Supplementary Material for:

Adaptive alterations in the mesoaccumbal network following peripheral nerve

injury

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Six supplementary figures.

Supplemental Figures



Figure S1 - Ren et al.



0.7768 for **f**). Whisker box plots are displayed as median, lower and upper quartiles, and whiskers representing minimum and maximum of the data.

Figure S2 - Ren et al.



Figure S2. SNI increased the proportion of calcium-permeable AMPARs at PL-cNAc synapses. *a-c*, Calcium-permeable AMPAR antagonist Naspm decreased AMPAR EPSC amplitudes in sham and SNI mice (n = 7 neurons from 5 mice per group; Wilcoxon test with W = -28, p = 0.0156 for *b* W = -28, p = 0.0156 for *c*). *d*, Naspm had bigger effect on the d2SPNs from SNI mice than those from sham mice (Mann–Whitney *U* test with U = 7, p = 0.0262). *e-f*: Naspm reversed enhanced A/N ratio at PL-cNAc d2SPNs synapse in SNI mice (n = 6 neurons from 5 mice per group; Mann– Whitney U test with U = 5, p = 0.0411; calibration: 50 pA, 100 ms). Data are presented as whisker box plots displaying median, lower and upper quartiles, and whiskers representing minimum and maximum of the data.

Figure S3 - Ren et al.



Figure S3. In open field test, chemogenetic activation of cNAc d2SPNs in PSAM-5HT3 expressing SNI mice by PSEM89S treatment unchanged locomotor activities (U = 17, p = 0.9773 for Sham versus Saline-SNI; U = 19, p = 0.9433 for Saline-SNI versus PSEM-SNI). Data are reported as median, first and third quartiles (box plots), and minimum and maximum of data set (whiskers), and are analyzed by Mann–Whitney test.

Figure S4 - Ren et al.



Figure S4. *a*, The Chemogenetic inhibition of cNAc projection VTA neurons by intraperitoneal injections of PSEM in RV-Cre (in cNAc) and AAV-PSAM-GlyR (VTA) viruses infected mice had no effect on SNI-induced tactile allodynia (n = 6 for each group; U = 15.50, p = 0.7359). *b*, activation msNAc projecting VTA neurons by the same virus strategy unchanged the social recognition deficits in SNI mice (n = 5 in control and n = 6 in PSEM; U = 20, p = 0.2159). Data are reported as median, first and third quartiles (box plots), and minimum and maximum of data set (whiskers), and are analyzed by Mann–Whitney test.

Figure S5 - Ren et al.



Figure S5. Biocytin visualized the SPNs' dendritic morphology in the cNAc slices from
Christmas (Xmas) transgenic mice. *a*, The d2SPNs (eGFP-positive, green) and d1SPNs (Td tomato-positive, red) are identified in the same cNAc slice taken from BAC transgenic mouse (Calibration: 20 μm). *b*, The biocytin-filled neuron overlapped with populations of d2SPNs. *c*, Another biocytin-filled neuron overlapped with populations of d1SPNs.





Figure S6. Morphological analysis in reconstructed d1SPNs from SNI and Sham animals. *a-c*, For d1SPNs, no significant difference in Sholl analysis or total tree length was detected between SNI and Sham (n = 8 from 5 mice in each group, U = 13639 and p = 0.5946 for *b* and U = 31 and p = 0.9319 for *c*, Mann–Whitney test). *d*: Representative images of d1SPN dendrites/spines from SNI/Sham animals. *e*, Spine density of d1SPNs were similar between SNI and Sham (n = 8 from 5 mice in each group, Mann–Whitney test with U = 21, p = 0.2747). Data for *b* are shown as median with shaded interquartile (quartile 1 to quartile 3); whisker box plots are displayed as median, lower and upper quartiles, and whiskers representing minimum and maximum of the data.