

Supplementary Table 4. Full data for ventromedial thalamus (VMthal) functional connectivity.

Brain Region	Wild-type (+/+)			<i>Myshkin</i> (<i>Myk</i> +/)		
	mean	±	SEM	mean	±	SEM
Caudal Motor (CMCTX)	0.46	±	0.04	0.48	±	0.06
Rostral Motor (RMCTX)	1.50	±	0.03	0.42*	±	0.09
Frontal Cortex (FCTX)	1.28	±	0.04	0.39*	±	0.05
Rostral Ventromedial Striatum (RVMStr)	1.39	±	0.03	0.90	±	0.09
Rostral Dorsolateral Striatum (RDLStr)	1.42	±	0.02	1.52	±	0.04
Rostral Dorsomedial Striatum (RDMStr)	1.43	±	0.02	1.47	±	0.05
Rostral Ventrolateral Striatum (RVLStr)	0.99	±	0.08	1.44	±	0.07
Caudal Centromedial Striatum (CCMStr)	1.33	±	0.03	0.85	±	0.06
Caudal Dorsolateral Striatum (CDLStr)	0.50	±	0.05	0.28	±	0.06
Caudal Dorsomedial Striatum (CDMStr)	1.01	±	0.07	0.26*	±	0.07
Caudal Ventrolateral Striatum (CVLStr)	0.82	±	0.09	0.67	±	0.08
Globus Pallidus (GP)	0.99	±	0.08	0.31*	±	0.08
Olivary Body (OB)	0.36	±	0.06	0.44	±	0.05
Auditory (AudC)	0.47	±	0.09	1.01	±	0.05
Substantia Nigra pars Reticulata (SNR)	0.33	±	0.03	0.46	±	0.09
CA3	0.45	±	0.08	0.84	±	0.07
Somatosensory (SSCTX)	1.33	±	0.03	0.30*	±	0.07
Ventrolateral Nucleus (VLthal)	1.69	±	0.04	1.75	±	0.05
Dorsolateral Geniculate (DLG)	0.42	±	0.06	0.82	±	0.13
CA1	0.90	±	0.09	0.53	±	0.06
Entorhinal (EC)	0.89	±	0.09	0.86	±	0.05
Rostral PAG (RPAG)	0.90	±	0.06	0.70	±	0.09
Pontine Reticular Formation (PRF)	0.88	±	0.10	0.76	±	0.12
Dorsolateral Entorhinal (DLECTX)	0.97	±	0.04	0.66	±	0.05
External Cortex of the Inferior Colliculus (ECIC)	1.10	±	0.04	0.54	±	0.08
Median Raphe (MR)	0.74	±	0.09	1.34	±	0.07
Superior Colliculus (SupC)	1.30	±	0.03	0.37	±	0.04
Caudal Pontine Reticular Nucleus (CPRt)	0.50	±	0.07	1.12	±	0.06
Superficial Grey Layer of the Superior Colliculus (SGSupC)	0.73	±	0.09	0.27	±	0.11
Caudal PAG (CPAG)	0.39	±	0.03	0.61	±	0.05
Locus Coeruleus (LC)	0.79	±	0.05	1.64	±	0.04
Dorsal Cortex of the Inferior Colliculus (DCIC)	1.07	±	0.05	0.61	±	0.09
Gigantocellular Reticular Nucleus (GRt)	1.18	±	0.04	0.89	±	0.05
Medial Vestibular nucleus (MVN)	0.94	±	0.05	0.53	±	0.04
Superior Cerebellar Peduncle (SupCPed)	1.24	±	0.06	0.62*	±	0.09
Dorsomedial PAG (DMPAG)	1.02	±	0.06	0.94	±	0.06
Medial Geniculate Nucleus (MG)	0.84	±	0.05	0.52	±	0.05
Paramedian Lobule (PML)	0.30	±	0.03	1.06*	±	0.03
Red Nucleus Parvocellular (RNPv)	0.93	±	0.10	0.34	±	0.05
Red Nucleus Magnocellular (RNMn)	0.35	±	0.11	0.20*	±	0.02
Deep Cerebellar Nuclei (DCN)	0.33	±	0.10	0.46	±	0.01
Medial Amygdala (MeA)	0.84	±	0.07	1.21	±	0.07
Ventral Posterolateral Nucleus (VPLthal)	0.66	±	0.09	2.20*	±	0.03
Ventral Posteromedial Nucleus (VPMthal)	0.68	±	0.07	2.05*	±	0.03
Ventromedial Nucleus (VMthal)	1.70	±	0.04	1.46	±	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.