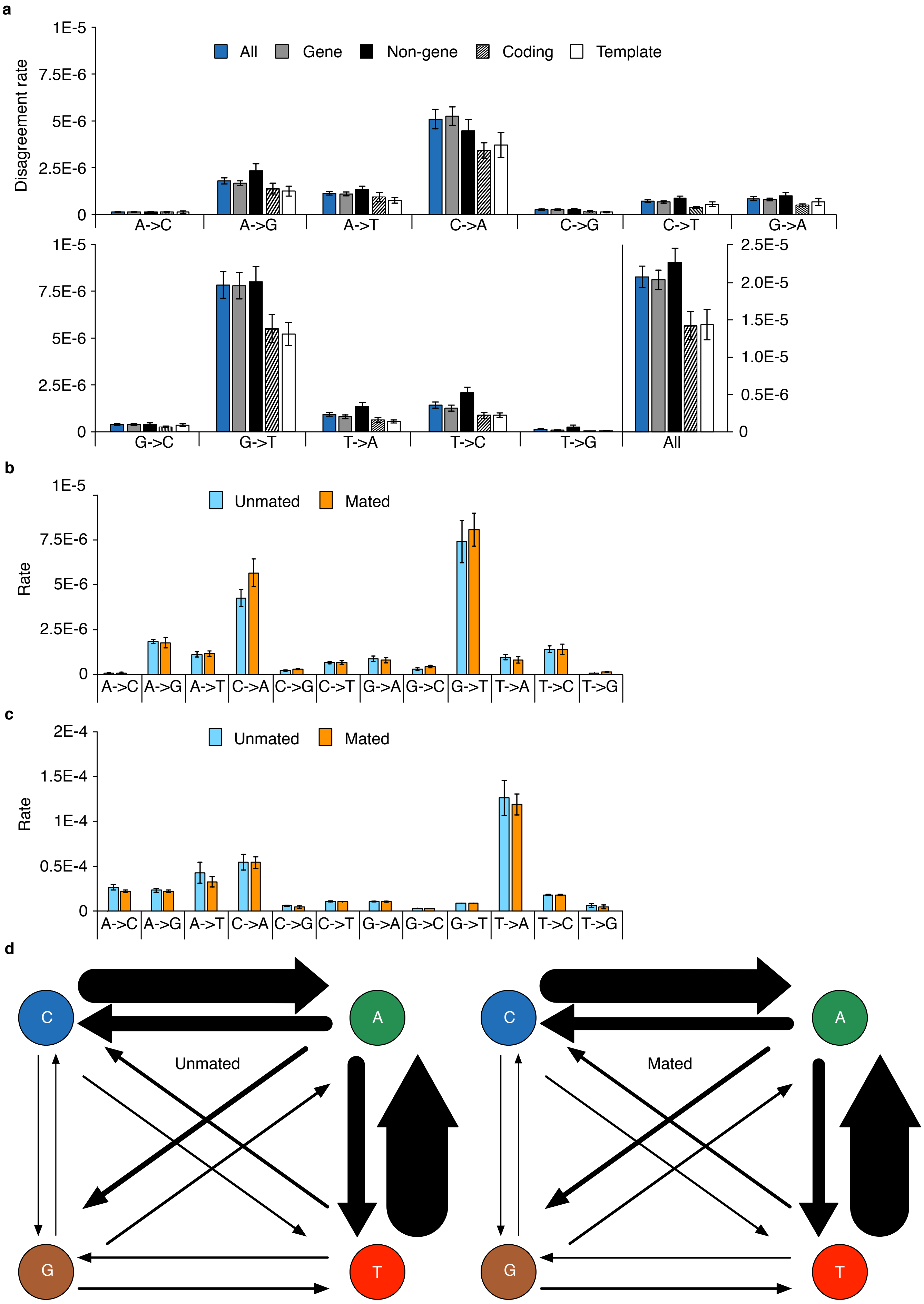

Supplemental Fig S6. Analysis of duplex substitution disagreements, and raw Q1 or Q2 mismatches.
(**a**) Duplex substitution disagreements pooled between mated and unmated samples, and broken down by genome location and coding or template strand type. (**b**) Distribution of duplex substitution disagreement rates as a function of mating status (see Fig 3 for ratios). (**c**) Distribution of raw Q2 substitution mismatch rates as a function of mating status. (**d**) Raw Q1 substitution mismatch spectra (compare to Supplemental Fig S7a-b).