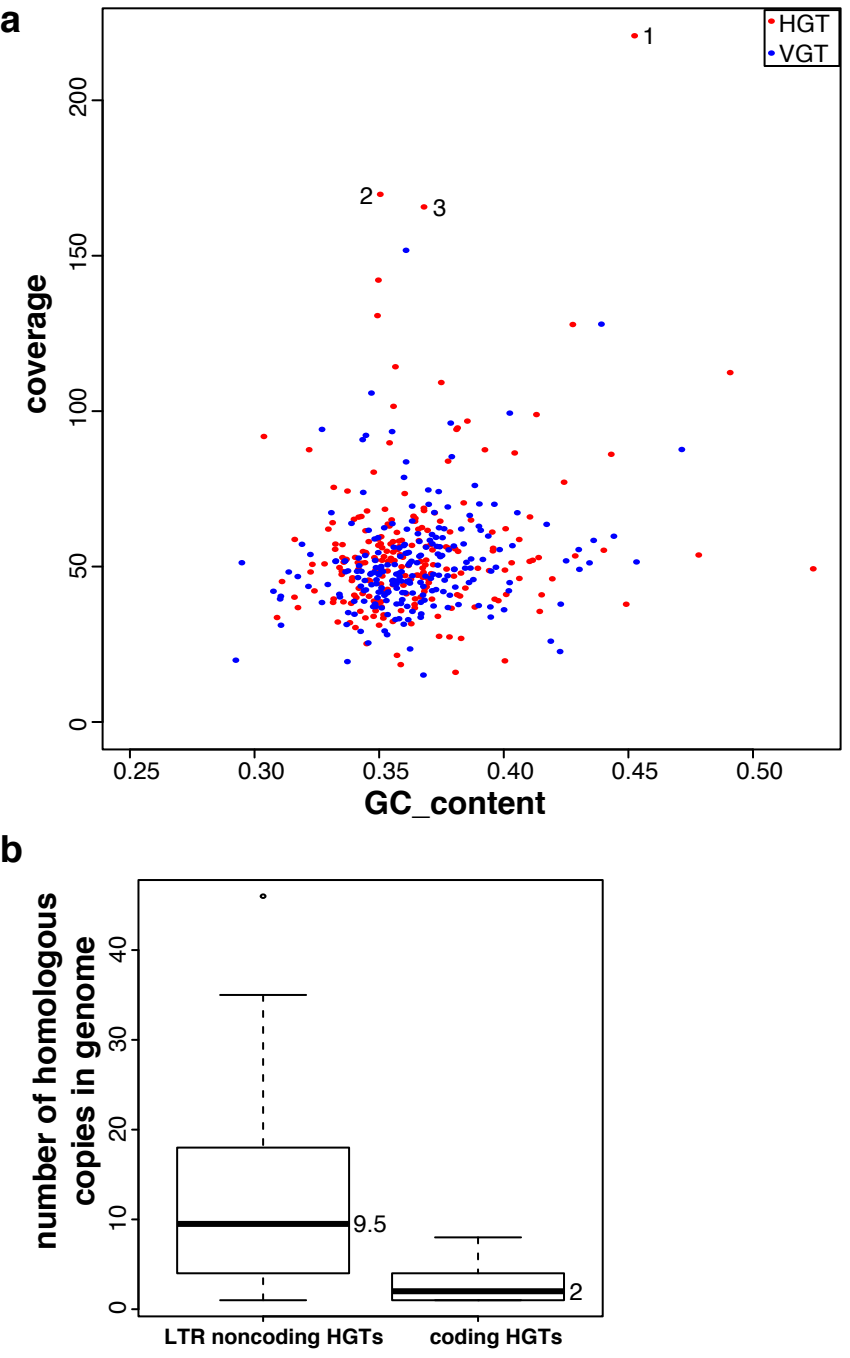

Fig. S5. Stoichiometry plot comparing the GC content and depth of coverage of HGT and vertically transmitted genomic scaffolds (a), and boxplot comparing the depth of coverage of LTR HGTs and coding HGTs (b). (a) X-axis and Y-axis refer to the GC_content and read depth coverage of the HGT and vertically transmitted genomic scaffolds, respectively. HGT genomic scaffolds were identified by taking the genomic contig with the HGT genes, whereas vertically transmitted genomic contigs (VGT) were identified by taking the vertically transmitted genes from the tree and searching against the *Cuscuta campestris* genome to identify the best BLASTN hits. The top three HGT contigs with the highest depth of coverage are labeled with "1", "2", and "3". Both 1 and 2 are HGT-derived LTR (Ty1/Copia) retrotransposon sequences of 307bp and 899 bp, respectively, likely from a Fabales ancestor; 3 is an expressed HGT gene encoding an uncharacterized protein likely from a Malpighiales ancestor. Although the HGT gene is not a retrotransposon, the genomic scaffold (~51k) on which the HGT gene is located contains a 1958bp-long Ty1/Copia retrotransposon sequence. **(b)** Boxplot compares the number of copies in the genome for 24 HGT-derived LTR (Ty1/Copia) retrotransposon sequences with copies for an equal number of 24 coding HGTs. The wilcoxon rank sum test with the the number of genome hits (>=80% coverage and >=80% identity) shows that LTR noncoding HGTs have significantly more copies in the genome than the coding HGTs (P-value = 2.136e-06), with the median number of copies being 9.5 and 2, for the former and latter, respectively. This analysis might explain the higher depth of coverage for the three HGT scaffolds (1 ,2, 3).