

Table S2

Seed	Comparison	Target peak	MNI Coordinates			Cluster size (voxels)	F/T - value	p ≤
			X	Y	Z			
Left Caudate	S-PMS < Control	Cerebellum, Right Crus I	34	-58	-34	142	4.17	0.050
		Precuneus	16	-86	32	120	3.81	0.050
	S-PMS > D-NSS	Superior parietal cortex	40	-58	60	137	4.21	0.050
	HMP < D-NSS	Medial frontal cortex	-4	50	-14	285	5.43	0.010
		Somatosensory cortex	-28	-24	18	161	4.81	0.050
Right Putamen	D-NSS > Control	Medial frontal cortex	0	50	-8	266	4.64	0.010
	S-PMS < Control	Frontal pole	20	46	22	166	4.49	0.050
	D-NSS > Control	Inferior temporal cortex	44	-2	-44	249	4.6	0.010
Left Thalamus	All cluster comparison	Insula	-42	-22	8	355	10.68	0.001
	S-PMS < HMP	Occipital Cortex	28	-100	4	164	4.33	0.050
		Heschl's gyrus	-40	-24	4	1035	6.51	0.001*
	S-PMS > HMP	Precuneus	12	-36	44	149	5.18	0.050
		Insula	40	-2	2	243	4.63	0.010
		Cingulate gyrus	-4	-2	38	271	4.59	0.010
		S-PMS > Control	Insula	-34	-4	10	311	5.04
Right Thalamus	All cluster comparison	Insula	-30	-2	14	171	11.51	0.010
		Insula	-30	-2	14	810	5.5	0.001*
		Somatosensory cortex	32	-6	16	292	5.5	0.001*
		Temporal cortex	-30	-2	-12	176	5.4	0.010
	S-PMS > HMP	Superior parietal cortex	14	-58	58	232	4.75	0.010
		Superior parietal cortex	-26	-50	64	601	4.48	0.001*
		Premotor cortex	0	-6	58	258	4.17	0.001*
		Premotor cortex	-30	-6	56	187	4.1	0.010
		Premotor cortex	30	-6	50	104	4.1	0.050
	S-PMS < HMP	Occipital cortex	8	-90	-6	660	5.53	0.001
		Insula	-36	-4	12	210	5.2	0.050
	S-PMS > Control	Premotor cortex	24	-6	50	162	4.61	0.050
		Superior parietal cortex	-40	-46	50	152	4.21	0.050
Primary Motor	S-PMS < D-NSS	Occipital cortex	22	-102	12	476	4.54	0.001*
	HMP < D-NSS	Anterior Cerebellum	6	-60	-12	193	5.32	0.010
		Inferior parietal cortex	56	-36	22	192	5.02	0.010
	HMP > D-NSS	Precuneus	0	-70	22	189	4.85	0.050
		Superior frontal cortex	18	24	50	113	4.65	0.050
		Inferior parietal cortex	52	-62	18	113	4.58	0.050
Supplementary Motor Area	S-PMS > Control	Supplementary motor area	14	6	48	426	4.56	0.001*
		Hippocampus	34	-8	-32	203	4.18	0.050

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Table S1: Seed to voxel results for one way ANOVAs and independent samples t-tests comparing the CHR subtypes and healthy controls on functional connectivity for each individual seed. The index of connectivity for each comparison was defined as either a between-subject T or F contrast using r-to-z transformed values. Each of the comparisons in the rsFMRI analysis were first thresholded at the voxel-level at $p_{\text{uncorr}} < 0.001$ and then corrected at the cluster-level to a false-discovery rate (FDR) of $p < 0.05$. *Indicates independent samples t-test results surviving Bonferroni correction $p(\text{FDR}) < 0.001$.