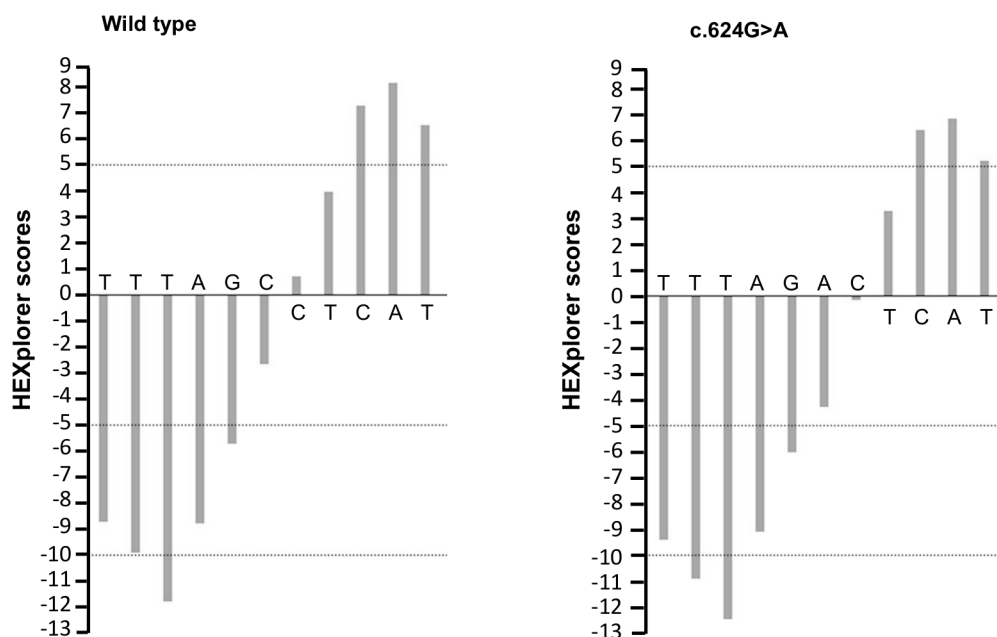# SUPPLEMENTARY FIGURES

Supplementary Figure 1: Predictions of exonic splicing regulator elements of the c.627C>T *TMC1* variant.

A

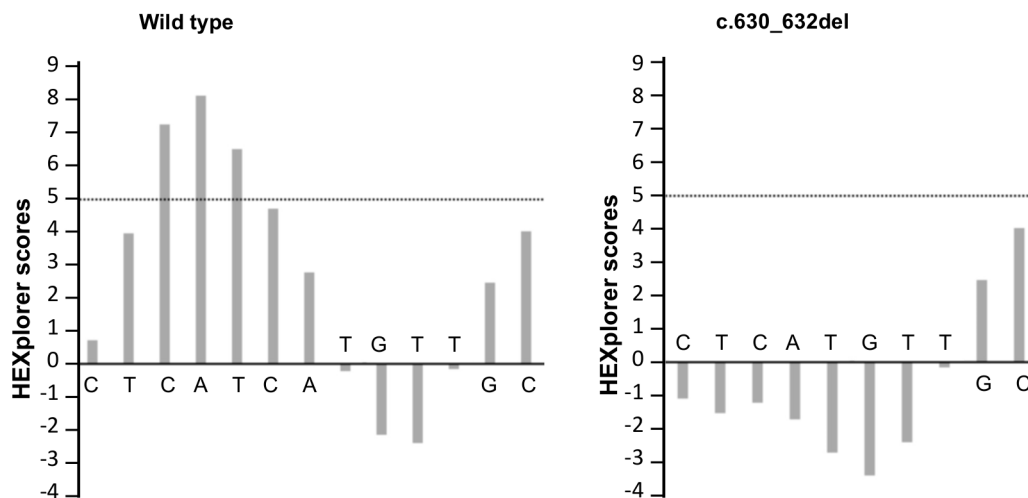| Positions (wild type)	Hexamer seq wild type	ESRseq score wild type	Hexamer seq variant	ESRseq score variant	ESRseq score change (variant vs wild type)
c.619-624	TTTAG**C**	-0.5510	TTTAG**A**	-0.4845	+0.0665
c.620-625	TTAG**C**C	-0.5749	TTAG**A**C	-0.3924	+0.1825
c.621-626	TAG**C**CT	-0.2658	TAG**A**CT	0	+0.2658
c.622-627	AG**C**CTC	0	AG**A**CTC	0	0
c.623-628	G**C**CTCA	0	G**A**CTCA	0	0
c.624-629	**C**CTCAT	0	**A**CTCAT	0	0
Total		-1.3917		-0.8769	**+0.5148**

B

A) Data obtained from the HExoSplice tool. The nucleotide change is indicated with underlined bold font; $\Delta tESR_{seq}$ score: -1.31. **B)** Graphical presentation of data extracted from the HEXplorer algorithm for the wild type (c.622-632) and mutated sequences; ΔHZ_{EI} value: -60.13.

Supplementary Figure 2: Predictions of exonic splicing regulator elements of the c.630_632del *TMC1* alteration.

A

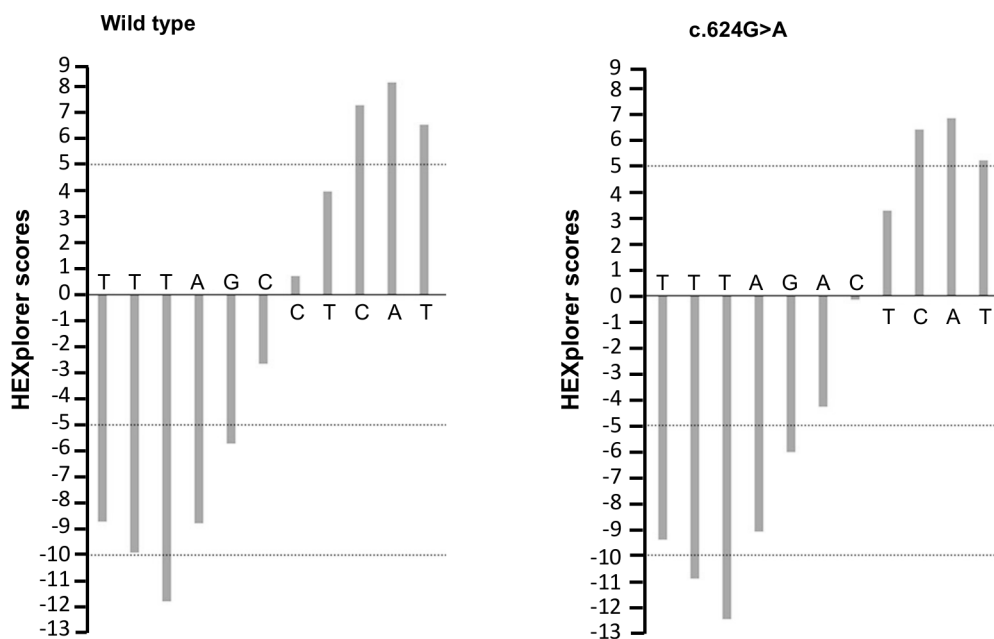| Positions (wild type)	Hexamer seq wild type	ESRseq score wild type	Hexamer seq variant	ESRseq score variant	ESRseq score change (variant vs wild type)
c.625-630	CTCAT**C**	0	CTCATG	0	
c.626-631	TCAT**CA**	0	TCATGT	0	
c.627-632	CAT**CAT**	0	CATGTT	0	
c.628-633	AT**CAT**G	0	ATGTTG	0	
c.629-634	T**CAT**GT	0	TGTTGC	0	
c.630-635	**CAT**GTT	0			
c.631-636	**AT**GTTG	0			
c.632-637	**T**GTTGC	0			
Total		0		0	**0**

B

A) Data obtained from the HExoSplice tool. The deletion is indicated with underlined bold font in the wild type sequence; ΔtESR$_{seq}$ score: 0. **B)** Graphical presentation of data extracted from the HEXplorer algorithm for the wild type (c.625-637) and mutated sequences; ΔHZ$_{EI}$ value: -43.76.

Supplementary Figure 3: Predictions of exonic splicing regulator elements of the c.624C>A _TMC1_ variant

A

Positions (wild type)	Hexamer seq wild type	ESRseq score wild type	Hexamer seq variant	ESRseq score variant	ESRseq score change (variant vs wild type)
c.619-624	TTTAG**C**	-0.5510	TTTAG**A**	-0.4845	+0.0665
c.620-625	TTAG**C**C	-0.5749	TTAG**A**C	-0.3924	+0.1825
c.621-626	TAG**C**CT	-0.2658	TAG**A**CT	0	+0.2658
c.622-627	AG**C**CTC	0	AG**A**CTC	0	0
c.623-628	G**C**CTCA	0	G**A**CTCA	0	0
c.624-629	**C**CTCAT	0	**A**CTCAT	0	0
Total		-1.3917		-0.8769	**+0.5148**

B

A) Data obtained from the HExoSplice tool. The nucleotide change is indicated with underlined bold font; ΔtESR$_{seq}$ score: +0.51. **B)** Graphical presentation of data extracted from the HEXplorer algorithm for the wild type (c.619-629) and mutated sequences; ΔHZ$_{EI}$ value: -9.82.