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Supplementary Information Appendix for

Behavioral traits that define social dominance are the same that reduce social influence in a consensus task

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Author Contributions

AJ, JD, and HAH designed experiments; AJ and JD wrote code for automated data acquisition; AJ, MRS, LKG and SFG performed experiments; AJ and SFG performed image-based tracking; PN performed computer vision tracking; PN, AJ, LKG, FAF, and MRS performed statistical analysis; AJ, PN, and MRS wrote the manuscript; AJ, LKG, HAH, and OD revised manuscript.

This file includes:

Supplementary Video 1; Supplementary Figures 1 to 5

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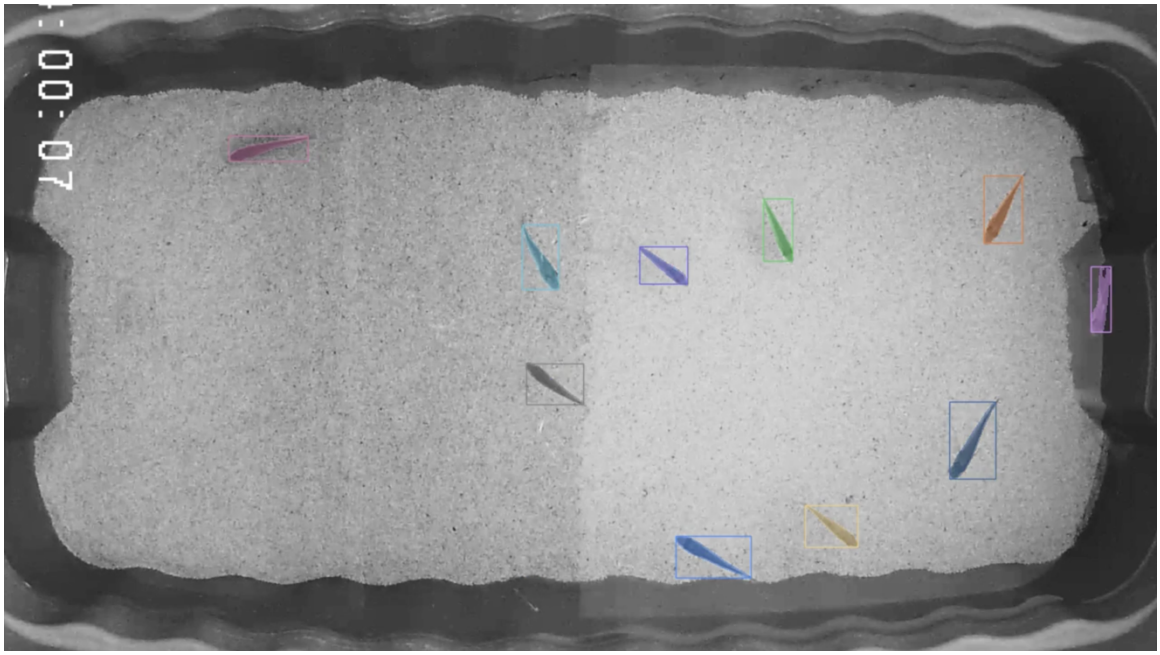
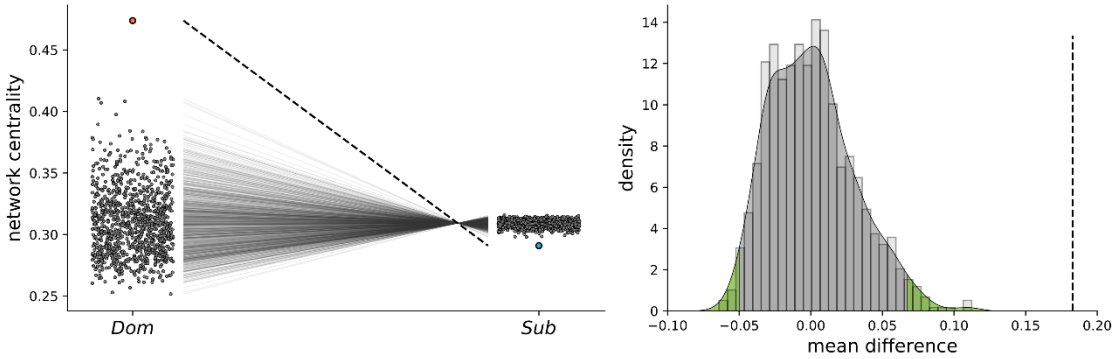
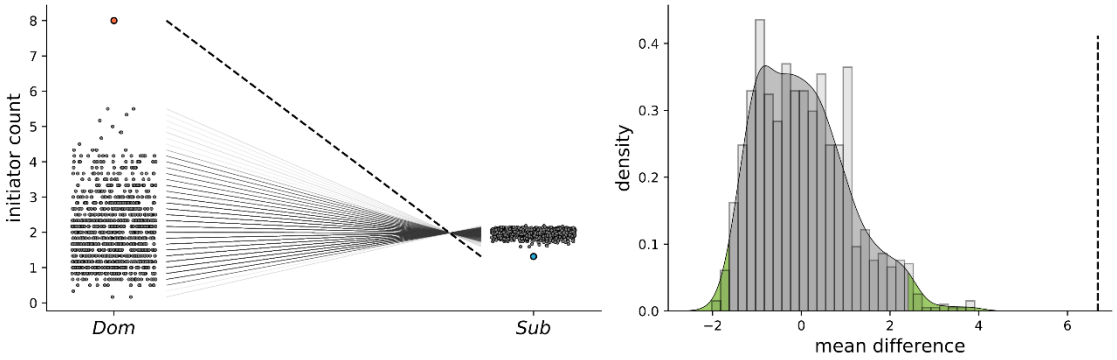


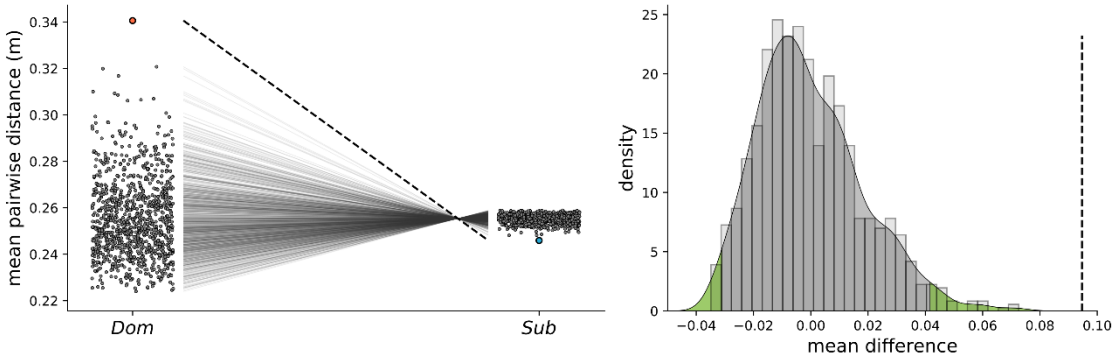
Supplementary Video 1. A still frame from supplementary video showing the sequence of our tracking and behavioral analyses. The first sequence shows raw video input, of which a subset of frames was annotated as the training set. After training the neural network with these annotations, fish in the video were then able to be automatically segmented with Mask R-CNN; this segmentation is here represented with a colored mask and corresponding bounding-box applied to each successfully detected fish in each frame of the video (second sequence). Identities of each fish were maintained in subsequent frames using a nearest neighbor linking approach. The third sequence displays the trajectories and estimated spine positions of each individual. A simplified model (colored 'fish') was then overlaid on actual positions of fish to compute visual field connectivity using a ray-casting approach, considering the visual fields of each eye of a focal individual (fourth sequence, gray-shaded areas) and occlusions (black-shaded areas).



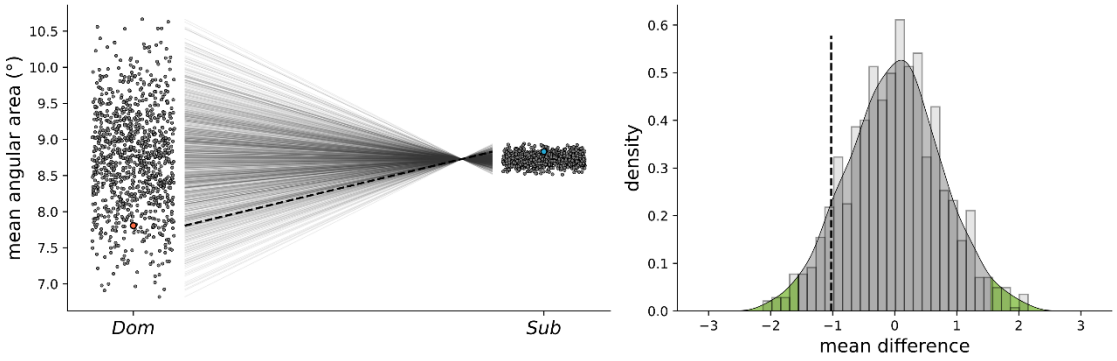
Supplementary Figure 1. Network randomization test for network centrality. left) Repeated node randomization (n = 1000) of the networks resulted in mean values (gray dots) for both dominant (*Dom*) and subordinate (*Sub*) network centrality (see Figure 1b for the observed distributions). For each randomization, a mean difference was calculated between *Dom* and *Sub* mean values, represented with the thin, gray lines. The observed difference is represented with the thick, dashed line. **right)** The distribution of mean differences (histogram and kernel density estimate) that resulted from node randomizations was used as the null distribution to calculate a two-tailed *p*-value for the observed difference (dashed line), yielding a value of $p < .001$ for the difference between *Dom* and *Sub* network centrality. The green areas represent mean differences that are as or more extreme than the .025 or .975 quantiles of the null distribution for a two-tailed test with a significance level of $\alpha = .05$. As the *p*-value for the observed difference is smaller than this significance level, the difference is evaluated to be statistically significant.



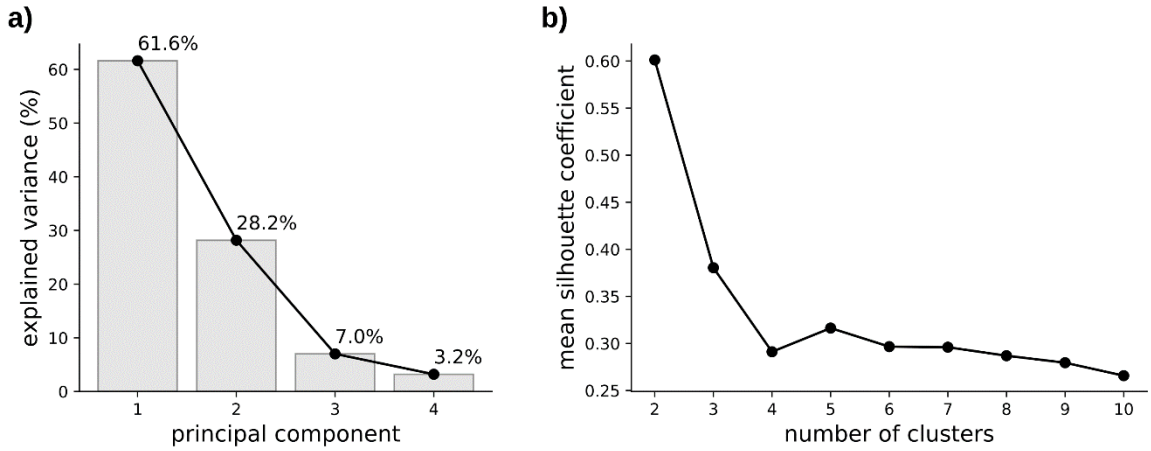
Supplementary Figure 2. Network randomization test for initiator count. A *p*-value (< .001) was obtained for the observed difference of dominant (*Dom*) and subordinate (*Sub*) event initiator counts using a network randomization test analogously to Supplementary Figure 1 (see also Figure 1c).



Supplementary Figure 3. Network randomization test for mean pairwise distance. A *p*-value (< .001) was obtained for the observed difference of dominant (*Dom*) and subordinate (*Sub*) mean pairwise distance using a network randomization test analogously to Supplementary Figure 1 (see also Figure 3b).



Supplementary Figure 4. Network randomization test for mean angular area. A *p*-value (= .196) was obtained for the observed difference of dominant (*Dom*) and subordinate (*Sub*) mean angular area using a network randomization test analogously to Supplementary Figure 1 (see also Figure 3c).



Supplementary Figure 5. PCA and clustering. a) Percentage of explained variance for each of the four principal components. **b)** A silhouette analysis was performed to determine the appropriate number of clusters (between 2 to 10) for *k*-means clustering. For each number of clusters (*k*), the mean silhouette coefficient was calculated. These values are ranged in the interval [-1, 1], a coefficient close to 1 indicates good cluster separation, 0 overlapping clusters and negative values wrong cluster assignments. Hence, $k = 2$ clearly results in the best separation of clusters. For visualization, see Figure 3e. The two clusters that were obtained through *k*-means clustering are identical to the categories of social status (dominant and subordinate) that we defined based on the phenotypic indicators of dominance (color of dominant male individuals).