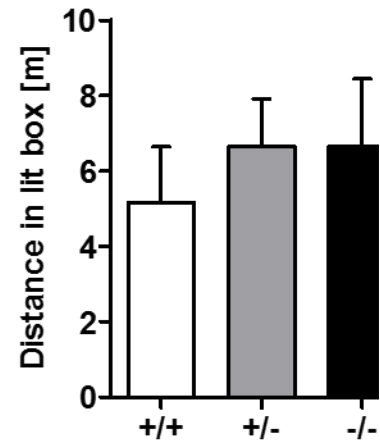


Fig. S1

a) Light-dark box



b) Open-field

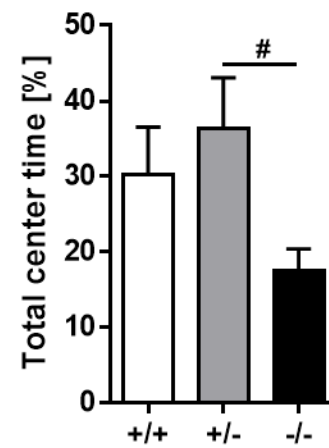
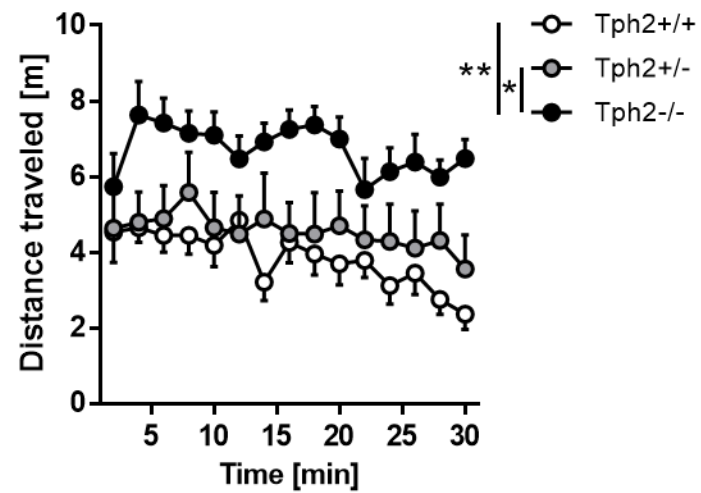
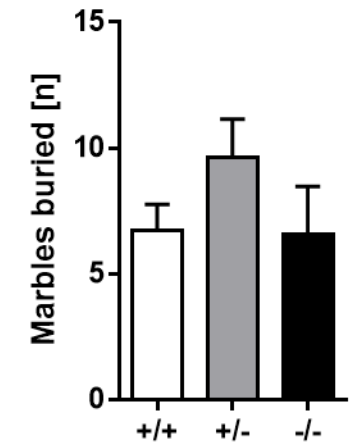
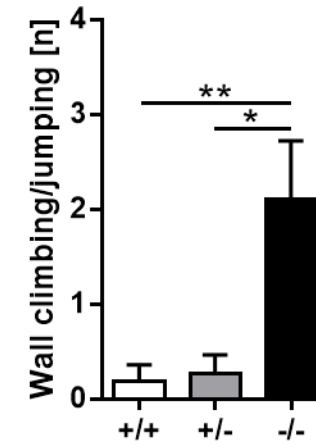
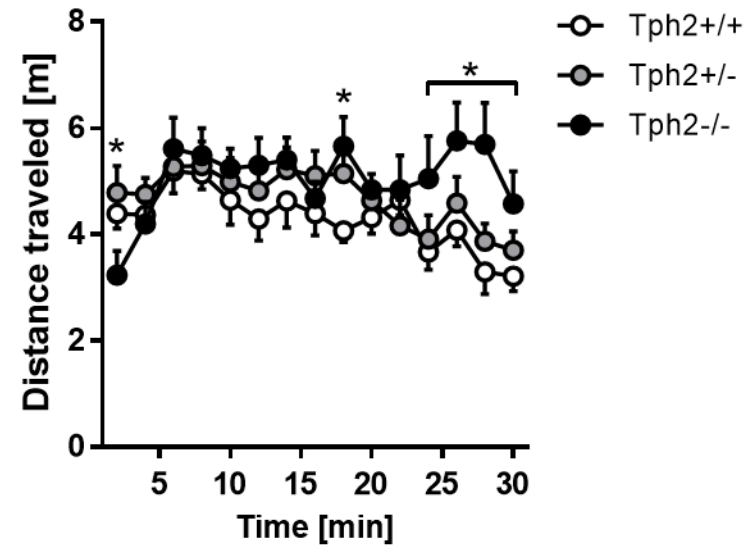


Fig. S2

a) Marble burying



b) Social interaction

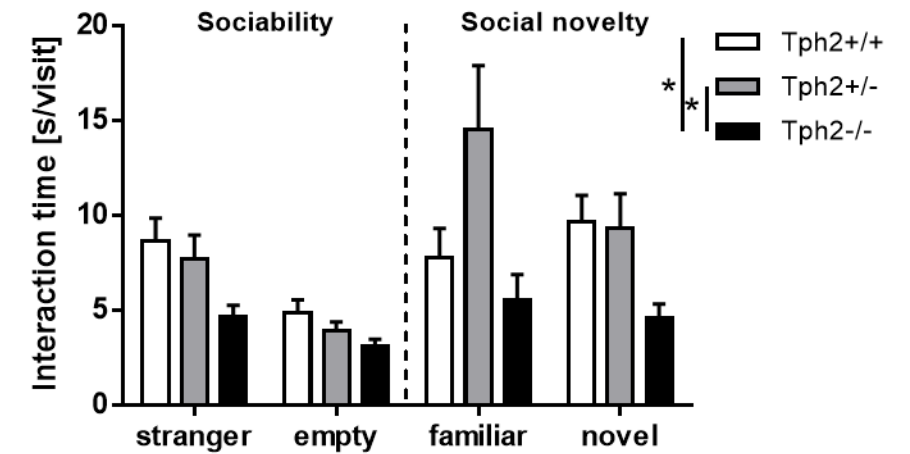
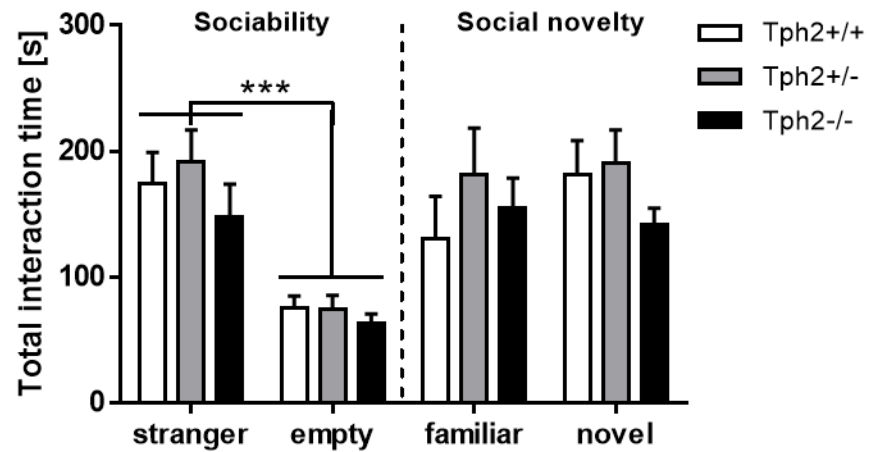


Fig. S3

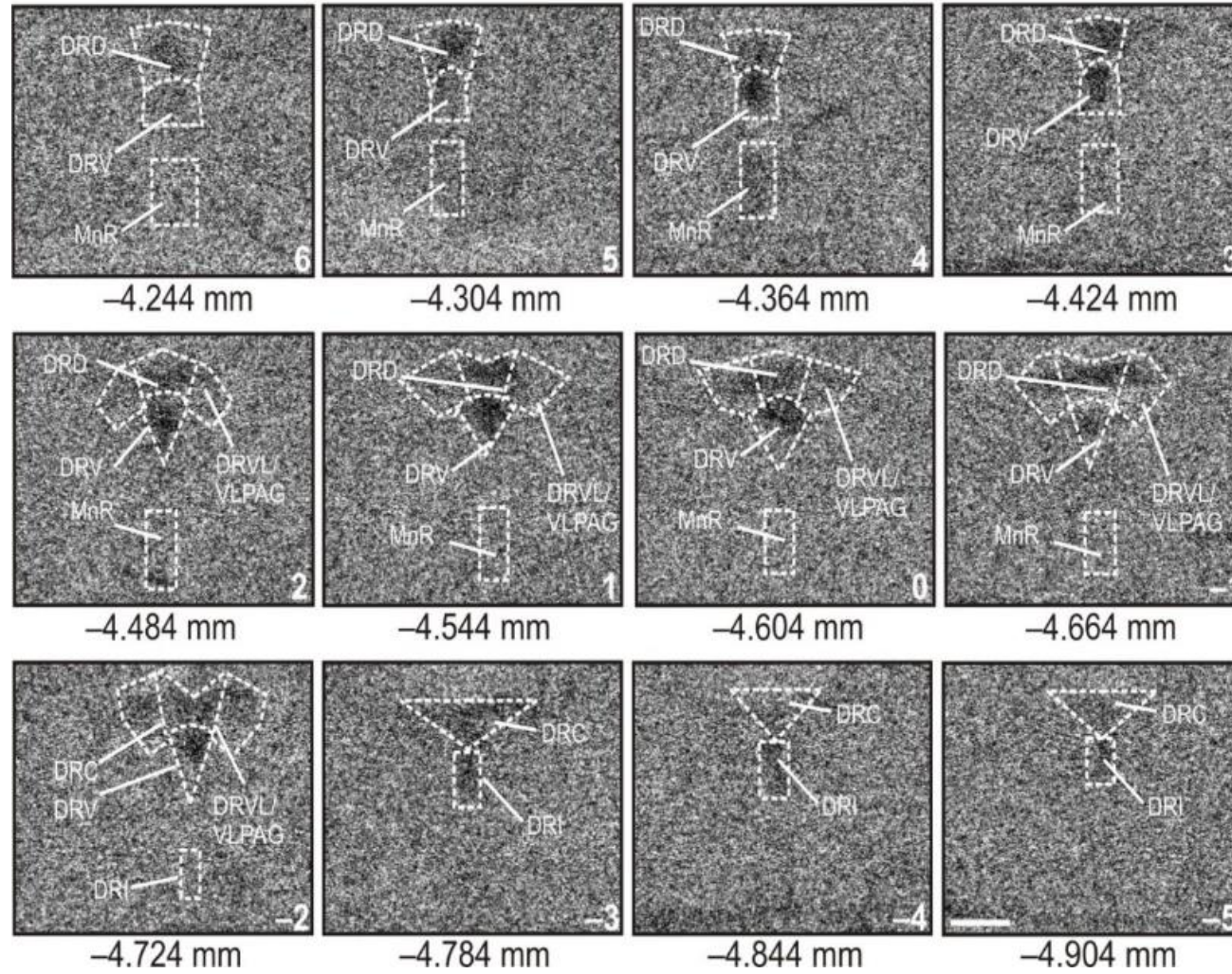


Fig. S4

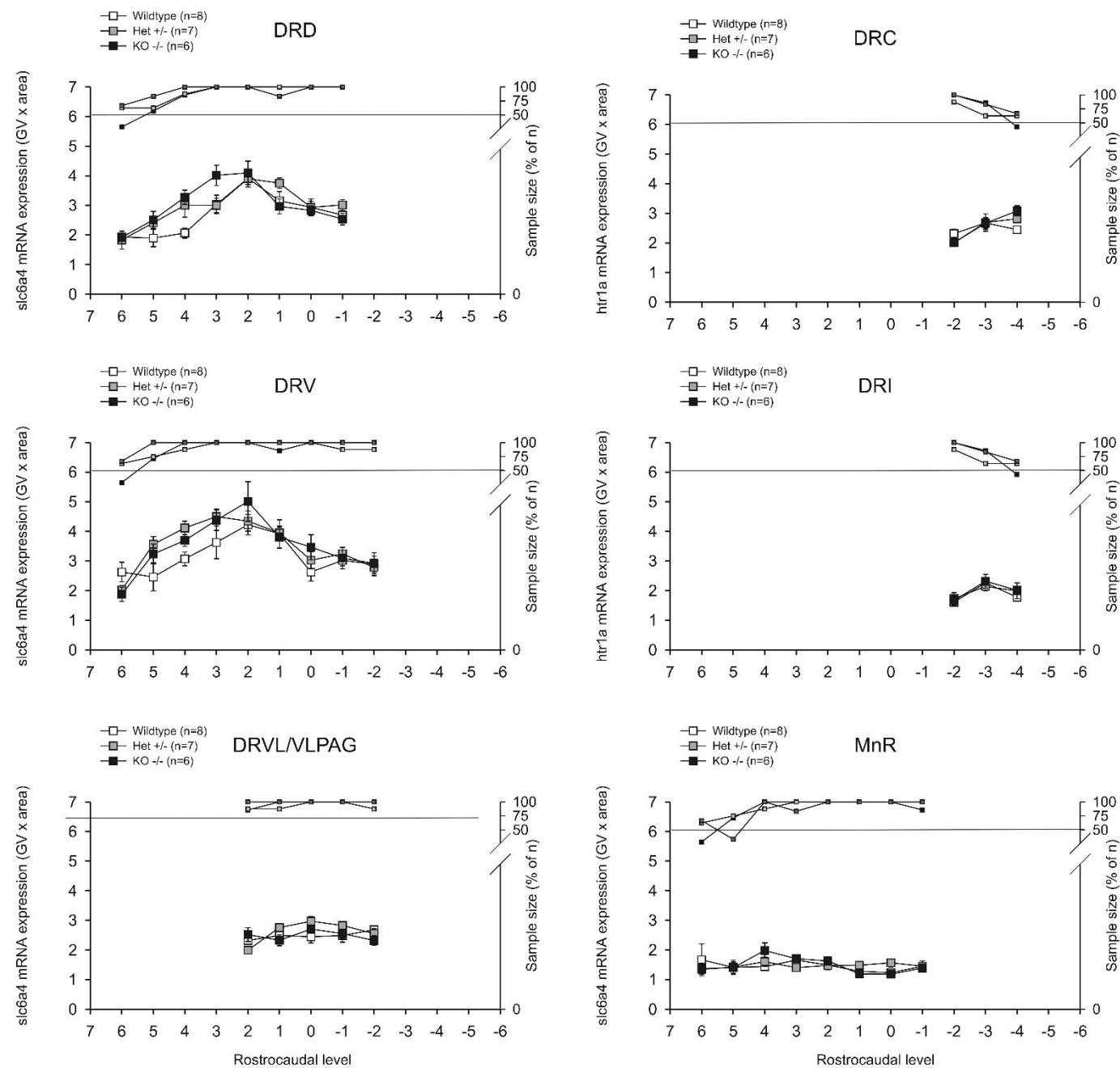


Table S1: Fixed effects of the Linear Mixed Models used to analyze *slc6a4* mRNA expression

Model	Source	Test statistic	p-value
Overall Analysis			
Entire dataset			
	Genotype	$F_{(2, 152.1)} = 8.9$	0.001
	Raphe subregion	$F_{(6, 119.8)} = 533.6$	0.001
	Rostrocaudal level	$F_{(10, 102.4)} = 51.8$	0.001
	Genotype*Rostrocaudal level(Raphe subregion)	$F_{(122, 56.2)} = 7.1$	0.001
Subregional Analyses			
Mean <i>slc6a4</i> mRNA expression in entire DR			
	Genotype	$F_{(2, 51.7)} = 4.3$	0.019
	Rostrocaudal level	$F_{(10, 30.8)} = 58.3$	0.001
	Genotype*Rostrocaudal Level	$F_{(20, 30.9)} = 1.536$	0.138
DRD			
	Genotype	$F_{(2, 40.9)} = 2.4$	0.060
	Rostrocaudal level	$F_{(7, 28.0)} = 15.7$	0.001
	Genotype*Rostrocaudal Level	$F_{(14, 31.3)} = 1.5$	0.156
DRV			
	Genotype	$F_{(2, 38.2)} = 3.0$	0.107
	Rostrocaudal level	$F_{(8, 32.5)} = 15.3$	0.001
	Genotype*Rostrocaudal Level	$F_{(16, 32.6)} = 1.5$	0.158
DRV/LPAG			
	Genotype	$F_{(2, 28.9)} = 1.1$	0.363
	Rostrocaudal level	$F_{(4, 30.4)} = 3.3$	0.024
	Genotype*Rostrocaudal Level	$F_{(8, 30.5)} = 2.7$	0.024
DRC			
	Genotype	$F_{(2, 16.3)} = .3$	0.749
	Rostrocaudal level	$F_{(2, 24.4)} = 22.3$	0.001
	Genotype*Rostrocaudal Level	$F_{(4, 26.4)} = 3.3$	0.025
DRI			
	Genotype	$F_{(2, 16.7)} = .3$	0.761
	Rostrocaudal level	$F_{(2, 16.1)} = 9.1$	0.002
	Genotype*Rostrocaudal Level	$F_{(4, 16.3)} = .3$	0.893
MnR			
	Genotype	$F_{(2, 35.3)} = .1$	0.94
	Rostrocaudal level	$F_{(7, 28.9)} = 3.2$	0.013
	Genotype*Rostrocaudal Level	$F_{(14, 26.8)} = 1.7$	0.112