

S15 Table. 3-chamber test for the 16p11.2 deletion model.

16p11.2											
3-Chamber	Measure	Genotype	Mean SE		Mean SE		n	Factor			
			Left	Right	Genotype	Stimulus		Genotype x Stimulus			
	Baseline % Time in Chambers	WT	21.8	3.1	31.5	3.8	16	F	2.7	8.4	0.2
		HET	28.3	1.9	35.6	3.2	16	p	ns	0.01	ns
			Mouse		Object						
	% Time in Chamber	WT	55.9	5.0	30.7	3.5	16	F	0.8	24.6	0.7
		HET	59.1	3.9	29.8	3.3	16	p	ns	0.0001	ns
	% Time Sniffing	WT	24.0	2.5	8.0	1.3	16	F	0.001	53.9	0.1
		HET	24.8	2.2	7.3	1.0	16	p	ns	0.0001	ns
	Entries to Chamber	WT	19.7	7.4	11.4	1.2	16	F	0.4	3.0	0.2
HET		15.4	2.1	10.8	1.0	16	p	ns	ns	ns	
		Mean SE		SE			Genotype				
Mouse Preference Time (%)	WT	63.0		5.3		16	F		0.3		
	HET	66.1		3.9		16	p		ns		
Mouse Sniffing (%)	WT	72.3		5.9		16	F		0.3		
	HET	76.1		3.4		16	p		ns		
			Novel		Familiar		n	Genotype	Stimulus	Genotype x Stimulus	
% Time in Chamber	WT	51.3	2.8	36.4	2.6	16	F	0.3	15.3	0.3	
	HET	49.9	2.1	38.7	2.2	16	p	ns	0.001	ns	
% Time Sniffing	WT	16.2	1.8	9.2	1.0	16	F	0.4	20.9	0.1	
	HET	14.9	1.3	9.0	0.8	16	p	ns	0.0001	ns	
Entries into Chamber	WT	30.1	9.4	28.4	12.2	16	F	0.3	0.2	1.4	
	HET	21.4	3.7	25.0	3.5	16	p	ns	ns	ns	
		Mean SE		SE			Genotype				
Novel Mouse Preference (%)	WT	58.5		2.9		16	F		0.3		
	HET	56.4		2.3		16	p		ns		
Novel Mouse Sniffing (%)	WT	62.7		3.7		16	F		0.04		
	HET	61.7		3.2		16	p		ns		