Supplementary Table 1. Coding single nucleotide polymorphisms (SNPs) in the *SATB1* locus used in this analysis*

Region	Contig position	mRNA position		dbSNP cluster ID	Function	dbSNP allele	Protein residue [single-letter code]	Codon position	Amino acid position
		Variant 1	Variant 2						
Exon 1	18402463		247		Start codon				1
Exon 2	18402353	1846	331	rs61760908	Synonymous	A	Gly [G]	3	37
					Contig reference	G	Gly [G]	3	37
Exon 3	18398486	2035	520	rs61751589	Synonymous	A	Leu [L]	3	100
					Contig reference	G	Leu [L]	3	100
Exon 5	18396697	2284	769	rs61733671	Missense	C	His [H]	3	183
					Missense	T	His [H]	3	183
					Contig reference	A	Gln [Q]	3	183
Exon 5	18396682	2299	784	rs55782480	Synonymous	G	Thr [T]	3	188
					Contig reference	A	Thr [T]	3	188
Exon 7	18376328	2571	1056	rs11717113	Missense	G	Gly [G]	2	279
					Contig reference	C	Ala [A]	2	279
Exon 8	18367928	3121	1606	rs9845303	Synonymous	A	Pro [P]	3	462
					Contig reference	C	Pro [P]	3	462
Exon 11	18331056	3637	2122	rs61733672	Synonymous	G	Pro [P]	3	634
					Contig reference	A	Pro [P]	3	634

*All gene identification information was obtained from NCBI GenBank with Genome Reference Consortium Human Build 37 (GRCh37) (reference genome build 37.1). mRNA variant 2 differs in the 5' untranslated region compared to variant 1, mRNA variants 1 and 2 encode the same SATB1 protein isoform. Heterozygosity was not determined. Contig = contiguous sequence of DNA providing a chromosome map; dbSNP = The Single Nucleotide Polymorphism Database; ID = identification number.