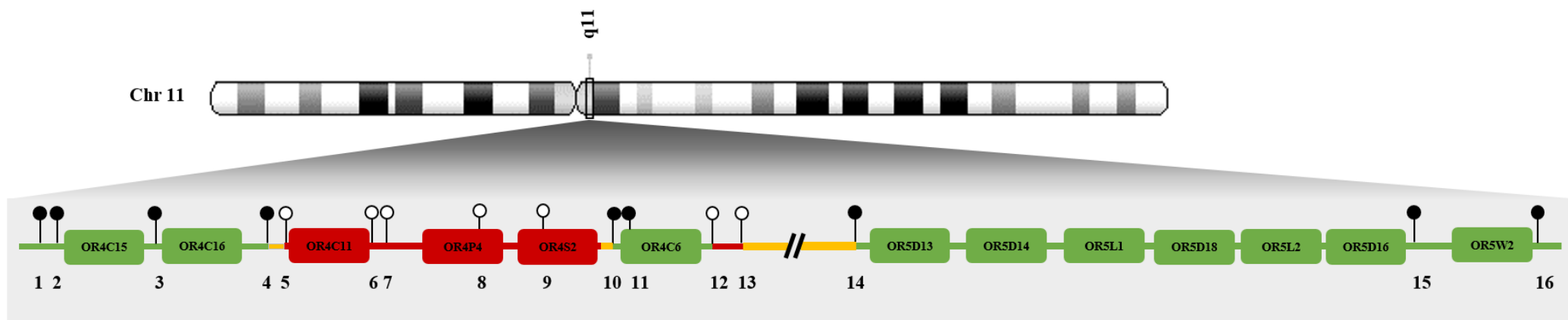


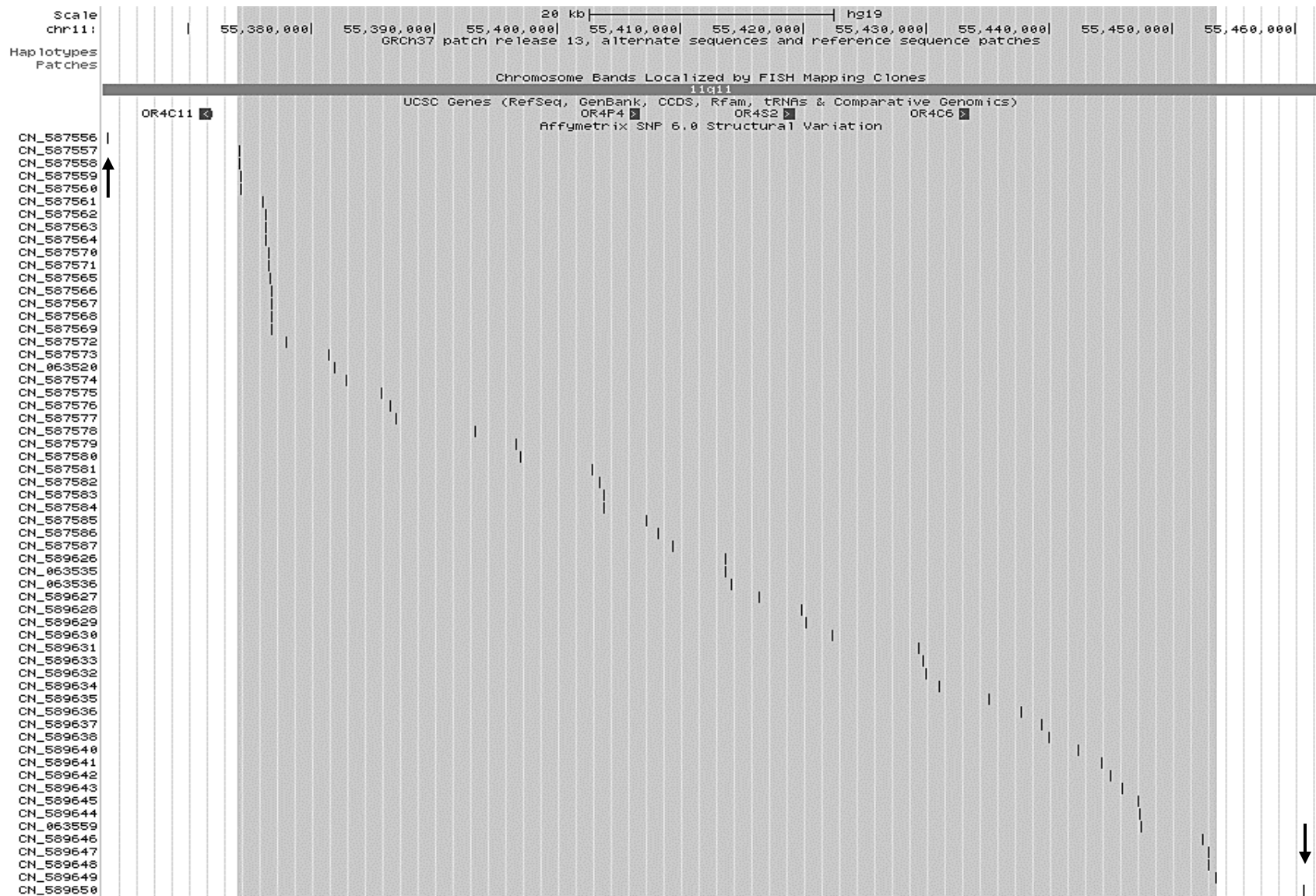
## Supplementary material



**Supplementary Figure 1. Positioning of the different primer pairs used for copy number variation screening.**

The position of each MAQ primer pair in the region of interest is schematically represented with  $\uparrow$ . Each pair is specified with its corresponding number (1-16). Primer pairs were designed with the MAQ primer design tool, which is accessible via <https://suremastrtools.agilent.com/maq-design/>. The target region was set at chr11:55,300,000-55,700,000 (genome build GRCh37/hg19) and includes a total of 13 olfactory receptor genes.

Screening of the 11q11 region resulted in copy number loss detection (white/black colored probes represent absence/presence of the MAQ primer pair); red coloring represents the minimal deleted region, yellow coloring signifies the maximal deleted region, and green coloring indicates genes that are not part of the deletion.



**Supplementary Figure 2. Visual representation of probe coverage in the 11q11 region by the Affymetrix Genome-Wide Human CNV Array 6.0.**

Individual probes of the Affymetrix Genome-Wide Human CNV Array 6.0 are represented in the 11q11 region. Each probe is specified by its probe identifier “CN\_.....”. The grey colored region indicates the minimal size deletion identified by Jarick et al (2011). None of the array probes are positioned within a gene. Arrows specify the boundaries of the maximal size deletion identified by Jarick et al (2011) and indicate the presence of *OR4C11* as potential extra gene involved in the deletion.