

Figure S18

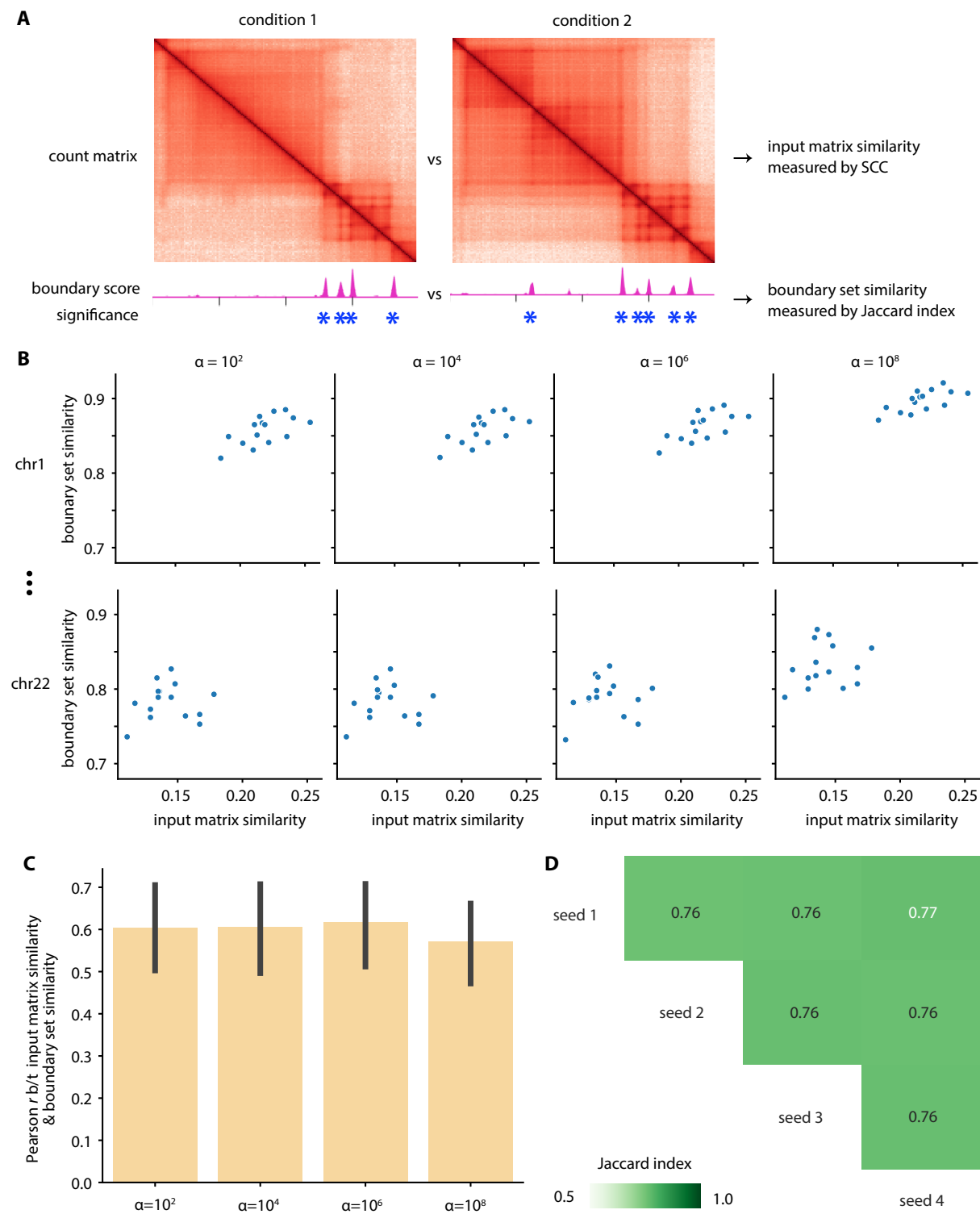


Figure S18. Hyperparameter α selection for TGIF-DB. **(A)** The similarity between the input matrices is measured by SCC and the output boundary set agreement measured by Jaccard index. **(B)** Plotting input matrix similarity vs output boundary set agreement for each α and each chromosome. Each dot represents one pairwise comparison. **(C)** Correlation between the input matrix similarity and the output boundary set agreement for different values of α . **(D)** Similarity of boundary sets from different random initialization seeds (with $\alpha = 10^6$), measured by Jaccard index.