

**Additional file 8 Table S5. Candidate variants located in MTRDHH1**

<b>Position</b>	<b>Ref/Alt</b>	<b>Quality score</b>	<b>Location Annotation</b>	<b>Functional Consequence<sup>a</sup></b>
23,436,234	G/GTCACA	385.8	Intergenic	Modifier
23,436,236	T/TTTGTG	385.8	Intergenic	Modifier
23,776,347	G/A	146.0	Exonic, <i>MMUT</i> (c.1225C>T)	High, stop-gain (p.Gln409*)
23,969,676	C/T	370.3	Intergenic	Modifier

<sup>a</sup>Variant annotation and effect predicted by SnpEff [23].

Ref: reference allele

Alt: alternate allele