Supplemental Table 6. Pyrimidine dinucleotide analyses at G:C>A:T substitution sites in six FN M_3 plant lines.

FN Line	Position	Substitution category	Substitution and flanking sequence	DiPyr±DiPyr Forward Strand	DiPyr±DiPyr Reverse Strand	Pyr-Pyr	Functional context	Substitution class	Substitution effect	Gene orientation	On transcribed strand
E125	Chr1:21445271	G:C→A:T	TTCTAACAAA**C**TATTAACTAT		**C**T	y	Intergenic			NA	NA
E125	Chr1:22289862	G:C→A:T	CATTGATGGA**C**ATCATTGGTT				Exon	synonomous	silent	Forward	yes
E128	Chr1:22959189	G:C→A:T	ATTGTCGAAG**C**GCTGTCATGT				Exon	synonomous	silent	Reverse	No
E125	Chr1:29219260	G:C→A:T	CTTCAAGCCT**C**TTTTTTATCT		T**C**, **C**T	y	UTR			NA	NA
E99	Chr1:29991776	G:C→A:T	AGCTTGGTCT**C**CCTGATTACT	T**C**, **C**T		y	Exon	synonomous	silent	Forward	yes
E71	Chr1:30242299	G:C→A:T	TAGGAGCAGC**C**TATGCAGCTG		C**C**, **C**T	y	Exon	synonomous	silent	Forward	yes
E216	Chr2:13496083	G:C→A:T	ATATATACTA**C**TATCTTACTG	**C**T		y	Intron			NA	NA
E125	Chr2:16150493	G:C→A:T	GTTTCTCACT**C**TCCCAAATCC	T**C**, **C**T		y	Exon	non-synonomous	missense	Forward	yes
E71	Chr2:17438544	G:C→A:T	ACACATGTCA**C**ATGAAGGGTG				Intron			NA	NA
E138	Chr2:19568871	G:C→A:T	AAATAATCAA**C**CTGCAAAAGA	**CC**		y	Exon	non-synonomous	missense	Forward	yes
E216	Chr2:8139800	G:C→A:T	TGAGAGTAAA**C**GAGATGATTT				Exon	non-synonomous	truncated	Forward	yes
E128	Chr3:15105689	G:C→A:T	CTTAATATTT**C**AGCTTTGAAT	T**C**		y	Intergenic			NA	NA
E138	Chr3:18755414	G:C→A:T	CTTCACGATC**C**TTCCGCCACC		C**C**, **C**T	y	Exon	non-synonomous	missense	Reverse	no
E71	Chr3:2496101	G:C→A:T	ATCGACTTGT**C**ATTTTGCCGG	T**C**		y	Intergenic			NA	NA
E71	Chr3:8303675	G:C→A:T	TAATACTTAA**C**CGACACTTCG	**C**C		y	Intergenic			NA	NA
E125	Chr3:9623429	G:C→A:T	GTTACGCTGA**C**GTCATTTGAG				Intergenic			NA	NA
E138	Chr4:12517099	G:C→A:T	GAAACGAATA**C**AGAAATAAAA				UTR			NA	NA
E125	Chr4:14565079	G:C→A:T	CTTGGTTTTT**C**TTTATGAAAA	T**C**, **C**T		y	Intron			NA	NA
E99	Chr4:891280	G:C→A:T	ATGGTCTCAT**C**GCTTCCCGCA	T**C**		y	Intron			NA	NA
E216	Chr5:8368874	G:C→A:T	ATATAAAATA**C**CTACGTCCTC		**C**C	y	Intergenic			NA	NA