



### BLAT alignments

All EST are aligned on the 4 fish species genomes (RNA, DNA, translated RNA and translated DNA modes; masked repeats).

Initial cutoff: score > 30, homology > 60%

For each EST, the best localization(s) (best score + scores > 0.95 \* [best scores]) on each genome are retained.

### UCSC Genome Browser

Corresponding Ensembl gene IDs are extracted using the ensGene files.

### Ensembl orthology:

The number (n) of orthologous genes matched by each EST is counted. Each clone is then annotated with the EST exhibiting the highest "n". In the case when several EST have the same "n", the best score is then considered.

### Ensembl Orthology and GeneOntology:

GeneOntology terms associated with fish as well as mouse, rat and human orthologous genes are inferred to the trout clone.

Are finally not considered:

- ESTs with multiple localizations
- ESTs with score < 50 and/or that mached a location > 500 bp from the gene, if "n" < 2