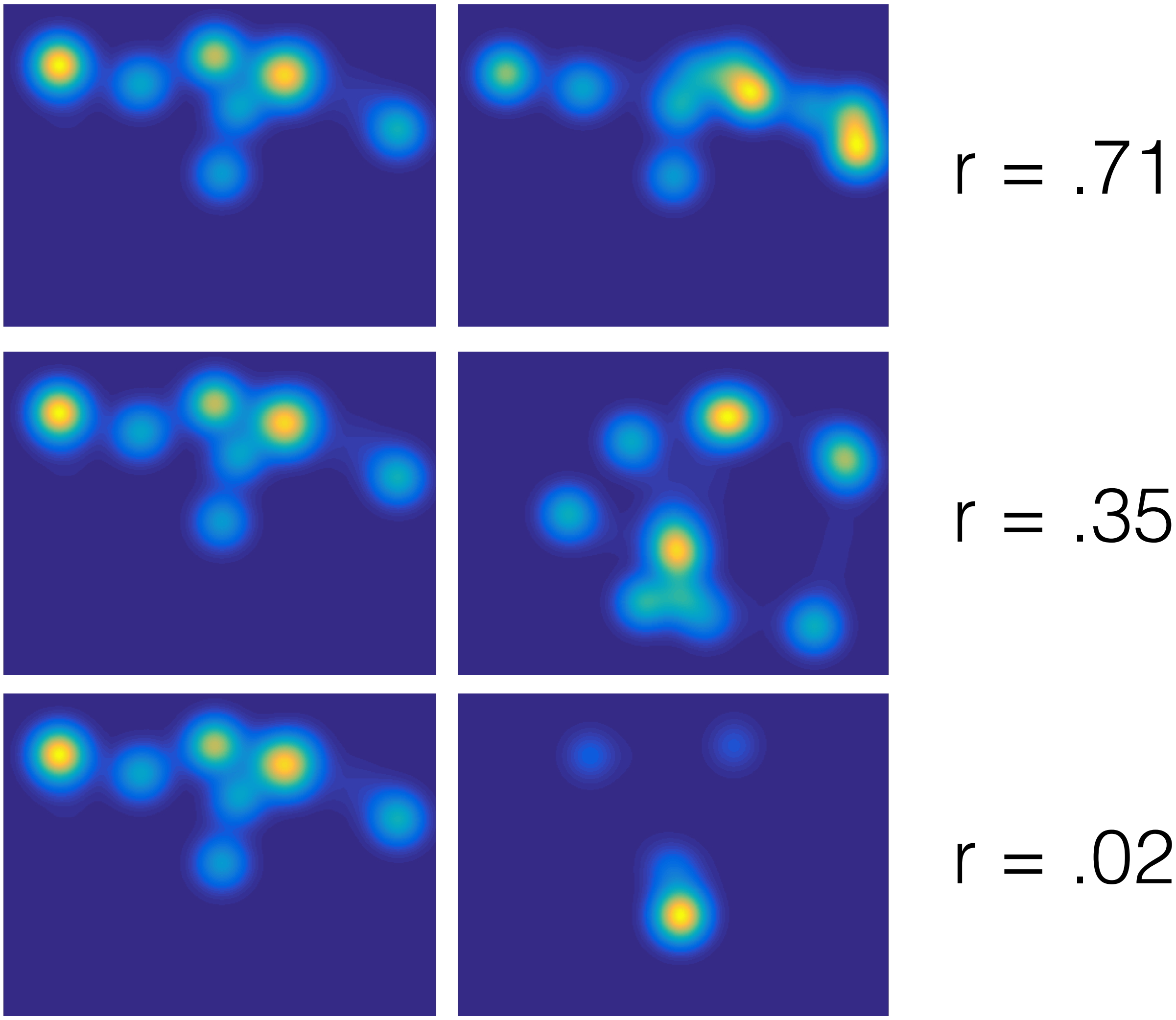

Figure S1. Illustrative examples of correlations between several of the heatmaps depicted in Figure 2a, ranging from highly similar to dissimilar gaze patterns. Related to **STAR Methods**, **Results**, and **Figure 2**.

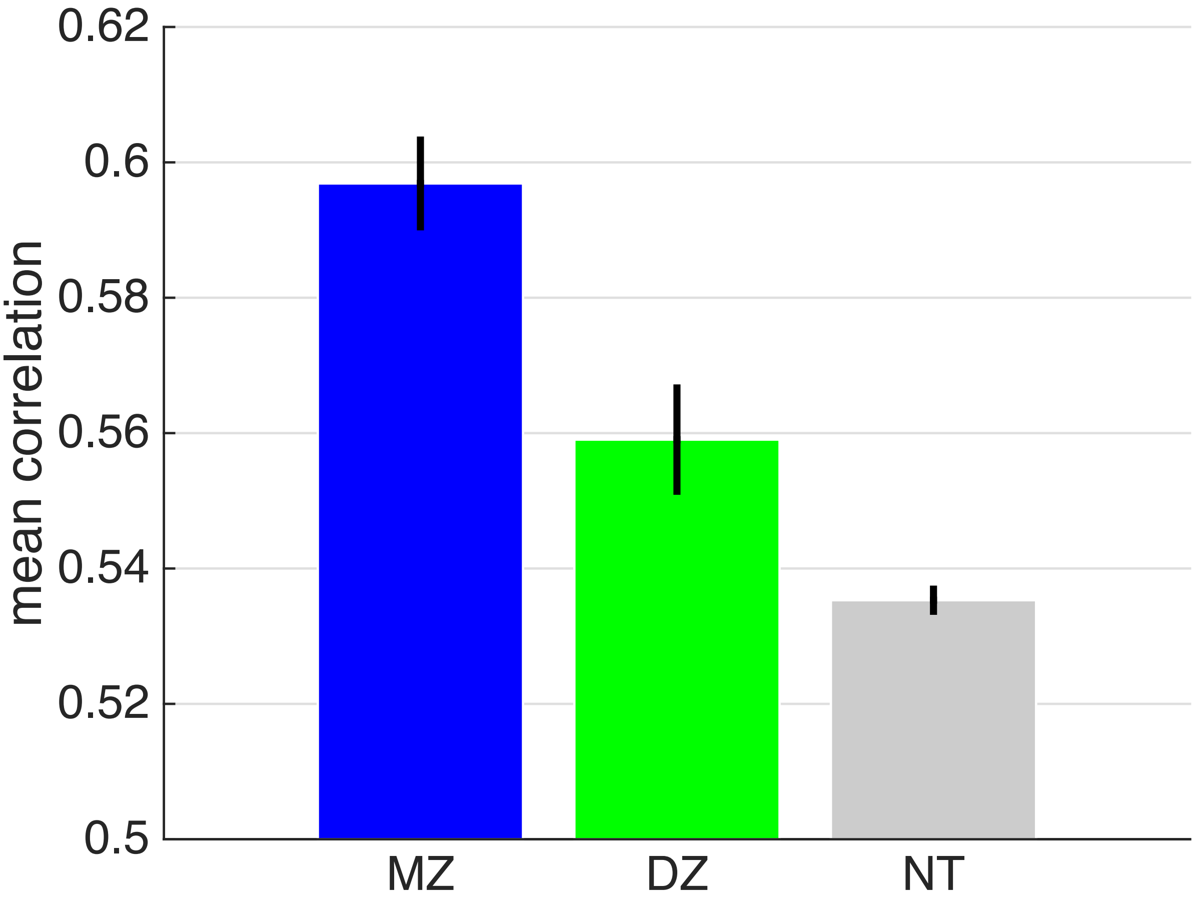

Figure S2. Bar graph depicting spatial similarity (mean heatmap correlation) in gaze in monozygotic twins (MZ), dizygotic twins (DZ), and non-twin (NT) pairs. Error bars = s.e.m. Related to **Results** and **Figure 3**.

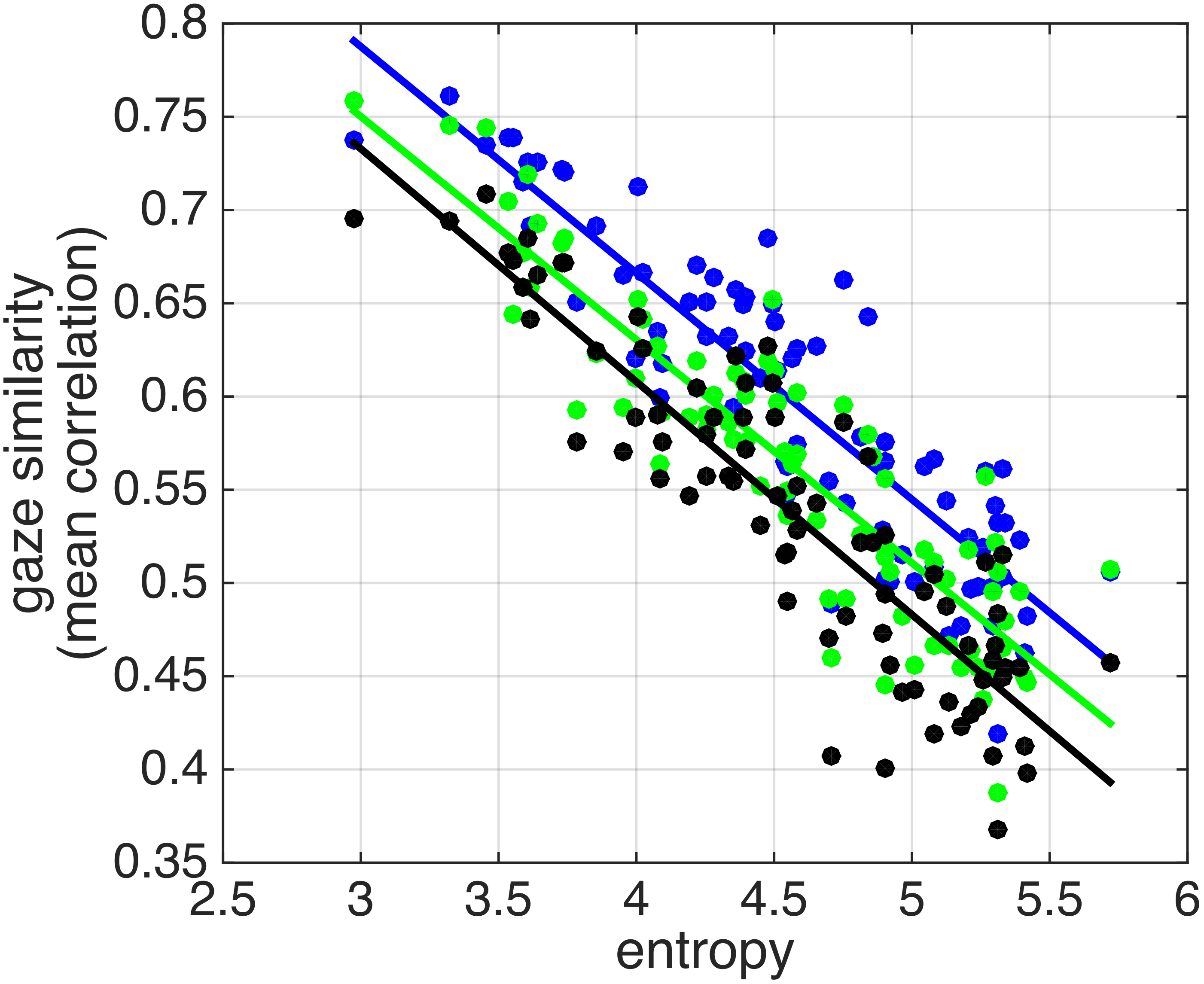

Figure S3. Gaze similarity as a function of heatmap complexity and group. Consistently across the different levels of heatmap complexity (quantified with Shannon entropy), the overall pattern of MZ>DZ>NT was preserved. For reference, the entropy of the heatmaps shown in **Figure 1** are as follows: social = [5.33, 4.28, 4.48, 3.59, 4.08, 5.33, 4.22, 5.04], non-social = [4.70, 4.97, 3.60, 4.35, 3.45, 4.86, 4.10, 4.90]. Related to **Figure 1**.

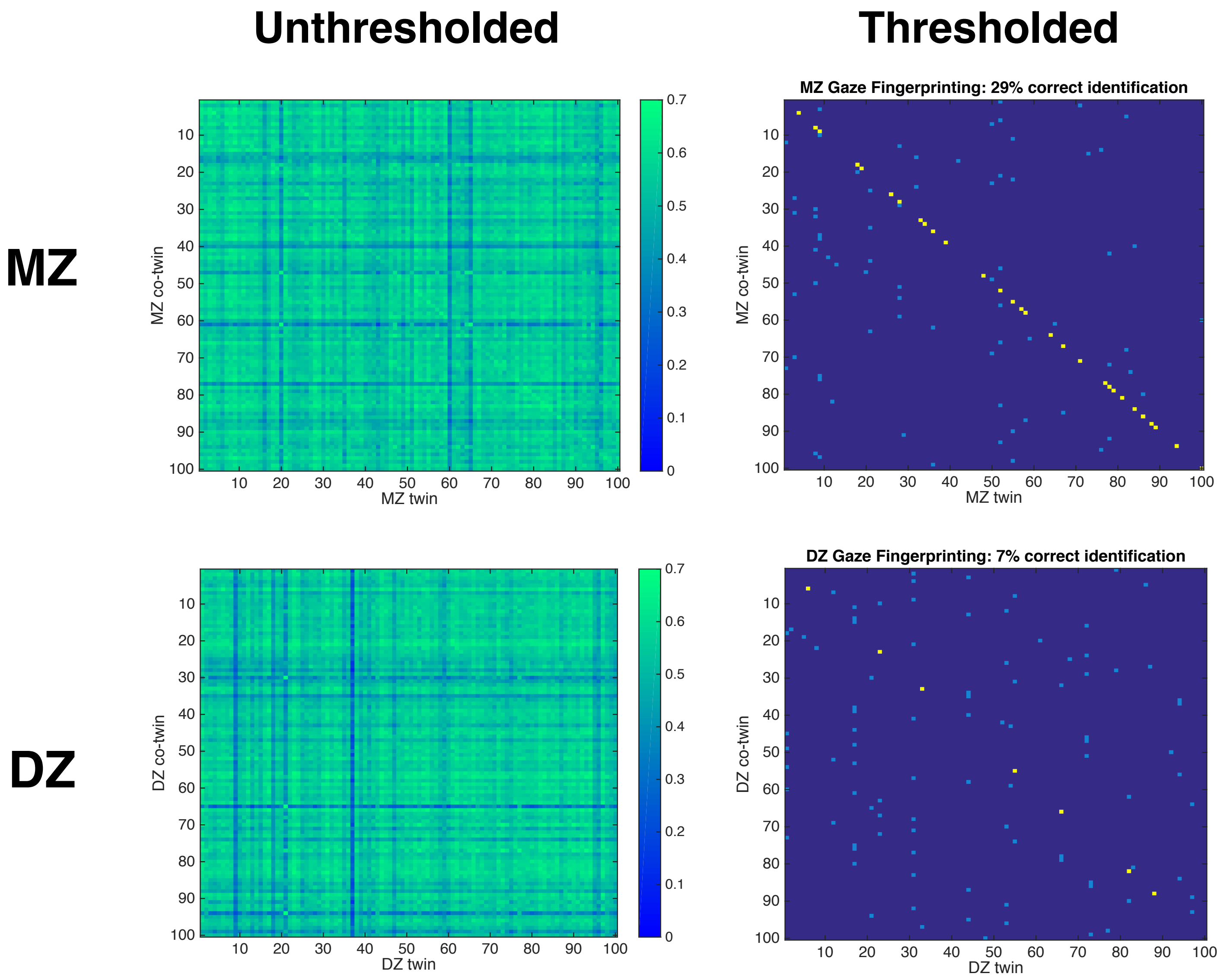

Figure S4. Unthresholded and thresholded examples of the cross-subject gaze fingerprinting procedure. As in Figure 4 from the main text, correlation matrices are calculated for 100 MZ or DZ individuals and their MZ or DZ co-twins (left). Then, the thresholding procedure (right) identifies the single individual with the most similar gaze within that row (i.e., the highest correlation for each row). The cells that fall on the diagonal indicate twin-co-twin matches and are highlighted in yellow, while the off-diagonal cells indicate non-matches. Note the generally higher similarities between MZ twin-co-twins (i.e., along the diagonal) even in the unthresholded correlation matrix (top left), and that this pronounced diagonal is largely absent in the DZ correlation matrix (bottom left). Related to **Figure 4**.

Analysis	Sample Size (pairs)		Twin Correlations		Model	Variance Components (95% Confidence Intervals)				Model Fit		
	MZ	DZ	MZ	DZ		Additive Genetic	Dominant Genetic	Shared Environment	Non-Shared Environment	RMSEA	AIC	BIC
Entropy	114	109	0.42	0.19	AE	**0.38 (0.25-0.51)**	**-**	**-**	**0.62 (0.49-0.75)**	0.099	508.653	518.874
					ACE	0.30 (-0.18-0.78)	-	0.08 (-0.34-0.49)	0.63 (0.49-0.77)	0.113	510.530	524.159
					ADE	0.38 (0.25-0.51)	0.00 (0.00-0.00)	-	0.62 (0.49-0.75)	0.114	510.653	524.282
					CE	-	-	0.32 (0.20-0.43)	0.69 (0.57-0.80)	0.108	510.071	520.292
Gaze Similarity	118	109	0.30	0.10	AE	**0.28 (0.12-0.43)**	**-**	**-**	**0.72 (0.57-0.88)**	0	-728.539	-718.264
					ACE	0.28 (0.12-0.43)	-	0.00 (0.00-0.00)	0.72 (0.57-0.88)	0	-726.539	-712.839
					ADE	0.05 (-0.70-0.80)	0.25 (-0.55-1.05)	-	0.70 (0.54-0.87)	0	-726.906	-713.206
					CE	-	-	0.19 (0.07-0.32)	0.81 (0.68-0.93)	0.021	-726.099	-715.824

Table S1. Results from behavior genetic analyses of the Entropy and Gaze Similarity Traits. The models were fit to the raw data using a maximum likelihood approach. AE, ACE, ADE, and CE models are shown for completeness, but the AE model (highlighted in gray) that includes only additive genetic and non-shared environmental factors is the best model for both Entropy and Gaze Similarity traits. This was as expected – because DZ twin correlations are less than half the MZ correlations, shared environmental factors do not influence these measures. RMSEA = root mean squared error of approximation. Related to **STAR Methods: Behavioral Genetic Analyses** and **Results**.