TBX1	*List of variants detected in affected subjects*												
	(GRCh38/hg38)			***NM_080647.1***	***NP_542378.1***								
chr	***chr pos start***	***chr pos end***	***Change type***	***HGVS_Transcript consequence***	***HGVS_Protein consequence***	***Variant effect***	***Domains - Amino acids***	***Variant class***	***Phenotype***	***Reference***	***PMID***	***Allele freq gnomAD***	***Comments***
22	19759558	19765825	Gross DEL	ex. 2-7	?	del ex.2-7		Patho.Var	TOF	Aguayo-Gómez *et al* (2015)	26036351	Not Found	De novo
22	19760999	19760055	Gross DEL	c.146_202del(57bp)	p.Arg49_Pro67del	deL 19 aa [mz]		Patho.Var	TOF	Griffin *et al* (2010)	20937753	Not Found	[c.146_202del] Descr.as c.129_185 (57bp), reduced transcriptional activity by 40%. Mother is a carrier
22	19761179	19761181	DEL	c.309_311delGAA	p.Lys103del	in-frame (-1aa) [mz]		Patho.Var	CHD	Xu *et al* (2017)	28272434	0.0004	Sig.reduced transcrptional activity and expression, parents DNA not available
22	19761255		SUB	c.385G>A	p.Glu129Lys	missense	T-Box 109-302	Patho.Var	CHD	Xu *et al* (2017)	24998776	Not Found	Sig. reduced transcriptional activity compared to Wt. (Fig. 2)
22	19763273		SUB	c.443T>A	p.Phe148Tyr	missense	T-Box 109-302	VUS	CTFA	Yagi *et al* (2003)	14585638	Not Found	
22	19764218		SUB	c.576C>T	p.Arg192Arg	synonymous_coding	T-Box 109-302	VUS	CHD	Gong *et al* (2001)	11748311	0.0449	
22	19764224		SUB	c.582C>G	p.His194Gln	missense	T-Box 109-302	Patho.Var	VCFS	Zweier *et al* (2007)	17273972	Not Found	
22	19765078		SUB	c.805C>T	p.Arg269*	stop-gained	T-Box 109-302	Patho.Var	VPI-isolated			Not Found	Identified in this study
22	19765102		SUB	c.829C>T	p.Gln277*	stop-gained	T-Box 109-302	Patho.Var	CHD	Pan *et al* (2015)	25860641	Not Found	
22	19765803		SUB	c.886C>A	p.Arg296Arg	synonymous_coding	T-Box 109-302	VUS	CHD	Gong *et al* (2001)	11748311	0.0481	
22	19765921		SUB	c.928G>A	p.Gly310Ser	missense			DGS	Yagi *et al* (2003)	14585638	0.0046	Unable to bind SMAD1 (Fig. 2), Fulcoli et al (2009) PubMed: 19557177; VCFS Soden et al (2014), PMID:25473035; Conotruncal heart defects, isolated ?; Homozygosis observed
22	19766428		SUB	c.1049G>A	p.Gly350Asp	missense		VUS	CHD	Gong *et al* (2001)	11748311	0.0004	
22	19766511		SUB	c.1132G>A	p.Gly378Ser	missense		VUS	MFDH	Simioni *et al* (2010)	20453311	0.0009	Father and daugher with a VSD
22	19766514	19766522	DEL	c.1135_1143delGCCGGCGGC	p.Ala379_Gly381del	in-frame (-3aa) [mz]		Patho.Var	CHD	Rauch *et al* (2004)	15060116	Not Found	
22	19766566		SUB	c.1187C>T	p.Pro396Leu	missense	NLS 394-448	VUS	CHD	Gong *et al* (2001)	11748311	0.0002	
22	19766602	19766602	DEL	c.1223delC	p.Ser408Trpfs*52	frame-shift [mz]		Patho.Var	CTFA	Yagi *et al* (2003)	14585638	Not Found	De novo
22	19766611		SUB	c.1232T>C	p.Leu411Pro	missense	NLS 394-448	Patho.Var	22q11.2 del features	Torres-Juan *et al* (2007)	17377518	Not Found	
22	19766632	19766632	DEL	c.1253delA	p.Tyr418Phefs*42	frame-shift [mz]		Patho.Var	22q11.2 del features	Ogata *et al* (2014)	24637876	Not Found	
22	19766653	19766660	DEL	c.1274_1281delACTATCTC	p.His425Argfs*189	frame-shift [mz]		Patho.Var	DGS	Gong *et al* (2001)	11748311	Not Found	[c.1321_1343del (23bp)] Descr. as c.1320_1342del (23bp)
22	19766700	19766721	Gross DEL	c.1321_1343del (23bp) [mz]	p.Leu441Alafs*168	frame-shift [mz]		Patho.Var	DGS/VCFS & psych disorder	Paylor *et al* (2006)	16684884	Not Found	
22	19766713	19766727	DEL	c.1334_1348del15	p.Gly445_His449del	in-frame (-5aa)		VUS	DGS	Gong *et al* (2001)	11748311	Not Found	
22	19766751	19766752	INS	c.1370_1372dupACC	p.His457dup	in-frame (+1aa)		VUS	VCFS	Gong *et al* (2001)	11748311	Not Found	[c.1399-1428dup (30bp)] Desc.r as c.1399-1427dup (30bp)
22	19766778	19766827	Gross Dup	c.1399-1428dup (30bp) [mz]	p.Ala467_Ala476dup	dup 10 aa		VUS	CHD	Gong *et al* (2001)	11748311	Not Found	
22	19766783	19766791	DEL	c.1404_1412delCGCTGCCGC	p.Ala474_Ala476del	in-frame (-3 aa) [mz]		VUS	DGS/VCFS	Gong *et al* (2001)	11748311	0.0359	

Legend:

Variant class

	Patho.Var: Pathogenic Variant	all LoF and missense either neomutation, co-segregagting in >=2,or funct validated as deleterious
	VUS: Variant of unknown significance	rare >0.5% gnomAD
	Assoc.Var: Associated Variant	>1% gnomAD frequent variant but losses some of it's activity compared to wild-type

Domains -Amino acids

T-Box	DNA-binding domain
NLS	Nuclear Localisation Signal

Associated disorders

MFDH	Midline facial defects with hypertelorism
CTFA	Conotruncal face anomaly syndrome
DGS	DiGeorge syndrome
VCFS	Velocardiofacial syndrome
CHD	Congenital heart defects
TOF	Tetralogy of Fallot
VPI	Velopharyngeal Insufficiency

Footnotes:

mt - stop codon predicted by mutationt@ster

mz - stop codon predicted by Mutalyzer