

eTable 1. Clinical and Genetic Features of Discovery Cohort

PCGP ID	Gender	Ethnicity	Stage	Age at Diagnosis (Years)	Event-free Survival (Years)	Overall Survival (Years)	Relapse yes/no	Survival Status	¹ ATRX (WGS)	² ATRX (IHC)
SJNBL001_D-SK-T205	Male	White Non Hispanic	4	7.0	1.0	1.4	Yes	Dead		Positive
SJNBL002_D-SK-T216	Female	White Non Hispanic	4	2.3	1.1	2.6	Yes	Alive	Exon 6-12 deletion	Mosaic
SJNBL003_D-SK-T221	Female	Black Non Hispanic	4	13.0	5.4	5.6	Yes	Alive	A1690D	Mosaic
SJNBL007_D-SK-T229	Male	White Non Hispanic	4s, then 4	0.1	0.8	2.6	Yes	Dead		n.d.
SJNBL008_D-SK-T232	Male	White Hispanic	4	3.1	1.5	2.2	Yes	Dead		Positive
SJNBL009_D-SK-T237	Male	Black Non Hispanic	4	3.6	5.9	5.9	No	Alive	L407F	n.d.
SJNBL010_D-SK-T238	Male	White Non Hispanic	4	3.0	6.8	6.8	No	Alive		Positive
SJNBL011_D-SK-T241	Male	White Non Hispanic	4	4.4	1.0	1.7	Yes	Dead		Positive
SJNBL012_D-SK-T244	Male	White Non-Hispanic	4	1.8	7.4	7.4	No	Alive		Positive
SJNBL013_D-SK-T247	Female	White Non Hispanic	4	0.7	12.4	12.4	No	Alive		n.d.
SJNBL014_D-SK-T256	Female	Black Non Hispanic	4	5.2	1.4	1.4	Yes	Dead		Positive
SJNBL015_D-SK-T260	Male	White Non Hispanic	4	9.7	3.0	5.2	Yes	Alive		Mosaic
SJNBL016_D-SK-T264	Female	Unknown	4	3.3	1.5	3.5	Yes	Alive		Positive
SJNBL017_D-SK-T270	Male	White Non Hispanic	4	3.6	2.3	3.5	Yes	Dead		n.d.
SJNBL018_D-SK-T278	Male	White Non Hispanic	4	4.2	1.2	3.1	Yes	Alive		n.d.
SJNBL019_D-SK-T279	Male	White Non Hispanic	4	0.7	1.4	3.0	Yes	Alive		Positive
SJNBL020_D-SK-T280	Male	White Non Hispanic	4	0.8	24.1	24.1	No	Alive		n.d.
SJNBL021_D-SK-T290	Female	White Non Hispanic	4	11.8	5.1	5.3	No	Alive		Positive
SJNBL022_D-SK-T291	Female	White Non Hispanic	4	4.0	2.1	2.1	No	Dead		n.d.
SJNBL023_D-SK-T292	Male	White Non Hispanic	4	1.6	6.4	6.4	No	Alive		Positive
SJNBL024_D-SK-T294	Male	White Non Hispanic	4	3.9	4.8	9.9	No	Alive	Exon 2-10 deletion	Negative
SJNBL025_D-SK-T296	Male	White Non Hispanic	2B then 4	6.5	2.6	7.5	Yes	Dead	E555*	Negative
SJNBL026_D-SK-T301	Male	White Non Hispanic	4	0.2	8.0	8.0	No	Alive		n.d.
SJNBL027_D-SK-T304	Male	Black Non Hispanic	4	1.9	1.8	3.0	Yes	Dead		Positive
SJNBL029_D-SK-T315	Male	White Non Hispanic	4	6.5	1.1	1.7	Yes	Dead		Schwannian stroma only
SJNBL030_D-SK-T318	Male	White Non-Hispanic	4	2.4	0.3	0.3	No	Dead		Positive
SJNBL031_D-SK-T322	Male	Black Non Hispanic	4	29.2	2.6	5.5	Yes	Dead	R2188Q	Negative
SJNBL032_D-SK-T325	Male	Black Hispanic	4	26.9	2.0	2.4	Yes	Alive	Exon 3-9 deletion	Negative

SJNBL033_D-SK-T329	Male	White Non Hispanic	4	3.8	0.9	1.4	Yes	Dead		Positive
SJNBL034_D-SK-T332	Female	White Non-Hispanic	4	5.6	0.7	1.1	Yes	Dead		Positive
SJNBL035_D-SK-T335	Male	White Non Hispanic	4	4.6	3.2	6.8	Yes	Dead		Positive
SJNBL036_D-SK-T341	Female	White Non Hispanic	4	0.9	4.2	4.2	No	Alive		Positive
SJNBL037_D-SK-T342	Female	White Non Hispanic	4	9.0	7.8	9.5	Yes	Dead		n.d.
SJNBL038_D-SK-T343	Female	White Non Hispanic	4	4.1	1.7	3.3	Yes	Dead	Exon 2-10 deletion	n.d.
SJNBL039_D-SK-T350	Male	Asian/Far East/Indian Subcontinent	4	25.1	1.0	3.8	Yes	Dead	K425_E426fs	Negative
SJNBL040_D-SK-T351	Female	White Non Hispanic	4	4.2	1.3	3.0	Yes	Alive		Positive
SJNBL041_D-SK-T354	Male	White Non Hispanic	4	13.3	1.2	4.0	Yes	Dead	Exon 2-10 deletion	Negative
SJNBL042_D-SK-T357	Female	White Non Hispanic	4	3.2	1.1	2.2	Yes	Dead		n.d.
SJNBL044_D-SK-T364	Female	Black Non Hispanic	4	6.1	0.7	1.7	Yes	Dead		n.d.
SJNBL045_D-SK-T369	Male	White Non Hispanic	4	2.9	1.9	6.8	Yes	Alive		Positive

¹ All ATRX lesions were validated by PCR and Sanger sequencing.

² IHC was performed on FFPE sections from the tumors that were used for sequence analysis. Mosaic samples had some nuclear ATRX and some tumor cells lacking ATRX nuclear stain. Positive samples retained nuclear ATRX and negative samples lost ATRX nuclear stain.

³ Telomere length was estimated for the tumor sample and compared to the matched normal sample. The criteria for longer telomeres was the (Tumor-Germline/Germline) value >0.05. WGS data was validated using telomere qPCR.

⁴ FISH results for telomeres were scored as abnormal if they showed evidence of large ultrabright signal characteristic of ALT.

⁵ qPCR telomere length was performed on tumor and matched normal whole genome amplified DNA. The criteria for longer telomeres was the (Tumor-Germline/Germline) value >0.05.

⁶ The copy numbers for MYCN were estimated from the WGS data. For samples with > 10 copies of MYCN from this analysis, the number of genes in the amplicon is specified as well as the copy number. For samples with ≤ 10 copies of MYCN, we analyzed the size of the amplified region as focal (≤ 5 genes), large segment (> 5 genes) or chromosomal (whole chromosome 2 gain).

⁷ MYCN amplification information was extracted from the clinical database and confirmed by pPCR. MYCN copy numbers > 10 was defined as amplified.

⁸ Tumor purity by WGS was estimated using CNV, deletion and allelic imbalance in LOH which may be an underestimate if CNV/LOH is subclonal. Purity for SJNBL022 was listed N/A because it does not have any CNV or LOH.

eTable 1. Clinical and Genetic Features of Discovery Cohort (cont.)

PCGP ID	³ Telomere (WGS)	⁴ Telomere (FISH)	⁵ Telomere (qPCR)	MYCN Copy (WGS) ⁶	MYCN Amplification (>10 copies by qPCR) ⁷	ALK	11q	1p	17q	X	⁸ Purity (WGS)	Purity (pathology)
SJNBL001_D-SK-T205	LONG	Abnormal (mosaic)	LONG	Unchanged	NO	NO	Loss	No change	Gain		78%	70-90%
SJNBL002_D-SK-T216	LONG	Abnormal (mosaic)	LONG	Unchanged	NO	NO	Loss	No change	Gain		81%	65%
SJNBL003_D-SK-T221	LONG	Abnormal (mosaic)	LONG	+1 copy, whole chromosome 2	NO	NO	Gain, whole chr11	No change/Weak gain	Gain	1 copy loss	91%	90%
SJNBL007_D-SK-T229	LONG	n.d.	n.d.	+1 copy, large segment +150 copies, 2 genes	NO	NO	No change	Loss	Gain		94%	85-90%
SJNBL008_D-SK-T232	SHORT	Normal	n.d.	+0.5 copy, large segment	Amplified	F1174L	No change	Loss	Gain		81%	85%
SJNBL009_D-SK-T237	SHORT	n.d.	SHORT	+65 copies, 2 genes	NO	NO	Loss	Loss	Gain		82%	70-75%
SJNBL010_D-SK-T238	SHORT	Normal	n.d.	+1 copy, large segment +160 copies, 2 genes	Amplified	NO	No change	Loss	Gain		83%	90%
SJNBL011_D-SK-T241	SHORT	Normal	n.d.	Unchanged	NO	NO	Loss	Loss	Gain		82%	60%
SJNBL012_D-SK-T244	SHORT	Normal	n.d.	+0.5 copy, large segment +3 copy, large segment +290 copies, 2 genes	Amplified	NO	No change	Loss	Gain		96%	85-90%
SJNBL013_D-SK-T247	LONG	n.d.	n.d.	Unchanged	NO	NO	Loss	No change	Gain		89%	95%
SJNBL014_D-SK-T256	SHORT	Normal	n.d.	+180 copies, 3 genes	Amplified	NO	Loss	No change	Gain	0.5 copy loss	81%	55-60%
SJNBL015_D-SK-T260	SHORT	Normal	n.d.	Unchanged	NO	NO	No change	No change	Gain		91%	85%
SJNBL016_D-SK-T264	SHORT	Normal	n.d.	+260 copies, 2 genes	Amplified	NO	No change	Loss	Gain		93%	80%
SJNBL017_D-SK-T270	LONG	n.d.	n.d.	Unchanged	NO	NO	Loss	Loss	Gain	0.5 copy gain	95%	65-70%
SJNBL018_D-SK-T278	SHORT	n.d.	n.d.	Unchanged	NO	NO	Loss	No change	Gain		82%	70%
SJNBL019_D-SK-T279	SHORT	Normal	n.d.	Unchanged	Amplified	NO	No change	Loss	Gain		97%	85%

SJNBL020_D-SK-T280	LONG	n.d.	n.d.	+1.5 copy, large segment	NO	F1174V	No change	Loss	Gain		93%	90%	
SJNBL021_D-SK-T290	LONG	Normal	n.d.	+7 copy, focal	NO	NO	No change	No change	No change		65%	50%	
SJNBL022_D-SK-T291	LONG	n.d.	LONG	Unchanged	NO	NO	No change	No change	No change		NA	90%	
SJNBL023_D-SK-T292	SHORT	Normal	n.d.	+50 copies, 2 genes	Amplified	NO	Loss	Loss	Gain		97%	80-85%	
SJNBL024_D-SK-T294	LONG	Abnormal	LONG	+1.5 copy, large segment	NO	NO	Loss	No change	Gain, whole chromosome 1	Gain	59%	50%	
SJNBL025_D-SK-T296	LONG	Abnormal (mosaic)	LONG	Unchanged	NO	NO	No change	No change	Gain, whole chromosome 1	Gain	85%	75-80%	
SJNBL026_D-SK-T301	LONG	n.d.	n.d.	+1 copy, whole chromosome 2	NO	NO	No change	No change	Gain, whole chromosome 1	Gain	79%	85%	
SJNBL027_D-SK-T304	SHORT	Normal	n.d.	+300 copies, 4 genes	Amplified	F1174L	No change	Loss	Gain	No change	95%	60%	
SJNBL029_D-SK-T315	LONG	Normal	n.d.	Unchanged	NO	NO	No change	No change	No change		89%	70%	
SJNBL030_D-SK-T318	SHORT	Normal	SHORT	+65 copies, 2 genes	Amplified	F1174L	No change	Loss	Gain		89%	65%	
SJNBL031_D-SK-T322	LONG	Abnormal	LONG	+0.5 copy, focal	NO	NO	No change	No change	Gain		80%	70-75%	
SJNBL032_D-SK-T325	LONG	Abnormal	LONG	+1 copy, whole chromosome 2	NO	NO	Loss	No change	Gain		68%	65%	
SJNBL033_D-SK-T329	SHORT	Normal	n.d.	+320 copies, 2 genes	Amplified	NO	No change	Loss	Gain	No change	96%	>90%	
SJNBL034_D-SK-T332	SHORT	Normal	n.d.	Unchanged	NO	NO	No change	Loss	Gain		83%	75-90%	
SJNBL035_D-SK-T335	SHORT	Normal	n.d.	Unchanged	NO	NO	Loss	Loss	Gain		81%	>95%	
SJNBL036_D-SK-T341	LONG	Normal	n.d.	+1.5 copy, focal	NO	NO	Loss	No change	Gain		52%	60%	
SJNBL037_D-SK-T342	LONG	n.d.	n.d.	+1 copy, whole chromosome 2	NO	NO	Gain, whole chr11	No change	Gain, whole chromosome 1	Gain	0.35 copy gain	87%	75-80%
SJNBL038_D-SK-T343	LONG	n.d.	LONG	Unchanged	NO	NO	Loss	No change	Gain		87%	85%	

SJNBL039_D-SK-T350	LONG	Abnormal (mosaic)	LONG	+2 copy, focal	NO	NO	Loss	Gain, whole chromosome 1	Gain		73%	65%
SJNBL040_D-SK-T351	SHORT	Normal		+0.5 copy, large segment	NO	NO	No change	No change/Weak loss	Gain	0.5 copy loss	47%	80%
SJNBL041_D-SK-T354	SHORT	Abnormal	LONG	Unchanged	NO	NO	Loss	Loss	Gain		74%	55-60%
SJNBL042_D-SK-T357	SHORT	n.d.	n.d.	Unchanged	NO	L1196M	Loss	No change	Gain		91%	90%
SJNBL044_D-SK-T364	LONG	n.d.	LONG	+80 copies, 4 genes	Amplified	R1275Q	Gain, whole chr11	No change	Gain	0.5 copy loss	48%	60%
SJNBL045_D-SK-T369	SHORT	Normal	n.d.	+1 copy, whole chromosome 2	NO	NO	Loss	No change	Gain		72%	80%

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² IHC was performed on FFPE sections from the tumors that were used for sequence analysis. Mosaic samples had some nuclear ATRX and some tumor cells lacking ATRX nuclear stain. Positive samples retained nuclear ATRX and negative samples lost ATRX nuclear stain.

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eTable 2. Clinical and Genetic Features of Validation Cohort

Sample #	Gender	Ethnicity	Stage	Age at Diagnosis (Years)	Event-Free Survival (Years)	Overall Survival (Years)	Relapse yes/no	Survival Status	ATRX	ALK	MYCN Amplification (>10 copies by qPCR)
D-SK-T204	Male	Black/ African American	4	1.2	3.9	3.9	no	alive		NO	NO
D-SK-T206	Male	Unknown	4	21.0	0.5	2.2	yes	Dead		NO	NO
D-SK-T209	Male	White Non Hispanic	4	0.5	0.2	0.2	yes	Dead		NO	YES
D-SK-T213	Female	White Non Hispanic	4	14.8	1.9	1.9	yes	Dead		NO	NO
D-SK-T217	Female	White Non Hispanic	4	17.1	13.8	13.8	no	alive		NO	NO
D-SK-T220	Female	White Non Hispanic	4	31.7	0.7	1.0	yes	Dead		NO	NO
D-SK-T222	Female	Asian/Far East/India	4	1.7	7.7	7.7	no	alive		NO	YES
D-SK-T228	Female	Black Non Hispanic	4	0.4	18.1	18.1	no	alive		NO	NO
D-SK-T235	Female	White Non Hispanic	4	10.5	0.5	0.9	yes	Dead		NO	NO
D-SK-T252	Female	White Non Hispanic	4	1.1	1.5	2.0	yes	Dead		NO	YES
D-SK-T261	Male	White Non Hispanic	4	8.9	13.7	13.7	no	alive		NO	YES
D-SK-T271	Female	Black/ African American	4	23.6	4.6	9.8	yes	Dead		NO	NO
D-SK-T276	Female	Unknown	4	10.8	0.6	0.6	yes	Dead	Exon 2-10 deletion	NO	NO
D-SK-T277	Male	Unknown	4	1.4	0.7	0.8	yes	Dead		NO	YES
D-SK-T289	Female	White Non Hispanic	4	10.1	1.0	2.8	yes	Dead		NO	NO
D-SK-T297	Female	Asian/Far East/India	4	1.6	10.6	10.6	no	alive		NO	NO
D-SK-T298	Female	White Non Hispanic	4	24.5	2.7	5.9	yes	alive	Y2083C	F1174L	NO
D-SK-T300	Male	White Hispanic	4	18.4	3.2	4.5	yes	Dead	Q2183L	F1245L	NO
D-SK-T305	Male	Black/ African American	4	13.9	0.9	1.6	yes	Dead		NO	NO
D-SK-T306	Male	White Non Hispanic	4	1.0	0.6	1.1	yes	Dead		NO	YES
D-SK-T307	Female	White Non Hispanic	4	7.5	2.6	4.2	yes	Dead		NO	NO
D-SK-T316	Female	White Non Hispanic	4	0.5	12.7	12.7	no	alive		NO	YES
D-SK-T319	Male	White Non Hispanic	4	7.4	18.5	18.5	no	alive		NO	NO
D-SK-T338	Male	White Non Hispanic	4	1.3	1.1	7.6	yes	alive		NO	YES
D-SK-T344	Male	White Non Hispanic	4	0.3	1.8	10.9	yes	alive		NO	YES
D-SK-T356	Female	White Non Hispanic	4	10.8	1.4	1.9	yes	Dead	K1701fs	NO	NO
D-SK-T363	Female	Unknown	4	8.0	1.0	1.0	yes	Dead		NO	NO
D-SK-T370	Female	White Non Hispanic	4	1.4	5.1	5.1	no	alive		NO	YES
D-SK-T505	Female	White Non Hispanic	4	14.4	0.6	0.6	no	alive		R1275Q	NO
D-SK-T508	Male	White Non Hispanic	4	13.8	1.0	3.4	yes	Dead	Exon 2-10 deletion	NO	NO
D-SK-T509	Female	White Non Hispanic	4	7.0	5.0	7.6	yes	Dead		NO	NO

D-SK-T542	Male	White Non Hispanic	4	41.9	1.7	2.6	yes	Dead		NO	NO
D-SK-T553	Male	White Non Hispanic	4	20.7	0.8	4.0	yes	alive	Exon 2-10 deletion	NO	NO
D-SK-T577	Male	White Non Hispanic	4	18.0	4.7	8.6	yes	Dead		NO	NO
D-SK-T583	Male	Other	4	5.7	2.0	7.2	yes	alive		NO	NO
D-SK-T586	Female	Unknown	4	14.6	7.2	14.5	yes	alive		NO	NO
D-SK-T588	Male	Unknown	4	7.4	1.8	2.9	yes	Dead		NO	NO
D-SK-T624	Female	White Non Hispanic	4	31.6	1.7	3.0	yes	Dead		R1275Q	NO
D-SK-T626	Male	White Non Hispanic	4	20.5	1.4	5.2	yes	alive		NO	NO
D-SK-T639	Female	White Non Hispanic	4	19.5	1.7	3.9	yes	Dead		NO	NO
D-SK-T659	Female	White Non Hispanic	4	1.0	10.5	10.6	yes	Dead		NO	NO
D-SK-T670	Male	Unknown	4	12.9	1.3	1.7	yes	Dead	Exon 2-10 deletion	R1275L	NO
D-SK-T672	Female	White Non Hispanic	4	7.4	1.2	7.4	yes	alive		NO	NO
D-SK-T679	Female	White Non Hispanic	4	11.6	9.5	9.5	no	alive	P2292fs	NO	NO
D-SK-T680	Female	White Non Hispanic	4	10.5	0.8	1.6	yes	Dead		NO	NO
D-SK-T683	Male	White Non Hispanic	4	12.7	1.0	3.9	yes	Dead	Exon 2-10 deletion	NO	NO
D-SK-T686	Male	White Non Hispanic	4	8.0	2.3	3.1	yes	Dead		NO	NO
D-SK-T701	Female	Black/ African American	4	10.8	4.5	4.5	yes	Dead		NO	NO
D-SK-T715	Male	White Non Hispanic	4	8.4	5.4	5.4	no	alive		NO	NO
D-SK-T727	Male	White Non Hispanic	4	14.6	0.7	0.7	no	alive		R1275Q	YES
D-SK-T814	Male	White Non Hispanic	4	6.8	4.0	11.7	yes	alive		NO	NO
D-SK-T815	Male	White Non Hispanic	4	7.8	0.3	0.6	yes	Dead		NO	YES
D-SK-T820	Male	Black/ African American	4	13.9	0.4	1.9	yes	Dead		F1174L	NO
D-SK-T823	Female	White Non Hispanic	4	21.2	3.6	5.4	yes	Dead	Exon 2-10 deletion	NO	NO
D-SK-T827	Female	White Non Hispanic	4	18.2	11.0	14.5	yes	Dead	Exon 2-10 deletion	F1245C	NO
D-SK-T839	Female	White Non Hispanic	4	13.9	0.9	1.1	yes	Dead		NO	NO
D-SK-T846	Male	Black/ African American	4	5.1	3.6	8.2	yes	Dead	Exon 3-12 deletion	NO	NO
D-SK-T860	Female	Black/ African American	4	7.1	7.2	16.3	yes	alive		NO	NO
D-SK-T866	Male	White Non Hispanic	4	4.6	3.1	7.7	yes	Dead		NO	NO
D-SK-T895	Female	Black/ African American	4	8.6	1.3	3.0	yes	alive		NO	NO
D-SK-T1098	Male	Unknown	4	21.0	0.0	0.0	yes	Dead		NO	NO
D-SK-T1113	Male	White Non Hispanic	4	1.3	0.7	2.2	yes	alive		NO	YES
D-SK-T1114	Female	Unknown	3	24.5	1.9	1.9	no	alive	E23_splice variant	NO	NO
D-SK-T1115	Male	White Non Hispanic	4	28.7	1.6	6.2	yes	alive		F1174C	NO