

1 Appendix: Variation in the propensity to diversify in  
2 experimental populations of *Escherichia coli*:

3 Consequences for adaptive radiation

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9 Running title: Appendix: Asymmetric propensities to diversify

## 10 **A. Mean pairwise Euclidean distance**

11 We conducted an analyses directly on the (log transformed) data, in addition to the rank-  
12 data that we described in the main text.

13 Briefly, we calculated the mean pairwise (Euclidean) distance among clones isolated from  
14 each evolved population. Subsequently, we used mean pairwise distance as response variables  
15 in an ANOVA to determine whether variance in mean pairwise distance differed among source  
16 populations or source ecotypes.

17 We found variation in mean pairwise distance that was explained by source ecotype  
18 (Slow-switcher v. Fast-switcher,  $F(1,24)=69.29$ ,  $p<1.5\times 10^{-8}$ ) but not source population  
19 (strain dst1018 v. dst1019 v. dst1020,  $F(2,24)=0.11$ ,  $p<0.90$ ). These results are shown in  
20 Figure S1.

21 In the main text, we elected to cluster similar derived ecotypes. This allowed us to more  
22 easily compare between evolved populations (to determine whether clones were of the same  
23 ranked cluster). Finally, analyses on rank data typically have less power – and thus are  
24 conservative – relative to absolute data.

## 25 **Ecotypes in phenotype space**

26 We plotted the ecotypes identified by cluster analysis in phenotype space (Figure S2).

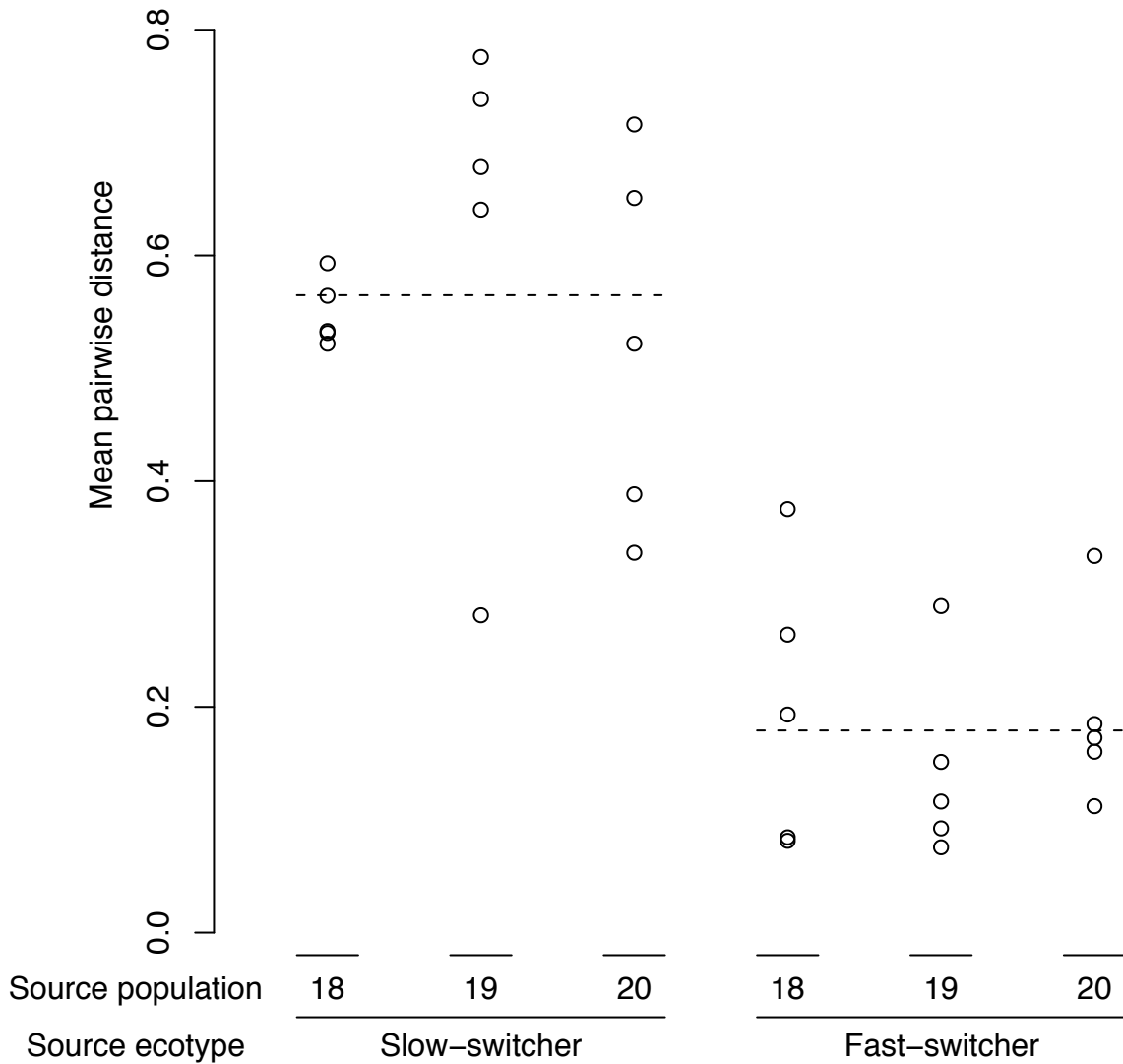


Figure S1. Mean pairwise distance was calculated on growth curve traits among clones isolated from each evolved population, identified by treatment: Source ecotype referred to either slow-switcher or fast-switcher and source population referred to one of three populations that had diversified at the 1,000 generation mark (18=dst1018, 19=dst1019, 20=dst1020). The dashed horizontal lines are the grand means of the mean pairwise distance for each source ecotype.

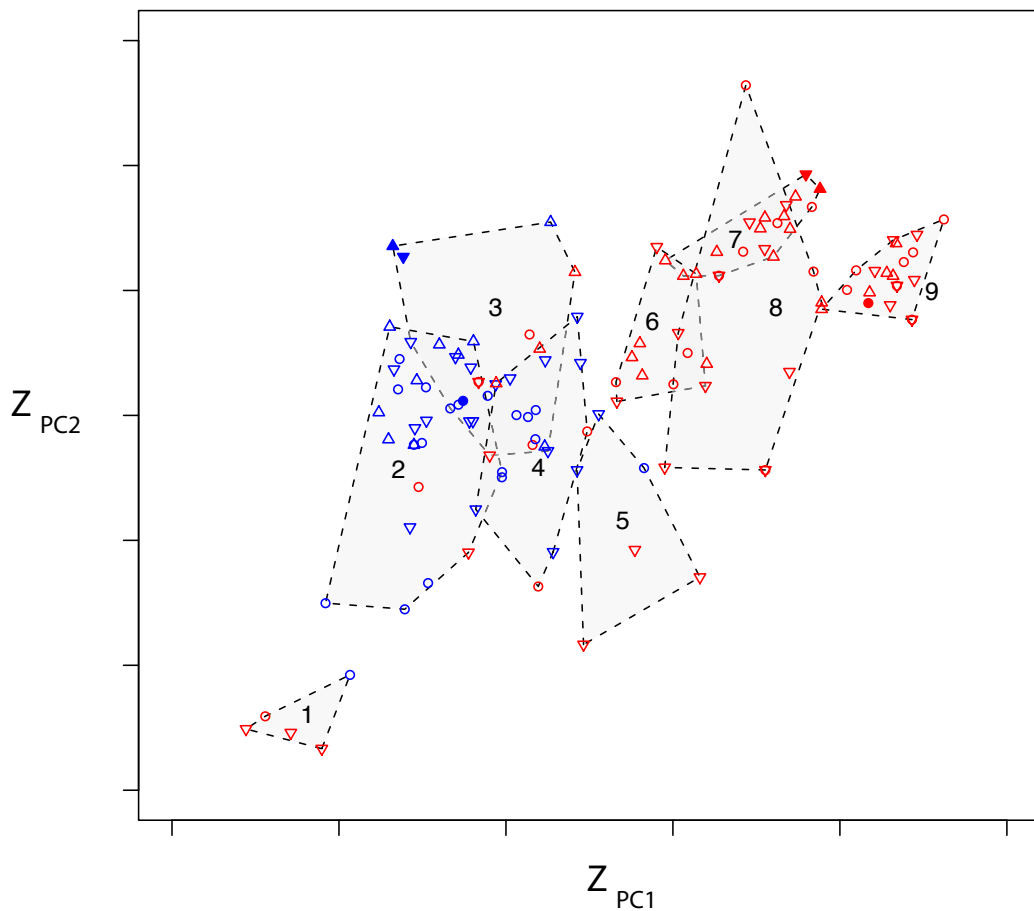


Figure S2. Cluster analysis identified nine clusters (shaded polygons), plotted in phenotype space ( $Z_{PC1}$  v.  $Z_{PC2}$ , see Figure 2 in main text). The numbers within or beside each polygon is the cluster identity (see main text for further description). Points indicate ecotypes isolated from derived populations (open symbols) or the ancestors (filled symbols). Red symbols indicate ecotypes isolated from populations derived from the slow-switcher ecotype, and blue symbols indicate ecotypes isolated from populations derived from the fast-switcher ecotype. Symbol shapes reflect the source population (circle=dst1018, up-triangle=dst1019, down-triangle=dst1020).