Supporting Information

Muehlenbachs *et al.* 10.1073/pnas.0803657105

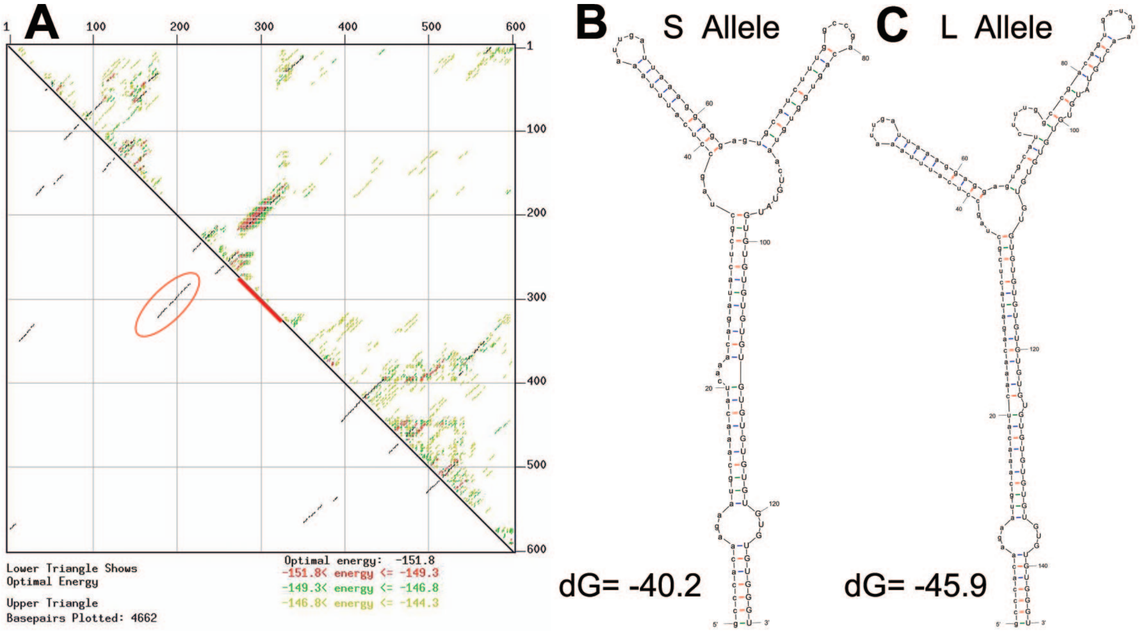

Fig. S1. Predicted secondary structure of the FLT1 3′ UTR. (*A*) Dot plot for FLT1 3′ UTR showing complementarity of RNA residues (upper right triangular graph section) and the optimal energy configuration (lower left triangular graph section), indicating that the dinucleotide repeat allele (S) (red line) forms a stem-loop structure (red circle) with upstream residues. (*B* and *C*) Predicted stem-loop structure for the S allele (24 repeats) (*B*) and for the L allele (32 repeats) (*C*), demonstrating an alternate structure. Predicted free energies of each structure are shown. All figures were generated using the Mfold algorithm [Zuker M (2003) Mfold web server for nucleic acid folding and hybridization prediction. *Nucleic Acids Res* 31:3406–3415.1].

Table S1. Genotype frequencies of mother and offspring, stratified by parity and by maternal genotype

		SS		SL		LL		
Group	f(S)	*n*	f(SS)	*n*	f(SL)	*n*	f(LL)	*P*
Mother P1	0.56	76	0.32	112	0.48	47	0.20	
Mother P≥3	0.57	104	0.32	166	0.50	60	0.18	0.793
Offspring P1	0.55	65	0.27	133	0.56	41	0.17	
Offspring P≥3	0.59	133	0.37	155	0.44	67	0.19	0.0112
SS Mother								
Offspring P1	0.75	38	0.50	38	0.50	—	—	
Offspring P≥3	0.84	67	0.67	33	0.33	—	—	0.0228
SL Mother								
Offspring P1	0.53	24	0.22	67	0.61	18	0.17	
Offspring P≥3	0.55	51	0.31	76	0.47	35	0.22	0.0612
LL Mother								
Offspring P1	0.26	—	—	24	0.52	22	0.48	
Offspring P≥3	0.27	—	—	30	0.55	25	0.45	0.8119

P1, nulliparous pregnancy; P≥3, multiparous pregnancy. *P* values were calculated using χ^2 test (2 × 3) across all genotypes or (2 × 2) for offspring of homozygous mothers.