	ID	SNVs	Gene	Wild-Type Size and (Charge)	Mutant Size and (Charge)	Characteristics & Features
Familial non-*RET* MTC	**MTC_1**	E1183G	*PTPRS*	Large & (+ve)	Small & (0)	Hydrophobicity: High Loss of interaction: High Protean folding: Affected
	MTC_3	S621L	*TBC1D4*	Small & (0)	Large & (0)	Hydrophobicity: High Loss of interaction: High Protean folding: Affected
	MTC_4	R411K	*UBA7*	Large & (0)	Small & (0)	The mutation is located within a stretch of residues annotated as a special region: 2 approximate repeats Loss of interaction: High Protean folding: Affected
		G19D	*NICN1*	Small & (0)	Large & (0)	Hydrophobicity: Lost Loss of interaction: High Protean folding: Affected
		L579P	*MROH2A*	Large & (0)	Small & (0)	The mutation is located within a stretch of residues that is repeated in the protein, HEAT 7 Loss of interaction: High Protean folding: Affected
		E571GfsTer7	*IL16*			
		P421L	*DDX51*	Small & (0)	Large & (0)	The mutation is located within a domain, Helicase ATP-binding Loss of interaction: High Protean folding: Affected
		L735fsTer29	*CCDC134*			
		E939Q	*ANKRD24*	Large & (-ve)	Large & (0)	Loss of interaction: High Protean folding: Affected
		Q639Ter	*DNAH11*			
		R76C	*MAPK12*	Large & (+ve)	Small & (0)	The mutation is located within a domain, Protein kinase; Hydrophobicity: High Loss of interaction: High Protean folding: Affected
	MTC_5	H183R	*ZNF19*	Small & (0)	Large & (+ve)	Mutant residue disturb the interaction with the metal-ion: "Zinc" Loss of interaction: High Protean folding: Affected
		A1111D	*USP40*	Small	Large	Hydrophobicity: Lost Protean folding: Affected
		R1076C	*MSH6*	Large & (+ve)	Small & (0)	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		P766S	*DGKQ*	Large	Small	Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		D96N	*COL4A4*	Small & (-ve)	Small & (0)	The mutation is located within a special motif: Cell attachment site and Triple-helical region Loss of interaction: High Protean folding: Affected
Familial NMTC	**NMTC _1**	P59Q	*FOXM1*	Small & (0)	Large & (-ve)	Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		R310W	*EpCAM*	Small & (+ve)	Large & (0)	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		W286SfsTer6	*KRT39*			
		E85Ter	*BTBD16*			
	NMTC _2	Q1076P	*CACNA2D1*	Small & (0)	Large & (0)	The residue is located in a region annotated as a transmembrane domain Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		H526Y	*SHISA6*	Small	Large	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		P448S	*AATK*	Large & (0)	Small & (0)	Loss of interaction: High Protean folding: Affected
	NMTC _4	Q1248R	*JMJD1C*	Small & (0)	Large & (+ve)	Loss of interaction: High Protean folding: Affected
		L276R	*AGXT*	Small & (0)	Large & (+ve)	Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
	NMTC_6	G483V	*HOOK3*	Small & (0)	Large & (0)	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		K432T	*RNF20*	Large & (+ve)	Small & (0)	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		S106C	*GGNBP2*	Small	Small	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
	NMTC_7	L435P	*NKD1*	Large	Small	Loss of interaction: High
		I309T	*ROBO1*	Large	Small	The mutation is located within a domain, Ig-like C2-type 3 Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		E1580K	*MYH10*	Small & (0)	Large & (+ve)	Loss of interaction: High Protean folding: Affected
		A1129V	*TTC28*	Small	Large	Loss of interaction: High Protean folding: Affected
		N2165K	*ZZEF1*	Small & (0)	Large & (+ve)	Loss of interaction: High Protean folding: Affected
		L455F	*CLIC6*	Small	Large	Loss of interaction: High Protean folding: Affected
		G2217S	*CSMD2*	Small	Large	The mutation is located within a domain, CUB 13 Loss of interaction: High Protean folding: Affected
		A213T	*STK32A*	Small	Large	The mutation is located within a domain, Protein kinase Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		W2251C	*TG*	Large	Small	The mutation is located within a special region: Cholinesterase-like (ChEL) Loss of interaction: High Protean folding: Affected
	NMTC_11	L313Q	*NTRK1*	Small	Large	The mutation is located within a domain, Ig-like C2-type 2 Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		Q623K	*TNKS*	Small & (0)	Large & (+ve)	The mutation is located within a stretch of residues that is repeated in the protein, ANK 12 Loss of interaction: High Protean folding: Affected
		Y815H	*ANKRD35*	Small	Large	Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		Q112H	*OR51M1*	Small	Large	The residue is located in a region annotated as a transmembrane domain Loss of interaction: High Protean folding: Affected
		W713Ter	*PPP6R2*			
	NMTC_12	W389Ter	*FN1B*			
		T2603M	*ITPR1*	Small	Large	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		G341E	*PRKG1*	Small & (0)	Large & (-ve)	The mutation is located within a domain, GMP-binding, low affinity Loss of interaction: High Protean folding: Affected
		S233del	*DENND2B*			
		M837T	*BMP1*	Large	Small	The mutation is located within a domain, CUB 4 Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		G657R	*THSD7A*	Small & (0)	Large & (+ve)	The mutation is located within a domain, TSP type-1 7 Loss of interaction: High Protean folding: Affected
		G323V	*INSC*	Small	Large	Loss of interaction: High Protean folding: Affected Hydrophobicity: High
		A4134T	*USH2A*	Large & (+ve)	Small & (0)	The mutation is located within a domain, Laminin EGF-like 3 Loss of interaction: High Protean folding: Affected Hydrophobicity: High
	NMTC_13	D202VfsTer20	*MPPE1*			
		L208H	*KTI12*	Small	Large	Loss of interaction: High Protean folding: Affected Hydrophobicity: Lost
		W120Ter	*BEAN1*			