

Supplementary Table 6. Full data for dorsomedial periaqueductal grey (DMPAG) functional connectivity.

Brain Region	Wild-type (+/+)		<i>Myshkin</i> (<i>Myk</i> +/+)	
	mean	SEM	mean	SEM
Caudal Motor (CMCTX)	0.92	± 0.09	0.57	± 0.06
Rostral Motor (RMCTX)	0.73	± 0.06	1.42	± 0.05
Frontal Cortex (FCTX)	0.79	± 0.07	1.30	± 0.05
Rostral Ventromedial Striatum (RVMStr)	0.59	± 0.06	0.90	± 0.08
Rostral Dorsolateral Striatum (RDLStr)	0.64	± 0.05	0.43	± 0.03
Rostral Dorsomedial Striatum (RDMStr)	0.63	± 0.05	0.32	± 0.07
Rostral Ventrolateral Striatum (RVLStr)	0.36	± 0.05	1.05	± 0.12
Caudal Centromedial Striatum (CCMStr)	0.59	± 0.04	0.41	± 0.04
Caudal Dorsolateral Striatum (CDLStr)	0.68	± 0.08	0.98	± 0.06
Caudal Dorsomedial Striatum (CDMStr)	0.61	± 0.03	0.72	± 0.05
Caudal Ventrolateral Striatum (CVLStr)	0.65	± 0.07	0.45*	± 0.08
Globus Pallidus (GP)	0.91	± 0.10	0.46	± 0.05
Olivary Body (OB)	0.28	± 0.05	0.81	± 0.04
Auditory (AudC)	1.30	± 0.03	1.72	± 0.06
Substantia Nigra pars Reticulata (SNR)	0.77	± 0.06	0.78	± 0.05
CA3	1.00	± 0.06	0.46*	± 0.16
Somatosensory (SSCTX)	0.60	± 0.05	0.70	± 0.08
Ventral Anterior Nucleus (VAthal)	1.20	± 0.05	1.01	± 0.06
Ventrolateral Nucleus (VLthal)	1.17	± 0.05	1.42	± 0.08
Dorsolateral Geniculate (DLG)	1.74	± 0.03	0.94*	± 0.07
CA1	0.90	± 0.09	0.43*	± 0.07
Entorhinal (EC)	1.06	± 0.10	0.65*	± 0.07
Rostral PAG (RPAG)	1.19	± 0.06	0.38	± 0.12
Pontine Reticular Formation (PRF)	0.83	± 0.07	0.50	± 0.04
Dorsolateral Entorhinal (DLECTX)	1.63	± 0.09	1.17	± 0.09
External Cortex of the Inferior Colliculus (ECIC)	0.90	± 0.06	0.61	± 0.06
Median Raphe (MR)	0.60	± 0.07	0.71	± 0.08
Superior Colliculus (SupC)	1.72	± 0.05	1.31	± 0.04
Caudal Pontine Reticular Nucleus (CPRt)	0.49	± 0.06	0.66	± 0.05
Superficial Grey Layer of the Superior Colliculus (SGSupC)	0.90	± 0.10	0.53	± 0.06
Caudal PAG (CPAG)	0.81	± 0.04	0.61	± 0.08
Locus Coeruleus (LC)	0.73	± 0.03	1.52*	± 0.04
Dorsal Cortex of the Inferior Colliculus (DCIC)	0.55	± 0.05	0.77	± 0.06
Gigantocellular Reticular Nucleus (GRt)	0.82	± 0.06	1.43	± 0.08
Medial Vestibular nucleus (MVN)	0.96	± 0.06	1.33	± 0.08
Superior Cerebellar Peduncle (SupCPed)	1.49	± 0.07	0.99*	± 0.07
Medial Geniculate Nucleus (MG)	1.46	± 0.10	0.67*	± 0.04
Paramedian Lobule (PML)	0.31	± 0.07	0.61	± 0.06
Red Nucleus Parvocellular (RNPv)	1.32	± 0.08	1.07	± 0.07
Red Nucleus Magnocellular (RNMn)	1.22	± 0.12	1.00	± 0.08
Deep Cerebellar Nuclei (DCN)	0.80	± 0.10	0.91	± 0.08
Medial Amygdala (MeA)	0.95	± 0.07	0.96	± 0.07
Ventral Posterolateral Nucleus (VPLthal)	0.40	± 0.14	0.61	± 0.08
Ventral Posteromedial Nucleus (VPMthal)	0.61	± 0.06	1.13	± 0.04
Ventromedial Thalamic Nucleus (VMthal)	0.93	± 0.07	0.82	± 0.06

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.