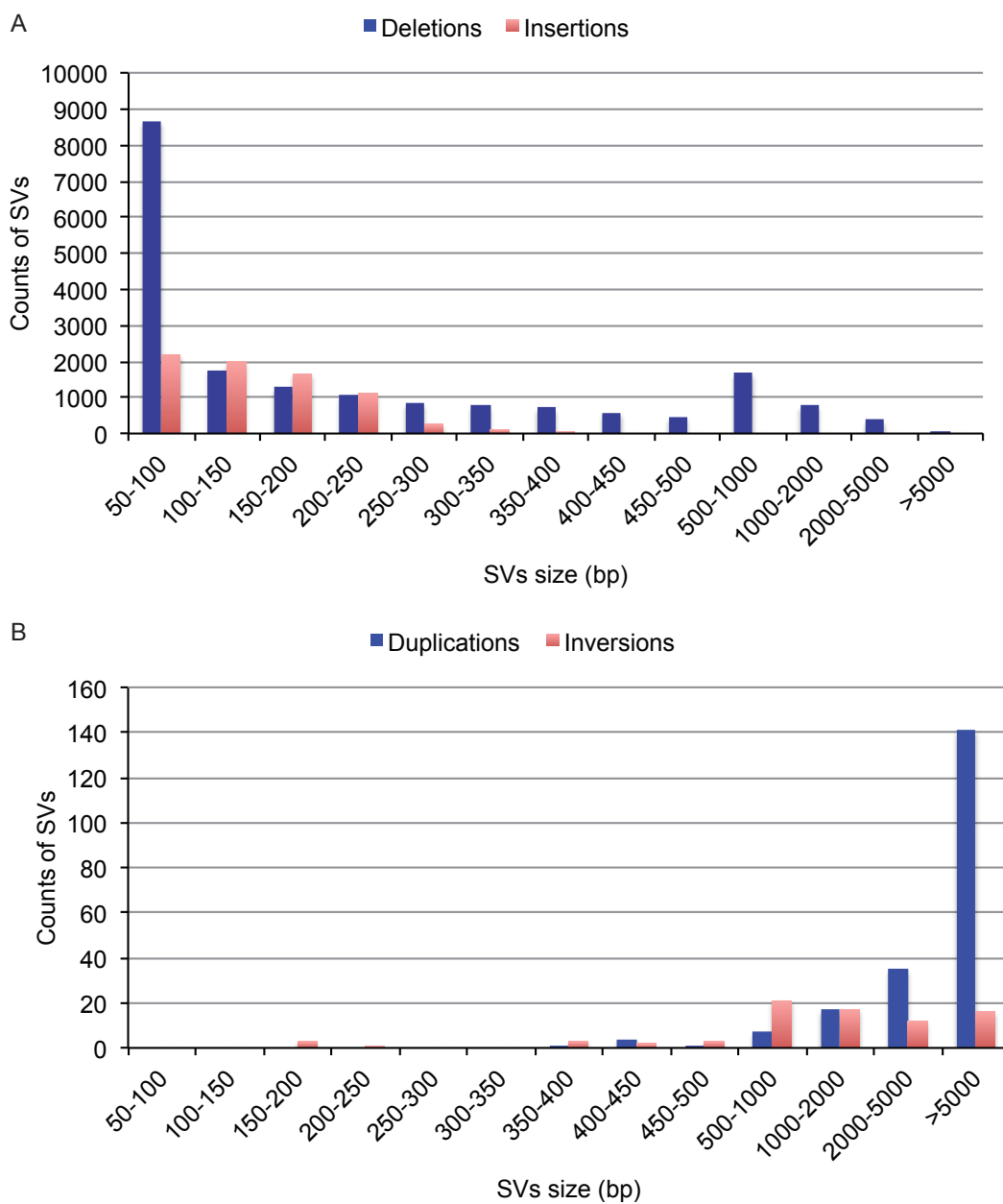
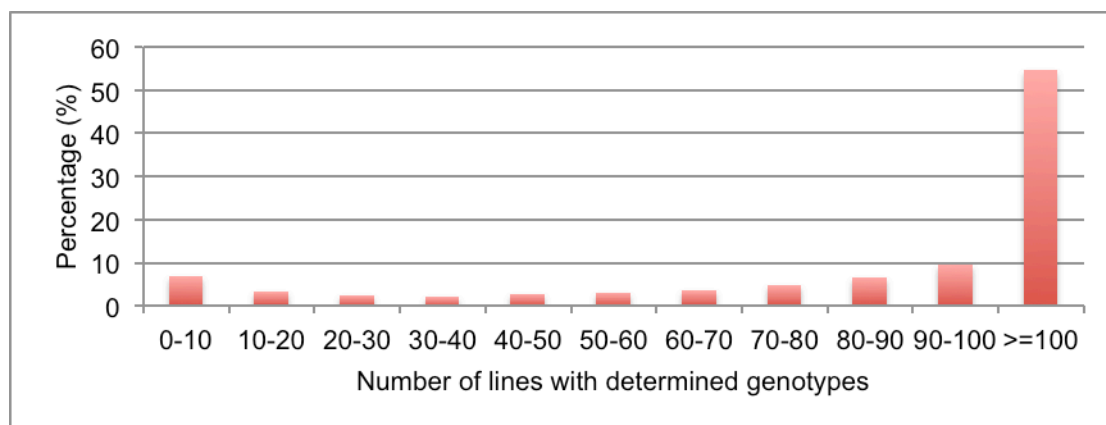


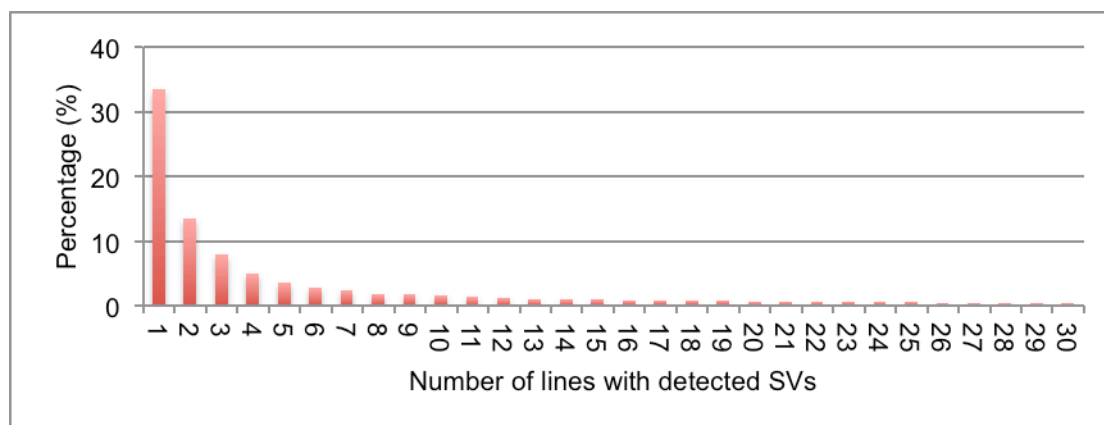
Supplemental Figure 1. SV discovery, filtering and genotyping. (A) Pipeline for SV discovery, filtering and genotyping. (B) Number of SVs in each of the 115 accessions after each filtering process. Potential false positive SVs were filtered sequentially by the five filters (gap→ratio→SNV→coverage→depth), thus SVs that could be filtered by more than one filter were only counted in the first applied filter. The accessions were ordered as listed in Supplemental Data Set 1.



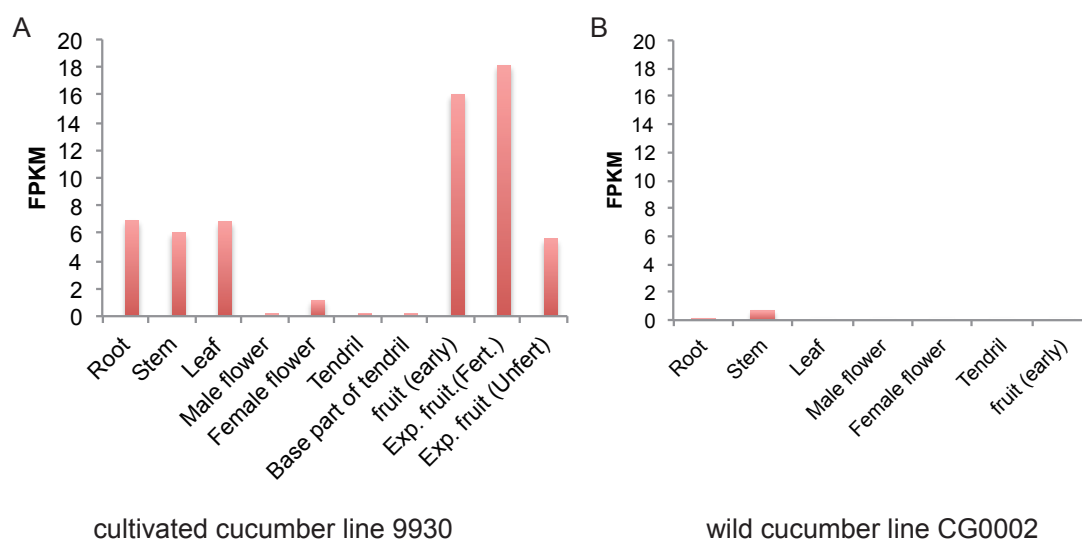
Supplemental Figure 2. Size distribution of identified SVs.



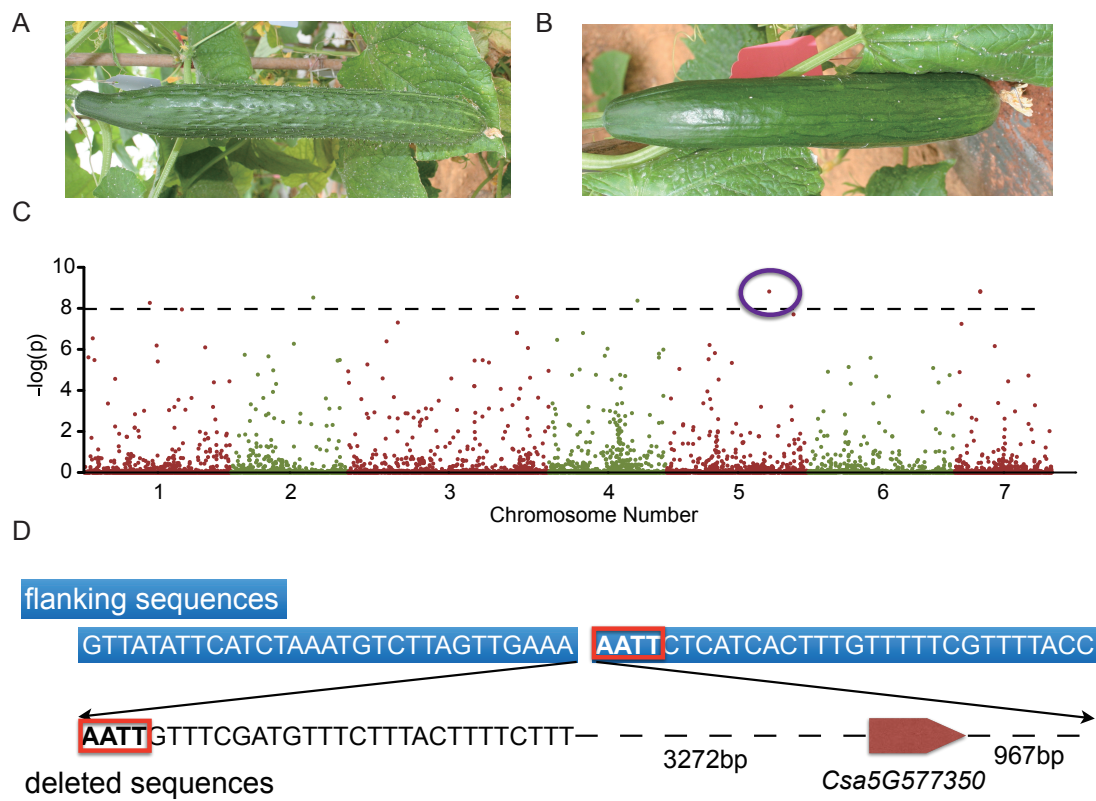
Supplemental Figure 3. Genotyping summary of cucumber SVs in the 115 accessions.



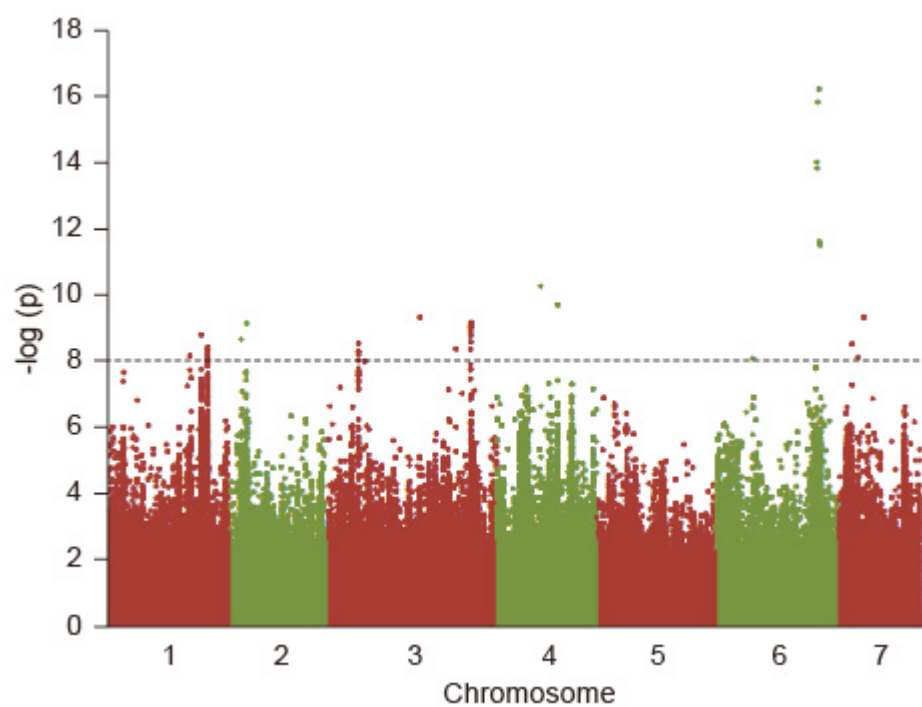
Supplemental Figure 4. Distribution of different numbers of accessions for which a structural variation was detected compared to the reference genome. About 33% of the SVs only occur in one accession of the core collection.



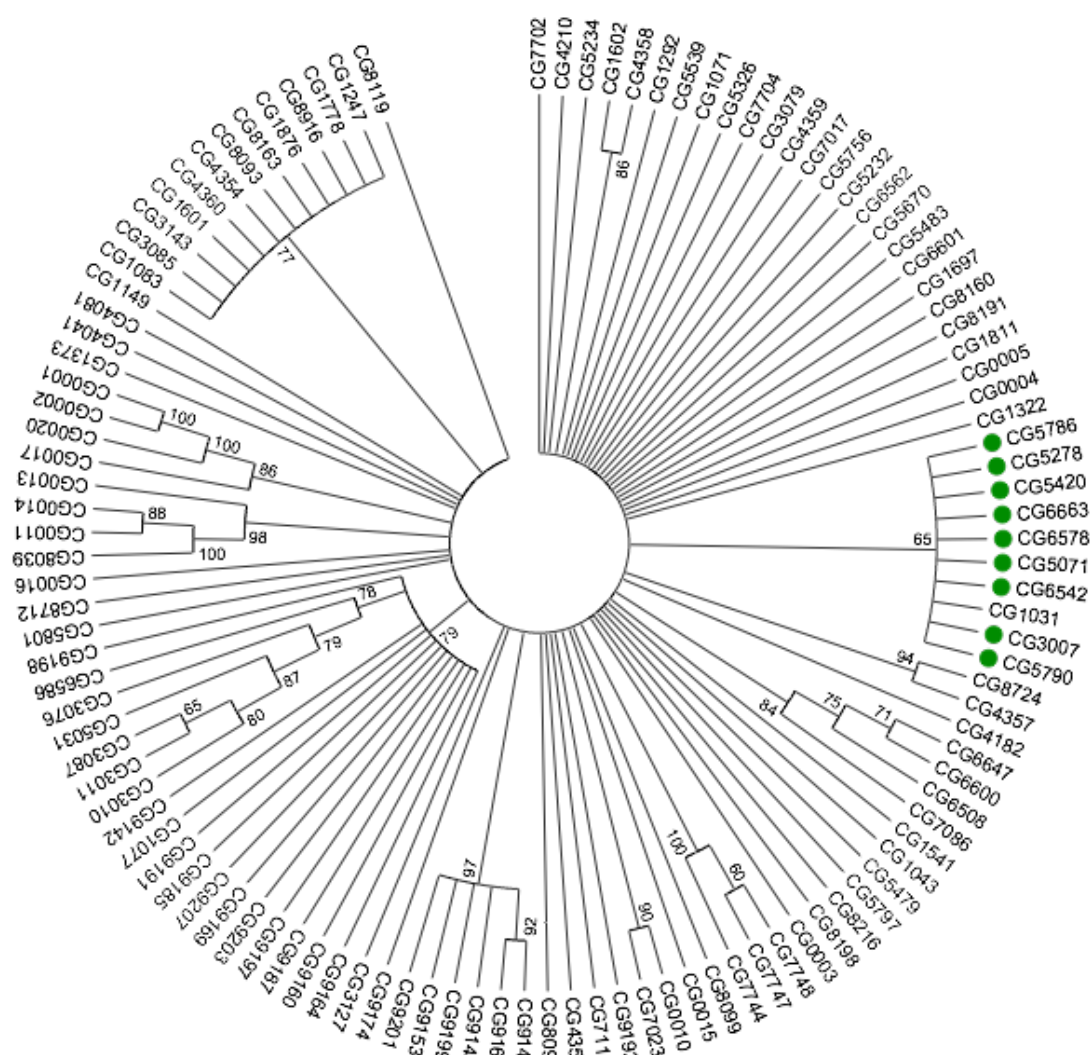
Supplemental Figure 5. Expression profile of *Csa2G237130* in cultivated cucumber line 9930 (A) and wild line CG0002 (B).



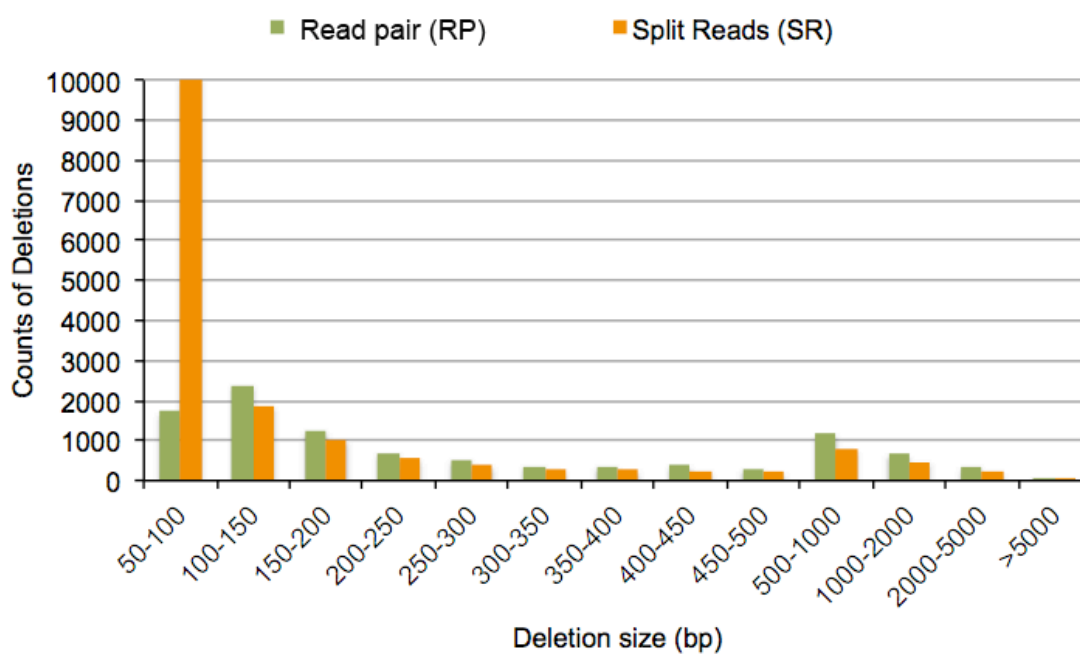
Supplemental Figure 6. SVs associated with tuberculate fruit in cucumber. Cucumber fruits with tubercles (A) and smoother appearance (B). (C) Manhattan plot of GWAS using the SV set for tuberculate fruit. (D) Sequences at the breakpoint of the deletion. The microhomologs AATT might be responsible for the formation of this deletion.



Supplemental Figure 7. Manhattan plot of GWAS using the SNP set for the gynoecy phenotype.



Supplemental Figure 8. Phylogenetic relationships of the 115 cucumber accessions based on the SNPs within the 30.2-kb duplicated region (*F* locus). Accessions marked by green circles are gynoecious. The branches with low support value (<60) were condensed to avoid the confusion of relationships with low confidence.



Supplemental Figure 9. Size distribution of deletions detected by read pair (RP) and split read (SR) approaches.

Supplemental Table 1. SVs predicted to be full-length LTR retrotransposons.

SV ID	chromosome	SV left window		SV right window		SV type
		Start	End	Start	End	
SV1G00237800	Chr1	16940777	16940777	16945383	16945383	deletion
SV1G00324300	Chr1	22186523	22186523	22188315	22188315	deletion
SV2G00261700	Chr2	18392804	18392804	18394273	18394273	deletion
SV3G00131400	Chr3	11152955	11152955	11154992	11154992	deletion
SV3G00301200	Chr3	22411125	22411125	22415576	22415576	deletion
SV3G00315300	Chr3	23465804	23465804	23471293	23471293	deletion
SV4G00149000	Chr4	10272463	10272463	10277765	10277765	deletion
SV5G00036800	Chr5	2617628	2617628	2634155	2634155	deletion
SV5G00135800	Chr5	10756388	10756388	10757931	10757931	deletion
SV5G00173600	Chr5	13536061	13536061	13539551	13539551	deletion
SV5G00242200	Chr5	19033877	19033877	19035220	19035220	deletion
SV6G00280500	Chr6	18939086	18939086	18940983	18940983	deletion