



Figure 3: Network level estimates of (A) host breadth, (B) potential cross-species transmission connections, and (C) graph density all indicate that parasites in these communities vary in their ability to infect and transmit between different host species. Networks were created using the host species present in each site as nodes and epidemic overlap for connections between hosts. Connections were summed across years, so each point in the figure shows data for a single site/lake. There was a significant difference in host breadth (Kruskal–Wallis test, $\chi^2 = 35.2$, $p < 0.001$, $df = 6$), proportion of potential cross-species transmissions (Kruskal–Wallis test, $\chi^2 = 38.3$, $p < 0.001$, $df = 6$), and graph density across parasite species (Kruskal–Wallis test, $\chi^2 = 36.2$, $p < 0.001$, $df = 6$). Letters show pairwise comparisons that were significantly different based on the Conover–Iman test with Bonferroni corrections. Note that the y-axes differ slightly between the three panels, as they are ordered based on the ranking for each particular metric.