

**Supplemental Table 2. Histologic and molecular data for all the nodules tested.**

Case	Cytology	Nucleotide Mutations	Amino Acid Alteration	Additional mutations	Allelic frequency of <i>PTEN</i> mutation	Chromosomal Copy Number Alteration (CNA)	Gene expression alterations	Gene Fusions	Surgical pathology of <i>PTEN</i> nodule
1	AUS/FLUS	c.517_518insA	p.R173Qfs*7	N	22%	N	N	N	FA
2	AUS/FLUS	c.70G>C	p.D24H	N	10-30%	N	N	N	Oncocytic FA
3	AUS/FLUS	c.208delC	p.L70Ffs*29	N	23%	Y	N	N	Oncocytic FA
4	AUS/FLUS	c.388C>T	p.R130*	N	20%	N	N	N	-
5	AUS/FLUS	c.750delT	p.C250Wfs*6	<i>BRAF</i> (19%). BRAFp.K601N c.1803A>T19.0%	72%	Y	N	N	FA
6	AUS/FLUS	c.994A>T, c.504delT	p.K332*, p.S170Vfs*13	2 <i>PTEN</i> mutations	15%, 15%	N	N	N	FA
7	AUS/FLUS	c.302T>A	p.I101N	N	10%	N	N	N	-
8	AUS/FLUS	c.1027-1G>C, c.389G>T	p.?, p.R130L	2 <i>PTEN</i> mutations	4%, 5%	N	N	N	-
9	FN/SFN	c.663_667delG GTGA	p.V222Dfs*19	N	13%	N	N	N	-
10	AUS/FLUS	c.955dupA11	p.T319Nfs*6	N	11%	N	N	N	-
11	AUS/FLUS	c.A755T	p.D252V	N	25%	N	N	N	-
12	AUS/FLUS	c.74T>A, c.323T>G	p.L25* , p.L108R	2 <i>PTEN</i> mutations	33%	N	N	N	FA
13	AUS/FLUS	c.195C>G	p.Y65*	N	24%	N	N	N	-
14	AUS/FLUS	c.49C>T	p.Q17*	N, limited RNA analysis	30%	Y	Failed	Failed	FA
15	FN/SFN	c.955dupA	p.T319Nfs*6	N	34%	N	N	N	FA

16	AUS/FLUS	c.198_206dup GATATACAA	p.K66_Y68dup	N	12.00%	N	N	N	-
17	FN/SFN	c.518G>C	p.R173P	N	33%	N	N	N	FA
18	AUS/FLUS	c.974T>C, c.295G>T	p.L325P, p.E99*	2 <i>PTEN</i> mutations	7%, 5%	N	N	N	-
19	AUS/FLUS	c.974T>C, c.295G>T	p.L325P, p.E99*	2 <i>PTEN</i> mutations	3%, 2%	N	N	N	-
20	FN/SFN	c.368A>C	p.H123P	N	24%	N	N	N	FA
21	Not available	c.30_52del	p.S10Rfs*26	N	37%	Y	N	N	Not available
22	AUS/FLUS	c.190_191del	p.H64Lfs*9	N	12%	N	N	N	-
23	AUS/FLUS	c.209_209+1del	p.L70_splice	N	19%	N	N	N	-
24	AUS/FLUS	c.1003C>T	p.R335*	N	19%	N	N	N	-
25	AUS/FLUS	c.661A>T	p.K221*	N	16%	N	N	N	-
26	AUS/FLUS	c.389G>A, c.49C>T	p.R130Q, p.Q17*	2 <i>PTEN</i> mutations	10%, 7%	N	N	N	FA
27	AUS/FLUS	c.388C>T, c.697C>T	p.R130*, p.R233*	2 <i>PTEN</i> mutations	51%, 3%	N	N	N	Multiple FAs
28	Nondiagnostic	c.385G>A	p.G129R	N	13%	N	N	N	FA
29	AUS/FLUS	c.389G>A	p.R130Q	N, limited RNA analysis	22%	N	Failed	Failed	-
30	AUS/FLUS	c.697C>T	p.R233*	N	18%	N	N	N	-
31	AUS/FLUS	c.741dupA	p.P248Tfs*5	N	23%	N	N	N	-
32	AUS/FLUS	c.940G>T, c.210-2A>T	p.E314*, p.L70_splice	2 <i>PTEN</i> mutations	23%, 12%	N	N	N	Oncocytic FA
33	AUS/FLUS	c.518G>C	p.R173P	N	13%	N	N	N	-
34	FN/SFN	c.253+1G>A	p.?	N	48%	N	N	N	-
35	Benign	c.35delA, c.384G>C	p.N12Tfs*12, p.K128N	2 <i>PTEN</i> mutations	35%, 29%	N	N	N	-
36	AUS/FLUS	c.762dupA, c.371G>C	p.V255Sfs*43 , p.C124S	2 <i>PTEN</i> mutations	18%, 16%	N	N	N	-

37	AUS/FLUS	c.319G>T, c.1012_1016de linsGAGA	p.D107Y, p.S338Efs*6	2 <i>PTEN</i> mutations	23%, 19%	N	N	N	-
38	AUS/FLUS	c.517C>G	p.R173G	N	18%	N	N	N	-
39	AUS/FLUS	c.389G>A, c.49C>T5	p.R130Q, p.Q17*	2 <i>PTEN</i> mutations, <i>NRAS</i> mutation	6%, 5%	N	N	N	EFVPTC
40	FN/SFN	c.210- 5_217delinsTT A	p.L70_splice	N	16%	N	N	N	Oncocytic FA
41	FN/SFN	c.18A>C	p.K6N	N	30%	N	N	N	-
42	AUS/FLUS	c.762dup	p.V255Sfs*43	N	59%	N	N	N	FA
43	FN/SFN	c.722_723delT T	p.F241*	N	5%	N	N	N	-
44	FN/SFN	c.943dupT	p.Y315Lfs*10	N	34%	N	N	N	-
45	AUS/FLUS	c.300_301insC	p.I101Hfs*	N	35%	Y	N	N	FA
46	FN/SFN	c.945T>G, c.69dupA	p.Y315*, p.D24Rfs*20	2 <i>PTEN</i> mutations, <i>EZH1</i> mutation	15%, 13%	N	N	N	-
47	AUS/FLUS	c.758T>A	p.I253N	N	14%	N	N	N	FA
48	AUS/FLUS	c.741dup	p.P248Tfs*5	N	19%	N	N	N	-
49	AUS/FLUS	c.1003C>T, c.253+2dup	p.R335*, splice-site	2 <i>PTEN</i> mutations	36%, 35%	N	N	N	Oncocytic hyperplastic nodule