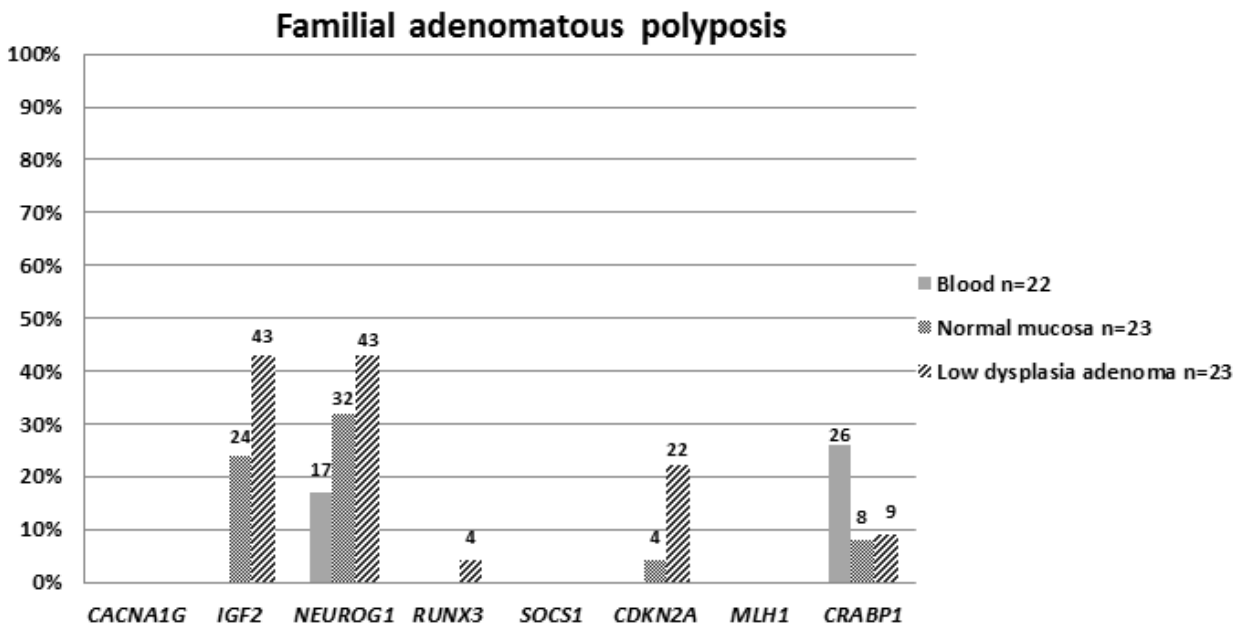
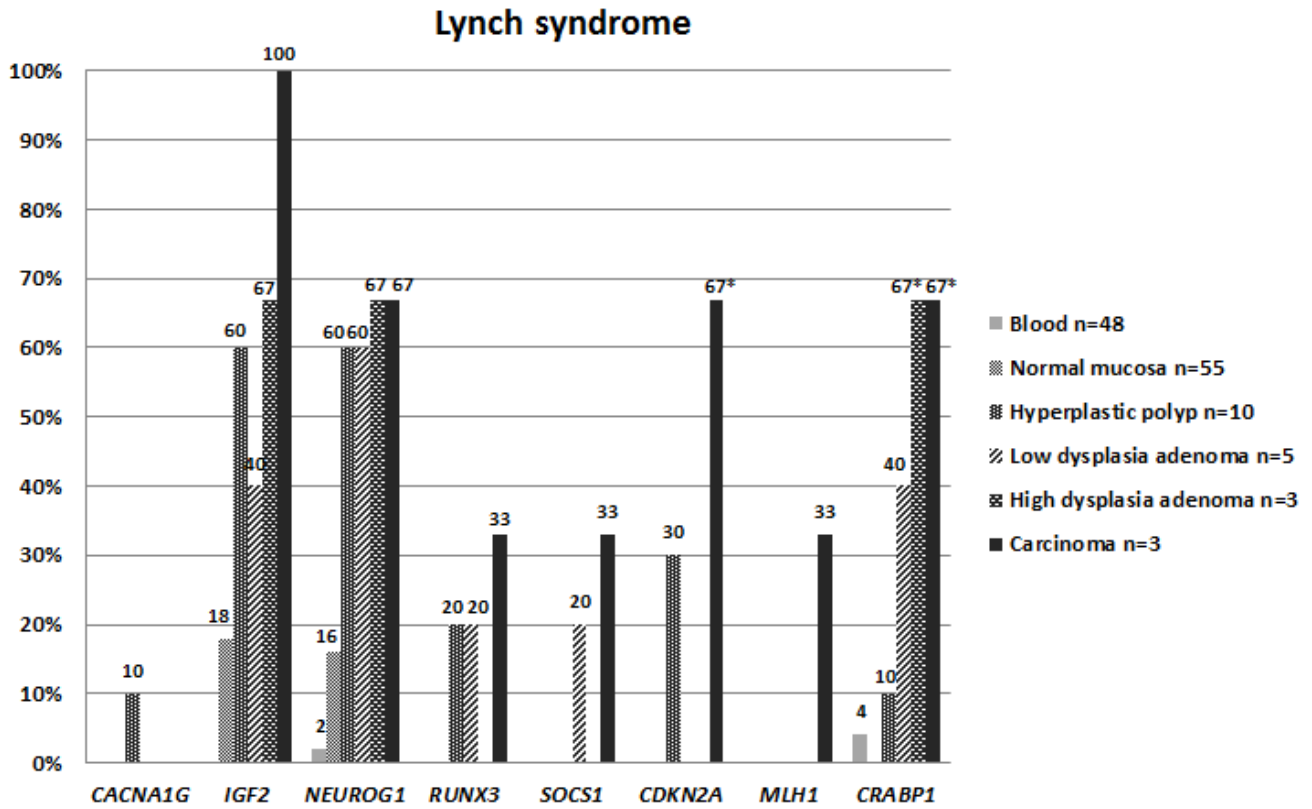


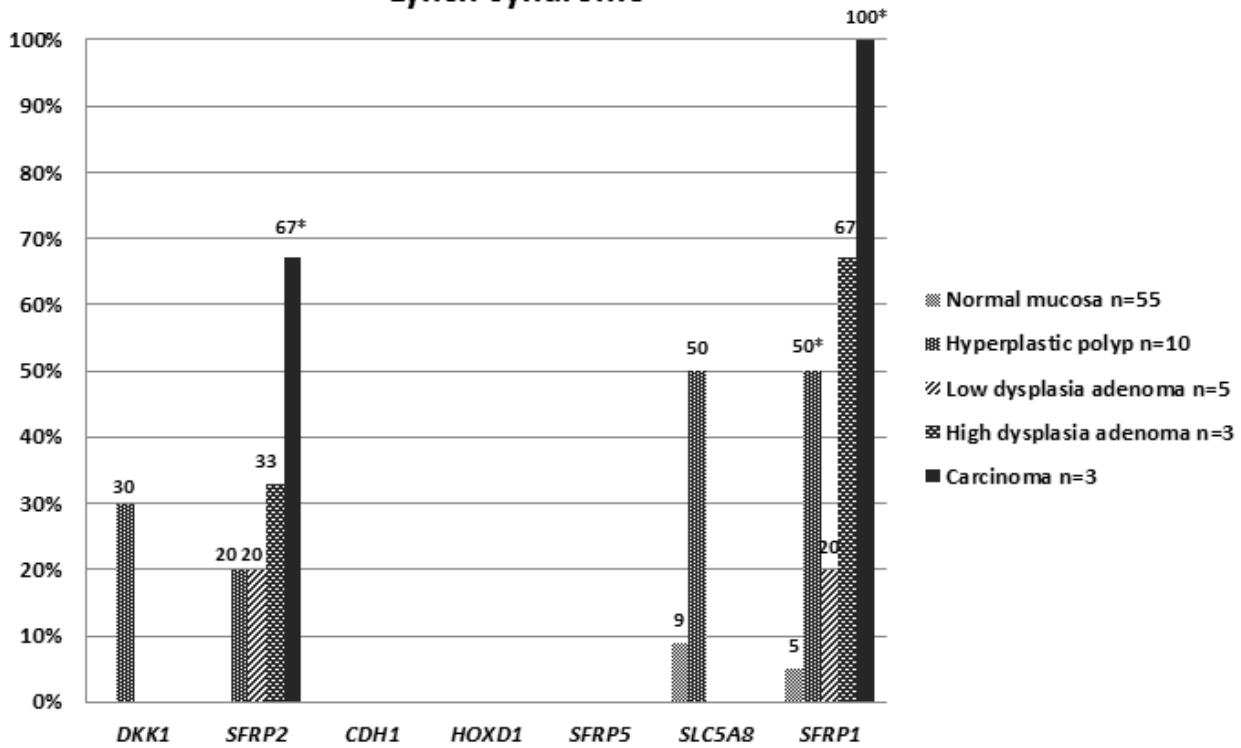
**Suppl. Fig.1.** Frequency of hypermethylated samples in the LS and FAP prospective series. Numerical values of percentages are given above each bar. Hypermethylation thresholds were calculated according to stringency level I, resulting in values below the technical threshold for all probes technical except *IGF2 I*, *IGF2 III*, *NEUROG1 I* and *NEUROG1 IV* that had calculated thresholds 0.44, 0.23, 0.20 and 0.16, respectively. Pairwise comparisons were calculated by Fisher's exact test (2-sided *p* values) and the *p* values were adjusted for multiple comparisons by Bonferroni correction. Significant increase (*p*<0.05) in the frequency of methylated specimen compared to normal colon tissue is indicated by \*.

**A. CIMP panel**



**B. Candidate panel**

**Lynch syndrome**



**Familial adenomatous polyposis**

