

Table S1: List of cilia genes and previously reported genes analyzed in the patients with transposition of the great arteries.

Motile cilia genes:

Central pair:

HYDIN, CCDC180, CFAP54, SPAG6, SPAG17, WDR93

Nexin-dynein regulator complex:

CCD39, CCDC65, CCDC40, DRC1, GAS8, CCDC164, CCDC40, CCDC65, DRC3, DRC7, FBXL13, TCTE1

Radial spoke:

DYDC2, DNAJB13, RSPH1, RSPH2, RSPH3, RSPH4A, RSPH9, PPIL6, RPON1L RSPH10B, RSPH10B2, RSPH14

Centrosomal:

CCDC113, C4orf47, CEP295, CCDC113, C4orf47, CEP104, CEP120, CEP162, CEP19, CEP192, CEP44, CEP76, CEP83, CEP83, CEP97

Centriole :

CFAP53, CFAP65, DEUP1, KIF24, NEK5, OFD1, POC1B

Centriolar satellite:

CCDC81, CCDC96, CCDC146, NEK10, TEX9

Ciliary tip:

ARMC9, CEP104

Outer dyneir arm:

CFAP70

Heavy chain

DNAH1, DNAH9, DNAH11, DNAH5, DNAH8

Intermediate chain

DNAI1, DNAI2

Light Chain

DNAL1, DYNLRB2, NME9

Inner dynein arm

CASC1, ZMNYD12

Heavy chain

DNAH2, DNAH3, DNAH6, DNAH10, DNAH12

Intermediate chain

WDR63, WDR78

Light intermediate chain

DNAL1

Cytoplasm region of cilia:

PIH1D3

Dynein pre-assembly:

DNAAF1, DNAAF2, DNAAF3, DNAAF4, DNAAF5, SPAG1, ZMYND10, LRCC6, C21Orf59

Axoneme:

AKAP14, CCDC173, CCDC33, CFAP43, EFHC1, EFHC2, LRGUK, PPP1R32, PACRG, RIBC2, SPACA9. TTCT29, TEK1, WDR66

Periaxoneme

SPATA6, TEK3

Outer dense fiber

TEKT2, TEK4H

Other gene related to Outer /inner dynein arm:

NME6, NME8, CLASP1

Cilia 96-nm repeat ruler:

CCDC39, CCDC40

Outer dynein arm attachment:

CCDC103

Docking complex:

ARMC4, CCDC114, CCDC151, MNS1, DZANK1

Dynein Motor Complex:

TTC25

Non-motile cilia:

Axoneme and signaling :

ADCY6, ANKS3, ANKS6, CEP41, CNG11, CNGA41, CNGB1, C2orf71, C2orf2, DCDC2, EFHC1, FLCN1, GPR161, ICK, INPP5E, IQCB1, LCA5, NEK1, OCRL, PIK3R4, PKD1, PKD2, PKD1L1, RAB23, SDCCAG8, SMO, USP9X

Dynein assembly docking :

ARMC4, CCDC114, DNAAF1, HEATR2, LRCC6, MNS1, ZMNYD10

Primary Cilia assembly:

PIBF1

Cilium tip:

CEP104, GLI2, GLI3, KIF7, SUFU

INV compartment:

EVC2, EVC, INVS, NPHP3, NEK8, IQCE

Other: Cytosol, Golgi, nucleus, etc

AK7, DDX59, GALNT11, GLIS2, PIK3R4, POMGNT1, TBC1D32, XPNPEP3, ZNF423

Transcription factor:

CRX, ZIC2

Other non motile-cilia related genes:

ALS2CR12, CFAP61, CFAP77, CFAP100, CFAP299, C9orf116, FANK1, IQCD, IQUB, LRRC34, EFCAB1, MYCBPAP, SPA17

Cilia tip

C1orf87

Golgi cilia network

PIFO

Cytoskeleton

CATIP, DCDC1, TTC23L

Transcription factors:

FOXJ1, RFX

Ciliogenesis:

Centriole or basal body:

ALMS1, ARL2BP, CENPF, CEP19, CEP41, EP78, CEP104, CEP120, CSPP1, C2CD3, C21orf2, FAM16A, FLCN, HYL51, INTU, KIAA0556, KIZ, NEK2, NME7, OCRL1, OFD1, PIBF1, PLK4, POC1B, POC1A, RAB2B, RP2, TALPID3, TAPT1, TOPORS, TTL5, TUB, WDPCP

Cilia assembly:

ARMC2, C9orf24, CCDC151, CFAP126, CFAP300, DAW1, DNAAF1, DNAAF3, LRRC6, MAK, MARCH10, PIH1D2, PIHD3, SAXO2, UBXN10, ZYMND10

Transition zone

AHI1, B9D1, B9D2, CC2D2A, CEP900, C5orf42, IQCB1, LCA5, MKS1, NPHP1, NPHP4, RP1, RP1L1, RPGRIP, RPGRIP1, RPGRIP1L, SDCCAG8, SPATA7, TCTN1, TTN1, TCTN3, TMEM17, TMEM67, TMEM107, TMEM138, TMEM216, TMEM231, TMEM237, TMEM67, MKS1, CCT2

Centriolar satellites

BBS4, CCDC28B, CFAP53, CEP290, KIAA0753, OFD1

Cilia base:

ARMC3, C5orf49, CCDC170, TSGA10

Basal body:

AGBL2, BBOF1, C11orf97, CABCO1, CCDC13, CFAF157, ENKUR, MAPK15, MORN1, PPP1R42, ARMC9

Tubulin modifying enzyme:

TUB1A, TTLL6

Distal appendage:
CEP83, CEP164, SCLT1, TTBK2

Unclear or various localization:
ATXN10, CFAP52, NEK9, TULP1

Subdistal appendage:
CC2D2A

Cilia trafficking:

IFT dynein subunits:
DYNC2H1, DYNC2LI1, TCTEX1D2, WDR34, WDR35, WDR60

IFT subcomplex A:
IFT43, IFT140, WDR19, IFT122, TTC21B, IFT121, IFT139, IFT14

Cytoplasm related:
IQCG, LRRRC23, MORN3, STK33
Nuclear related:
CCNA1, CFAP45, FOXJ1, MAP3K19, NEK11, SPATA4, ZEB2

BBS proteins
BBSome:
ARL, BBS1, BBS2, BBS4, BBS5, BBS7, BBS8, BBS9, TTC8
Bbsome regulatoris:
BIBP1, BBS10, BBS12, CEP290, C8orf37, LZFTL1, MKKS, MKS, SDCCAG8, TRIM32,

IFT Cilia regulators:
FAM58A, ICK, MAK

IFT subcomplex B:
CLUAP1, ITF23, ITF57, IFT52, IFT80, IFT81, IFT172, TRAF3IP1, IFT20, IFT46, IFT52, IFT57, IFT80, IFT88, IFT172, DISC1, RABL5, TRAF3LP1, TTC26, TTC30B, KIF3A, KIF3B, KIFAP3

LIFT:
ARL13B, ARL3, PDE6D, RP2, UNC119

Ciliary receptor :
TRPV4

TGA previously related genes:

Laterality:
ZIC3, PITX2, LEFTY2, FOXH1, GDF1, ACVR2B, NODAL, CFC1, LEFTY1, CCT2, CEP57, SLC4A1, AK7, ARL13B, POC1B, DISC1, DNAI1, CLASP1, DNAAF2, MLF1, IFT43, PRKAR1A, GPR161, NME8, B9D1, TMEM260, PLB1, SLC4A1.

Heart development:
CITED2, HIF1A, TBX1, HSPG2, MED13L, ISL1, MYH6, MYH10, MEF2C

Table S2: Complete abnormalities of ciliary genes in TGA. Missense anomalies of ciliary genes found in patients with transposition of great arteries.

Patient	Gene	dbSNP	NT change	AA change	SIFT	PP2. HumDiv	PP2. HumVar	Mutation Assesor	Allele Freq	OMIM	Mend	¿Del?	Entity Associated
T1801 Male	<i>DNAH6</i>	rs77489911 3	c.637A>G	p.I213V	T (1)	B (0.01)	B (0.008)	L (1.71)	2.75E x 10 ⁻⁴	NR	HETO	No	No
	<i>FOXH1</i>	rs89918950 5	c.187G>A	p.V63I	T (0.69)	B (0.251)	B (0.083)	N (-1.43)	5.81E x 10 ⁻⁵	NR	HETO	No	No
	<i>DNAH10</i>	rs75210353 2	c.2489G>A	p.R830Q	T (0.37)	B (0.135)	B (0.011)	M (2.11)	1.77 x 10 ⁻⁵	NR	HETO	No	No
	<i>SAXO2</i>	rs11632427 9	c.1111T>C	p.S371P	T (0.04)	PD (0.879)	PD (0.635)	M (2.14)	5.65 x 10 ⁻⁴	ND	HETO	Yes	No
	<i>WDR93</i>	rs28727970	c.238G>A	p.A80T	T (0.37)	B (0.028)	B (0.014)	N (0.74)	3.17 x 10 ⁻³	ND	HETO	No	No
	<i>DRC7</i>	rs19982808 7	c.1819C>T	p.R607C	D (0.04)	D (0.912)	PD (0.992)	L (1.81)	2.83 x 10 ⁻⁵	NR	HETO	Yes	No
	<i>TTC25</i>	rs78233380 6	c.218C>T	p.S73L	D (0)	PD (1)	PD (0.976)	M (2.54)	5.94 x 10 ⁻⁴	AR	HETO	Yes	No
	<i>RSPH14</i>	rs78097110 4	c.488A>G	p.E163G	D (0)	B (0.026)	B (0.028)	M (2.71)	4.63 x 10 ⁻⁴	NR	HETO	Yes	No
	<i>RIOK1</i>	rs55698032	c.341G>A	p.R115Q	T (0.22)	B (0.007)	B (0.004)	L (1.2)	5.85 x 10 ⁻⁵	NR	HETO	No	No
	<i>PIBF1</i>	rs17089782	c.1214G>A	p.R405Q	D (0)	PD (1)	PD (0.996)	M (2.56)	0.1021	AR	HETO	Yes	Joubert
	<i>KATNB1</i>	rs14182060 7	c.1841A>G	p.H614R	T (0.07)	B (0.42)	B (0.018)	L (0.9)	1.31 x 10 ⁻⁴	AR	HETO	No	No
	<i>KDM6A</i>	rs78023827 0	c.232C>T	p.R78C	T (0.15)	B (0.05)	b (0.009)	L (1.31)	3.95 x 10 ^{-5*}	XL	HEMY	No	No
T180201 Male	<i>UBXN10</i>	rs11556959	c.794A>G	p.H265R	D (0.01)	PD (0.982)	PD (0.824)	M (2.32)	2.60 x 10 ⁻⁴	NR	HETO	Yes	No
	<i>PLB1</i>	rs62131028	c.2710A>T	p.N904Y	T (0.13)	PD (0.966)	PD (0.942)	M (2.05)	5.96 x 10 ⁻³	NR	HETO	Yes	No
	<i>NEK5</i>	rs35465612	c.1420C>T	p.R474C	D (0)	PD (1)	PD (0.959)	M (2.44)	9.27 x 10 ⁻³	NR	HETO	Yes	No
	<i>ALDH6A1</i>	rs18306644 2	c.1604G>A	p.R535H	D LC (0)	B (0)	B (0.001)	L (1.04)	7.9 x 10 ^{-6 *}	AR	HETO	No	No
	<i>IQCE</i>	rs20064808 6	c.1688T>C	p.L563S	D (0)	B (0.193)	B (0.207)	M (2.31)	5.23 x 10 ⁻⁴	AR	HETO	Yes	No
	<i>KMT2D</i>	New	c.547C>T	p.P183S	T (0.62)	PD (0.959)	PD (0.6)	N (0.55)	New	AD	HETO	Yes	No
	<i>MEGF8</i>	rs76986297 5	c.1315C>T	p.R439W	D (0)	PD (1)	PD (0.948)	M (2.27)	6.13 x 10 ^{-4*}	AR	HETO	Yes	No

T180301 Male	<i>RSPH10B2</i>	rs2711191	c.212G>C	p.S71T	T (1)	B (0)	B (0.0)	N (-2.04)	9.51 x 10 ⁻⁴	ND	HOMO	No	No
	<i>RSPH10B2</i>	rs20194368 7	c.1835A>G	p.Y612C	T (0.13)	PD (0.761)	B (0.24)	L (1.59)	4.24 x 10 ⁻³	ND	HETO	No	No
	<i>LRGUK</i>	rs14017512 9	c.2044C>T	p.R682C	D (0)	PD (0.965)	B (0.270)	N (0)	3.44 x 10 ⁻²	NR	HETO	Yes	No
	<i>CFAP43</i>	rs15037811 0	c.3935G>A	p.R1312H	T (0.12)	PD (0.997)	PD (0.855)	M (2.59)	1.21 x 10 ⁻³	AD/AR	HETO	Yes	No
	<i>DNAH10</i>	rs77989738 4	c.1468C>A	p.P490T	D (0.01)	PD (0.999)	PD (0.97)	M (3.04)	1.98 x 10 ⁻³	NR	HETO	Yes	No
	<i>DNAH3</i>	rs76611408 9	c.6556G>A	p.V2186M	T (0.7)	PD (0.924)	PD (0.967)	L (1.55)	4.35 x 10 ⁻³	NR	HETO	No	No
	<i>DNAH3</i>	rs18246251 4	c.608T>C	p.M203T	T (0.1)	PD (0.454)	B (0.073)	M (2.17)	3.95 x 10 ⁻³	NR	HETO	Yes	No
	<i>TTLL6</i>	rs18436295 5	c.517C>T	p.R173W	D (0)	PD (1)	PD (1.0)	H (4.64)	8.89X 10 ⁻³	NR	HETO	Yes	No
	<i>DZANK1</i>	rs13970057 5	c.1142G>A	p.R381Q	T (0.1)	B (0.106)	B (0.018)	L (1.06)	3.59 x 10 ⁻²	ND	HETO	No	No
	<i>DZANK1</i>	rs11774037 7	c.1019A>C	p.Y340S	T (0.13)	B (0.001)	B (0.0)	N-(2.82)	3.50 x 10 ⁻²	ND	HETO	No	No
	<i>STX19</i>	rs14512441 8	c.70T>G	p.S24A	T (0.81)	B (0)	B (0.0)	N (0)	1.03 x 10 ⁻³	ND	HETO	No	No
	<i>IQCE</i>	rs18096184 1	c.1148G>T	p.R383L	T (0.63)	PD (0.924)	B (0.366)	L (1.445)	1.074 x 10 ⁻³	AR	HETO	No	No
	<i>CEP76</i>	rs14680859 6	c.985G>A	p.A329T	T (0.08)	B (0.222)	B (0.117)	L (1.54)	2.68 x 10 ^{-4*}	ND	HETO	No	No
	<i>KMT2D</i>	rs20162835 7	c.15686G> A	p.R5229H	D(0.04)	PD (1)	PD (0.98)	N (0.255)	2.49 x 10 ^{-5**}	AD	HETO	Yes	No
T180401 Male	<i>WDR35</i>	rs13014514 24	c.721C>G	p.H241N	T (0.6)	B (0)	B (0)	L (1.08)	5.84 x 10 ⁻⁵	AR	HETO	No	No
	<i>CFAP100</i>	rs14951102 3	c.589G>A	p.A197T	T (0.04)	PD (0.998)	PD (0.850)	M (2.715)	6.85 x 10 ⁻³	ND	HETO	Yes	No
	<i>CFAP77</i>	rs11243798	c.551G>A	p.R184H	D (0.04)	PD (1)	PD (0.994)	M (2.65)	5.03 x 10 ⁻³	ND	HETO	Yes	No
	<i>TTC8</i>	rs92816564 0	c.595A>G	p. I199V	T LC (0.26)	B (0.146)	B (0.116)	N (0.6)	4.76 x 10 ⁻⁵	AR	HETO	No	No
	<i>DNAH3</i>	rs14471790 0	c.4878T>G	p.S1626R	D (0.01)	B (0.187)	B (0.103)	L (1.64)	6.18 x 10 ⁻²	NR	HETO	No	No
	<i>HYDIN</i>	New	c.3332C>T	p.P1111L	D (0)	PD (0.999)	PD (0.988)	M (2.76)	New	AR	HOMO	Yes	No

T180701 Female	DNAH9	rs139596704	c.3050A>G	p.Y1017C	D (0)	PD (0.981)	PD (0.827)	M (2.93)	5.30 x 10 ⁻²	AR	HETO	Yes	No
	MYCBPAP	rs73334009	c.886C>T	p.R296C	T (0.17)	B (0)	PD (0.556)	N (0.69)	9.96 x 10 ⁻⁴	NR	HETO	No	No
	PRSS54	rs143446844	c.626C>T	p. T209M	T (0.27)	B (0.017)	B (0.010)	N (0.755)	5.8 x 10 ⁻³	NR	HETO	No	No
	TRPV4	rs187864727	c.649G>T	p.A217S	T (0.13)	PD (1)	PD (0.99)	M (2.00)	6.85 x 10 ⁻²	AD	HETO	Yes	Neuromus c dyspl
	WDR63	rs1056616254	c.1742C>A	p.T581N	D (0)	PD (0.984)	PD (0.649)	M (2.58)	1.19 x 10 ^{-5*}	NR	HETO	Yes	No
	CFAP100	rs754767651	c.1292G>C	p.R430T	D (0)	PD (0.997)	PD (0.84)	L (1.76)	3.76 x 10 ⁻⁴	ND	HETO	Yes	No
	DNAH8	rs752099198	c.7906A>G	p.T2636A	T (0.31)	B (0.099)	B (0.101)	L (1.35)	3.73 x 10 ⁻⁴	AR	HETO	No	No
	CFAP43	rs117768807	c.589G>A	p.V197M	D (0)	PD (0.999)	PD (0.973)	L (1.76)	3.05 x 10 ⁻³	AD/AR	HETO	Yes	No
	IFT46	rs145438119	c.454C>G	p.P152A	D (0.01)	PD (1)	PD (1)	M (3.25)	3.16 x 10 ⁻³	AR	HETO	Yes	No
	MORN3	rs782293129	c.616G>C	p.A206P	D (0)	PD (1)	PD (1)	M (2.87)	2.03 x 10 ⁻⁴	ND	HETO	Yes	No
	TMEM260	rs753356578	c.469A>T	p.M157L	T (0.44)	B (0.002)	B (0.002)	L (1.01)	2.04 x 10 ⁻⁴	AR	HETO	No	No
	BBOF1	rs190718961	c.248G>A	p.S83N	T (0.2)	B (0.001)	B (0.003)	N (0.74)	4.35 x 10 ⁻³	NR	HETO	No	No
	CCDC113	rs144246110	c.300A>T	p.K100N	D (0)	PD (1)	PD (0.997)	M (2.855)	2.03 x 10 ⁻³	NR	HETO	Yes	No
	DZANK1	rs139700575	c.1142G>A	p.R381Q	T (0.1)	B (0.106)	B (0.018)	L (1.06)	3.59 x 10 ⁻²	ND	HETO	No	No
	DZANK1	rs117740377	c.1019A>C	p.Y340S	T (1)	B (0.01)	B (0.018)	N (-2.82)	3.50 x 10 ⁻²	ND	HETO	No	No
	TRAF3IP1	rs761035757	c.838C>T	p.R280W	D (0.01)	PD (0.999)	PD (0.913)	L (1.79)	2.56 x 10 ⁻⁴	AR	HETO	Yes	No
	MIB1	rs759658918	c.1694C>G	p.T565S	T (0.06)	PD (0.843)	PD (0.893)	L (0.9)	9.14 x 10 ⁻⁵	AD	HETO	No	No
T180801 Male	TRPV4	rs187864727	c.649G>T	p.A217S	T (0.13)	PD (1)	PD (0.99)	M (2.00)	6.85 x 10 ⁻²	AD	HETO	Yes	Neuromus c dyspl
	RSPH10B2	rs2711191	c.212G>C	p.S71T	T (1)	B (0)	B (0)	N (-2.04)	9.51 x 10 ⁻⁴	ND	HOMO	No	No
	RSPH10B2	rs759234050	c.2510C>T	p.P837L	T (0.06)	PD (0.998)	PD (0.871)	L (1.79)	5.32 x 10 ^{-5**}	ND	HOMO	No	No

	<i>DNAH10</i>	rs755673190	c.8228C>T	p.P2743L	D (0.05)	B (0.005)	B (0.005)	M (2.53)	2.83 × 10 ⁻⁵	NR	HETO	Yes	No
	<i>DNAH10</i>	rs199619464	c.10258G>A	p.V3420I	T (0.51)	B (0.132)	B (0.078)	N (0.11)	9.08 × 10 ⁻⁴	NR	HETO	No	No
	<i>PIBF1</i>	rs17089782	c.1214G>A	p.R405Q	D (0)	PD (1)	PD (0.966)	M (2.56)	0.1021	AR	HOMO	Yes	Joubert
	<i>IQCE</i>	rs375144768	c.784C>T	p.L262F	D (0)	PD (1)	PD (0.998)	M (2.595)	2.60 × 10 ⁻⁴	AR	HETO	Yes	No
	<i>INPP5E</i>	rs138150684	c.1360G>A	p.D454N	T (0.06)	PD (1)	PD (0.885)	M (1.995)	1.96 × 10 ^{-4*}	AR	HETO	Yes	No
	<i>OFD1</i>	rs779051357	c.2482T>G	p.F828V	T (0.07)	PD (0.903)	PD (0.591)	M (2.43)	5.17 × 10 ⁻⁵	XLD	HEMY	Yes	No
T180901 Male	<i>MORN1</i>	rs34587196	c.757C>T	p.R253W	D (0)	PD (1)	PD (0.999)	M (2.25)	6.57 × 10 ⁻³	NR	HETO	Yes	No
	<i>WDR63</i>	rs138379333	c.922G>A	p.A308T	D (0.04)	PD (0.792)	B (0.14)	M (2.49)	5.39 × 10 ⁻²	NR	HETO	Yes	No
	<i>CFAP65</i>	rs144604393	c.3079C>T	p.R1027C	T (0.14)	B (0.481)	B (0.032)	M (2.04)	5.65 × 10 ⁻⁵	AR	HETO	No	No
	<i>CFAP100</i>	rs199685364	c.209G>A	p.R70Q	D (0.04)	B (0.105)	B (0.027)	L (1.53)	2.82 × 10 ⁻⁴	ND	HETO	No	No
	<i>NEK11</i>	rs141777290	c.1915C>A	p.Q639K	T (0.14)	B (0.068)	B (0.014)	M (1.995)	1.98 × 10 ⁻⁴	NR	HETO	No	No
	<i>CCDC96</i>	rs181515863	c.721C>A	p.R241S	D (0.04)	B (0.322)	B (0.034)	L (0.805)	2.18 × 10 ⁻²	ND	HETO	No	No
	<i>CFAP70</i>	rs575812060	c.3079T>A	p.C1027S	D (0.02)	PD (0.986)	PD (0.906)	M (2.43)	2.60 × 10 ⁻³	AR	HETO	Yes	No
	<i>ALDH6A1</i>	rs183066442	c.1604G>A	p.R535H	D LC (0)	B (0)	B (0.001)	L (1.04)	1.75 × 10 ⁻²	AR	HETO	No	No
	<i>DNAH3</i>	rs144845767	c.9329A>G	p.N3110S	T (0.07)	B (0.004)	B (0.024)	L (1.89)	1.86 × 10 ⁻³	NR	HETO	No	No
	<i>DNAH3</i>	rs141197402	c.8597A>G	p.H2866R	D (0)	PD (0.833)	PD (0.499)	L (1.29)	1.87 × 10 ⁻³	NR	HETO	Yes	No
	<i>PRSS54</i>	rs143678998	c.1121G>A	p.R374K	T (0.15)	PD (0.919)	B (0.214)	M (2.00)	5.08 × 10 ⁻⁴	ND	HETO	Yes	No
	<i>DNAH9</i>	rs267604735	c.7150G>A	p.G2384R	D (0.04)	PD (0.999)	D (0.918)	H (3.71)	5.79 × 10 ⁻⁵	AR	HETO	Yes	No
	<i>MARCH10</i>	rs141504034	c.1961G>C	p.G654A	T (0.47)	PD (0.887)	B (0.251)	L (1.84)	7.90 × 10 ⁻⁴	NR	HETO	No	No
T181001 Female	<i>NPHP4</i>	rs202179978	c.1331G>A	p.R444Q	T (1)	B (0.008)	B (0.001)	N (-0.34)	6.79 × 10 ⁻⁴	AR	HETO	No	No

	<i>ARMC9</i>	rs386656198	c.878C>T	p.T293M	T (1)	PD (1)	D (0.984)	M (2.33)	5.24 × 10 ⁻⁴	AR	HETO	Yes	No
	<i>NEK11</i>	rs140058289	c.127G>C	p.V43L	D (0.01)	PD (0.934)	PD (0.528)	M (3.41)	4.80 × 10 ⁻²	NR	HETO	Yes	No
	<i>DNAH11</i>	rs199789835	c.8521A>G	p.S2841G	D (0.02)	PD (0.957)	PD (0.796)	M (2.95)	2.23 × 10 ⁻⁴	AR	HETO	Yes	No
	<i>FBXL13</i>	New	c.253C>A	p.H85N	T (0.2)	B (0.204)	B (0.068)	N (0.69)	New	NR	HETO	No	No
	<i>ENKUR</i>	rs144669094	c.372T>G	p.I124M	B (0.06)	B (0.204)	B (0.055)	M (2.32)	7.96E-6*	NR	HETO	No	No
	<i>DNAH3</i>	rs766114089	c.6556G>A	p.V2186M	T (0.7)	PD (0.924)	B (0.342)	L (1.55)	4.35 × 10 ⁻³	NR	HETO	No	No
	<i>DRC3</i>	rs761307066	c.652C>G	p.L218V	T (0.57)	B (0.001)	B (0.003)	N (0.67)	1.40 × 10 ⁻³	NR	HETO	No	No
	<i>NRK</i>	rs192589373	c.2365C>T	p.P789S	T (0.25)	B (0)	B (0)	N (0)	4.39 × 10 ⁻²	NR	HETO	No	No
	<i>TTLL6</i>	rs149873082	c.893G>A	p.R298H	T (0.93)	B (0)	B (0)	N (0.205)	2.23 × 10 ⁻³	NR	HETO	No	No
	<i>OFD1</i>	New	c.2610G>C	p.Q870H	D (0.04)	PD (0.899)	PD (0.639)	M (2.125)	New	XL	HEMY	Yes	No
	<i>KIF3B</i>	rs1166002310	c.1666C>T	p.H556Y	D (0.03)	B (0.331)	B (0.112)	L (0.895)	1.40 × 10 ⁻⁴	AD	HETO	No	No
	<i>CEP295</i>	rs763108226	c.512C>T	p.P171L	D (0.04)	PD (0.728)	B (0.25)	NF	5.37 × 10 ⁻³	ND	HETO	Yes	No
	<i>MEGF8</i>	rs1281253733	c.2344C>T	p.R782W	D (0.085)	PD (0.962)	D (0.898)	N (0.345)	8.11 × 10 ⁻⁶	AR	HETO	Yes	No
T181101 Male	<i>SPAG17</i>	rs140959339	c.430C>T	p.R144W	D (0)	PD (1)	PD (0.99)	M (2.70)	2.37 × 10 ⁻²	NR	HETO	Yes	No
	<i>RIOK1</i>	rs1228728066	c.333G>C	p.K111N	T (0.12)	B (0.129)	B (0.067)	M (1.985)	5.78 × 10 ⁻⁵	NR	HETO	No	No
	<i>DNAI1</i>	rs771320807	c.203G>A	p.R68Q	D (0)	PD (0.998)	PD (0.917)	M (2.45)	2.89 × 10 ⁻⁵	AR	HETO	Yes	No
	<i>DYNC2H1</i>	rs200264343	c.12937A>G	p.N4313D	D (0.09)	B (0.064)	B (0.015)	N (0.34)	1.19 × 10 ⁻³	AR/DR	HETO	No	No
	<i>CCDC33</i>	rs189088694	c.52G>A	p.A18T	T (1)	B (0.01)	B (0.01)	N (-1.245)	2.21 × 10 ⁻³	NR	HETO	No	No
	<i>C2CD3</i>	rs150676400	c.6343C>T	p.P2115S	T (0.51)	B (0.01)	B (0.01)	N (0.77)	5.00 × 10 ⁻³	AR	HETO	No	No
T181201 Male	<i>SPAG17</i>	rs102826158	c.1700C>A	p.P567Q	D (0.01)	PD (0.979)	PD (0.848)	M (2.62)	1.74 × 10 ⁻⁴	NR	HETO	Yes	No

T181401 Male	<i>PLB1</i>	rs62131028	c.2710A>T	p.N904Y	T (0.13)	PD (0.996)	PD (0.942)	M (2.05)	5.96 x 10 ⁻³	NR	HOMO	Yes	No
	<i>RSPH10B2</i>	rs27111191	c.212G>C	p.S71T	T (1)	B (0)	B (0.0)	N (-2.04)	9.51 x 10 ⁻⁴	ND	HOMO	No	No
	<i>AGBL2</i>	rs7941404	c.956G>A	p.R319H	T (0.09)	PD (0.999)	PD (0.917)	M (2.49)	9.9E-5*	NR	HETO	Yes	No
	<i>CFAP54</i>	rs14235805 55	c.1964A>G	p.H655R	T (0.07)	B (0.124)	B (0.124)	NF	9.37E-6*	ND	HETO	No	No
	<i>DNAH9</i>	rs13959670 4	c.3050A>G	p.Y1017C	D (0)	PD (0.981)	PD (0.827)	M (2.93)	5.30 x 10 ⁻²	AR	HETO	Yes	No
	<i>PIBF1</i>	rs17089782	c.1214G>A	p.R405Q	D (0)	PD (1)	PD (0.996)	M (2.56)	0.1021	AR	HOMO	Yes	Joubert
	<i>LZTFL1</i>	rs75196880 7	c.724A>G	p.T242A	T (0.47)	B (0.01)	B (0.02)	N (0.4)	0.001721	AR	HETO	No	No
	<i>RPGRIP1L</i>	New	c.2957A>G	p.D986G	T (0.035)	B (0)	B (0.0)	N (0)	New	AR	HETO	No	No
	<i>CEP192</i>	rs11790167 7	c.6737T>C	p.F2246S	T (0.24)	B (0.036)	B (0.030)	NF	5.56 x 10 ⁻³	NR	HETO	No	No
	<i>TEKT2</i>	rs14449798 4	c.1114C>T	p.R372W	D (0.01)	PD (1)	PD (0.99)	M (2.86)	2.21 x 10 ⁻²	NR	HETO	Yes	No
	<i>CCDC13</i>	rs34234072	c.164A>G	p.D55G	D (0.05)	B (0.001)	B (0.003)	L (1.64)	4.74 x 10 ⁻³	ND	HETO	No	No
	<i>BBS7</i>	rs19989133 0	c.508A>G	p.R170G	D (0.02)	PD (1)	PD (0.994)	M (2.66)	9.84 x 10 ⁻⁴	AR	HETO	Yes	No
	<i>SPATA4</i>	rs76503401 7	c.599A>C	p.N200T	D (0.02)	PD (0.984)	PD (0.884)	M (2.17)	8.67 x 10 ⁻⁵	ND	HETO	Yes	No
	<i>IFT140</i>	New	c.60T>G	p.F20L	T (0.52)	B (0)	B (0.0)	N (-0.97)	New	AR	HETO	No	No
	<i>DZANK1</i>	rs79400176	c.848G>A	p.S283N	T (0.47)	B (0.077)	B (0.026)	L (1.76)	3.76 x 10 ⁻³	ND	HETO	No	No
	<i>TTBK2</i>	rs20077324 8	c.1936C>G	p.Q646E	T (0.05)	B (0.304)	B (0.072)	M (2.38)	3.92 x 10 ⁻⁴	AD	HETO	No	No
	<i>CEP44</i>	rs13933169 6	c.556A>G	p.I186V	T (0.61)	B (0.017)	B (0.11)	L (1.245)	6.75 x 10 ⁻⁴	ND	HETO	No	No
	<i>EVC2</i>	rs75438004 1	c.209G>T	p.G70V	T (0.19)	B (0.082)	B (0.276)	N (0)	4.57 x 10 ⁻⁴	AR/AD	HETO	No	No
	<i>KIFAP3</i>	rs12030924 09	c.646C>G	p.H216D	T (0.07)	B (0.44)	B (0.138)	M (2.05)	3.25 x 10 ⁻⁵	NR	HETO	No	No

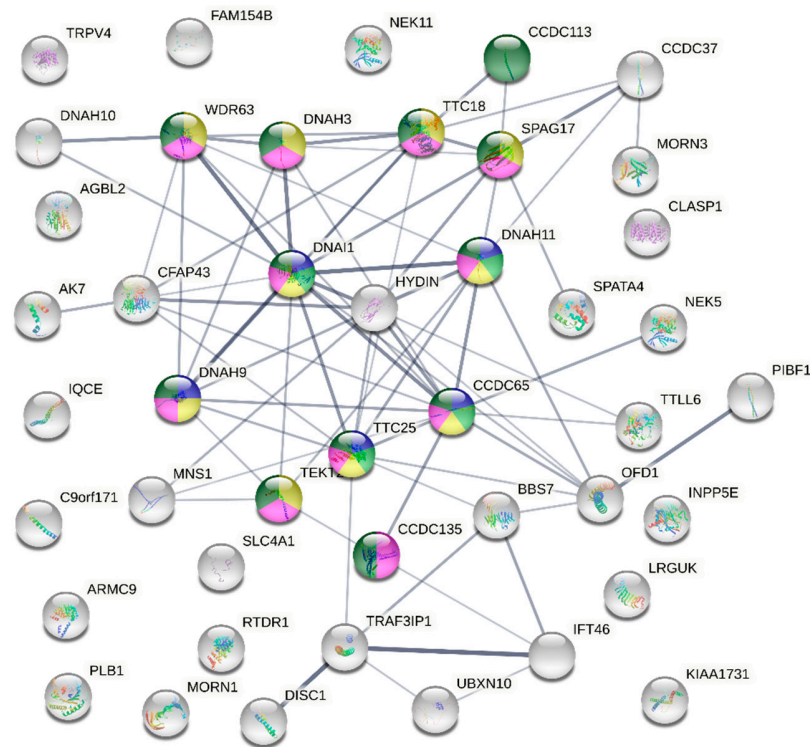
The algorithms could display several differences for a single variant, and the deleteriousness should be interpreted in this context. *TRPV4* and *PIBF1* genetic variants had been previously reported to other genetic diseases. dbSNP: Single Nucleotide Polymorphism database ; AA: Amino acid; NT: Nucleotide; SIFT: PP2: Polyphen2; Freq: Frequency; Mend: Mendelian inheritance; OMIM: Online Mendelian Inheritance of Man; PD: Probably/Possibly damaging; B: Benign; L: Lo; M: Medium; H: High; N: Neutral; T: Tolerated; Del/D: Deleterious. AD: Autosomic dominant; AR:

Autosomal recessive; NF: Not found; HETO: Heterozygous; HOMO: Homozygous; HEMY: Hemizygous; Neuromusc dyspl: Neuromuscular dysplasia. Allele frequency in latin population or if data is not available an asterisk (*) represent global frequency

Table S3: Protein clusters of selected genes in TGA patients. The analysis was performed in String using the Markov clustering algorithm.

#Clustering method	Cluster number	Cluster color	Gene count	Protein name	protein identifier
MCL	1	Red	8	DNAH10	9606.ENSP00000386770
MCL	1	Red	8	DNAH11	9606.ENSP00000475939
MCL	1	Red	8	DNAH3	9606.ENSP00000261383
MCL	1	Red	8	DNAH9	9606.ENSP00000262442
MCL	1	Red	8	DNAI1	9606.ENSP00000480538
MCL	1	Red	8	TTC18	9606.ENSP00000310829
MCL	1	Red	8	TTC25	9606.ENSP00000478589
MCL	1	Red	8	WDR63	9606.ENSP00000294664
MCL	2	Brown	7	CCDC135	9606.ENSP00000353942
MCL	2	Brown	7	CCDC65	9606.ENSP00000312706
MCL	2	Brown	7	HYDIN	9606.ENSP00000377197
MCL	2	Brown	7	MNS1	9606.ENSP00000260453
MCL	2	Brown	7	NEK5	9606.ENSP00000347767
MCL	2	Brown	7	TEKT2	9606.ENSP00000207457
MCL	2	Brown	7	TTLL6	9606.ENSP00000377043
MCL	3	Olive	5	BBS7	9606.ENSP00000264499

MCL	3	Olive	5	DISC1	9606.ENSPO0000355593
MCL	3	Olive	5	IFT46	9606.ENSPO0000264020
MCL	3	Olive	5	TRAF3IP1	9606.ENSPO0000362424
MCL	3	Olive	5	UBXN10	9606.ENSPO0000364240
MCL	4	Green	3	CCDC113	9606.ENSPO0000219299
MCL	4	Green	3	SPAG17	9606.ENSPO0000337804
MCL	4	Green	3	SPATA4	9606.ENSPO0000280191
MCL	5	Blue	2	OFD1	9606.ENSPO0000344314
MCL	5	Blue	2	PIBF1	9606.ENSPO0000317144
MCL	6	Light Sky Blue	2	AK7	9606.ENSPO0000267584
MCL	6	Light Sky Blue	2	CFAP43	9606.ENSPO0000349568
MCL	7	Medium Blue	2	CCDC37	9606.ENSPO0000344749
MCL	7	Medium Blue	2	MORN3	9606.ENSPO0000347486



Local network cluster (STRING)				
cluster	description	count in network	strength	false discovery rate
CL:10812	Axonemal dynein complex	3 of 15	1.95	0.0048
CL:10696	Kartagener syndrome	3 of 16	1.92	0.0050
CL:10690	Primary ciliary dyskinesia, and axonemal central apparatus	7 of 41	1.88	1.08e-08
CL:10692	Primary ciliary dyskinesia	5 of 30	1.87	1.05e-05
CL:10694	Primary ciliary dyskinesia	4 of 24	1.87	0.00028
CL:10689	Primary ciliary dyskinesia, and COPI-independent Golgi-to-E...	10 of 78	1.76	6.49e-12
CL:10687	Mixed, incl. primary ciliary dyskinesia, and copi-independent...	11 of 107	1.66	3.43e-12
CL:10686	Mixed, incl. primary ciliary dyskinesia, and copi-independent...	12 of 130	1.61	1.02e-12

Figure S1: Genetic anomalies aggregation of transposition of the great arteries by String. Further Ciliary dyskinesia, genetic variants are accumulated in COPI independent Golgi to ER retrograde traffic.