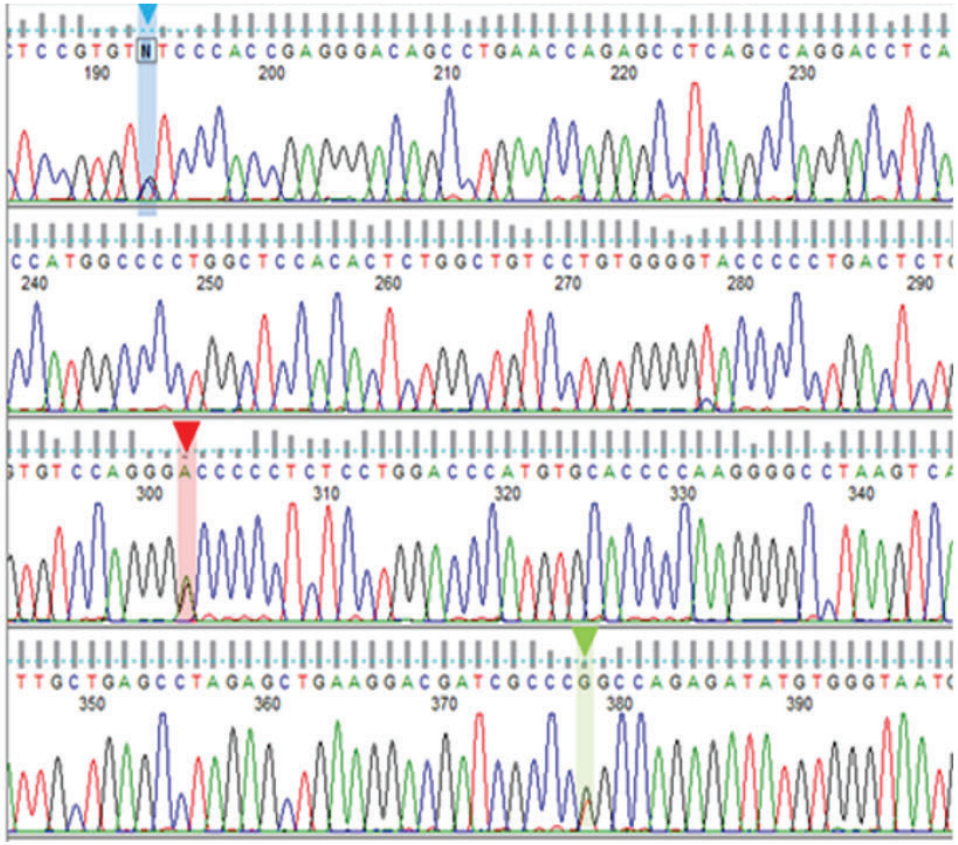
Supplemental figure 1. Mutations in CD19 in pre and post-CART biopsies. A) Sequencing of CD19-cDNA from exon2 to exon8 was performed. Mutation in exon3 results in change of a Leucine to Valine, and it matches an annotated SNP with an allele frequency of 50% heterozygosity in the Caucasian population. Mutation in exon 4 results in substitution of a small amino acid Glycine by a negatively charged Aspartic Acid that is predicted to be a highly damaging mutation. Mutation in exon 4 does not result in amino acid change (Proline to Proline) and it also corresponds with and annotated SNP. B) Conservation of the CD19 protein residue 210 among mammals. C) SIFT prediction of non-synonymous substitution of residue G210 of CD19 by any other amino acid. According to this algorithm, substitution by Aspartic Acid would be "very damaging". D) Measurement of the impact of the substitution of the residue G210 of CD19 as measured by Polyphen 2.

Supplemental figure 2. Immunohistochemistry for mismatch repair proteins. Immunostains for mismatch repair proteins reveals intact expression of MLH1 and PMS2 (brown nuclear staining) while there is no expression of MSH2 and MSH6 corresponding with SNP data of loss of 2p locus containing these genes.

A) Post CART-19

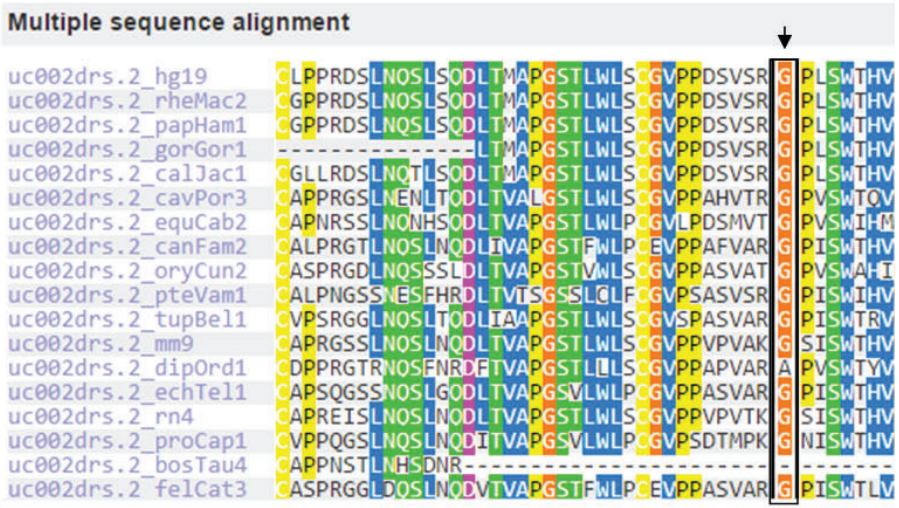


Exon 3: C/G → L174V, SNP rs2904880 50% frequency of heterozygous. in Caucasian population.

Exon 4: G/A→ G210D, pathologic mutation.

Exon 4: G/T → SNP rs35979293, 42% frequency of heterozygous. in Caucasian population.

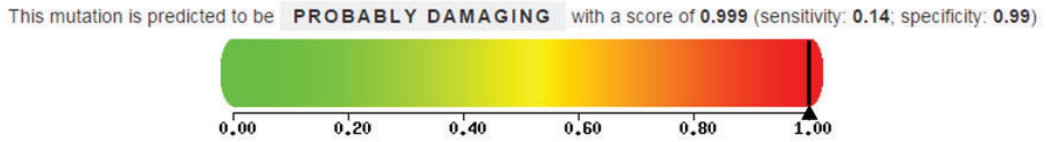
B) Multiple sequence alignment

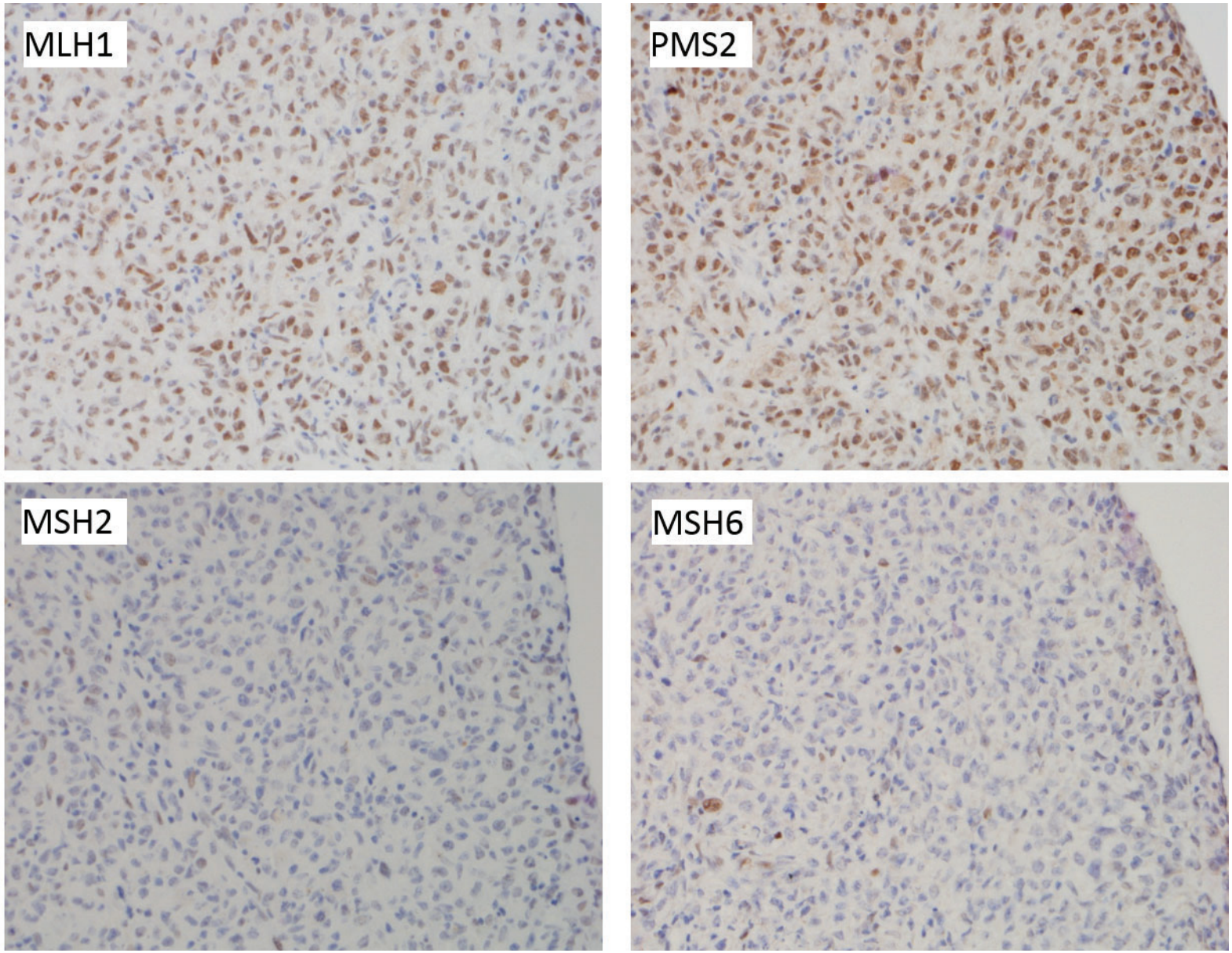


C) SIFT analysis of mutations in residue G210

User Input	ENSP	Pos	Ref	Subst	Prediction	SIFT Score	Median Information Content	# Seqs
ENSP00000313419.G210	ENSP00000313419	210	G	A	TOLERATED	0.09	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	C	*DAMAGING	0.01	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	D	*DAMAGING	0.01	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	E	TOLERATED	0.12	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	F	*DAMAGING	0	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	G	TOLERATED	1	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	H	*DAMAGING	0	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	I	*DAMAGING	0	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	K	*DAMAGING	0.01	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	L	*DAMAGING	0.01	3.6	29
ENSP00000313419.G210	ENSP00000313419	210	G	M	*DAMAGING	0	3.6	29

D) Polyphen-2 analysis of change G210D




MLH1
PMS2
MSH2
MSH6