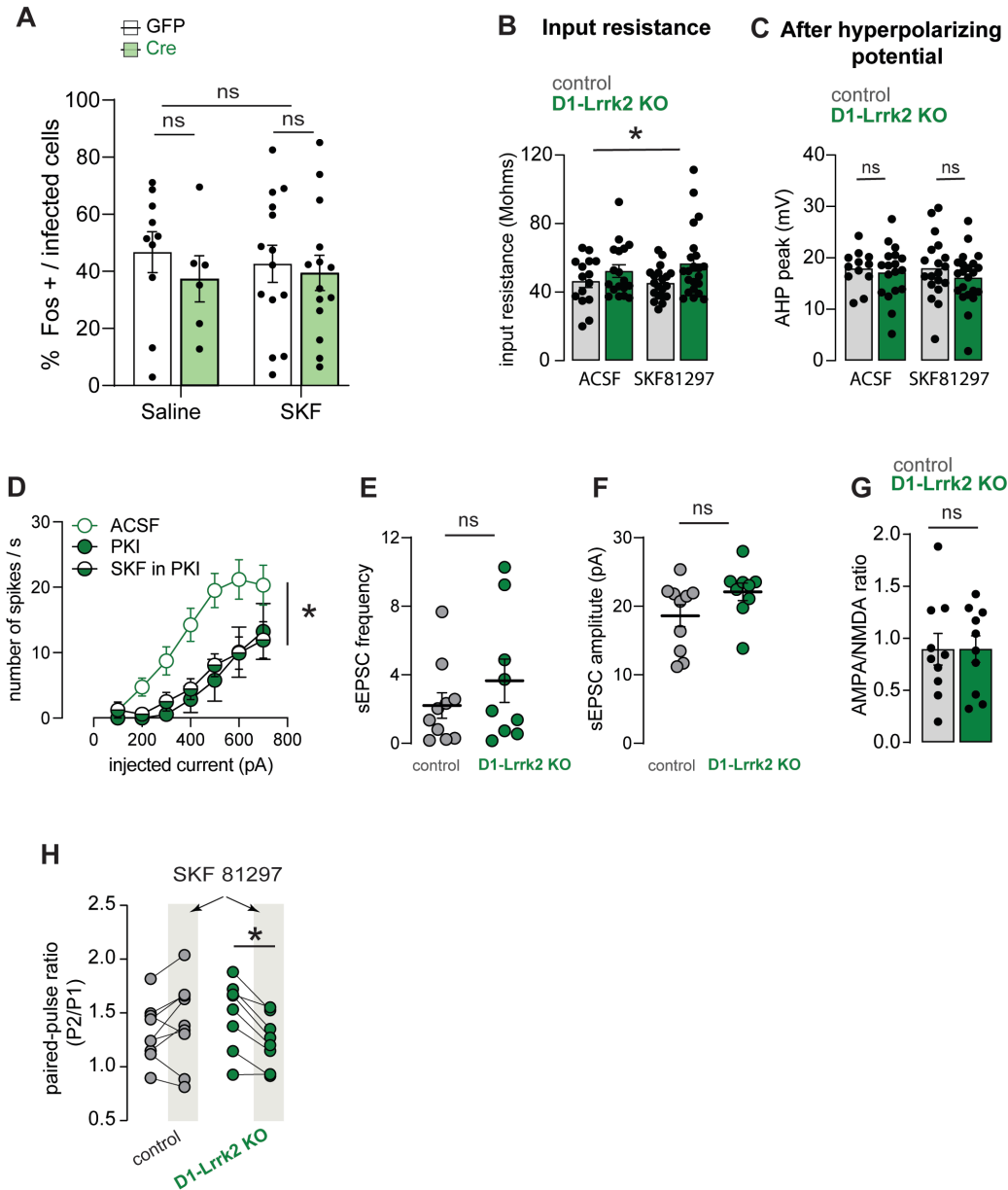


# “Leucine-Rich Repeat Kinase 2 limits dopamine D1 receptor signaling in striatum and biases against heavy persistent alcohol drinking”

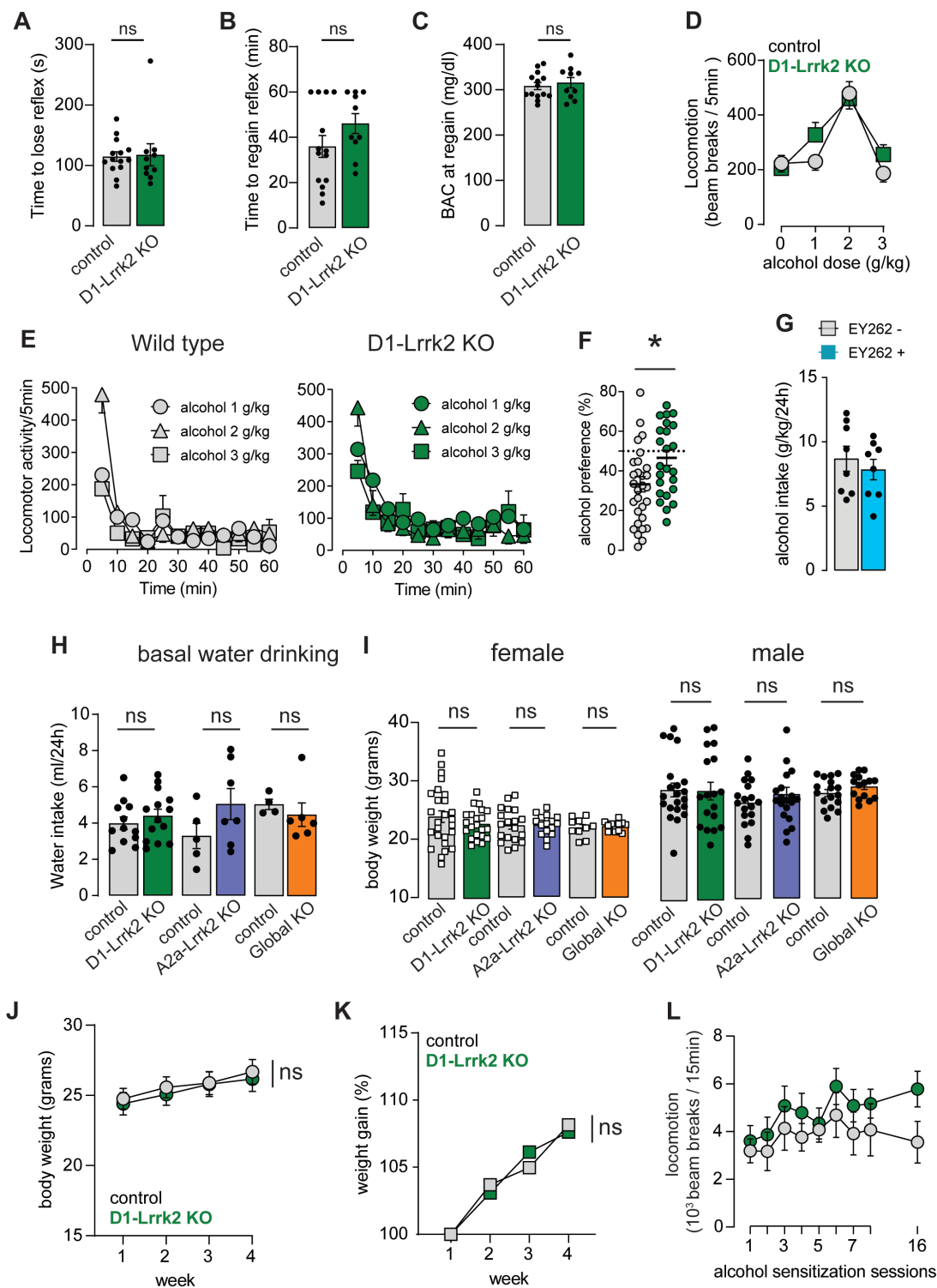
da Silva et al.



**Fig S1: c-Fos quantification and assessment of D1R, Glutamatergic, and GABAergic function in D1-Lrrk2-KO mice.**

**A**, Quantification of c-Fos positive cells in the striatum of  $Lrrk2^{floxP/floxP}$  mice injected with either Cre-eGFP or GFP after systemic administration of saline or SKF81297 (2 mg/kg; no virus, treatment or interaction effect:  $F_{(1,40)}=0.17, 0.017, 0.72, P_S>0.4$ ). **B**, Input resistance recorded in baseline conditions and in the presence of SKF81297 (main effect of treatment:  $F_{(1,71)}=5.6, P<0.05$ ). **C**, After hyperpolarizing current measured in baseline conditions and in the presence of SKF81297 (no genotype effect:  $F_{(1,67)}=1.0$ ; no

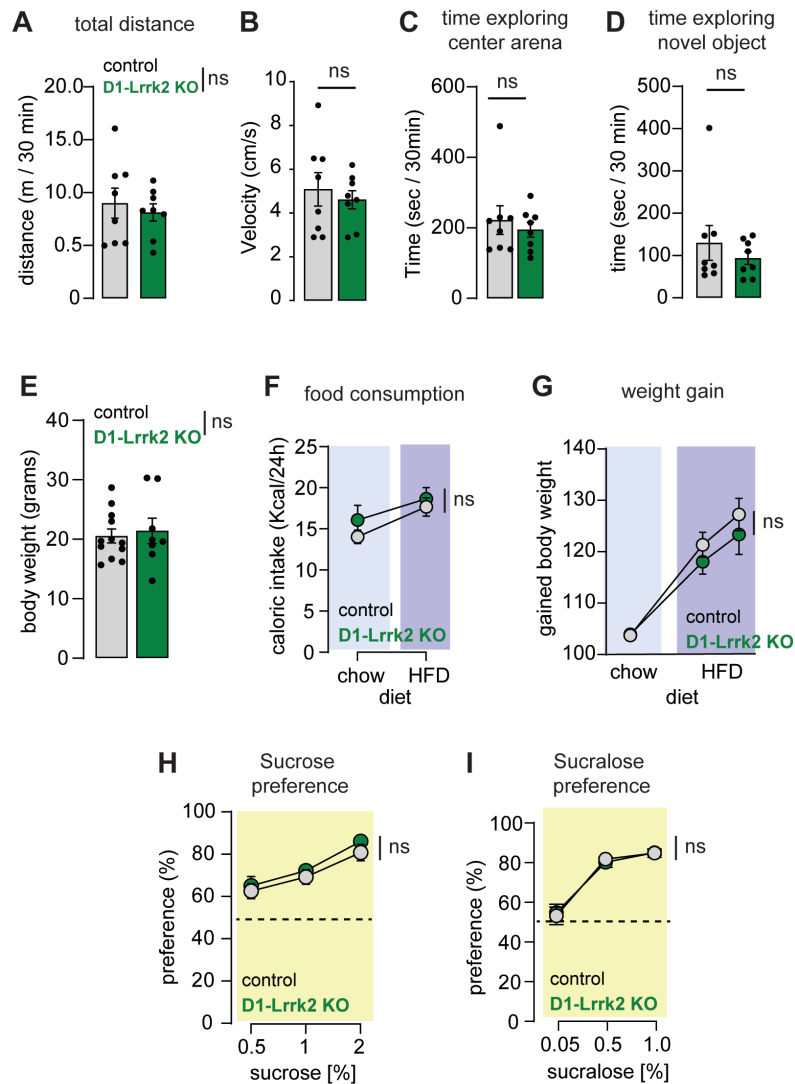
interaction:  $F_{(1,67)}=0.16$ ;  $P_S>0.05$ ). **D**, Input-output curve of firing rate from D1-MSNs in response to current steps of increasing amplitude after incubation of slices with SFK81297 and PKA inhibitor PKI (PKI effect:  $F_{(1,26)}=8.7$ ,  $P<0.01$ ; interaction:  $F_{(6,156)}=2.2$ ,  $P<0.05$ ;  $n=9$  cells, 3 mice) E-F, spontaneous postsynaptic current frequency (E,  $t_{(17)}=1$ ,  $P=0.33$ ) and amplitude (F,  $t_{(17)}=1.7$ ,  $P=0.11$ ) in D1-Lrrk2 KO and control mice. **G**, Average AMPAR/NMDAR ratio  $t_{(18)}=0.01$ ,  $P=0.99$ ,  $n=10/10$  cells, 4/3 mice. **H**, Paired pulse ratio of the synaptic responses before and after (shaded area) bath application of D1-like agonist (interaction:  $F_{(1,15)}=16$ ,  $P<0.001$ ; Sidak's test: control,  $P=0.26$ ; D1-Lrrk2-KO,  $P<0.005$ ). For all panels, bars represent mean  $\pm$  S.E.M and symbols represent values from individual mice. \* denotes  $P < 0.05$ ;



**Fig S2: LORR and consummatory behaviors in cell-specific Lrrk2-KO mice.**

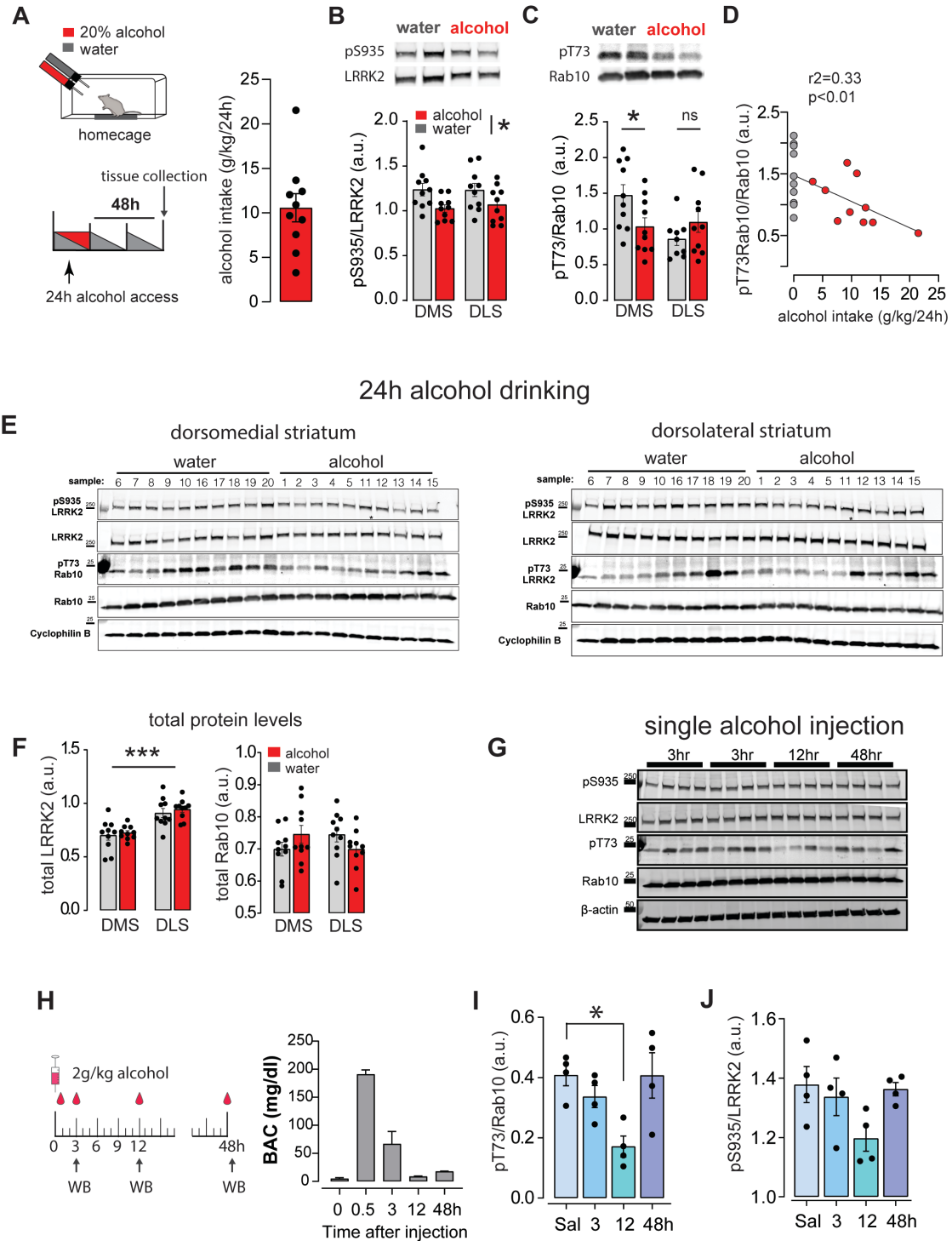
**A**, Latency to lose the righting reflex ( $t_{(22)}=0.16$ ,  $P=0.87$ ). **B**, Time to regain the righting reflex ( $t_{(22)}=1.5$ ,  $P=0.15$ ). **C**, BAC at the time of regaining the righting reflex ( $t_{(22)}=0.56$ ,  $P=0.6$ ). **D**, Raw data of dose-dependent locomotor response induced by systemic administration of alcohol. **E**, Time course of the effects of different doses of alcohol on locomotion. **F**, Mean alcohol preference during 2-bottle-choice sessions for

D1-Lrrk2 KO (green) and littermate controls (gray) ( $t_{(53)}=2.4, P<0.05$ ). **G**, Mean alcohol intake (g/kg/24h) during 2-bottle-choice sessions for EY262 (blue) and littermate controls (gray) ( $t_{(14)}=0.7 P=0.51$ ). **H**, Bar graphs showing basal water drinking (ml/24h) for D1-Lrrk2-KO (green;  $t_{(24)}=0.83$ ), A2a-Lrrk2-KO (blue;  $t_{(10)}=1.5$ ), Global-Lrrk2-KO (orange;  $t_{(8)}=0.7$ ) and their respective littermate controls (gray). **I**, Bar graphs showing average body weight for females (left) and males (right) for D1-Lrrk2-KO (green;  $t_{(37)}=0.17$ ;  $t_{(46)}=1.1$ ), A2a-Lrrk2-KO (blue;  $t_{(36)}=0.9$ ;  $t_{(33)}=0$ ), Lrrk2-Global-KO (orange;  $t_{(30)}=1.4$ ;  $t_{(20)}=0.2$ ), and their respective littermate controls. **J-K**, Raw (J) and percentage (K) of weight gain for D1-Lrrk2-KO and controls during 4 weeks of drinking procedure. **L**, Locomotor response to eight consecutive daily injections of alcohol followed by a challenge injection after eight days of incubation. For all panels, data from  $Lrrk2^{loxP/loxP}$  is shown in gray and from D1-Lrrk2-KO in green; bars represent mean  $\pm$  S.E.M and symbols represent values from individual mice.



**Fig S3: Exploration and caloric intake are largely unchanged following selective deletion of *Lrrk2* in D1-MSN.**

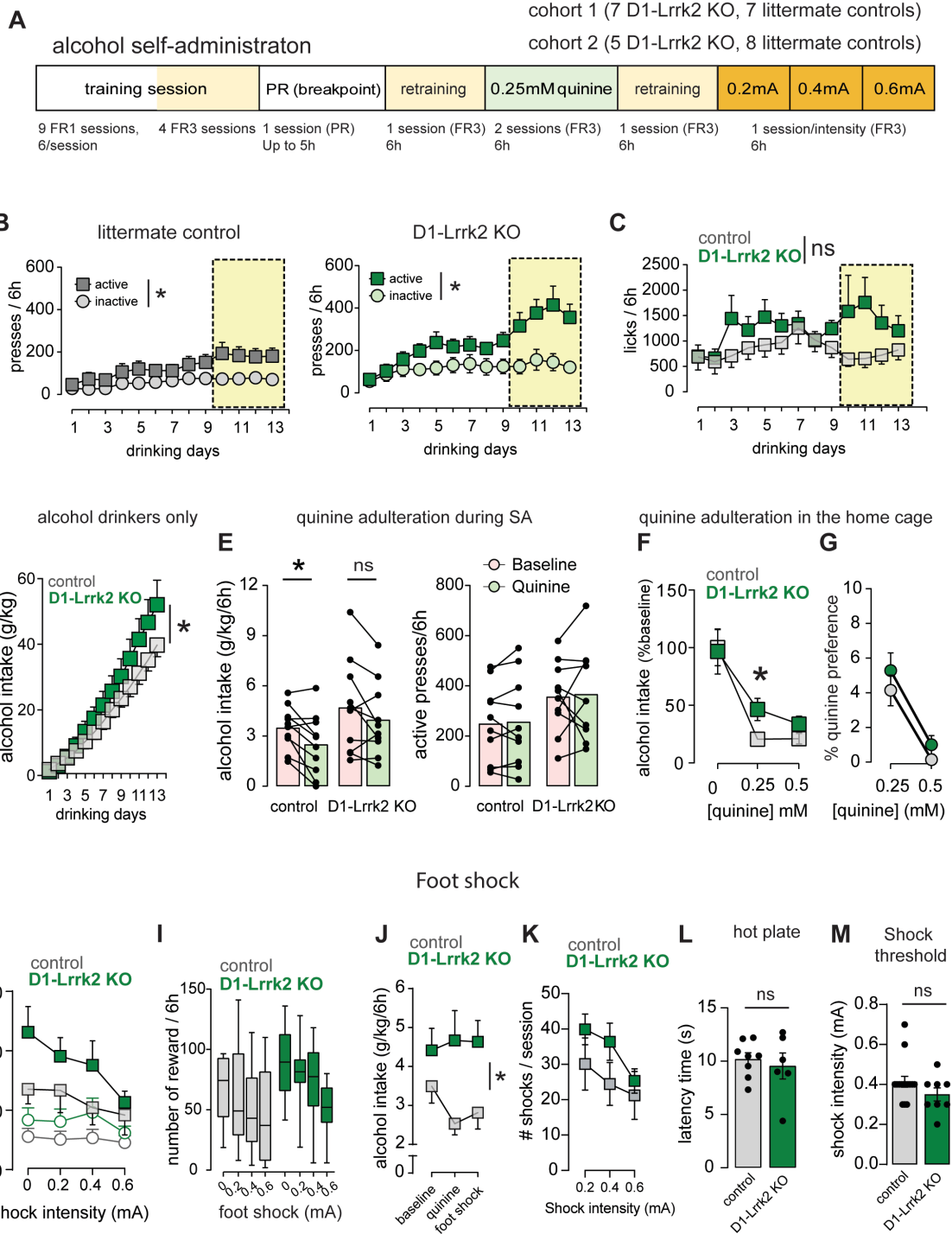
**A-D**, Distance travelled ( $t_{(14)}=0.53$ ,  $P=0.6$ ), velocity ( $t_{(14)}=0.55$ ,  $P=0.59$ ), time in center ( $t_{(14)}=0.6$ ,  $P=0.56$ ) and novel object exploration ( $t_{(14)}=0.8$ ,  $P=0.42$ ) assessed in an open field arena. **E**, average body weight for age-matched mice of each genotype ( $t_{(18)}=0.4$ ,  $P=0.7$ ). **F**, Caloric intake in Kcal/day when given unrestricted access to normal chow diet and high fat diet (HFD) for littermate control (gray) and D1-Lrrk2-KO mice (green) (genotype:  $F_{(1,18)}=1.3$ ,  $P=0.26$ ; diet:  $F_{(1,18)}=6.8$ ,  $P<0.05$ ). **G**, change in body weight during access to regular chow diet or HFD diet (no genotype:  $F_{(1,18)}=0.6$ ,  $P=0.44$ ; no interaction:  $F_{(2,36)}=0.7$ ,  $P=0.7$ ). **H**, Sucrose preference during 0.5%, 1% and 2% sucrose solution access using a two-bottle choice procedure (REML, no genotype effect:  $F_{(1,42)}=1.7$ ,  $P=0.2$ ; dose effect:  $F_{(2,62)}=18$ ,  $P<0.0001$ ). **I**, Sucralose preference using two-bottle choice procedure (concentration effect:  $F_{(1,35,44,8)}=68$ ,  $P<0.0001$ ; no genotype effect:  $F_{(1,33)}=0.001$ ,  $P=0.97$ ). For all panels, data from  $Lrrk2^{\text{loxP/loxP}}$  is shown in gray and from D1-Lrrk2-KO in green.



**Fig S4: Alcohol modulates LRRK2 activity in mouse striatum.**

**A**, *Top*, schematic diagram of the two-bottle-choice paradigm used to measure volitional alcohol drinking over 24h. *Bottom*, time course of the experiment outlines 24h alcohol drinking and brain tissue collection for western blots (WB) 48h after the single drinking session. *Right*, Average alcohol consumed over 24h. **B-C**, *Top*, Images of Western Blots for pS935 LRRK2 and total LRRK2 and pT73-Rab10 and total Rab10

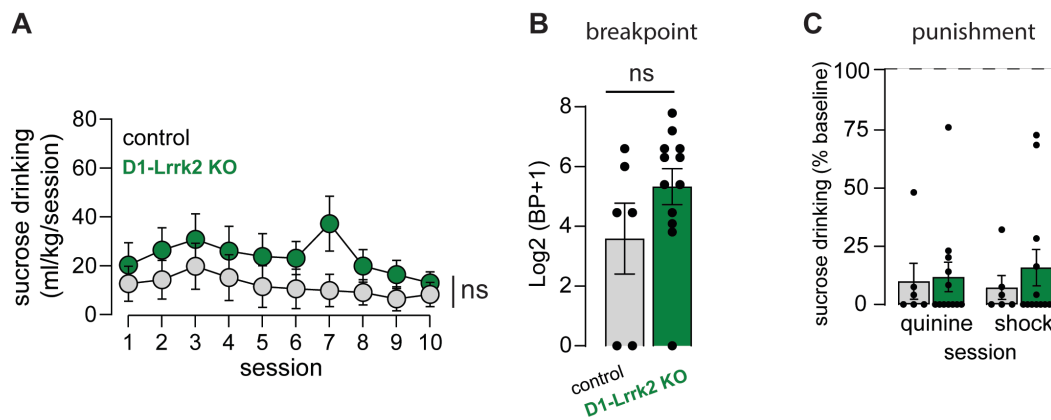
in samples from DMS and DLS of water and alcohol drinking mice. *Bottom*, bar graphs showing the ratio of labeling density for the phosphorylated forms of LRRK2 (alcohol effect:  $F_{(1,18)}=5.3$ ,  $P<0.05$ ; no interaction:  $F_{(1,18)}=0.4$ ,  $P=0.53$ ) and Rab10 (interaction:  $F_{(1,17)}=14.4$   $P<0.005$ ; DMS Sidak's test  $P<0.05$ ) over the total protein levels. **D**, pT73-Rab10 as a function of the amount of alcohol consumed over a single 24h drinking session ( $r^2 = 0.33$ ,  $P<0.01$ ). **E**, Western Blots for pS935 LRRK2, LRRK2, pT73 RAB10, RAB10, and Cyclophilin B in the DMS (*left*) and DLS (*right*) for alcohol and water drinking mice. **F**, Bar graphs showing labeling density for total LRRK2 (*left*; no genotype effect:  $F_{(1,18)}=0.56$ ; region effect:  $F_{(1,18)}=42$ ,  $P<0.0001$ ) and total Rab10 (*right*; no genotype effect  $F_{(1,18)}=0$ ,  $P=0.99$ ) in the DMS and DLS of water (gray) and alcohol (red) drinking mice. **G**, Western Blots for pS935 LRRK2, LRRK2, pT73 RAB10, RAB10, and  $\beta$ -actin in the DMS of mice injected with saline or 2g/kg alcohol. **H**, *Left*, Schematic diagram of systemic injections of 2g/kg alcohol and time points of tissue collections for Western blot. *Right*, Blood alcohol levels in different time points after systemic injection of 2g/kg alcohol. **I-J**, Time-dependent changes in pS935 LRRK2 (**I**; effect of time:  $F_{(3,12)}=2.7$ ,  $P=0.09$ ) and pT73 RAB10 (**J**; time effect:  $F_{(3,12)}=5.2$ ,  $P<0.05$ ; Tukey's test: Saline vs 12h,  $P<0.05$ ) levels after systemic injection of 2g/kg alcohol. For all panels, bars represent mean  $\pm$  S.E.M and symbols represent values from individual mice. \* denotes  $P < 0.05$ , \*\*\* denotes  $P < 0.0001$



**Fig S5: Operant alcohol self-administration in D1-Lrrk2-KO mice.**



**A**, Detailed schematic diagram of the operant training schedule. **B**, Mean number of active and inactive lever presses (lever response:  $F_{(1,14)}=16$ ,  $P<0.005$ ). **C**, Mean number of licks (no genotype effect:  $F_{(1,25)}=1.38$ ,  $P=0.21$ ). **D**, Average cumulative daily alcohol intake (g/kg/6h) among the population of alcohol drinking mice (interaction:  $F_{(12,204)}=2.3$ ;  $P<0.05$ ). **E**, Average alcohol intake (main effect of dose  $F_{(1,17)}=11$ ,  $P<0.005$ ) and active lever presses (right; no effect of dose  $F_{(1,17)}=0.22$ ,  $P=0.65$ ) during baseline (pink) and quinine adulteration (*green*) sessions. **F**, Non-operant alcohol intake (g/kg/24h) during baseline sessions with access to 20% alcohol solution (0) and during quinine-adulteration sessions (genotype effect:  $F_{(1,19)}=5.0$ ,  $P<0.05$ ; Sidak's test,  $P<0.05$ ). **G**, Quinine preference (taste aversion) tested using two bottle choice for tap water or quinine solution (no genotype effect  $F_{(1,12)}=1.4$ ,  $P=0.25$ ). **H**, Mean number of lever presses during foot shock sessions (main effect of shock intensity:  $F_{(1.5,38.2)}=2.6$ ,  $P=0.1$ ; interaction:  $F_{(2,50)}=2.3$ ,  $P=0.1$ ). **I**, Average number of earned rewards during baseline and foot shock sessions (effect of shock intensity  $F_{(2,41)}=10.6$ ,  $P<0.0001$ ). **J**, Alcohol intake (g/kg) during baseline, quinine adulteration and foot shock SA sessions (main effect of genotype  $F_{(1,17)}=6.2$ ,  $P<0.05$ ). **K**, Average number of shocks received during foot shock punishment sessions. **L**, Average withdrawal latency in the hot plate test ( $t_{(12)}=0.51$ ,  $P=0.6$ ). **M**, Average threshold sensitivity to foot shock (Mann Whitney  $U=41.5$ ;  $P=0.18$ ). For all panels, data from  $Lrrk2^{loxP/loxP}$  is shown in gray and from D1-Lrrk2-KO in green; bars represent mean  $\pm$  S.E.M and symbols represent values from individual mice. \* denotes  $P < 0.05$



**Fig S6: Operant sucrose self-administration in D1-Lrrk2-KO mice.**

**A**, Sucrose consumption during operant self-administration task (no genotype effect:  $F_{(1,44)}=1.4$ ,  $P=0.24$ ;  $t_{(44)}=1.1$ ,  $P=0.26$ ). **B**, Breakpoint for sucrose ( $U(23)$ ,  $P=0.23$ ). **C**, Sucrose drinking during quinine adulteration ( $t_{(16)}=0.17$ ,  $P=0.86$ ) and foot shock ( $t_{(16)}=0.73$ ,  $P=0.48$ ) punishment sessions. Data from  $Lrrk2^{loxP/loxP}$  is shown in gray and from D1-Lrrk2-KO in green.

## **“Leucine-Rich Repeat Kinase 2 limits dopamine D1 receptor signaling in striatum and biases against heavy persistent alcohol drinking”**

**da Silva et al.**

### **Supplementary Material and Methods**

**Electrophysiology:** Slices used for the excitability experiments were incubated in SKF81297 (1  $\mu$ M), ethanol (50 mM), ethanol (100 mM), and PKI (1  $\mu$ M) for 20 mins before the start of recordings (maximum time 120 min). tdTomato positive D1-MSN were visualized with a 40x water-immersion objective on an upright fluorescent microscope (BX51WI, Olympus USA). Membrane responses to 1s current injection between 0-700 pA (100 pA increment) were collected using an Axopatch-200B amplifier (Molecular Devices). Current was adjusted to keep  $V_m$  at -90 mV. Patch pipettes (2.0-3.5 M $\Omega$ ) were filled with internal solution containing (in mM): 120 K-MeSO<sub>4</sub>, 20 KCl, 2 MgCl<sub>2</sub>, 10 HEPES, 0.2 K-EGTA, 4 Na-ATP, and 0.4 Na-GTP, pH 7.35, 290 mOsm. For whole-cell voltage clamp recordings, neurons were voltage clamped at -60 mV. Paired pulse light (0.2-2 ms) and electrical stimulation (20 Hz every 30 s) were used to trigger GABA-A IPSCs in GABA neurons in SNr. Physiological identification of GABA neurons was based on the rate of spontaneous action potential (>5 Hz) with spike widths <1.2 ms. Internal solution contained (in mM): 57.5 KCl, 57.5 K-methylsulfate, 20 NaCl, 1.5 MgCl<sub>2</sub>, 5 HEPES, 10 BAPTA, 2 ATP, 0.2 GTP, 10 phosphocreatine, pH 7.35, 290 mOsM. To isolate GABA-A currents, NBQX (5  $\mu$ M) and CPP (5  $\mu$ M) were added to aCSF. Series resistance was monitored throughout the experiment (range; 3-15 M $\Omega$ ). AMPAR/NMDAR ratio was recorded using patch pipette filled with internal solution containing (in mM): 120 CsMeSO<sub>3</sub>, 10 CsCl, 10 HEPES, 0.2 EGTA, 4 ATP, 0.4 GTP, and 10 phosphocreatine, pH 7.35 (290 mOsM). Evoked EPSCs were generated by electrical stimulation and recorded in presence of gabazine (5  $\mu$ M). AMPAR current was recorded at -60 mV and NMDAR current was measured at 40 mV in the presence of NBQX (5  $\mu$ M). Data were acquired using pClamp 10 software, sampled at 50 kHz and filtered at 1 kHz. Analysis was performed with AxoGraphX (Axograph Scientific).

**c-Fos Immunostaining:** D1-Lrrk2-KO and littermate control mice expressing tdTomato under the *Drd1a* promoter were injected with either SKF 81297 (2mg/kg) or saline (10 ml/kg) 90 mins

prior to transcardial perfusion with 4% PFA. Brains were removed and post-fixed in 4% PFA overnight at 4 °C. Coronal sections (50 µm) from each treatment and genotype groups were processed in parallel using a vibratome (Ted Pella). Sections were washed in PBS (3 × 10 min) and blocked with 10% normal goat serum for 2 h at RT. Sections were incubated in primary antibody rabbit mAb cFos (1:500, Cell Signaling Technology, #2250S) for 48 h at 4 °C, washed in PBS (3 x 10 min), then incubated in the secondary antibody anti-rabbit Alexa Fluor 488 (1:500, Invitrogen, #A11008) or Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Cyanine5 (1:500, ThermoFisher, #A10523) for 2 h at RT and washed with PBS (1 x 10 min), and 0.1 M PB (1 x 10 min). Slices from the microinjection experiments were additionally incubated with primary antibody Chicken IgY GFP Polyclonal Antibody (1:100, ThermoFisher, #A10262) for 48 h at 4 °C and with secondary antibody Goat anti-Chicken IgY (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor Plus 488 (1:100, ThermoFisher, #A32931). Sections were mounted with Vectashield with DAPI (Vector Laboratories).

**Drugs and chemicals:** Alcohol (Decon Laboratories, 190 proof, glass container) was dissolved in tap water for drinking experiments or ACSF for electrophysiology. Quinine hemisulfate monohydrate (Sigma-Aldrich) was dissolved in the 20% alcohol solution or in tap water. SKF81297, NBQX, CPP, and PKI were purchased from Tocris. SCH23390, gabazine, and kynurenic acid (sodium salt) were obtained from Abcam.

**Lrrk2 mRNA expression:** FASTQ files were downloaded (GSE81672: Nac, PFC, BLA, vHipp; GSE89692: PFC, VTA and PRJEB36194: DMS) using SRA toolkit. Only naïve C57BL6/J wild type mice were used in this analysis. Read quality, length, and composition were assessed using FastQC before trimming low quality bases (Phred < 20) and adapters using Fastp. Alignment to the GRCm39 Gencode genome assembly and gene-level counts were generated using STAR with default options. BiomaRt in the R (version 4.0.3) was used to calculate FPKM of gene counts.

**Stereotaxic virus injections:** Mice were anesthetized with isoflurane and placed in the stereotaxic apparatus (Kopf Instruments). Adeno-associated viral (AAV) vectors for ChR2 expression (rAAV5-CaMKIIhChR2(H134R)-EYFP;  $1.5 \times 10^{13}$ , Penn Vector Core), Cre expression (pAAV.CMV.HI.eGFP-Cre.WPRE.SV40) and eGFP expression

(pENN.AAV.CB7.CI.eGFP.WPRE.rBG) were bilaterally injected into DMS (276 nl, from bregma: AP, +1.1; ML,  $\pm$ 1.2; DV, -3.0 mm for ChR2 expression and AP, +0.6, +1.1; ML,  $\pm$ 1.4,  $\pm$ 1.2; DV, -3.2 mm for Cre and eGFP expression) using a Nanoject II (Drummond Scientific).