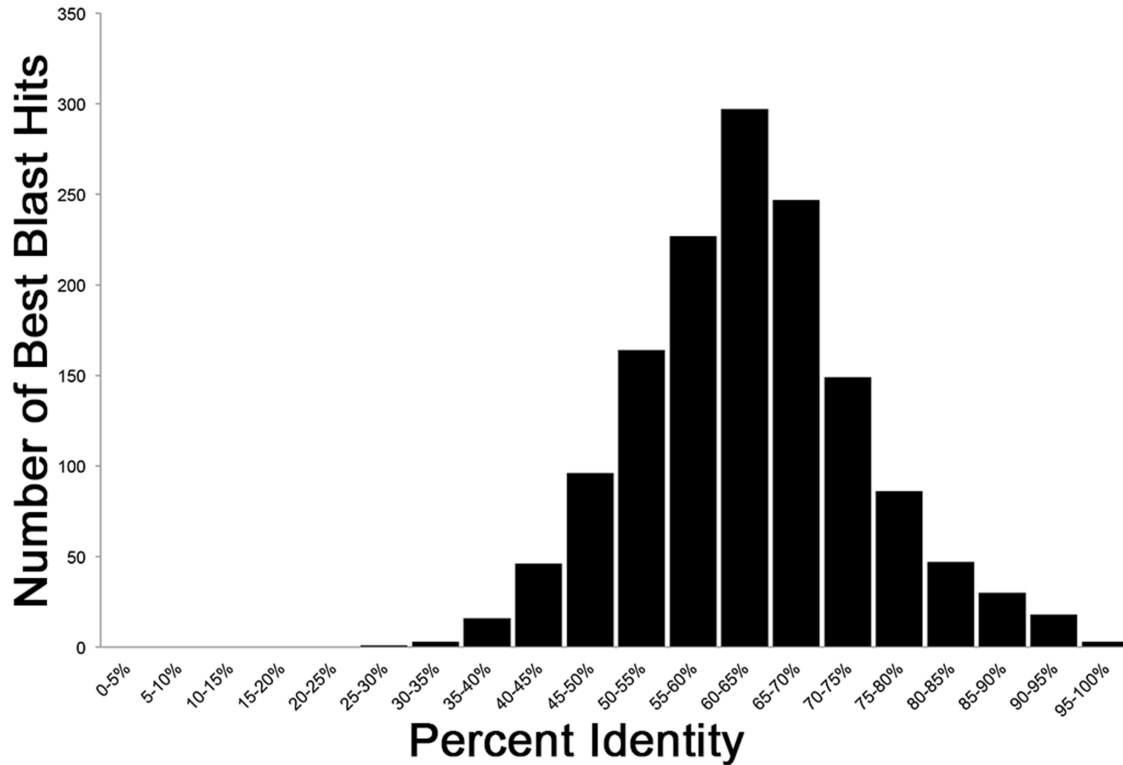


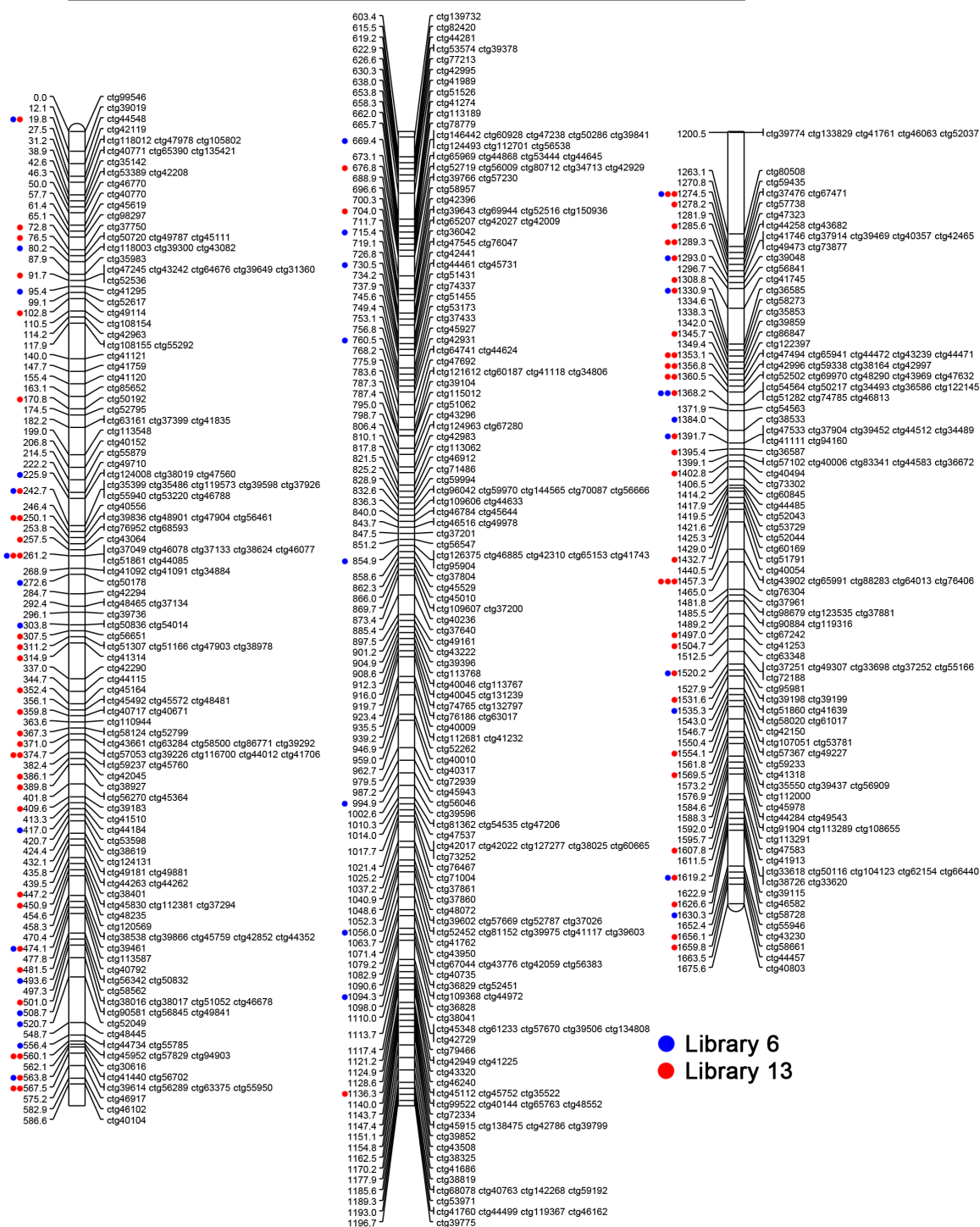
Supplementary Figures

Keinath et al, "A Linkage Map for the Newt *Notophthalmus viridescens*: Insights in Vertebrate Genome and Chromosome Evolution"

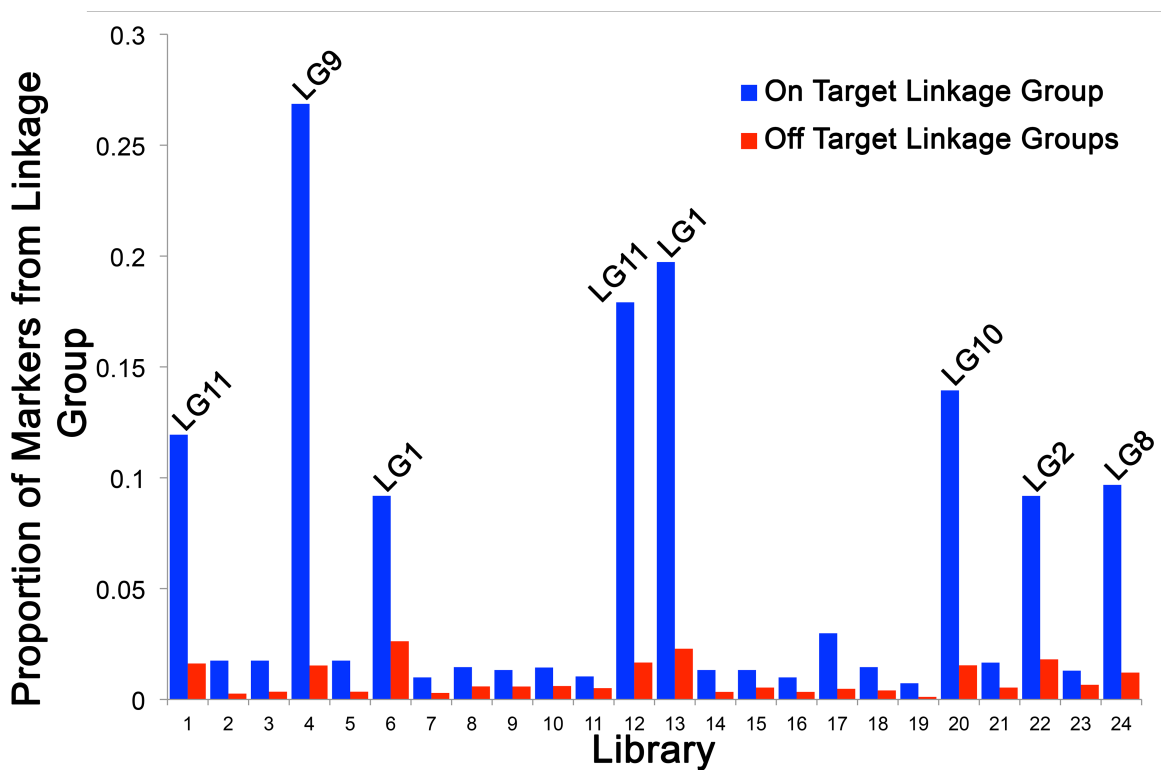


Supplementary Figure 1 – Amino acid identity between newt/chicken best blast hits. This chart shows the distribution of percent identity of best blast hits between the newt linkage map and the chicken genome with a minimum combined alignment length of 40 amino acids and a bitscore of at least 100.

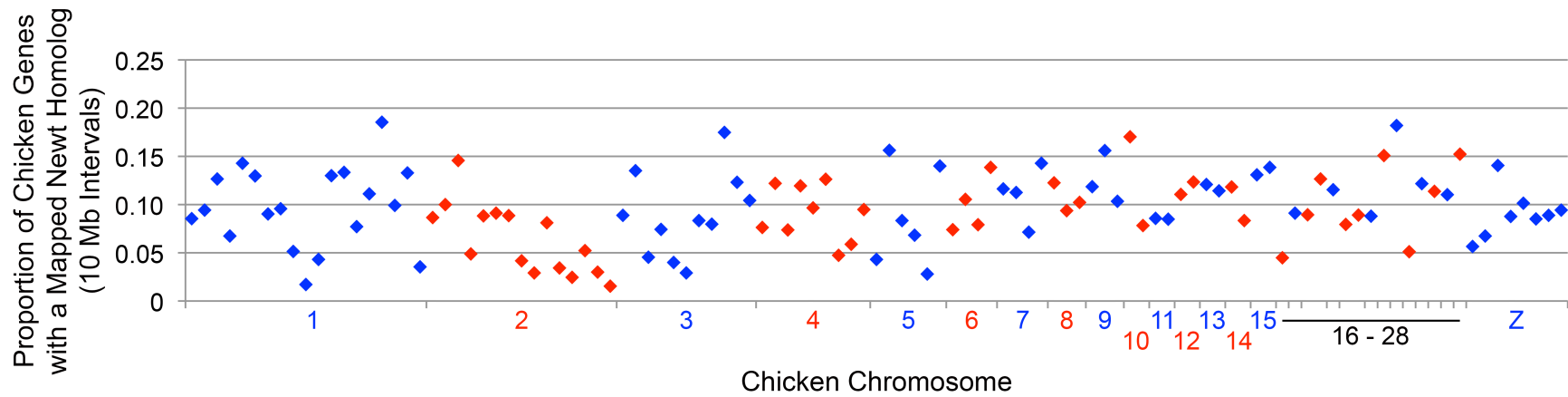
Preliminary Maternal LG2



Supplementary Figure 2 (Previous Page) – Preliminary linkage group 2. This linkage group was manually curated to yield new linkage groups 1 and 5. Laser-capture chromosome sequencing data (colored dots) indicated that the first ~570 cM and last ~400 cM were portions of the same chromosome, exclusive of a ~700 cM internal segment that was flanked by large gaps in the linkage map. Colored dots represent markers that were sampled by libraries from two independently captured and amplified dyads (libraries 6 and 13 from Supplementary Figure 3).



Supplementary Figure 3 – Mapping of reads generated by laser capture sequencing. Read mapping from genomic libraries of individual laser captured dyads was used to validate marker content of linkage groups. The X-axis shows the proportion of *Notophthalmus viridescens* markers with nearly identical reads recovered from chromosome-targeted sequencing. The proportions of markers identified from each target linkage group (linkage group showing the highest degree of enrichment, in blue) vs. all other off target linkage groups (in red) are presented separately for each library. Each library targeted a single dyad, although many libraries yielded insufficient sequence to identify a corresponding linkage group at the current sequence depth. Libraries yielding sufficient sequence information are labeled with their corresponding linkage group.



Supplementary Figure 4 – Sampling of newt/chicken homologs along the chicken genome. This chart shows the proportion of annotated chicken genes for which a homologous gene was placed on the newt linkage map. Proportions are shown for all all non-overlapping 10 Mb intervals along the length of each chicken chromosome.