Reference of the olfactory genes:

**1) study about vertebrate ORs:**

Niimura, Y. (2009). On the origin and evolution of vertebrate olfactory receptor genes: comparative genome analysis among 23 chordate species. Genome Biology and Evolution, 1(2006), 34–44. http://doi.org/10.1093/gbe/evp003

7 types - alfa, beta, gama, delta, epsilon, zéta, éta + théta, kappa, lambda (as non-OR)

Supplementary - they provide AA sequences (can we retrieve it from genomes??).



**2) mudskipper genome study (OR part of it, uses the names following Niimura):**

You, X., Bian, C., Zan, Q., Xu, X., Liu, X., Chen, J., … Shi, Q. (2014). Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. *Nature Communications*, *5*, 1–8. http://doi.org/10.1038/ncomms6594







**3) cichlid OR**:

Azzouzi, N., Barloy-Hubler, F., & Galibert, F. (2014). Inventory of the cichlid olfactory receptor gene repertoires: Identification of olfactory genes with more than one coding exon. BMC Genomics, 15(1), 1–16. http://doi.org/10.1186/1471-2164-15-586

14 families: Fam A, Fam D, Fam E, Fam G, Fam H, Fam I, Fam K, Fam L, Fam N, Fam O, Fam P, Fam R, Fam S, Fam W

(each with several subfamilies)

**Methods**:

1) Azzouzi et al: TBLASTN, reference OR + a lot of related GPCR genes.

... TBLASTN results were filtered with a homemade python script so that candidate OR sequences conformed to the following rules: (1) one or more matches with the positive dataset and (2) no match with the negative data- set using an e-value cut-off of 1e−50. Selected candidates were re-checked using both BLASTX and BLASTP against the fish protein database (NCBI, taxiD: 7898) using default parameters with a cut-off of 1.e-100

2) mudskippers: BLASTP on proteomes...

3) Libor suggested: xxx + bedtools extract from coordinates

Idea: Extraction from the raw reads?

- map raw reads against ref, assemble?