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

**Lynch syndrome**

![Graph showing frequency of hypermethylated samples in LS.]

![Graph showing frequency of hypermethylated samples in Lynch syndrome.]

**Familial adenomatous polyposis**

![Graph showing frequency of hypermethylated samples in FAP.]

**Graph showing frequency of hypermethylated samples in Familial adenomatous polyposis.**
B. Candidate panel

**Lynch syndrome**

- Normal mucosa n=55
- Hyperplastic polyp n=10
- Low dysplasia adenoma n=5
- High dysplasia adenoma n=3
- Carcinoma n=3

**Familial adenomatous polyposis**

- Normal mucosa n=23
- Low dysplasia adenoma n=23