Table S1. Pairwise statistical analysis of Rasgrf1 transcript levels in olfactory bulb.

Rasgrf1 transcript levels in P8 neonatal olfactory bulb were quantified for each genotype tested (see Methods). Transcript levels found in each genotype were compared using Students *t*-test; alpha levels were Bonferroni-corrected for ten multiple comparisons such that $p < 0.005$ indicates significance. The *t*-statistic and *p*-value for each pairwise comparison are depicted (df = 26 in all cases).

t statistic **p-value**	**B**	**MM**	**+/*tm2***	**MP**	**N**
B	--	$t = 3.60$ **$p = 0.0013$**	$t = 4.74$ **$p < 0.0001$**	$t = 0.25$ **$p = 0.8007$**	$t = 12.73$ **$p < 0.0001$**
MM		--	$t = 1.14$ **$p = 0.2655$**	$t = 3.48$ **$p = 0.0018$**	$t = 9.13$ **$p < 0.0001$**
+/*tm2*			--	$t = 4.66$ **$p < 0.0001$**	$t = 7.99$ **$p < 0.0001$**
MP				--	$t = 12.96$ **$p < 0.0001$**

Table S2. Pairwise statistical analysis of Rasgrf1 transcript levels in hippocampus.

Rasgrf1 transcript levels in P8 neonatal hippocampus were quantified for each genotype tested (see Methods). Transcript levels found in each genotype were compared using Students *t*-test; alpha levels were Bonferroni-corrected for ten multiple comparisons such that $p < 0.005$ indicates significance. The *t*-statistic and *p*-value for each pairwise comparison are depicted (df = 26 in all cases).

t statistic **p-value**	**B**	**MM**	**+/*tm2***	**MP**	**N**
B	--	$t = 5.83$ **$p < 0.0001$**	$t = 8.07$ **$p < 0.0001$**	$t = 3.38$ **$p = 0.0023$**	$t = 28.04$ **$p < 0.0001$**
MM		--	$t = 2.24$ **$p = 0.0338$**	$t = 2.67$ **$p = 0.0128$**	$t = 22.21$ **$p < 0.0001$**
+/*tm2*			--	$t = 5.00$ **$p < 0.0001$**	$t = 19.97$ **$p < 0.0001$**
MP				--	$t = 25.72$ **$p < 0.0001$**

Table S3. Pairwise statistical analysis of Rasgrf1 transcript levels in the remainder of the brain. *Rasgrf1* transcript levels in the remainder of the P8 neonatal brain (ROB, comprising the whole brain excepting olfactory bulbs, hippocampus, hypothalamus and pituitary gland; see Methods for details) were quantified for each genotype tested (see Methods). Transcript levels found in each genotype were compared using Students *t*-test; alpha levels were Bonferroni-corrected for ten multiple comparisons such that $p < 0.005$ indicates significance. The *t*-statistic and *p*-value for each pairwise comparison are depicted (df = 26 in all cases).

t statistic **p-value**	**B**	**MM**	***+/tm2***	**MP**	**N**
B	--	$t = 6.51$ $p < 0.0001$	$t = 13.53$ $p < 0.0001$	$t = 3.67$ $p = 0.0011$	$t = 37.65$ $p < 0.0001$
MM		--	$t = 7.02$ $p < 0.0001$	$t = 3.09$ $p = 0.0047$	$t = 31.14$ $p < 0.0001$
+/tm2			--	$t = 10.37$ $p < 0.0001$	$t = 24.12$ $p < 0.0001$
MP				--	$t = 35.40$ $p < 0.0001$