Figure S1. Detailed methylation analyses of the pan-cancer methylation status of data sets from The Cancer Genome Atlas (TCGA) using the Shiny Methylation Analysis Resource Tool (SMART). β-values for olfactory receptors (ORs) show median, cancer (red) and normal (grey), data sets between 0.5-0.9. A high range (0.1-0.9) of β-values between individual samples, represented by the scatter; OR1J4 stands out as having β-values lower than 0.5; OR2A1, OR10Q1 and OR4M1 exhibit the highest level (median β-value 0.75) of tumour and normal methylation. Significant change in methylation indicated as: *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001, while non-significant change as: N/S: P>0.05. It must be noted that control data are absent for: AAC, DLBC, KICH, OV, MESO, USC and UVM.

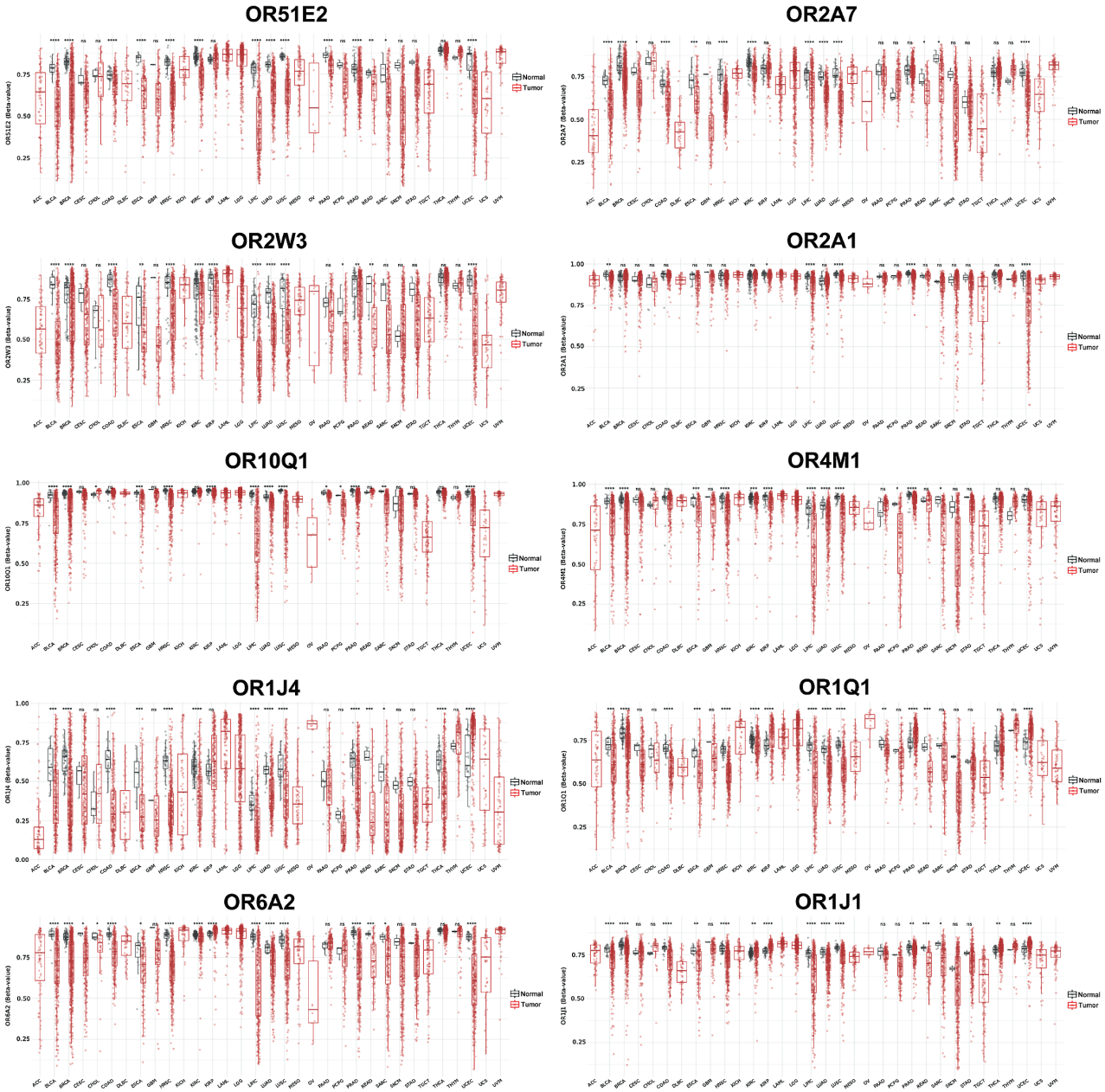

Figure S2. Pan-cancer distribution of olfactory receptor (OR) mutation types from RNAseq data (cBioportal). OR2A7, OR2W3 and OR2A1 exhibit a high distribution of amplification/gain of function throughout the range of tumour groups (red); OR51E2, OR10Q1, OR1J4, OR1Q1, OR6A2 and OR1J1 primarily exhibit mutations in the form of shallow deletions (blue) across the range of tumours; OR4M1 presents with limited sample size, expressing a range of shallow deletions and amplification across the data set.