

Supplementary Table 3. Full data for ventral anterior thalamus (VAthal) 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.