Supplementary Table 3: *Molecular alterations and their prognostic value.*

		Disease-free survival		**Overall survival**	
	Patients (%)	**Recurrence (%)**	**p-value***	**Death (%)**	**p-value***
Total	151 (100%)	50 (33%)		77 (51%)	
Oncogenes					
HRAS			0.38 (NS)	76 (99%)	0.21 (NS)
Wild type	145 (96%)	49 (98%)		1 (1%)	
Mutated	6 (4%)	1 (2%)			
NFE2L2			0.80 (NS)		0.93 (NS)
Wild type	142 (94%)	47 (94%)		73 (95%)	
Mutated	9 (6%)	3 (6%)		4 (5%)	
PIK3CA			0.87 (NS)		0.64 (NS)
Wild type	130 (86%)	43 (86%)		65 (84%)	
Mutated	21 (14%)	7 (14%)		12 (16%)	
TERT			0.30 (NS)		0.56 (NS)
Wild type	75 (50%)	21 (42%)		36 (47%)	
Mutated	76 (50%)	29 (58%)		41 (53%)	
Tumor Suppressor Genes					
CDKN2A			0.81 (NS)		0.75(NS)
Wild type	113 (75%)	37 (74%)		59 (77%)	
Mutated	38 (25%)	13 (26%)		18 (23%)	
FAT1			0.73 (NS)		0.36 (NS)
Wild type	125 (83%)	42 (84%)		67 (87%)	
Mutated	26 (17%)	8 (16%)		10 (13%)	
FAT2			0.09 (NS)		0.06 (NS)
Wild type	142 (94%)	49 (98%)		75 (97%)	
Mutated	9 (6%)	1 (2%)		2 (3%)	
KMT2B			0.72 (NS)		0.62 (NS)
Wild type	143 (95%)	47 (94%)		74 (96%)	
Mutated	8 (5%)	3 (6%)		3 (4%)	
KMT2D			0.57 (NS)		0.95 (NS)
Wild type	137 (91%)	44 (8%)		69 (90%)	
Mutated	14 (9%)	6 (12%)		8 (10%)	
TP53			0.53 (NS)		0.06 (NS)
Wild type	44 (29%)	13 (26%)		16 (21%)	
Mutated	107 (71%)	37 (74%)		61 (79%°	
CASP8			0.44 (NS)		0.44 (NS)
Wild type	145 (96%)	47 (94%)		75 (97%)	
Mutated	6 (4%)	3 (6%)		2 (3%)	
Both oncogenes and tumor suppressor genes					
NOTCH1			0.88 (NS)		0.58 (NS)
Wild type	129 (85%)	42 (84%)		65 (84%)	
Mutated	22 (15%)	8 (16%)		12 (16%)	
NSD1			0.32 (NS)		0.53 (NS)
Wild type	145 (96%)	49 (98%)		74 (96%)	
Mutated	6 (4%)	1 (2%)		3 (4%)	

Abbreviations: DFS, disease-free survival; OS, overall survival; NS, not significant
** Log-rank test*