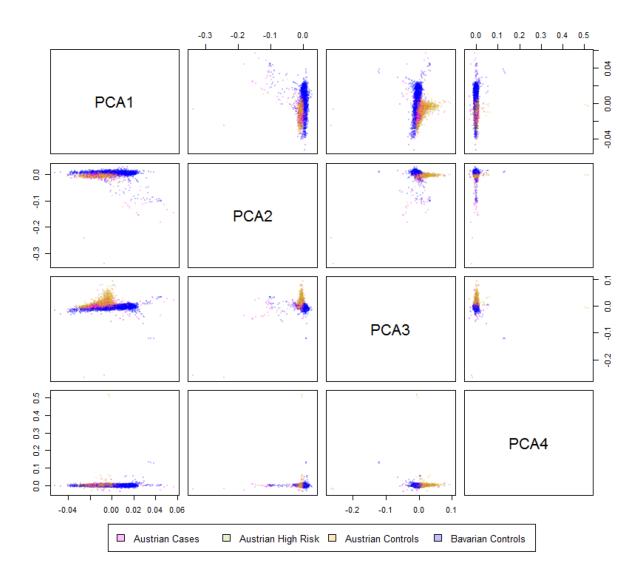
## Bayesian and frequentist analysis of an Austrian genome-wide association study of colorectal cancer and advanced adenomas

## **SUPPLEMENTARY MATERIALS**



**Supplementary Figure 1: PCA plot.** The first 4 PCs are plotted against each other. Case-control status is indicated by coloured shading.

Supplementary Table 1: UICC staging and localization of post-QC samples

	CRC (A)	AA (B)
UICC Stage		
I	153	-
II	224	-
III	376	-
IV	112	-
$\mathbf{X}^{1}$	66	-
Missing	47	-
Location		
Colon – distal <sup>2</sup>	296	288
Colon – proximal³	257	215
Rectal <sup>4</sup>	401	113
Missing	24	20
Amount of polpys		
one	-	436
two	-	93
more than two	-	88
Missing	-	19

CRC Colorectal cancer cases.

AA Advanced adenomas.

Supplementary Table 2: The 200 top ranking SNPs for each case-control contrast. The four different case and control groups were colorectal cancer cases (A), advanced colorectal adenomas (B), CORSA controls (C) and KORA controls (D).

## See Supplementary File 1

<sup>&</sup>lt;sup>1</sup> UICC staging not possible (e.g. incomplete TNM or palliative surgery).

<sup>&</sup>lt;sup>2</sup> sigmoid colon, descending colon, splenic flexure.

<sup>&</sup>lt;sup>3</sup> transverse colon, hepatic flexure, ascending colon, cecum, appendix.

<sup>&</sup>lt;sup>4</sup> rectum, rectosigmoid junction.