

Supplementary Table 5. Full data for ventral posteromedial nucleus (VPMthal) functional connectivity.

Brain Region	Wild-type (+/+)		<i>Myshkin</i> (<i>Myk</i> +/+)	
	mean	SEM	mean	SEM
Caudal Motor (CMCTX)	0.52	± 0.05	0.51	± 0.03
Rostral Motor (RMCTX)	1.02	± 0.06	0.26*	± 0.06
Frontal Cortex (FCTX)	0.95	± 0.09	0.41	± 0.03
Rostral Ventromedial Striatum (RVMStr)	1.00	± 0.03	0.51*	± 0.05
Rostral Dorsolateral Striatum (RDLStr)	0.93	± 0.04	0.94	± 0.03
Rostral Dorsomedial Striatum (RDMStr)	0.92	± 0.04	0.98	± 0.06
Rostral Ventrolateral Striatum (RVLStr)	1.02	± 0.07	1.03	± 0.08
Caudal Centromedial Striatum (CCMStr)	0.75	± 0.05	0.79	± 0.06
Caudal Dorsolateral Striatum (CDLStr)	0.52	± 0.05	0.36	± 0.04
Caudal Dorsomedial Striatum (CDMStr)	0.93	± 0.09	0.29*	± 0.03
Caudal Ventrolateral Striatum (CVLStr)	0.72	± 0.07	0.61	± 0.05
Globus Pallidus (GP)	0.73	± 0.07	0.25*	± 0.05
Olivary Body (OB)	1.26	± 0.14	0.50*	± 0.08
Auditory (AudC)	0.78	± 0.10	0.81	± 0.03
Substantia Nigra pars Reticulata (SNR)	1.48	± 0.07	1.06*	± 0.12
CA3	1.37	± 0.09	0.68*	± 0.09
Somatosensory (SSCTX)	0.85	± 0.05	0.60	± 0.05
Ventral Anterior Nucleus (VAthal)	1.09	± 0.07	2.12*	± 0.04
Ventrolateral Nucleus (VLthal)	0.92	± 0.09	1.74	± 0.03
Dorsolateral Geniculate (DLG)	0.53	± 0.12	1.02	± 0.08
CA1	1.04	± 0.07	0.51	± 0.05
Entorhinal (EC)	0.84	± 0.07	0.64	± 0.06
Rostral PAG (RPAG)	1.74	± 0.09	0.90	± 0.04
Pontine Reticular Formation (PRF)	1.23	± 0.12	0.54*	± 0.05
Dorsolateral Entorhinal (DLECTX)	1.19	± 0.12	0.77	± 0.03
External Cortex of the Inferior Colliculus (ECIC)	0.96	± 0.02	0.96	± 0.03
Median Raphe (MR)	0.79	± 0.06	1.16	± 0.04
Superior Colliculus (SupC)	0.87	± 0.07	0.65	± 0.05
Caudal Pontine Reticular Nucleus (CPRt)	1.12	± 0.08	0.87	± 0.06
Superficial Grey Layer of the Superior Colliculus (SGSupC)	0.66	± 0.06	0.35	± 0.06
Caudal PAG (CPAG)	0.55	± 0.08	0.72	± 0.04
Locus Coeruleus (LC)	1.04	± 0.08	1.44	± 0.02
Dorsal Cortex of the Inferior Colliculus (DCIC)	0.65	± 0.06	0.82	± 0.11
Gigantocellular Reticular Nucleus (GRt)	1.40	± 0.13	1.27	± 0.02
Medial Vestibular nucleus (MVN)	0.91	± 0.05	0.93	± 0.02
Superior Cerebellar Peduncle (SupCPed)	0.88	± 0.08	1.02	± 0.06
Dorsomedial PAG (DMPAG)	0.78	± 0.08	1.08	± 0.05
Medial Geniculate Nucleus (MG)	0.94	± 0.09	0.70	± 0.12
Paramedian Lobule (PML)	1.21	± 0.05	1.16	± 0.02
Red Nucleus Parvocellular (RNPv)	0.88	± 0.08	0.40*	± 0.05
Red Nucleus Magnocellular (RNMn)	0.46	± 0.06	0.32*	± 0.05
Deep Cerebellar Nuclei (DCN)	0.54	± 0.07	0.48	± 0.08
Medial Amygdala (MeA)	0.94	± 0.09	0.68	± 0.06
Ventral Posterolateral Nucleus (VPLthal)	1.20	± 0.07	2.12	± 0.04
Ventromedial Thalamic Nucleus (VMthal)	0.92	± 0.07	1.76*	± 0.04

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.