

**Table A1. Primer pairs used in Quantitative RT-PCR of olfactory receptors (ORs)**

<b>OR Family`</b>	<b>Receptors amplified*</b>	<b>Forward primer (5'-3')</b>	<b>Reverse Primer (5'-3')</b>
4	4.1	TTGACACCAGGACTATGTCGTT	CATATGCCATTGCAGTCAAGAT
5	5.1, 5.2 <sup>^</sup> , 5.4	TGCTGGGATTTCCAGGACTCC	CAGAAGATTACATAGGTGGGTT
7	7.1	TGTCCTCATGAACTCCAGCTTA	CAGGCGCCAAATGAGATATAGT
9	9.1 <sup>^</sup> ,9.3,9.4	ATATGCAATCCACTGCGATAC	TTGAATCACAGATCTGCAGTGG

` Primer pairs were designed for all OR families (2,4,5,7,9 and 13) however, primers for families 2 and 13 did not work in QRT-PCR despite working in conventional PCR. Therefore, the following receptors were not tested by either QT-PCR or microarray: 2.1-2.4, 2.6, 2.9-2.11 and 13.2.

\* PCR products were cloned into a vector and randomly chosen clones were sequenced to verify amplification of ORs.

<sup>^</sup> Though the primers amplify multiple family members, in our analysis they showed a preference for these receptors. Receptors 5.3 and 9.2 are the most divergent receptors in families 5 and 9 and were not amplified using these primers. ORs 5.3 and 9.2 were also not represented on the microarray and were not tested in our experiments.