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polymorphic regions were associated with village-level prevalence of infection (Supplementary Figure 4).

No SNPs were associated with village-level prevalence of TF (Figure 3A). However, 8 polymorphic regions from positions 774 000–791 000 were associated with TF prevalence (Figure 3B). SNPs in these regions were focused in CTA0743/*pbpB* (harboring 29 SNPs), CTA0747/*sufD* (10 SNPs), and CTA0742/*ompA* (7 SNPs). All SNP

Simpson D and adjusting for number of genomes sampled per district. We used published *Ct* infection, TF, and TI prevalence estimates [6, 28] (Table 3). *Ct* infection and TI prevalence were signi cantly higher with increasing *ompA* diversity; a similar trend was found for TF prevalence. In a multivariate model, only *Ct* infection prevalence was associated with increasing *ompA* diversity.

DISCUSSION

This study sequenced *Ct* from ocular samples collected from districts in Amhara, Ethiopia, which had received approximately 5 years of the SAFE strategy, as part of trachoma control efforts. We found that sequences were typical of ocular *Ct*, at both the whole-genome level and in tropism-associated genes, yet phylogenetically distinct from most previously sequenced *Ct* genomes. There was no evidence of macrolide-resistance alleles in this ocular *Ct* population. Greater *ompA* diversity at the district level was associated with increased *Ct* infection prevalence. A continued commitment to the implementation of the SAFE strategy with consideration of enhanced MDA accompanied by further longitudinal investigation is warranted in Amhara.

Almost 900 million doses of azithromycin have been distributed by trachoma control programs since 1999, and in Amhara 15 million doses are administered annually [3]. Mass distri-
m711 (u)-5 (t)-5 (m).9 (f)0.5 (en)-5 9-4.9 ((d a)9 (nn)19 (u)-3 ()13 40

have been associated with trachoma; therefore, resistance in other bacteria may be important.

No *Ct* genomes in this study had acquired azithromycin-resistance alleles, but there may be other genomic factors that support *Ct* transmission a er treatment. To explore this, we compared Amharan *Ct* genomes with previously sequenced *Ct* to nd polymorphism(s) speci c to this population that could explain continued transmission. e few SNPs identified as speci c to Amhara were dispersed across the genome in known polymorphic genes, rather than being overrepresented in genes related to *Ct* survival. e typical nature of this *Ct* population was supported by phylogenetic clustering with other ocular 10 ( )]TJ0.109 Tw 0 -1.368 Td[(in g)8 (en)46id5(si1 (or)2 (p

can increase nasopharyngeal carriage of macrolide-resistant *Staphylococcus* [35] and *Streptococcus* [36] and alters the fecal microbiome [37, 38], with reports of increased macrolide-resistant *Escherichia coli* [39]. is study, in agreement with previous work [16–18], found no evidence of macrolide resistance in this *Ct* population. While encouraging, it does not rule out macrolide resistance as a potential problem in these communities. Carriage of macrolide-resistant pathogens in the gut and nasopharynx may be impacted by antibiotic treatment. Additionally, presence of additional species of *Chlamydia* [40, 41] and nonchlamydial bacteria [42–45] in the ocular niche

We identi ed several polymorphic regions associated with village-level TF prevalence. e polymorphisms were .9 (p)X)

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