

README

Zip file contains 3 directory and 2 files:

- *.gmap.f2.gff3 All mapped query sequences in GFF3 format
the code “f2” mean the filtering condition:
trimmed coverage \geq 90%
identity \geq 90%
and only best path (match) is selected to output
- alignment All mapped query sequences were saved in GMAP Alignment format
and output files were separated in different types as described in GMAP
- blat.psl All mapped query sequences were saved in BLAT PSL format
and output files were same as above
- *.gmap.f2.nomap.seq The remaining nomapped sequences in FASTA format
- fosmid Nomapped sequences mapping to fosmid contigs (>5 kb) using GMAP
and then alignments were saved in GMAP Alignment format.
Output files were same as above