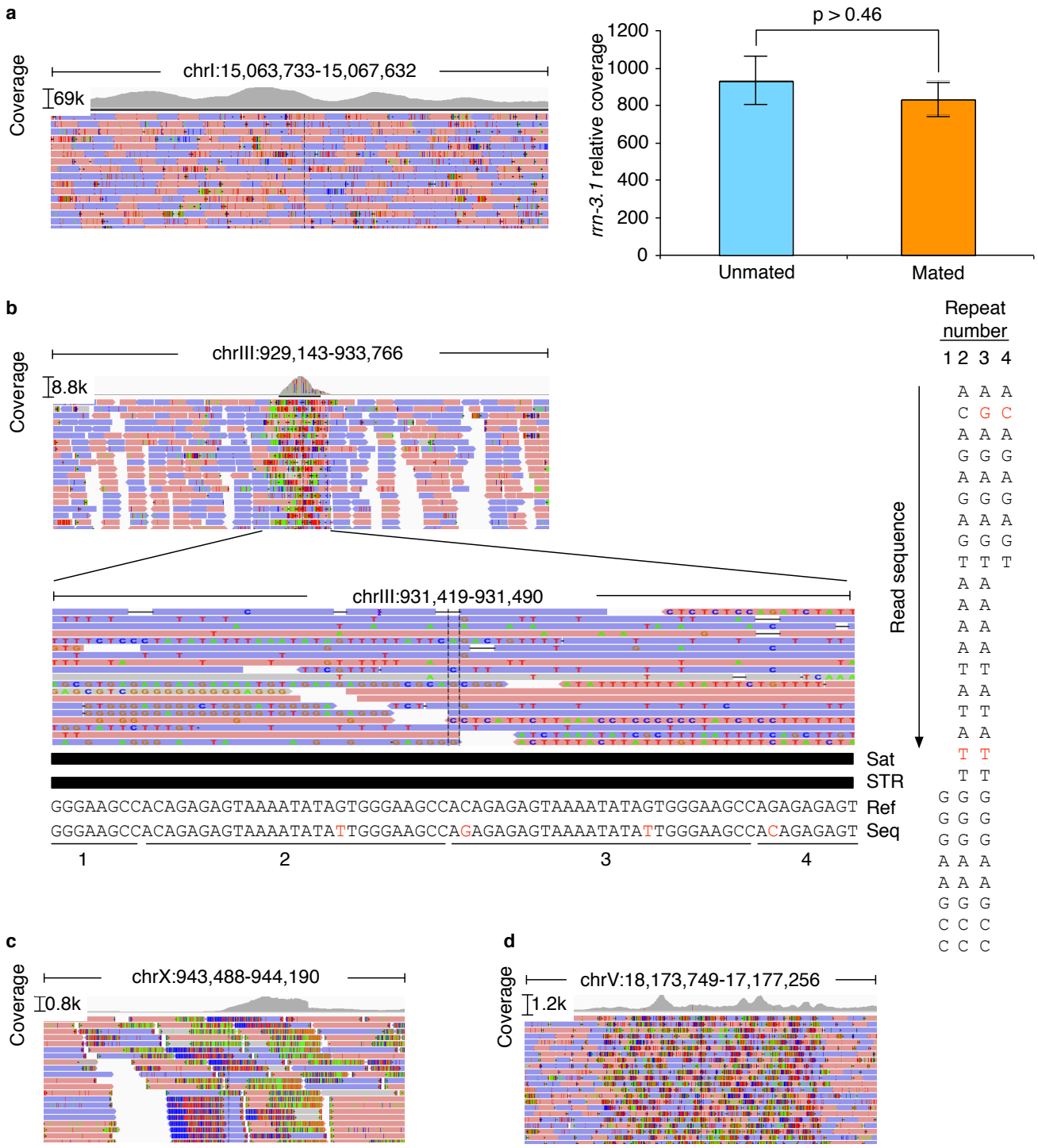

Supplemental Fig S3. Identification of problematic genome regions.
(**a**) Left: Display by the Integrative Genomics Viewer (Thorvaldsdóttir et al. 2013) of sequencing reads from a single MZ mapping to the *rrn-3.1* rDNA region; coverage (~69,000) is ~800-fold higher than average coverage over the whole genome. Right: average relative *rrn-3.1* coverage across samples, computed by dividing coverage over a ~50 bp portion of the region by average coverage. (**b**) Representative satellite DNA region showing a peak of abnormally high coverage and mismatches between genome and aligned reads. Mismatches are highlighted in red, and RepeatMasker tracks as black stripes (Sat: satellite DNA; STR: simple tandem repeat). Ref: reference sequence; Seq: our sequence data. Repeats aligned against each other are shown on the right. (**c**) Representative simple tandem repeat and satellite DNA region showing high clipping rate. (**d**) Representative simple tandem repeat region showing frequent mismatches.