 / Os03g0706900* | *OsRHC1, OsDGS1* | 3 | 28448846 - 28456395 | zinc finger, C3HC4 type domain containing protein, expressed |
| *LOC_Os03g49910 / -* | - | 3 | - | retrotransposon protein, putative, Ty1-copia subclass, expressed |
| *LOC_Os03g49920 / -* | - | 3 | - | expressed protein |
| *LOC_Os03g49930 / -* | - | 3 | - | pentatricopeptide, putative, expressed |
| *LOC_Os03g49940 / Os03g0707200* | *OsTT3.2* | 3 | 28470552 - 28473673 | integral membrane protein, putative, expressed |
| *LOC_Os03g49960 / Os03g0707300* | - | 3 | 28474312 - 28483670 | expressed protein |

**Table S3.** Continued

**Table S3.** Continued

| MSU ID / RAP ID | Gene | Chromosome | Position (IRGSP – 1.0) (bp) | Function |
|---|---|---|---|---|
| *LOC_Os03g49970 / Os03g0708600* | *OsRH21* | 3 | 28568746 - 28571308 | transposon protein, putative, CACTA, En/Spm sub-class, expressed protein<br>expressed |
| *LOC_Os03g49980 / Os03g0708700* | - | 3 | 28572774 - 28575246 | retrotransposon protein, putative, unclassified, expressed<br>expressed |
| *LOC_Os03g49990 / Os03g0708800* | *OsSLR17* | 3 | 28577263 - 28580786 | GRAS family transcription factor domain containing protein, transcription regulator, putative, expressed<br>expressed |
| *LOC_Os03g50010 / Os03g0708900* | *OsTOC64* | 3 | 28588605 - 28591841 | toc64, putative, expressed<br>toc64, putative, expressed |
| *LOC_Os03g50030 / Os03g0709000* | - | 3 | 28594360 - 28596338 | microsomal glutathione S-transferase 3, putative, expressed<br>microsomal glutathione S-transferase 3, putative, expressed |
| ***LOC_Os03g50040 / Os03g0709100*** | ***OsUCL8*** | **3** | **28598319 - 28599921** | **plastocyanin-like domain containing protein, putative,** phospholipase A2, putative, expressed<br>**expressed** |
| *LOC_Os03g50050 / Os03g0709200* | *OMT7* | 3 | 28600956 - 28603981 | NB-ARC domain containing protein, putative, expressed<br>phytanoyl-CoA dioxygenase, putative, expressed |
| *LOC_Os03g50060 / Os03g0709300* | *OsFBL69* | 3 | 28604758 - 28606325 | plastocyanin-like domain and DUF1639 domain containing protein, putative,<br>expressed |
| *LOC_Os03g50080 / Os03g0709400* | - | 3 | 28561107 - 28564805 | DUF1295 domain containing protein, putative, unclassified, expressed<br>retrotransposon protein, putative, unclassified, expressed |
| *LOC_Os03g50090 / Os03g0708500* | *OsFKBP17-2* | 3 | 28565482 - 28566757 | peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed protein<br>expressed |

**Table S3.** Continued

| MSU ID / RAP ID | Gene | Chromosome | Position (IRGSP – 1.0) (bp) | Function |
|---|---|---|---|---|
| *LOC_Os03g50210 / Os03g0710000* | - | 3 | 28631644 - 28633235 | DUF292 domain containing protein, expressed |
| *LOC_Os03g50220 / Os03g0710100-02* | *OsHOP2* | 3 | 28633286 - 28636276 | homologous-pairing protein meu13, putative, expressed |
| *LOC_Os03g50230 / Os03g0710100-01* | - | 3 | 28633318 - 28643842 | protein kinase, putative, expressed |
| *LOC_Os03g50240 / -* | - | 3 | - | hypothetical protein |
| *LOC_Os03g50250 / Os03g0710500* | *OsBIP2* | 3 | 28647086 - 28649570 | DnaK family protein, putative, expressed |
| *LOC_Os03g50260 / -* | - | 3 | - | expressed protein |
| *LOC_Os03g50270 / Os03g0710600* | - | 3 | 28651110 - 28653063 | expressed protein |
| *LOC_Os03g50280 / Os03g0710700* | - | 3 | 28655240 - 28657433 | GLTP domain containing protein, putative, expressed |
| *LOC_Os03g50290 / Os03g0710800* | *OsGF14F* | 3 | 28664068 - 28667703 | 14-3-3 protein, putative, expressed |
| *LOC_Os03g50300 / Os03g0710900* | - | 3 | 28671127 - 28678954 | CASP, putative, expressed |

**Table S3.** Continued

| MSU ID / RAP ID | Gene | Chromosome | Position (IRGSP – 1.0) (bp) | Function |
|---|---|---|---|---|
| *LOC_Os03g50310 / Os03g0711100* | *OsCCT14* | 3 | 28686958 - 28689501 | CCT/B-box zinc finger protein, putative, expressed |
| *LOC_Os03g50320 / Os03g0711200* | - | 3 | 28690392 - 28695611 | phosphatidylinositol 4-kinase PI4K, putative, expressed |
| *LOC_Os03g50325 / -* | - | 3 | - | phosphatidylinositol 4-kinase, putative, expressed |
| *LOC_Os03g50330 / Os03g0711300* | - | 3 | 28708952 - 28716214 | CAMK_KIN1/SNF1/Nim1_like.18 - CAMK includes calcium/calmodulin dependent protein kinases, expressed |
| *LOC_Os03g50340 / Os03g0711400* | *OsWD40-84* | 3 | 28719395 - 28724712 | coatomer alpha subunit, putative, expressed |
| *LOC_Os03g50350 / Os03g0711500* | *OsWD40-85* | 3 | 28730960 - 28732934 | coatomer alpha subunit, putative, expressed |
| *LOC_Os03g50355 / -* | - | 3 | - | AT hook-containing DNA-binding protein, putative, expressed |
| *LOC_Os03g50364 / Os03g0711600* | - | 3 | 28751264 - 28742402 | expressed protein |
| *LOC_Os03g50380 / Os03g0711700* | - | 3 | - | DNA-directed RNA polymerase I subunit RPA12, putative, expressed |
| *LOC_Os03g50390 / Os03g0711800* | *OsAGC8* | 3 | 28750215 - 28762250 | AGC_AGC_other_GWLd.2 - ACG kinases include homologs to PKA, PKG and PKC, expressed |

**Table S3.** Continued

| MSU ID / RAP ID | Gene | Chromosome | Position (IRGSP – 1.0) (bp) | Function |
|---|---|---|---|---|
| *LOC_Os03g50400 / -* | - | 3 | - | expressed protein |
| *LOC_Os03g50410 / -* | - | 3 | - | lipase family protein, expressed |
| *LOC_Os03g50420 / Os03g0712100* | - | 3 | 28769963 - 28772120 | expressed protein |
| *LOC_Os03g50430 / Os03g0712200* | - | 3 | 28774588 - 28777241 | zinc finger family protein, putative, expressed |
| *LOC_Os03g50440 / Os03g0712300* | *OsUEV1A* | 3 | 28781652 - 28786598 | ubiquitin-conjugating enzyme, putative, expressed |
| *LOC_Os03g50450 / Os03g0712400* | *OsRLK902-1* | 3 | 28797570 - 28798180 | inactive receptor kinase At2g26730 precursor, putative, expressed |
| *LOC_Os03g50470 / Os03g0712600* | - | 3 | 28804844 - 28810296 | expressed protein |

Candidate gene related to SPAD value is indicated in bold.

**Table S4.** Information on the SNP marker (dCAPS) for selecting SPAD values.

| Oligo name | SNP | Position | Allele | Sequence (5’ → 3’) | Type | Tm (℃) | Product size (bp) |
|---|---|---|---|---|---|---|---|
| qSV3-2_F1 | AX-154973481 | 3: 28,612,703 | G/A | TCTTGTTACGCTTAATGGGAAACTGCCTAA | dCAPS | 60 | 212/186 |
| qSV3-2_R1 | | | | GACCGAGTTCTTCTGTGCCA | | | |

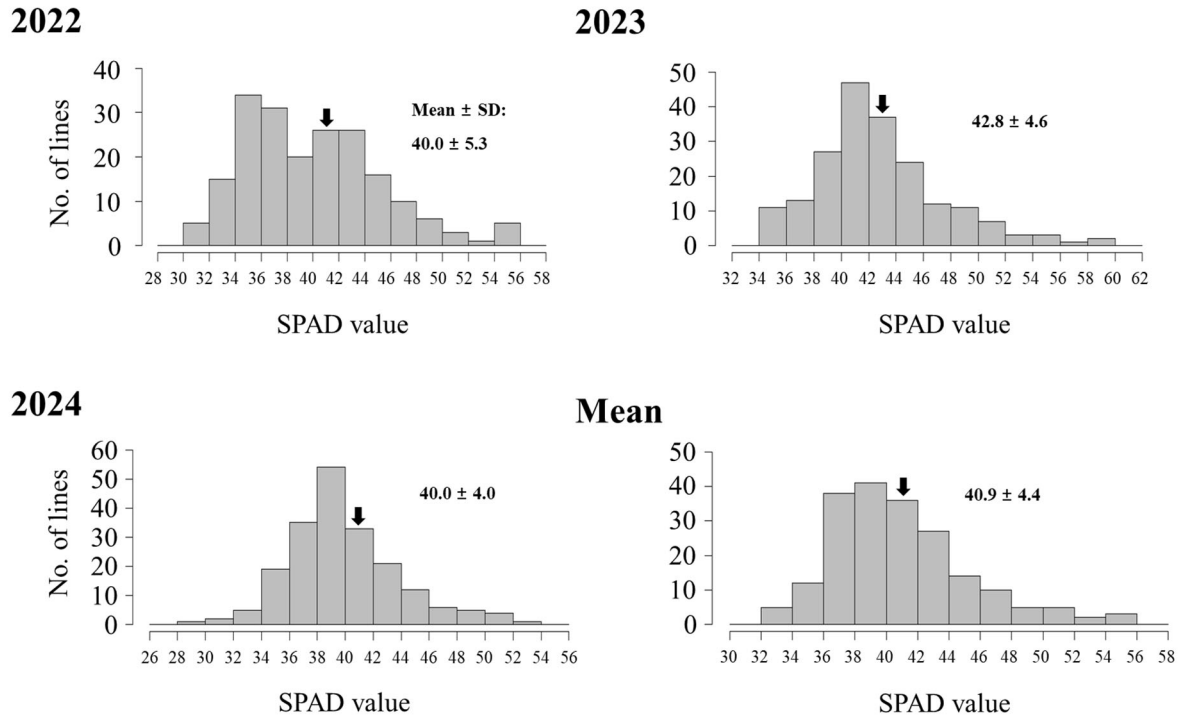



**Figure S1.** Distribution of SPAD values in 198 rice genetic resources across three years (2022–2024) and their mean values. *Arrow with smooth end* represents mean ± SD.

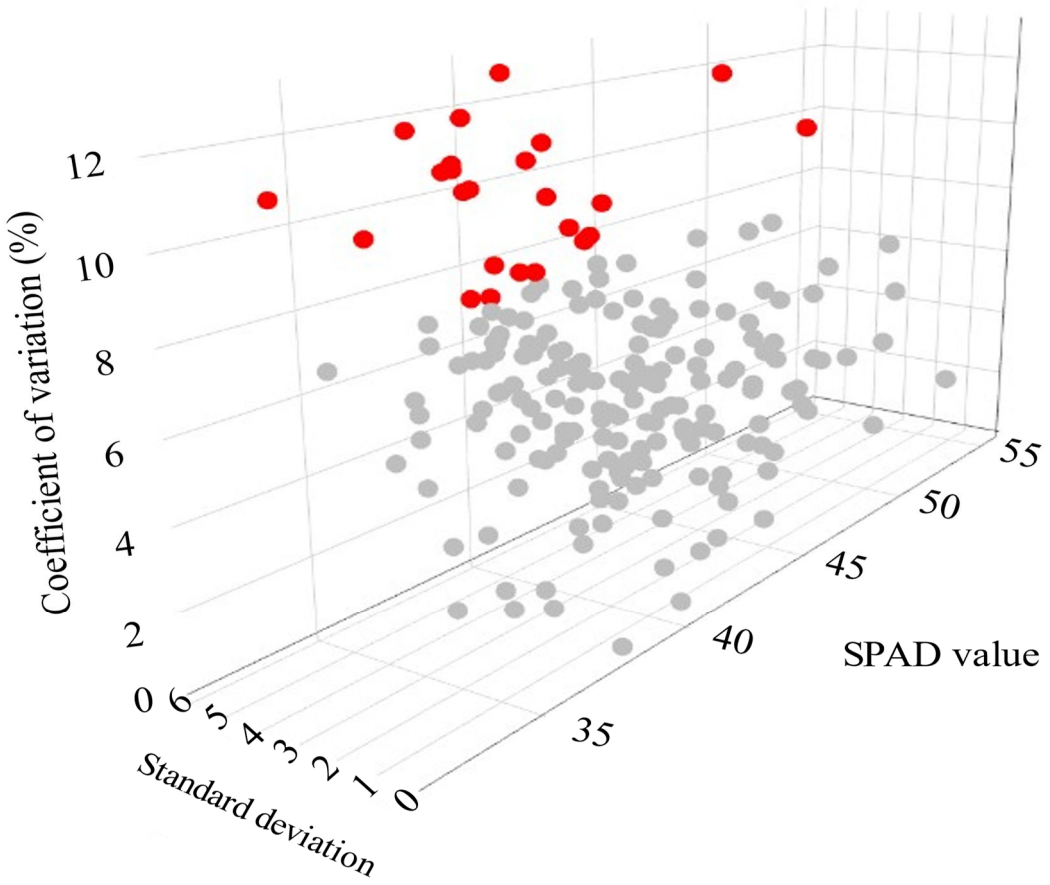



**Figure S2.** Scatter plot of 198 genetic resources showing the relationship between coefficient of variation (CV) and standard deviation (SD). Red points indicate outliers with CV ≥8.3, which were excluded from subsequent selection, resulting in 175 genetic resources chosen for further analysis.

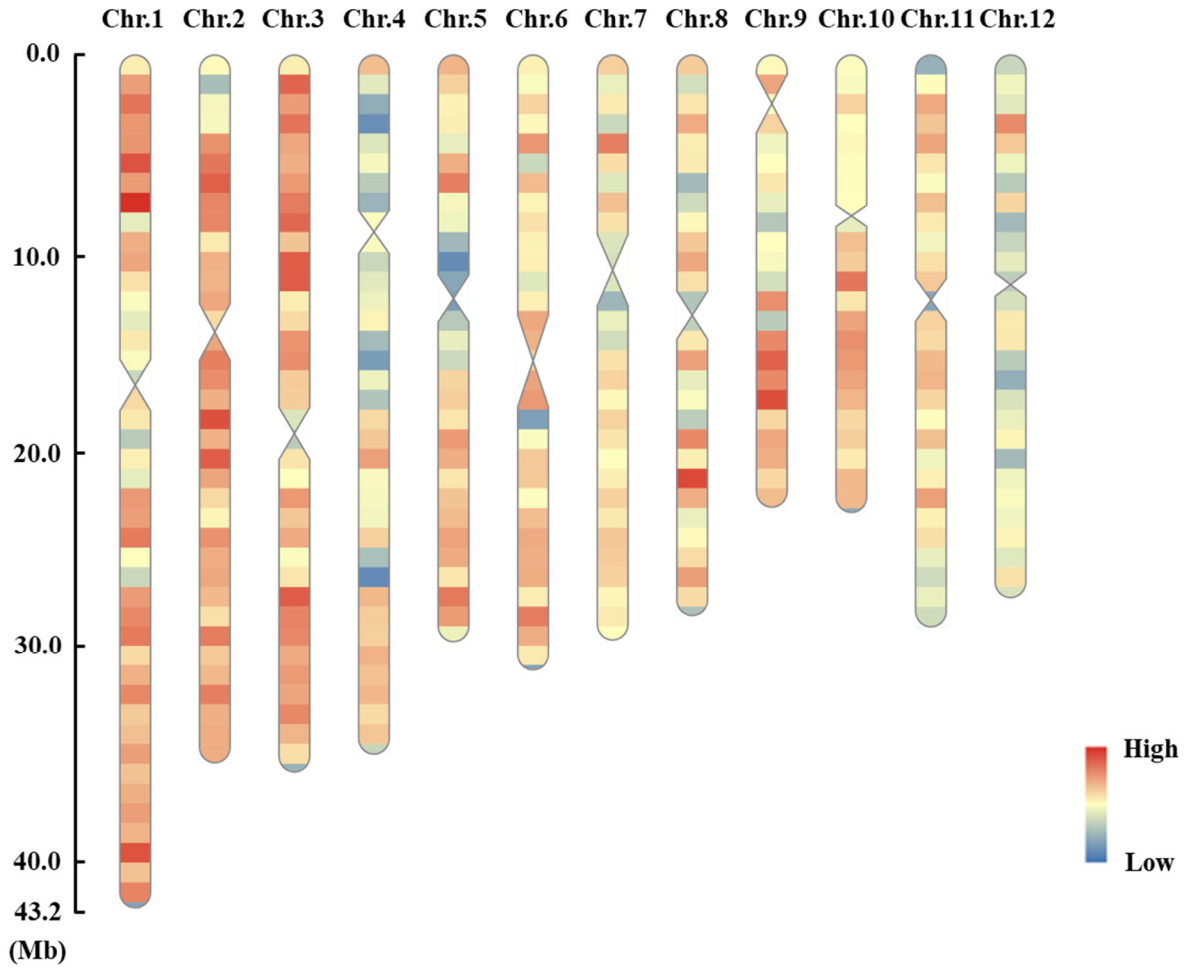



**Figure S3.** Distribution of SNP density on each chromosome. SNP density plot chromosome-wise represents number of SNPs within 1 Mb window size. The vertical axis shows the chromosome length (Mb); the color depicts SNP density. As the color changes from red to blue, the number of SNPs decreases.

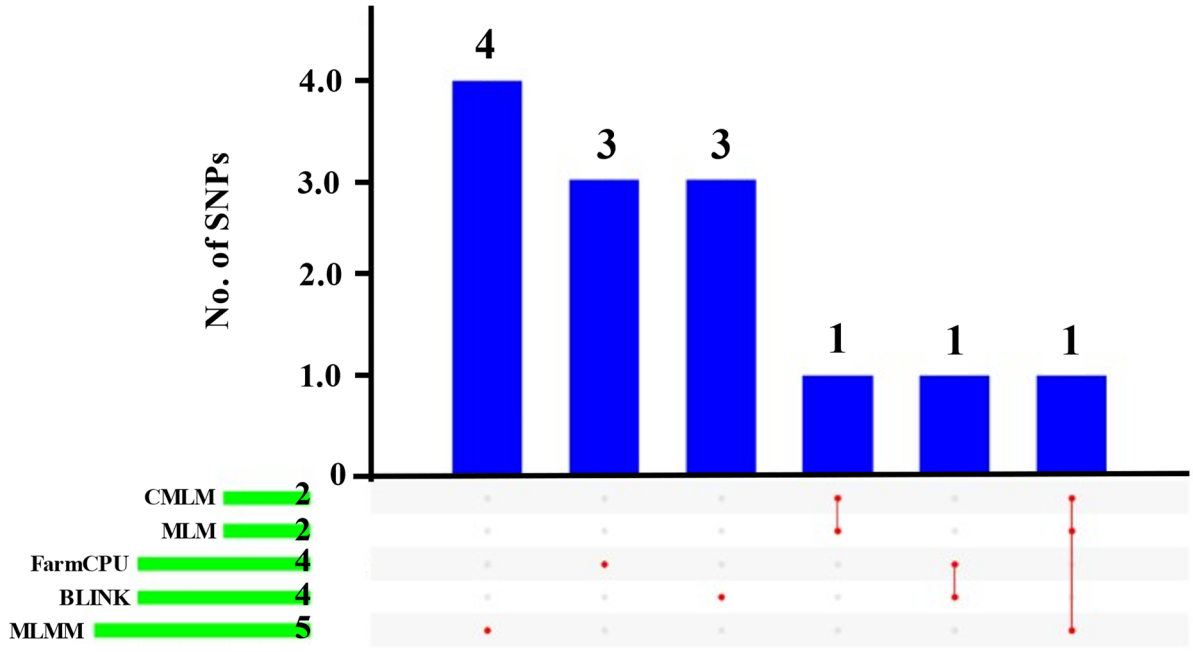



**Figure S4.** Distribution of lead SNPs associated with SPAD values using 5 models (BLINK, CMLM, FarmCPU, MLM, and MLMM) in GWAS. Vertical bars represent the number of SNPs identified by each model. SNP identified by multiple models were counted only once. Horizontal bars and corresponding numbers represent the number of SNPs in each model. The number of SNPs for each model was calculated by summing the counts of vertical bars that include a red dot corresponding to that model. Vertical bars represent the number of SNPs commonly identified by two or more models, while red dots indicate the corresponding models.

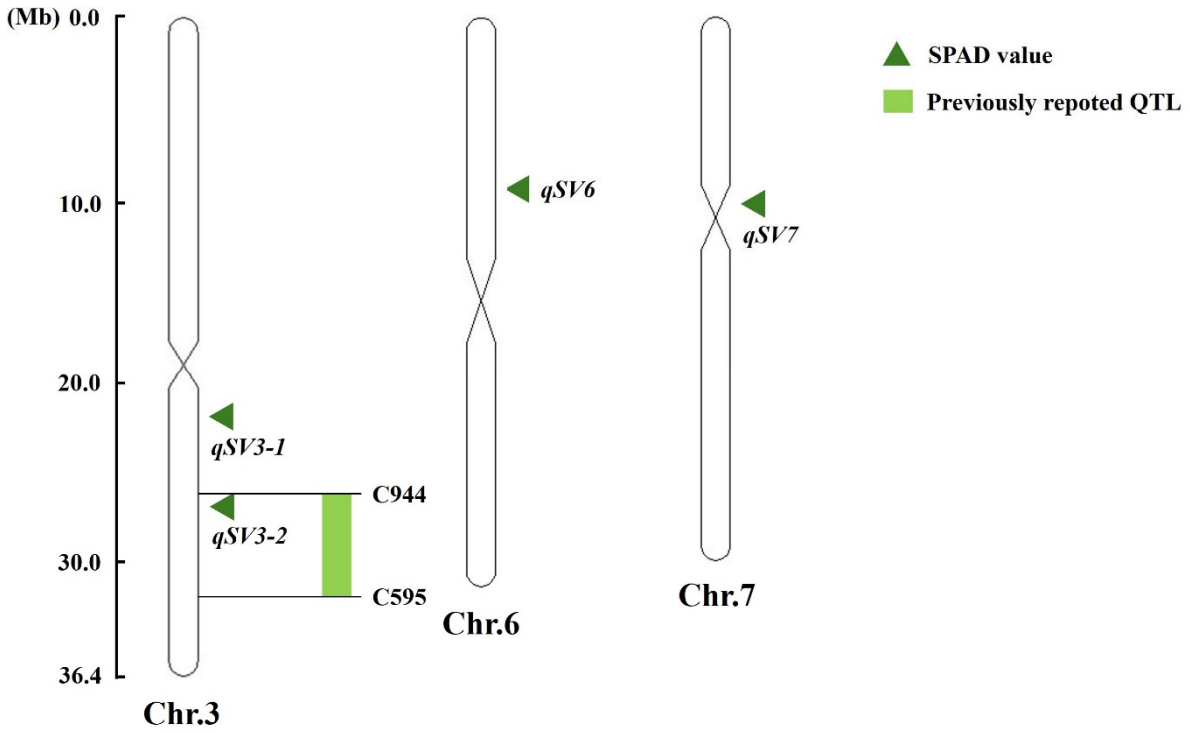



**Figure S5.** Phenogram plot showing significant QTLs (−log10(p) > 5.46) associated with SPAD values. Triangles indicate their QTL positions on chromosomes and rectangle indicates previously identified QTL, with a scale of chromosome lengths on the left.