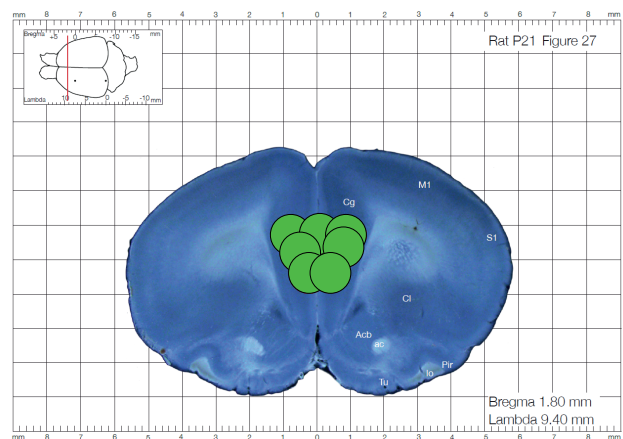
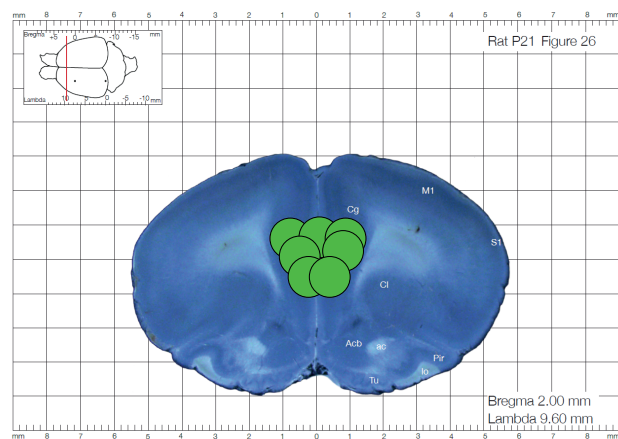
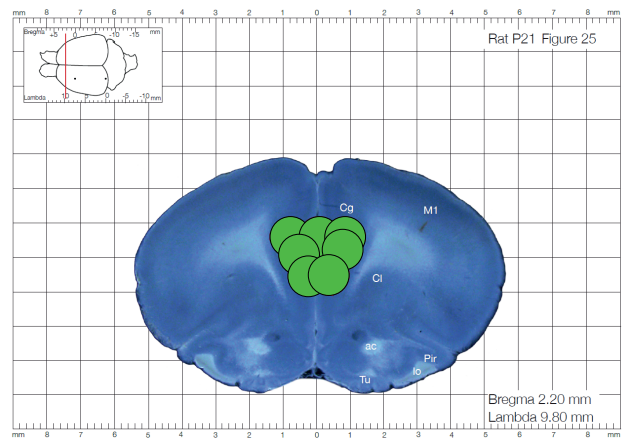
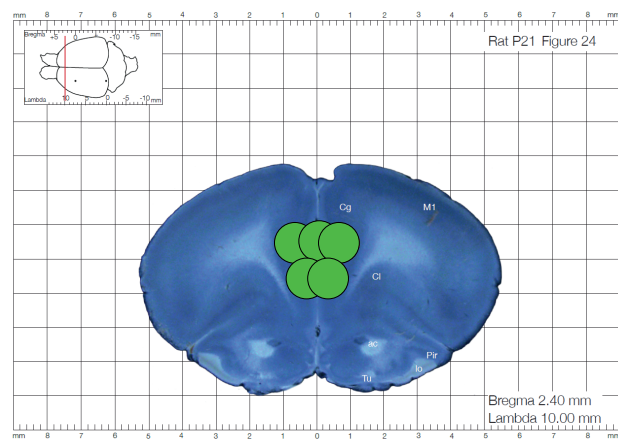
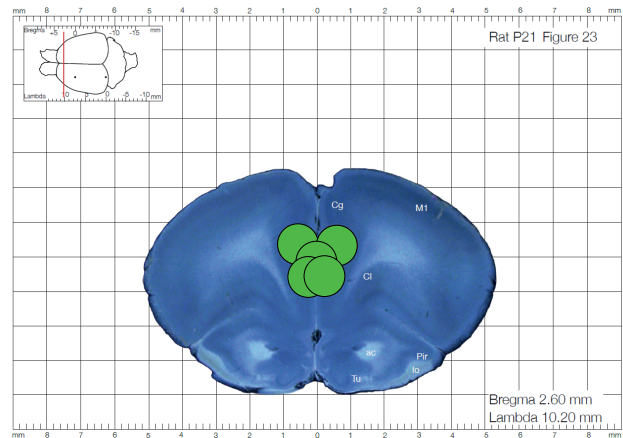
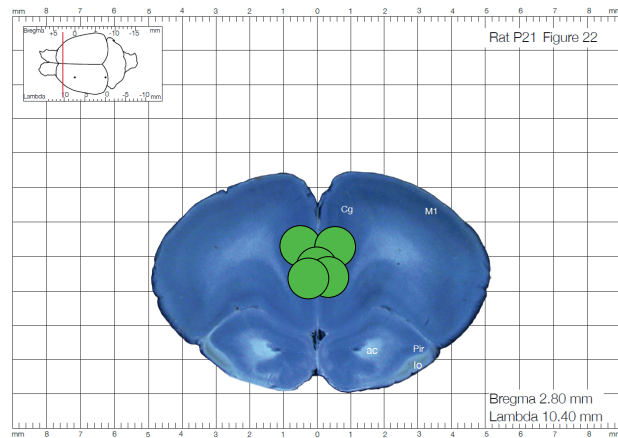
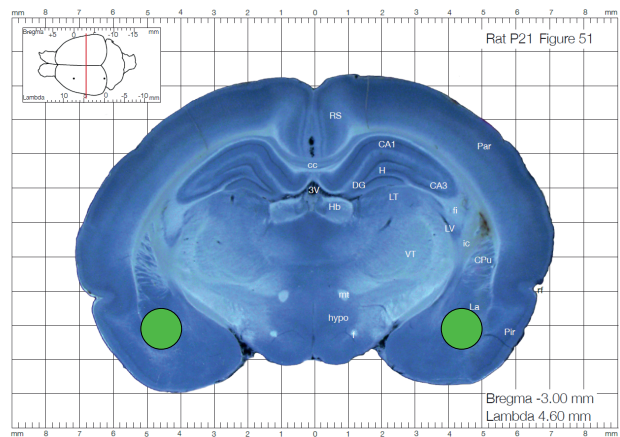
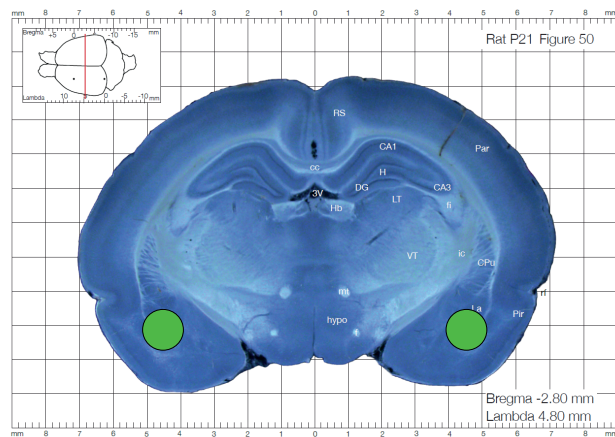
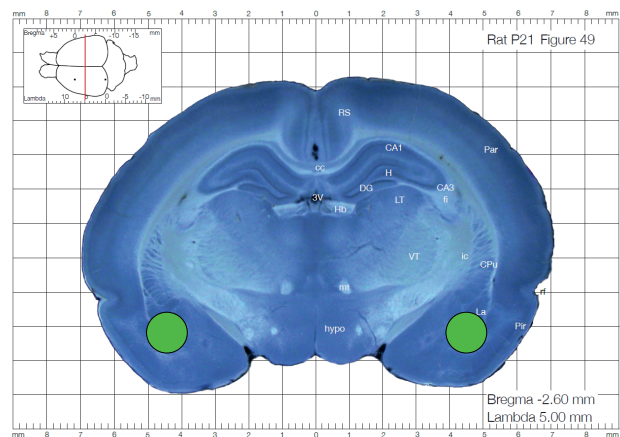
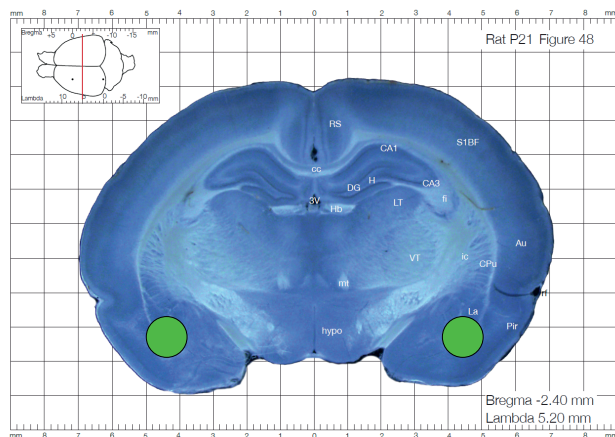
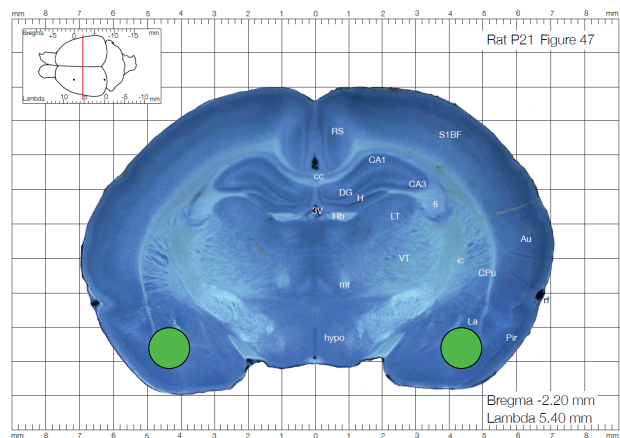
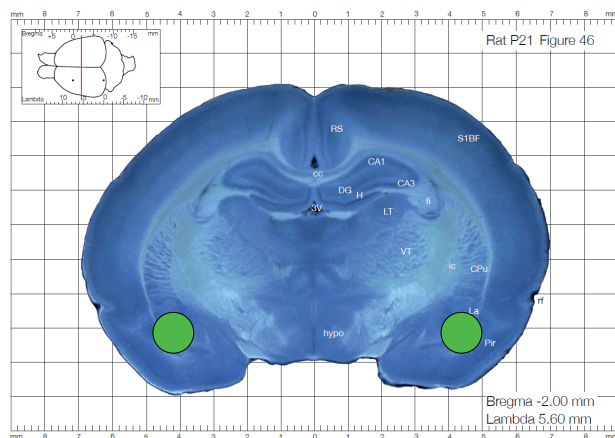
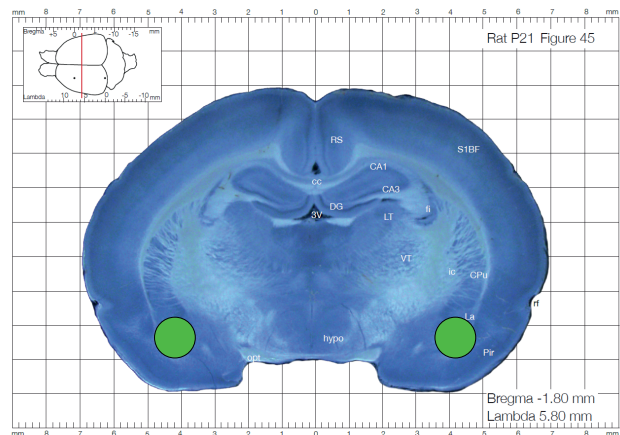
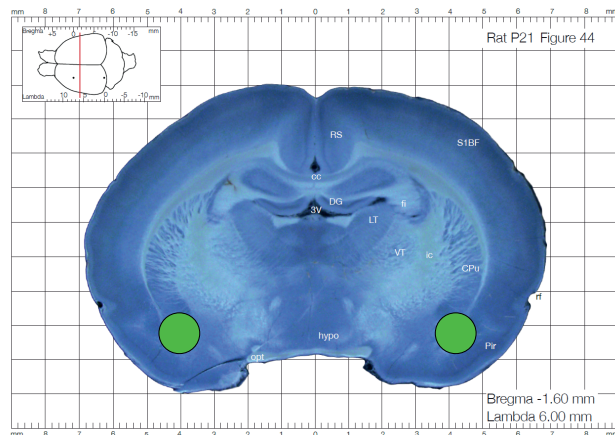


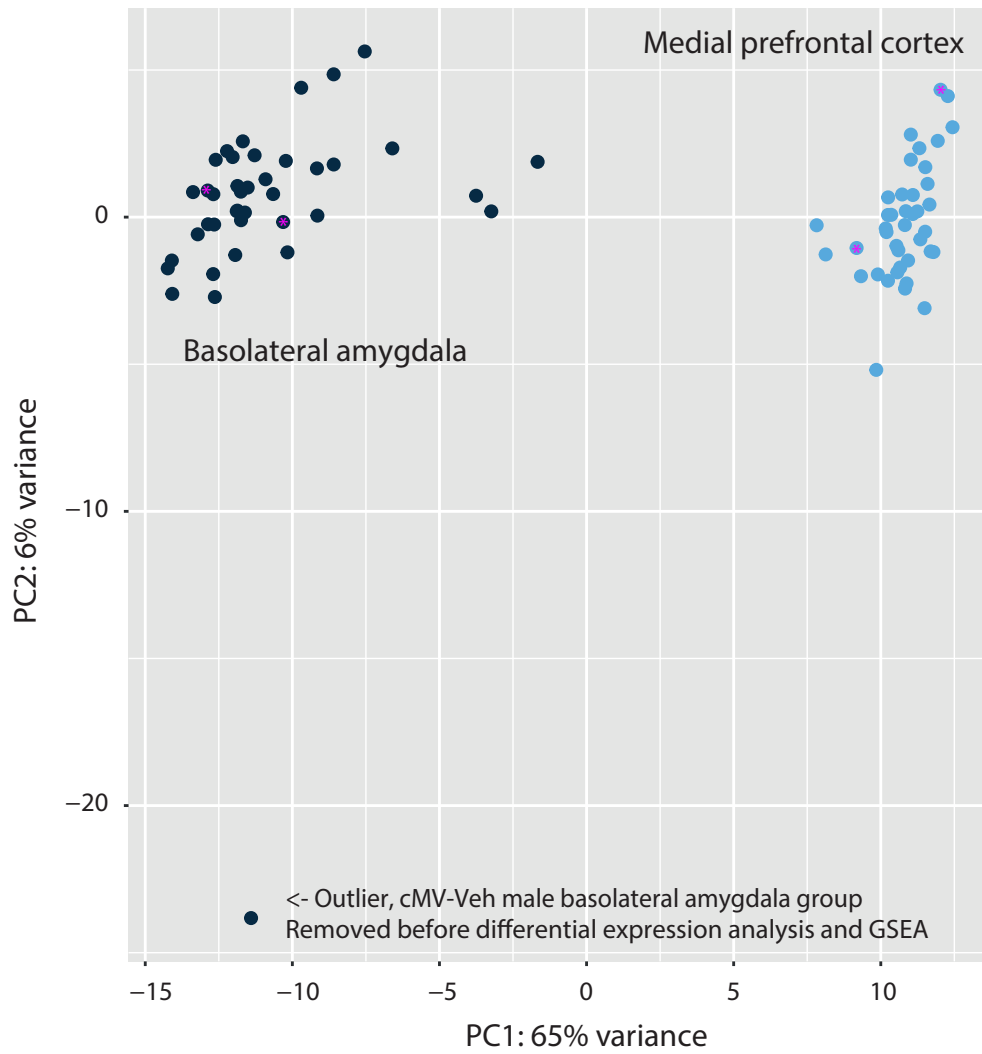
A. Location punches PFC



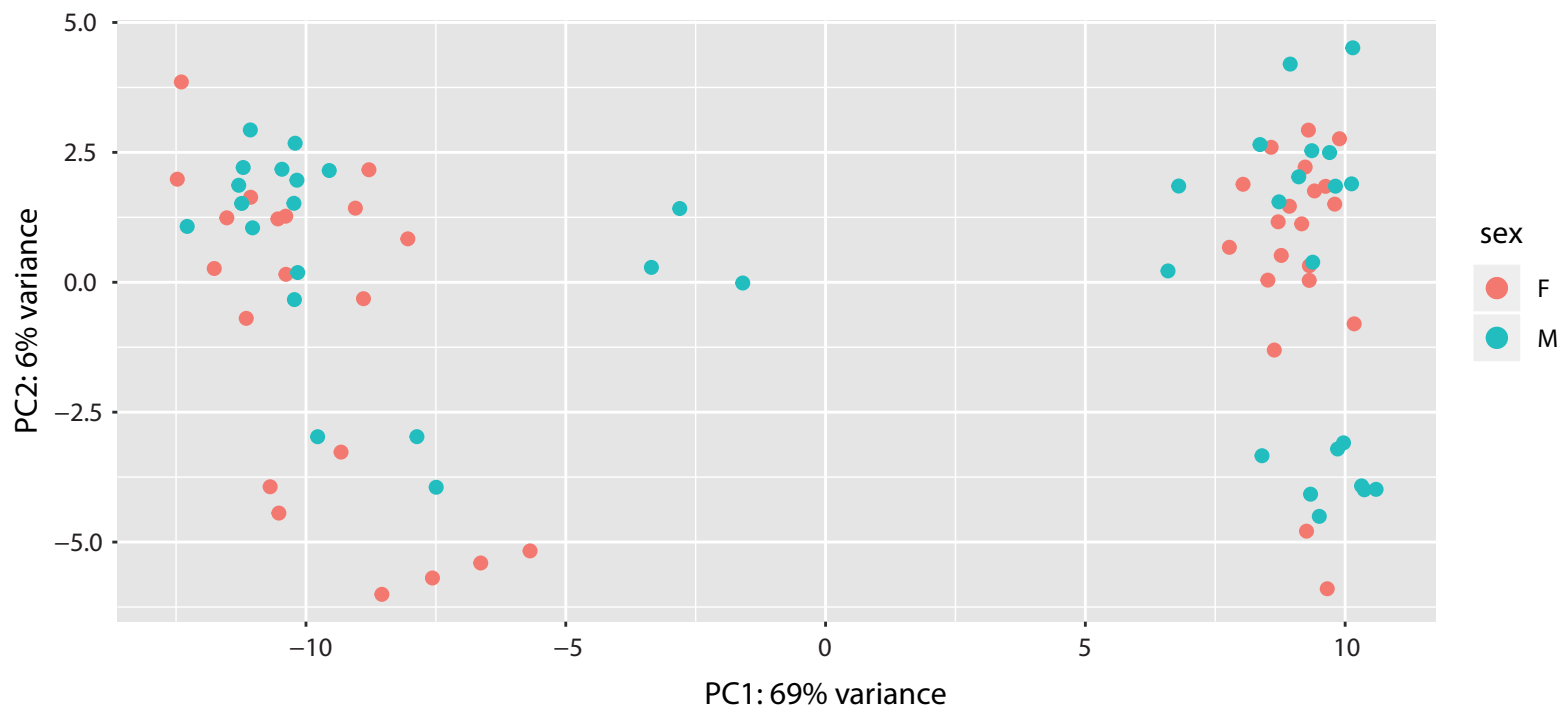
B. Location punches BLA

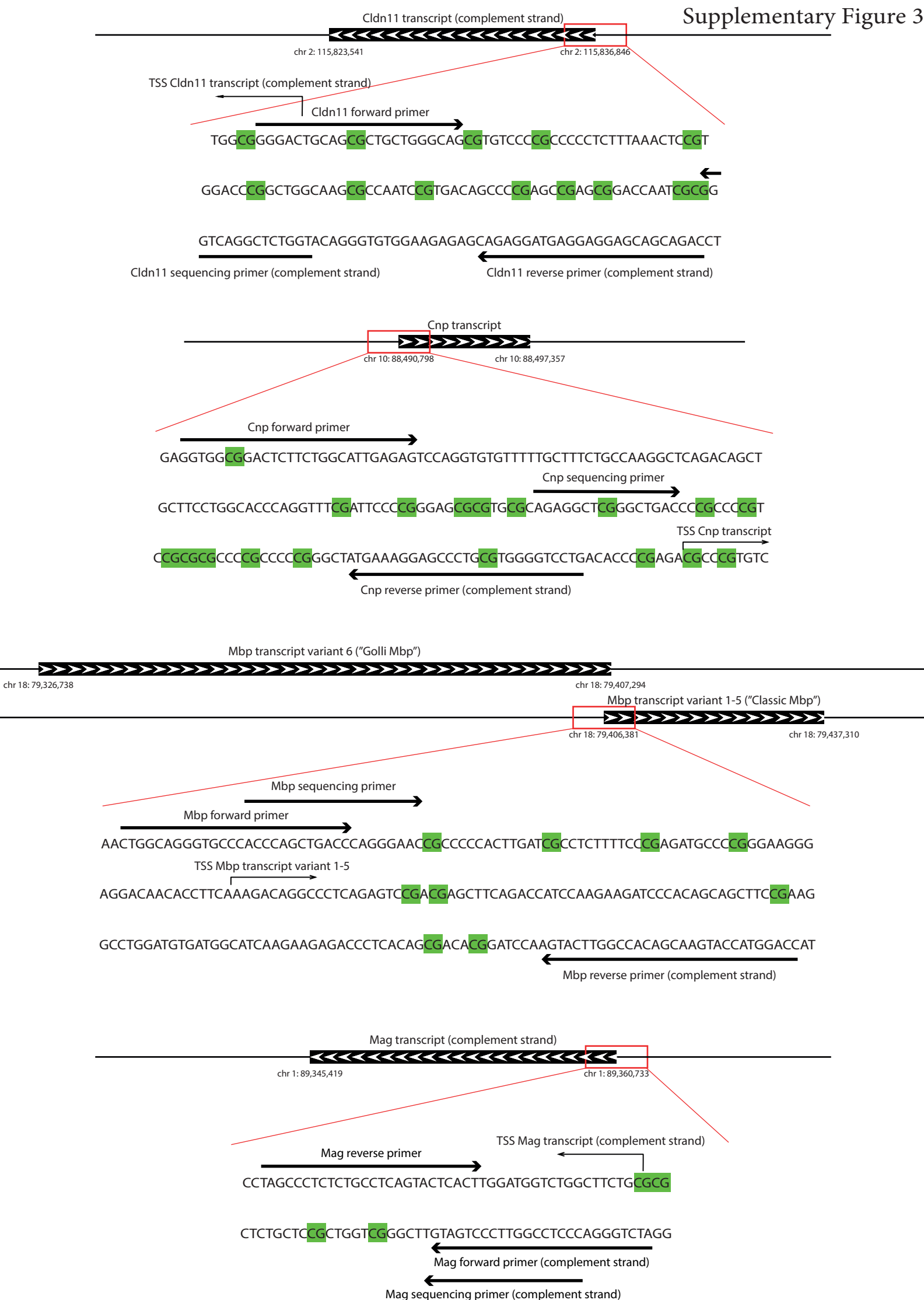


A

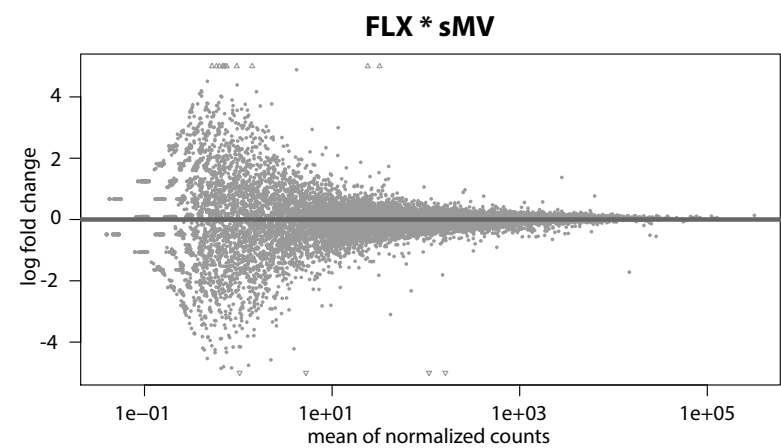
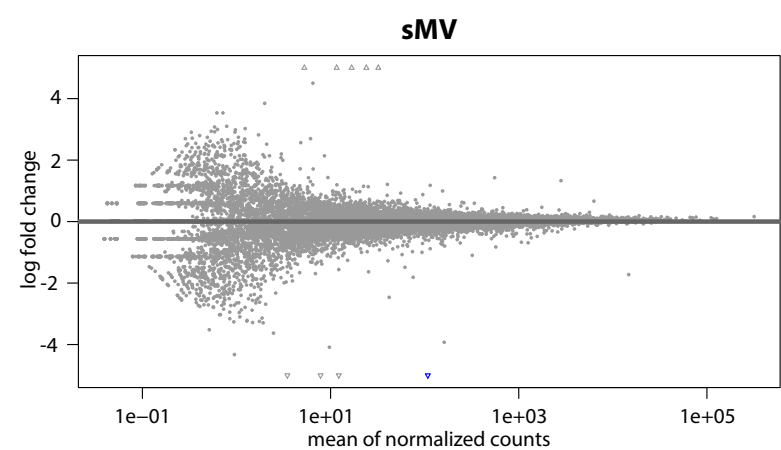
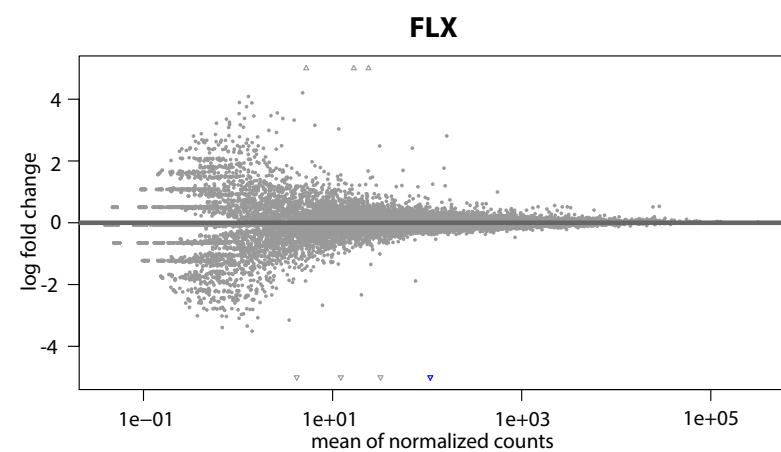


B



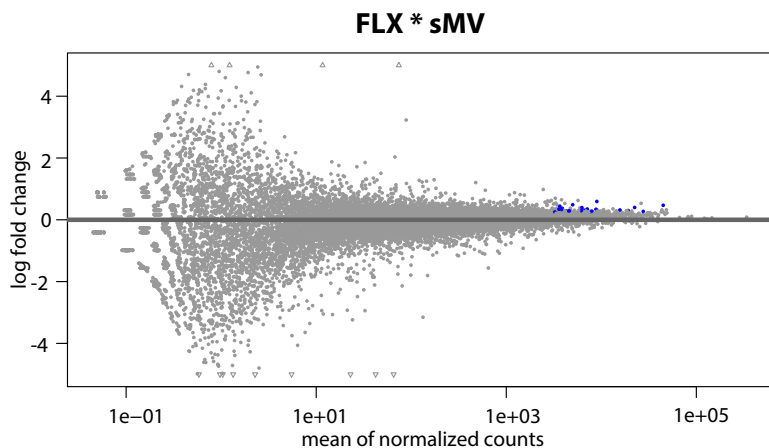
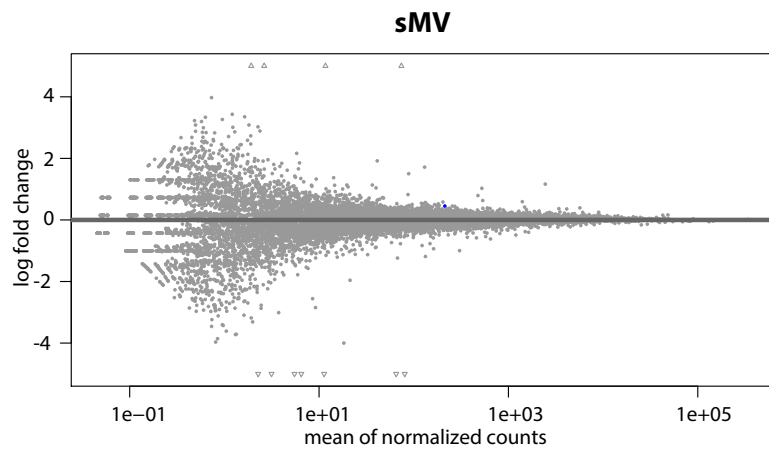
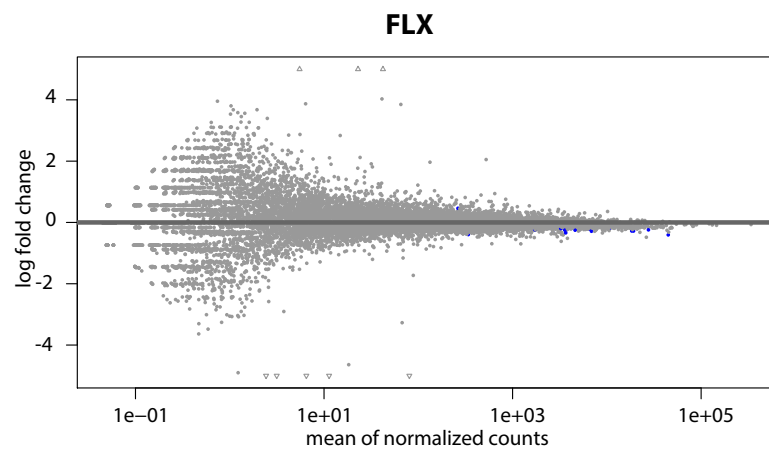


A PFC ♂

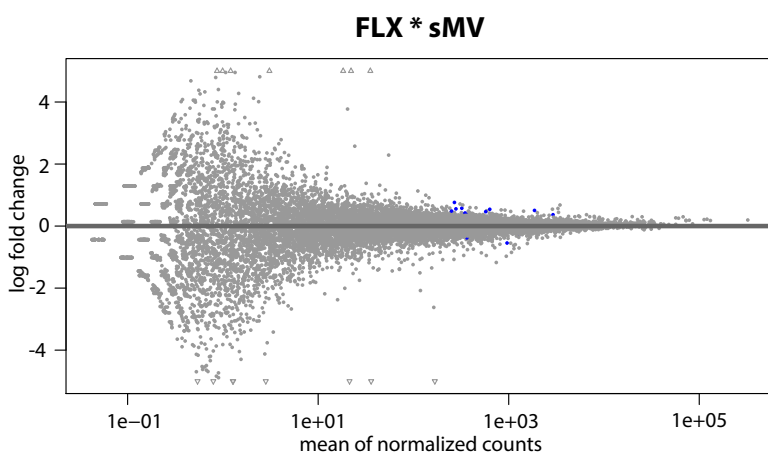
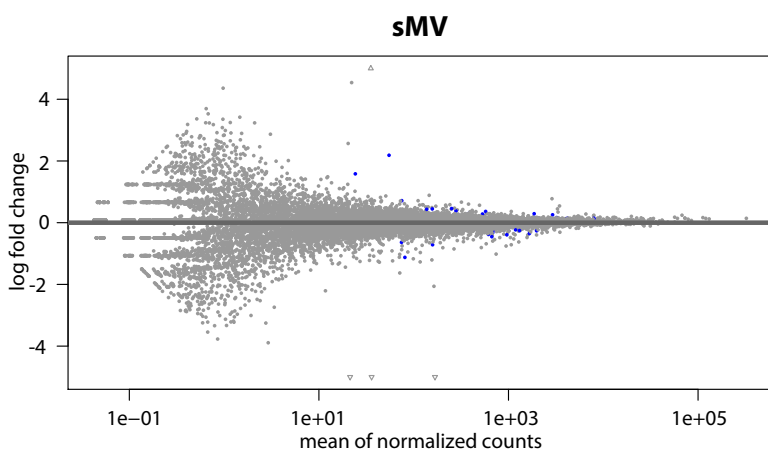
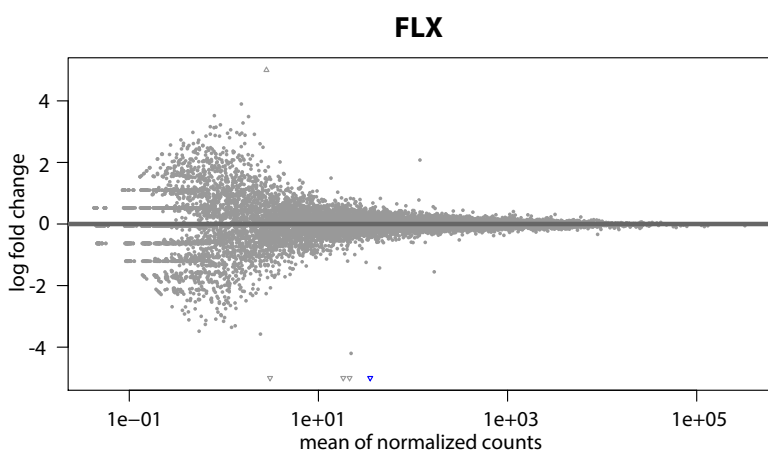


B BLA ♂

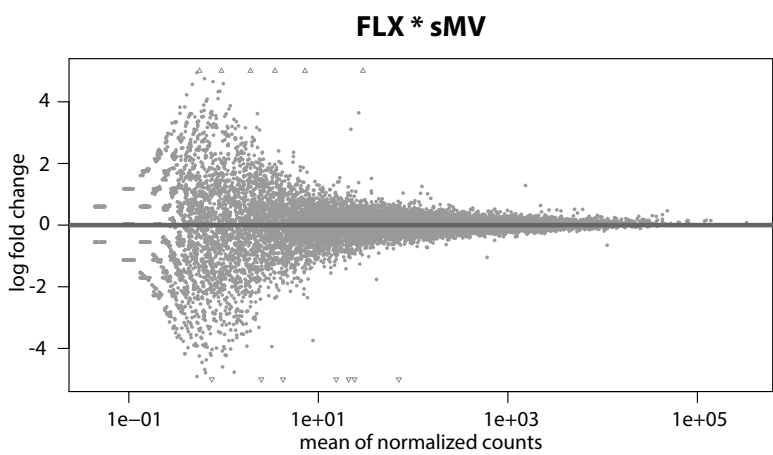
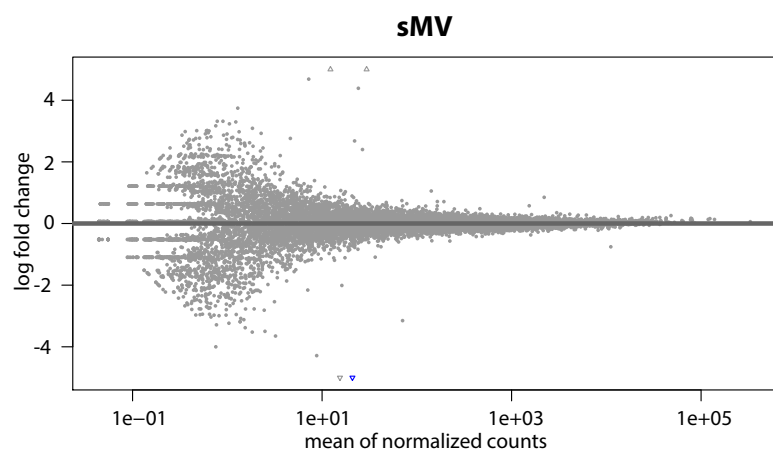
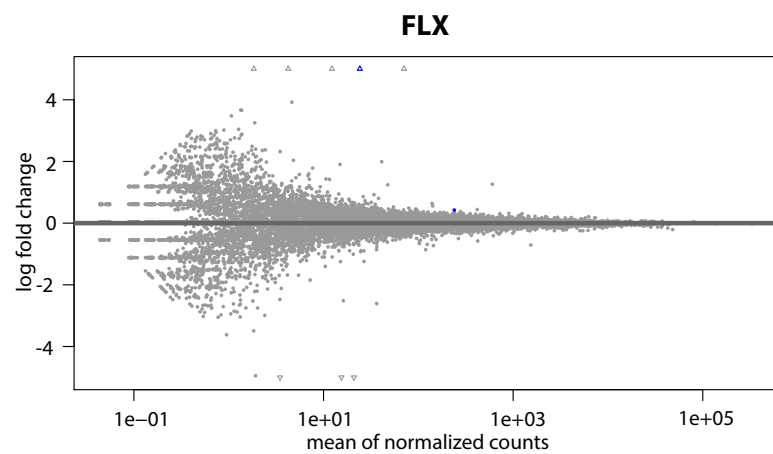
Supplementary Figure 4



C PFC ♀

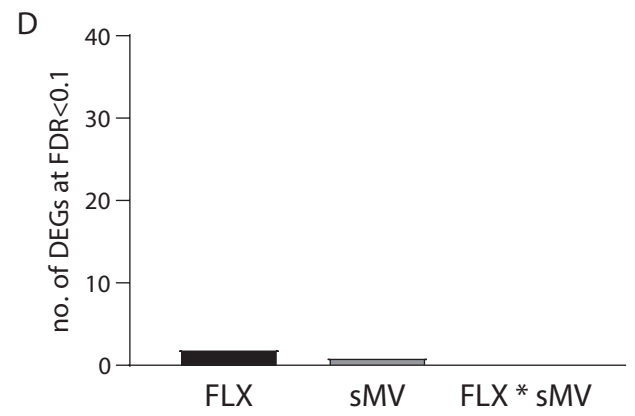
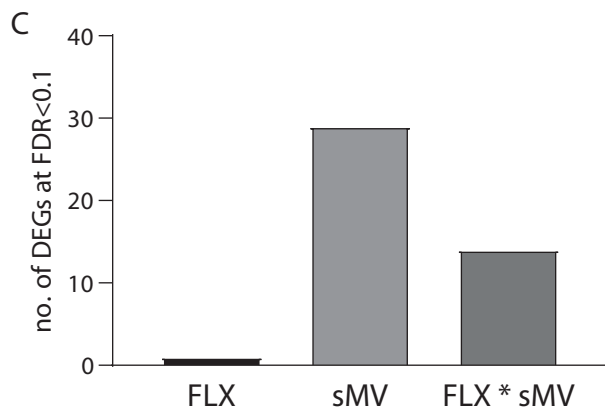
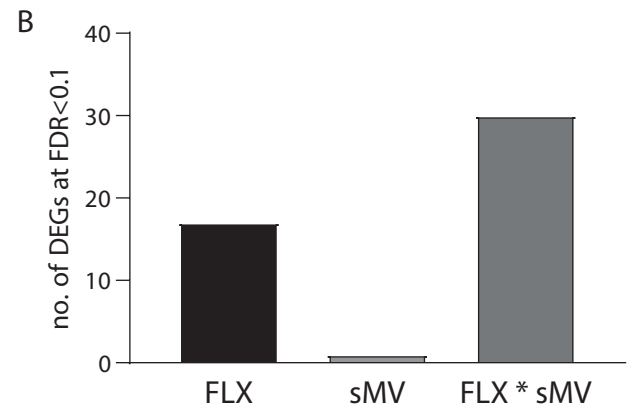
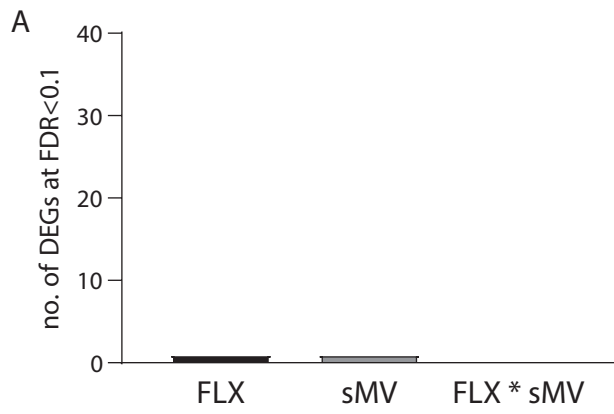


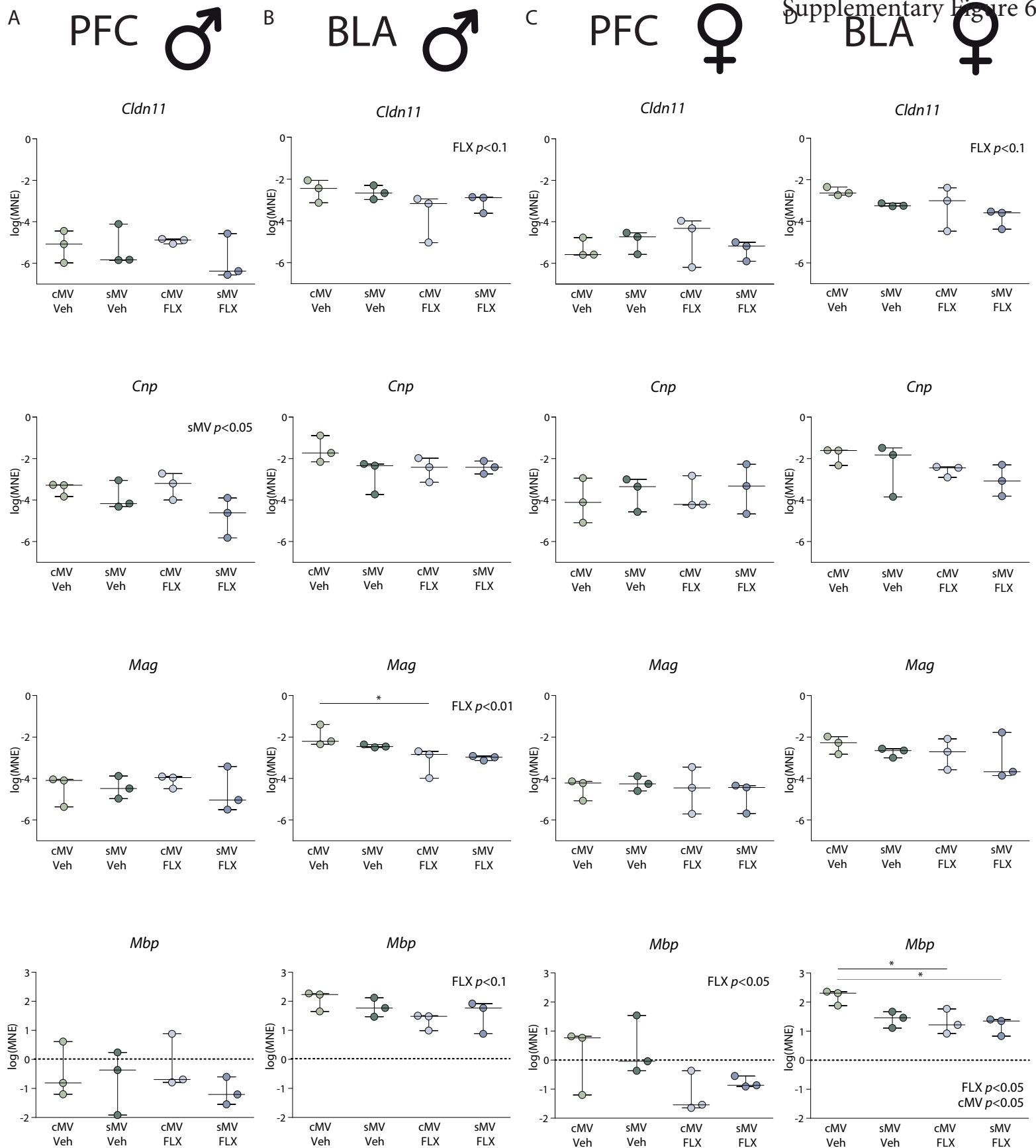
D BLA ♀



PFC

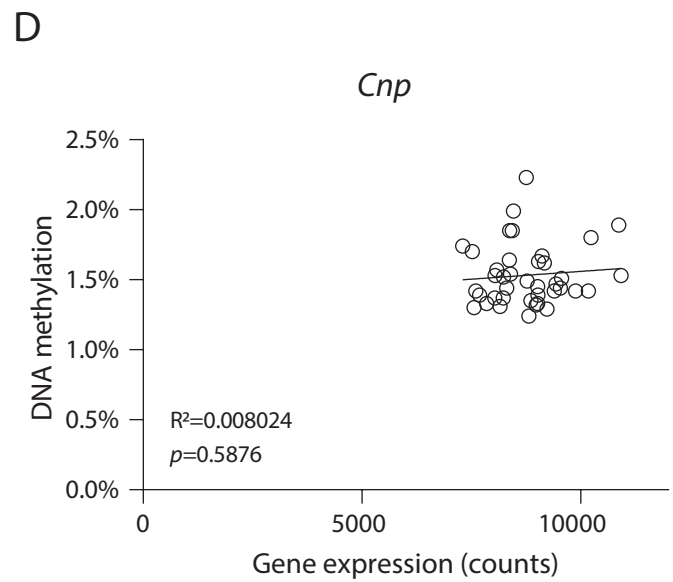
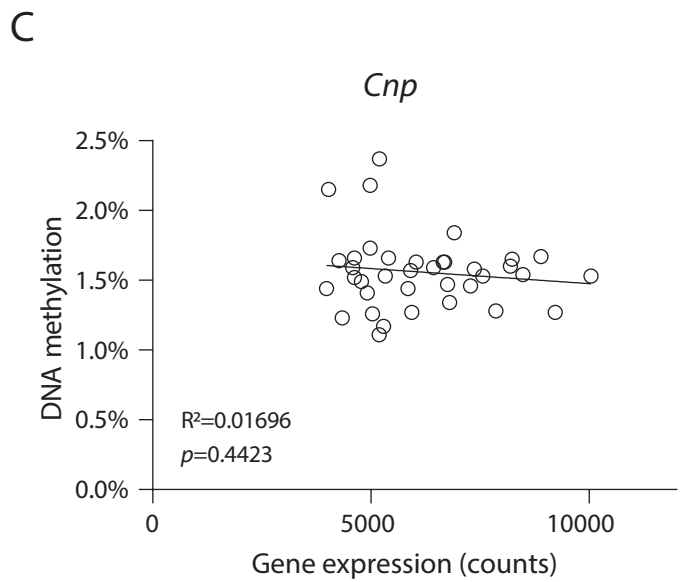
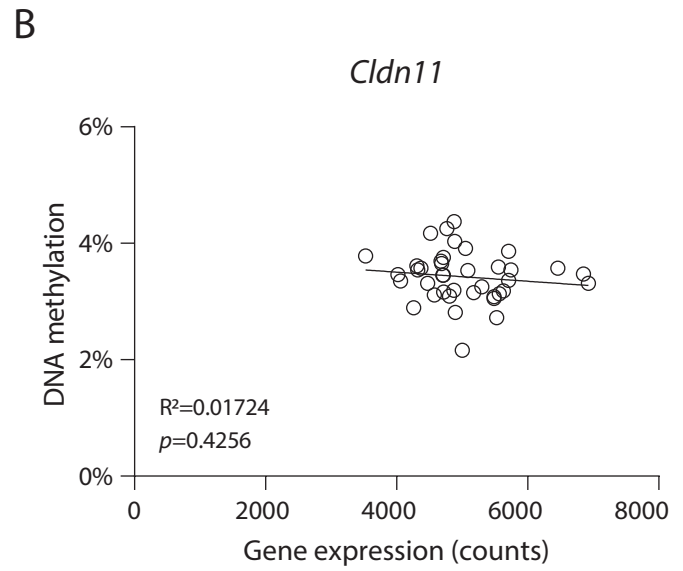
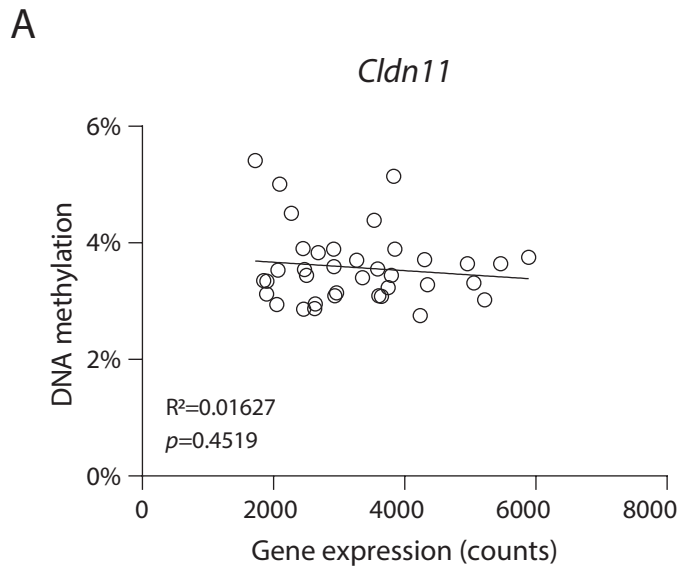
BLA





PFC

BLA



Overview of groups and samples

Sex	cMV/sMV	Veh/FLX	Brain area	N collected	N for RNAseq and DNA methylation	N for qPCR
M	cMV	Veh	PFC	8	5	3
M	cMV	Veh	BLA	8	5	3
M	sMV	Veh	PFC	8	5	3
M	sMV	Veh	BLA	8	5	3
M	cMV	FLX	PFC	8	5	3
M	cMV	FLX	BLA	8	5	3
M	sMV	FLX	PFC	8	5	3
M	sMV	FLX	BLA	8	5	3
F	cMV	Veh	PFC	8	5	3
F	cMV	Veh	BLA	8	5	3
F	sMV	Veh	PFC	8	5	3
F	sMV	Veh	BLA	8	5	3
F	cMV	FLX	PFC	8	5	3
F	cMV	FLX	BLA	8	5	3
F	sMV	FLX	PFC	8	5	3
F	sMV	FLX	BLA	8	5	3

Primer sequences qPCR

Primer name	Sequence (5' to 3')/product code	Final reaction concentration
Actb forward primer	ACCCGCGAGTACAACCTTC	500 nM
Actb reverse primer	ATCGTCATCCATGGCGAACTG	650 nM
Actb probe	FAM- CGTCGCCGGTCCACACCCGC-TAMRA	100 nM
Gapdh	Rn01775763_g1	1X
Cldn11	Rn00584941_m1	1X
Cnp	Rn01399463_m1	1X
Mag	Rn01457782_m1	1X
Mbp	Rn00690431_m1	1X

Primer sequences DNA methylation analysis

Primer name	Primer code	Sequence (5' to 3')
Cldn11 forward primer	r_Cldn11_Fwd_biotin	GGGATTGTAGAGTTGTTGGGTAG
Cldn11 reverse primer	r_Cldn11_Rev	ATCTACTACTCCTCCTCATCCTCTA
Cldn11 sequencing primer	r_Cldn11_seq	ACCAAAACCTAACCC
Cnp forward primer	r_Cnp_Fwd	GGTGGAGGATTTTTTGGTATTGAGAG
Cnp reverse primer	r_Cnp_Rev_biotin	CAAAACCCACCCAAAACCTCCTTCAT
Cnp sequencing primer	r_Cnp_seq3	AGAGGTTAGGGTTGAT
Mag forward primer	r_Mag_Fwd2	TAGATTTTGGGAGGTTAAGGGATTAT
Mag reverse primer	r_Mag_biotin_Rev2	TAACCCTCTCTACCTCAATACTCACT
Mag sequencing primer	r_Mag_seq2	GGGAGGTTAAGGGATTATA
Mbp forward primer	r_Mbp_Fwd	TTGGTAGGGTGTTTATTTAGTTGATT
Mbp reverse primer	r-Mbp_Rev_biotin	AATCCATAATACTTACTATAACCAAATACT
Mbp sequencing primer	r_Mbp_seq	ATTTAGTTGATTTAGGGAAT

PCR conditions

Primer pair	Annealing temperature (°C)	Number of cycles
Cldn11	60	45
Cnp	58	45
Mag	56	45
Mbp	54	50

Supplementary Figure 1: Location of the tissue punches, depicted in green in: A.) The PFC. B.) The BLA.

Supplementary Figure 2: Principal coordinates (PC) plot of gene expression data, depicting: A.) The PFC and BLA cluster separately. One male cMV-Veh sample was determined to be an outlier and was removed before further analyses. The pink asterisks identify samples from cross-fostered offspring (see Methods section under heading “Maternal adversity and fluoxetine treatment”) and show that these samples cluster with all other samples. B.) Males and females do not cluster separately. Related to Supplementary File 2.

Supplementary Figure 3: The genomic location of the primer targets used for DNA amplification and bisulfite sequencing. CpG locations are highlighted in green. A.) *Cldn11*. B.) *Cnp*. C. *Mag*. D. *Mbp*. Related to Supplementary File 4.

Supplementary Figure 4: MA plots of read counts based on FLX, sMV, or FLX*sMV, in: A.) The male PFC. B.) The male BLA. C.) The female PFC. D.) The female BLA. Differentially expressed genes (DEGs) at $FDR < 0.1$ are colored blue. Related to Supplementary Figure 5 and Supplementary File 6.

Supplementary Figure 5: The number of differentially expressed genes (DEGs) at $FDR < 0.1$ associated with FLX, sMV, or FLX*sMV, in: A.) The male PFC. B.) The male BLA. C.) The female PFC. D.) The female BLA. Related to Supplementary Figure 4 and Supplementary File 6.

Supplementary Figure 6: qPCR results of *Cldn11*, *Cnp*, *Mag* and *Mbp* in: A.) The male PFC. B.) The male BLA. C.) The female PFC. D.) The female BLA. Error bars represent median and range. * indicates $p < 0.05$ analyzed with two-way ANOVA. Related to Supplementary File 3 and 8.

Supplementary Figure 7: Scatter plots of DNA methylation percentages and gene counts for: A.) *Cldn11* in the PFC. B.) *Cldn11* in the BLA. C.) *Cnp* in the PFC. D.) *Cnp* in the BLA. Related to Supplementary File 2 and 9.

Supplementary File 1: Overview of groups and samples.

Supplementary File 2: Annotated read counts.

Supplementary File 3: Primer information qPCR.

Supplementary File 4: Primer information DNA methylation analysis.

Supplementary File 5: Gene Set Enrichment Analysis results.

Supplementary File 6: Differential expression analysis.

Supplementary File 7: Gene Set Enrichment Analysis results for Myelin sheath.

Supplementary File 8: qPCR results.

Supplementary File 9: DNA methylation results.