Figure S1. Variable of importance analysis of the random forest classification of tissue samples.

Supplemental Table S1. **Primer Sequences, Sequence to analyse and genomic position of analysed region by pyrosequencing**

Gene	Primer Sequences			Chromosome	Genomic position		Sequence to analyze	Coordinates in UCSC table browser
	Sequencing	Forward	Reverse		Genomic Start	Genomic End		
INA	AAACCCAAATCAA ATCTAATTTAAC	AGGAGGTAGTAGA GTTGTTGGTTA	TCTCCCTCAAAAC CCAAATCAAATCTA ATT	10	105037678	105037737	CACAATCACRTCCACCTCRAC CRCRACCTACRACRACRCCT ACAACRTAACCAACAACTC	chr10:105037678-105037737
NHLH2	GGGAAGGTTTTTT GGAT	GTTGGGGGAGGG AAGGTT	AACTCCCCCACCT TTATTTAATCATTT CTT	1	116381641	116381682	TTTTYGYGTTTTTTYGAAATYG TAAAGAAATGATTAAATAAA	chr1:116381641-116381682
THBS4	GGGGTGGGTGTA GATA	GAGGATGGGAAG GAGTTTG	TCTCCCCTATAATC TCTACTCAAC	5	79330905	79330970	YGGTTTYGAYGYGYGAGGGT AGGGGYGAAGATGGGTAGTY GGGGTTGGAGAGAAAGGGGT GTTGAG	chr5:79330905-79330970