

**Figure S1. Principal coordinates analysis based on 14 microsatellite loci for *Nannoperca obscura* individuals from each genetic lineage.** A) pure Eastern.Eigen values for the first and second axes have been plotted, which explain 38% and 23% of the variance, respectively. E1, E2 and E3 refer to genetic clusters identified within this lineage; B) Merri/Curdies. Eigen values for the first and second axes explain 40% and 26% of the variance, respectively. M1, M2, and M3 refer to genetic clusters identified within this lineage; C) Central. Eigen values for the first and second axes explain 34% and 26% of the variance, respectively. C1, C2, C3, and C4 refer to genetic clusters identified within this lineage; D) Murray-Darling basin. Eigen values for the first and second axes explain 24% and 22% of the variance, respectively. No genetic structure was apparent within this ESU