

Supplementary Table 7. Full data for rostral periaqueductal grey (RPAG) functional connectivity.

Brain Region	Wild-type (+/+)			<i>Myshkin</i> (<i>Myk</i> +/+)		
	mean	±	SEM	mean	±	SEM
Caudal Motor (CMCTX)	0.76	±	0.05	0.46	±	0.06
Rostral Motor (RMCTX)	1.00	±	0.05	0.59	±	0.05
Frontal Cortex (FCTX)	0.93	±	0.05	0.81	±	0.10
Rostral Ventromedial Striatum (RVMStr)	0.90	±	0.07	0.61	±	0.04
Rostral Dorsolateral Striatum (RDLStr)	0.88	±	0.08	0.31*	±	0.03
Rostral Dorsomedial Striatum (RDMStr)	0.88	±	0.07	0.55	±	0.07
Rostral Ventrolateral Striatum (RVLStr)	0.63	±	0.05	1.26	±	0.09
Caudal Centromedial Striatum (CCMStr)	0.74	±	0.06	1.58*	±	0.04
Caudal Dorsolateral Striatum (CDLStr)	0.71	±	0.04	1.02	±	0.09
Caudal Dorsomedial Striatum (CDMStr)	0.67	±	0.03	1.04	±	0.07
Caudal Ventrolateral Striatum (CVLStr)	0.68	±	0.09	1.30	±	0.07
Globus Pallidus (GP)	1.07	±	0.03	0.42*	±	0.06
Olivary Body (OB)	0.95	±	0.08	1.04	±	0.07
Auditory (AudC)	0.73	±	0.06	0.57*	±	0.08
Substantia Nigra pars Reticulata (SNR)	1.82	±	0.06	0.83*	±	0.08
CA3	1.08	±	0.06	1.19	±	0.13
Somatosensory (SSCTX)	0.76	±	0.06	0.76	±	0.07
Ventral Anterior Nucleus (VAthal)	1.12	±	0.05	0.86	±	0.11
Ventrolateral Nucleus (VLthal)	1.10	±	0.05	0.41*	±	0.13
Dorsolateral Geniculate (DLG)	0.89	±	0.08	0.53*	±	0.09
CA1	0.70	±	0.07	0.36*	±	0.05
Entorhinal (EC)	0.64	±	0.03	0.75	±	0.06
Pontine Reticular Formation (PRF)	1.55	±	0.05	0.49	±	0.09
Dorsolateral Entorhinal (DLECTX)	1.11	±	0.05	1.32	±	0.04
External Cortex of the Inferior Colliculus (ECIC)	0.82	±	0.06	0.47	±	0.09
Median Raphe (MR)	0.65	±	0.07	0.86	±	0.08
Superior Colliculus (SupC)	1.34	±	0.06	1.96*	±	0.06
Caudal Pontine Reticular Nucleus (CPRt)	0.62	±	0.04	0.72	±	0.09
Superficial Grey Layer of the Superior Colliculus (SGSupC)	0.73	±	0.08	2.02*	±	0.08
Caudal PAG (CPAG)	0.43	±	0.07	0.91	±	0.09
Locus Coeruleus (LC)	0.59	±	0.03	1.33	±	0.08
Dorsal Cortex of the Inferior Colliculus (DCIC)	0.64	±	0.04	0.81	±	0.09
Gigantocellular Reticular Nucleus (GRt)	1.74	±	0.04	0.43	±	0.10
Medial Vestibular nucleus (MVN)	1.49	±	0.04	0.41	±	0.08
Superior Cerebellar Peduncle (SupCPed)	0.82	±	0.03	0.45	±	0.11
Dorsomedial PAG (DMPAG)	1.16	±	0.06	0.40*	±	0.13
Medial Geniculate Nucleus (MG)	0.84	±	0.06	1.58	±	0.07
Paramedian Lobule (PML)	0.58	±	0.06	1.54	±	0.08
Red Nucleus Parvocellular (RNPv)	1.15	±	0.07	1.74	±	0.06
Red Nucleus Magnocellular (RNMn)	0.76	±	0.03	1.31	±	0.06
Deep Cerebellar Nuclei (DCN)	0.48	±	0.09	0.75	±	0.06
Medial Amygdala (MeA)	0.76	±	0.06	0.45*	±	0.03
Ventral Posterolateral Nucleus (VPLthal)	0.57	±	0.09	1.05	±	0.13
Ventral Posteromedial Nucleus (VPMthal)	1.57	±	0.12	1.01	±	0.05
Ventromedial Thalamic Nucleus (VMthal)	0.97	±	0.07	0.57	±	0.12

Data shown as the mean ± SEM of the VIP statistic as determined through PLSR analysis. Bold denotes significant functional connection with the defined seed region in given experimental group (95% CI VIP>0.80). *denotes $P < 0.05$ significant difference in VIP statistic between genotypes (1000 random permutations). Red highlights regions showing increased and blue decreased functional connectivity with the given seed brain region in *Myshkin* (*Myk*+/+) mice relative to wild-type (+/+) controls.