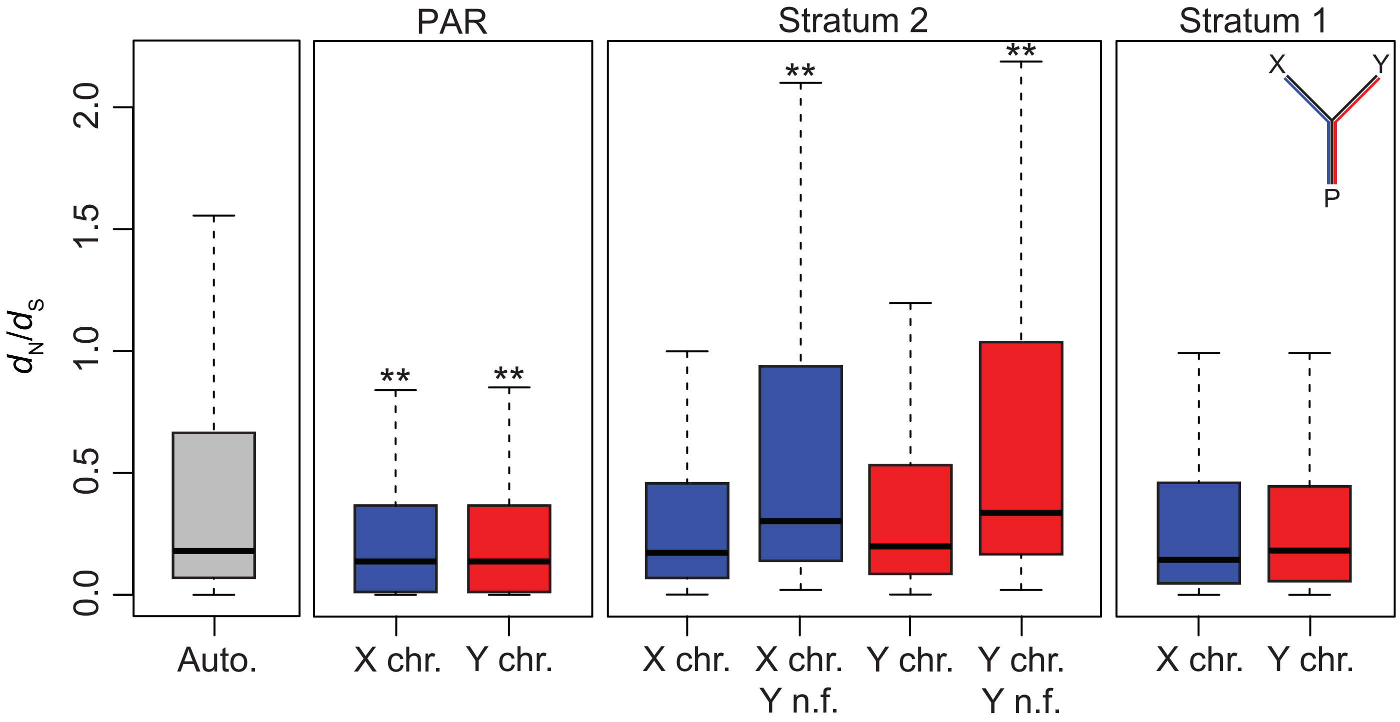
Figure S1. Lineage-specific divergence of the X and Y chromosomes. The X chromosome, Y chromosome, and autosomes of *G. aculeatus* were aligned to the ninespine stickleback *(P. pungitius)* to quantify d_N/d_S ratios between the sex chromosomes and *P. pungitius* orthologs (autosomes, N = 27,328 genes; PAR, N = 87 genes; stratum two, N = 471 genes; stratum two n.f., N = 91 genes; stratum one, N = 74 genes). Non-functional (n.f.) genes are those that include frameshifts or nonsense mutations on the Y chromosome. Significant differences among groups were determined using a Kruskal-Wallis test. Groups significantly different from the autosomes using a post-hoc Mann-Whitney U test (corrected for multiple comparisons) are indicated with asterisks (** $P < 0.05$). Whiskers are 1.5x the interquartile range. Sample sizes are the same as in Figure 2. Outliers are not shown.

Figure S1



PAR
Stratum 2
Stratum 1
d_N/d_S
0.0
0.5
1.0
1.5
2.0
**
**
**
**
X
Y
P
Auto.
X chr.
Y chr.
X chr.
X chr.
Y n.f.
Y chr.
Y chr.
Y n.f.
X chr.
Y chr.