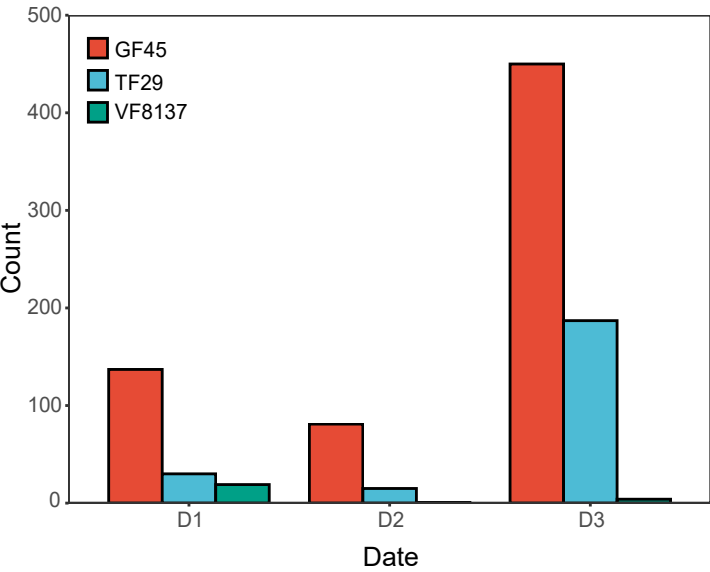


a



b

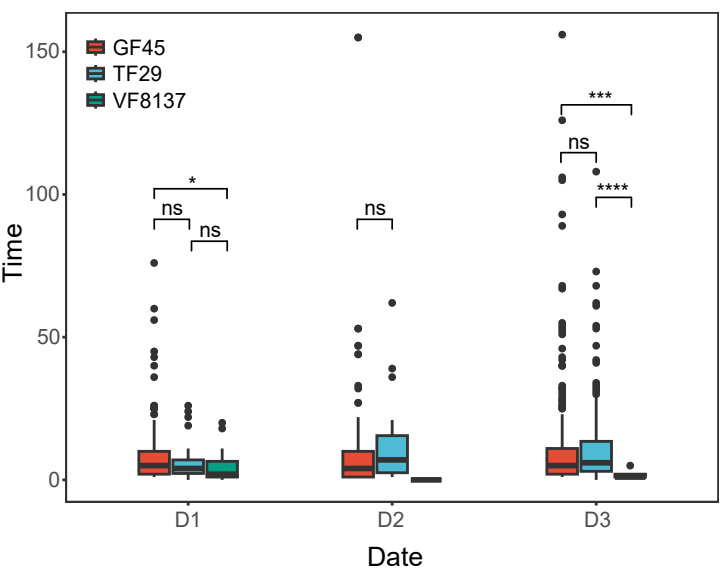
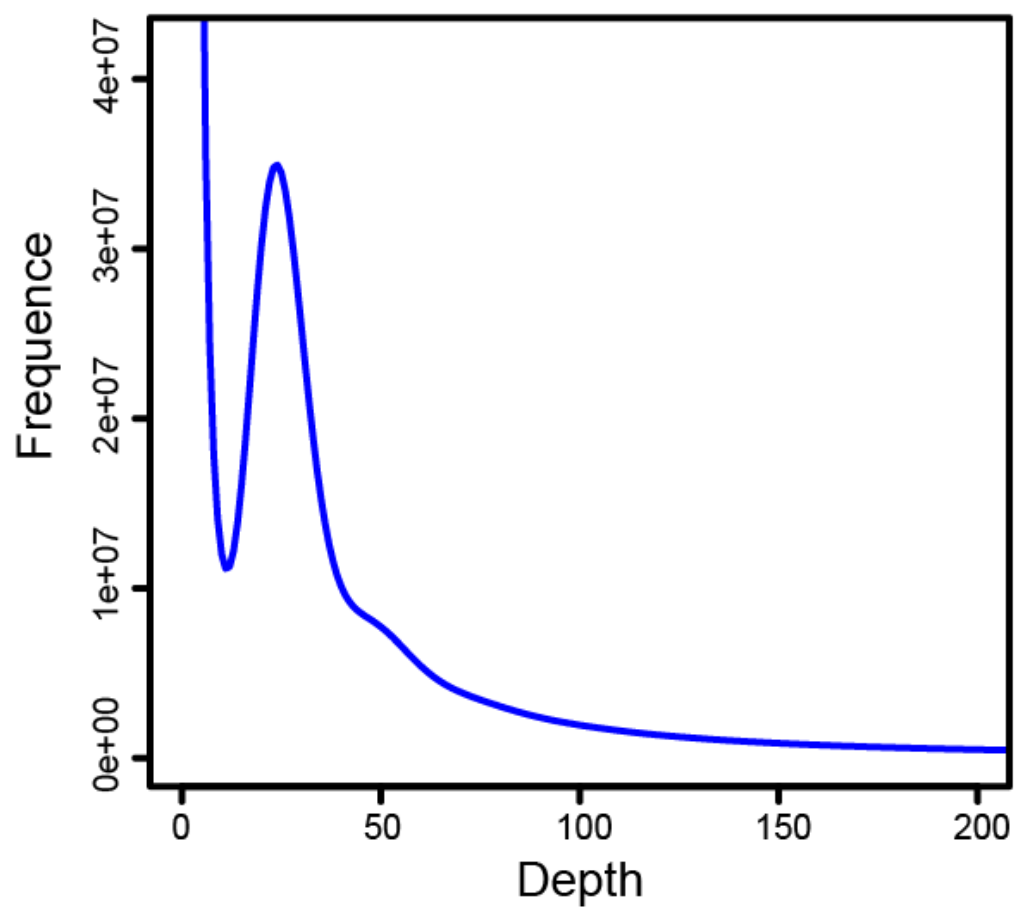


Fig. S1 Differences in the visiting frequency (a) and time (b) of bees for three varieties of faba beans with different wing petal lengths. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.



K-mer	Genome size (MB)	Heterozygous ratio (%)	Repeat sequence (%)
17	11,772.94	0.49	92.34

Fig.S2 Depth distribution of 17-mers in the genome VF8137 according to K-mer analysis.

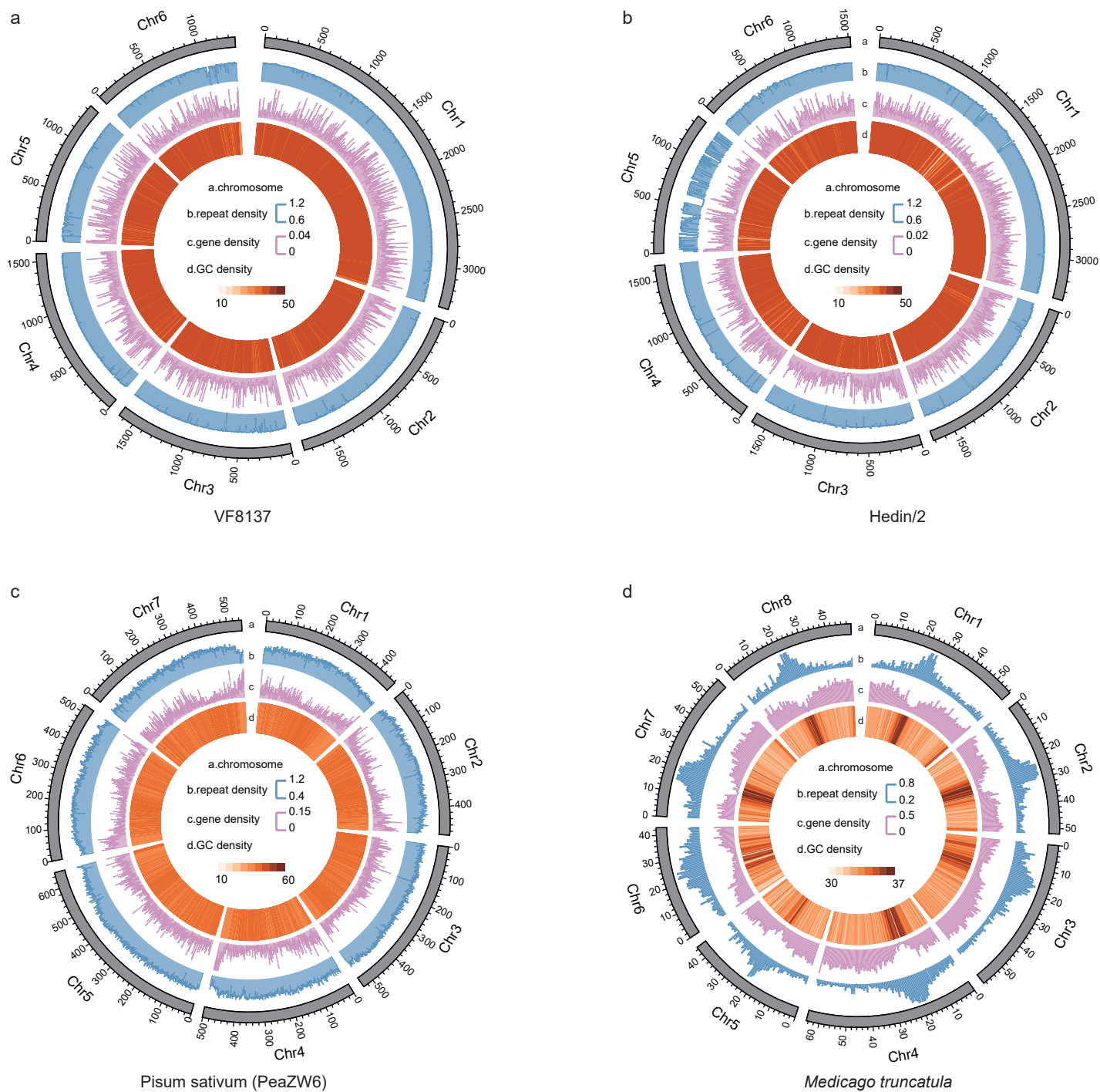


Fig. S3 Genome features of two assemblies of faba bean including VF8137 (a) and Hedini/2 (b) and one assembly of *Pisum sativum* (c) and *Medicago truncatula* (d). Bin size of 5 Mb, 1Mb and 500 Kb were applied for two genome assemblies of faba bean including VF8137 and Hedini/2, *Pisum sativum* and *Medicago truncatula*, respectively.

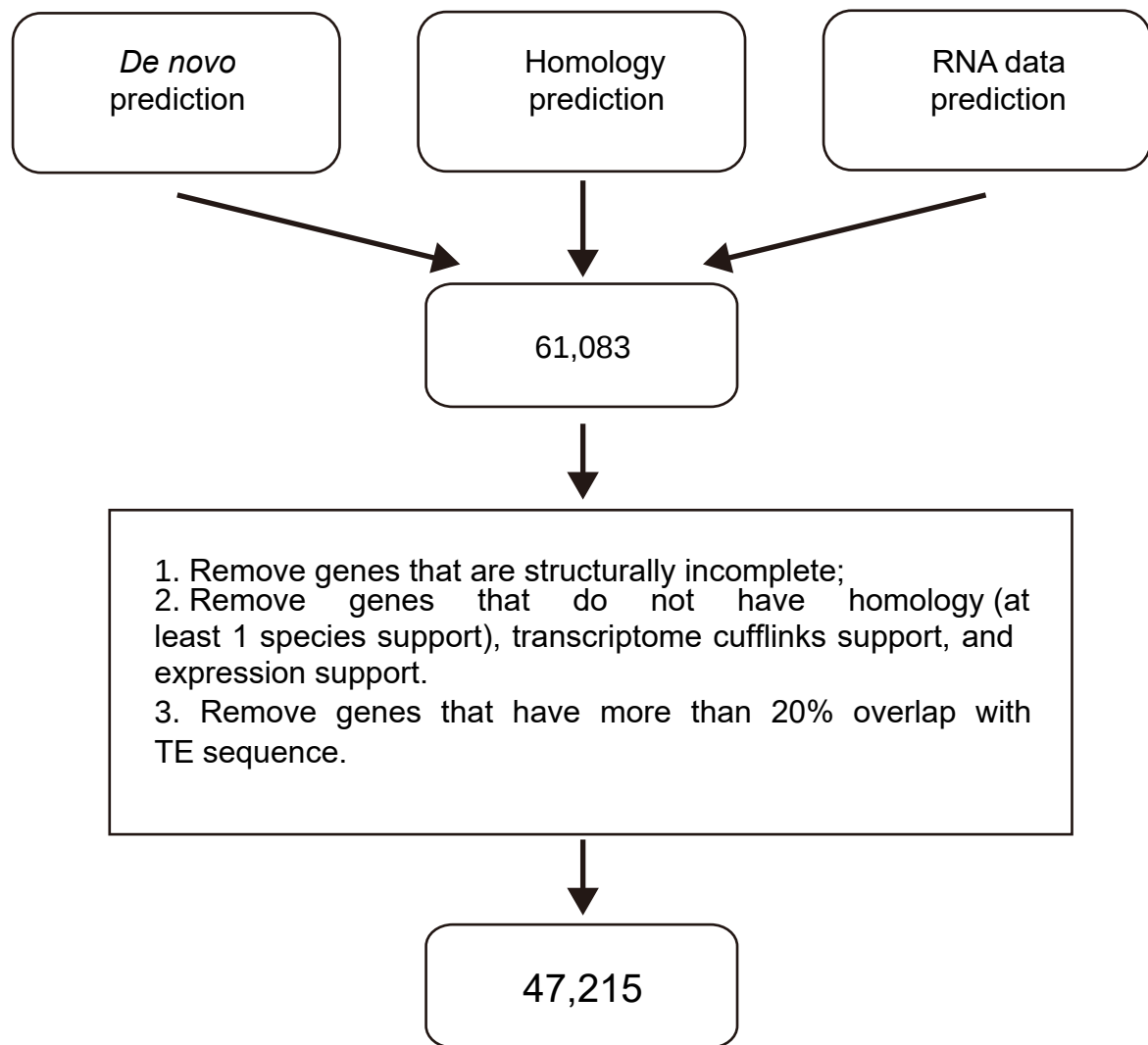
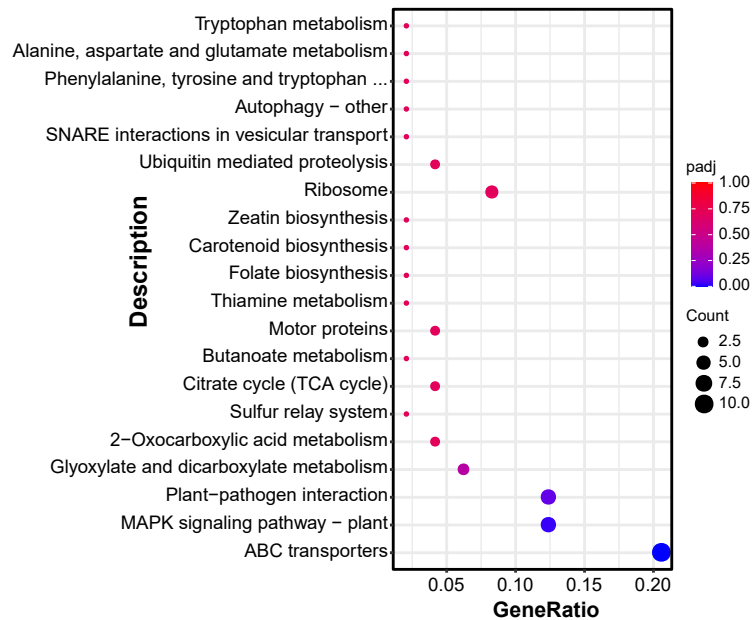


Fig. S4 Gene annotation pipeline for genome assembly VF8137 of Faba bean.

a



b

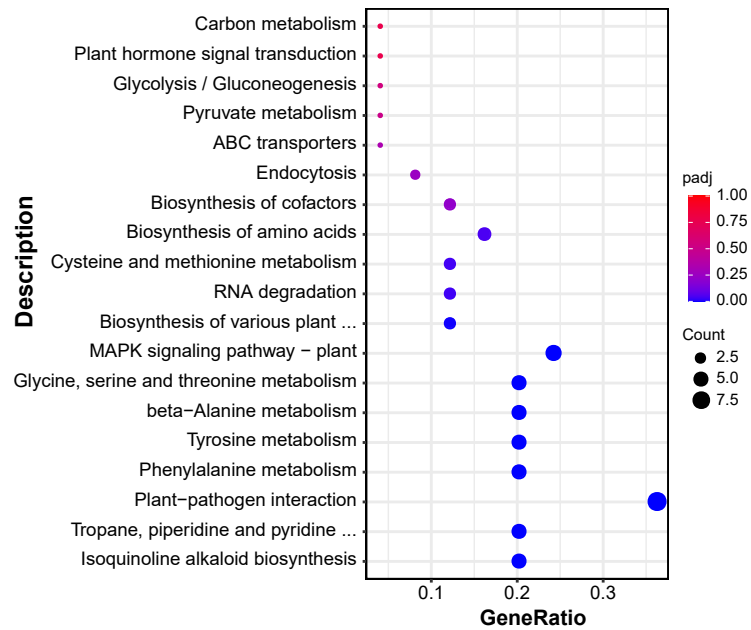


Fig. S6 KEGG enrichment of the contracted gene family in Galegoids (a) and Millettoids (b). The circle color and size indicate padj values and the number of genes involved, respectively. Padj value less than 0.05 is considered statistically significant.

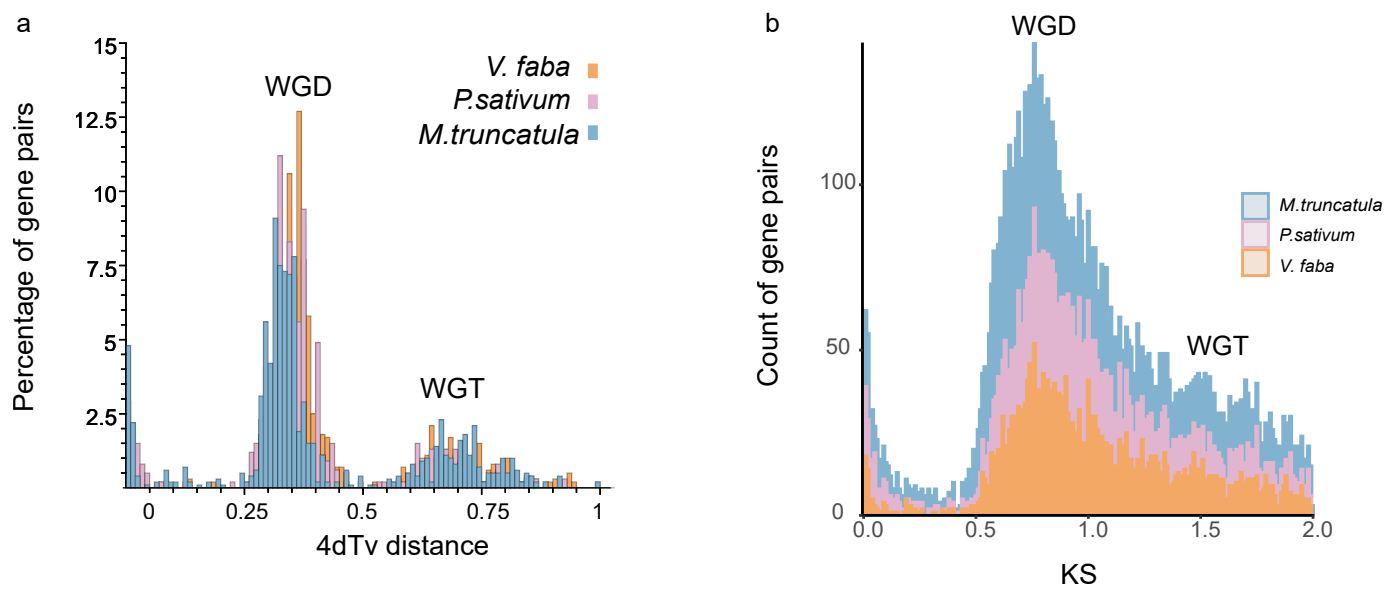


Fig.S7 WGD estimation for *V. faba*, *P. sativum* and *M. truncatula* using 4dTv distance (a) and Ks analysis (b).

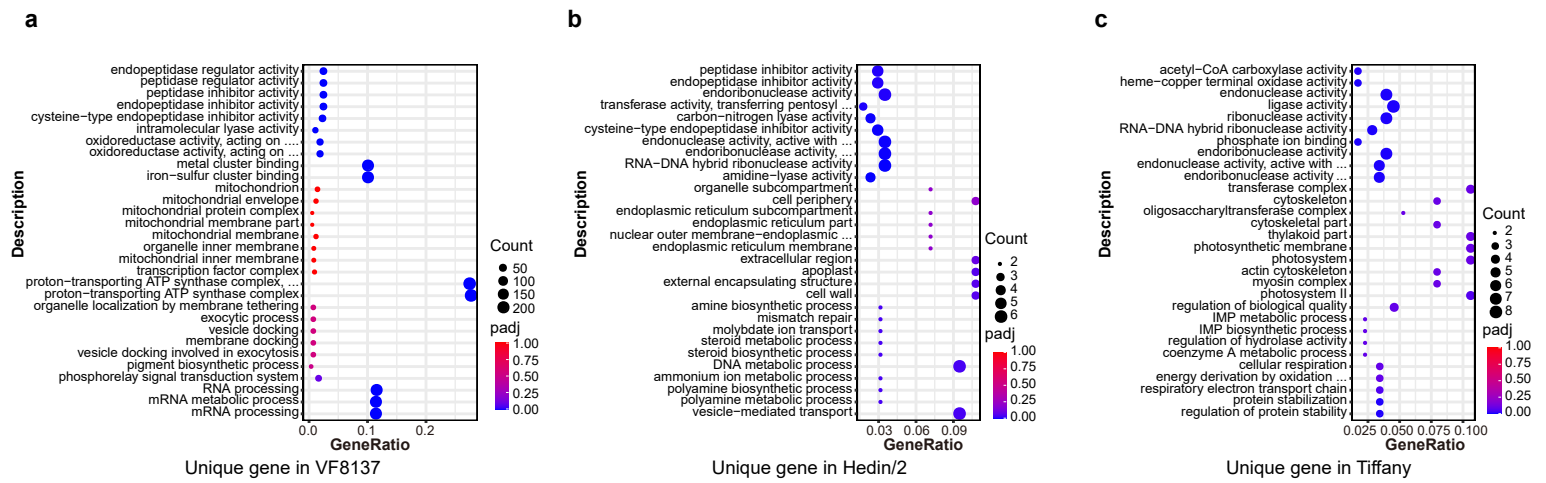


Fig. S8 GO analysis of the unique genes identified in one of the three genome assemblies VF8137 (a), Hedin/2 (b), and Tiffany (c). The circle color and size indicate padj values and the number of genes involved, respectively. Padj value less than 0.05 is considered statistically significant.

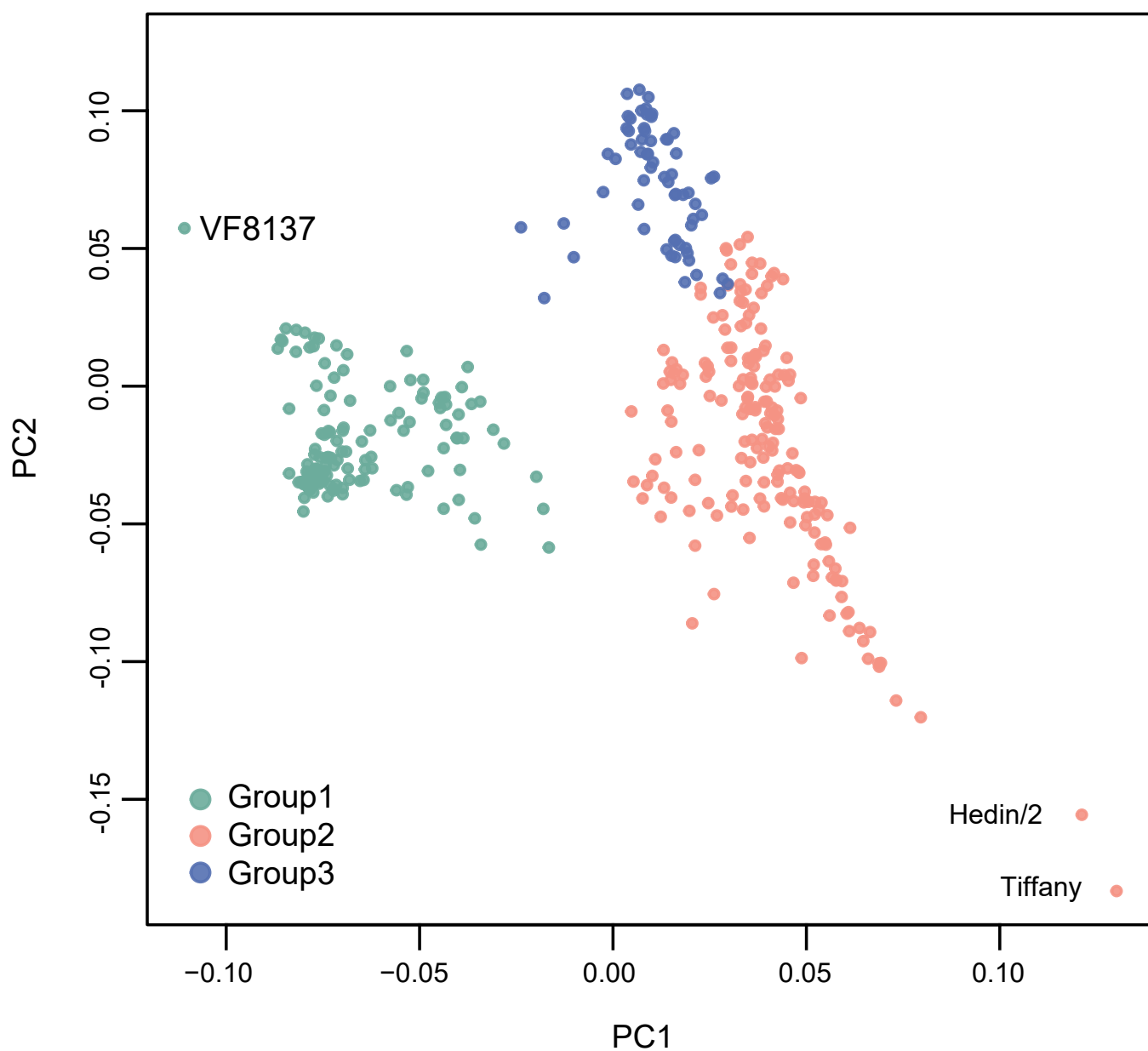


Fig. S9 PCA analysis using SNPs integrating with the variation from the three genome assemblies of VF8137, Hedini/2, and Tiffany and the 558 faba bean germplasms. Green, pink and blue represent Group 1, Group 2 and Group 3, respectively, which is corresponded to the three genetic groups obtained from ADMIXTURE results.

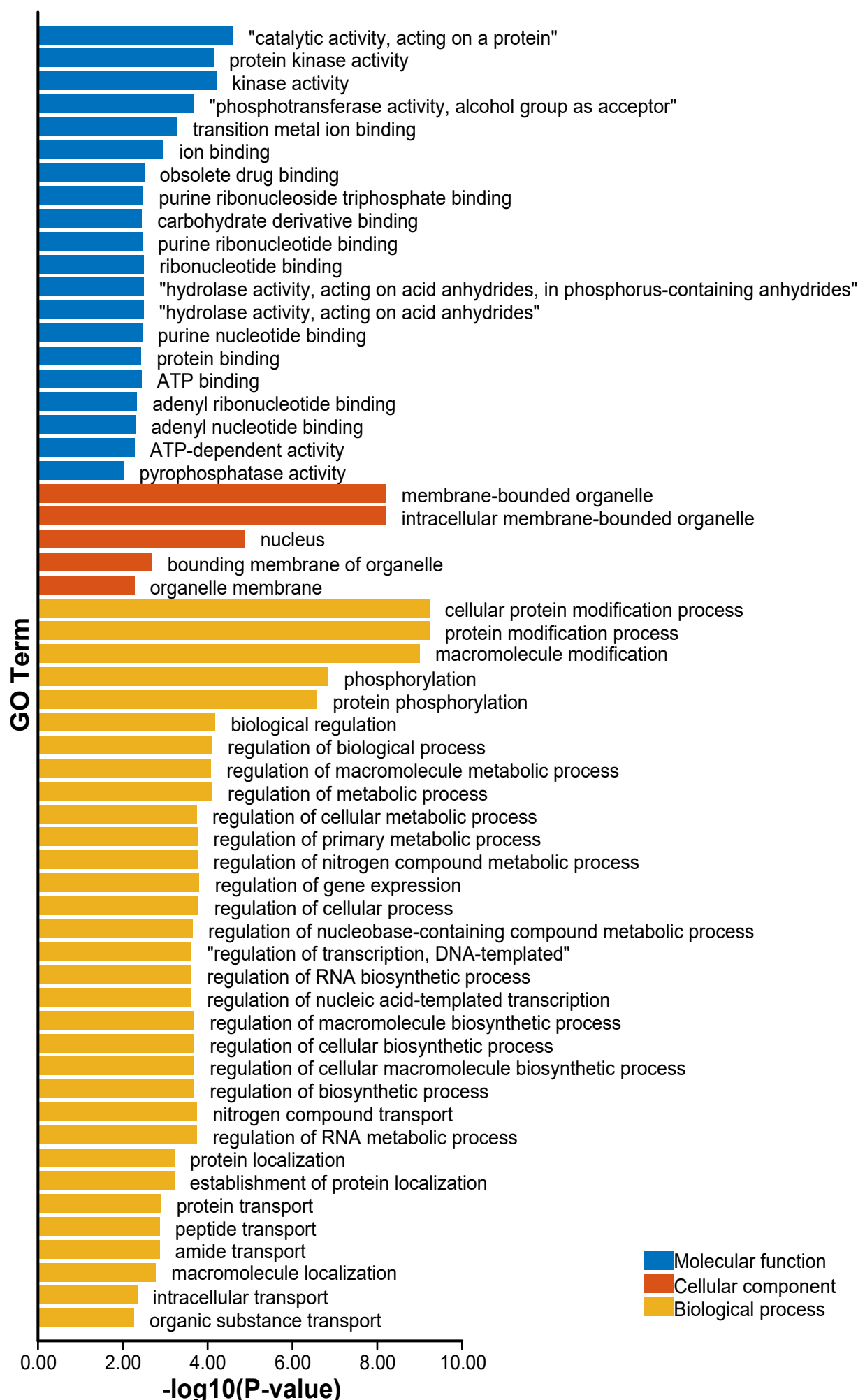


Fig.S10 GO analysis of the 3248 candidate selected genes between group 1 and group 2. Blue, red and orange represent Molecular function, Cellular component and Biological process, respectively.

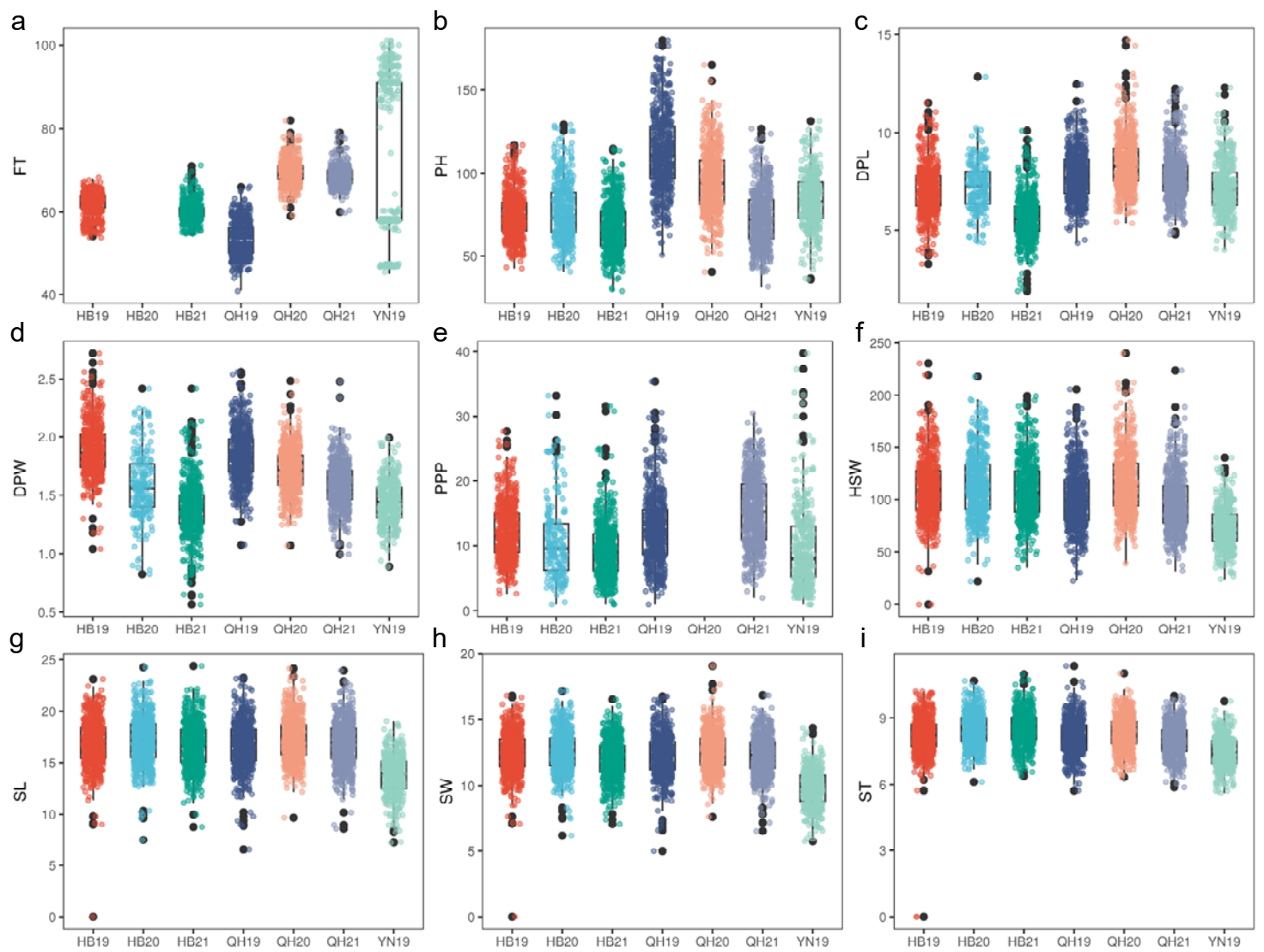


Fig.S11 Distribution of nine quantitative traits of 558 accessions of faba bean germplasm used in the seven phenotyping experiments (HB19, HB20, HB21, QH19, QH20, QH21, and YN19) at Hebei, Qinghai and Yunnan sites between 2019 and 2021. FT = Flowering time, PH = Plant height, DPL = Dry pod length, DPW = Dry pod width, PPP = Pods number per plant, HSW = 100-seed weight, SL = Seed length, SW = Seed width, ST = Seed thickness.

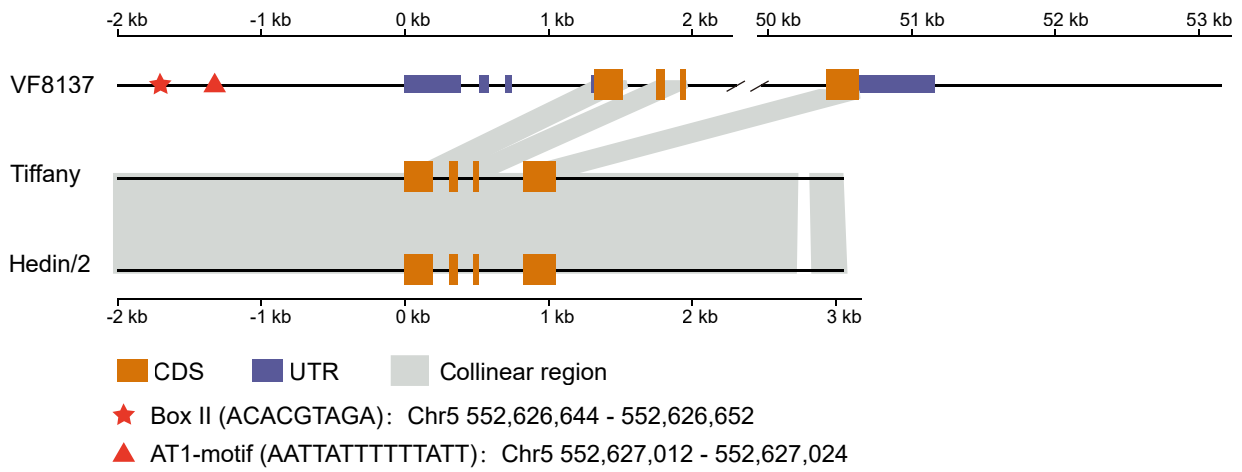


Fig. S12 Collinearity analysis of *FT* gene in three faba bean genome assemblies of VF8137, Hedin/2, and Tiffany. Blue and orange boxes represent UTR and CDS of gene, whereas the red star and triangle represent the two unique photoperiod related regulation elements of the *FT* gene in VF8137.

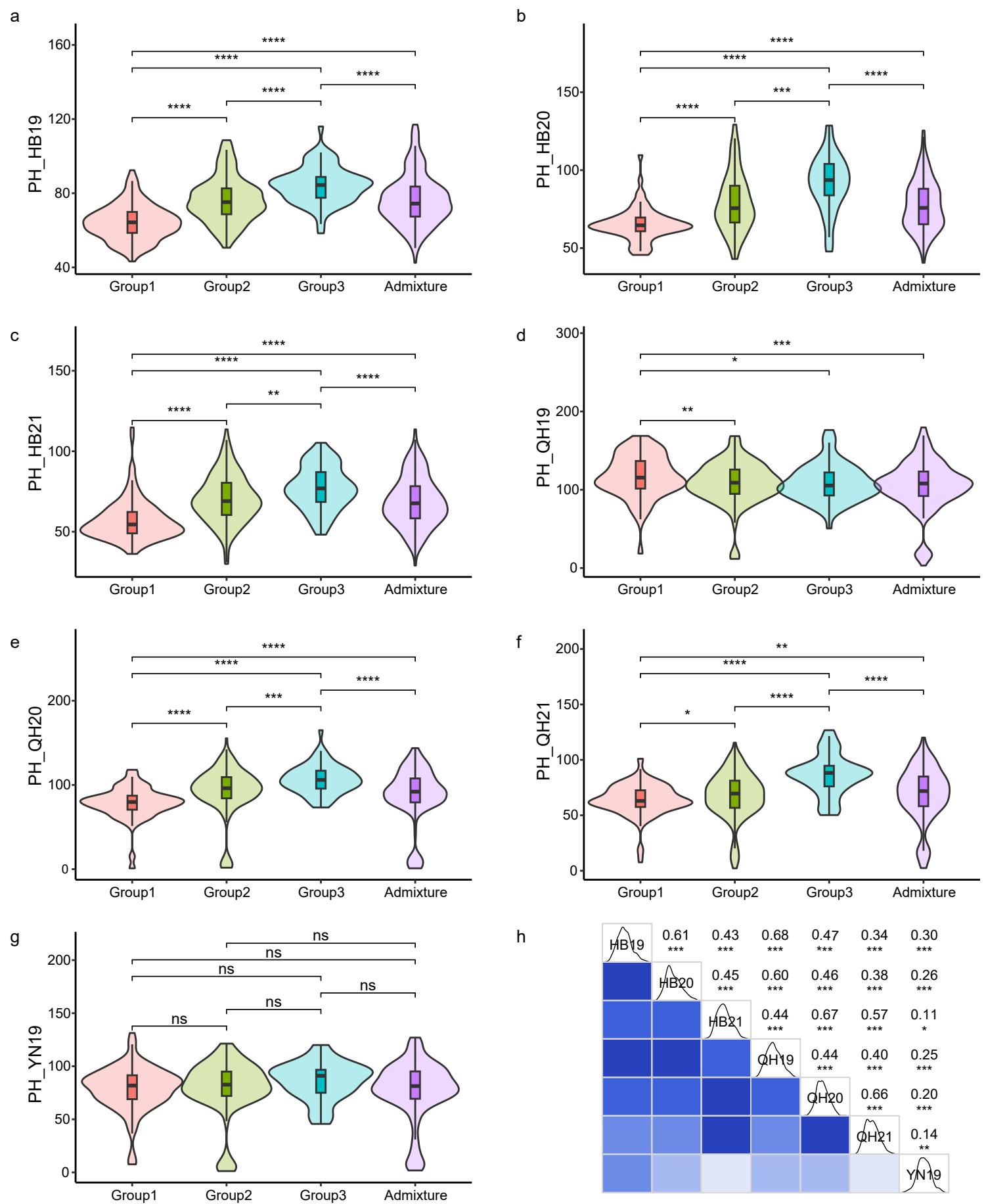


Fig. S13 Phenotypic differences among different genetic groups (a, b, c, d, e, f, g) and correlations (h) of PH in seven experiments. a, b, c, d, e, f, g, Pink, green, blue and purple represent Group 1, Group 2, Group 3 and Admixture, respectively. h, The darker the color intensity, the higher the correlation; whereas the weaker the color intensity, the lower the correlation. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.

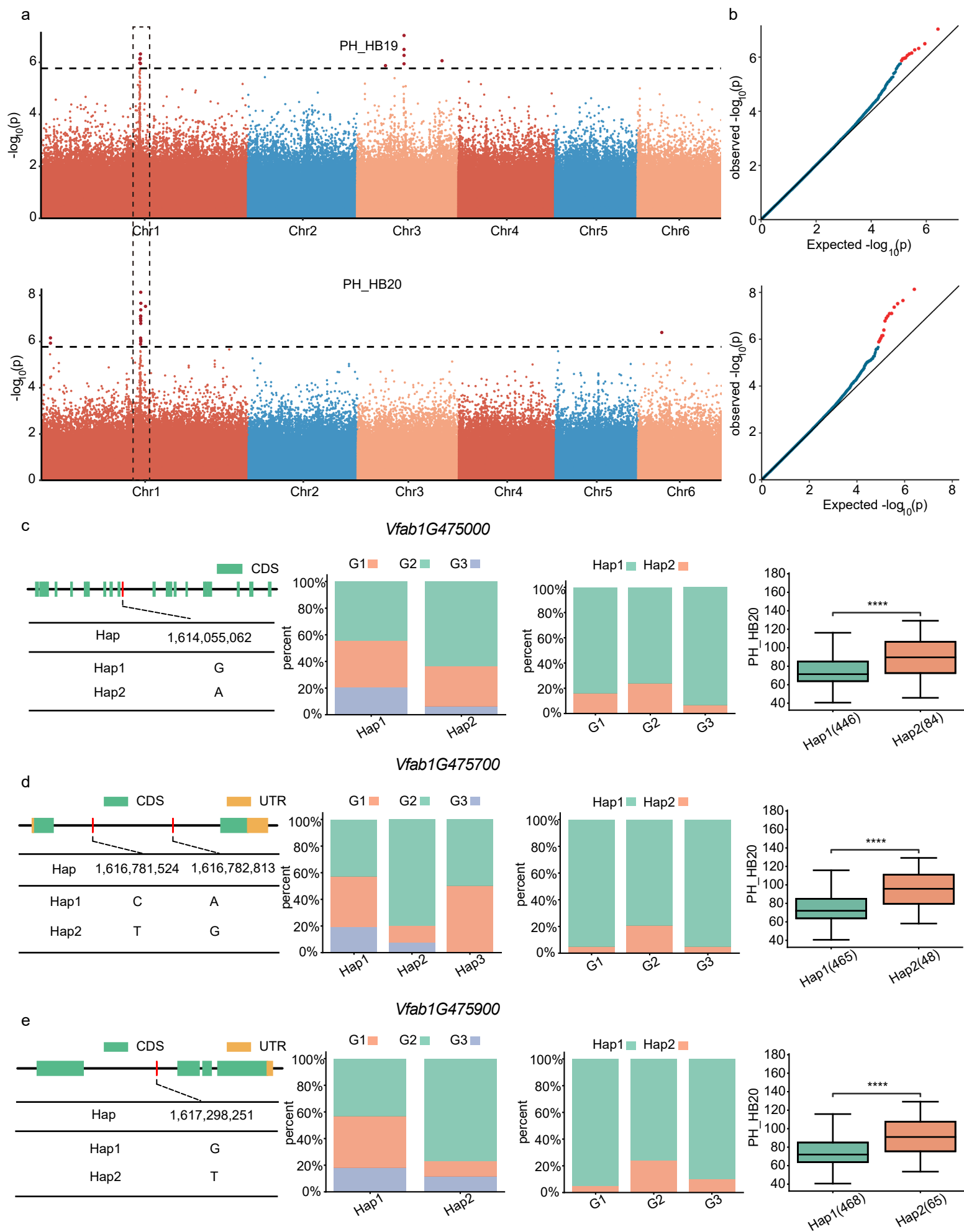


Fig.S14 GWAS and genetic analyses of candidate genes associated with PH. a and b, GWAS results of PH in HB19 (a) and HB20 (b). c, d, and e, Genotype distribution in three genetic groups and phenotypic differences of distinct haplotypes in *Vfab1G475000* (c), *Vfab1G475700* (d), and *Vfab1G475900* (e).

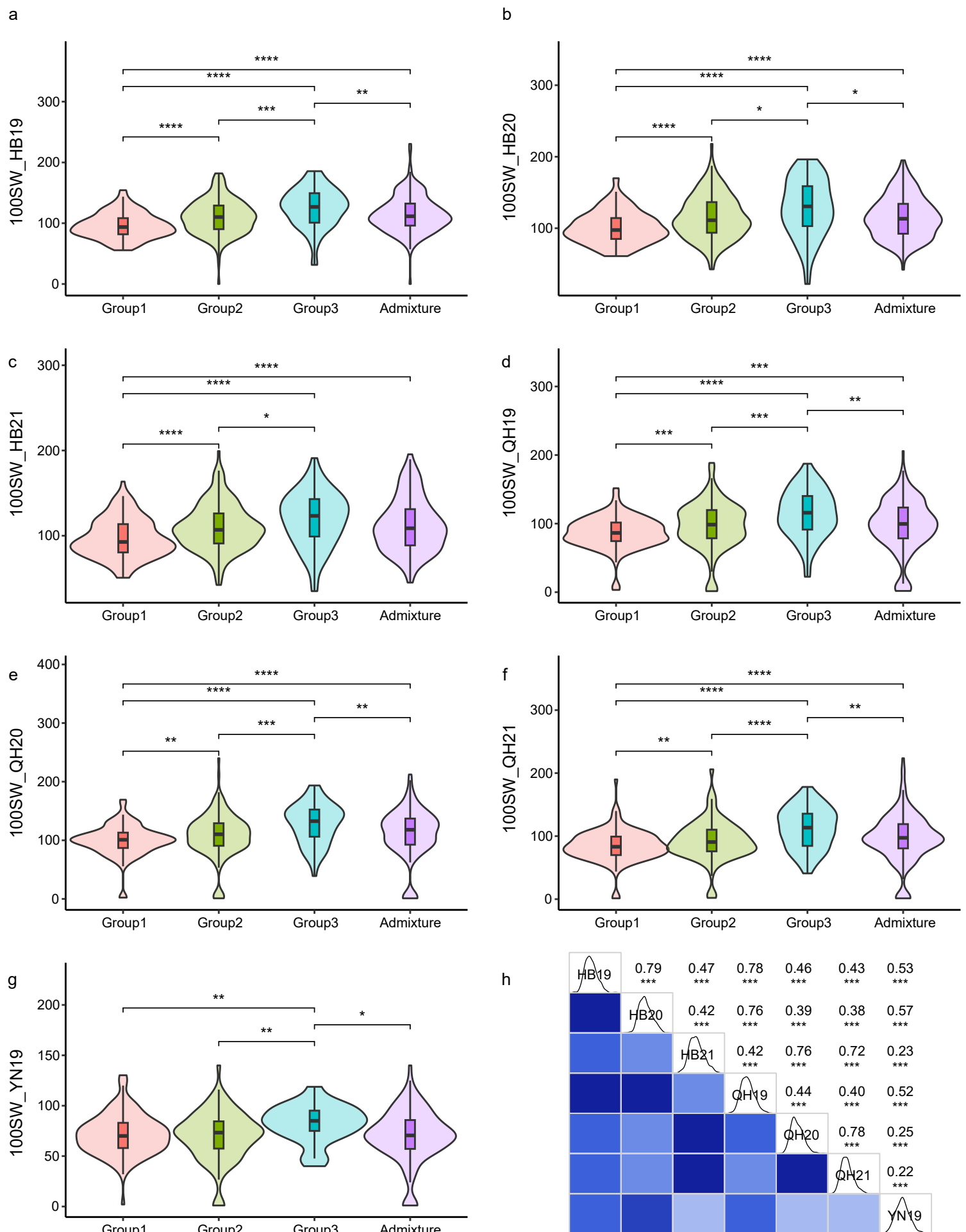


Fig. S15 Phenotypic differences among different genetic groups (a, b, c, d, e, f, g) and correlations (h) of 100SW in seven experiments. a, b, c, d, e, f, g, Pink, green, blue and purple represent Group 1, Group 2, Group 3 and Admixture, respectively. h, The darker the color intensity, the higher the correlation; whereas the weaker the color intensity, the lower the correlation. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$.

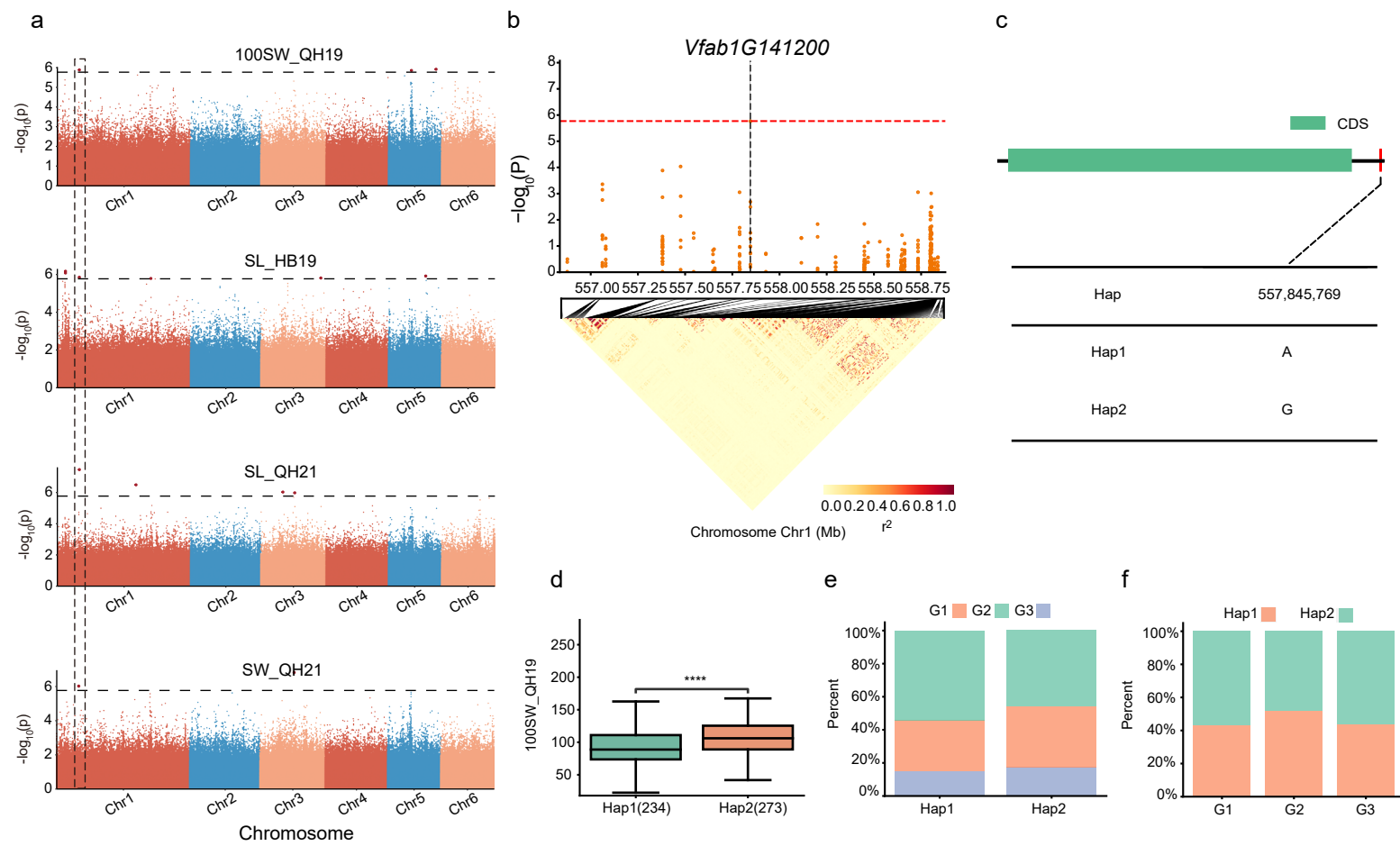


Fig.S16 GWAS and genetic analyses of the candidate gene *Vfab1G141200* associated with seed size and seed weight. a, GWAS results of seed size and seed weight at different sites across years. b, LD block analysis for the SNPs significantly associated with 100SW. c, Genotype of the SNP significantly associated with 100SW. d, Phenotypic differences in distinct haplotypes of 100SW. e and f, Haplotype composition in different genetic groups of 558 accessions of faba bean germplasm.

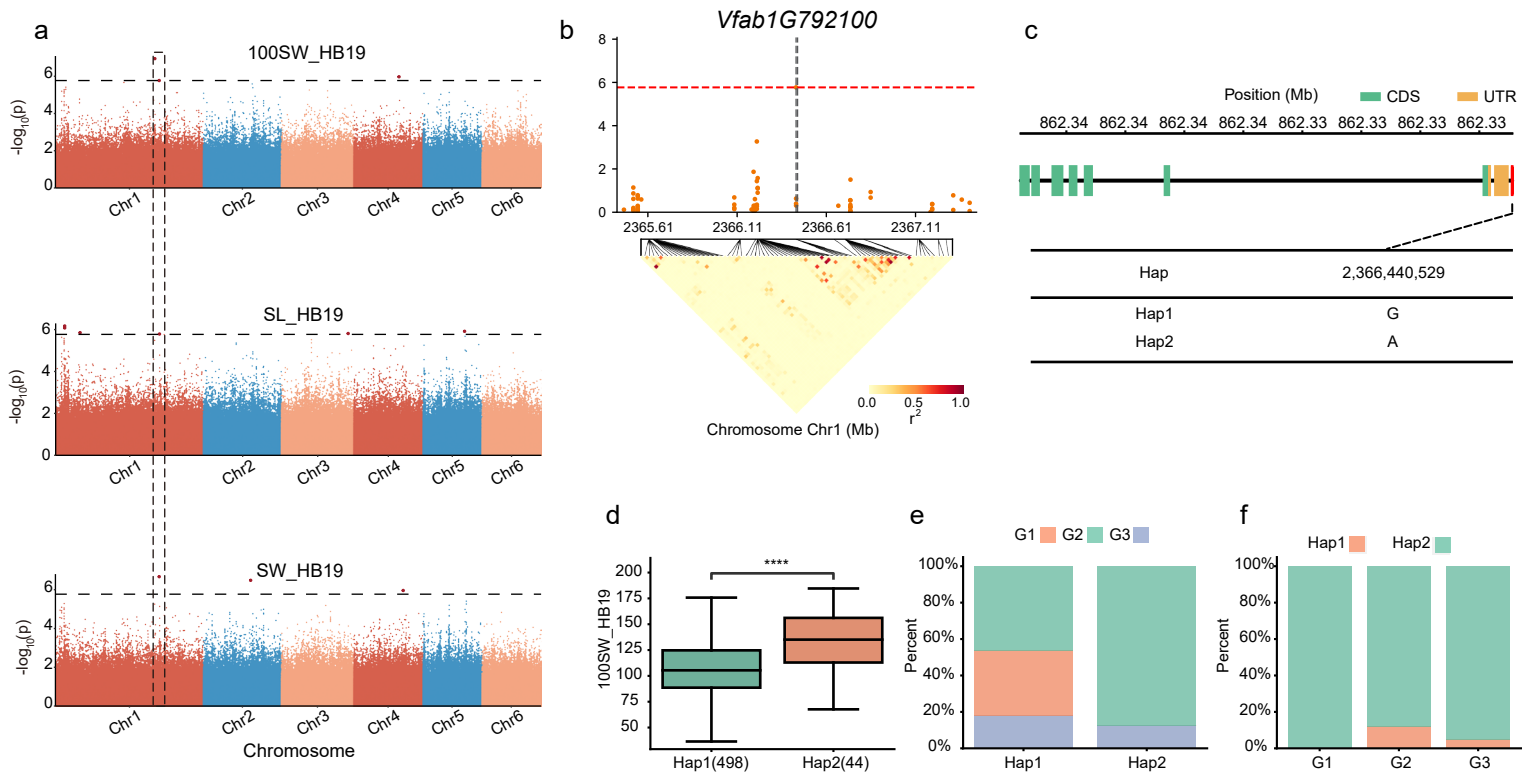


Fig.S17 GWAS and genetic analyses of the candidate gene *Vfab1G792100* associated with seed size and seed weight. a, GWAS results of seed size and seed weight at different sites across years. b, LD block analysis for the SNPs significantly associated with 100SW. c, Genotype of the SNP significantly associated with 100SW. d, Phenotypic differences in distinct haplotypes of 100SW. e and f, Haplotype composition in different genetic groups of 558 accessions of faba bean germplasm.

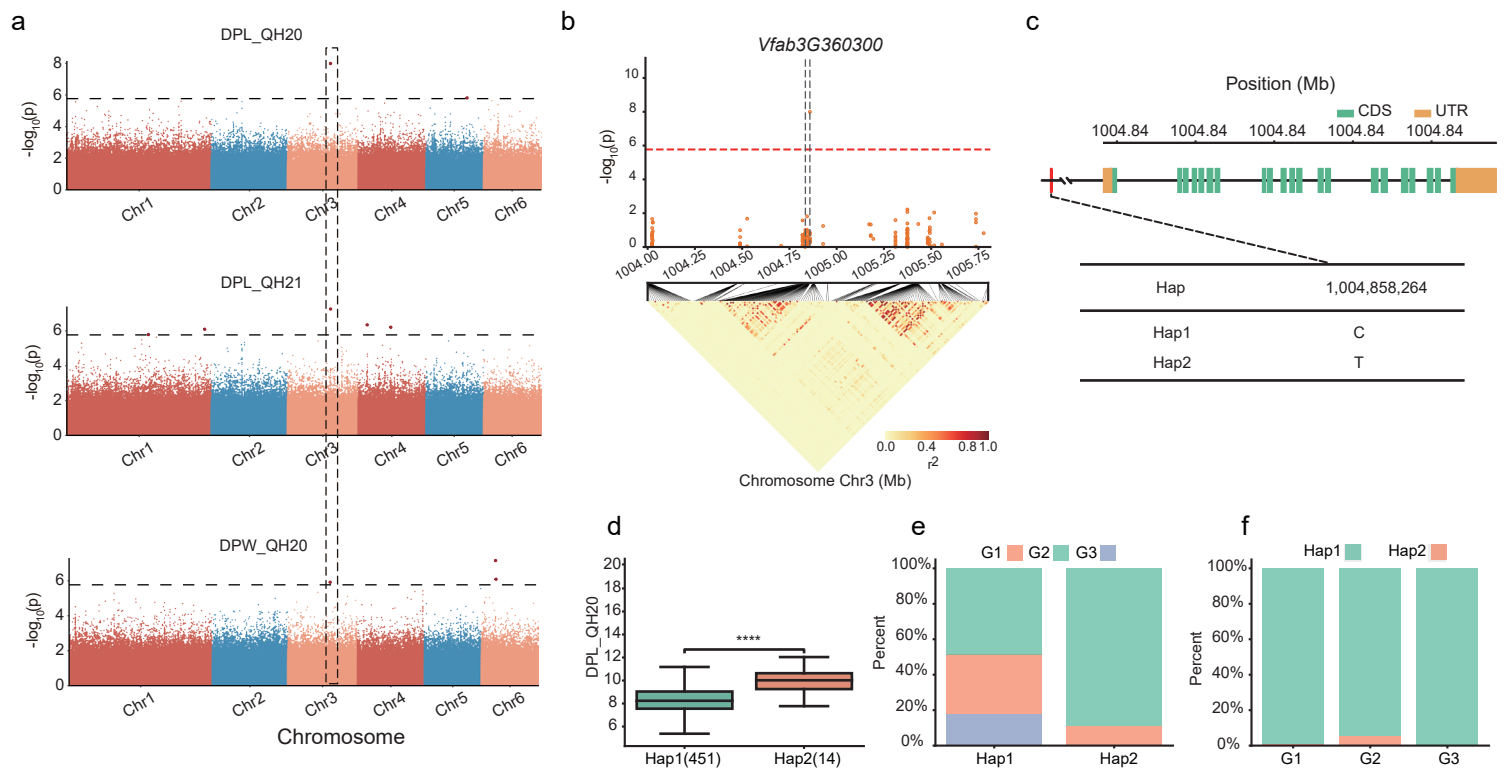


Fig.S18 GWAS and genetic analyses of variations and genes associated with pod size. a, GWAS results of dry pod length (DPL) and dry pod width (DPW) across years. b, LD block analysis for the SNPs significantly associated with DPL. c, Genotype of the SNP significantly associated with DPL. d, Phenotypic difference in DPL among distinct haplotypes. e and f, Haplotype composition in different genetic groups of 558 accessions of faba bean germplasm.

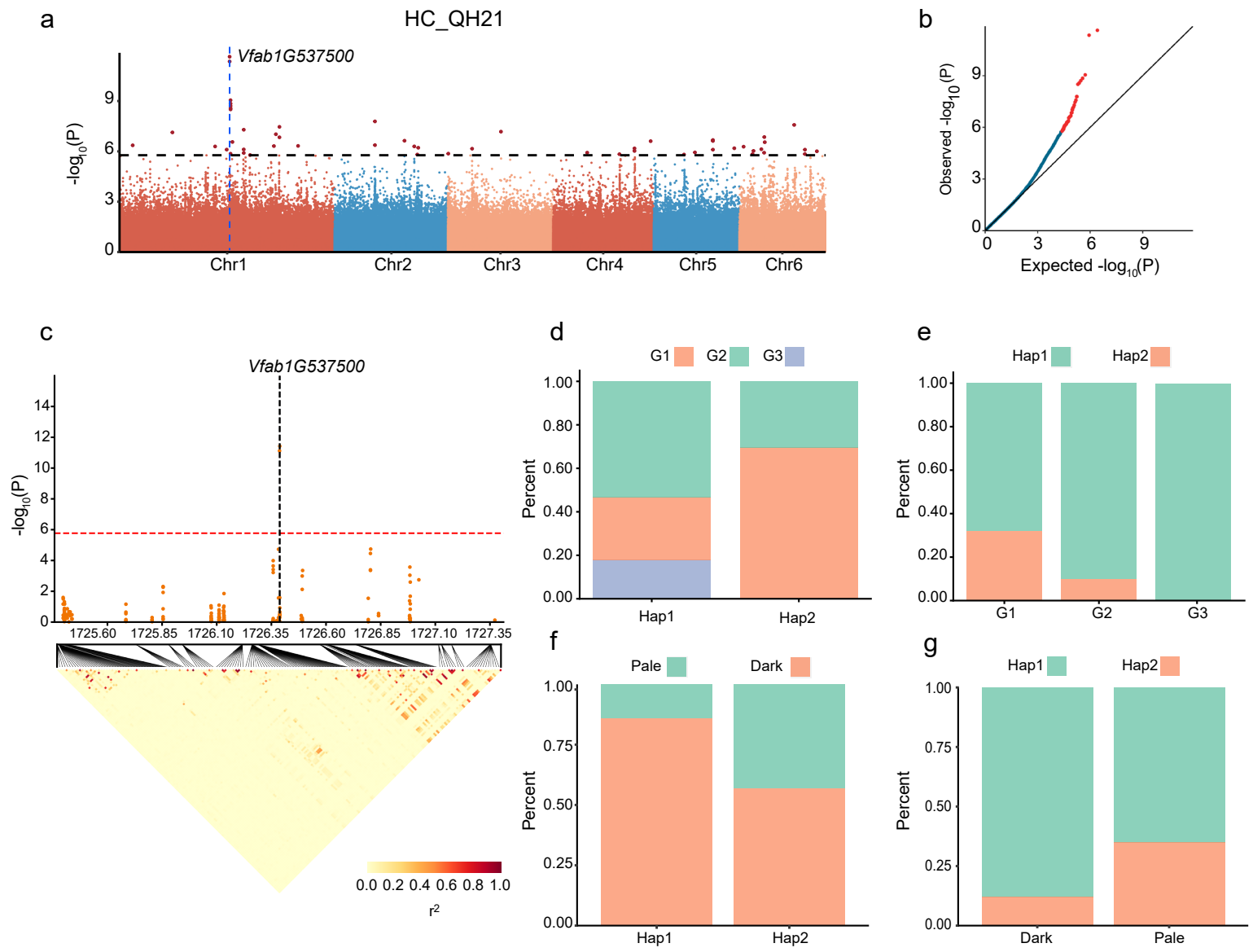


Fig.S19 GWAS analyses and genetic dissection of candidate genes associated with HC. a, SNPs significantly associated with HC according to GWAS. b, QQ plot of HC in GWAS analysis. c, LD block analysis for SNPs significantly associated with HC. d and e, Haplotype composition of *Vfab1G537500* (*PPO*) in different genetic groups of 558 accessions of faba bean germplasm. f and g, Phenotypic differences in HC among distinct haplotypes of *Vfab1G537500* (*PPO*).

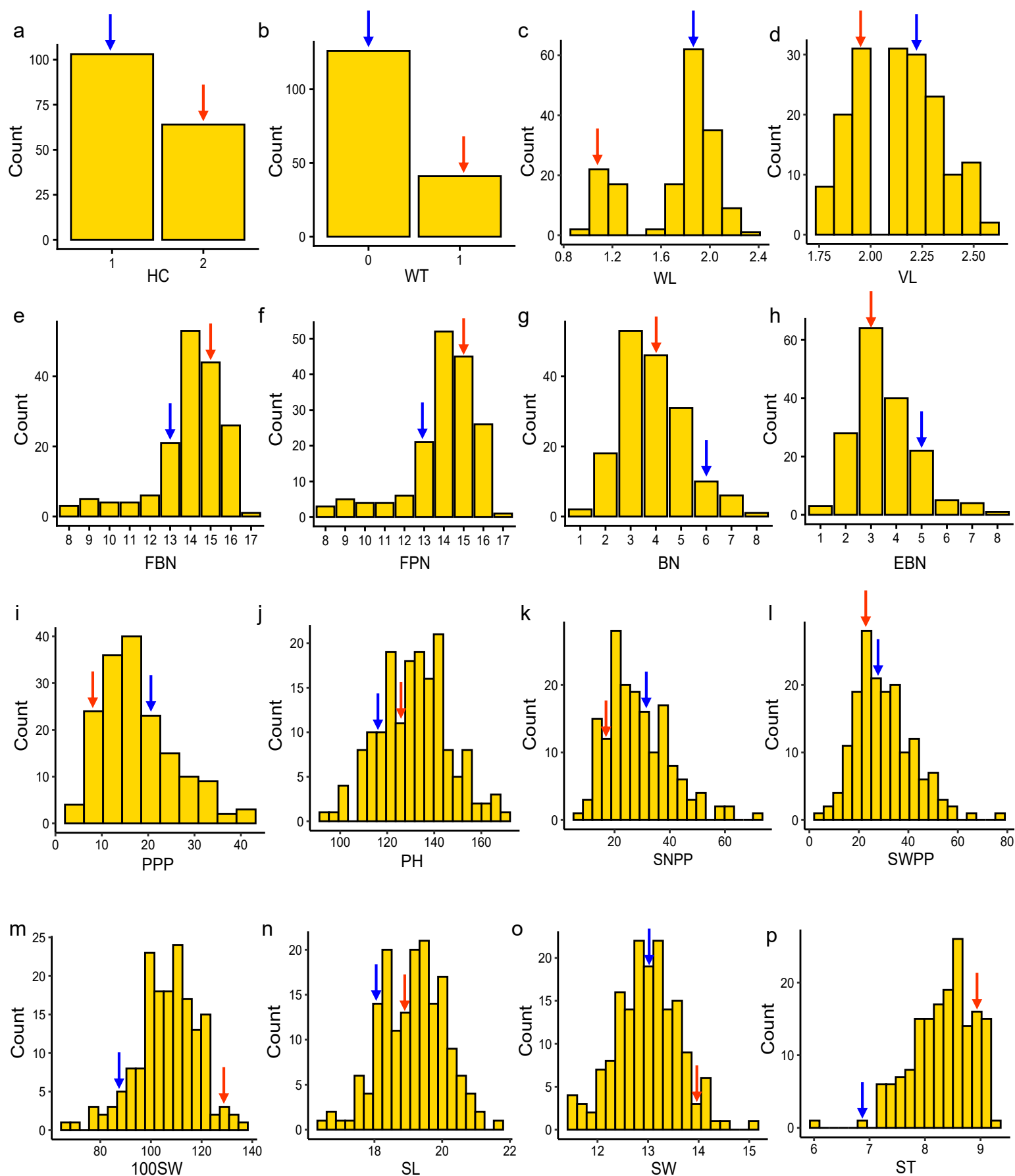


Fig. S20 Frequency distribution of 16 agronomic traits in 167 F₂ population of faba beans. The black and red arrows indicate the parents (VF8137 and H3712) of the F population, respectively. HC = Hilum color, WT = Wing type, WL = Wing length, VL = Vexil length, FBN = First bud node, FPN = First pod node, BN = Branch number, EBN = Effective branch number, PPP = Pods per plant, PH = Plant height, SNPP = Seeds number per plant, SWPP = Seeds weight per plant, 100SW = 100-Seed weight, SL = Seed length, SW = Seed width, ST = Seed thickness.

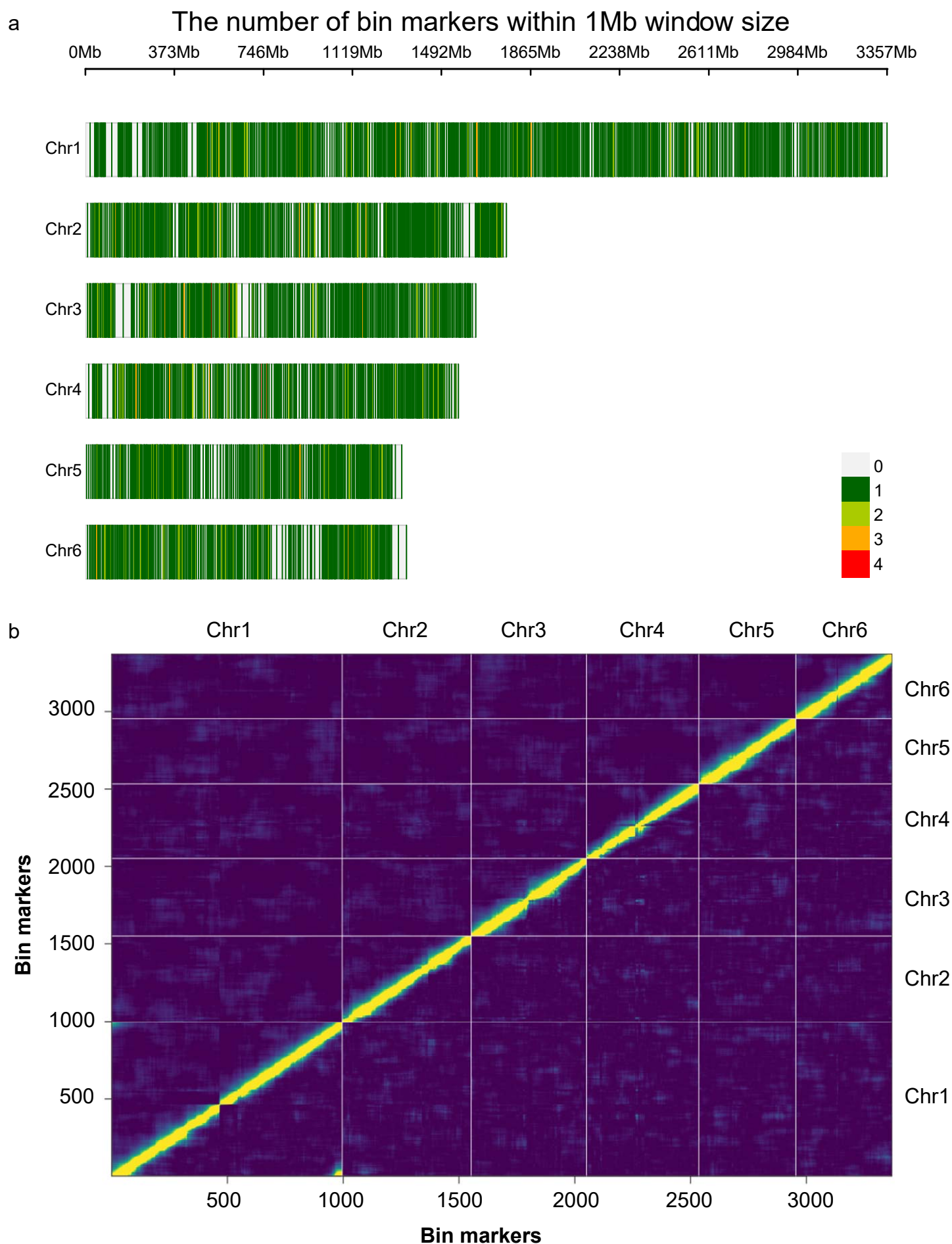


Fig.S21 Genome distribution (a) and estimated recombination fractions (b) for 3369 bin markers in faba beans. A bin size of 1 Mb is applied for genetic marker density.

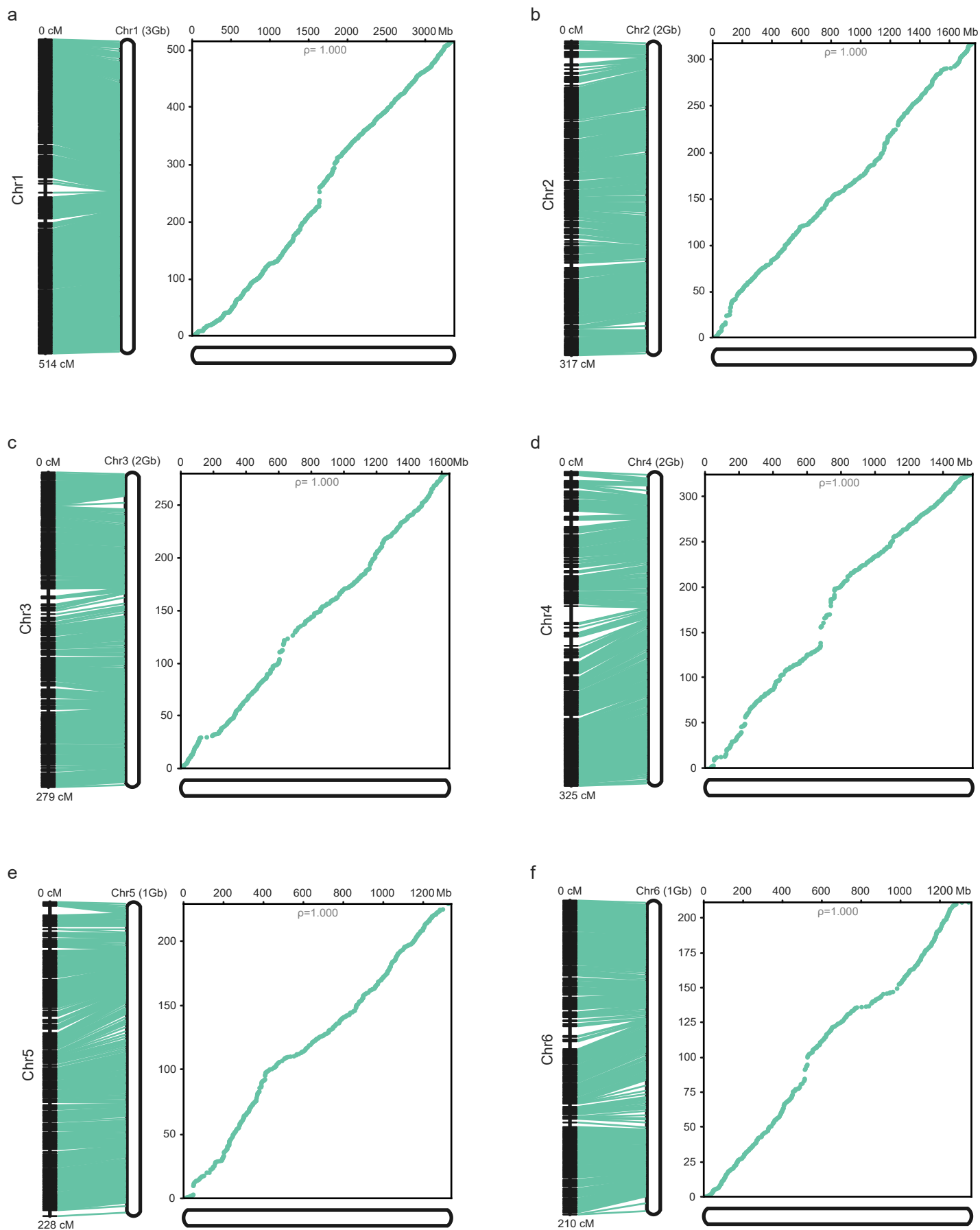


Fig.S22 High consistency between the assembly of VF8137 and the genetic map. a, Chr1; b, Chr2; c, Chr3; d, Chr4; e, Chr5; f, Chr6.

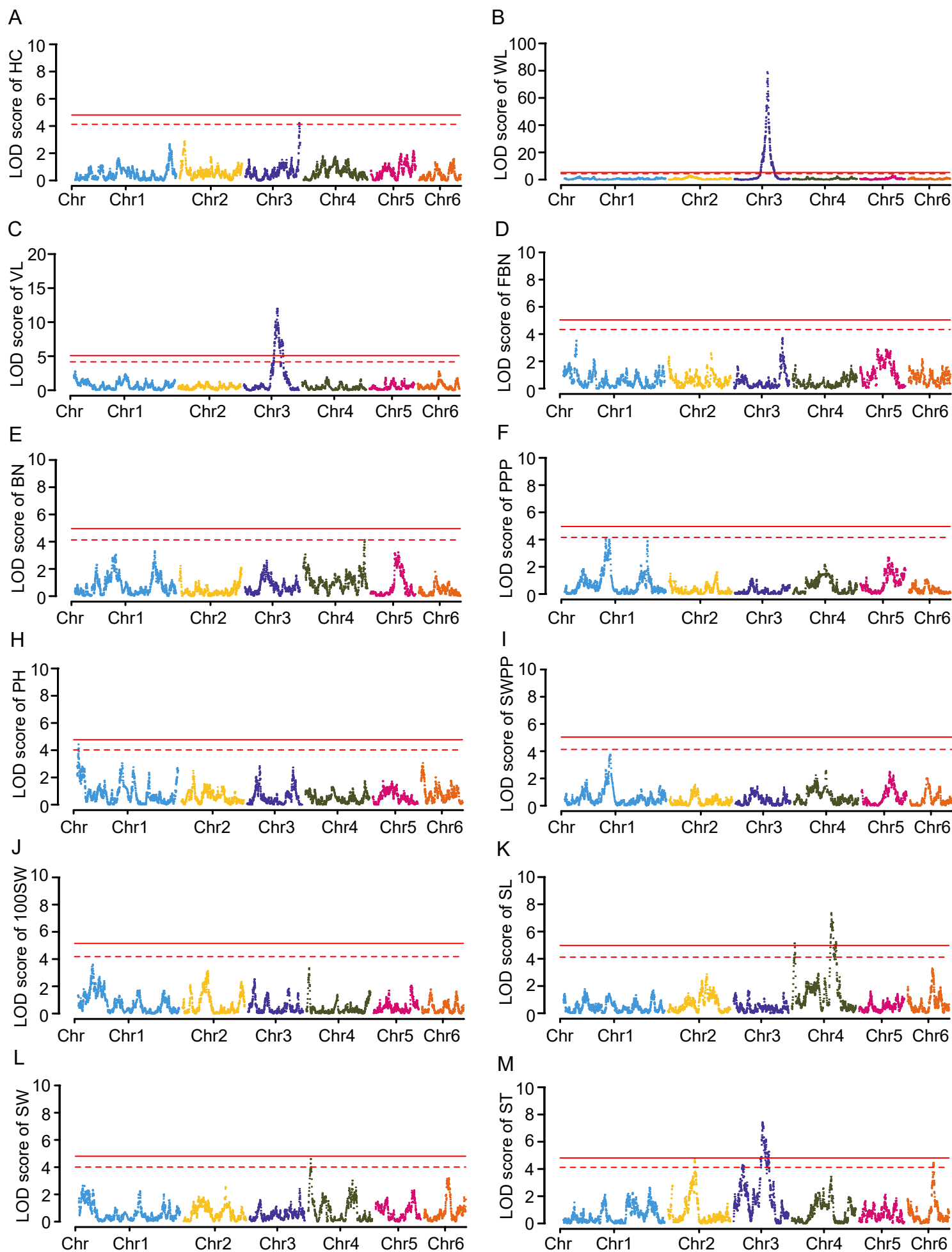


Fig. S23 LOD distribution across the genome for 12 agronomic traits in QTL analyses of faba bean. The red solid and broken lines indicate thresholds of 0.01 and 0.05, respectively. HC = Hilum color, WL = Wing length, VL = Vexil length, FBN = First bud node, BN = Branch number, PPP = Pods per plant, PH = Plant height, SWPP = Seeds weight per plant, 100SW = 100-Seed weight, SL = Seed length, SW = Seed width, ST = Seed thickness.

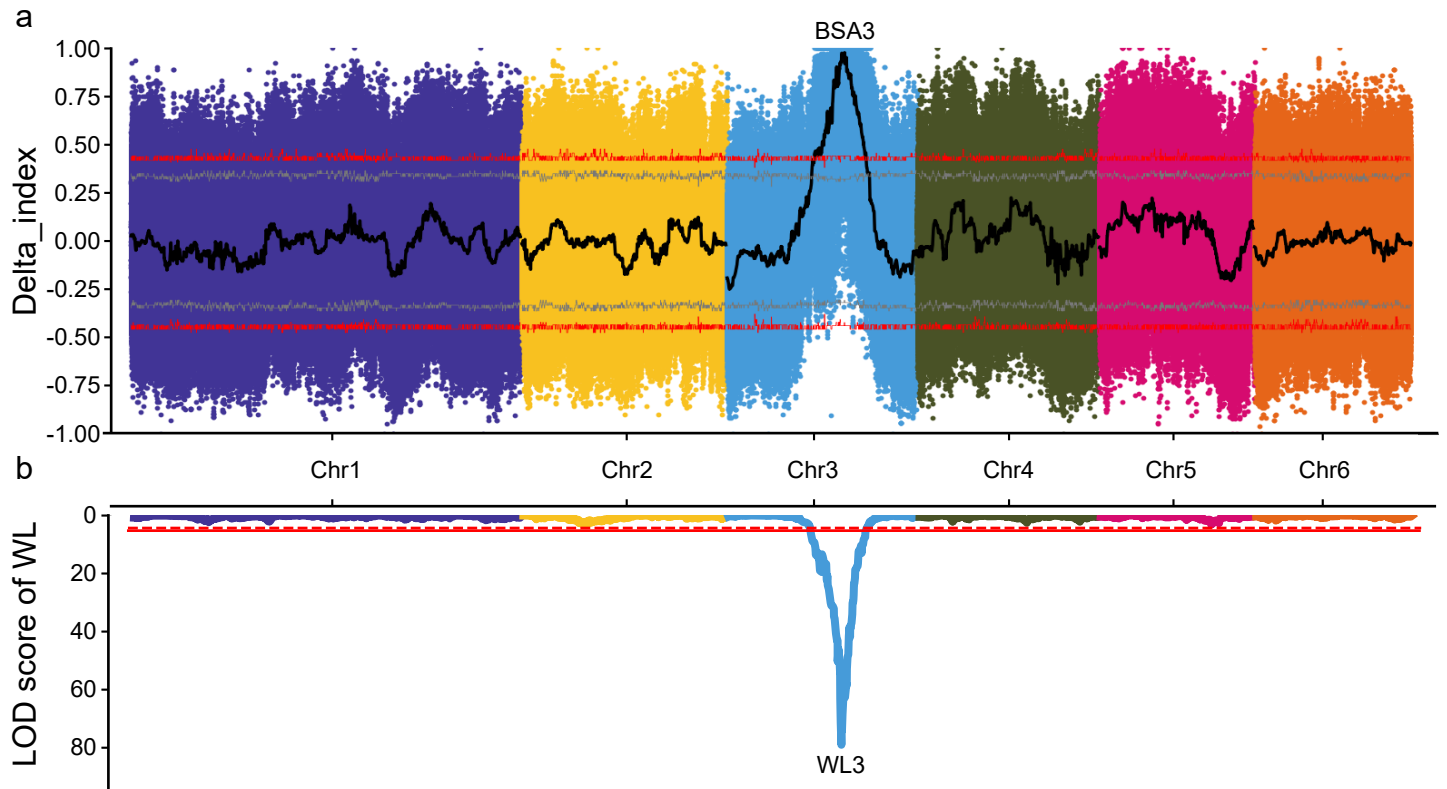


Fig. S24 Delta index distribution across the genome for WL in the BSA analysis (a) and LOD score of WL across the genome in QTL mapping (b) of faba beans. a, The red and grey lines indicate confidence intervals of 99% and 95%, respectively. b, The red solid and broken lines indicate thresholds of 0.01 and 0.05, respectively.

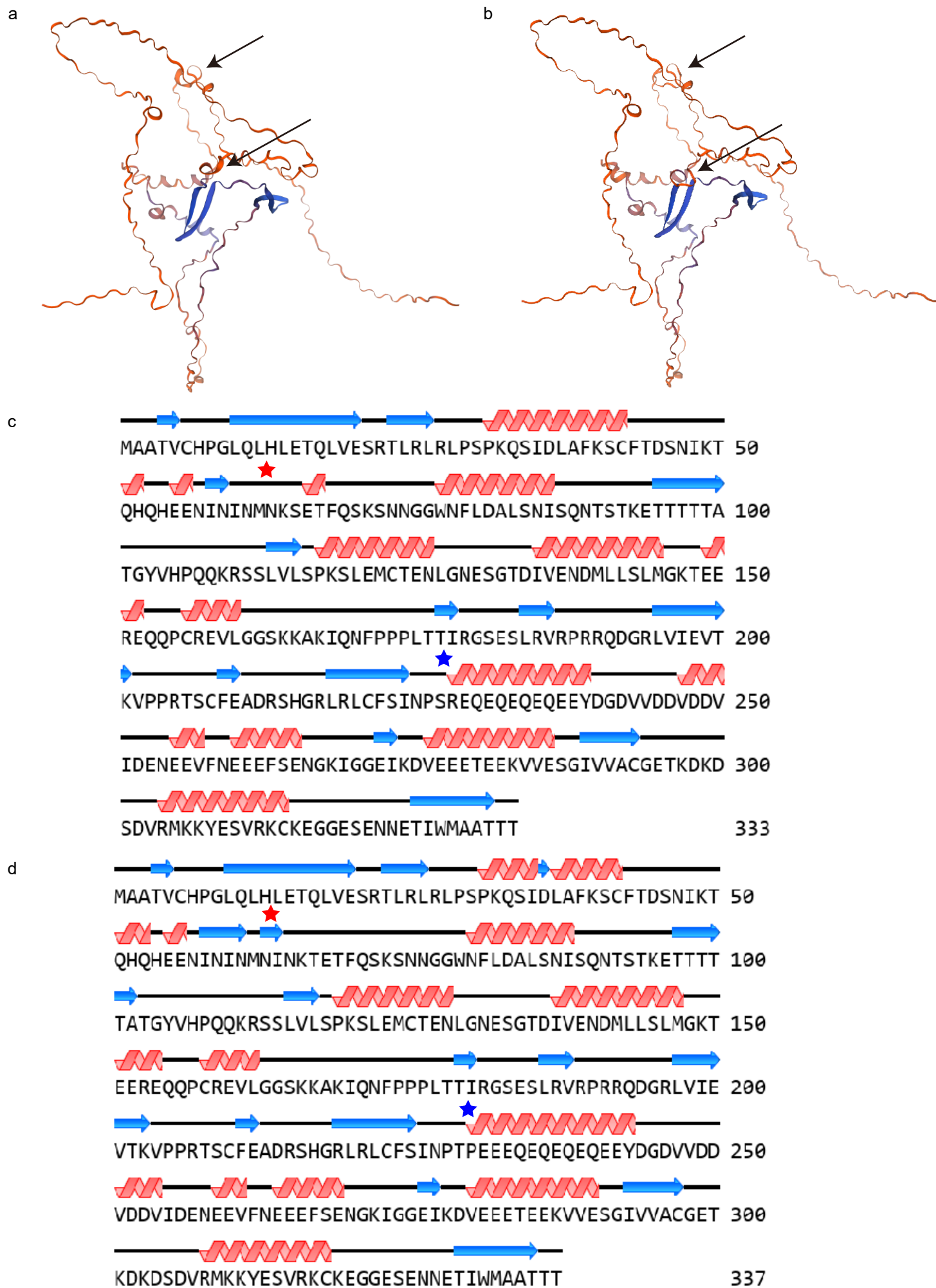


Fig.S25 Differences in three-dimensional structure and secondary structure prediction of FAF3 protein in H3712 (a and c) and VF8137 (b and d). The black arrows in a & b depict disparities in three-dimensional structure, whereas the red and blue asterisks in c & d illustrate variations in secondary structure.