Supplementary data

Table 1.

Differentially expression mRNA related to recovery of olfactory disturbance. (fold change, 1.5; log2 normalized read counts of ≥ 4 were selected; $p < 0.05$). OT: Olfactory training, 2w: after 2 weeks OT, 3w: after 3 weeks OT. *: significantly higher than control.

Gene (2w)	Anosmia /control	OT /control	Gene (3w)	Anosmia /control	OT/control
GDNF	0.510	0.503	GDNF	1.912	0.256
ADCY1	0.018	0.370	ADCY1	7.607*	2.564
ADCY3	0.403	0.536	ADCY3	0.635	0.382
ADCY8	0.133	14.615*	ADCY8	6.355*	0.604
ADCY10	0.540	54.666*	ADCY10	1	1.005
BDNF	2.435	0.1159	BDNF	1.940	0.604
NGFR	0.104	0.102	NGFR	1.133	2.376*
NGFRAP	0.0129	0.160*	NGFRAP	1.346	2.175*

MATERIALS AND METHODS

Data analysis

QuantSeq 3' mRNA-Seq reads were aligned using Bowtie2 (Langmead and Salzberg, 2012). Bowtie2 indices were either generated from genome assembly sequence or the representative

transcript sequences for aligning to the genome and transcriptome. The alignment file was used for assembling transcripts, estimating their abundances and detecting differential expression of genes. Differentially expressed gene was determined based on counts from unique and multiple alignments using coverage in Bedtools (Quinlan AR, 2010). The RC (Read Count) data were processed based on quantile normalization method using EdgeR within R (R development Core Team, 2016) using Bioconductor (Gentleman*et al*.,2004). Gene classification was based on searches done by DAVID (http://david.abcc.ncifcrf.gov/) and Medline databases (http://www.ncbi.nlm.nih.gov/).