

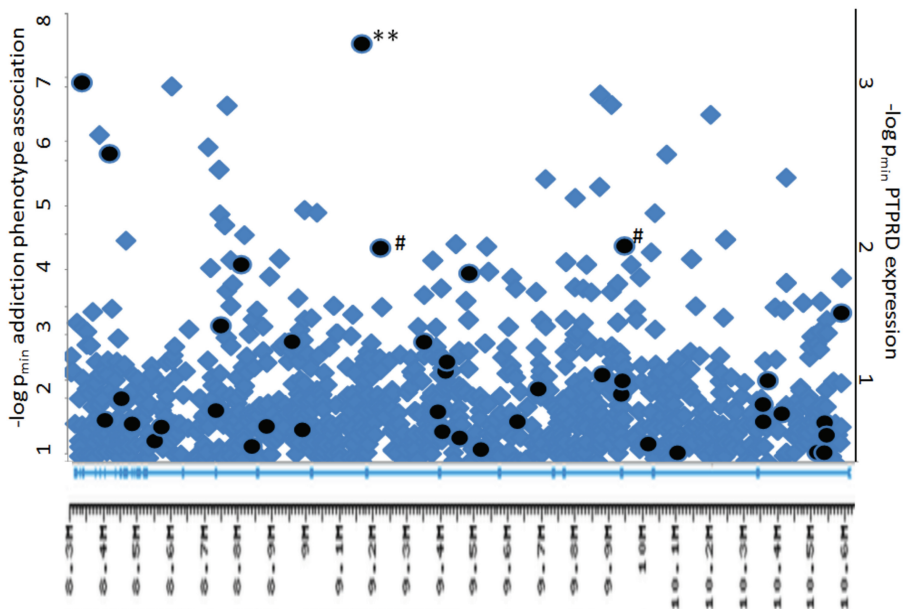
Supplemental Data

Mouse Model for Protein Tyrosine Phosphatase D (*PTPRD*) Associations with Restless Leg Syndrome or Willis-Ekbom Disease and Addiction: Reduced Expression Alters Locomotion, Sleep Behaviors and Cocaine-Conditioned Place Preference

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Supplementary Figure S1. Plots of $-\log p_{\min}$ association with addiction -related phenotypes from samples noted above vs chromosomal distance at *PTPRD* locus, with *PTPRD* exons and chromosomal basepairs from Mapviewer (diamonds, left axis) and of $-\log p$ values for association with level of *PTPRD* mRNA expression in human postmortem cerebral cortical samples (filled circles, right axis). #- RLS-associated SNPs. ** SNP with strongest association with *PTPRD* mRNA expression.

Supplementary Table S1. Data from which pmin association values are obtained.

Columns: rs_id: SNP rs identifier; CHR: chromosome; position: bp (build 37) of SNP; pmin: lowest association p value for this SNP; strand: which chromosomal strand the gene/SNP is located on; allele_a: the defined allele a for Affymetrix genotyping; allele_b: the defined allele b for Affymetrix genotyping; nidaii_aa_P: p value for association with polysubstance dependence/use v controls with little use and no dependence (Af Am samples) (Drgon *et al.*, 2010); nidaii_aa_Phase: phase of association; nidaii_ea_P: p value for association with polysubstance dependence/use v controls with little use and no dependence (Eu Am samples) (Drgon *et al.*, 2010); nidaii_ea_Phase: phase of association; nida600k_aa_P: p value for association with polysubstance dependence/use v controls with little use and no dependence (Af Am samples) (Liu *et al.*, 2006); nida600k_aa_Phase: phase of association; nida600k_ea_P: p value for association with polysubstance dependence/use v controls with little use and no dependence (Eu Am samples) (Liu *et al.*, 2006); nida600k_ea_Phase: phase of association; jgida_P: p value for association with methamphetamine dependence v controls with little use and no dependence (Japanese samples) (Uhl *et al.*, 2008); jgida_Phase: phase of association; taiw_P: p value for association with methamphetamine dependence v controls with little use and no dependence (Taiwanese samples) (Uhl *et al.*, 2008); taiw_Phase: phase of association; hm_dep_P: p value for association with nicotine dependence (FTND) v controls with little use and no dependence (EuAm samples) (Johnson *et al.*, 2009); hm_dep_Phase: phase of dependence; eca_P: p value for association with dependence on at least one addictive substance v controls with no abuse or dependence (EuAm samples) (Johnson *et al.*, 2009); eca_Phase: phase of association; PS_P: p value for association with dependence on any addictive substance v controls with little use and no dependence (EuAm samples) (Uhl *et al.*, 2014); PS_Phase: phase of dependence; BRN_P: p value for association with ability to quit smoking in a randomized controlled clinical trial (EuAm samples) (Uhl *et al.*, 2008); BRN_Phase: phase of association; CNIII_PVAL p value for association with ability to quit smoking in a randomized controlled clinical trial (EuAm samples) (Uhl *et al.*, 2014); CNIII_Phase: phase of association; HM_P: p value for association with ability to quit smoking in the community (former vs current smokers) (EuAm samples) (Johnson *et al.*, 2007); HM_Phase: phase of association; LER_P p value for association with ability to quit smoking in a randomized controlled clinical trial (EuAm samples) (Uhl *et al.*, 2008); LER_Phase: phase of association; PIP_P: p value for association with ability to quit smoking in a clinical setting (UK samples) (Uhl *et al.*, 2010); PIP_Phase: phase of association; R1_P: p value for association with ability to quit smoking in a randomized controlled clinical trial (EuAm samples) (Uhl *et al.*, 2007); ROSE2_PVAL: p value for association with ability to quit smoking in a randomized controlled clinical trial (EuAm samples) (Uhl *et al.*, 2010); ROSE2_Phase: phase of association; VEC_P: p value for association with ability to quit smoking in a randomized controlled clinical trial (EuAm samples) (Drgon *et al.*, 2010); VEC_Phase: phase of association; SAGE_EA_COC_pval: p value for association with cocaine dependence v controls with little use and no dependence (Eu Am samples) (Drgon *et al.*, 2010); SAGE_EA_COC_phase: phase of association; SAGE_WH_ALC_pval: p value for association with alcohol dependence v controls with little use and no dependence (EuAm samples) (Drgon *et al.*, 2010); SAGE_WH_ALC_phase: phase of association; SAGE_AA_COC_pval p value for association with cocaine dependence v controls with little use and no dependence (Af Am samples) (Drgon *et al.*, 2010); SAGE_AA_COC_phase: phase of association; SAGE_BL_ALC_pval p value for association with alcohol dependence v controls with little use and no dependence (Af Am samples) (Drgon *et al.*, 2010); SAGE_BL_ALC_phase: phase of association; Treut_pval: p value for association with alcohol dependence v controls with little use and no dependence (German samples) (Treutlein *et al.*, 2009, kindly provided by M Reitschul); Treut_phase: phase of association. lmnStrand: Strand assessed in Immulina assays (SAGE). ACTG: base.

rs_id	CHR	position	p_min	strand	allele_a	allele_b	nidaii_aa_P	nidaii_ea_P	nida600k_aa_P	nida600k_ea_P	jgida_P	taiw_P	hm_dep_P	eca_P	PS_P	PS_Phase	BRN_P	CNIII_PVAL	HM_P	HM_Phase	LER_P	Lerman_Phase	PIP_P	R1_P	ROSE2_PVAL	VEC_P	SAGE_EA_COC_pval	SAGE_EA_COC_phase	SAGE_WH_ALC_pval	SAGE_WH_ALC_phase	SAGE_AA_COC_pval	SAGE_AA_COC_phase	SAGE_BL_ALC_pval	SAGE_BL_ALC_phase	Treut_pval	lmnStrand	ACTG																	
rs7872830	9	8274789	0.003988095	-	A	G	0.966996466	A	0.347611788	A	0.966736473	A	0.217613045	B	0.923838402	A	0.448319119	A	0.873378308	B	0.236939945	A	0.01133	B	0.495982219	A	0.758700013	B	0.758268983	B	0.056335509	B	0.003988095	0.103562452	B	0.818000019	0.863741191	B	0.279300004	T	0.3565	T	0.987600029	G	0.594900012	G		Top	(A/C)					
rs7872172	9	8274965	0.002235398	-	A	T																																																

Supplementary Table S1. Continued.

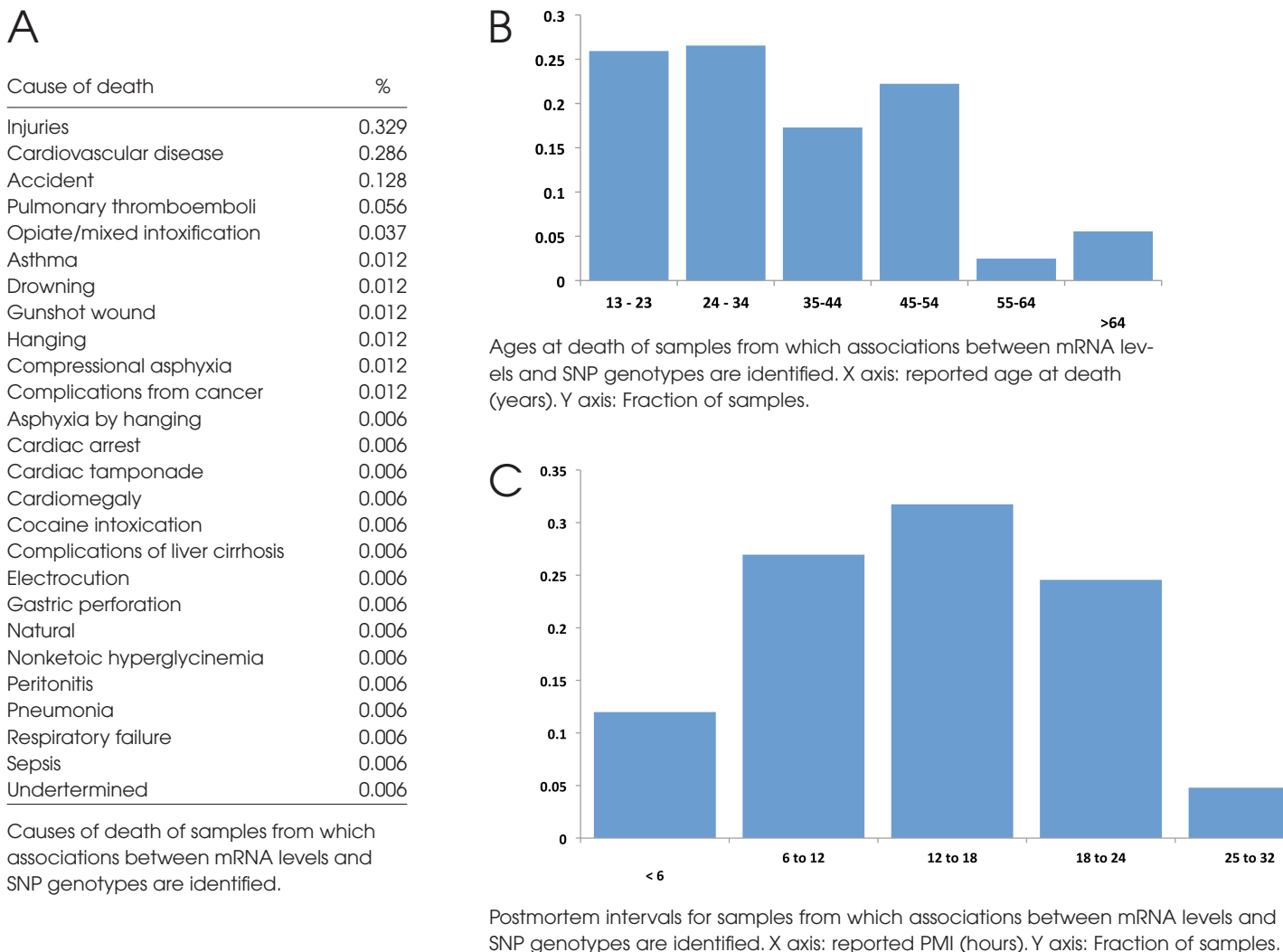
Table with columns: rs_id, CHR, position, P_val, strand, allele_a, allele_b, and numerous other variant-related fields including strand, phase, and recombination rates.

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Supplementary Table S1. Continued.

Table with columns: rs_id, CHR, position, P_min, strand, allele_a, allele_b, nidal, nidal_ac_P, nidal_ac_Phase, nidal_ac_Phase, nidal_ac_Phase, nidal_ac_Phase, jgld_a, jgld_a_Phase, talw_P, talw_Phase, hm_dep_P, hm_dep_Phase, eoa_P, eoa_Phase, PS_P, PS_Phase, BRN_P, BRN_Phase, CNIL_PVAL, CNIL_Phase, HM_P, HM_Phase, LER_P, LER_Phase, Lemman_Phase, PIP_P, PIP_Phase, RI_P, RI_Phase, rose_phase, ROSE2_PVAL, ROSE2_Phase, VEC_P, VEC_Phase, SAGE_EA_COX_pval, SAGE_EA_COX_phase, SAGE_WHL_ALC_pval, SAGE_WHL_ALC_phase, SAGE_AA_COX_pval, SAGE_AA_COX_phase, SAGE_BB_ALC_pval, SAGE_BB_ALC_phase, TruT_pval, TruT_phase, ltrmstrand, ACTG.

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Supplementary Figure S2. Causes of death (A), ages of death (B) and postmortem intervals (C) for samples used for study of PTPRD mRNA expression levels in individuals with different PTPRD haplotype.