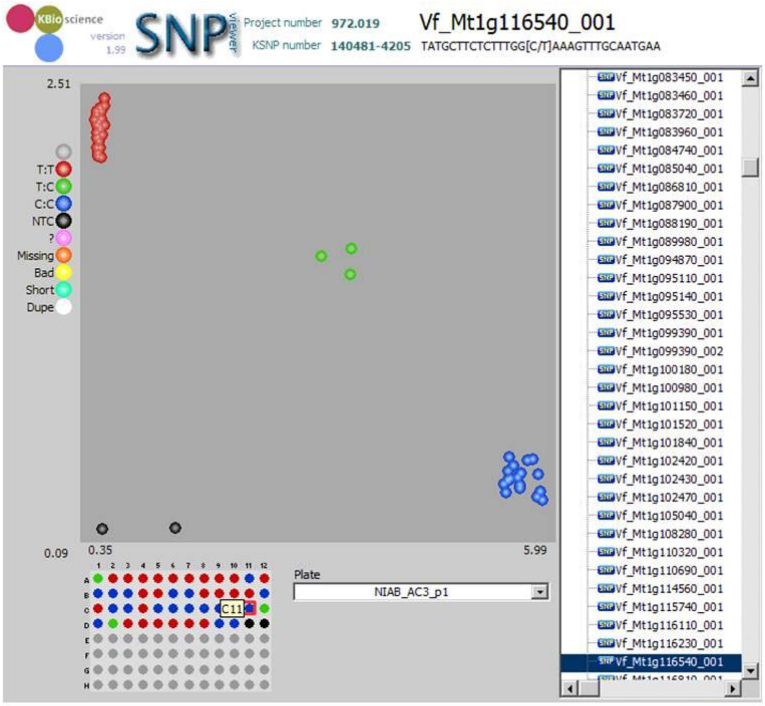
Supplementary Figures

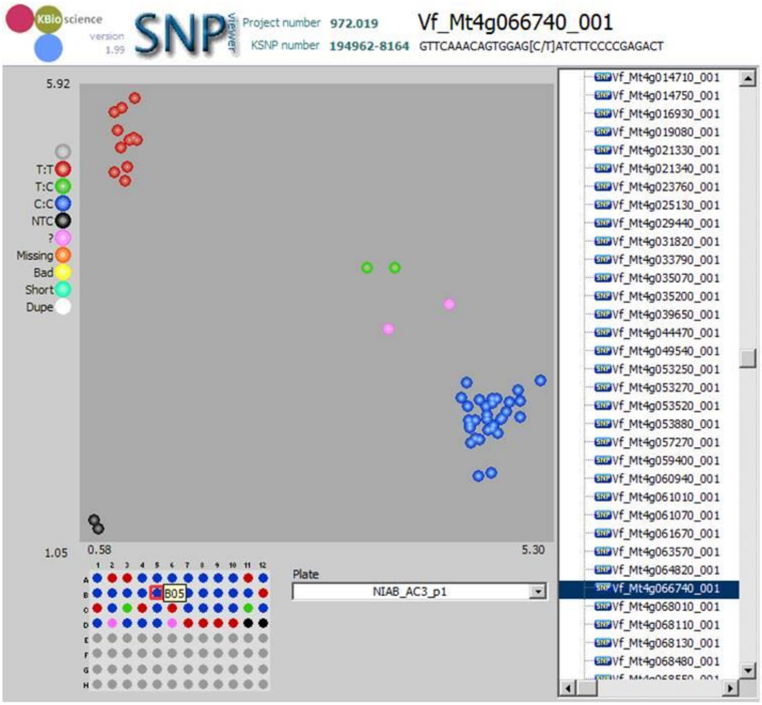


Vf_Mt1g116540_001

Project number 972.019

KSNP number 140481-4205 TATGCTTCTCTTTGG[C/T]AAAGTTTGCAATGAA

Plate NIAB_AC3_p1



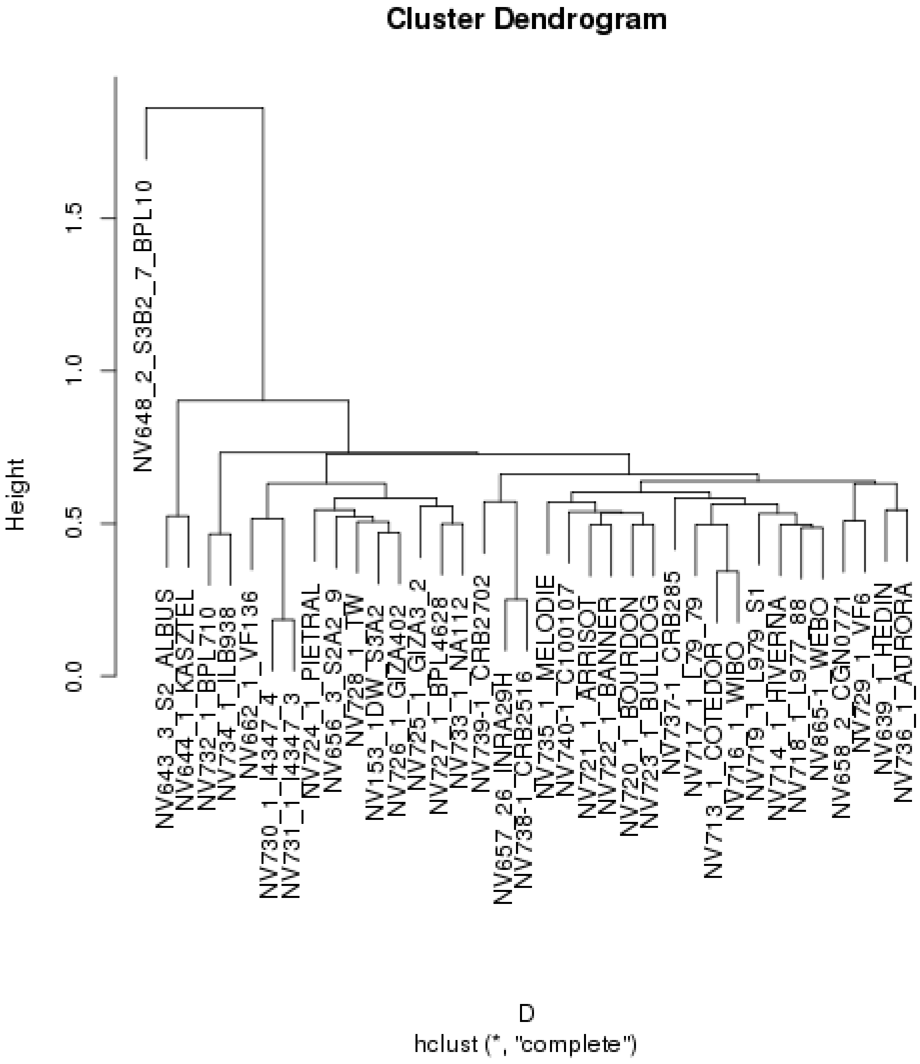
Vf_Mt4g066740_001

Project number 972.019

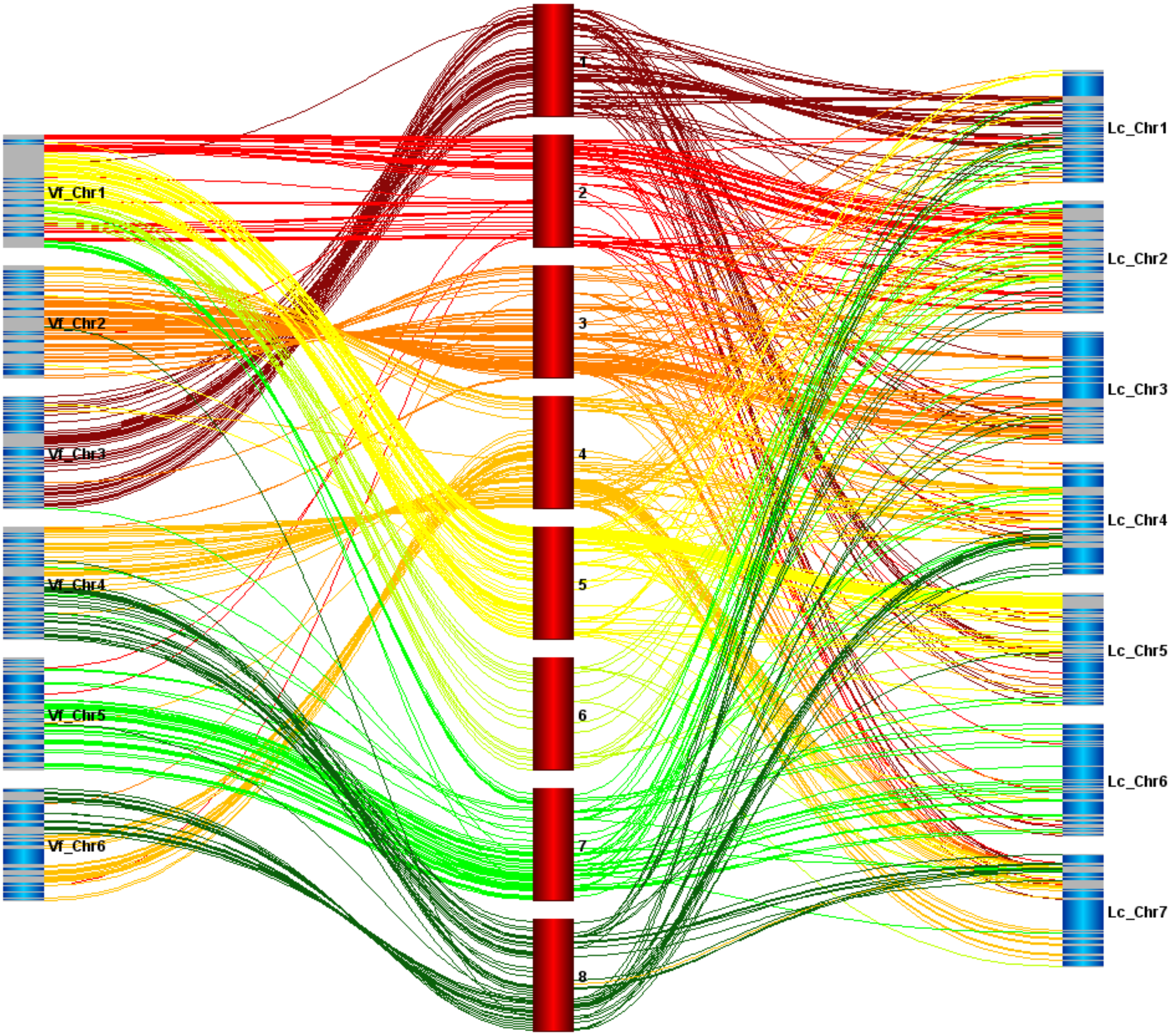
KSNP number 194962-8164 GTTCAAACAGTGGAG[C/T]ATCTTCCCCGAGACT

Plate NIAB_AC3_p1

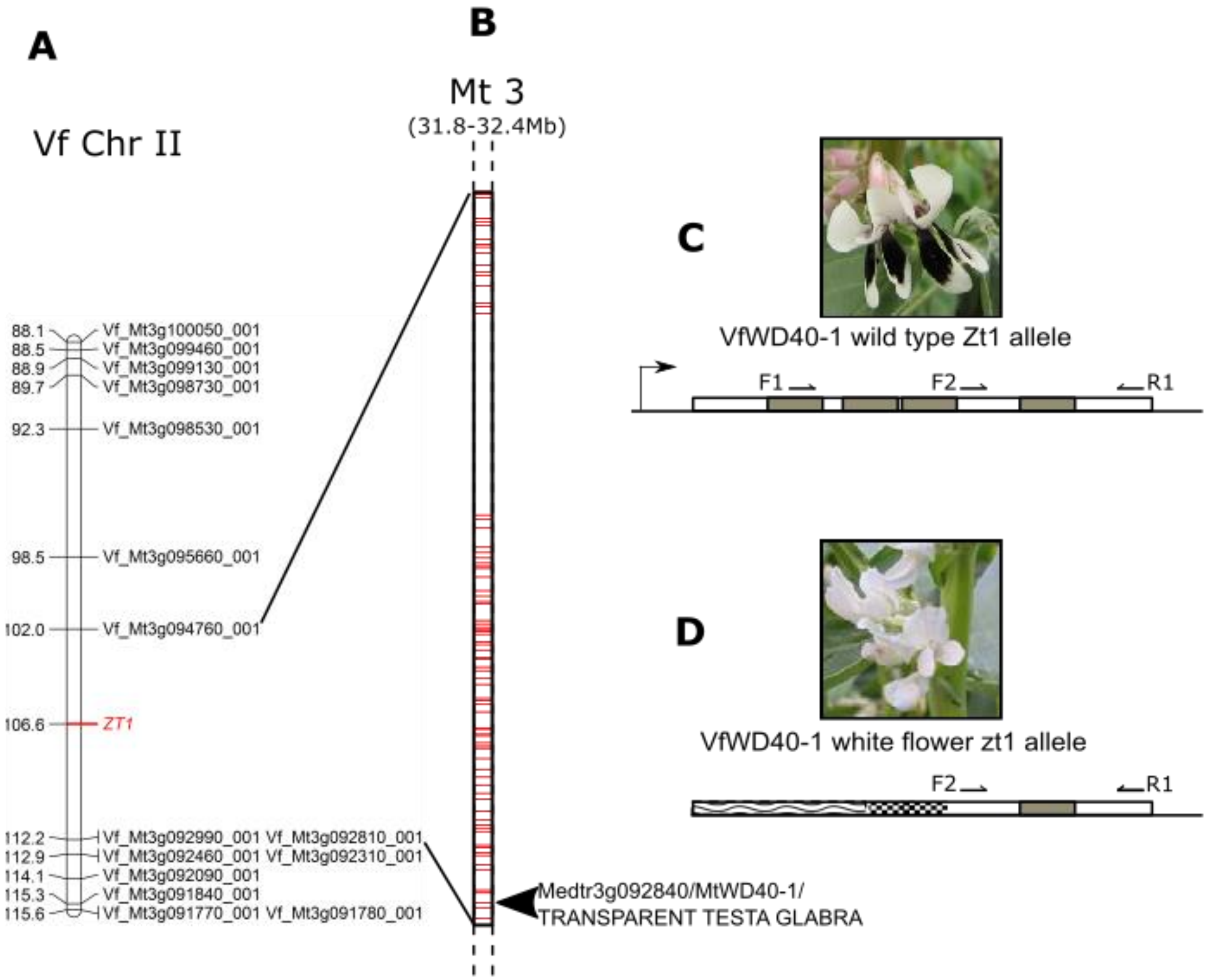
Supplementary Figure 1: Examples of SNP calls for the SNP validation panel of 37 inbred *Vicia faba* lines (Table 3) displayed in SNPViewer (LGC Genomics Ltd., UK) for a marker assigned to quality class I (top) and IV (bottom).



Supplementary Figure 2: UPGMA dendrogram of the SNP-validation panel of 37 inbred *V. faba* lines , based on the panel of SNP markers developed in this study. Line identifiers shown here are a concatenation of the NIAB Vicia (NV) accession number and given name of the inbred shown in Table 3.



Supplementary Figure 3: Display of synteny between chromosomes of *Medicago truncatula* (centre) and linkage groups likely to represent chromosomes of *Vicia faba* (left) and *Lens culinaris* (Sharpe et al. 2013) (right). For *Vicia faba,* only markers syntenous to one locus on *M. truncatula* were mapped, markers of *L. culinaris* may map to more than one locus in *M. truncatula*.



Supplementary Figure 4: **A.** A portion of the linkage map from the F_2 population 1 (NV643-1 x NV648-1) showing the map location of ZT1 between flanking markers Mt3g094760_001 and Vf_Mt3g092810_001. **B.** A schematic of the collinear region of M. truncatula showing the locations of the 78 predicted genes between Medtr3g098210 and Medtr3g09470 (horizontal red ticks). The most obvious candidate functional orthologue for *ZT1* in this interval is Medtr3g092840, annotated as TRANSPARENT TESTA GLABRA and functionally characterised as MtWD40-1 (ref). **C.** The wild-type *Zt1*/VfWD40-1 allele from NV648 with normal flower pigmentation. Primer pairs F1/R1 and F2/R1 amplify 1032bp and 582bp fragments respectively. Grey boxes show the locations of the 4 WD40 repeats. **D.** The recessive *zt1*/VfWD40-1 allele from white-flowered parent NV643 amplifies only the 582bp F2/R1 fragment in common with the wild-type allele and genome walking from the conserved 3' end shows that it contains only one WD40 domain (grey box) and strong homologies in the 5' flanking sequence to *Pisum sativum* adenylate isopentenyltransferase (PsITP1,Genbank Sequence ID AB194606.1; wavy pattern fill) and VfENOD12 (AJ277288.1; checkerboard pattern fill).