

**Supplemental Table 1.** Novel *PITX2* and *FOXC1* alleles reported in this study.

Nucleotide change	Predicted effect	MAF <sup>1</sup>	In silico analysis <sup>2</sup>	CADD / REVEL <sup>3</sup>	ACMG/AMP classification	Family history
<b><i>PITX2</i> (NM_153427.2)</b>						
c.137T>C	p.(Phe46Ser)	NP	Dam by 5/5	32/0.951	Likely Pathogenic ( <i>PM1, PM2, PP1, PP2, PP3, PP4</i> )	AD, cosegregates
c.253-2A>G	Splicing defect	NP	Acceptor loss ( $\Delta$ score 0.99)	N/A	Pathogenic ( <i>PVS1, PM2, PP3</i> )	NA
c.344_347del	p.(Asn115Serfs*39)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP4</i> )	NA
c.504delC	p.(Asn169Thrfs*6)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP1, PP4</i> )	AD, cosegregates
c.631delG	p.(Val211Cysfs*28)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PS2, PM2, PP4</i> )	De novo (ES)
c.632_633dup	p.(Pro212Cysfs*28)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PM6, PP4</i> )	De novo
<b><i>FOXC1</i> (NM_001453.2)</b>						
c.65dupA	p.(Gln23Alafs*60)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PS2, PM2, PP4</i> )	De novo (ES)
c.176dup	p.(Met60Hisfs*23)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP1, PP4</i> )	AD, cosegregates
c.241T>C	p.(Tyr81His)	NP	Dam by 5/5	28.7/0.894	Pathogenic ( <i>PS2, PM1, PM2, PP2, PP3</i> )	De novo (ES)
c.246C>G	p.(Ser82Arg)	NP	Dam by 5/5	26.5/0.967	Pathogenic ( <i>PS1, PM1, PM2, PM5, PP1, PP2, PP3, PP4</i> )	AD, cosegregates
c.257T>G	p.(Leu86Arg)	NP	Dam by 5/5	31/0.969	Pathogenic ( <i>PS2, PM1, PM2, PM5, PP2, PP3</i> )	De novo (ES)
c.263C>T	p.(Thr88Ile)	NP	Dam by 5/5	28.9/0.899	Likely Pathogenic ( <i>PM1, PM2, PP1, PP3, PP4</i> )	AD, cosegregates
c.269C>T	p.(Ala90Val)	NP	Dam by 5/5	31/0.970	Likely Pathogenic ( <i>PM1, PM2, PM5, PP1, PP3</i> )	AD, cosegregates
c.354del	p.(Asn118Lysfs*63)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP1</i> )	AD, not tested
c.366G>	p.(Trp122*)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PS2, PM2, PP4</i> )	De novo (ES)
c.407T>C	p.(Phe136Ser)	NP	Dam by 5/5	32/0.976	Likely Pathogenic ( <i>PM1, PM2, PP1, PP2, PP3, PP4</i> )	AD, cosegregates
c.470A>T	p.(Asp157Val)	NP	Dam by 5/5	29.4/0.824	Likely Pathogenic ( <i>PM1, PM2, PP2, PP3</i> )	AD, variable phenotype
c.486C>G	p.(Phe162Leu)	NP	Dam by 5/5	25.5/0.891	Likely Pathogenic ( <i>PM1, PM2, PP2, PP3, PP4</i> )	AD, not tested
c.502del	p.(Leu168Cysfs*13)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PM6, PP4</i> )	De novo
c.816_817delCCinsA	p.(Ser272Argfs*43)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP1</i> )	AD, cosegregates
c.965_977dup	p.(Leu328Argfs*204)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP4</i> )	AD, not tested
c.1430del	p.(Gln477Argfs*42)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP1, PP4</i> )	AD, cosegregates
c.1508del	p.(Asn503Thrfs*16)	NP	PTC	N/A	Pathogenic ( <i>PVS1, PM2, PP1, PP4</i> )	AD, cosegregates

<sup>1</sup>frequency in gnomAD v2.1.1; <sup>2</sup>SIFT, Polyphen2, Mutation Assessor, Mutation Taster, FATHMM-MKL (from dbNSFP v4.1a accessed through VEP) or SpliceAI analysis, Dam= Damaging; <sup>3</sup>CADDphredhg19 and REVEL scores (from dbNSFP v4.1a accessed through VEP); CADD score >20 and REVEL score >0.5 indicates predicted pathogenicity. AD = autosomal dominant; ES = exome sequencing; N/A = not available; NP = not present; PTC = premature truncating variant.

**Supplemental Table 2. Clinical features in individuals with *PITX2*-related Axenfeld Rieger syndrome from this cohort.**

Paper ID	relation	Variant <sup>a</sup>	Predicted effect	ASD	GL	Dental	Umbilicus	Heart	Hearing	GI	GU	Endo	Brain	Joints	Other	Age (y)	Sex	Race/Ethnicity
<b>DELETIONS</b>																		
Individual 1	Proband	0.015 Mb deletion (4:111539233-111554198)	Deletion of PITX2 (ENPEP to PITX2)	+	U	+	+	-	-	-	-	-	-	-	+	5-10	M	W
Reis 2012 Case 24	Proband	0.020 Mb deletion (4:111758031-111777957)	Deletion of regulatory region of PITX2 only	+	U	+	+	-	-	+	-	-	+	-	+	1-5	M	SA
Individual 2	Proband	0.674 Mb deletion (4:110880453-111554198)	Deletion of PITX2 (EGF to PITX2)	+	U	+	U	-	-	-	-	-	-	-	-	40-45	F	W
Reis 2012 Case 20	Proband	1.1 Mb deletion (4:110825068-111897193)	Deletion of PITX2 (EGF to PITX2)	+	+	+	+	-	-	+	+	+	+	-	+	50-55	M	W
Reis 2012 Case 22	Proband	1.93 Mb deletion (4:111427788-113362412)	Deletion of PITX2 (ENPEP (partial) to ALPK1 (partial))	+	U	+	+	-	-	-	-	-	-	-	-	2-5	M	EA/W
Reis 2012 Case 23	Proband	3.3 Kb deletion (4:111539233-111542544)	Deletion of PITX2 only	+	+	+	+	-	-	+	-	-	-	-	-	65-70	M	W
Individual 3	Proband	3.78 Mb deletion (4:111119388-114899976)	Deletion of PITX2 (ELOVL6 (partial) to ARSJ (partial))	+	U	+	+	+	+	+	+	+	+	+	+	10-15	F	U
Reis 2012 Case 19	Proband	6.4 Mb deletion (4:111334607-117695772)	Deletion of PITX2 (ENPEP to NDST4)	+	+	+	+	-	-	-	-	+	-	-	-	20-25	F	W
Volkmann 2011	Proband	7.6 Mb deletion (4:111666637-119311524)	Deletion of PITX2 regulatory region (AP1AR to PRSS12)	+	-	+	+	-	-	+	-	+	+	-	-	5-10	M	W
Reis 2012 Case 21	Proband	19.2 Mb deletion (4:111119401-130032948)	Deletion of PITX2 (ELOVL6 to SCLT1)	+	+	+	+	+	+	+	-	-	+	-	-	10-15	F	W
<b>PREMATURE TERMINATION CODONS</b>																		
Individual 4	Proband	c.61C>T	p.(Gln21*)	+	+	+	+	-	-	+	-	+	-	+	-	40-45	F	W
Reis 2012 Case 1	Proband	c.134dupA	p.(His45Glnfs*154)	+	-	+	+	-	-	-	-	-	-	-	-	1-2	F	H
Reis 2012 Case 2A	Proband	c.143_144delGC	p.(Ser48Thrfs*150)	+	U	+	+	-	-	-	-	-	-	-	-	30-35	M	W
Reis 2012 Case 2B	Child	c.143_144delGC	p.(Ser48Thrfs*150)	+	U	+	+	-	-	-	-	-	-	-	-	2-5	F	W
Reis 2012 Case 2C	Child	c.143_144delGC	p.(Ser48Thrfs*150)	+	U	U	+	-	+	-	-	-	-	-	-	<1	M	W
Reis 2012 Case 4A	Proband	c.225G>A	p.(Trp75*)	+	+	+	+	-	-	-	+	-	-	-	-	35-40	M	U
Reis 2012 Case 4B	Child	c.225G>A	p.(Trp75*)	+	-	U	+	-	-	-	-	-	-	-	+	<1	F	U
Individual 5	Child	c.225G>A	p.(Trp75*)	+	-	U	+	+	-	+	-	+	-	-	-	1-2		U
Reis 2012 Case 5	Proband	c.225G>A	p.(Trp75*)	+	-	+	+	-	-	+	-	-	-	-	-	10-15	M	U
Individual 6	Parent	c.225G>A	p.(Trp75*)	+	+	+	+	-	-	-	+	-	-	-	-	adult	M	U
Individual 7	Proband	c.252+1G>A	splicing defect	+	+	+	+	-	-	+	+	-	+	-	-	50-55	F	W

Paper ID	relation	Variant <sup>a</sup>	Predicted effect	ASD	GL	Dental	Umbilicus	Heart	Hearing	GI	GU	Endo	Brain	Joints	Other	Age	Sex	Race/ Ethnicity
<b>MISSENSE</b>																		
Individual 15	Proband	c.137T>C	p.(Phe46Ser)	+	+	+	+	-	-	-	+	-	-	-	+ Preemie (EGA 25 w)	15-20	F	W
Individual 16	Parent	c.137T>C	p.(Phe46Ser)	+	+	+	+	-	-	-	+	-	-	-	-	50-55	F	W
Reis 2012 Case 3	Proband	c.185G>A	p.(Arg62His)	+	U	+	+	-	-	-	-	-	-	-	-	40-45	F	U
Reis 2012 Case 6	Proband	c.247G>T	p.(Val83Phe)	+	-	+	+	-	-	-	+	-	-	-	-	2-5	F	W
Reis 2012 Case 12	Proband	c.257G>C	p.(Trp86Ser)	+	U	+	+	-	-	-	-	-	-	-	-	40-45	M	U
Reis 2012 Case 13	Proband	c.258G>T	p.(Trp86Cys)	+	U	+	+	-	-	+	-	-	-	-	-	2-5	F	U
Reis 2012 Case 7	Proband	c.253-11A>G	splicing defect	+	+	+	+	-	-	+	+	-	-	+	+	5-10	M	W
Reis 2012 Case 8	Proband	c.253-11A>G	splicing defect	+	+	+	+	+	-	-	-	+	-	-	+ ECMO x 3 mo	25-30	F	W
Reis 2012 Case 9	Proband	c.253-11A>G	splicing defect	+	U	-	+	-	-	-	-	+	-	-	-	10-15	F	W
Individual 8	Proband	c.253-2A>G	splicing defect	+	U	U	U	U	U	U	U	U	U	U	U	U	F	U
Reis 2012 Case 10	Proband	c.253-1G>A	splicing defect	+	U	+	+	-	-	+	-	-	-	-	-	2-5	F	U
Reis 2012 Case 11	Proband	c.253-1G>A	splicing defect	+	-	+	+	-	-	-	-	-	-	-	-	15-20	F	W
Reis 2012 Case 15	Proband	c.289_290delAG	p.(Arg97Glyfs*101)	+	-	U	+	-	-	-	-	-	-	-	-	<1	F	W
Individual 9	Proband	c.344_347delATGG	p.(Asn115Serfs*39)	+	U	U	U	U	U	U	U	U	U	U	U	U	M	U
Hendee 2018 Patient 3A	Proband	c.356delA	p.(Gln119Argfs*36)	+	+	+	+	+	+	-	-	-	-	-	-	50-55	F	W
Hendee 2018 Patient 3B	Child	c.356delA	p.(Gln119Argfs*36)	+	+	+	+	+	-	+	-	-	+	+	+	25-30	M	W
Individual 10	Proband	c.363C>G	p.(Tyr121*)	+	U	+	+	-	-	-	-	-	-	-	-	2-5	M	U
Reis 2012 Case 16	Proband	c.366delC	p.(Asp122Glufs*33)	+	+	+	-	-	-	-	-	-	-	-	-	25-30	M	U
Reis 2012 Case 17	Proband	c.398G>A	p.(Trp133*)	+	+	+	+	-	-	-	+	-	-	-	-	1-2	M	AI, B, W
Semina Family 6	Proband	c.399G>A	p.(Trp133*)	+	U	U	+	-	-	+	-	-	-	-	-	adult	F	U
Semina Family 6	Brother	c.399G>A	p.(Trp133*)	+	U	U	U	-	-	-	-	-	-	-	-	adult	M	U
Semina Family 6	Brother	c.399G>A	p.(Trp133*)	+	U	U	+	-	-	-	-	-	-	-	-	adult	M	U
Semina Family 6	Child	c.399G>A	p.(Trp133*)	+	U	U	+	-	-	-	-	-	-	-	-	child	F	U
Semina Family 6	Nephew	c.399G>A	p.(Trp133*)	+	U	U	+	-	-	+	-	-	-	-	-	child	M	U
Individual 11	Proband	c.504delC	p.(Asn169Thrfs*6)	+	+	-	-	-	-	-	-	-	-	-	-	35-40	F	W
Individual 12	Brother	c.504delC	p.(Asn169Thrfs*6)	+	+	-	-	-	-	+	-	-	-	-	-	35-40	M	W
Individual 13	Proband	c.631delG	p.(Val211Cysfs*28)	+	-	U	+	-	-	+	+	-	-	-	+	<1	F	W
Individual 14	Proband	c.632_633dup	p.(Pro212Cysfs*28)	+	-	+	+	-	-	+	+	+	+	+	-	5-10	M	W
Reis 2012 Case 18	Proband	c.708_730del	p.(Ser237Alafs*48)	+	U	U	+	-	-	+	-	-	-	-	+	<1	F	W

Hendee 2018 Patient 2A	Proband	c.259T>C	p.(Phe87Leu)	+	+	U	U	-	-	-	-	-	-	-	-		45-50	M	W
Hendee 2018 Patient 2B	Child	c.259T>C	p.(Phe87Leu)	+	+	U	+	-	-	-	-	-	-	-	+ neonatal asphyxiation	10-15	M	W	
Reis 2012 Case 14	Proband	c.269G>C	p.(Arg90Pro)	+	+	+	+	-	-	+	-	-	-	-	-		30-35	M	W
<b>Individual 17</b>	Proband	c.269G>C	p.(Arg90Pro)	+	+	-	+	-	-	+	-	-	-	-	+		5-10	M	W
Hendee 2018 Patient 1A	Proband	c.271C>T	p.(Arg91Trp)	+	+	+	+	-	-	-	-	-	-	-	-		5-10	M	W
Hendee 2018 Patient 1B	Parent	c.271C>T	p.(Arg91Trp)	+	-	+	U	-	-	-	-	-	-	-	-		30-35	F	W
Hendee 2018 Patient 1C	Grandparent	c.271C>T	p.(Arg91Trp)	+	+	+	U	-	-	+	-	-	-	-	-		55-60	F	W
<b>Individual 18</b>	Proband	c.272G>A	p.(Arg91Gln)	+	+	+	+	-	-	+	-	+	-	-	-		65-70	F	W
<b>Individual 19</b>	Proband	c.272G>C	p.(Arg91Pro)	+	+	+	+	-	-	+	-	-	-	-	+		15-20	F	W

<sup>a</sup>coordinates: hg19; c.DNA: NM\_153427.2

AI American Indian; B Black; F female; M male; SA South Asian; U unknown; W white

Bold rows: novel variants; Bold ID only: new cases

**Supplemental Table 3. Clinical features in Individual individuals with FOXC1-related Axenfeld-Rieger syndrome from this cohort.**

Paper ID	Relation	Variant <sup>a</sup>	Predicted effect	ASD	GL	Dental	Umbilicus	Heart	Hearing	GI	GU	Growth/ Endo	Brain	Joints	Other	Age (y)	Sex	Race/ Ethnicity	
<b>DELETIONS</b>																			
Individual 20	Proband	0.001 Mb del (6:1515346-1613196)	deletion of FOXC1 only	+	+	-	-	+	-	-	+	-	-	-	-	-	2-5	F	W
Individual 21	Proband	deletion	Deletion of FOXC1 only	+	U	U	U	U	U	U	U	U	U	U	U	U	U	M	U
Individual 22	Proband	0.001 MB del (6:1610679-1612344)	Deletion of FOXC1 only	+	+	-	-	-	-	+	-	-	-	-	-	+	10-15	M	W
Individual 23	Proband	0.001 MB del (6:1610679-1612344)	Deletion of FOXC1 only	+	+	+	-	+	+	+	-	-	-	+	+	-	55-60	F	W
Individual 24	Proband	0.0016 Mb del (6:1610473-1612132)	Deletion of FOXC1 only	+	U	U	U	U	U	U	U	U	U	U	U	U	U	M	U
Individual 25	Proband	0.350 Mb del (6:1610679-1961202)	Deletion of FOXC1 & GMDS (partial)	+	+	+	-	+	+	+	+	-	-	+	+	+	35-40	F	W
Individual 26	Proband	0.541 Mb del (6:1610679-2124967)	Deletion of FOXC1 & GMDS	+	U	U	U	U	U	U	U	U	U	U	U	U	U	F	U
Reis 2012 Case 25	Proband	0.98 Mb del (6:1570594-2546932)	Deletion of FOXC1 & GMDS	+	+	-	-	+	+	+	-	-	-	-	-	-	1-2	M	AI/W
Individual 27	Proband	1.2 Mb del (6:391769-1624777)	Deletion of FOXC1 (IRF4 (partial) to GMDS (partial))	+	-	+	+	-	-	-	-	-	-	-	-	-	10-15	M	W
Individual 28	Parent	1.2 Mb del (6:391769-1624777)	Deletion of FOXC1 (IRF4 (partial) to GMDS (partial))	+	-	+	-	-	Y	-	+	-	-	-	-	-	40-45	F	W
Reis 2012 Case 28	Proband	1.3 Mb del (6:893508-2204627)	Deletion of FOXC1 (LINC01622 to GMDS)	+	-	+	-	-	+	-	-	+	-	+	+	+ De Hauwere syndrome	45-50	F	W
Individual 29	Proband	1.44 Mb del (6:486669-1930466)	Deletion of FOXC1 (EXOC2 to GMDS partial)	+	+	-	-	+	+	-	-	-	-	+	-	+	5-10	F	W
Reis 2012 Case 27	Proband	1.5 Mb del (6:1538121-3071609)	Deletion of FOXC1 (FOXC1 to RIPK1 (partial))	+	+	U	-	-	-	-	-	-	-	-	-	-	5-10	F	H/W
Individual 30	Proband	1.9 Mb del (6:348747-2245681)	Deletion of FOXC1 (DUSP22 (partial) to GMDS)	+	U	-	-	-	-	-	-	-	-	-	-	-	Adult	F	H
Individual 31	Proband	2.2 Mb del (6:156,974-2,400,023)	Deletion of FOXC1 (DUSP22-GMDS)	+	-	-	-	+	+	-	-	-	-	+	-	+	10-15	M	H
Individual 32	Proband	2.7 Mb del (6:366602-3090996)	Deletion of FOXC1 (IRF4 to RIPK1 (partial))	+	+	+	-	-	+	-	-	-	-	+	+	+	60-65	F	W
Individual 33	Proband	2.89 Mb del (6:665234-3559813)	deletion of FOXC1 (EXOC2 (partial) to SLC22A23))	+	-	+	-	-	+	+	-	+	-	+	+	+	5-10	M	W
Paper ID	Relation	Variant <sup>a</sup>	Predicted effect	ASD	GL	Dental	Umbilicus	Heart	Hearing	GI	GU	Growth/ Endo	Brain	Joints	Other	Age (y)	Sex	Race/ Ethnicity	

Individual ID	Relationship	Variant <sup>a</sup>	Predicted effect	ASD	GL	Dental	Umbilicus	Heart	Hearing	GI	GU	Growth/ Endo	Brain	Joints	Other	Age (y)	Sex	Race/ Ethnicity
Individual 34	Proband	3.15 Mb del 6pter-315094)	Deletion of FOXC1 (DUSP22 to SERPINB9)	+	-	+	-	-	+	-	-	-	+	+	+	5-10	F	W
Individual 35	Proband	4.34 Mb del (6:393110-5113651)	Deletion of FOXC1 (IRF4 to LYRM4 (partial))	+	-	+	-	-	-	-	-	-	-	-	-	2-5	F	W
Individual 36	Proband	5.93 Mb del (6:393173-6318916)	Deletion of FOXC1 (IRF4 (partial) to F13A1 (partial))	+	U	-	-	-	-	-	-	+	+	-	+	U	F	W
Reis 2012 Case 26A	Proband	6p25 del (extent ND)	Deletion of FOXC1; other genes ND	+	+	+	-	-	+	-	-	-	-	-	+	30-35	F	W
Reis 2012 Case 26B	Child	6p25 del (extent ND)	Deletion of FOXC1; other genes ND	+	+	U	+	-	-	+	+	-	-	+	-	+<1	M	W
<b>PREMATURE TERMINATION CODONS</b>																		
Individual 37	Proband	c.65dupA	p.(Gln23Alafs*60)	+	+	-	-	+	-	-	-	+	+	-	-	15-20	F	W
Individual 38	Proband	c.176dupG	p.(Met60Hisfs*23)	+	-	+	-	+	-	-	-	-	-	-	-	2-5	F	W
Individual 39	Brother	c.176dupG	p.(Met60Hisfs*23)	+	+	+	-	-	-	-	-	+	-	-	-	2-5	M	W
Individual 40	Father	c.176dupG	p.(Met60Hisfs*23)	-	-	+	-	+	-	+	-	-	-	-	+	30-35	M	W
Individual 41	Proband	c.274C>T	p.(Gln92*)	+	+	+	-	-	-	-	+	+	-	-	+ adopted 8 yo, delayed treatment	10-15	F	EA
Individual 42	Proband	c.354delC	p.(Asn118Lysfs*63)	+	+	-	-	-	-	-	-	-	-	-	-	25-30	F	W
Individual 43	Child	c.354delC	p.(Asn118Lysfs*63)	+	-	U	-	-	-	-	-	-	-	-	-	<1	M	W
Individual 44	Proband	c.366G>A	p.(Trp122*)	+	+	+	-	-	+	-	+	-	-	-	+	20-25	F	H
Individual 45	Proband	c.366G>A	p.(Trp122*)	-	-	-	-	+	-	+	-	+	+	U	+	2-5	F	H
Individual 46	Proband	c.502delC	p.(Leu168Cysfs*13)	+	-	-	-	-	-	+	-	+	+	-	-	1-2	F	W
Individual 47	Proband	c.718_719del	p.(Leu240Valfs*65)	-	-	+	-	-	+	-	-	-	+	-	-	40-45	F	W
Individual 48	Father	c.718_719del	p.(Leu240Valfs*65)	U	-	+	-	-	+	-	+	-	+	-	-	Adult	M	W
Individual 49	Child	c.718_719del	p.(Leu240Valfs*65)	-	-	-	-	-	-	-	-	-	+	-	-	15-Oct	M	W
Individual 50	Proband	c.816_817delCCinsA	p.(Ser272Argfs*43)	+	+	-	-	-	-	-	-	-	-	-	-	30-35	M	H
Individual 51	Child	c.816_817delCCinsA	p.(Ser272Argfs*43)	+	+	U	-	U	-	-	-	-	-	-	-	<1	M	H
Individual 52	Proband	c.821del	p.(Pro274Argfs*41)	+	-	U	+	+	-	+	-	+	+	+	+	<1	M	W
Individual 53	Proband	c.965_977dup	p.(Leu328Argfs*204)	+	+	+	-	-	+	-	-	-	-	-	+	35-40	F	W
Individual 54	Proband	c.1141dupG	p.(Ala381Glyfs*147)	+	+	-	-	-	+	+	+	-	+	+	+	15-20	F	W
Reis 2016 Patient 3	Proband	c.1193_1196dupAAGC	p.(Met400Serfs*129)	+	+	-	-	-	+	-	-	-	+	+ 18q23del	<1	M	W	
Reis 2016 Patient 3B	Parent	c.1193_1196dupAAGC	p.(Met400Serfs*129)	+	+	-	-	-	+	-	-	-	-	+	-	50-55	M	W
Individual 55	Proband	c.1430delA	p.(Gln477Argfs*42)	+	+	+	+	-	-	-	-	+	-	+	-	5-10	M	W
Individual 56	Twin	c.1430delA	p.(Gln477Argfs*42)	+	+	-	+	-	-	-	-	+	-	+	-	5-10	M	W
Individual 57	Brother	c.1430delA	p.(Gln477Argfs*42)	+	+	-	-	+	-	-	-	-	-	+	-	2-5	M	W
Individual 58	Parent	c.1430delA	p.(Gln477Argfs*42)	+	-	-	-	-	-	-	-	-	-	-	-	40-45	M	W
Individual 59	Proband	c.1508delA	p.(Asn503Thrfs*16)	+	+	-	-	U	-	-	-	-	-	-	-	10-15	F	W

		MISSENSE																				
Individual	Relationship	ID	Variants	p.(Tyr81His)	+	-	-	-	-	+	+	-				+	+		2-5	F	W	
Individual 62	Proband	<b>c.241T&gt;C</b>	<b>p.(Tyr81His)</b>	+	-	-	-	-	+	+	-					+	+		2-5	F	W	
Individual 63	Proband	<b>c.246C&gt;G</b>	<b>p.(Ser82Arg)</b>	+	+	-	-	-	+	-	-	-	-	-	-	+	-		35-40	F	H	
Individual 64	Sister	<b>c.246C&gt;G</b>	<b>p.(Ser82Arg)</b>	+	+	-	-	-	-	-	-	-	-	-	-	-	-		<1	F	H	
Individual 65	Proband	<b>c.257T&gt;G</b>	<b>p.(Leu86Arg)</b>	+	+	-	+	+	+	-	-	+	+	-	-	+	t(3;4)(q13.2;q21.1)pat	1-2	F	H		
Individual 66	Proband	<b>c.263C&gt;T</b>	<b>p.(Thr88Ile)</b>	+	+	-	-	-	-	-	-	-	-	-	-	-	-		30-35	F	U	
Individual 67	Sister	<b>c.263C&gt;T</b>	<b>p.(Thr88Ile)</b>	+	U	-	-	-	+	U	-	-	-	-	-	-	-		30-35	F	U	
Individual 68	Child	<b>c.263C&gt;T</b>	<b>p.(Thr88Ile)</b>	+	+	-	-	-	+	U	-	-	-	+	U	+	+		<1	M	U	
Individual 69	Proband	<b>c.269C&gt;T</b>	<b>p.(Ala90Val)</b>	+	+	-	-	-	-	-	-	-	-	-	-	+	-		10-May	M	H/W	
Individual 70	Sister	<b>c.269C&gt;T</b>	<b>p.(Ala90Val)</b>	+	+	-	-	-	+	-	-	-	-	-	-	-	-		<2	F	H/W	
Individual 71	Mother	<b>c.269C&gt;T</b>	<b>p.(Ala90Val)</b>	+	-	-	-	-	-	-	-	-	+	-	-	-	-		30-35	F	H/W	
Individual 72	proband	<b>c.335T&gt;C</b>	<b>p.(Phe112Ser)</b>	+	U	U	U	U	U	U	U	U	U	U	U	U	U		Adult	M	U	
Individual 73	Proband	<b>c.380G&gt;A</b>	<b>p.(Arg127His)</b>	+	+	U	U	U	+	U	U	U	U	U	U	U	U	U	U	F	U	
Individual 74	Proband	<b>c.407T&gt;C</b>	<b>p.(Phe136Ser)</b>	+	+	-	-	-	+	+	-	-	-	-	-	-	-		35-40	M	W	
Individual 75	Child	<b>c.407T&gt;C</b>	<b>p.(Phe136Ser)</b>	+	+	U	-	-	+	-	-	-	-	-	-	+	-		2-5	F	W	
Individual 76	Proband	<b>c.470A&gt;T</b>	<b>p.(Asp157Val)</b>	+	+	+	-	-	+	-	+	-	+	+	+	-	-		5-10	F	W	
Individual 77	Father	<b>c.470A&gt;T</b>	<b>p.(Asp157Val)</b>	-	-	-	-	-	-	-	-	+	-	-	-	+	-		40-45	M	W	
Individual 78	Brother	<b>c.470A&gt;T</b>	<b>p.(Asp157Val)</b>	-	-	-	-	-	+	-	-	-	-	-	-	+	-		15-20	M	W	
Individual 79	Proband	<b>c.486C&gt;G</b>	<b>p.(Phe162Leu)</b>	+	+	U	-	-	U	U	-	U	U	U	U	U	U		1-2	F	W	
Individual 80	Proband	<b>c.508C&gt;T</b>	<b>p.(Arg170Trp)</b>	+	+	+	-	-	+	-	-	-	-	-	-	-	+		10-15	F	H	
Individual 81	Parent	<b>c.508C&gt;T</b>	<b>p.(Arg170Trp)</b>	+	+	-	-	-	-	-	+	-	-	-	-	-	-		30-35	M	H	

<sup>a</sup>coordinates: hg19; c.DNA: NM\_001453.2

AI American Indian; B Black; F female; H Hispanic; M male; SA South Asian; U unknown; W white

Bold rows: novel variants; Bold ID only: new cases

**Supplemental Table 4. Previously reported heterozygous *PITX2* variants in ARS and related conditions.**

Nucleotide variant (NM_153427.2)	Protein effect	Reference
c.47-1G>A	splicing	1
c.47-1G>C	splicing	2
c.47-1G>T	splicing	3 4
c.61C>T	p. Gln21*	5
c.64C>T	p. Gln22*	1 6
c.88G>T	p. Ala30Ser	7
c.90delC	p. Glu31Argfs*124	1
c.103A>T	p. Lys35*	8
c.104_127del	p. Lys35_Gln42del	7
c.108delG	p. Lys37Serfs*118	1
c.114delG	p. Gln39Lysfs*116	3
c.127C>T	p. Arg43Trp	9
c.130_150dup	p. Thr44_Gln50dup	10
c.134_137delACTT	p. His45Leufs*109	11
c.134dupA	p. His45Glnfs*154	1 12
c.137_138delTT	p. Phe46Tyrfs*152	13
c.143_144delGC	p. Ser48Thrfs*150	12
c.148C>T	p. Gln50*	14
c.155A>G	p. Gln52Pro	8
c.157_158insGGT	p. Glu53_Val271delinsGly	8
c.161T>A	p. Leu54Gln	15
c.163G>T	p. Glu55*	16
c.172T>C	p. Phe58Leu	13
c.173T>G	p. Phe58Cys	8
c.173T>C	p. Phe58Ser	8
c.174C>G	p. Phe58Leu	16
c.175C>T	p. Gln59*	13
c.184_205del22	p. Arg62Alafs*86	17
c.185G>A	p. Arg62His	12 18 19
c.190C>G	p. Pro64Ala	8
c.191C>G	p. Pro64Arg	20 21
c.191C>T	p. Pro64Leu	17 22-24
c.198_201delGTCCinsTTTCT	p. Met66Ilefs*133	25
c.202A>C	p. Thr68Pro	15
c.205C>G	p. Arg69Cys	26
c.205C>T	p. Arg69Gly	27
c.206G>A	p. Arg69His	6 28 29
c.211G>T	p. Glu71*	1

c.217G>A	p. Ala73Thr	30
c.224G>A	p. Trp75*	12 13
c.233T>C	p. Leu78Pro	30
c.247G>C	p. Val83Leu	10
c.247G>T	p. Val83Phe	12
c.250C>T	p. Arg84Trp	19 31
c.251G>C	p. Arg84Pro	1
c.252+1G>A	splicing	17 32
c.252+5G>C	splicing	4 15
c.253-11A>G	splicing	1 8 12 13 15 33 34
c.253-2A>T	splicing	2 35
c.253-1G>A	splicing	8 12
c.257G>A	p. Trp86*	14
c.257G>C	p. Trp86Ser	12
c.258G>T	p. Trp86Cys	12 36
c.259T>C	p. Phe87Leu	37
c.262A>G	p. Lys88Glu	2 38
c.268C>T	p. Arg90Cys	2
c.269G>C	p. Arg90Pro	8 12 22
c.271C>G	p. Arg91Gly	17
c.271C>T	p. Arg91Trp	37
c.272G>A	p. Arg91Gln	39
c.272G>C	p. Arg91Pro	15
c.274G>C	p. Ala92Pro	17
c.279delA	p. Lys93Asnfs*62	30
c.282G>A	p. Trp94*	8 13
c.286_287delAA	p. Lys96Glufs*102	2
c.289_290delAG	p. Arg97Glyfs*101	12
c.296delG	p. Arg99Profs*56	6
c.300_301delCCinsT	p. Gln101Serfs*54	40
c.301C>T	p. Gln101*	13
c.304C>T	p. Gln102*	13 41
c.313C>G	p. Leu105Val	22
c.317G>A	p. Cys106Tyr	7
c.323A>C	p. Asn108Thr	22
c.341 dup	p. Asn115Glnfs*84	19
c.348delG	p. Leu117Serfs*38	8
c.356delA	p. Gln119Argfs*36	1 2 37 42
c.363C>A	p. Tyr121*	16
c.363_364delinsAA	p. Tyr121*	43
c.366delC	p. Asp122Glufs*33	12 44

c.377delC	p.Pro126Glnfs*29	8
c.398G>A	p.Trp133*	12
c.399G>A	p.Trp133*	15
c.410G>T	p.Gly137Val	45
c.416delC	p.Thr139Asnfs*16	3
c.475_476delCT	p.Leu159Valfs*39	1 6 46 47
c.484C>T	p.Gln162*	1
c.487_488delAG	p.Ser163Hisfs*35	17
c.500dupC	p.Pro168Thrfs*31	2
c.539_551del	p.Met180Lysfs*2	8
c.555_576del	p.Thr186Serfs*4	17
c.573_574delCA	p.Leu193Glnfs*5	48
c.629_630dupCG	p.Val211Argfs*29	14
c.648T>A	p.Cys216*	17
c.649C>A	p.Pro217Thr	49
c.652_653delTAinsAAG	p.Tyr218Lysfs*11	2
c.663_670dupGACTCCTC	p.Pro224Argfs*18	16
c.679delT	p.Tyr227Ilefs*12	50
c.690delG	p.Cys231Valfs*8	34
c.698C>T	p.Ser233Leu	51
c.708_730del	p.Ser237Alafs*48	12
Regulatory region deletion	Decreased dosage	12 52 53
Partial gene deletion	Haploinsufficiency	17 54 55
Full gene deletion	Haploinsufficiency	12-14 17 55-59

Reference transcript NM\_153427.1. Gray shading indicates variants in the homeodomain (aa38-98) or OAR domain (aa233-246)

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**Supplemental Table 5. Previously reported heterozygous *FOXC1* variants in ARS and related conditions.**

Nucleotide variant (NM_001453.2)	Protein effect	References
c.4C>T	p. Gln2*	1
c.12delC	p.Tyr5Thrfs*40	2
c.30_51dup	p.Tyr18Glnfs*72	3 4
c.67C>T	p. Gln23*	5
c.75C>G	p. Tyr25*	6
c.99_108del10	p.Gly34Thrfs*8	3 7
c.100_109del10	p.Gly34Thrfs*8	8
c.116_123delCCATGCCG	p.Ala39Glyfs*41	3 8
c.141C>G	p. Tyr47*	9
c.143C>A	p. Ser48*	10
c.149_156delCTGCGCAC	p.Pro50Argfs*30	3
c.153_163del11	p.His52Valfs*27	11
c.192C>G	p. Tyr64*	6 12
c.206delC	p.Pro69Argfs*9	13
c.210delG	p.Gln70Hisfs*8	14
c.235C>A	p. Pro79Thr	15
c.236C>G	p. Pro79Arg	10
c.236C>T	p. Pro79Leu	3
c.240_243dup	p.Tyr81dup	13
c.240_284del	p.Tyr81_Pro95del	16
c.245G>C	p. Ser82Thr	7
c.246C>A	p.Ser82Arg	13 17
c.247T>C	p.Tyr83His	13
c.253G>C	p. Ala85Pro	18
c.255_256delGCinsTT	p.Leu86Phe	19
c.256C>T	p. Leu86Phe	8
c.257T>C	p.Leu86Pro	13
c.261C>G	p. Ile87Met	7
c.264dupC	p.Met89Hisfs*217	3
c.268G>A	p. Ala90Thr	8
c.269C>A	p. Ala90Asp	20
c.272T>C	p. Ile91Thr	21
c.272T>G	p. Ile91Ser	4
c.274C>T	p. Gln92*	22
c.275A>C	p.Gln92Pro	13
c.286dupG	p.Asp96Glyfs*210	4 23
c.302T>C	p. Leu101Pro	24

c.316C>T	p. Gln106*	8 9 23
c.317delA	p.Gln106Argfs*75	25
c.325A>G	p. Met109Val	23
c.335delT	p.Phe112Serfs*69	23
c.335T>C	p. Phe112Ser	11
c.344A>C	p. Tyr115Ser	26
c.349delG	p.Asp117Thrfs*64	27
c.358C>T	p. Gln120*	26
c.363delC	p.Trp122Glyfs*59	28
c.364T>G	p.Trp122Gly	13
c.365_366insCT	p.Trp122Cysfs*60	6
c.367C>T	p. Gln123*	1 6 22
c.368_370delAGAinsC	p.Gln123Profs*182	6
c.377T>G	p. Ile126Ser	9
c.378C>G	p. Ile126Met	11 29
c.379C>T	p. Arg127Cys	30
c.380G>A	p. Arg127His	4 13
c.380G>T	p. Arg127Leu	31
c.383A>G	p. His128Arg	2
c.387C>A	p. Asn129Lys	6
c.388C>T	p. Leu130Phe	13 28
c.392C>A	p. Ser131*	23
c.392C>G	p. Ser131Trp	23
c.392C>T	p. Ser131Leu	11 13 32
c.399C>G	p.Asn133Lys	13
c.404G>A	p. Cys135Tyr	2
c.405C>A	p.Cys135*	32
c.409_411delGTC	p.Val137del	33
c.412A>G	p. Lys138Glu	23
c.430A>T	p.Lys144*	13
c.437_453del17	p.Pro146Leufs*154	18
c.446G>A	p. Gly149Asp	10
c.453_454delCTinsAA	p.Tyr151*	34
c.454T>A	p. Trp152Arg	22
c.454T>G	p. Trp152Gly	35
c.456G>A	p. Trp152*	36
c.457A>C	p. Thr153Pro	8 20
c.477C>G	p. Tyr159*	37
c.478_482 dup	p.Met161Ilefs*22	38
c.481A>G	p. Met161Val	10
c.482T>A	p. Met161Lys	1 13 39 40

c.487G>T	p. Glu163*	20
c.493G>C	p. Gly165Arg	41
c.506G>C	p. Arg169Pro	41
c.508C>T	p. Arg170Trp	42
c.513_518del	p.Arg172_Arg173del	13
c.518G>A	p. Arg173His	38
c.592_593delinsC	p.Gly198Profs*117	13
c.599_617del19	p.Gln200Argfs*109	8
c.605delC	p.Pro202Argfs*113	23
c.609delC	p.Ala204Argfs*111	43
c.666_681del16	p.Ile223Profs*87	8
c.692delG	p.Gly231Valfs*84	23
c.718_719delCT	p.Leu240Valfs*65	6 13 36
c.719delT	p.Leu240Argfs*75	44
c.740delG	p.Gly247Alafs*68	10
c.780dupC	p.Asp261Argfs*45	23
c.816_817delCCinsG	p.Ser272Argfs*43	23
c.821delC	p.Pro274Argfs*41	45
c.848_872dup	p.Pro292Glnfs*22	2
c.925_949del	p.Ser309Cysfs*84	8
c.980_981delAG	p.Glu327Alafs*200	23
c.1053_1056dupCGCC	p.Tyr353Argfs*176	6
c.1086delC	p.Ser363Profs*38	2
c.1193_1196dupAAGC	p.Met400Serfs*129	46
c.1200delG	p.Met400Ilefs*45	47
c.1265C>A	p. Ser422*	8
c.1399C>T	p.Gln467*	38
c.1491C>G	p. Tyr497*	8 23
c.1496delG	p.Gly499Alafs*20	48
c.1511delT	p.Phe504Serfs*15	10
c.1513delC	p.His505Thrfs*14	3
c.1540delC	p.Gln514Argfs*5	13
Full gene deletion	haploinsufficiency	6 8 13 20 23 24 49- 64
Full gene duplication	Increased dosage	3 6 8 56 65

Reference transcript NM\_001453.2. Gray shading indicates variants affecting the forkhead domain (aa 77-168)

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