

S16 Table. 3-chamber test for the Cntnap2 knockout model.

Cntnap2											
3-Chamber	Measure	Genotype	Mean SE		Mean SE		n	Factor			
			Left	Right	Genotype	Stimulus		Genotype x Stimulus			
	Baseline % Time in Chambers	WT	38.1	2.4	36.4	1.9	13	F	5.3	1.2	0.1
		KO	36.5	1.2	33.1	1.5	13	p	0.03	ns	ns
			Mouse		Object						
	% Time in Chamber	WT	51.2	2.4	35.6	1.8	13	F	7.1	22.9	0.9
		KO	46.1	2.0	35.6	1.9	13	p	0.01	0.0001	ns
	% Time Sniffing	WT	20.8	1.4	8.9	0.7	13	F	11.7	110.7	1.1
		KO	15.7	1.4	6.0	0.6	13	p	0.002	0.0001	ns
	Entries to Chamber	WT	17.4	1.4	15.9	1.1	13	F	3.0	4.6	0.6
KO		22.4	2.7	19.2	1.9	13	p	ns	0.04	ns	
		Mean SE		SE			Genotype				
Mouse Preference Time (%)	WT	58.8		2.3		13	F		0.6		
	KO	56.4		2.2		13	p		ns		
Mouse Sniffing (%)	WT	69.4		2.5		13	F		1.0		
	KO	72.3		1.6		13	p		ns		
			Novel		Familiar		n	Genotype	Stimulus	Genotype x Stimulus	
% Time in Chamber	WT	51.1	1.6	33.7	1.7	13	F	7.6	23.9	2.0	
	KO	44.0	2.7	34.4	2.3	13	p	0.01	0.0001	ns	
% Time Sniffing	WT	16.1	1.3	7.3	1.0	13	F	10.1	37.5	3.7	
	KO	10.4	1.3	5.8	0.7	13	p	0.004	0.0001	ns	
Entries into Chamber	WT	21.3	1.7	18.8	1.8	13	F	2.3	4.9	0.1	
	KO	24.8	2.2	23.0	2.1	13	p	ns	0.04	ns	
		Mean SE		SE			Genotype				
Novel Mouse Preference (%)	WT	60.3		1.7		13	F		1.7		
	KO	55.9		3.0		13	p		ns		
Novel Mouse Sniffing (%)	WT	68.8		3.4		13	F		1.3		
	KO	63.6		3.0		13	p		ns		