

Supplementary Table 8. Full data for caudal motor cortex (CMCTX) functional connectivity.

Brain Region	Wild-type (+/+)			<i>Myshkin</i> (<i>Myk</i> /+)		
	mean	±	SEM	mean	±	SEM
Rostral Motor (RMCTX)	0.71	±	0.10	1.46	±	0.03
Frontal Cortex (FCTX)	0.89	±	0.11	0.52	±	0.02
Rostral Ventromedial Striatum (RVMStr)	0.56	±	0.11	0.73	±	0.09
Rostral Dorsolateral Striatum (RDLStr)	0.58	±	0.09	0.43	±	0.04
Rostral Dorsomedial Striatum (RDMStr)	0.58	±	0.09	0.61	±	0.08
Rostral Ventrolateral Striatum (RVLStr)	0.48	±	0.14	0.53	±	0.04
Caudal Centromedial Striatum (CCMStr)	1.26	±	0.07	1.72	±	0.04
Caudal Dorsolateral Striatum (CDLStr)	1.99	±	0.03	2.10	±	0.01
Caudal Dorsomedial Striatum (CDMStr)	1.39	±	0.07	2.15	±	0.02
Caudal Ventrolateral Striatum (CVLStr)	1.55	±	0.03	1.35*	±	0.05
Globus Pallidus (GP)	0.75	±	0.04	2.07*	±	0.03
Olivary Body (OB)	0.63	±	0.08	1.00	±	0.05
Auditory (AudC)	1.34	±	0.05	0.31*	±	0.11
Substantia Nigra pars Reticulata (SNR)	0.98	±	0.06	0.44*	±	0.05
CA3	0.59	±	0.06	1.25	±	0.05
Somatosensory (SSCTX)	0.92	±	0.09	0.91	±	0.06
Ventral Anterior Nucleus (VAthal)	0.55	±	0.06	0.50	±	0.08
Ventrolateral Nucleus (VLthal)	0.57	±	0.06	0.62	±	0.08
Dorsolateral Geniculate (DLG)	1.35	±	0.07	1.70	±	0.06
CA1	1.20	±	0.08	0.95	±	0.08
Entorhinal (EC)	0.84	±	0.08	0.50	±	0.13
Rostral Periaqueductal Grey (RPAG)	0.59	±	0.05	0.36	±	0.05
Pontine Reticular Formation (PRF)	0.39	±	0.04	1.08*	±	0.10
Dorsolateral Entorhinal (DLECTX)	0.87	±	0.08	0.43	±	0.02
External Cortex of the Inferior Colliculus (ECIC)	0.62	±	0.09	0.98	±	0.13
Median Raphe (MR)	1.75	±	0.03	1.10	±	0.08
Superior Colliculus (SupC)	0.52	±	0.05	1.09*	±	0.08
Caudal Pontine Reticular Nucleus (CPRt)	1.72	±	0.07	0.39*	±	0.07
Superficial Grey Layer of the Superior Colliculus (SGSupC)	0.82	±	0.06	1.03	±	0.07
Caudal PAG (CPAG)	1.11	±	0.09	0.93	±	0.12
Locus Coeruleus (LC)	1.53	±	0.04	0.48*	±	0.10
Dorsal Cortex of the Inferior Colliculus (DCIC)	1.65	±	0.03	0.60	±	0.11
Gigantocellular Reticular Nucleus (GRt)	0.51	±	0.04	0.65	±	0.06
Medial Vestibular nucleus (MVN)	0.49	±	0.06	0.69	±	0.04
Superior Cerebellar Peduncle (SupCPed)	0.41	±	0.07	0.44	±	0.11
Dorsomedial PAG (DMPAG)	0.86	±	0.08	0.48	±	0.06
Medial Geniculate Nucleus (MG)	0.38	±	0.03	0.70	±	0.10
Paramedian Lobule (PML)	1.37	±	0.11	0.46*	±	0.03
Red Nucleus Parvocellular (RNPv)	0.45	±	0.05	0.44	±	0.03
Red Nucleus Magnocellular (RNMn)	0.59	±	0.09	0.45	±	0.07
Deep Cerebellar Nuclei (DCN)	1.31	±	0.10	1.45	±	0.07
Medial Amygdala (MeA)	0.92	±	0.10	0.95	±	0.07
Ventral Posterolateral Nucleus (VPLthal)	0.35	±	0.09	0.44	±	0.09
Ventral Posteromedial Nucleus (VPMthal)	0.37	±	0.04	0.50	±	0.05
Ventromedial Thalamic Nucleus (VMthal)	0.68	±	0.07	0.35	±	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.