Table S2. WGS variants identified in 20x coverage of an affected Devon Rex.

Variant		Analysis performed to prioritize variants**		
Impact*	**Functional Class**	**WGS Cat**	**Segregation**	**GWAS haplotype**
High	Stop gain	296	8	-
	Start / Stop loss	56	4	-
	Splice donor / acceptor	1,350	43	-
	Exon deletion	2	-	-
	Frameshift	3,013	69	-
	Rare amino acid	-	-	-
Moderate	Codon alteration	577	35	-
	Missense	22,905	820	5
	Splice branch	-	-	-
	5' or 3' UTR Deletion	-	-	-
Low		41,926	1,301	8
Modifier		11,646,620	535,250	1,570

*Variant impact as defined by http://snpeff.sourceforge.net/SnpEff_manual.html#eff. **Feline reference genome sequence (V6.2) is included in the analyses. GWAS haplotype indicates the variants within the haplotype that was identified via the GWAS. Effect counts are higher than variant counts because a given variant can potentially affect both the flanking upstream and downstream genes. The full genome sequence of this Devon Rex cat is under submission to the NCBI SRA database (http://www.ncbi.nlm.nih.gov/sra) and the variant has been submitted to dbSNP.