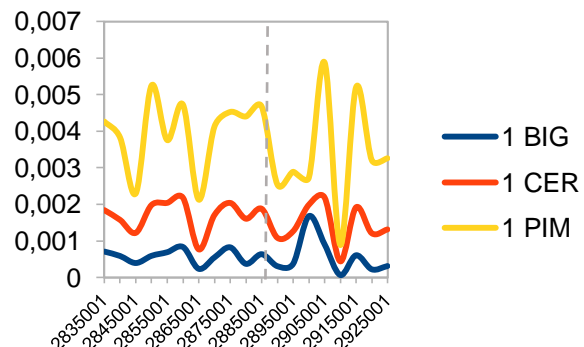
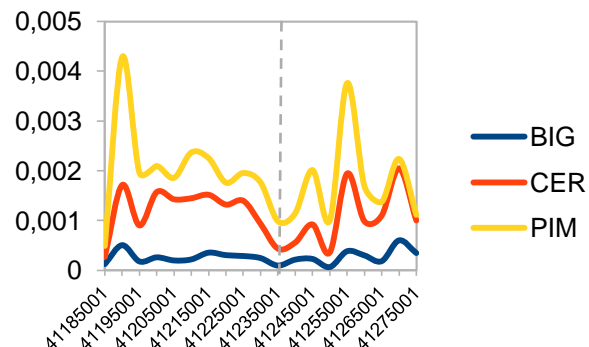


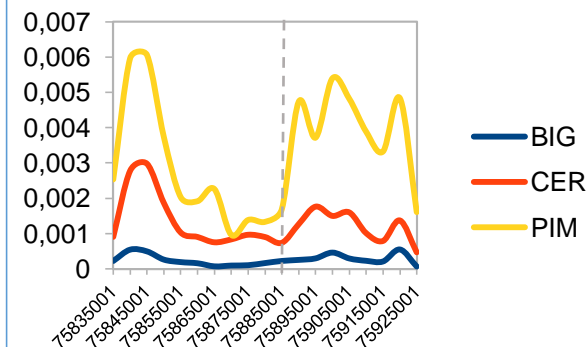
BIK - Solyc01g008860 – chr1



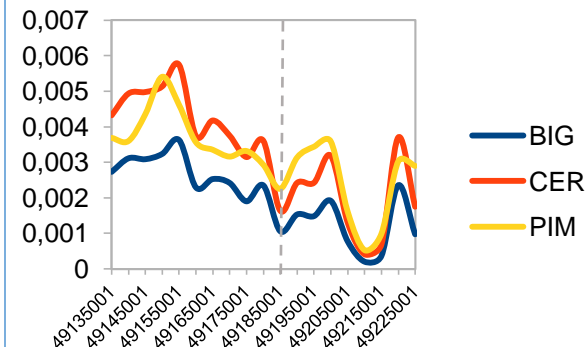
BIK - Solyc01g028830 – chr1



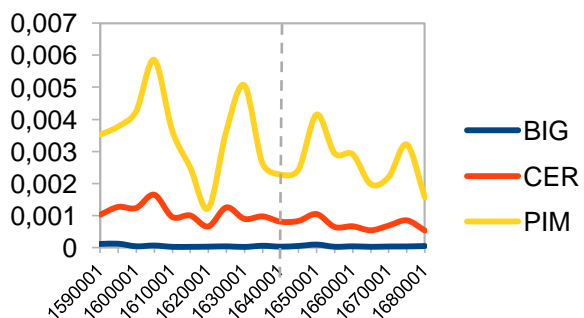
BIK - Solyc01g067400 - chr1



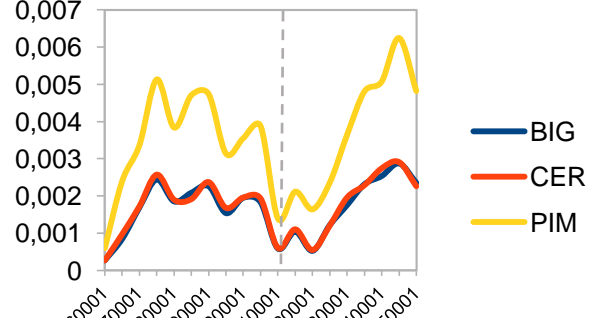
BIK - Solyc04g050970 – chr4



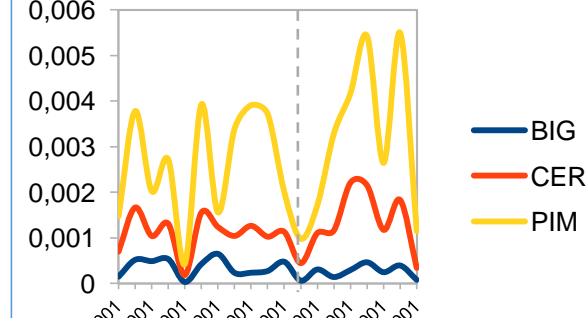
BIK - Solyc05g007050 - chr5



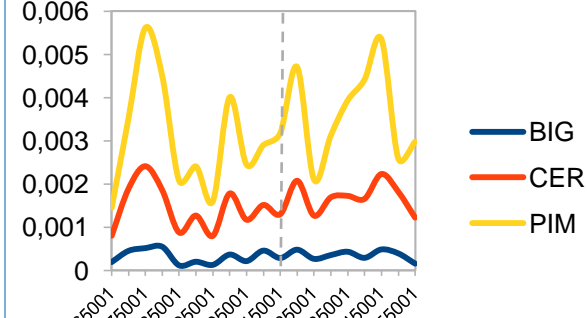
BIK - Solyc05g024290 - chr5



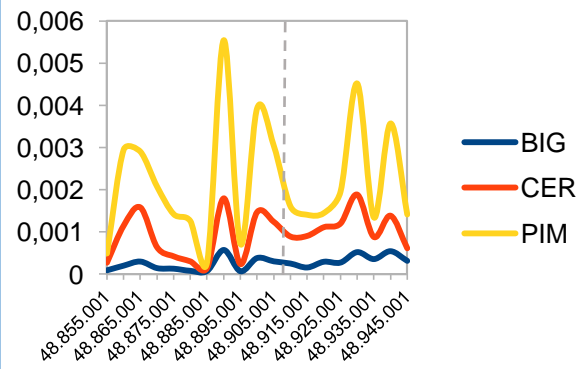
BIK - Solyc06g005500 - chr6



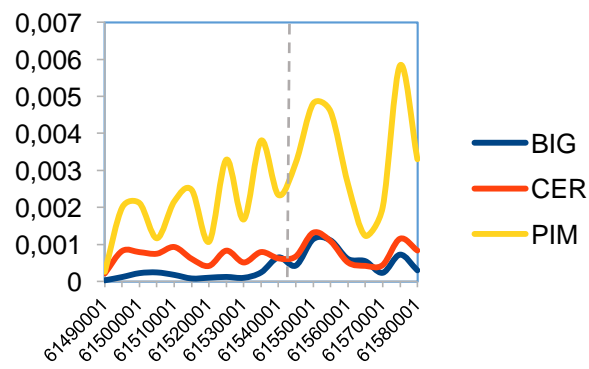
BIK - Solyc06g062920 - chr6



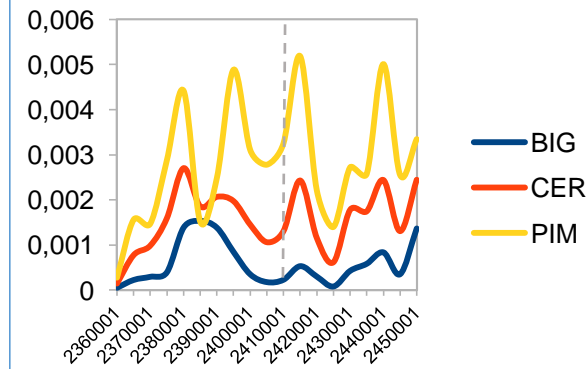
BIK - Solyc06g083500 - chr6



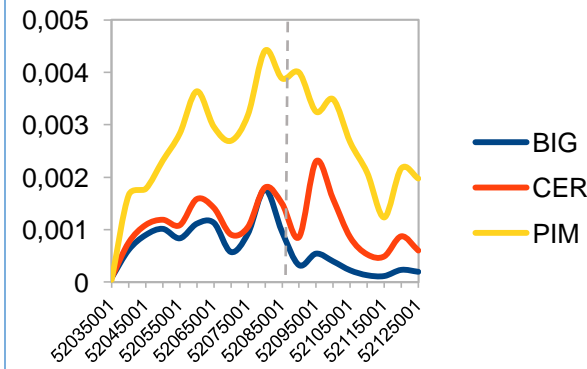
BIK - Solyc08g077560 - chr8



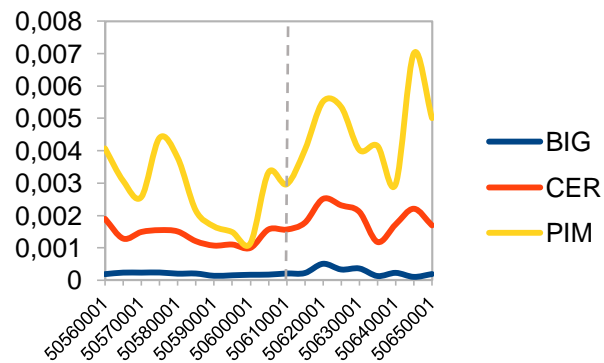
DMR1 - Solyc04g008760 - chr8



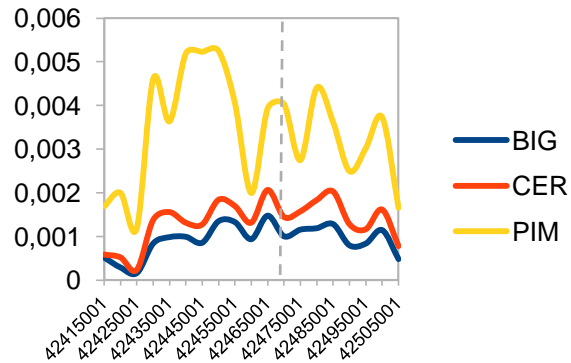
DMR6 - Solyc03g080190 - chr3



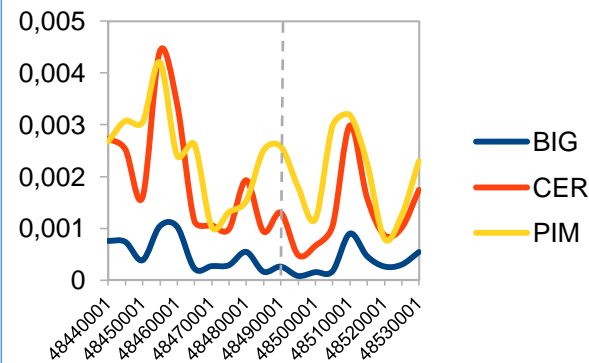
DND - Solyc02g088560 - chr2



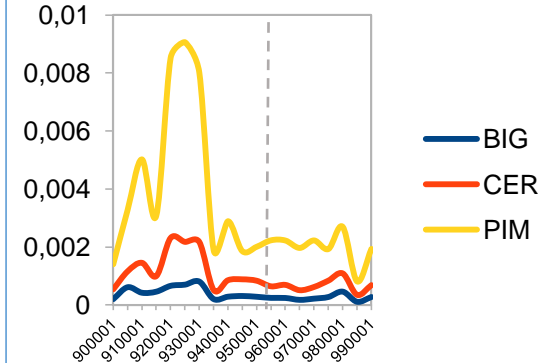
MLO - Solyc02g077570 - chr2



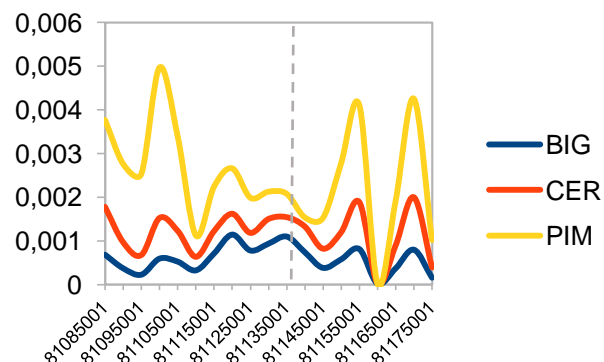
MLO - Solyc06g082820 - chr6



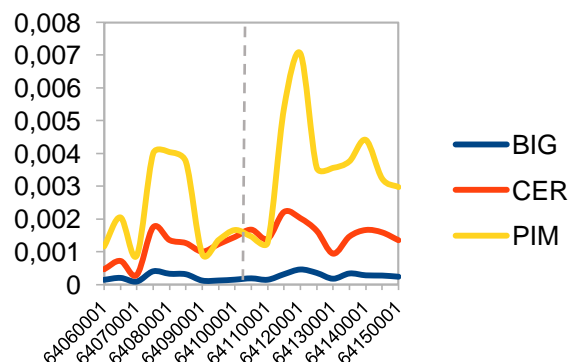
PMR4 - Solyc01g006350 - chr1



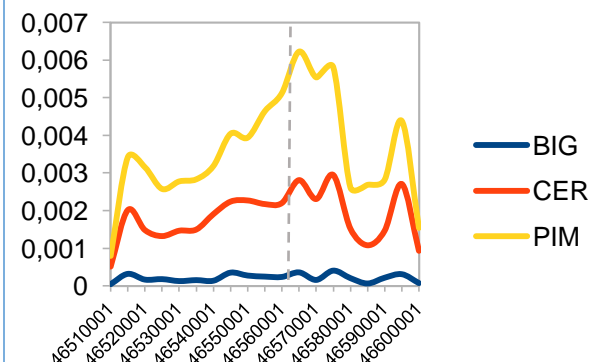
PMR4 - Solyc01g073750 - chr1



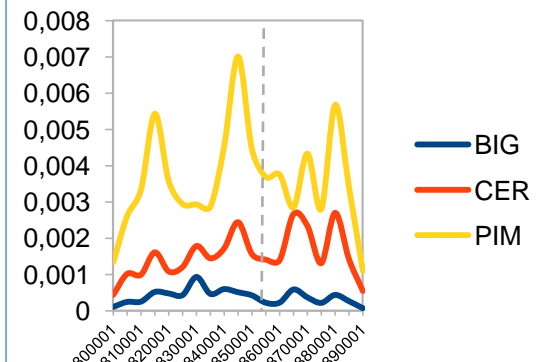
PMR4 - Solyc07g056260 - chr7



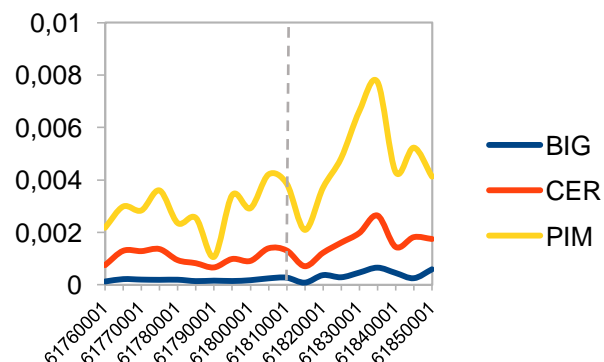
PMR5 - Solyc02g082950 - chr2



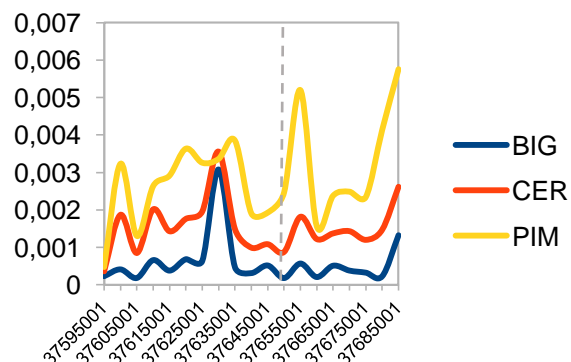
PMR5 - Solyc03g006220 - chr3



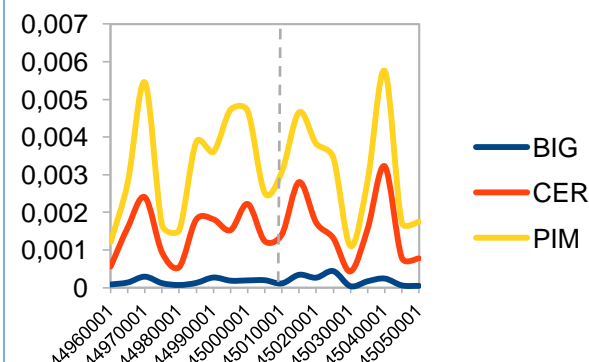
PMR5 - Solyc07g053350 - chr7



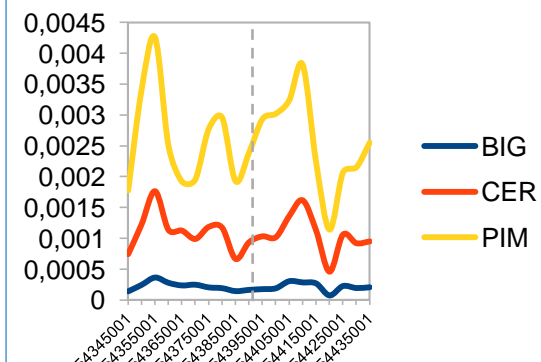
PMR6 - Solyc02g067450 - chr2



PMR6 - Solyc02g080910 - chr2



PMR6 - Solyc02g093580 - chr2



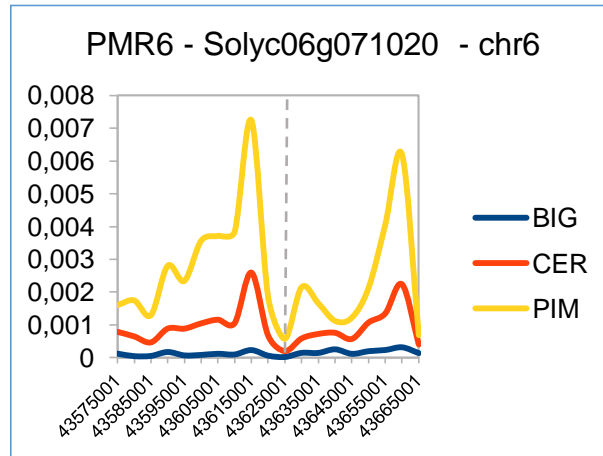
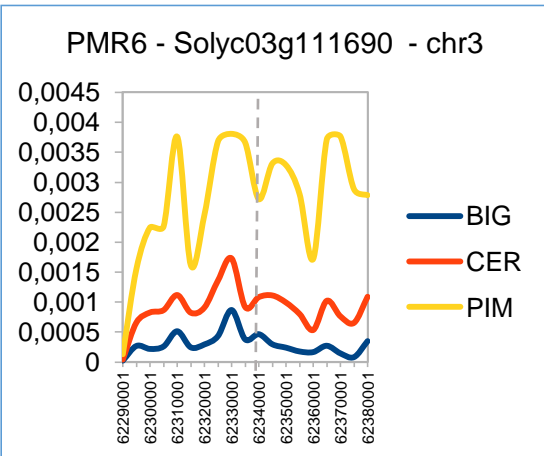


Figure S2. Nucleotide Diversity Analysis of S-Genes around Deleterious SNPs in PIM, CER, and BIG Groups. The genetic variation around of S alleles was analysed using the nucleotide diversity (π) index implemented in vcfTools (<https://vcftools.github.io>), among different tomato groups (PIM, CER, and BIG), focusing on a 100kb region, centered around each deleterious SNP with a 5k window