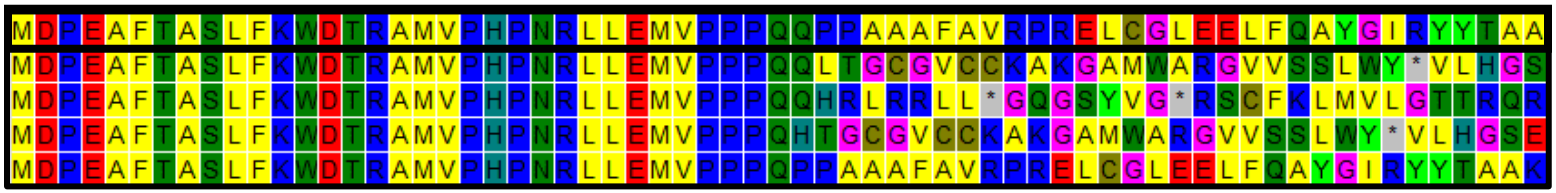
Amino acid modifications in *PLFY* for *LFY*-sg1

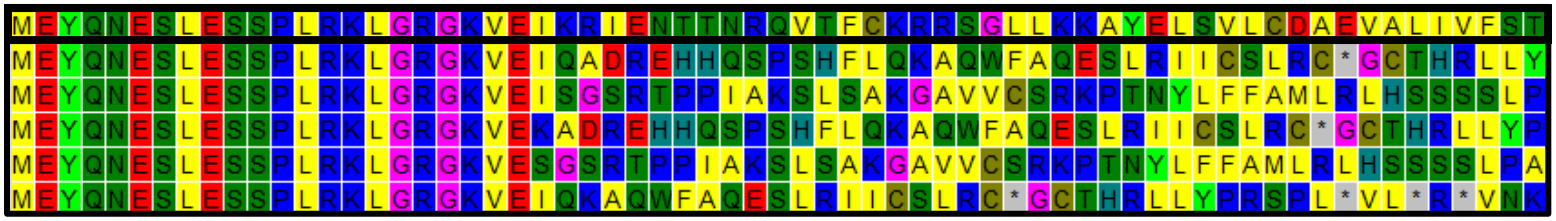


Genotype
WT
+1 bp
-1 bp
-2 bp
-3 bp

Amino acid modifications in *PLFY* for *LFY*-sg1sg2

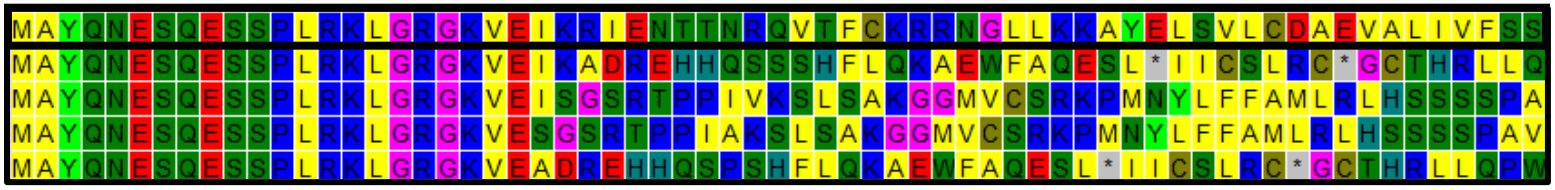
Genotype
WT
120 bp inversion
121 bp inversion
-120 bp
-121 bp
-130 bp

Amino acid modifications in *PAG1* for *AG*-sg1sg2



Genotype
WT
+1 bp
-1 bp
-2 bp
-4 bp
-41 bp

Amino acid modifications in *PAG2* for *AG*-sg1sg2



Genotype
WT
+1 bp
-1 bp
-4 bp
-5 bp

Fig S1. Diversity in putative amino acid modifications to the WT peptide sequence in 717. These peptide alignments are the partial translation of the sequence alignment from the most common mutations seen in events with *LFY*-sg1, *LFY*-sg1sg2, and *AG*-sg1sg2. The first line in each alignment shows the WT sequence. Stop codons are shown with a *. The tables to the right identify the specific mutation that led to the peptide modification in each row.