

SUPPLEMENTAL INFORMATION

Central Role of Intestinal Epithelial Glucocorticoid Receptor in Alcohol and Corticosterone-Induced Gut Permeability and Systemic Response

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Table S1: PCR primer sequences	
Gene	5'-3' Sequence
IL-1 β	Forward: GCAACTGTTTCCTGAACTCAACT Reverse: ATCTTTTGGGGTCCGTCAACT
IL-6	Forward: TAGTCCTTCCTACCCCAATTTCC Reverse: TTGGTCCTTAGCCACTCCTTC
TNF- α	Forward: CCCTCACACTCAGATCATCTTCT Reverse: GCTACGACGTGGGCTACAG
MCP-1/CCL2	Forward: TTAAAAACCTGGATCGGAACCAA Reverse: GCATTAGCTTCAGATTTACGGGT
GAPDH	Forward: CTGCACCACCAACTGCTTAG Reverse: GGGCCATCCACAGTCTTCT
16S rDNA, (universal)	Forward: ACTCCTACGGGAGGCAGCAGT Reverse: ATTACCGCGGCTGCTGGC
23S rDNA (<i>Enterobacteriaceae</i>) <i>En-lsu-1</i>	Forward: TGCCGTA ACTTCGGGAGAAGGCA Reverse: TCAAGGACCAGTGTT CAGTGTC
16S rDNA (<i>E. coli</i>) <i>Ecoli</i>	Forward: CATGCCGCGTGTATGAAGAA Reverse: CGGGTAACGTCAATGAGCAA
All <i>Lactobacillus</i>	Forward: AGGGTGAAGTCGTAACAAGTAGCC Reverse: CCACCTTCCTCCGGTTTGTC

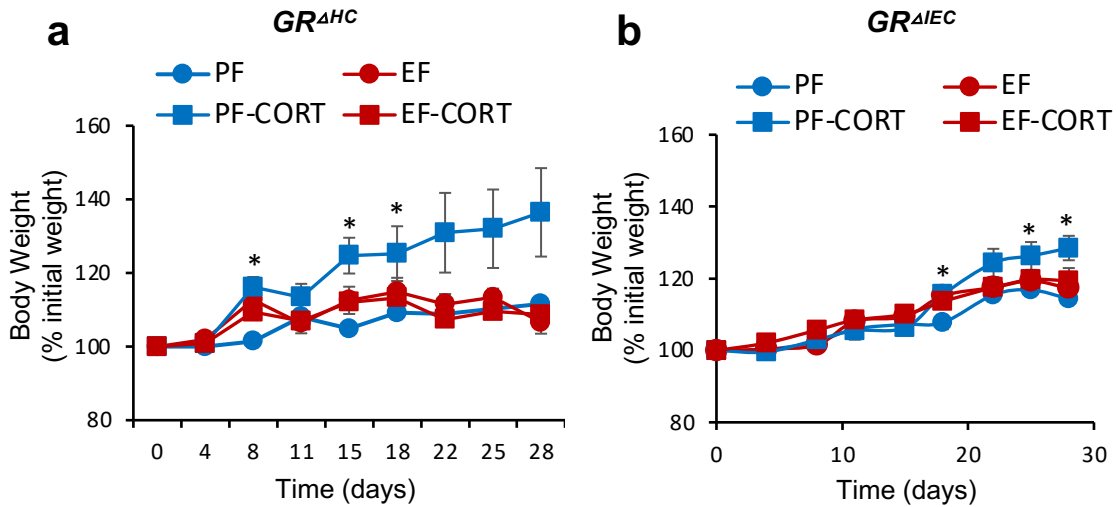


Figure S1

Intestinal glucocorticoid receptor mediates alcohol and corticosterone-induced effects on body weight changes.

Adult $GR^{\Delta HC}$ (a) and $GR^{\Delta IEC}$ (b) mice were fed a liquid diet with (EF) or without (PF) ethanol for four weeks. In some groups, animals were injected with corticosterone (Cort) daily; the other groups received the vehicle. Body weights were recorded twice a week. Values are Mean \pm SEM (n = 6). Asterisks indicate the values that significantly ($p < 0.05$) differ from corresponding PF values.

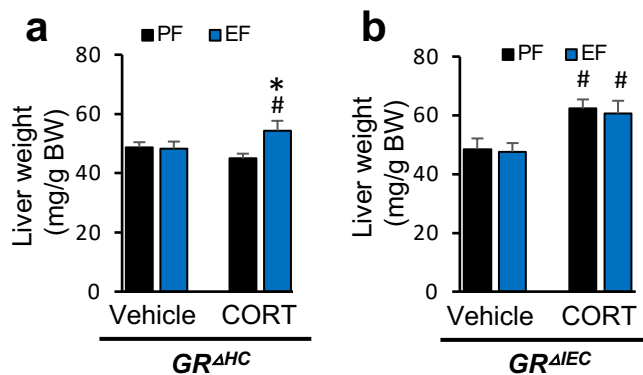


Figure S2
Intestinal glucocorticoid receptor mediates alcohol and corticosterone-induced effects on the liver.

Adult $GR^{\Delta HC}$ (a) and $GR^{\Delta IEC}$ (b) mice were fed a liquid diet with (EF) or without (PF) ethanol for four weeks. In some groups, animals were injected with corticosterone (Cort) daily; the other groups received the vehicle. At the end of treatments, liver weights recorded (a & b). Values are mean \pm SEM (n = 6). Asterisk indicates the value that significantly ($p < 0.05$) differ from corresponding PF value; hashtags indicate the values that differ from corresponding “Vehicle” values.

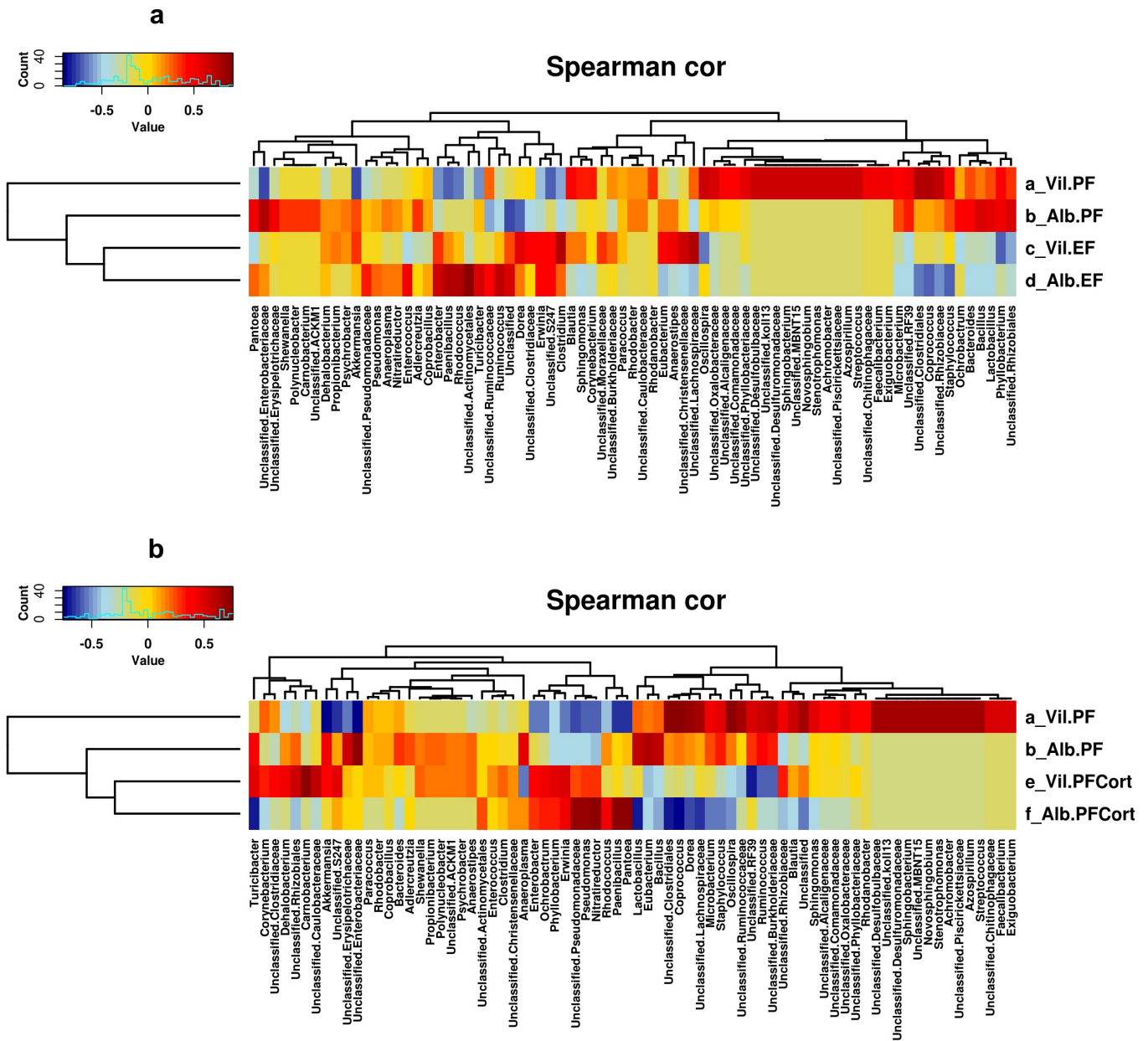


Figure S3
Intestinal glucocorticoid receptor mediates alcohol and corticosterone-induced effects on microbiota composition.

Adult *GR^{AHC}* and *GR^{AEC}* mice were fed a liquid diet with (EF) or without (PF) ethanol for four weeks. In some groups, animals were injected with corticosterone (Cort) daily; the other groups received the vehicle. The composition of microbiota in colonic flushing was analyzed by 16S rRNA-sequencing and metagenomics. Spearman's correlation of microbiota at the genus level was analyzed PF vs EF (a) and PF vs Cort (b).

LEfSe

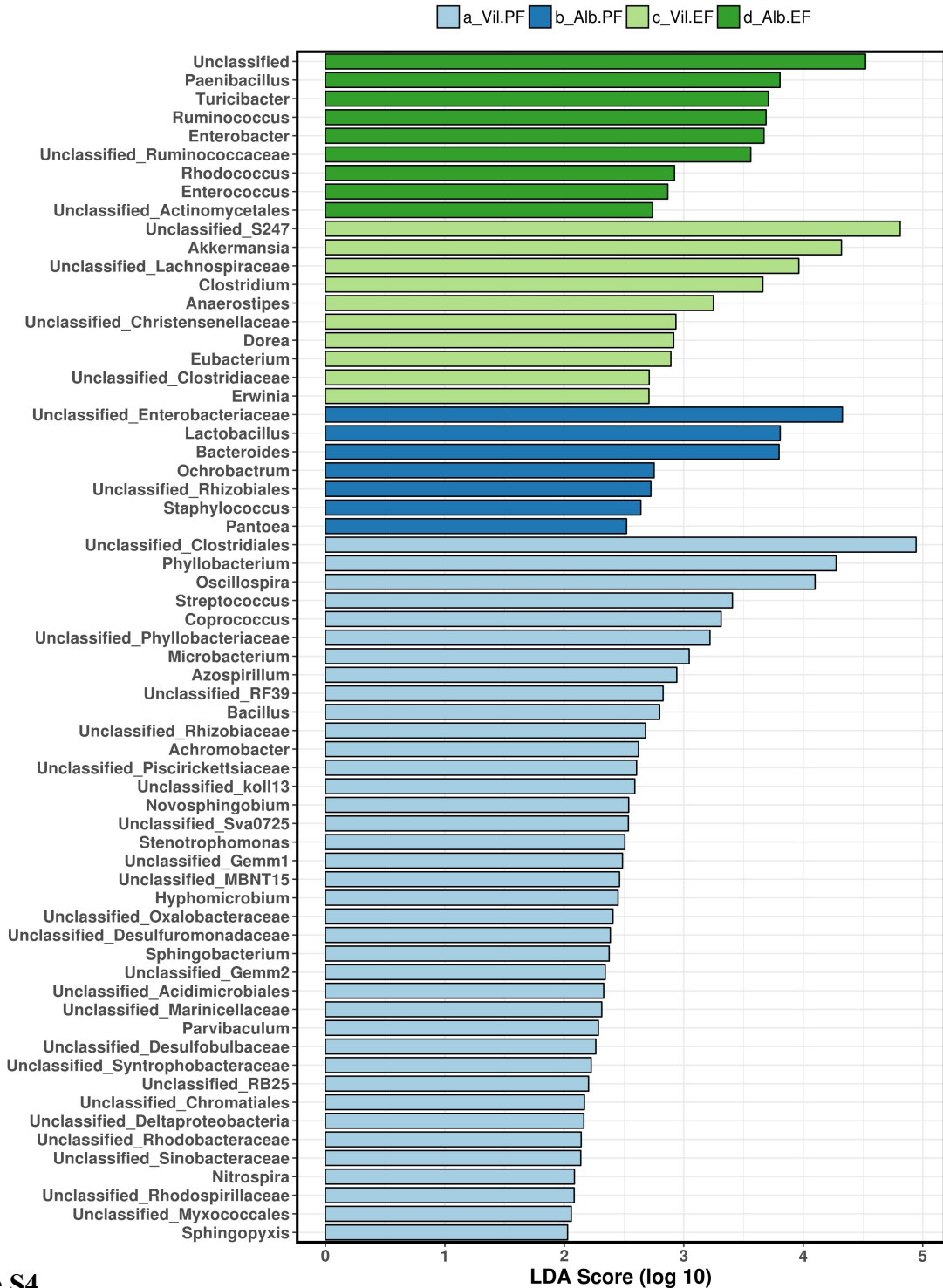


Figure S4

Intestinal glucocorticoid receptor mediates alcohol-induced effects on microbiota composition.

Adult GR^{AHC} and GR^{AEC} mice were fed a liquid diet with (EF) or without (PF) ethanol for four weeks. The composition of microbiota in colonic flushing was analyzed by 16S rRNA-sequencing and metagenomics. Linear discriminate analysis of effect size (LefSe) was used to identify enriched taxa following ethanol feeding.

LefSe

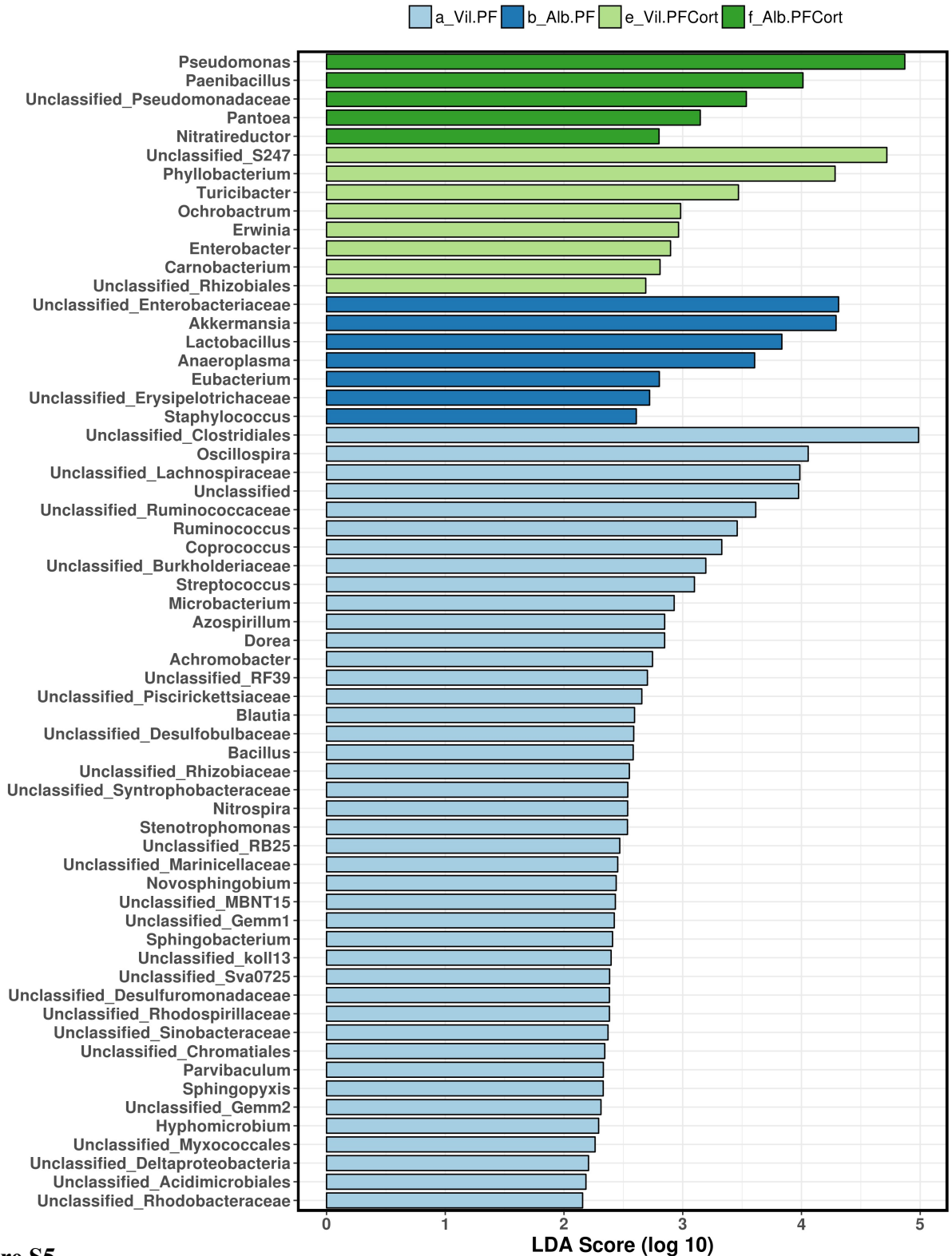


Figure S5

Intestinal glucocorticoid receptor mediates corticosterone-induced effects on microbiota composition.

Adult GR^{AHC} and GR^{AEC} mice were injected with corticosterone (Cort) daily; the other groups received the vehicle. The composition of microbiota in colonic flushing was analyzed by 16S rRNA-sequencing and metagenomics. Linear discriminate analysis of effect size (LefSe) was used to identify enriched taxa following corticosterone.

LefSe

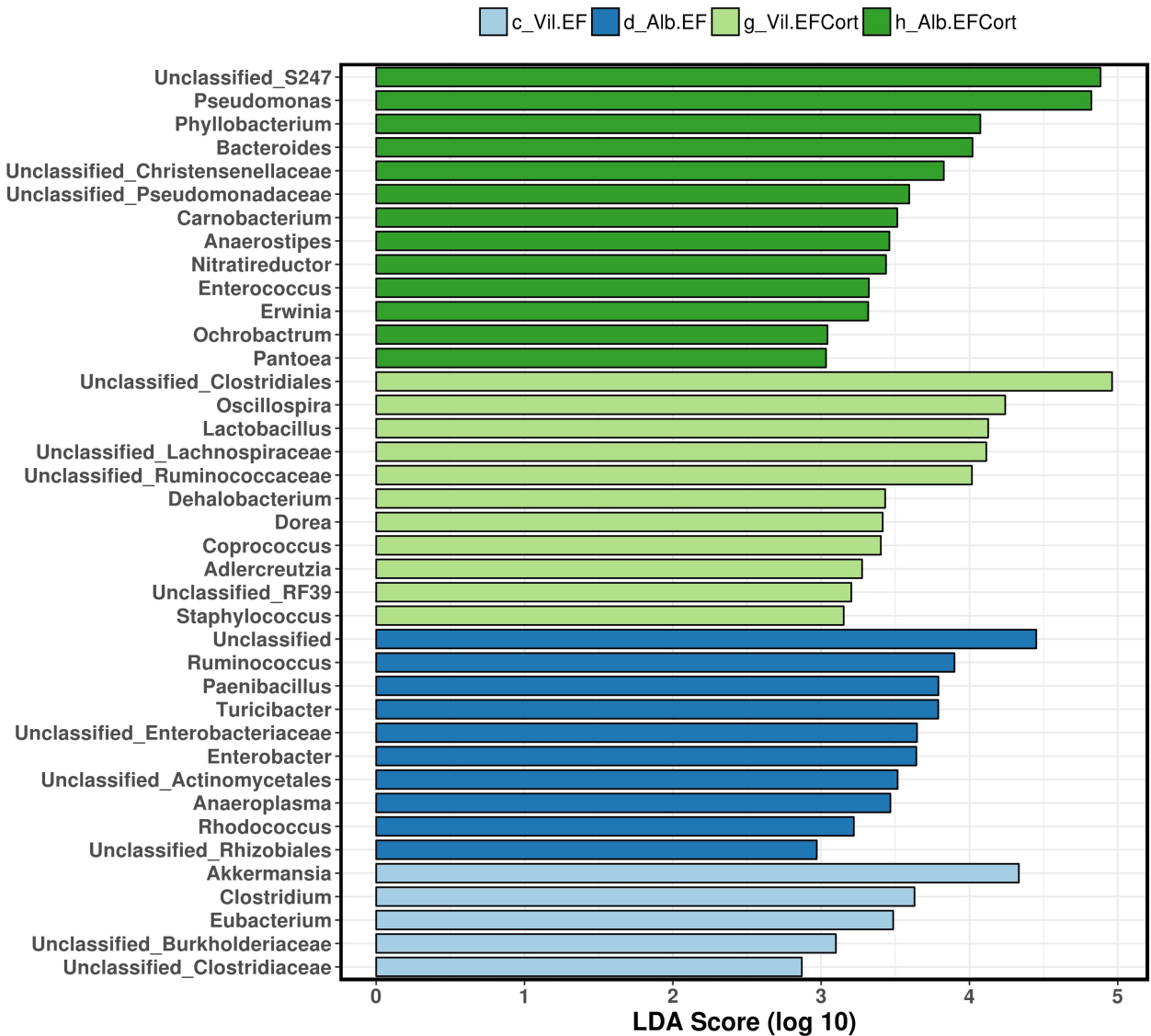


Figure S6

Intestinal glucocorticoid receptor mediates alcohol and corticosterone-induced effects on microbiota composition. Adult GR^{AHC} and GR^{AEC} mice were fed a liquid diet with (EF) or without (PF) ethanol for four weeks. In some groups, animals were injected with corticosterone (Cort) daily; the other groups received the vehicle. The composition of microbiota in colonic flushing was analyzed by 16S rRNA-sequencing and metagenomics. Linear discriminate analysis of effect size (LefSe) was used to identify enriched taxa following corticosterone.