Supplementary material.

Supplementary Figure 1.

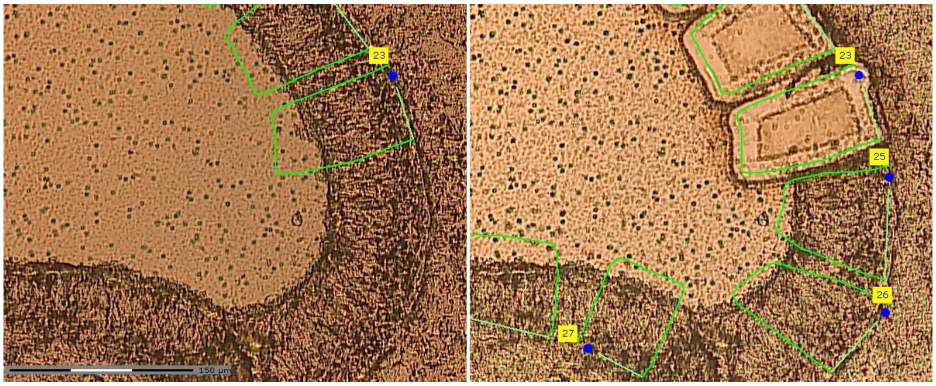
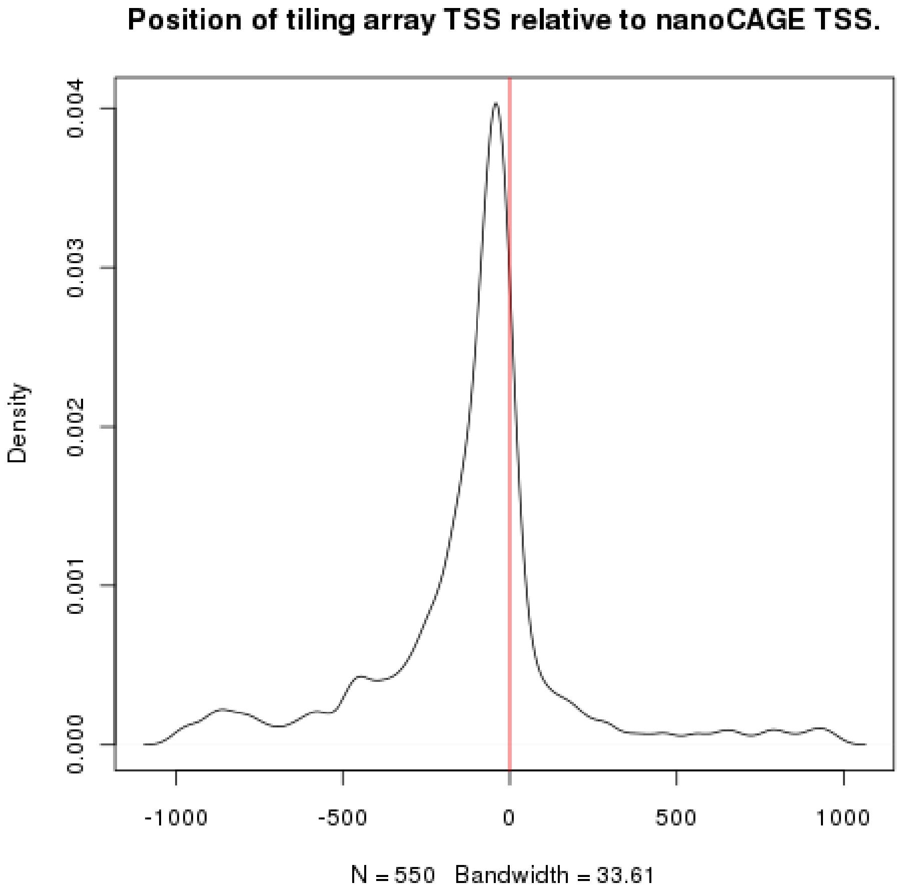


Figure S1: Laser capture microdissection of the olfactory epithelium. Fixed histological sections of olfactory epithelium were microdissected with a Zeiss P.A.L.M LCM microscope. The olfactory epithelium was divided in square blocks (left screen capture), that were cut with a computer-assisted laser and catapulted in microtubes. The screen capture on the right side shows two regions already harvested, and four others selected for dissection.

Supplementary Figure 2

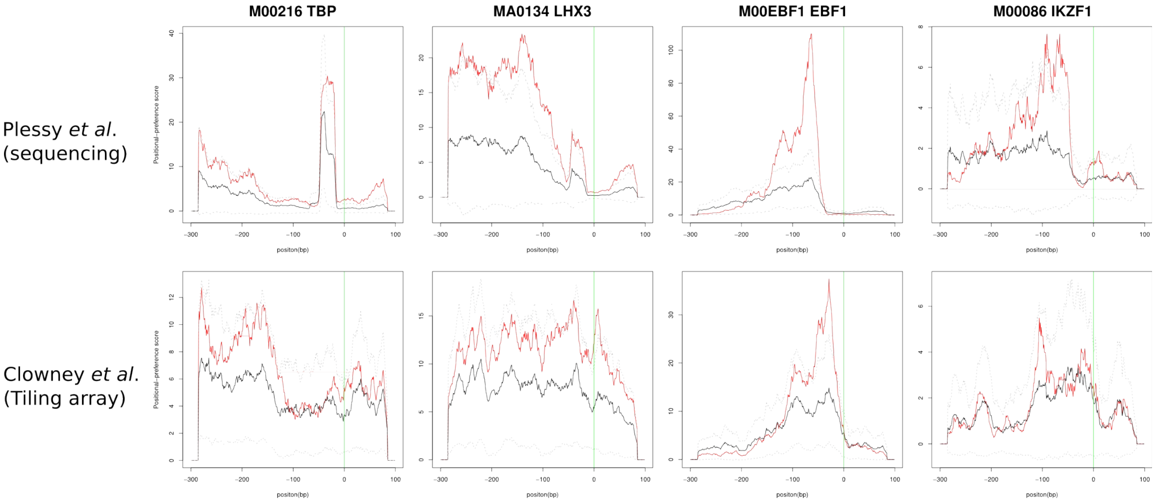
Figure S2: Position of Clowney *et al.*'s tilling array TSS relative to this work's nanoCAGE TSS.



Clowney et al's TSS for olfactory receptors were downloaded from http://genome.cshlp.org/content/suppl/2011/06/17/gr.120162.110.DC1/Clowney_olfrnamedproms.txt and compared to the TSS distributed in this supplementary material (see "Extended loci for olfactory receptors" below). For each OR where a TSS is defined in both studies, the position of the tilling array TSS were calculated by subtracting the coordinates of the nanoCAGE TSS with those of the tilling array TSS. Coordinates on the minus strand were used as negative values. 27 ORs had more than one tilling TSS and a position was computed for each TSS. The figure above shows a kernel density estimate of the positions of 550 tilling array TSS relative to the nanoCAGE TSS. 334 other TSS are assigned to the same OR in both studies, but their distance was higher than one kilobase.

Supplementary Figure 3

Transcription factor binding profile over nanoCAGE and tilling array promoters.



TF binding site motif profiles in this work's TSS based on sequencing (red lines, upper row, also displayed in Figure 3), and in the TSS based on tilling array from Clowney *et al.* (red lines, lower row). The same method and the same background set were used to produce the profiles. The background (black line) is calculated by random samplings of the target set and the background set, and therefore differs for the same PWM in the two analyzed TSS sets (nanoCAGE and tilling array). The gray lines are 99.99 % confidence intervals around the mean.

Supplementary Text

This section of the supplemental material contains links to download the CAGE data as well as the new promoters of the OR genes, in a format that can be used for display in the online genome browser of the University of California, Santa Cruz.

Tracks for use with the UCSC browser

The CAGE tracks can be directly used in the UCSC browser, either by:

- Instructing the UCSC browser to load the tracks from our servers by using the pre-established links shown below. Clicking one of the links will add that track as custom track to the UCSC genome browser without having to download the file on your computer. It will also open the browser. If desiring both tracks, close the genome browser window and repeat for other one: all the tracks will then be whown in the genome browser.
- Or, by first downloading the track files of interest and then, at the main UCSC site, clicking Genomes->add custom track, and upload the files in this page.

A tutorial on how to use the genome browser can be found at the UCSC browser help page.

Resource tracks for the study of the promotome of the MOE

- Expression track (in WIG format).
  [Download on your computer] [Load in UCSC browser] *Note that this will take some time.*
- Extended loci for olfactory receptors (in GFF format). *This file is also available as TableS6 from the Genome Research website*.
  [Download on your computer] [Load in UCSC browser]

All track coordinates refer to the mm9 assembly.

Other uses

Our tracks can be used in other browsers, like GBrowse, and can be loaded into Galaxy as a starting point for further analysis, for instance for extracting sequences upstream to the promoters.

The *extended loci* track in GFF format contains the expression value for each olfactory receptor in the column number 6 (score). Using programs like the BEDTools (http://code.google.com/p/bedtools/), this GFF track can be used to extract the promoter's sequences from the mouse genome.

Visit the OR clusters from:

After loading the CAGE data and the OR promoters in the UCSC browser, you can use the following links to explore the olfactory clusters.

We recommend the following configuration:

- Turn on the *full* display of the expression track (OE_12Feb09).
- Use either *dense* or *squish*ed display for the extended locus track (User Track).
- *Hide* the redundant Other RefSeq, MGC Genes and Ensembl Genes tracks.

- CLIC 1 (chromosome chr4)
- CLIC 2 (chromosome chr3)
- CLIC 3 (chromosome chr3)
- CLIC 4 (chromosome chr1)
- CLIC 5 (chromosome chr11)
- CLIC 5 (chromosome chr16)
- CLIC 5 (chromosome chr7)
- CLIC 7 (chromosome chr1)
- CLIC 8 (chromosome chr14)
- CLIC 9 (chromosome chr16)
- CLIC 10 (chromosome chr11)
- CLIC 11 (chromosome chr11)
- CLIC 12 (chromosome chr13)
- CLIC 12 (chromosome chr17)
- CLIC 14 (chromosome chr6)
- CLIC 15 (chromosome chr6)
- CLIC 16 (chromosome chr6)

- CLIC 17 (chromosome chr4)
- CLIC 18 (chromosome chr13)
- CLIC 19 (chromosome chr4)
- CLIC 20 (chromosome chr4)
- CLIC 21 (chromosome chr2)
- CLIC 22 (chromosome chr6)
- CLIC 22 (chromosome chr7)
- CLIC 23 (chromosome chr7)
- CLIC 24 (chromosome chr7)
- CLIC 25 (chromosome chr7)
- CLIC 26 (chromosome chr2)
- CLIC 27 (chromosome chr19)
- CLIC 28 (chromosome chr7)
- CLIC 29 (chromosome chr9)
- CLIC 30 (chromosome chr15)
- CLIC 31 (chromosome chr10)
- CLIC 32 (chromosome chr14)
- CLIC 32 (chromosome chr2)
- CLIC 33 (chromosome chr14)
- CLIC 34 (chromosome chr14)
- CLIC 35 (chromosome chr14)
- CLIC 36 (chromosome chr14)
- CLIC 37 (chromosome chr7)
- CLIC 38 (chromosome chr16)
- CLIC 39 (chromosome chr11)
- CLIC 40 (chromosome chr11)
- CLIC 42 (chromosome chr9)
- CLIC 42 (chromosome chr9)
- CLIC 43 (chromosome chr8)
- CLIC 44 (chromosome chr8)
- CLIC 45 (chromosome chr10)

- CLIC 46 (chromosome chr8)
- CLIC 47 (chromosome chr7)
- CLIC 48 (chromosome chrX)