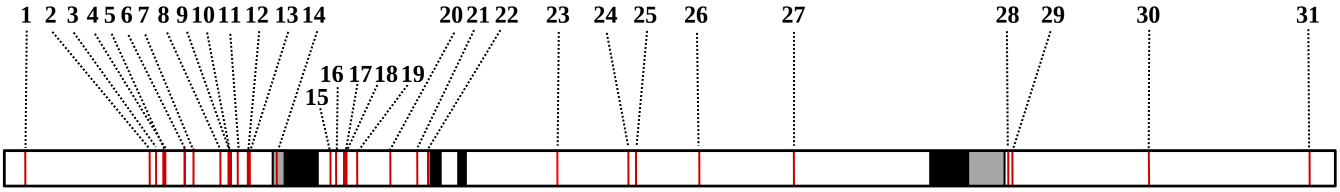

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
	Promoter													5' UTR
	-1544	-772	-731	-698	-694	-571	-544	-402	-379	-375	-349	-279	-274	-47
Toyomusume	A	T	43 bp	A	T	G	AT	G	G	G	T	-	-	-
TK780	A	T	43 bp	A	T	G	AT	G	G	G	T	-	-	-
Hayahikari	T	T	43 bp	A	T	G	AT	G	G	G	T	-	GATC	10 bp
Hidaka 4	A	A	-	T	-	T	AT	A	G	G	C	-	-	10 bp
Harosoy	A	A	-	T	T	G	-	G	A	A	T	G	-	10 bp

	15	16	17	18	19	20	21	22
	Intron I							
	294	315	398	403	475	710	965	988
Toyomusume	G	C	C	T	T	T	SORE-1	T
Hayahikari	G	C	A	T	C	C	-	C
Harosoy	T	T	A	A	T	T	-	T

	23	24	25	26	27	28	29	30	31
	Intron II					3' downstream region			
	2150	2604	2648	3022	3783	4606	4628	5300	6630
Toyomusume	$(C)_{10}$ A $(C)_{8}$ $(A)_{6}$	$(T)_{11}$ T	$(AT)_{8\text{-}11}$	$(A)_{10}$	-	A	$(A)_{6}$	G	A
Hayahikari	$(C)_{10}$ A $(C)_{8}$ $(A)_{6}$	$(T)_{10}$ A	$(AT)_{18}$	$(A)_{10}$	9 bp	A	$(A)_{7}$	G	G
Harosoy	$(C)_{16}$ $(A)_{9}$	$(T)_{11}$ A	$(AT)_{27\text{-}30}$	$(A)_{9}$	-	G	$(A)_{6}$	T	A

43 bp-indel	CCCCTGCTAATCTTCTTCCTCCTCACACATTGCTTCTCACCCC
10 bp-indel	GAAAGCATAA
SORE-1	*Ty1/copia-like* retrotransposon (6,224 bp)
9 bp-indel	AAAGAAAAA

Additional file 1. DNA polymorphisms detected in the *FT2a* genomic region for four soybean cultivars or breeding line and a wild soybean accession.