**Table S1.** Descriptive statistics of grain phenotypic traits from image analysis in the rice landrace panel.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Mean | Median | Std | 1st Qu | 3rd Qu | Min | Max |
| awn length | 1.04 | 0.00 | 2.73 | 0.00 | 0.66 | 0.00 | 16.83 |
| hull color | 149.42 | 148.80 | 17.71 | 140.48 | 157.57 | 97.19 | 188.38 |
| projected area | 23.63 | 23.74 | 2.64 | 22.26 | 24.81 | 17.54 | 41.84 |
| PC1 | 0.00 | -0.05 | 0.27 | -0.16 | 0.11 | -0.56 | 1.38 |
| PC2 | 0.00 | 0.00 | 0.07 | -0.04 | 0.05 | -0.19 | 0.22 |
| PC3 | 0.00 | 0.00 | 0.05 | -0.03 | 0.03 | -0.15 | 0.15 |
| PC4 | 0.00 | 0.00 | 0.05 | -0.03 | 0.02 | -0.14 | 0.15 |
| PC5 | 0.00 | 0.00 | 0.04 | -0.03 | 0.03 | -0.09 | 0.14 |

Note:“hull color” values represent the mean value computed in OpenCV’s CIELAB space. OpenCV rescales the conventional range to 0–255.

**Table S2.** The annotated genes in candidate genomic region for projected grain area regulation in chr 12.

|  |  |
| --- | --- |
| Model | Putative Function |
| LOC\_Os12g0254201 | Hypothetical conserved gene. |
| LOC\_Os12g0254400 | Hypothetical protein. |
| LOC\_Os12g0254601 | Hypothetical gene. |
| LOC\_Os12g0254700 | Similar to H-ATPase. |
| LOC\_Os12g0254825 | Conserved hypothetical protein. |
| LOC\_Os12g0255000 | Hypothetical gene. |
| LOC\_Os12g0255200 | Staphylococcal nuclease (SNase‐like), OB‐fold domain containing protein |
| LOC\_Os12g0255701 | Conserved hypothetical protein. |
| LOC\_Os12g0255850 | Conserved hypothetical protein. |
| LOC\_Os12g0256000 | Alpha/beta hydrolase fold-3 domain containing protein. |
| LOC\_Os12g0256300 | Similar to Schizosaccharomyces pombe (Fragment). |
| LOC\_Os12g0256400 | Conserved hypothetical protein. |
| LOC\_Os12g0256600 | Conserved hypothetical protein. |
| LOC\_Os12g0256800 | Aminotransferase‐like, plant mobile domain domain containing protein |
| LOC\_Os12g0256900 | Pentatricopeptide repeat domain containing protein. |
| LOC\_Os12g0257000 | Serine carboxypeptidase I precursor (EC 3.4.16.5) (Carboxypeptidase C). |
| LOC\_Os12g0257400 | Similar to Endochitinase A2. |
| LOC\_Os12g0257450 | Non-protein coding transcript. |
| LOC\_Os12g0257500 | Conserved hypothetical protein. |
| LOC\_Os12g0257600 | Similar to Laccase-25. |
| LOC\_Os12g0257900 | Similar to Receptor-like kinase. |
| LOC\_Os12g0258200 | ER-resident J-protein, ER quality control in rice endosperm, Translocation of secretory proteins and protein degradation of unfolded or misfolded protein |

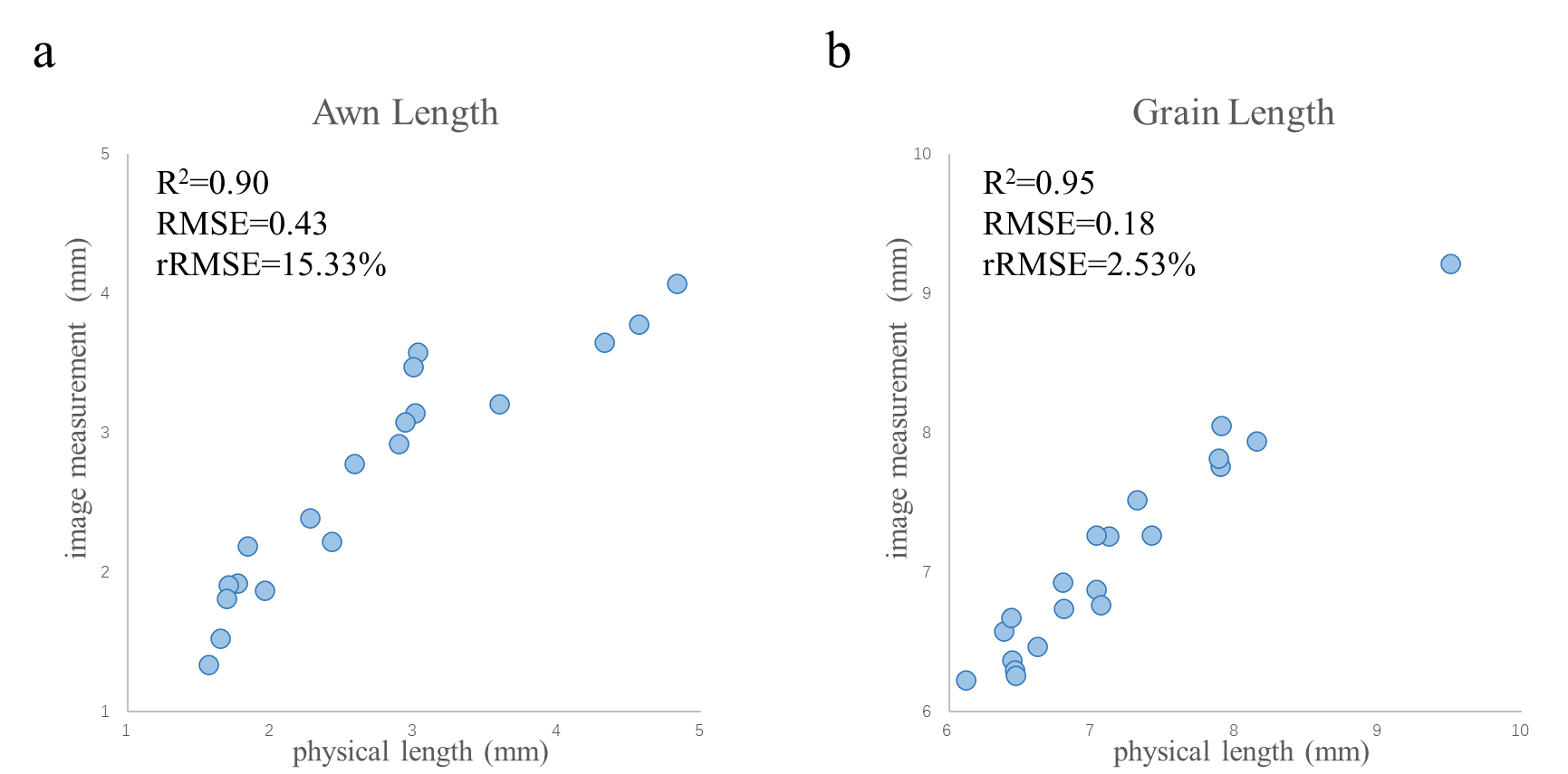


Figure S1: Validation of image-based measurements for awn length and grain length. Each panel shows a scatter plot of image-derived values versus manual caliper measurements (in millimetres) for 20 randomly selected rice grains. (a) Awn length R2=0.90, RMSE = 0.43 mm, rRMSE = 15.33 %. (b) Grain length R2=0.95, RMSE = 0.18 mm, rRMSE = 2.53 %.

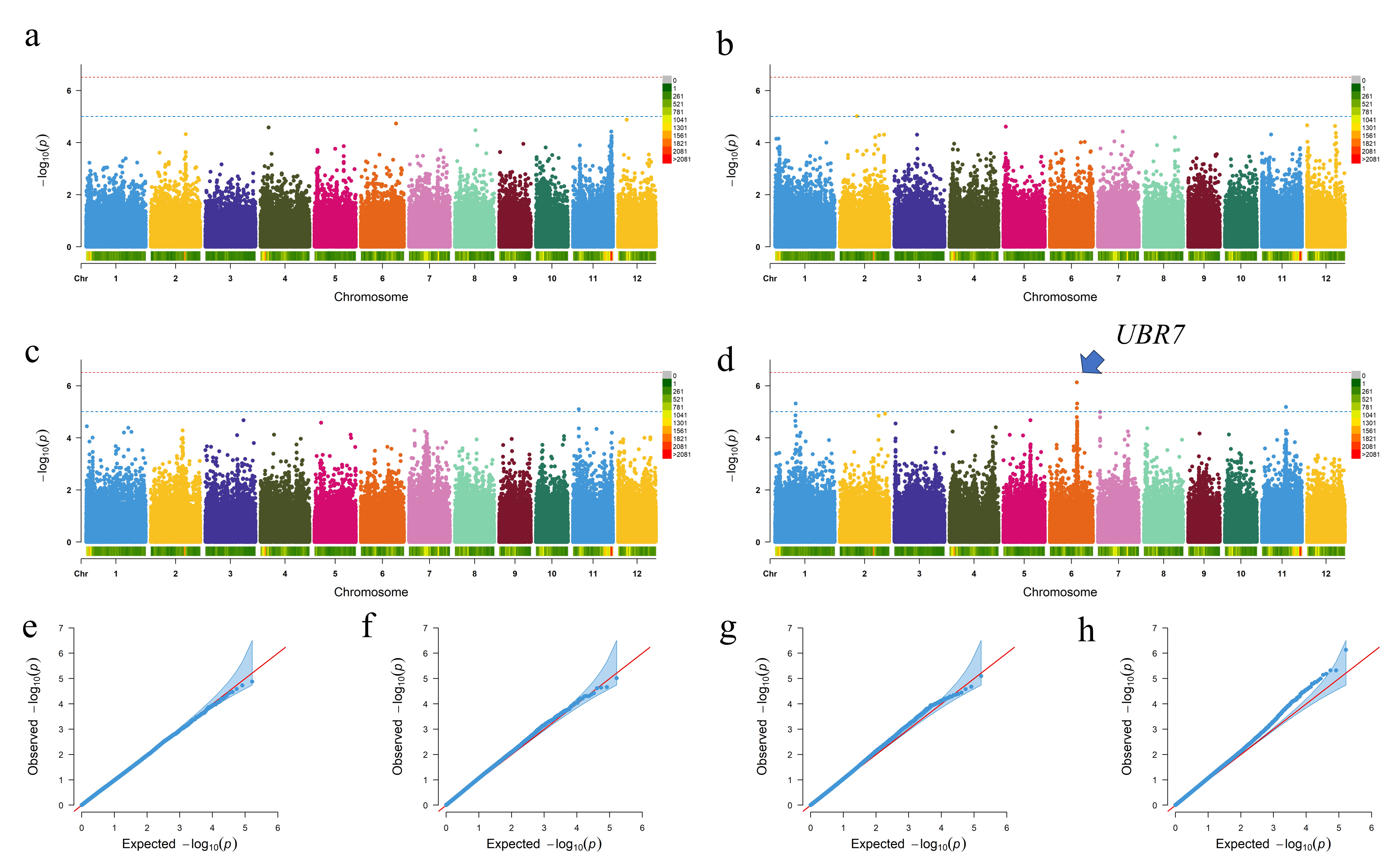


Figure S2: Results of association analyses for PC2–PC5 using a GLM with the first two principal components as covariates. Panels (a–d) are Manhattan plots of –*log*10(*P*) versus genomic position for PC2 (a), PC3 (b), PC4 (c), and PC5 (d). The horizontal blue line marks the genome-wide significance threshold of –*log*10(*P*) = 5. Major peaks are annotated with candidate gene names, including UBR7 for PC5. Panels (e–h) show Q–Q plots comparing the observed distribution of P values (y‑axis) with the expected null distribution (x‑axis).

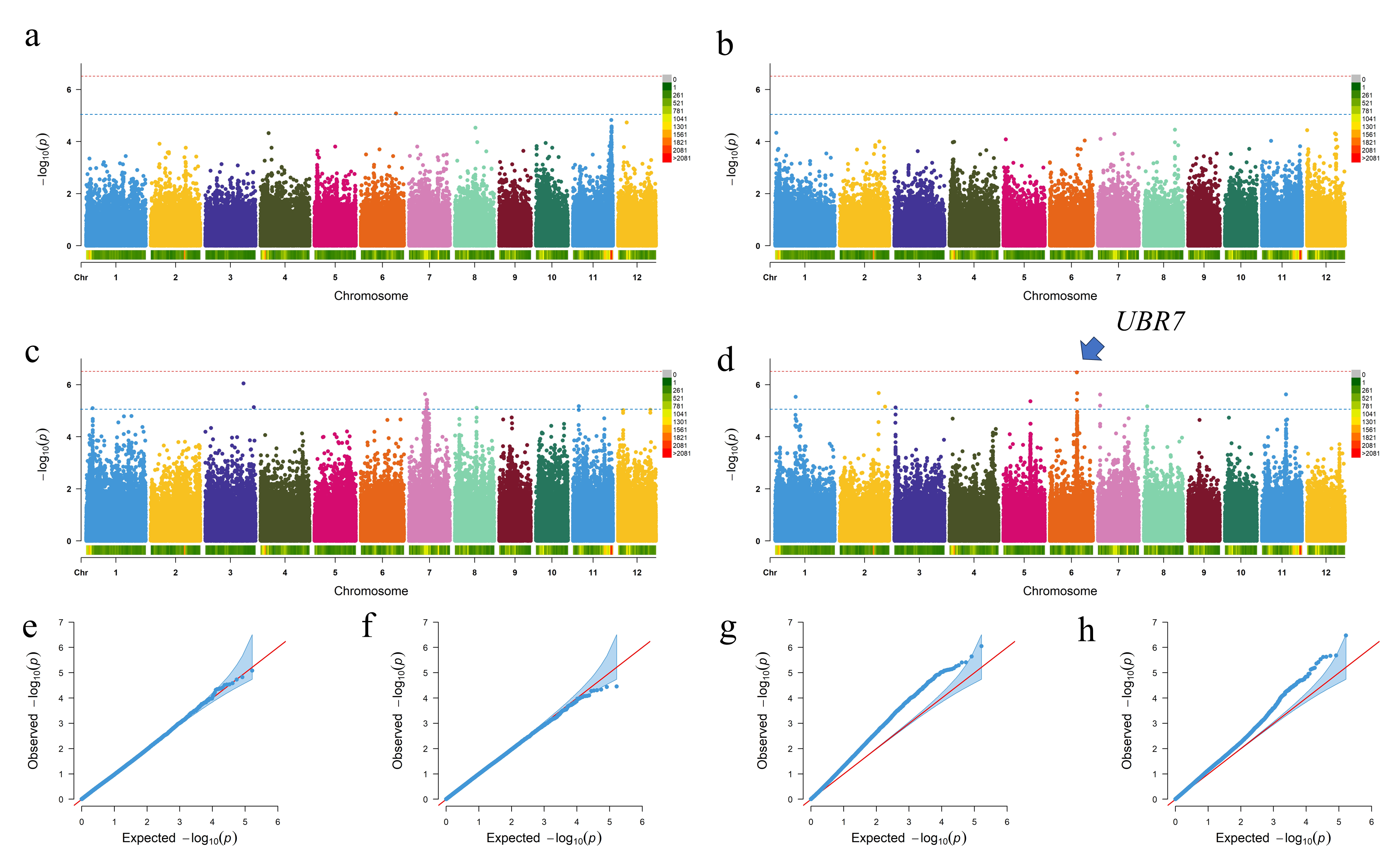


Figure S3: Results of association analyses for PC2–PC5 using a FarmCPU. Panels (a–d) are Manhattan plots of –*log*10(*P*) versus genomic position for PC2 (a), PC3 (b), PC4 (c), and PC5 (d). The horizontal blue line marks the genome-wide significance threshold of –*log*10(*P*) = 5. Major peaks are annotated with candidate gene names, including UBR7 for PC5. Panels (e–h) show Q–Q plots comparing the observed distribution of P values (y‑axis) with the expected null distribution (x‑axis).