

Figure S1. Immunohistochemistry demonstrated negative staining for (A) P53, (B) EMA, (C) GFAP, and (D) Vimentin in atypical choroid plexus papilloma tumor (all magnifications, x4).

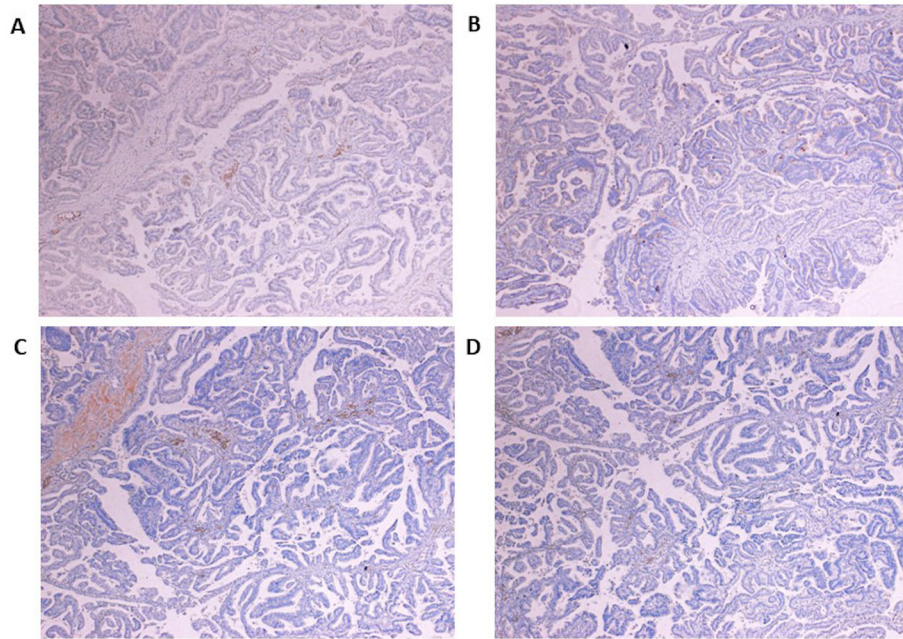


Figure S2. Immunohistochemistry demonstrated negative staining for (A) epidermal growth factor receptor, (B) thyroid transcription factor 1 and (C) CK-7, in atypical choroid plexus papilloma tumor (all x4 magnification).

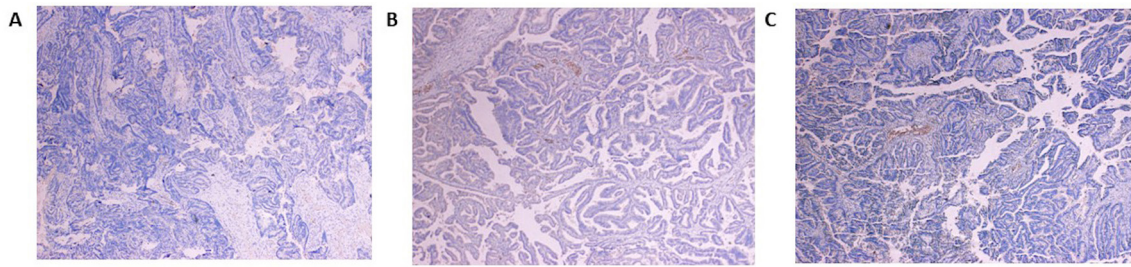


Figure S3. Positive control staining for antibodies. Known positive control tissues were stained with antibodies for (A) P53 (x40 magnification), (B) EMA (x20 magnification), (C) GFAP (x40 magnification), (D) vimentin (x20 magnification), (E) EGFR (x20 magnification), (F) TTF1 (x20 magnification) and (G) CK7 (x20 magnification).

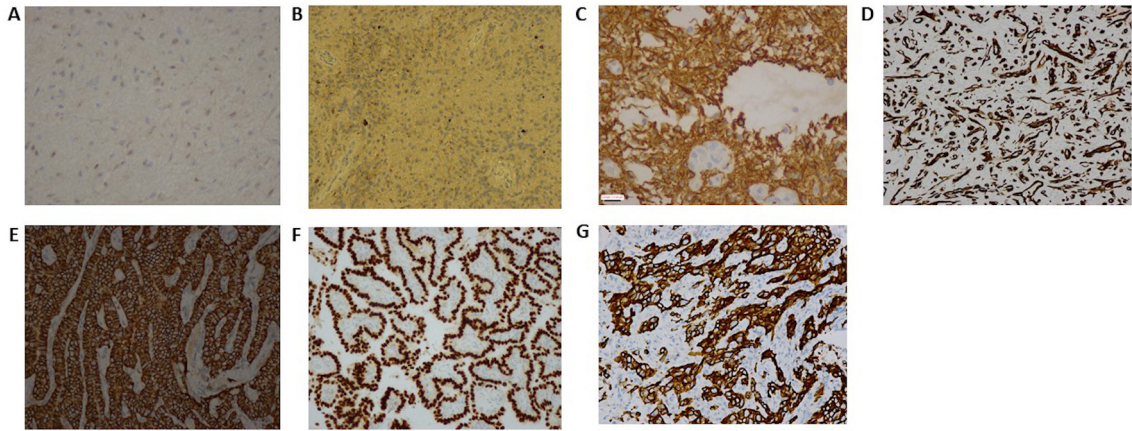


Table SI. Sequencing coverage analysis report from Torrent Suite software.

Target base coverage		Amplicon read coverage	
Variable	Value	Variable	Value
Bases in target regions	1,688,650	Number of amplicons	15,992
Percent base reads on target	83.18%	Percent assigned amplicon reads	82.30%
Average base coverage depth	459.4	Average reads per amplicon	466.5
Uniformity of base coverage	85.58%	Uniformity of amplicon coverage	85.61%
Target base coverage at 1x	99.66%	Amplicons with at least 1 read	99.74%
Target base coverage at 20x	96.55%	Amplicons with at least 20 reads	99.59%
Target base coverage at 100x	84.35%	Amplicons with at least 100 reads	84.62%
Target base coverage at 500x	32.99%	Amplicons with at least 500 reads	34.39%
Target bases with no strand bias	95.63%	Amplicons with no strand bias	96.20%
Percent end-to-end reads	92.13%	Amplicons reading end-to-end	93.10%

Table SII. Quality statistics of Novel Exonic Variants found in an atypical choroid plexus papilloma patient.

Genes	Coding	Allele coverage	Allele ratio	PolyPhen	P-value	Coverage (x)
<i>NOTCH1</i>	c.4214C>A	G=44, T=8	G=0.8462, T=0.1538	0.429	0.00002	52
<i>ATM</i>	c.5808A>T	A=1930, T=69	A=0.9655, T=0.0345	0.097	0.00407	1999
<i>STK36</i>	c.2439A>T	A=18, T=6	A=0.75, T=0.25	0.076	0.00021	24
<i>MAGI1</i>	c.2026A>G	T=439, C=109	T=0.8011, C=0.1989	0.06	0.00001	548
<i>DST</i>	c.15347A>T	T=144, A=58	T=0.7129, A=0.2871	0.999	0.00001	202
<i>RECQL4</i>	c.1412A>C	T=76, G=10	T=0.8837, G=0.1163	0.917	0.00003	86
<i>NUMA1</i>	c.4159C>G	G=97, C=10	G=0.9065, C=0.0935	0.979	0.00014	107
<i>THBS1</i>	c.2646G>T	G=10, T=50	G=0.1667, T=0.8333	1.0	0.00001	62
<i>MYH11</i>	c.1968G>A	C=40, T=5	C=0.8889, T=0.1111	0.983	0.00283	45
<i>MALT1</i>	c.1015T>G	T=231, G=12	T=0.9506, G=0.0494	0.007	0.00946	243
<i>CDH20</i>	c.2354G>A	G=243, A=30	G=0.8901, A=0.1099	0.006	0.00001	273
<i>SMARCA4</i>	c.2729C>T	C=266, T=2	C=0.9925, T=0.0075	0.99	0.00543	268

Table SIII. Quality statistics of Reported Exonic Variants found in an atypical choroid plexus papilloma patient.

Genes	Coding	Allele coverage	Allele ratio	PolyPhen	P-value	Coverage (x)
<i>ATM</i>	c.5948A>G	A=1, G=127	A=0.0078, G=0.9922	0.00	0.00001	128
<i>GATA2</i>	c.967C>T	G=5, A=60	G=0.0769, A=0.9231	0.933	0.00001	65
<i>FGFR3</i>	c.2044G>A	G=21, A=304	G=0.0646, A=0.9354	0.987	0.00001	325
<i>KDM5C</i>	c.3791C>T	G=173, A=14	G=0.9251, A=0.0749	0.958	0.00012	187
<i>ALK</i>	c.4381A>G	T=0, C=581	T=0.0, C=1.0	0.0	0.00001	581
<i>APC</i>	c.7858T>A	T=215, A=53	T=0.8022, A=0.1978	0.0	0.00001	268
<i>EGFR</i>	c.2506C>T	C=354, T=3	C=0.9916, T=0.0084	0.95	0.00172	357
<i>EGFR</i>	c.2551G>A	G=377, A=3	G=0.9921, A=0.0079	0.99	0.00094	380
<i>EGFR</i>	c.2569G>A	G=390, A=5	G=0.9873, A=0.0127	0.99	0.00632	395
<i>EGFR</i>	c.3263C>T	C=163, T=128	C=0.5601, T=0.4399	0.009	0.00001	291

Table SIV. Quality statistics of Novel INDELS Variants found in an atypical choroid plexus papilloma patient.

Genes	Coding	Allele coverage	Allele ratio	P-value	Coverage (x)
<i>NOTCH1</i>	c.4732_4734delGTG	GCACCACCACCA=1920, GCACCACCA=18, GCACCACCACCAC=0	GCACCACCACCA=0.9907, GCACCACCA=0.0093, GCACCACCACCAC=0.0	0.00001	1938
<i>PARP1</i>	c.1056_1057insG, c.1056_1057insA	G=0, GC=381, GT=332	G=0.0, GC=0.5344, GT=0.4656	0.00001	713
<i>MIR3163,</i> <i>SYNE1</i>	c.21904_21905insG	A=0, AC=225	A=0.0, AC=1.0	0.00001	225
<i>MET</i>	c.525T>A	T=889, A=80	T=0.9174, A=0.0826	0.00001	969
<i>RNF213</i>	c.6967C>T	C=423, T=62	C=0.8722, T=0.1278	0.00001	485

Table SV. Quality statistics of Novel Intronic Variants found in an atypical choroid plexus papilloma patient.

Genes	Coding	Allele coverage	Allele ratio	P-value	Coverage (x)
<i>ERBB4</i>	c.1946+18T>G	A=137, C=120	A=0.5331, C=0.4669	0.00001	257
<i>RET</i>	c.2392+32C>T	C=46, T=3	C=0.9388, T=0.0612	0.04513	49
<i>FGFR1</i>	c.2141+20T>G	A=133, C=9	A=0.9366, C=0.0634	0.0062	142
<i>FGFR3</i>	c.2169-32G>A	G=16, A=7	G=0.6957, A=0.3043	0.00003	23
<i>PMS1</i>	c.132+1G>C	G=1647, C=133	G=0.9253, C=0.0747	0.00001	1780
<i>PMS1</i>	c.700-41A>C	A=1219, C=101	A=0.9235, C=0.0765	0.00001	1320
<i>PAX3</i>	c.586+449GAG>G	CTC=372, C=27, CTA=0	CTC=0.9323, C=0.0677, CTA=0.0	0.00001	399
<i>SDHA</i>	c.896-88T>C	T=156, C=26	T=0.8571, C=0.1429	0.00001	182
<i>LIFR</i>	c.2065+47A>T	T=493, A=29	T=0.9444, A=0.0556	0.00319	522
<i>PDGFRB</i>	c.2698+45T>A	A=609, T=247	A=0.7114, T=0.2886	0.00001	856
<i>MAP3K7</i>	c.1524+39TTCT>T	AGAA=100, AA=0, A=32, AGAAA=0	AGAA=0.7576, AA=0.0, A=0.2424, AGAAA=0.0	0.00001	132
<i>PRKDC</i>	c.1448-52TG>GT	CA=894, AC=45	CA=0.9521, AC=0.0479	0.00002	939
<i>BRD3,</i> <i>LOC100130548</i>	c.-7C>T	G=17, A=4	G=0.8095, A=0.1905	0.0084	21
<i>WT1</i>	c.1644A>G	T=267, C=65	T=0.8042, C=0.1958	0.00001	332
<i>AKT2</i>	c.709-53G>T	C=135, A=12	C=0.9184, A=0.0816	0.00014	147
<i>SMARCB1</i>	c.986+30T>C	T=26, C=10	T=0.7222, C=0.2778	0.00001	36

Table SVI. Quality statistics of Novel Synonymous Variants found in atypical choroid plexus papilloma.

Genes	Coding	Allele coverage	Allele ratio	P-value	Coverage (x)
<i>PIK3CA</i>	c.3144T>C	T=1898, C=99	T=0.9504, C=0.0496	0.00001	1997
<i>FGFR3</i>	c.1953G>A	G=0, A=1997	G=0.0, A=1.0	0.00001	1997
<i>PDGFRA</i>	c.1701A>G	A=0, G=1996	A=0.0, G=1.0	0.00001	1996
<i>RET</i>	c.2307G>T	G=0, T=1994	G=0.0, T=1.0	0.00001	1994
<i>NOTCH2</i>	c.3963G>T	C=1232, A=48	C=0.9625, A=0.0375	0.00306	1280
<i>IGF2R</i>	c.6948G>A	G=22, A=122	G=0.1528, A=0.8472	0.00001	144
<i>ADGRA2</i>	c.2817C>G	C=89, G=136	C=0.3956, G=0.6044	0.00001	225
<i>PRKDC</i>	c.2319A>G	T=932, C=852	T=0.5224, C=0.4776	0.00001	1784
<i>PAX5</i>	c.42G>A	C=649, T=650	C=0.4996, T=0.5004	0.00001	1299
<i>TET1</i>	c.3900C>A	C=165, A=36	C=0.8209, A=0.1791	0.00001	201
<i>IDH2</i>	c.519C>T	G=249, A=16	G=0.9396, A=0.0604	0.00049	265