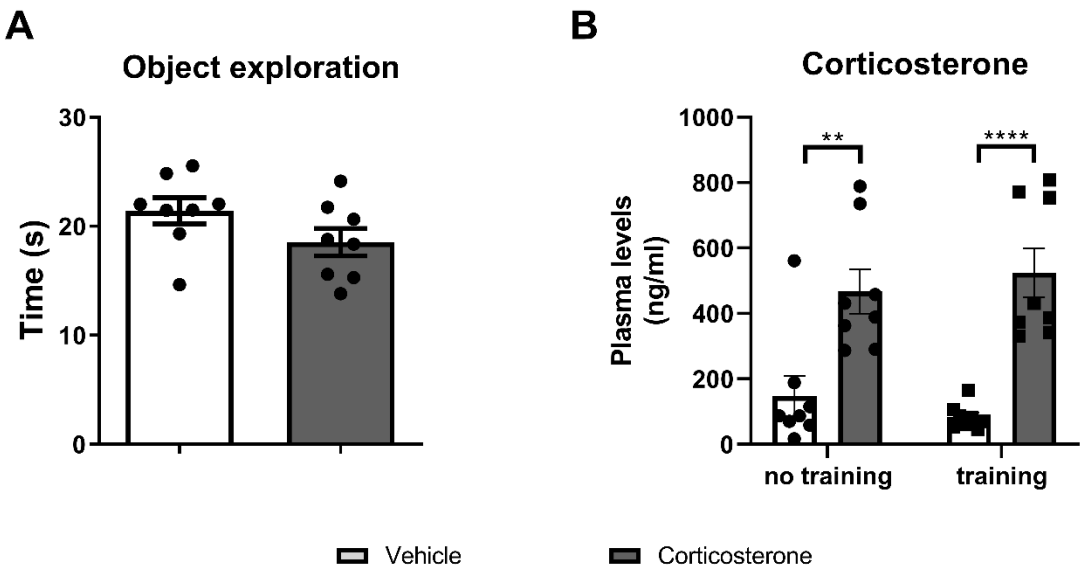
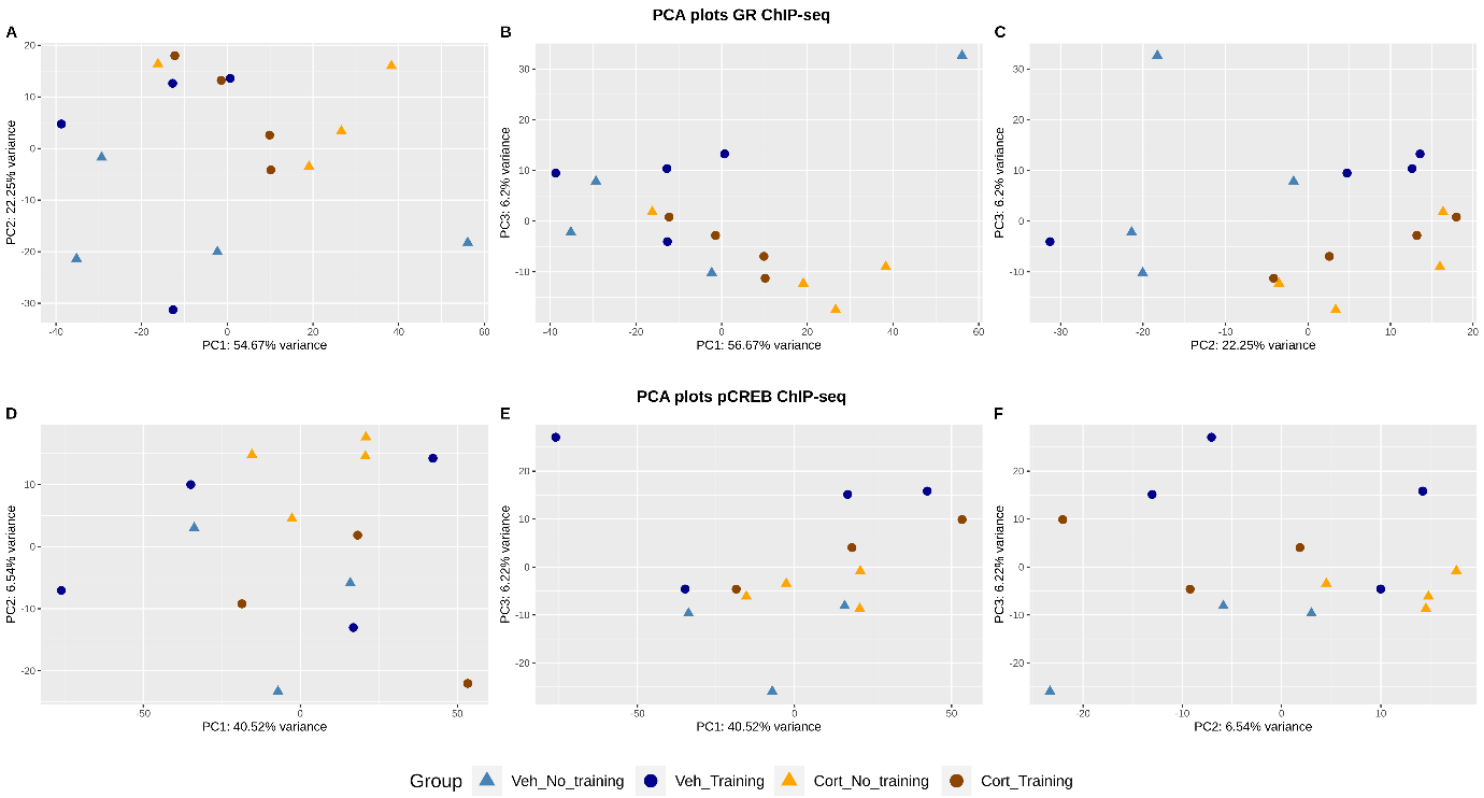


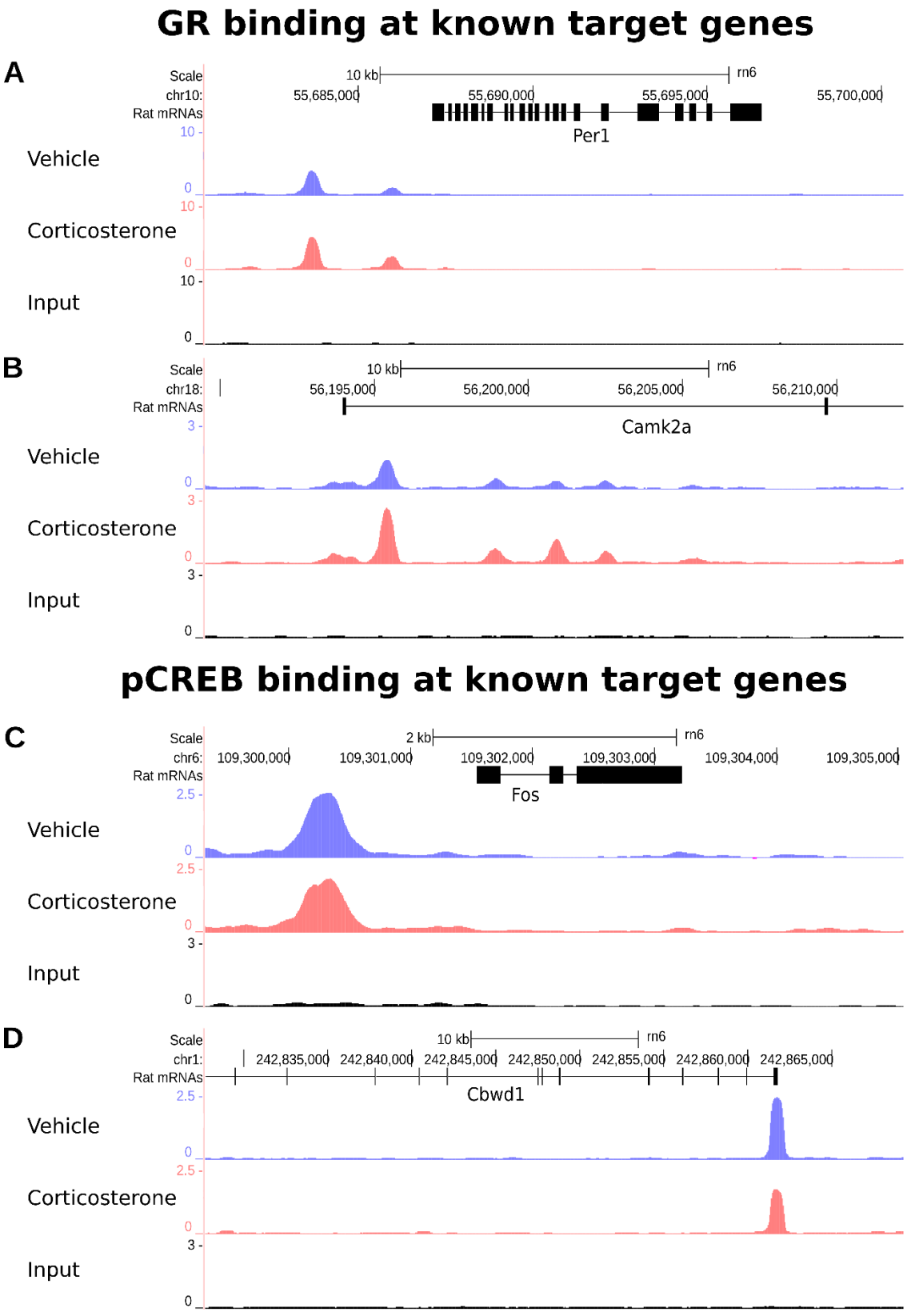
Supplementary Figure s1. Object exploration and corticosterone plasma levels in ChIP-seq cohort.

(A) Total object exploration time in seconds (s) of two identical objects during the object location memory training trial for training groups (vehicle and 3.0 mg/kg corticosterone, n=8 per group). **(B)** Plasma corticosterone levels at endpoint, 45 minutes after injection (n=8 per group). Data shown as mean ± SEM. ChIP = chromatin immunoprecipitation; training = object exploration training; s = seconds; ** = P<0.01; **** = P<0.0001.



Supplementary Figure s2. PCA plots of ChIP-seq data.

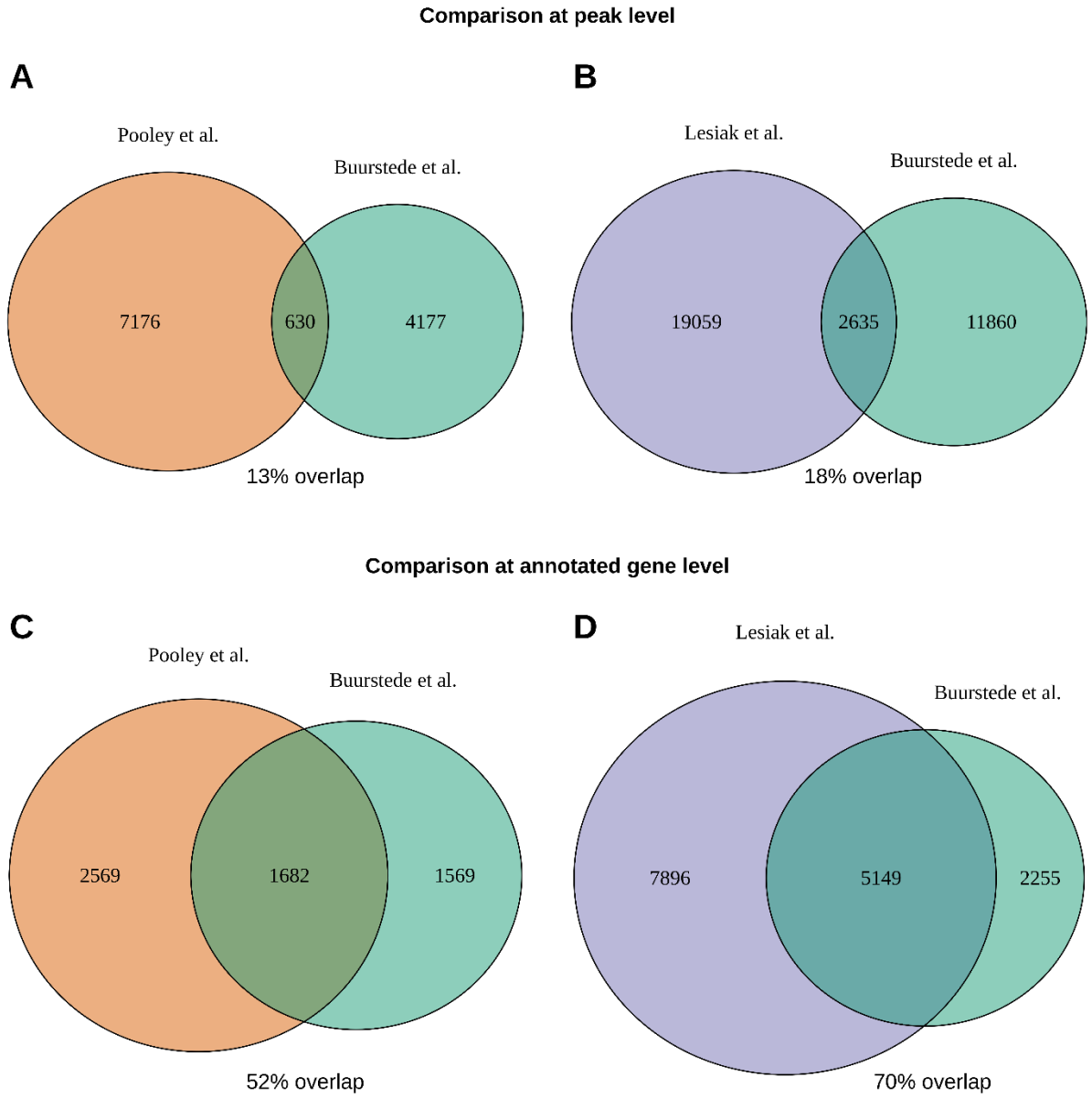
PCA plots visualizing the first three principal components of **(A-C)** GR and **(D-F)** pCREB ChIP-seq data. ChIP = chromatin immunoprecipitation; Cort = corticosterone; GR = glucocorticoid receptor; pCREB = phosphorylated cAMP response element-binding protein; PCA = principal component analysis; Training = object exploration training; Veh = vehicle.



Supplementary Figure s3. Validating ChIP-seq signal at known GR and pCREB target genes.

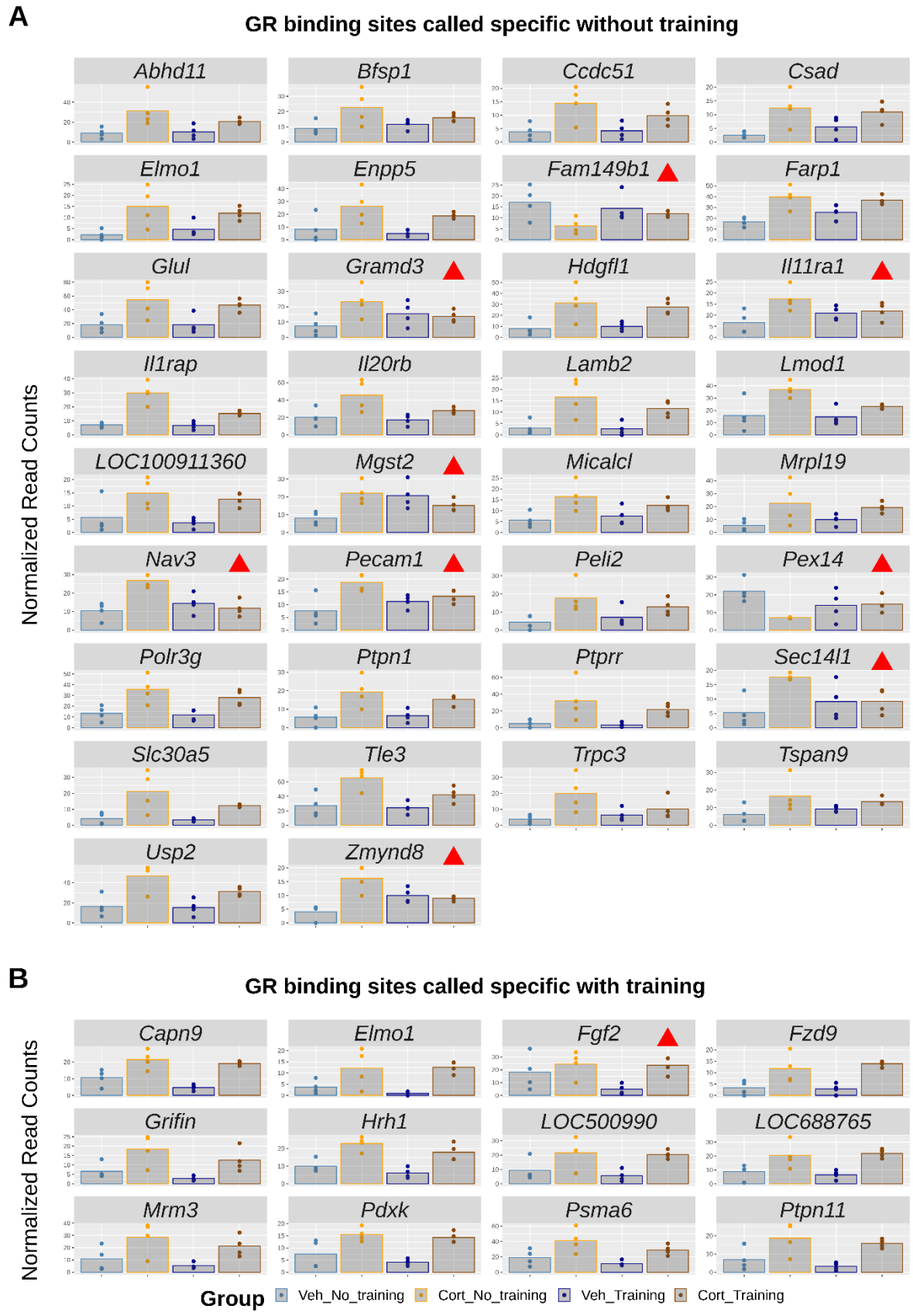
Genomic tracks showing GR and input signal at known GR target genes **(A)** *Per1* and **(B)** *Camk2a* and pCREB and input signal at known pCREB target genes **(C)** *Fos* and **(D)** *Cbwd1*. Displayed ChIP-seq

tracks are overlays of all biological replicates per group: vehicle = blue, corticosterone = red and input = black. ChIP = chromatin immunoprecipitation; GR = glucocorticoid receptor; pCREB = phosphorylated cAMP response element-binding protein.



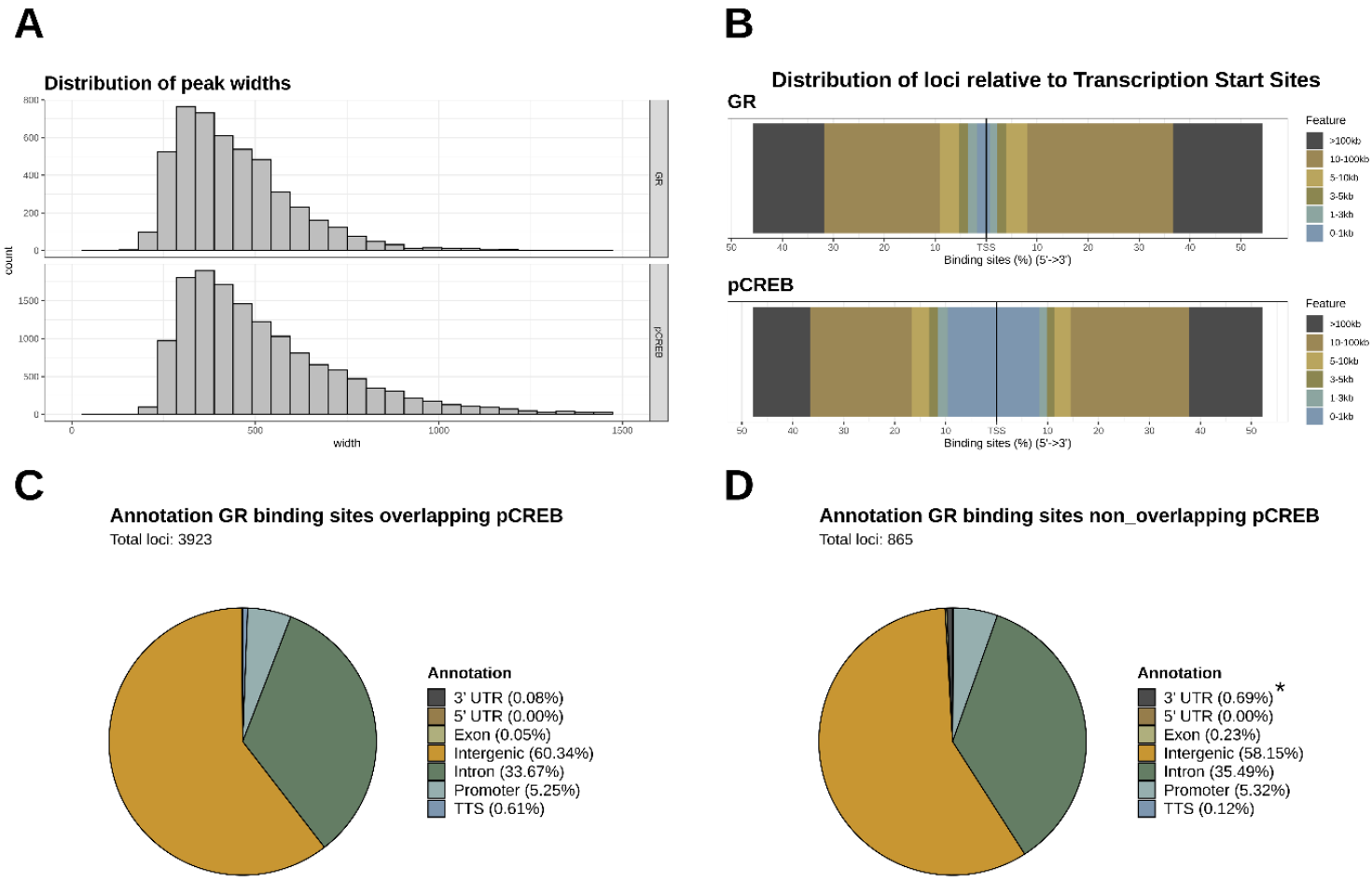
Supplementary Figure s4. Validation of ChIP-seq data with published datasets of GR and pCREB.

Our GR and pCREB ChIP-seq data were compared to publicly available GR ChIP-seq data by Pooley et al. and pCREB Chip-seq data by Lesiak et al. at **(A & B)** a peak level and at **(C & D)** an annotated gene level. Numbers in venn diagrams indicate the amount of identified **(A & B)** binding sites or **(C & D)** unique genes associated to these binding sites. Percentages below venn diagrams indicate the amount of our data that overlaps with the reference dataset. ChIP = chromatin immunoprecipitation; GR = glucocorticoid receptor; pCREB = phosphorylated cAMP response element-binding protein.



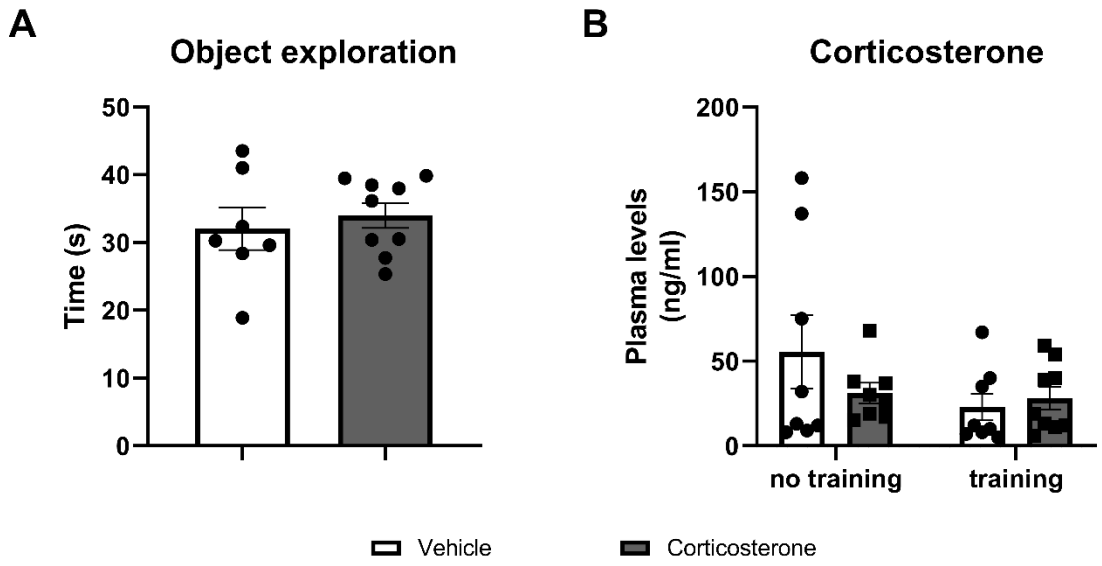
Supplementary Figure s5. Overview of "context-specific GR DNA-binding"

Normalized read count plots of GR DNA-binding sites with context-specificity. Differential GR DNA-binding was detected specifically **(A)** after corticosterone in untrained animals or **(B)** after corticosterone in trained animals. Red triangles behind the name of the gene associated to the binding site indicates that significance was lost in the pooled analysis. Cort = corticosterone; GR = glucocorticoid receptor; Training = object exploration training; Veh = vehicle.



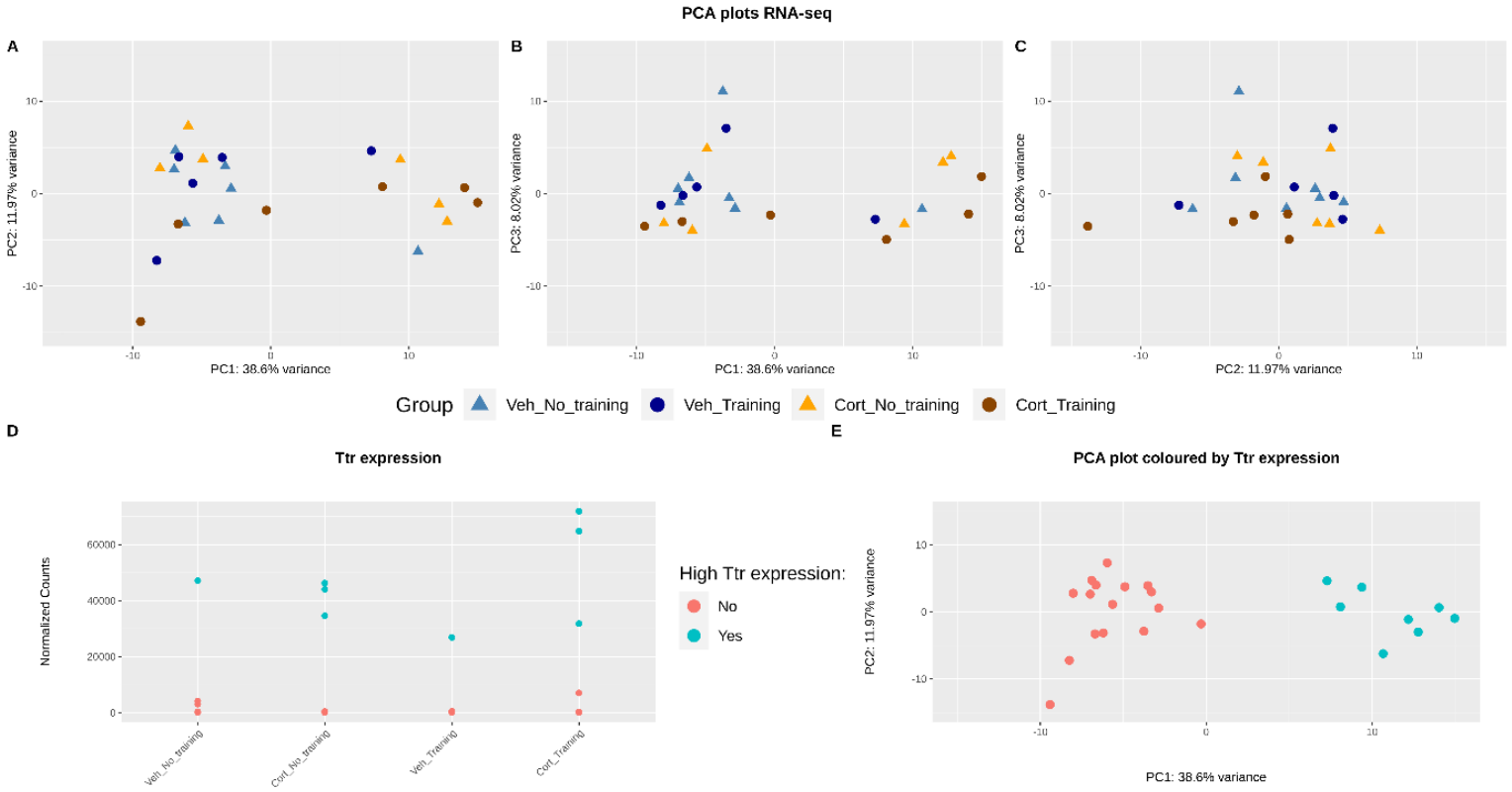
Supplementary Figure s6. GR and pCREB peak width and genomic distribution

(A) Distribution of GR and pCREB peaks widths, with the abundance displayed as count on the y-axis. **(B)** Distance to transcription start sites plot for all GR and pCREB binding sites. Annotation and distribution of GR binding sites that **(C)** do and **(D)** do not overlap with pCREB peaks. GR binding was significantly increased in the 3'UTR region in absence of pCREB co-binding. GR = glucocorticoid receptor; pCREB = phosphorylated cAMP response element-binding protein; TSS = transcription start site; TTS = transcription termination site; UTR = untranslated region; * = Bonferroni corrected P<0.05.



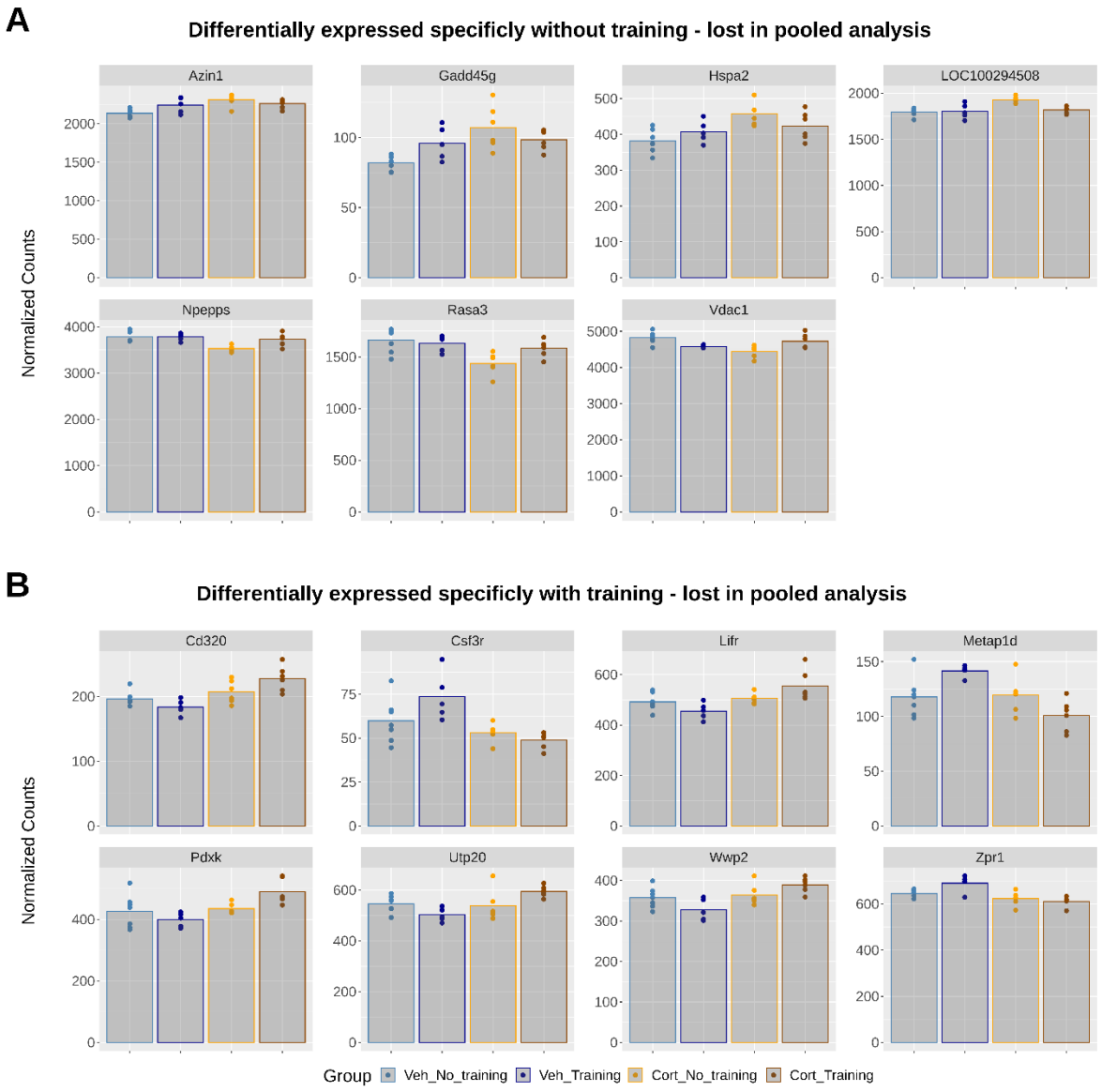
Supplementary Figure s7. Object exploration and corticosterone plasma levels in RNA-seq cohort.

(A) Total object exploration time in seconds (s) of two identical objects during the object location memory training trial for training groups (vehicle and 3.0 mg/kg corticosterone, n=7-9 per group). **(B)** Plasma corticosterone levels at endpoint, three hours after injection (n=8-9 per group). Data shown as mean ± SEM. training = object exploration training; s = seconds.



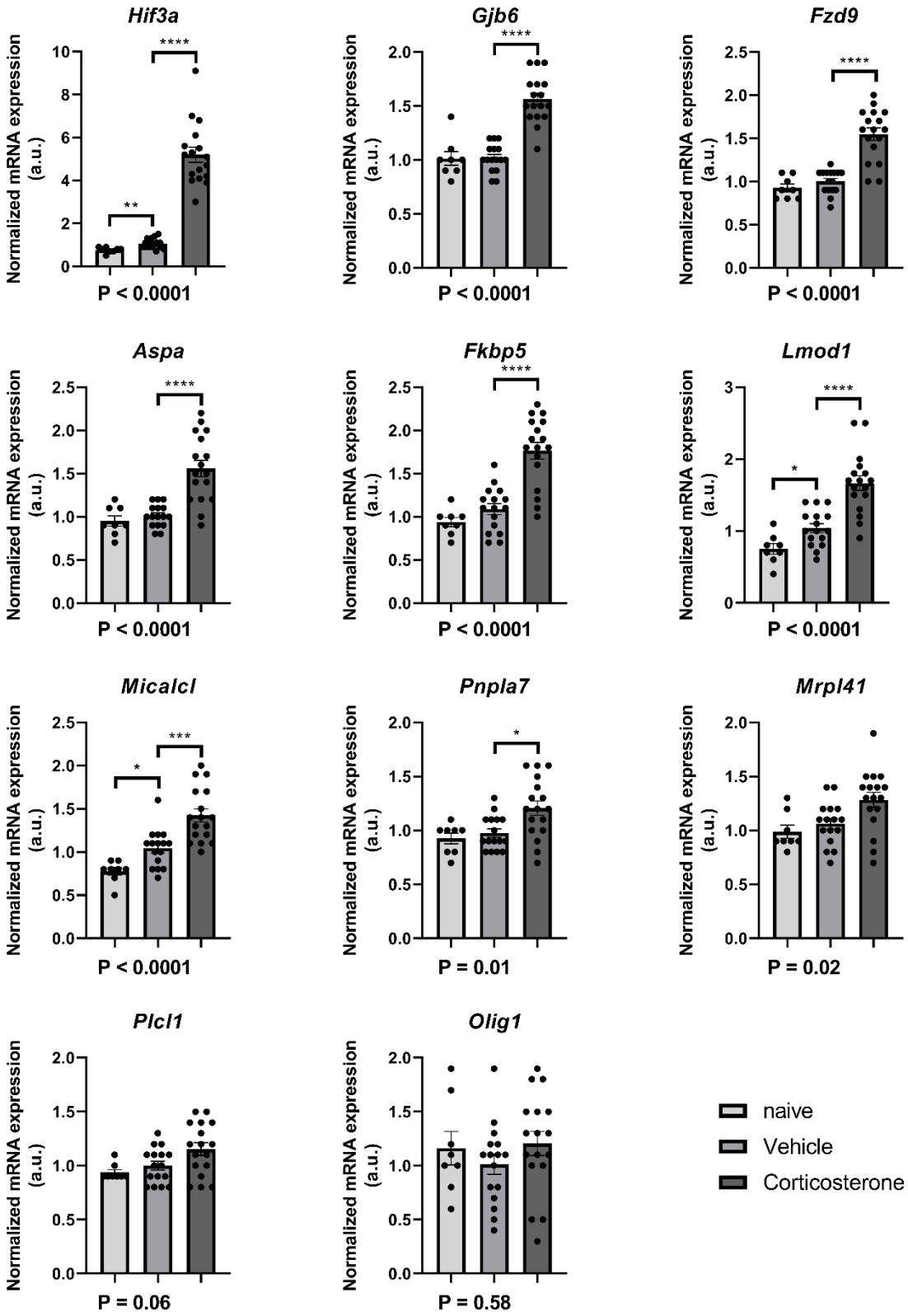
Supplementary Figure s8. PCA plots of RNA-seq data.

(A-C) PCA plots visualizing the first three principal components of the transcriptome data. **(D)** Expression plot with normalized counts of choroid plexus marker gene *Ttr* in the hippocampal samples, indicating a degree of tissue contamination. **(E)** PCA plot coloured according to high or low *Ttr* expression levels in the samples, explaining observed clustering in PCA plots. Cort = corticosterone; PCA = principal component analysis; Training = object exploration training; Veh = vehicle.



Supplementary Figure s9. Overview of lost "context-specific" transcriptome changes.

Normalized count expression plots of genes differentially expressed **(A)** without trained or **(B)** with training that were lost in the pooled transcriptome analysis. Cort = corticosterone; Training = object exploration training; Veh = Vehicle.



Supplementary Figure s10. qPCR validation of transcriptional effects of a set of GR-associated target genes.

mRNA expression of a set of identified GR target genes selected based on transcriptome data and associated differential GR DNA-binding (n=8 for naïve group and 16-17 for treated groups). Data shown as mean ± SEM, p-value of one-way ANOVA is displayed below the graphs. * = P<0.05, *** P<0.001, **** P<0.0001.