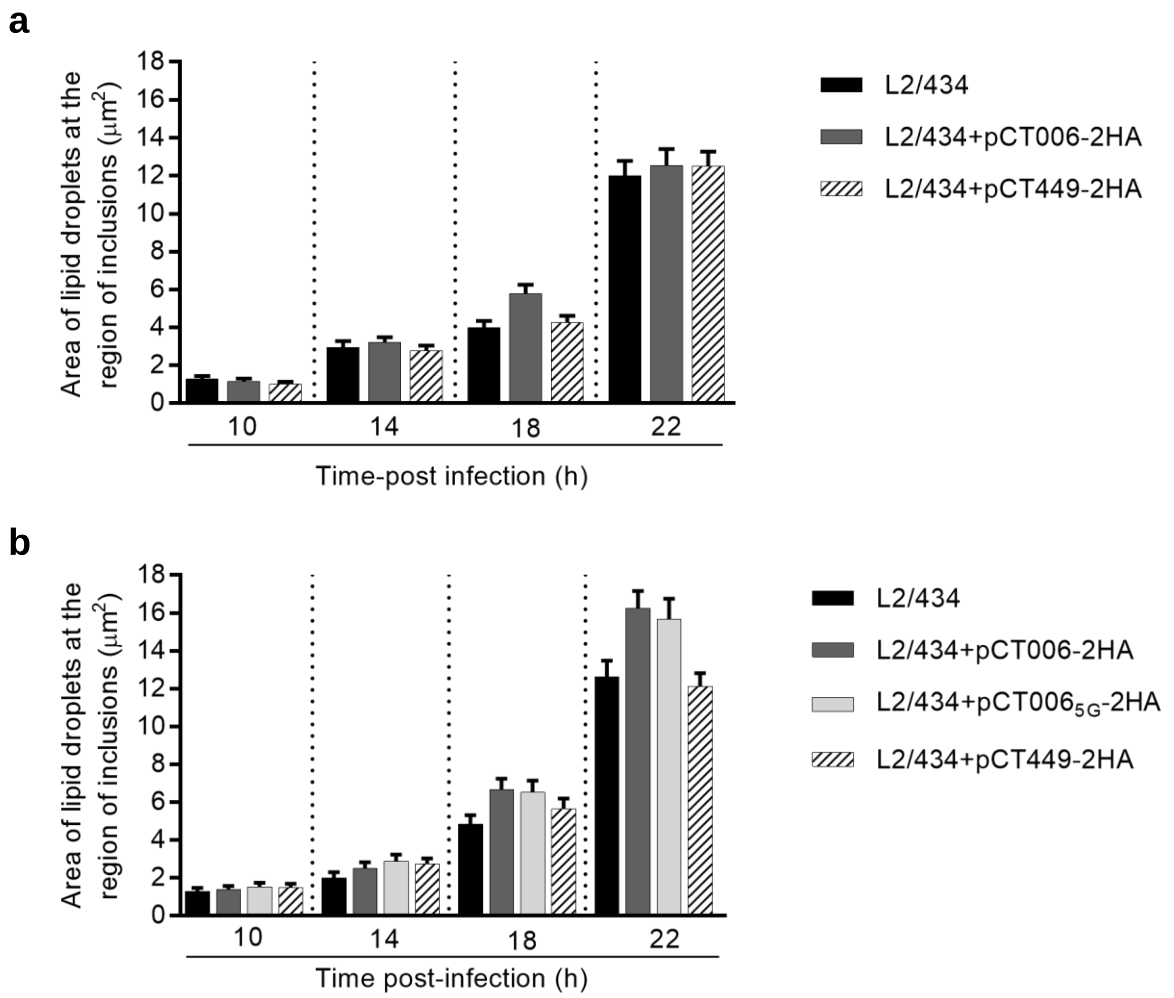

S15 Fig. Analysis of the area of LDs at the region of inclusions. (a) HeLa 229 cells were infected by the *C. trachomatis* L2/434 parental strain or by *C. trachomatis* L2/434 strains harboring pCT006-2HA (L2/434+pCT006-2HA) or pCT449-2HA (L2/434+pCT449-2HA). (b) HeLa 229 cells were infected by the *C. trachomatis* L2/434 parental strain or by *C. trachomatis* L2/434 strains harboring pCT006-2HA (L2/434+pCT006-2HA), pCT006$_{5G}$-2HA (L2/434+pCT006$_{5G}$-2HA) or pCT449-2HA (L2/434+pCT449-2HA). The area of BODIPY-positive LDs at the region of chlamydial inclusions was measured from randomly selected images, as those depicted in Figs 7a and S14, using Fiji software (Schindelin J, Arganda-Carreras I, Frise E, Kaynig V, Longair M, Pietzsch T, *et al.* Fiji: An open-source platform for biological-image analysis. Nat Methods. 2012;9(7):676–682). Data are represented as the mean and standard error of the mean from three independent experiments (n=60). Statistical analysis was performed using Kruskal-Wallis test with Dunn's multiple comparison test. * Represents $P<0.05$ by comparison to the L2/434 strain; ϕ represents $P<0.05$ by comparison to the L2/434+pCT006-2HA.