Supplemental Table 1. List of mutations identified in six FN M_3 plant lines.

FN Line	Variant type	Chromosome	Variant start position	SBS category	INDEL length	Nucleotide/s inserted or deleted	Variant position and flanking sequences; substitution (_) or INDEL (*)	Functional context	Notes	Dipyrimidine sequence
E125	SNP	Chr1	Chr1:17758232	G:C→T:A			TGTCGTATCA**C**TCATCACGTA	Genic	Non-synonomous	CT
E125	SNP	Chr1	Chr1:21445271	G:C→A:T			ATAGTTAATA**G**TTTGTTAGAA	Intergenic		CT*
E125	SNP	Chr1	Chr1:22289862	G:C→A:T			CATTGATGGA**C**ATCATTGGTT	Genic	Synonomous	
E125	SNP	Chr1	Chr1:27574935	A:T→T:A			TAGAACCGAT**A**TGCAGTTTCC	Genic	Non-synonomous	
E125	SNP	Chr1	Chr1:29219260	G:C→A:T			AGATAAAAAA**G**AGGCTTGAAG	UTR		TC*
E125	SNP	Chr1	Chr1:3445251	A:T→T:A			ATATTGCCCA**T**TTTTCTAAAA	Intergenic		TT
E125	SNP	Chr1	Chr1:4583389	A:T→G:C			GCACTAAAAG**T**AACTCATTCT	Intergenic		
E125	SNP	Chr2	Chr2:11891834	A:T→G:C			CAGTTAATGG**T**CCACCCAAAC	Intergenic		TC
E125	SNP	Chr2	Chr2:12056256	G:C→T:A			ATAAGAAGCA**C**CCTACAATTG	Intron		CC
E125	SNP	Chr2	Chr2:16150493	G:C→A:T			GTTTCTCACT**C**TCCCAAATCC	Genic	Non-synonomous	TC
E125	SNP	Chr2	Chr2:2426521	A:T→C:G			TGATTTCTTC**T**CCATAGAACC	Genic	Non-synonomous	CT
E125	SNP	Chr2	Chr2:4161552	A:T→T:A			TCTTATACCT**A**AAACATAGAT	Intergenic		TT*
E125	SNP	Chr2	Chr2:5592045	A:T→G:C			ACTTTTCAAT**A**CACATATCCA	Intergenic		
E125	SNP	Chr2	Chr2:6514329	G:C→C:G			TTTACCATCT**C**AATTCTCATT	Intergenic		TC
E125	SNP	Chr3	Chr3:142061	A:T→C:G			TGCCAATTCT**T**GATGCTACAC	Intron		TT
E125	SNP	Chr3	Chr3:7380300	G:C→T:A			ATATTCCACG**G**TCAATGGTGA	Genic	Non-synonomous	CC*
E125	SNP	Chr3	Chr3:9623429	G:C→A:T			GTTACGCTGA**C**GTCATTTGAG	Intergenic		
E125	SNP	Chr4	Chr4:14565079	G:C→A:T			CTTGGTTTTT**C**TTTATGAAAA	Intron		TC
E125	Insertion	Chr2	Chr2:10220586		1	T	CAGGGATAGC*TTTTTTTTTT	Intergenic		
E125	Insertion	Chr5	Chr5:25236520		1	A	GCAAATCTTG*AAAAAAAAAA	Intergenic		
E125	Deletion	Chr1	Chr1:17747994		-4	AATA	GAAAATAATT*AAATTAGCAC	Intron		
E125	Deletion	Chr1	Chr1:18669688		-2	GA	TAATATGGGC*AGAGGTTTGG	Intergenic		
E125	Deletion	Chr2	Chr2:13691669		-11	AATATGCTCGA	TTCTACAGAG*TCAGTGGGAT	Genic		
E125	Deletion	Chr2	Chr2:13804210		-12	TACAGAGCTAGC	CAGGAACCAA*TATAGCTAAT	Genic		
E125	Deletion	Chr2	Chr2:9135557		-7	AAGAAGC	CTATGTGCGT*AAGCTTTCTC	Genic		
E125	Deletion	Chr3	Chr3:17229771		-3	TTC	TCCTCTCTTT*TTCTGTTTCA	Genic		
E125	Deletion	Chr3	Chr3:487491		-4	TGGT	CCTTGATCCG*CTTATCTCTG	Genic		
E125	Deletion	Chr4	Chr4:16632942		-6	CTAACT	GTTGGAGAAA*CTAAACAAGA	Genic		
E125	Deletion	Chr5	Chr5:19925087		-32	ATGAAGATCATATATTAAATGCATATATGAAC	GTTTTGAACA*AATGCATATA	Intergenic		
E125	Deletion	Chr5	Chr5:3438719		-1	C	GTGAGATTGA*AGTTCGGTGC	UTR		
E125	Deletion	Chr5	Chr5:3727272		-17	AAGCCATGGCCAAAATT	ATCCCATGAC*AGGGCTAATT	Genic		
E125	Deletion	Chr5	Chr5:8315154		-1	C	AGTTCGGTAA*CAAAATTTAT	Intergenic		
E128	SNP	Chr1	Chr1:16212366	A:T→G:C			TATAATGTTA**A**CCTTTTTTTC	Intron	Splice site affected (second intron base changed to a G)	TT*
E128	SNP	Chr1	Chr1:22959189	G:C→A:T			ATTGTCGAAG**C**GCTGTCATGT	Genic	Synonomous	
E128	SNP	Chr1	Chr1:26345333	A:T→C:G			TTCCATACAT**T**AGCATTTCCA	Genic	Non-synonomous	TT
E128	SNP	Chr1	Chr1:4143027	A:T→G:C			ATCTGGAGGA**T**TTAATAAGCA	Genic	Synonomous	TT
E128	SNP	Chr3	Chr3:15105689	G:C→A:T			CTTAATATTT**C**AGCTTTGAAT	Intergenic		TC
E128	SNP	Chr4	Chr4:10672876	A:T→G:C			TTTCTCTTCT**T**TGTACTGAAC	Intron		TT
E128	Deletion	Chr1	Chr1:2199360		-8	CAAACCCT	GAGTCCGATC*AGGTTAGCCG	Genic		
E128	Deletion	Chr3	Chr3:2804349		-4	GGGA	CTTTCCCATG*GGGAAATTGA	Genic		
E128	Deletion	Chr5	Chr5:7998106		-3	TCA	GAGCTGTTTT*TGGAATATGT	Genic		
E138	SNP	Chr1	Chr1:29089661	A:T→G:C			TTTATGCTAT**A**GACCATCCTG	Intergenic		CT*
E138	SNP	Chr1	Chr1:8533634	A:T→G:C			GACCAGAGAG**T**GTTTCTTGTC	Genic	Non-synonomous	
E138	SNP	Chr2	Chr2:1261693	A:T→G:C			CCAAATGTTG**T**AGCTAAGACC	Genic	Non-synonomous	
E138	SNP	Chr2	Chr2:19568871	G:C→A:T			AAATAATCAA**C**CTGCAAAAGA	Genic	Non-synonomous	CC
E138	SNP	Chr3	Chr3:18755414	G:C→A:T			GGTGGCGGAA**G**GATCGTGAAG	Genic	Non-synonomous	CC*
E138	SNP	Chr4	Chr4:12517099	G:C→A:T			GAAACGAATA**C**AGAAATAAAA	UTR		
E138	SNP	Chr5	Chr5:24838815	G:C→C:G			TTATCAAATT**G**ATTCGGTTTT	Intergenic		TC*
E138	Insertion	Chr1	Chr1:7137500		1	A	AGAAAAAAAG*AAAAAAAAAA	Intergenic		

E138	Deletion	Chr1	Chr1:24646357		-1	A	AAACAAAATC*AAATTTAATA	Intergenic		
E138	Deletion	Chr3	Chr3:267625		-1	C	AAAGTGCACT*ATTATCCCTC	Intergenic		
E138	Deletion	Chr4	Chr4:1885738		-1	T	TTCTGAATGG*TTAGAATAGG	Intergenic		
E138	Deletion	Chr4	Chr4:2999448		-3	TGC	TTGTTCTTAA*TAGTTCTAGA	Intergenic		
E138	Deletion	Chr4	Chr4:5723251		-43	GGTTCTGTATCTGGTTGTGGTTCTGGTGGTTGTAGTATT	TGAGAGATGT*ATTGTATGGT	Genic		
E138	Deletion	Chr5	Chr5:5256590		-6	GACCAA	AAGAACCAGT*ATAACTTCCT	Intron		
E216	SNP	Chr2	Chr2:13496083	G:C→A:T			ATATATACTA**C**TATCTTACTG	Intron		CT
E216	SNP	Chr2	Chr2:8139800	G:C→A:T			TGAGAGTAAA**C**GAGATGATTT	Genic	Non-synonomous	
E216	SNP	Chr4	Chr4:12041956	A:T→G:C			TTAGTCCTAG**A**GAATCTGCGT	Genic	Synonomous	CT*
E216	SNP	Chr5	Chr5:5935167	A:T→T:A			TTTATGAATT**A**AGAGAACGTT	UTR		TT
E216	SNP	Chr5	Chr5:8368874	G:C→A:T			GAGGACGTAG**G**TATTTTATAT	Intergenic		CC*
E216	Deletion	Chr2	Chr2:1354114		-1	T	GAAAGATGAC*CTACAAGCCA	Genic		
E216	Deletion	Chr5	Chr5:1930240		-1	C	ATCTGTAAAT*TTTTTACAGG	Intron		
E216	Deletion	Chr5	Chr5:22317677		-1	G	TAATTGGTTG*CTCTTATACA	Intron		
E71	SNP	Chr1	Chr1:22719878	A:T→C:G			CTGATTCCTG**A**AGCAAGATCG	UTR		TT*
E71	SNP	Chr1	Chr1:26890288	A:T→C:G			CTACCTCGTC**T**CTGCATCACA	UTR		CT
E71	SNP	Chr1	Chr1:30242299	G:C→A:T			CAGCTGCATA**G**GCTGCTCCTA	Genic	Synonomous	CC*
E71	SNP	Chr2	Chr2:13657399	A:T→T:A			AGAAATTTGG**A**TTCTCAGAAA	Genic	Synonomous	TC*
E71	SNP	Chr2	Chr2:17438544	G:C→A:T			CACCCTTCAT**G**TGACATGTGT	Intron		
E71	SNP	Chr2	Chr2:19586780	G:C→C:G			ACTACTTTGA**C**TCTCTAACTG	Genic	Non-synonomous	CT
E71	SNP	Chr2	Chr2:5460139	A:T→C:G			GAGTTCCCAT**T**GTAGACTAAT	Intergenic		TT
E71	SNP	Chr2	Chr2:9891502	A:T→G:C			ATATATATAT**A**TAGGATTGGT	Intron		
E71	SNP	Chr3	Chr3:17368260	A:T→T:A			GTTGTAACAT**T**TAATAACAAA	Intergenic		TT
E71	SNP	Chr3	Chr3:17368261	A:T→T:A			TTGTAACATT**T**AATAACAAAA	Intergenic		TT
E71	SNP	Chr3	Chr3:1789378	A:T→T:A			TGAGGGATAC**A**GGATAAAATA	Intron		CT*
E71	SNP	Chr3	Chr3:1789379	G:C→T:A			GAGGGATACA**G**GATAAAATAA	Intron		CC
E71	SNP	Chr3	Chr3:2496101	G:C→A:T			ATCGACTTGT**C**ATTTTGCCGG	Intergenic		TC
E71	SNP	Chr3	Chr3:7208532	A:T→G:C			GAAGTCACCT**T**TTTCAGTTAC	Intergenic		TT
E71	SNP	Chr3	Chr3:8303675	G:C→A:T			TAATACTTAA**C**CGACACTTCG	Intergenic		CC
E71	SNP	Chr3	Chr3:977616	G:C→T:A			ATGAACAGTA**C**TTGAACACAG	Intergenic		CT
E71	SNP	Chr5	Chr5:10221002	G:C→T:A			ACCGCAGTCG**G**TGGTGACCAT	TE		CC*
E71	SNP	Chr5	Chr5:6957427	G:C→T:A			GCTTAGCTTT**C**TTGTTGGAAG	Genic	Non-synonomous	TC
E71	Insertion	Chr3	Chr3:7761881		1	T	AATTTTTTTG*TTTTTTTTAC	Intergenic		
E71	Insertion	Chr5	Chr5:4105018		1	A	CCCAGACTAT*AAGGGTTCGA	UTR		
E71	Deletion	Chr1	Chr1:24826965		-4	AAAT	GGCTTTGGAA*TCCTCTAATT	Intergenic		
E71	Deletion	Chr5	Chr5:15965758		-1	G	TGATTTTCTA*GAAAAACACA	Intergenic		
E71	Deletion	Chr5	Chr5:3594216		-1	T	CTCTCGCTGC*TGATGGTAAA	Genic		
E71	Deletion	Chr5	Chr5:4105012		-1	G	TTTCTGCCCA*ACTATAAGGG	UTR		
E99	SNP	Chr1	Chr1:2896318	A:T→C:G			TTTATGCACC**A**GGGTAAGACA	Intron		CT*
E99	SNP	Chr1	Chr1:2896383	G:C→T:A			AAGCAGAAGT**C**ATCGAGATTC	Genic	Non-synonomous	TC
E99	SNP	Chr1	Chr1:29991776	G:C→A:T			AGCTTGGTCT**C**CCTGATTACT	Genic	Synonomous	TC
E99	SNP	Chr1	Chr1:5260429	G:C→C:G			ACCTGTAAAA**G**CATGAAATCA	Intron		CT*
E99	SNP	Chr2	Chr2:1799992	G:C→T:A			ATGGTGAAAC**C**AATTGGGTTT	UTR		CC
E99	SNP	Chr3	Chr3:12725829	A:T→T:A			ACACGGTCCA**T**ATATCATACA	TE		
E99	SNP	Chr4	Chr4:10806229	A:T→T:A			GAAATTTTGA**A**ATTTGTTTCT	Intergenic		TT*
E99	SNP	Chr4	Chr4:3109275	G:C→T:A			GCGGAACCTA**G**AGGAGAACCA	TE		TC*
E99	SNP	Chr4	Chr4:891280	G:C→A:T			ATGGTCTCAT**C**GCTTCCCGCA	Intron		TC
E99	SNP	Chr5	Chr5:4973333	A:T→C:G			GAATTAATGA**A**AAAAAAAAAC	Intergenic		TT
E99	Deletion	Chr1	Chr1:2896321		-14	GTAAGACAACACCA	ATGCACCAGG*GTAAAGGCTA	Intron		
E99	Deletion	Chr1	Chr1:5288028		-1	G	TACTGCTGTT*TTCGATCAGT	UTR		
E99	Deletion	Chr1	Chr1:5288030		-2	TC	CTGCTGTTGT*GATCAGTCCA	UTR		
E99	Deletion	Chr1	Chr1:6220669		-7176	CGCCATTCATGATTCATTCCACGTATATATTGTTTGTTCG	AGTTTGAACT*TGCACACGCA	Genic		
E99	Deletion	Chr2	Chr2:11340050		-28	TTTTCTATTCCGATCAAACCATGGCGTA	CTGTAACCAT*TTTAGCTCCG	Genic		
E99	Deletion	Chr2	Chr2:8735136		-2	GG	TTTGTGGATC*TCTTATTTAG	Genic		
E99	Deletion	Chr2	Chr2:8735139		-1	C	GTGGATCGGT*TTATTTAGGG	Genic		

E99	Deletion	Chr4	Chr4:3109274		-1	A	CGCGGAACCT*GAGGAGAACC	TE		
E99	Deletion	Chr5	Chr5:13714219		-55	GCTATCATCTCCTGGACAAAGGAGACTCAGAGAAACAG	CTTAGTCGAT*CATAGAGGCG	TE		
E99	Deletion	Chr5	Chr5:9194110		-6	TACCAT	ATTACCAACT*CGGACACAAA	Intergenic		
E99	Deletion	Chr5	Chr5:9469535		-10	GATAATGGAT	AATATGTTCG*TGACGAGTTA	Intergenic		

(Dipyrimidine analyses: * = on reverse strand)