

axtToMaf

Use Kent tools to convert alignment
AXT files for galGal3:anoCar1 to MAF
files

**MAF-
formatted
alignments**

genome/summary.py (v0.1)

find perfectly conserved regions in
genome:genome alignments

sqlite-db
"DB1"

genome/summaryBlast.py (v0.1)

BLAST sequence regions to another
genome (zebra finch) to validate.

sqlite-db
"DB1"