Supplementary Table 2. *Overview of identified CTNNB1 and WT1 variants*

Patient ID	WT1 germline variant	WT1 germline HGVSg	WT1 germline HGVSc	WT1 germline HGVSp	WT1 somatic variant 1	WT1 somatic variant 1 HGVSg	WT1 somatic variant 1 HGVSc	WT1 somatic variant 1 HGVSp	WT1 somatic variant 1 Classification	WT1 somatic variant 2	WT1 somatic variant 2 HGVSg	WT1 somatic variant 2 HGVSc	WT1 somatic variant 2 HGVSp	WT1 somatic variant 2 Classification	WT1 LOH	Copy number variation Chr11	CTNNB1 somatic variant 1	CTNNB1 somatic variant 1 HGVSg	CTNNB1 somatic variant 1 HGVSc	CTNNB1 somatic variant 1 HGVSp	CTNNB1 somatic variant 2	CTNNB1 somatic variant 2 HGVSg	CTNNB1 somatic variant 2 HGVSc	CTNNB1 somatic variant 2 HGVSp
AA	None				None					None					ChrLOH	NC_000011.10:g.[50691219-50949954](3C)T08AFratio	Exon 3 Missense (Stabilising; other biomaterial)	NC_000003.12:g.41227265A>T	NC_000003.12(NM_001904.4):c.998A>T	NC_000003.12(NP_001895.1):p.(Tyr333Phe)	None			
AB	None				None					None					ChrLOH	NC_000011.10:g.[47439275-47519793](3C)+LOH					None				
AC	None									None					ChrLOH	NC_000011.10:g.[53780660-54346787](3C)T08AFratio	None				None				
AD	Truncating/Deletion	NC_000011.10:g.32434889C=A	NC_000011.10(NM_024426.5):c.472G>T	NM_024426.5(NP_077744.4):p.(Glu158Ter)	None					None					ChrLOH	NC_000011.10:g.[36728918-36768855](3C)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41216457C	NC_000003.12(NM_001904.4):c.1337C	NC_000003.12(NP_001895.1):p.(Ser446Pro)	None			
AE	None				None					None					ChrLOH	NC_000011.10:g.[47470466-47538253](3C)+LOH	None				None				
AF	None				None					None					None		None				None				
AG	None				None					None					None		None				None				
AH	Truncating/Deletion	NC_000011.10:g.32434847G>A	NC_000011.10(NM_024426.5):c.514C>T	NM_024426.5(NP_077744.4):p.(Gln172Ter)	Truncating/Deletion					None					LOH	NC_000011.10:31104921_(48880079_48900310)del	None				None				
AI	None				Truncating/Deletion	NC_000011.10:g.32433266_32444887del		NC_000011.10(NM_024426.6):c.-9527_661+1434del	NC_000011.10(NP_077744.4):p.0?	Franklin_LikelyPathogenic	Complex	Multiple rearrangements with chr 2	Complex	Complex		ChrLOH		Exon 3 Missense (Stabilising)	NC_000003.12:g.41216457C	NC_000003.12(NM_001904.4):c.1337C	NC_000003.12(NP_001895.1):p.(Ser446Pro)	None			
AJ	None				No SNVs (WXS)					No SNVs (WXS)					None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41227275A>T	NC_000003.12(NM_001904.4):c.1004A>T	No SNVs (WXS)	No SNVs (WXS)				
AK	None				None					None					None		None				None				
AL	None				None					None					None		None				None				
AM	None				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
AN	None				None					None					None		None				None				
AO	None (not checked in research)				None					None					None		None				None				
AP	None				No SNVs (WXS)					No SNVs (WXS)					ChrLOH	NC_000011.10:g.[:63875135-69062461](4S)T08AFratio	No SNVs (WXS)				No SNVs (WXS)				
AQ	None (not checked in research)				No data					No data					No data		No data				No data				
AR	None (not checked in research)				No data					No data					No data		No data				No data				
AS	None				None					None					None		None				None				
AT	None (not checked in research)				Truncating/Deletion	NC_000011.10:g.32396401G>A		NC_000011.10(NM_024426.6):c.1120C>T	NC_000011.10(NP_077744.4):p.(Arg374Ter)	ChrVar_Pathogenic	None				ChrLOH	NC_000011.10:g.[:]33112004-36338731](3C)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41216457C	NC_000003.12(NM_001904.4):c.1337C	NC_000003.12(NP_001895.1):p.(Ser446Pro)	None			
AU	None				None					None					ChrLOH	NC_000011.10:g.[:]36163192_32527590]N-LOH	None				None				
AV	None (not checked in research)				Truncating/Deletion	NC_000011.10:g.32396279_32396282del		NC_000011.10(NM_024426.6):c.1240_1243del	NC_000011.10(NP_077744.4):p.(Gln414Cysfs*39)	Franklin_LikelyPathogenic	None				None		None				None				
AW	None (not checked in research)				No data					No data					No data		No data				No data				
AX	Truncating/Deletion	NC_000011.10:g.[32026549_34934458]del	whole gene deletion		NC_000011.10(NP_077744.4):p.0?	No data				No data					No data		No data				No data				
AY	None				None					None					None		None				None				
AZ	Truncating/Deletion	NC_000011.10:g.32396401G>A	NC_000011.10(NM_024426.6):c.1120C>T	NC_000011.10(NP_077744.4):p.(Arg374Ter)	None					None					ChrLOH	NC_000011.10:g.[:]47332397-47416663](3C)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41224633A>G	NC_000003.12(NM_001904.4):c.1214A>G	NC_000003.12(NP_001895.1):p.(Thr414Ala)	None			
BA	None				None					None					ChrLOH	NC_000011.10:g.[:]33087622]N-LOH	None				None				
BB	None				None					None					None		Exon 3 545del (Stabilising)	NC_000003.12:g.41224644del	NC_000003.12(NM_001904.4):c.134_136del	NC_000003.12(NP_001895.1):p.(Ser45del)	None			
BC	None				No data					No data					No data		No data				No data				
BD	None				None					None					None		None				None				
BE	None				Truncating/Deletion	NC_000011.10:g.32008000_33165998del		whole gene deletion		NC_000011.10(NP_077744.4):p.0?	Franklin_Pathogenic	Truncating/Deletion	NC_000011.10:g.32353743_32460068del		whole gene deletion	NC_000011.10(NP_077744.4):p.0?	Franklin_Pathogenic	None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41224633A>G	NC_000003.12(NM_001904.4):c.1214A>G	NC_000003.12(NP_001895.1):p.(Thr414Ala)	None			
BF	None				None					None					None		None				None				
BG	None				None					None					None		None				None				
BH	None				None					None					ChrLOH	NC_000011.10:g.[:]33087622]N-LOH	None				None				
BI	None				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
BJ	None				Complex		Complex*		Complex		Complex				None		Exon 3 545del (Stabilising)	NC_000003.12:g.41224645_41224647del	NC_000003.12(NM_001904.4):c.131_133del	NC_000003.12(NP_001895.1):p.(Ser45del)	None			
BL	None				None					None					No data		None				None				
BM	None				None					None					LOH	NC_000011.10:g.[:]33087622]LOH	None				None				
BN	None				None					None					No data		None				None				
BO	None				None					None					None		None				None				
BP	None				None					None					ChrLOH	NC_000011.10:g.[:]46036521-46684939](7S)T08AFratio	None				None				
BQ	None				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
BR	None				Splice	NC_000011.10:g.32434409C>T		NC_000011.10(NM_024426.6):c.641+1G>A	NC_000011.10(NP_077744.4):p.0?	Franklin_LikelyPathogenic	None				ChrLOH	NC_000011.10:g.[:]32445675-32504567](7S)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41224634C>A	NC_000003.12(NM_001904.4):c.1222C>A	NC_000003.12(NP_001895.1):p.(Thr414Asn)	Exon 3 Missense (Stabilising; other biomaterial)	NC_000003.12:g.41224646C>T	NC_000003.12(NM_001904.4):c.1234C>T	NC_000003.12(NP_001895.1):p.(Ser412Phe)
BS	None				Missense	NC_000011.10:g.32392011G>A		NC_000011.10(NM_024426.6):c.1408C>T	NC_000011.10(NP_077744.4):p.(His470Tyr)	ClinVar_PathogenicBasedOnOneClassification	None				None		None				None				
BT	None (not checked in research)				None					None					None		None				None				
BU	None				None					None					None		None				None				
BV	None				None					None					None		None				None				
BW	None				No SNVs (WXS)					No SNVs (WXS)					No data		No SNVs (WXS)				No SNVs (WXS)				
BX	None				Truncating/Deletion	NC_000011.10:g.32434718_32435763del		NC_000011.10(NM_024426.6):c.403_643del	NC_000011.10(NP_077744.4):p.0?	Franklin_LikelyPathogenic	None				ChrLOH	NC_000011.10:g.[:]46256463-46533984](7S)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41216616C	NC_000003.12(NM_001904.4):c.1076C	NC_000003.12(NP_001895.1):p.(Ala359Val)	None			
BY	None				None					None					LOH	NC_000011.10:g.[:]33087622]LOH	None				None				
BZ	None				None					None					None		None				None				
CA	None				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
CB	None				None					None					LOH	NC_000011.10:g.[:]33087622]LOH	None				None				
CC	None				Truncating/Deletion	NC_000011.10:g.32428551_32428569del		NC_000011.10(NM_024426.6):c.714_732del	NC_000011.10(NP_077744.4):p.(His239Profs*6)	Franklin_LikelyPathogenic	None				None		None				None				
CD	None				None					None					LOH	NC_000011.10:g.[:]33087622]LOH	None				None				
CE	None				None					None					None		None				None				
CF	None (not checked in research)				None					None					None		None				None				
CG	None				None					None					ChrLOH	NC_000011.10:g.[:]57162570-57700286](4S)T08AFratio	None				None				
CH	None				None					None					No data		Exon 3 545del (Stabilising)	NC_000003.12:g.41224645_41224647del	NC_000003.12(NM_001904.4):c.133_135del	NC_000003.12(NP_001895.1):p.(Ser45del)	None			
CI	None				Complex	Multiple rearrangements between chr 11, affecting both alleles		Complex		Complex					ChrLOH	NC_000011.10:g.[:]35541448-35913128](3C)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41224646C>T	NC_000003.12(NM_001904.4):c.1234C>T	NC_000003.12(NP_001895.1):p.(Ser412Phe)	None			
CJ	None				None					None					None		None				None				
CK	None				None					None					ChrLOH	NC_000011.10:g.[:]33087622]N-LOH	None				None				
CL	None				Truncating/Deletion	NC_000011.10:g.32352737G>A		NC_000011.10(NM_024426.6):c.1303C>T	NC_000011.10(NP_077744.4):p.(Arg435Ter)	ClinVar_Pathogenic	None				ChrLOH	NC_000011.10:g.[:]47677963-50810330](3C)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41224646C>T	NC_000003.12(NM_001904.4):c.1234C>T	NC_000003.12(NP_001895.1):p.(Ser412Phe)	None			
CM	None				None					None					None		None				None				
CN	Not tested				Truncating/Deletion (VUS)	NC_000011.10:g.32396384_32396393dup		NC_000011.10(NM_024426.6):c.1131_1140dup	NC_000011.10(NP_077744.4):p.(Pro381Tyrfs*12)	Franklin_VUS	Truncating/Deletion	NC_000011.10:g.32399999del		NC_000011.10(NM_024426.6):c.1062del	NC_000011.10(NP_077744.4):p.(Cys354Valfs*25)	Franklin_LikelyPathogenic	None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41224645T>C	NC_000003.12(NM_001904.4):c.1133T>C	NC_000003.12(NP_001895.1):p.(Ser45Pro)	None			
CO	None				None					None					None		None				None				
CP	None				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
CQ	None				None					None					None		None				None				
CR	None				None					None					None		None				None				
CS	None				None					None					None		Exon 3 545del (Stabilising)	NC_000003.12:g.41224645_41224647del	NC_000003.12(NM_001904.4):c.133_135del	NC_000003.12(NP_001895.1):p.(Ser45del)	None			
CT	None				None					None					No data		None				None				
CU	None				None					None					None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41234207T>G	NC_000003.12(NM_001904.4):c.1163T>G	NC_000003.12(NP_001895.1):p.(Asn387Tyr)	None			
CV	None				None					None					None		None				None				
CW	None				No data					No data					No data		No data				No data				
CX	None (not checked in research)				None					None					None		None				None				
CY	None (not checked in research)				None					None					None		None				None				
CZ	None (not checked in research)				None					None					ChrLOH	NC_000011.10:g.[:]47480774-47709624](3C)+LOH	None				None				
DA	None (not checked in research)				No data					No data					No data		No data				No data				
DB	None (not checked in research)				None					None					None		None				None				
DC	None (not checked in research)				No data					No data					No data		No data				No data				
DD	None (not checked in research)				None					None					None		None				None				
DE	None (not checked in research)				No data					No data					No data		No data				No data				
DF	Truncating/Deletion	NC_000011.10:g.32399916_32405112del	NC_000011.10(NM_024426.6):c.1017-5068_1113+32del	NC_000011.10(NP_077744.4):p.(Asn339Lysfs*6)	Truncating/Deletion	NC_000011.10:g.32348526_35522440del		NC_000011.10(NM_001001991.3):c.73+3073_*30383806del	NC_000011.10(NP_001001991.1):p.(Glu25Aspfs*3e30)	Franklin_Pathogenic	None				None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41233420T>A	NC_000003.12(NM_001904.4):c.1167+A	NC_000003.12(NP_001895.1):p.(Asn387Tyr)	None			
DG	None (not checked in research)				Missense	NC_000011.10:g.32392014C>A		NC_000011.10(NM_024426.6):c.1405G>T	NC_000011.10(NP_077744.4):p.(Asp469Tyr)	ClinVar_Pathogenic	None				ChrLOH	NC_000011.10:g.[:]32519852-32613646](3C)N-LOH	None				None				
DH	None (not checked in research)				Truncating/Deletion (VUS)	NC_000011.10:g.32389113_32389114dup		NC_000011.10(NM_024426.6):c.1514_1515dup	NC_000011.10(NP_077744.4):p.(His507Profs*8e96)	Franklin_VUS	Truncating/Deletion	NC_000011.10:g.[32396367C>T;32396372_32396378del]		NC_000011.10(NM_024426.6):c.[1154G>A;1144_1150del]	NC_000011.10(NP_077744.4):p.[Arg385Gln;Thr382Tyrfs*3]	Franklin_LikelyPathogenic	None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41224646C>T	NC_000003.12(NM_001904.4):c.1234C>T	NC_000003.12(NP_001895.1):p.(Ser412Phe)	None			
DI	None (not checked in research)				No data					No data					No data		No data				No data				
DJ	None (not checked in research)				No data					No data					No data		No data				No data				
DK	None (not checked in research)				No data					No data					No data		No data				No data				
DL	None				None					None					Gain	NC_000011.10:g.[:]41131081-41424231]Gain	None				None				
DM	None (not checked in research)				None					None					None		None				None				
DN	None (not checked in research)				No data					No data					No data		No data				No data				
DO	None (not checked in research)				No data					No data					No data		No data				No data				
DP	None				Truncating/Deletion	NC_000011.10:g.31974353_32544075del		whole gene deletion		NC_000011.10(NP_077744.4):p.0?	Franklin_Pathogenic	Truncating/Deletion	NC_000011.10:g.29583148_33274783del		whole gene deletion	NC_000011.10(NP_077744.4):p.0	Franklin_Pathogenic	None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41224646C>T	NC_000003.12(NM_001904.4):c.1234C>T	NC_000003.12(NP_001895.1):p.(Ser412Phe)	None			
DQ	None (not checked in research)				No data					No data					No data		No data				No data				
DR	None (not checked in research)				No data					No data					No data		No data				No data				
DS	None (not checked in research)				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
DT	None (not checked in research)				None					None					None		None				None				
DU	None (not checked in research)				No data					No data					No data		No data				No data				
DV	None				Truncating/Deletion (VUS)	NC_000011.10:g.32428603_32428607dup		NC_000011.10(NM_024426.6):c.675_679dup	NC_000011.10(NP_077744.4):p.(Pro227Serfs*6e56)	Franklin_VUS	Truncating/Deletion	NC_000011.10:g.[31161405_32652492]del (Breakpoints not found in exome, both coordinates estimated based on DNAm CNV plots)	whole gene deletion		NC_000011.10(NP_077744.4):p.0	Franklin_Pathogenic	None		Exon 3 545del (Stabilising)	NC_000003.12:g.41224645_41224647del	NC_000003.12(NM_001904.4):c.133_135del	NC_000003.12(NP_001895.1):p.(Ser45del)	None			
DW	None (not checked in research)				No data					No data					No data		No data				No data				
DX	Not tested				None					None					None		None				None				
DY	None (not checked in research)				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
DZ	None (not checked in research)				No data					No data					No data		No data				No data				
EB	None (not checked in research)				None					None					None		None				None				
EC	None (not checked in research)				No data					No data					No data		No data				No data				
ED	Not tested				No data					No data					No data		No data				No data				
EE	None (not checked in research)				None					None					None		None				None				
EF	None (not checked in research)				None					None					None		None				None				
EG	None				None					None					ChrLOH (Other biomaterial)	NC_000011.10:g.[:]46609425-46747413](3C)+LOH_otherBiomaterial	None				None				
EH	None (not checked in research)				Truncating/Deletion	NC_000011.10:g.32428582G>T		NC_000011.10(NM_024426.6):c.699C>A	NC_000011.10(NP_077744.4):p.(Tyr233Ter)	ClinVar_LikelyPathogenic	Truncating/Deletion	NC_000011.10:g.32428616dup		NC_000011.10(NM_024426.6):c.665dup	NC_000011.10(NP_077744.4):p.(Tyr222Ter)	Franklin_LikelyPathogenic	None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41224646C>T	NC_000003.12(NM_001904.4):c.1234C>T	NC_000003.12(NP_001895.1):p.(Ser412Phe)	None			
EI	None (not checked in research)				No data					No data					No data		No data				No data				
EJ	None (not checked in research)				No data					No data					No data		No data				No data				
EK	None (not checked in research)				No data					No data					No data		No data				No data				
EL	None (not checked in research)				No data					No data					No data		No data				No data				
EM	None (not checked in research)				No data					No data					No data		No data				No data				
EN	None (not checked in research)				No data					No data					No data		No data				No data				
EO	None (not checked in research)				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
EP	None (not checked in research)				No data					No data					No data		No data				No data				
EQ	None (not checked in research)				No data					No data					No data		No data				No data				
ER	None (not checked in research)				No data					No data					No data		No data				No data				
ES	None				None					None					None		None				None				
ET	None (not checked in research)				No data					No data					No data		No data				No data				
EU	None (not checked in research)				No data					No data					No data		No data				No data				
EV	None (not checked in research)				No data					No data					No data		No data				No data				
EW	None (not checked in research)				None					None					None		None				None				
EX	None (not checked in research)				No data					No data					No data		No data				No data				
EY	None (not checked in research)				No data					No data					No data		No data				No data				
EZ	None (not checked in research)				None					None					None		None				None				
FA	None (not checked in research)				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
FB	Truncating/Deletion	NC_000011.10:g.32396307_32396308del	NC_000011.10(NM_024426.6):c.1213_1214del	NC_000011.10(NP_077744.4):p.(Lys405Glufs*64)	None					None					ChrLOH	NC_000011.10:g.[:]47122757-47276652](3C)+LOH	Partial deletion exon 3 (VUS)	NC_000003.12:g.41222965_41224646del	NC_000003.12(NM_001904.4):c.48-1052_1546del	NC_000003.12(NP_001895.1):p.?				
FC	None (not checked in research)				No SNVs (WXS)					No SNVs (WXS)					None		No SNVs (WXS)				No SNVs (WXS)				
FD	None				None					None					ChrLOH	NC_000011.10:g.[:]34910570-35118841](3C)+LOH	Exon 3 545del (Stabilising; other biomaterial)	NC_000003.12:g.41224645_41224647del	NC_000003.12(NM_001904.4):c.133_135del	NC_000003.12(NP_001895.1):p.(Ser45del)	Exon 3 Missense (Stabilising; other biomaterial)	NC_000003.12:g.41216645T>C	NC_000003.12(NM_001904.4):c.1337>C	NC_000003.12(NP_001895.1):p.(Ser446Pro)
FE	None				None					None					None		None				None				
FF	None				None					None					No data		No data				None				
FH	None				None					None					ChrLOH	NC_000011.10:g.[:]33087622]N-LOH	None				None				
FI	None				None					None					ChrLOH	NC_000011.10:g.[:]111578-32758357](7S)T08AFratio11p	None				None				
FL	None				None					None					ChrLOH	NC_000011.10:g.[:]33087622]N-LOH	None				None				
FK	Splice	NC_000011.10:g.32416401C>T	NC_000011.10(NM_024426.6):c.1016+8G>A	NC_000011.10(NP_077744.4):p.(?)	None					None					ChrLOH	NC_000011.10:g.[:]47949541-48269911](3C)+LOH	Exon 3 Missense (Stabilising)	NC_000003.12:g.41233408G>T	NC_000003.12(NM_001904.4):c.1149G>T	NC_000003.12(NP_001895.1):p.(Trp383Cys)	None			
FL	None				None					None					ChrLOH	NC_000011.10:g.[:]47073950-48478849](3C)+LOH	Exon 3 Missense (Stabilising; other biomaterial)	NC_000003.12:g.41227275A>T	NC_000003.12(NM_001904.4):c.1004A>T	NC_000003.12(NP_001895.1):p.(Lys335Ile)	None			
FM	None				None					None					None		None				None				
FN	None (not checked in research)				No data					No data					No data		No data				No data				
FP	None				None					None					None		Exon 3 Missense (Stabilising; other biomaterial)	NC_000003.12:g.41224660G>T	NC_000003.12(NM_001904.4):c.940>T	NC_000003.12(NP_001895.1):p.(Asp314Tyr)	None			
FQ	None				None					None					None		None				None				
FR	None				Truncating/Deletion	NC_000011.10:g.32399985dup		NC_000011.10(NM_024426.6):c.1076dup	NC_000011.10(NP_077744.4):p.(Tyr359Ter)	Franklin_LikelyPathogenic	SV_VUS	NC_000011.10:g.32396197_32396461dup		NC_000011.10(NM_024426.6):c.1114-54_1264+606dup	NC_000011.10(NP_077744.4):p.?	Franklin_VUS	None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41233408G>T	NC_000003.12(NM_001904.4):c.1149G>T	NC_000003.12(NP_001895.1):p.(Trp383Cys)	None			
FS	None				Missense (VUS)	NC_000011.10:g.32389120C>T		NC_000011.10(NM_024426.6):c.1507G>A	NC_000011.10(NP_077744.4):p.(Gly503Ser)	Franklin_VUS	None				None		None				None				
FT	None				None					None					ChrLOH	NC_000011.10:g.[:]50738669-50928105](3B)T08AFratio11p	None				None				
FU	None				None					None					ChrLOH	NC_000011.10:g.[:]33087622]p70CNLOHNo data	None				None				
FV	None				None					None					None		None				None				
FW	None				None					None					None		None				None				
FX	None				Complex	Multiple rearrangements between chr 11, affecting both alleles		Complex		Complex					Complex		None		Exon 3 Missense (Stabilising)	NC_000003.12:g.41216645C>T	NC_000003.12(NM_001904.4):c.1134C>T	NC_000003.12(NP_001895.1):p.(Ser446Phe)	None			
FY	Truncating/Deletion	NC_000011.10:g.32429516_32435759del	NC_000011.10(NM_024426.6):c.-410_662-897del	NC_000011.10(NP_077744.4):p.?	None					None					ChrLOH	NC_000011.10:g.[:]33305527-33332790](3C)N-LOH	None				None				
GC	None				None					None					LOH	NC_000011.10:g.[:]33087622]LOH	None				None				
GE	None				None					None					LOH	NC_000011.10:g.[:]48377745-48477764](3C)H	None				None				

Legend: WGS: whole genome sequencing; WES: whole exome sequencing; Ch-LOH: copy neutral loss-of-heterozygosity; *WGS revealed a localised drop in read coverage across the WT1 locus on chr11. Discordant and split reads support rearrangements between chr11:(~32.419 MB) and regions on chr8 (~26 Mb and ~56 Mb), consistent with a structural rearrangement involving this locus. Paired-end reads spanning the interval with an insert size of ~956 bp were observed, indicating that at least one allele remains structurally intact. RNA-seq analysis shows preserved expression of WT1, further supporting the presence of a functional allele. Together, these findings are consistent with a likely monoallelic rearrangement affecting the chr11 locus.