

S6 Table. Summary of *Notch1* HD Domain Sequence Mutations

Mutation Class	Location ^a	Alteration	Predicted Protein Change	No Tumours (if >1)
Deletion	+4821-4829	del 9 bp	del R1608-A1610	
Insertion	+5142-5188	dup 48 bp	dup H1725-G1741	
	+4814	ins 'GGT'	V1605ins VV	
	+4999	ins 'CAACCT'	V1666ins VST	
Point-Mutation	+4721	T>C	L1574P	
	+5003	T>C	L1668P	11 ^b
	+5009	T>G	I1670S	
	+5092	T>C	S1698P	
	+5096	T>C	L1699P	

^a Location relative to 'A' of translation start 'ATG' codon.

^b 8 tumours were C-TL, 3 were G-TL.