

**Supplementary Table 2.** Full data for frontal cortex (FCTX) functional connectivity.

Brain Region	Wild-type (+/+)		<i>Myshkin</i> ( <i>Myk</i> /+)	
	mean	SEM	mean	SEM
Caudal Motor (CMCTX)	<b>0.88</b>	± 0.10	0.52	± 0.02
Rostral Motor (RMCTX)	<b>1.84</b>	± 0.04	<b>1.43</b>	± 0.04
Rostral Ventromedial Striatum (RVMStr)	<b>1.73</b>	± 0.05	<b>1.91</b>	± 0.03
Rostral Dorsolateral Striatum (RDLStr)	<b>1.53</b>	± 0.05	<b>1.85</b>	± 0.02
Rostral Dorsomedial Striatum (RDMStr)	<b>1.52</b>	± 0.05	<b>1.74</b>	± 0.04
Rostral Ventrolateral Striatum (RVLStr)	<b>1.64</b>	± 0.05	<b>1.68</b>	± 0.06
Caudal Centromedial Striatum (CCMStr)	0.67	± 0.09	0.49	± 0.03
Caudal Dorsolateral Striatum (CDLStr)	0.75	± 0.11	0.49	± 0.04
Caudal Dorsomedial Striatum (CDMStr)	0.59	± 0.07	0.75	± 0.03
Caudal Ventrolateral Striatum (CVLStr)	0.47	± 0.05	0.44	± 0.03
Globus Pallidus (GP)	0.65	± 0.05	<b>0.94</b>	± 0.06
Olivary Body (OB)	<b>1.25</b>	± 0.05	<b>0.93</b>	± 0.05
Auditory (AudC)	0.54	± 0.07	0.42*	± 0.05
Substantia Nigra pars Reticulata (SNR)	0.61	± 0.07	<b>0.85</b>	± 0.07
CA3	0.69	± 0.08	0.31*	± 0.15
Somatosensory (SSCTX)	0.77	± 0.07	0.30	± 0.12
Ventral Anterior Nucleus (VAthal)	<b>1.42</b>	± 0.03	0.41*	± 0.06
Ventrolateral Nucleus (VLthal)	<b>1.28</b>	± 0.03	0.75*	± 0.06
Dorsolateral Geniculate (DLG)	0.32	± 0.08	0.58	± 0.04
CA1	0.58	± 0.04	0.83	± 0.07
Entorhinal (EC)	0.62	± 0.08	<b>0.99</b>	± 0.07
Rostral PAG (RPAG)	<b>0.86</b>	± 0.05	0.77	± 0.11
Pontine Reticular Formation (PRF)	0.74	± 0.05	0.31	± 0.03
Dorsolateral Entorhinal (DLECTX)	<b>0.95</b>	± 0.06	<b>1.14</b>	± 0.06
External Cortex of the Inferior Colliculus (ECIC)	<b>0.99</b>	± 0.10	<b>1.09</b>	± 0.06
Median Raphe (MR)	0.50	± 0.09	0.41	± 0.03
Superior Colliculus (SupC)	<b>0.84</b>	± 0.06	<b>1.81*</b>	± 0.03
Caudal Pontine Reticular Nucleus (CPRT)	<b>0.89</b>	± 0.08	0.67	± 0.04
Superficial Grey Layer of the Superior Colliculus (SGSupC)	<b>0.85</b>	± 0.09	<b>1.06</b>	± 0.10
Caudal PAG (CPAG)	<b>1.13</b>	± 0.06	0.61	± 0.05
Locus Coeruleus (LC)	0.61	± 0.05	<b>0.99</b>	± 0.03
Dorsal Cortex of the Inferior Colliculus (DCIC)	0.55	± 0.06	0.79	± 0.05
Gigantocellular Reticular Nucleus (GRt)	<b>1.15</b>	± 0.05	<b>1.38</b>	± 0.06
Medial Vestibular nucleus (MVN)	<b>0.84</b>	± 0.05	<b>1.67</b>	± 0.05
Superior Cerebellar Peduncle (SupCPed)	<b>1.37</b>	± 0.06	0.42*	± 0.04
Dorsomedial PAG (DMPAG)	0.73	± 0.06	<b>1.38</b>	± 0.06
Medial Geniculate Nucleus (MG)	0.43	± 0.03	0.58	± 0.05
Paramedian Lobule (PML)	<b>1.42</b>	± 0.04	<b>0.96</b>	± 0.07
Red Nucleus Parvocellular (RNPr)	0.62	± 0.03	0.44	± 0.07
Red Nucleus Magnocellular (RNMr)	0.48	± 0.04	0.35*	± 0.09
Deep Cerebellar Nuclei (DCN)	<b>0.93</b>	± 0.04	0.72	± 0.04
Medial Amygdala (MeA)	<b>1.63</b>	± 0.05	<b>1.41</b>	± 0.06
Ventral Posterolateral Nucleus (VPLthal)	<b>1.01</b>	± 0.06	0.42*	± 0.06
Ventral Posteromedial Nucleus (VPMthal)	0.52	± 0.07	0.42	± 0.04
Ventromedial Nucleus (VMthal)	<b>1.28</b>	± 0.04	<b>1.13</b>	± 0.05

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.