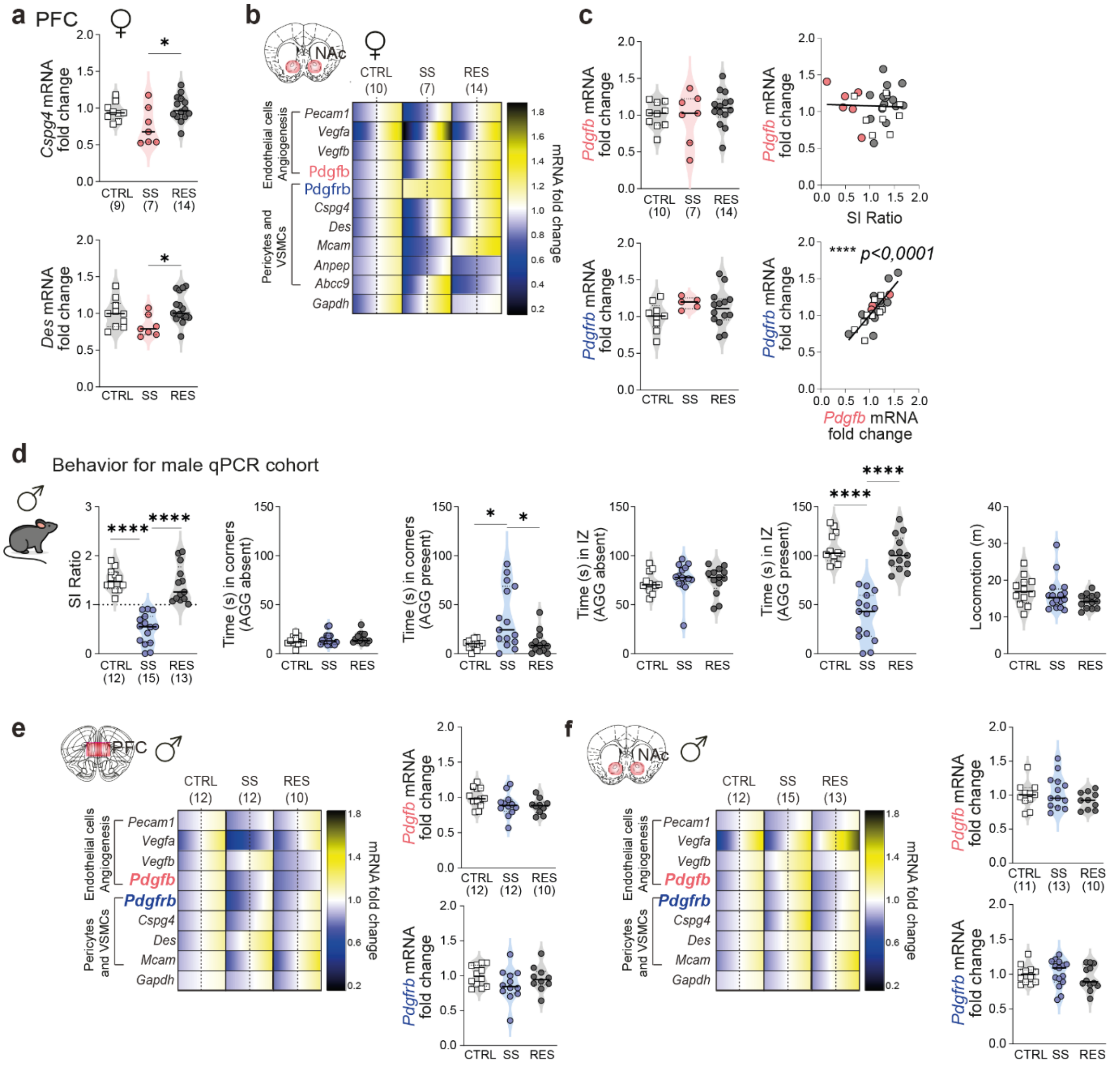
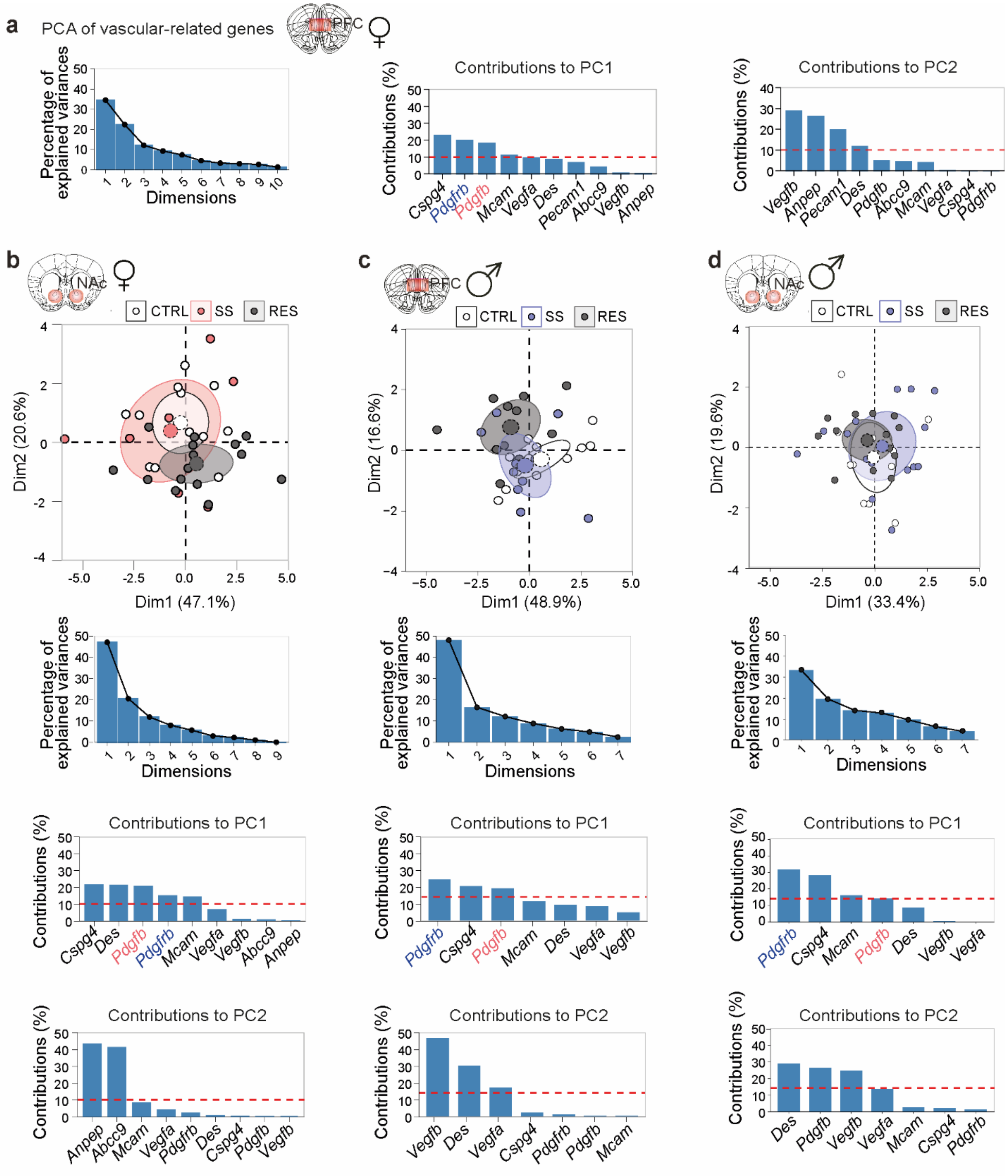
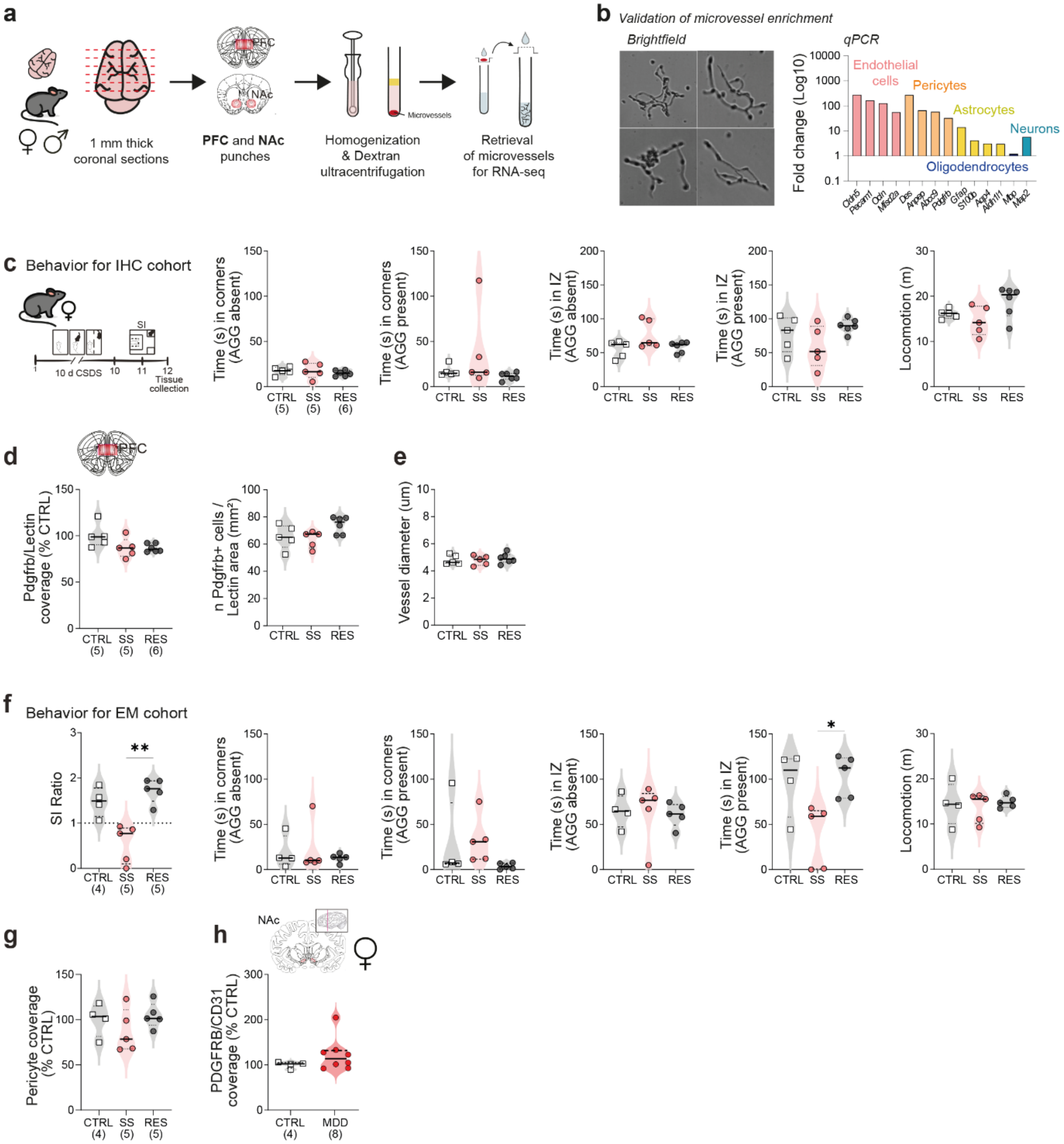


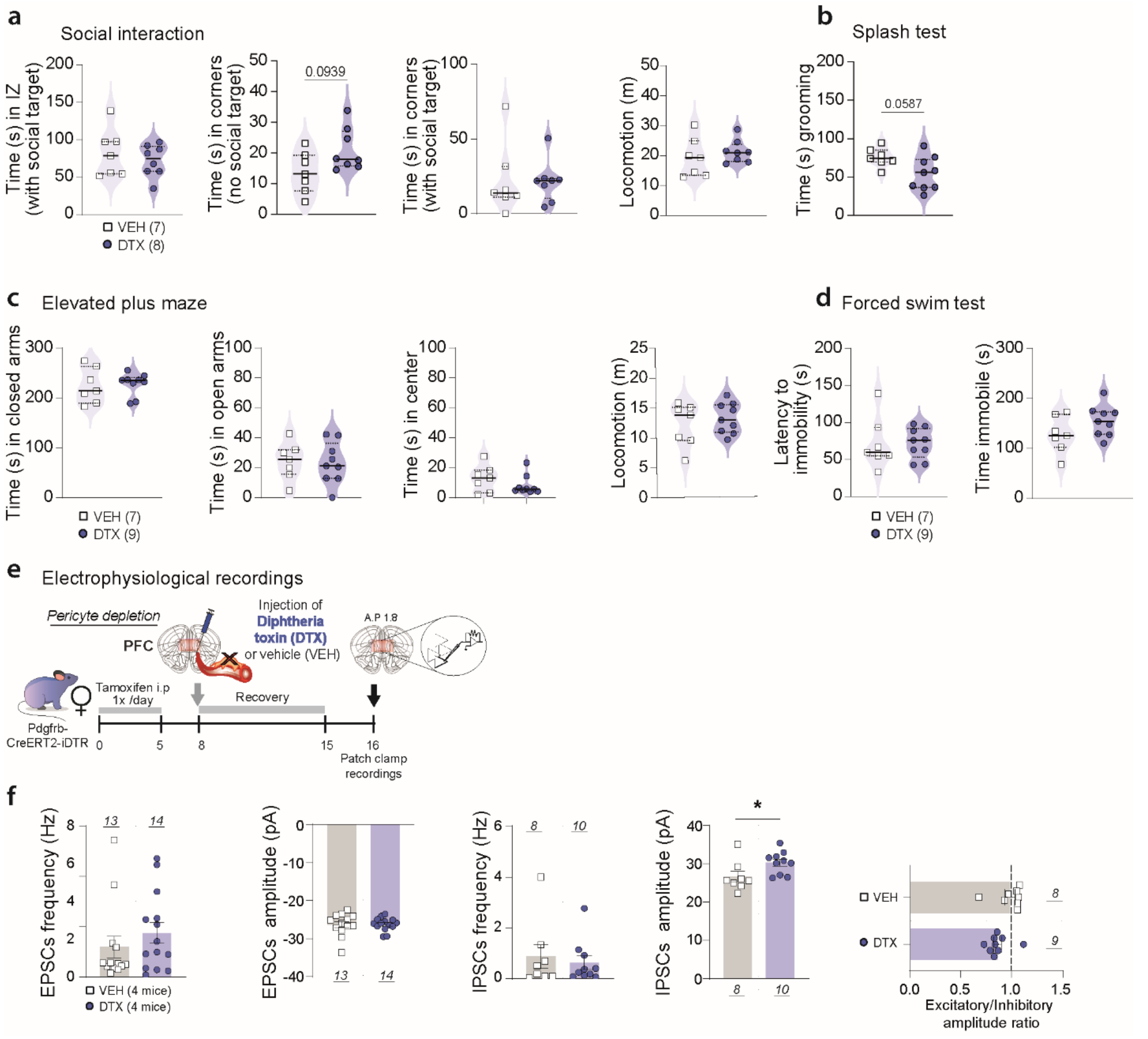
**Supp.Fig.1 - Supplementary data and behavior for qPCR cohorts. a** Additional significant quantitative (q)PCR results for the female prefrontal cortex (PFC). **b** qPCR results for female nucleus accumbens (NAc). Color range in the heatmap indicates individual differences within a group; average represented by the dashed line. **c** *Pdgfb* and *Pdgfrb* and associated correlations for the female NAc. **d** Social interaction (SI) test results for the male chronic social defeat stress (CSDS) cohort. **e-f** Heatmap of qPCR results and graphs for *Pdgfb* and *Pdgfrb* for the male PFC (**e**) and NAc (**f**) respectively, following CSDS. Color range in the heatmap indicates individual differences within a group; average represented by the dashed line. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Number of animals or subjects (n) is indicated on graphs. Correlations were evaluated with Spearman's correlation coefficient; One-way ANOVA followed by Tukey's multiple comparison test for other graphs. $^*p < 0.05$; $^{**}p < 0.01$; $^{****}p < 0.0001$. Source data are provided as a Source Data file.



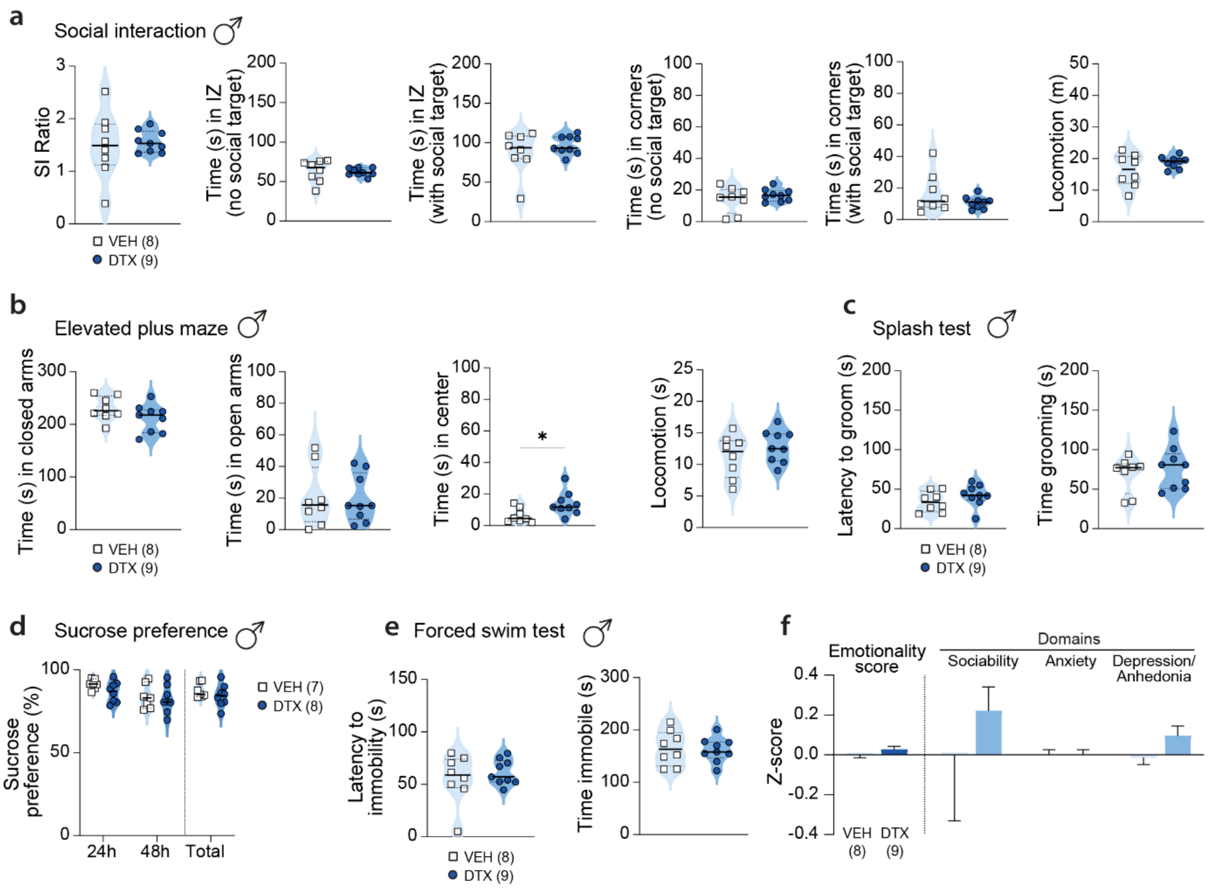
**Supp.Fig.2 – Extended graphs for principal component analysis (PCA). a** Percentage of variance explained by dimension for the female prefrontal cortex (PFC). **b-d** PCA of quantitative (q)PCR genes related to endothelial cells, angiogenesis, pericytes and vascular smooth muscle cells (VSMCs) in the female nucleus accumbens (NAc, **b**), male PFC (**c**) and male NAc (**d**). Dotted circles represent group average. Bar graphs represent percentage of explained variance across dimensions as well as genes contributing to principal component (PC) 1 and PC2, respectively. PCAs computed using the FactoMineR package. Source data are provided as a Source Data file.



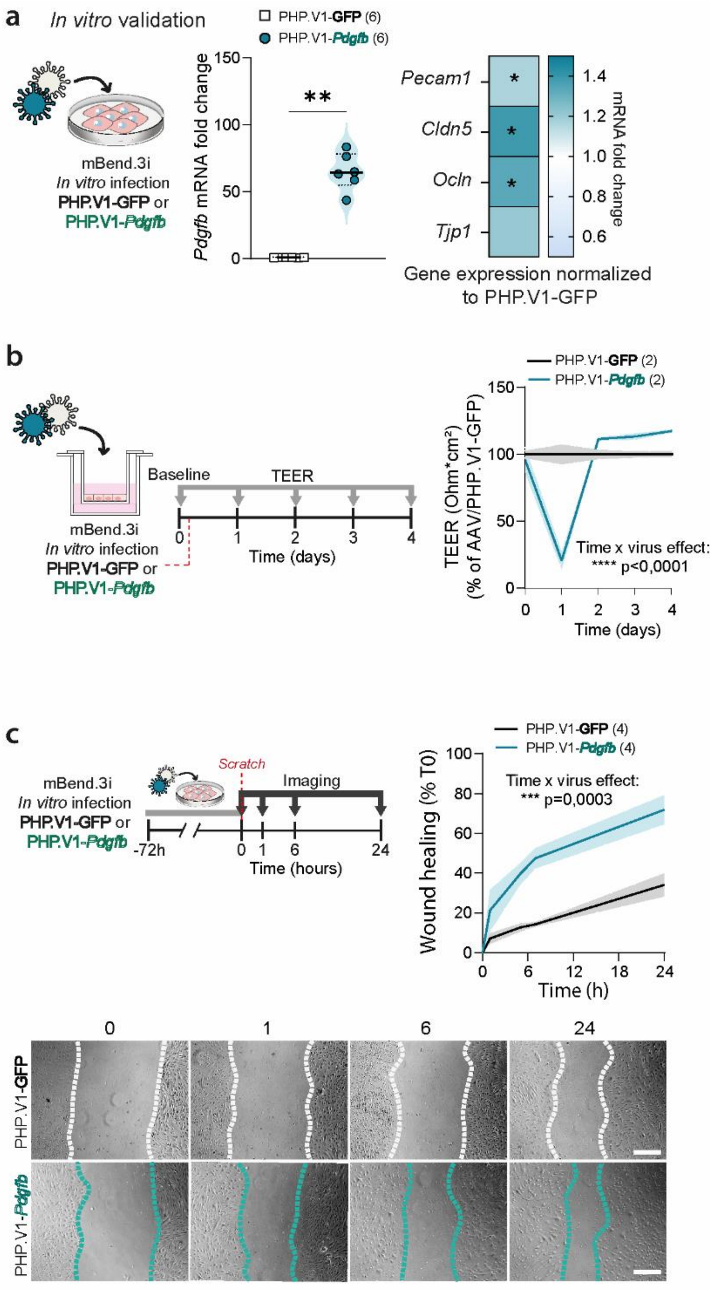
**Supp.Fig.3 – Supplementary data for RNA-sequencing and for mouse and human imaging cohorts. a** Schematic representation of microvessel isolation strategy for male and female prefrontal cortex (PFC) and nucleus accumbens (NAc). **b** Validation of microvessel enrichment in brightfield microscopy and quantitative (q)PCR (n=2). **c** Experimental timeline of chronic social defeat stress (CSDS) and social interaction (SI) test results for the female immunohistochemistry (IHC) cohort. **d** PFC Pdgfrb/lectin coverage and number of Pdgfrb+ cells against Lectin+ area. **e** Diameter of blood vessels analyzed in the female PFC. **f** SI test results for the female electron microscopy (EM) cohort (SI Ratio ***p=0.0010). **g** Pericyte coverage in the female PFC assessed by EM and **h** PDGFRB/CD31 coverage in the woman NAc. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Number of animals or subjects (n) is indicated on graphs. 2-group comparisons evaluated with unpaired Mann-Whitney test; Kruskal-Wallis tests followed by Dunn's multiple comparison test for other graphs. $^*p < 0.05$; $^{**}p < 0.01$. Source data are provided as a Source Data file.



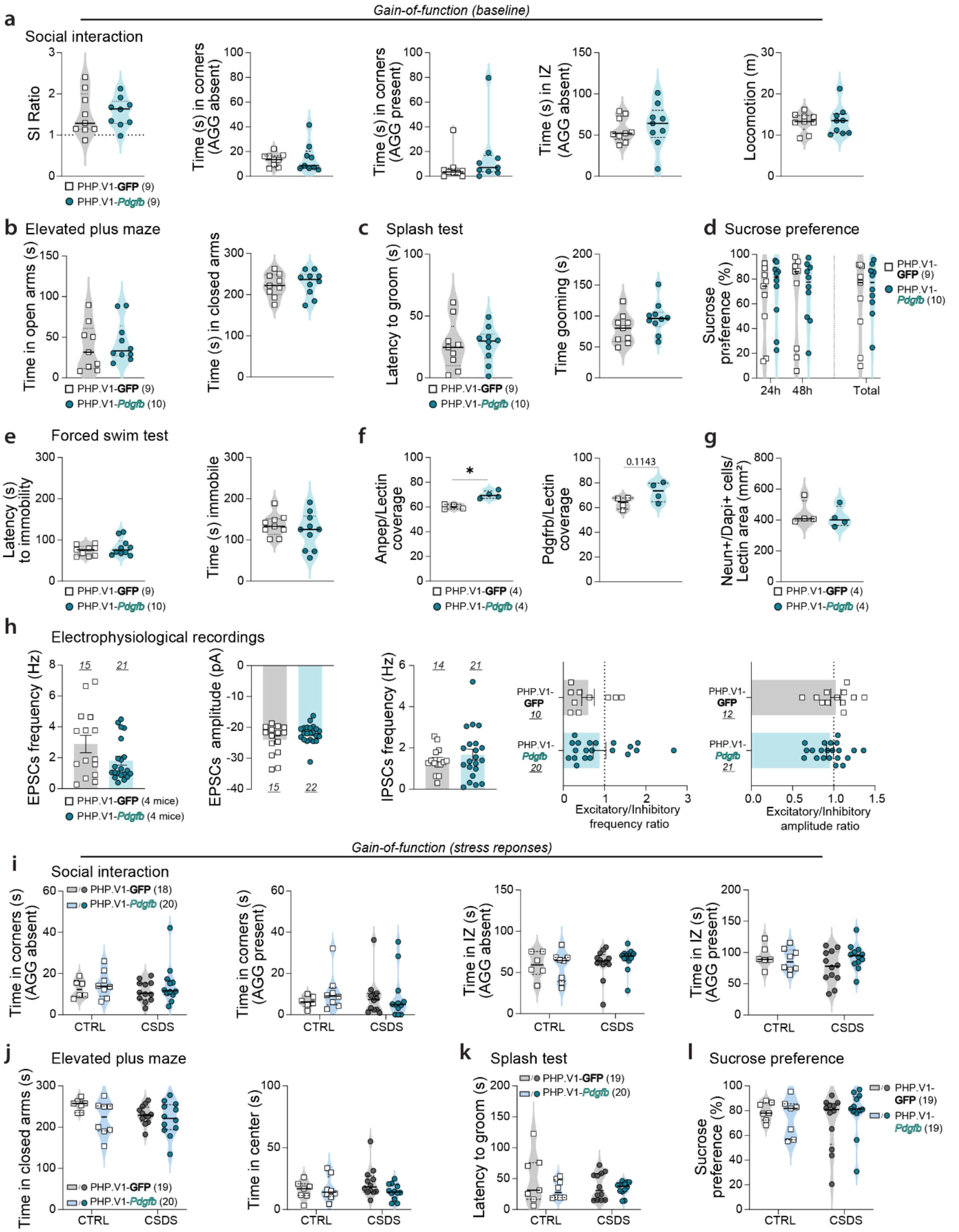
**Supp.Fig.4 - Supplementary data for pericyte ablation experiments in females. a-d** Supplementary results for the social interaction (SI) (**a**), splash test (**b**), elevated plus maze (**c**) and forced swim tests (**d**). **e** Experimental timeline for electrophysiological recordings cohort and **g** extended electrophysiological recordings of PFC pyramidal neurons in the female PFC. Numbers on graph represent total number of recorded cells, across 3 animals per group. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Bar graphs display mean and standard deviation of the mean (±SEM). Number of replicates (n) is indicated on graphs. 2-group comparisons evaluated with unpaired T-test or Mann-Whitney test. *$p < 0.05$. Source data are provided as a Source Data file.



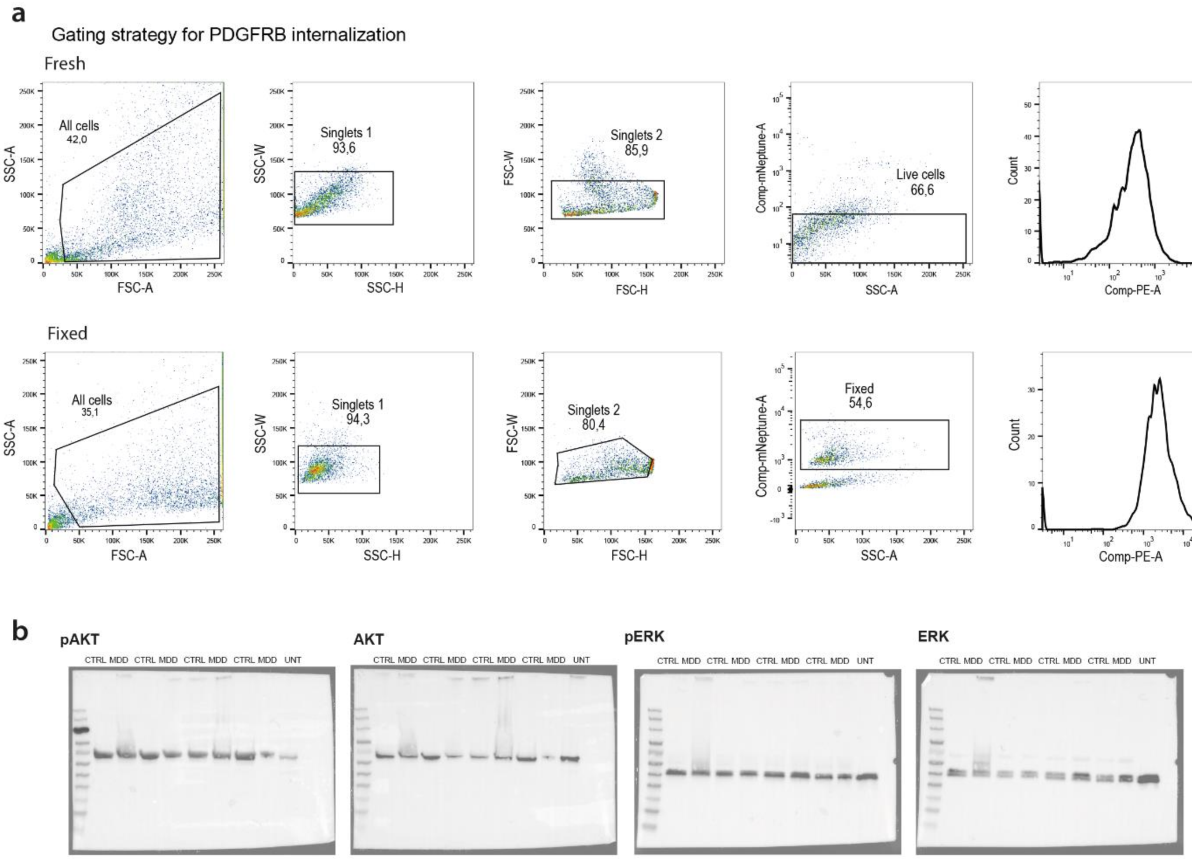
**Supp.Fig.5 - Supplementary data for pericyte ablation experiments in male mice. a-e** Behavioral results of male mice for pericyte ablation experiments in the SI (**a**), elevated plus maze (**b**), splash (**c**), sucrose preference (**d**) and forced swim tests (**e**), respectively. **f** Male emotionality Z-score generated from behavioral datapoints and separated domains. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Bar graphs display mean and standard deviation of the mean (±SEM). Number of animals or subjects (n) is indicated on graphs. 2-group comparisons evaluated with unpaired Mann-Whitney test; *p < 0.05. Source data are provided as a Source Data file.



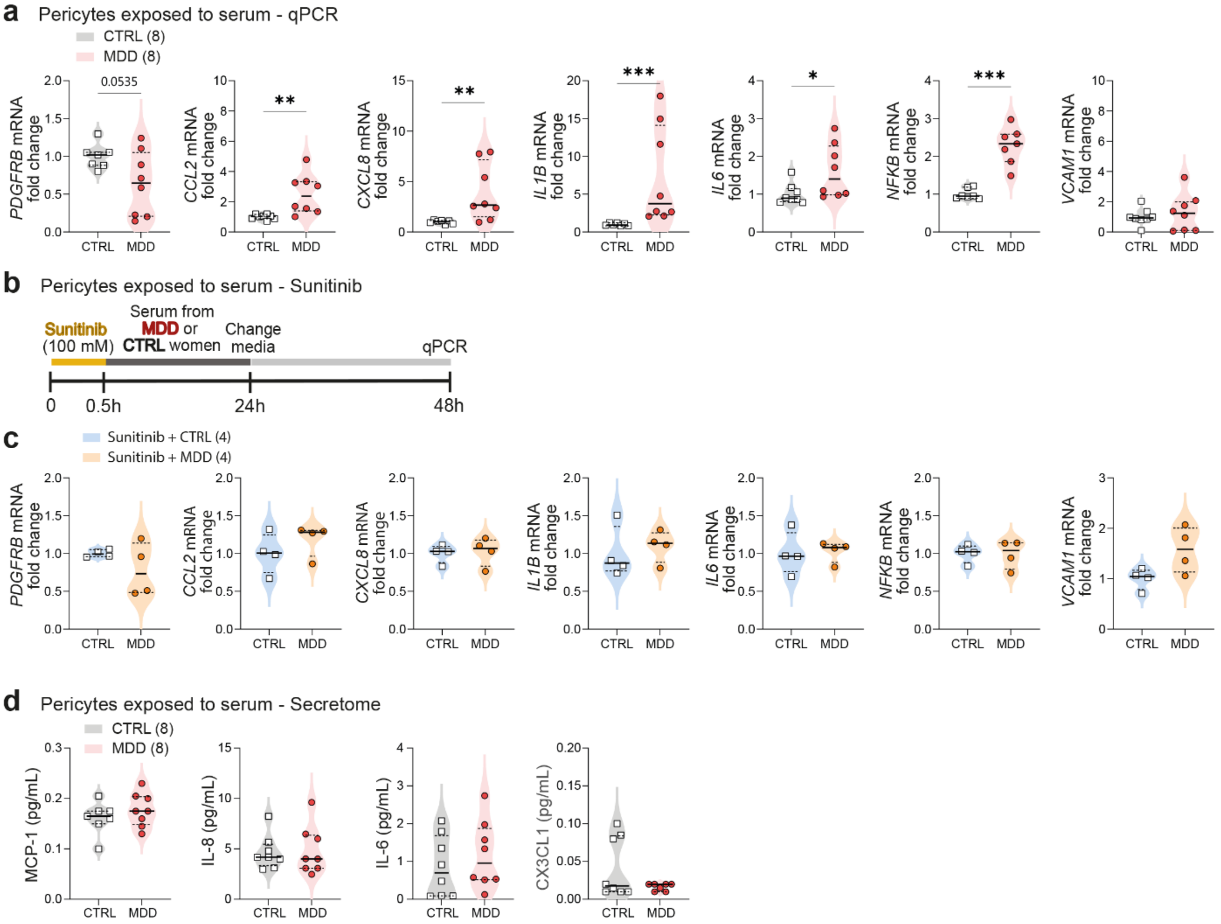
**Supp.Fig.6 – In vitro validation of PHP.V1-*Pdgfb* virus. a** Quantitative (q)PCR results of *in vitro* mouse endothelial cells (mBend.3i) exposed to PHP.V1-*Pdgfb* or PHP.V1-GFP viruses for 72h (*Pdgfb* **p=0.0022, Pecam*1* *p=0.0411, *Cldn5* *p=0.0152, *Ocln* *p=0.0152) **b** Experimental timeline and results of transendothelial electrical resistance (TEER) of mBend.3i exposed to PHP.V1 viruses across time (Time x Virus: ****$p<0.0001$). **c** Experimental timeline and results of wound healing assay of mBend.3i cells exposed to PHP.V1 viruses across time (Time x Virus ***p=0.0003) and representative images. Scale bar= 300 µm. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. For other graphs, full line represents group average and shadowed area around represents standard deviation of the mean (±SEM). Number of replicates (n) is indicated on graphs. 2-group comparisons evaluated with unpaired Mann-Whitney test. Grouped analyses with repeated measures across time were assessed with two-way ANOVA followed by Sidak multiple comparison test. *$p < 0.05$; **$p < 0.01$; ***$p < 0.001$; ****$p < 0.0001$. Source data are provided as a Source Data file.



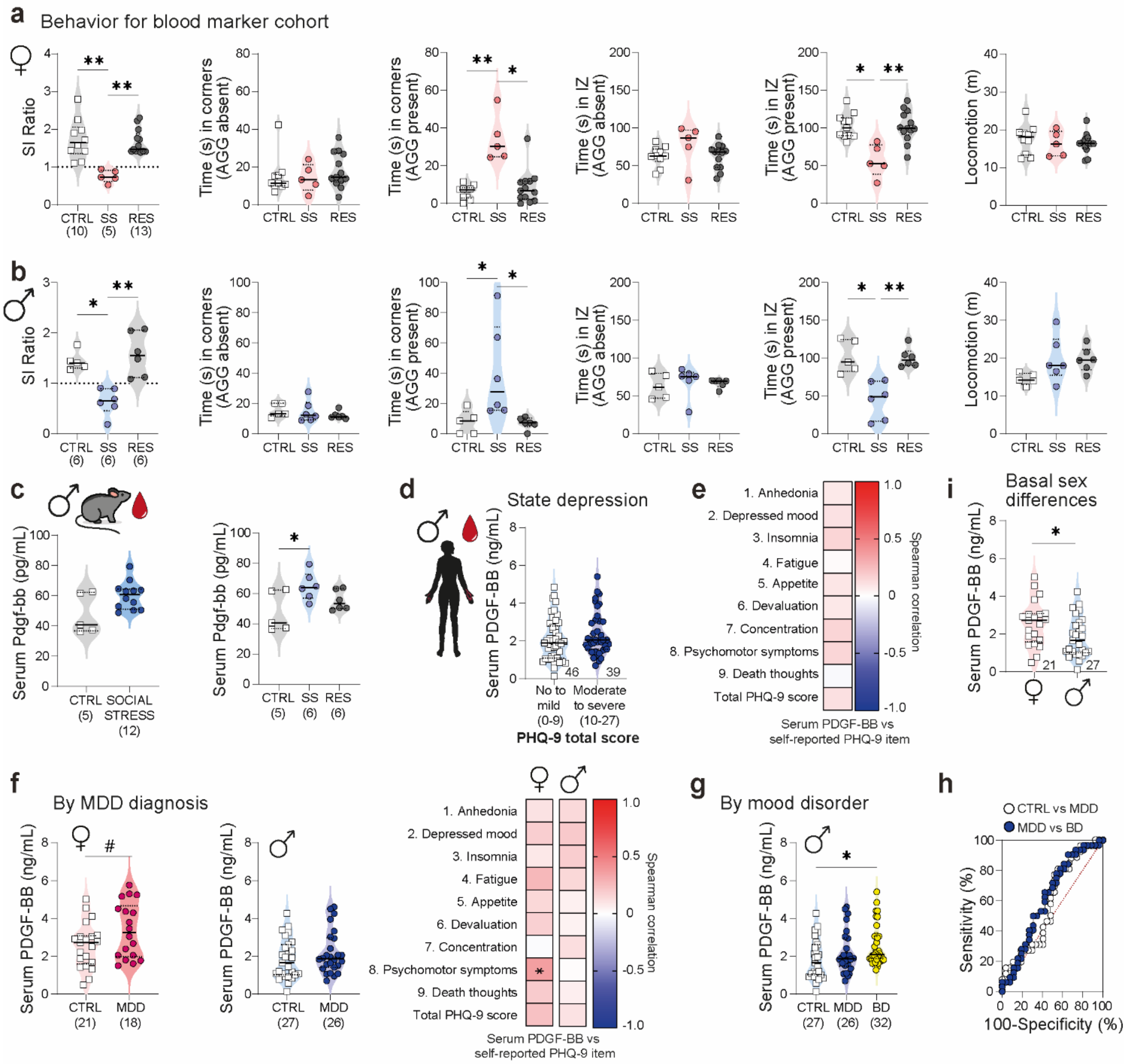
**Supp.Fig.7 – Supplementary data for PHP.V1-Pdgfb baseline and chronic stress cohorts. a-f** Extended behavioral data for gain-of-function baseline cohort for the social interaction (SI) (**a**), elevated plus maze (EPM, **b**), splash (**c**), sucrose preference (**d**) and forced swim (**e**) tests, respectively. **f** Immunohistochemistry (IHC) quantification of Anpep/Lectin coverage (*p=0.0286) and Pdgfrb/Lectin coverage in the female prefrontal cortex (PFC) following behavioral assessments. **g** IHC quantification of neuron (Neun+Dapi+) density per Lectin area in the female PFC. **h** Extended electrophysiological recordings of PFC pyramidal neurons in the female PFC. Numbers on graph represent total number of recorded cells, across 4 animals per group **i-l** Extended behavioral data for gain-of-function chronic social defeat stress cohort in the SI (**i**), EPM (**j**), splash (**k**) and sucrose preference (**l**) tests, respectively. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Bar graphs display mean and standard deviation of the mean (±SEM). Number of replicates (n) is indicated on graphs. 2-group comparisons evaluated with unpaired T-test or Mann-Whitney test. 4-group comparisons were assessed with two-way ANOVA followed by Sidak multiple comparison test. *$p < 0.05$. Source data are provided as a Source Data file.



**Supp.Fig.8 – Gating strategy for flow cytometry and full blots. a** Representative gating strategy for flow cytometry PDGFRB kinetics experiments for fresh (membrane) and fixed (total) cell fractions. **b** Full blots for phosphorylated (p)AKT, AKT, pERK and ERK after 3h of serum stimulation. Source data are provided as a Source Data file.



**Supp.Fig.9 – Supplementary transcriptomic and secretome results for *in vitro* experiments. a** Quantitative (q)PCR results for pericyte, inflammatory and cell adhesion-related genes (*CCL2* **p=0.0019, *CXCL8* **p=0.0059, *IL1B* ***p=0.0003, *IL6* *p=0.0281, *NFKB* ***p=0.0006). **b** Experimental timeline for PDGFRB inhibition (Sunitinib) experiments. **c** qPCR for results for pericyte, inflammatory and cell adhesion-related genes for Sunitinib treatment cohort. **d** Quantification of pericyte secretome following serum stimulation. Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Number of replicates (n) is indicated on graphs. 2-group comparisons evaluated with Mann-Whitney test. *$p < 0.05$; **$p < 0.01$; ***$p < 0.001$. Source data are provided as a Source Data file.



**Supp.Fig.10 – Supplementary data for mouse and human blood marker cohorts. a-b** Social interaction (SI) test data for female (**a**, SI Ratio **p=0.0025) and male (**b**, SI Ratio ***p=0.0005) blood marker cohorts. **c** Serum Pdgf-bb levels (pg/mL) for males (CTRL vs SS *p=0.0381). **d** Serum levels of PDGF-BB in men reporting no to mild vs moderate to severe depressive symptoms on the Patient Health Questionnaire (PHQ-9). **e** Correlation between serum PDGF-BB levels and PHQ-9 item score for men. **f** Serum PDGF-BB levels for women and men with or without a major depressive disorder (MDD) diagnosis (women MDD vs CTRL #p=0.0626) and correlation between serum PDGF-BB levels and PHQ-9 item score for individuals with MDD. **g** Serum PDGF-BB levels for men stratified by mood disorder diagnosis (CTRL vs bipolar disorder [BD] *p=0.0411). **h** Receiver operating characteristic (ROC) curve of serum PDGF-BB levels between CTRL and MDD (white) and BD and MDD (blue). Violin plots show the frequency distribution of the data. Full lines represent the median and dotted lines represent the first and third quartiles. Number of animals or subjects (n) is indicated on graphs. Correlations evaluated with non-parametric Spearman test, 2-group comparisons were evaluated with unpaired t-Test or Mann-Whitney test, 3-group comparisons with Kruskall-Wallis followed by Dunns's multiple comparison test. *p < 0.05; **p < 0.01. Source data are provided as a Source Data file.