Supplemental Information

An ancient influenza genome from Switzerland allows deeper insights into host adaptation during the 1918 flu pandemic in Europe

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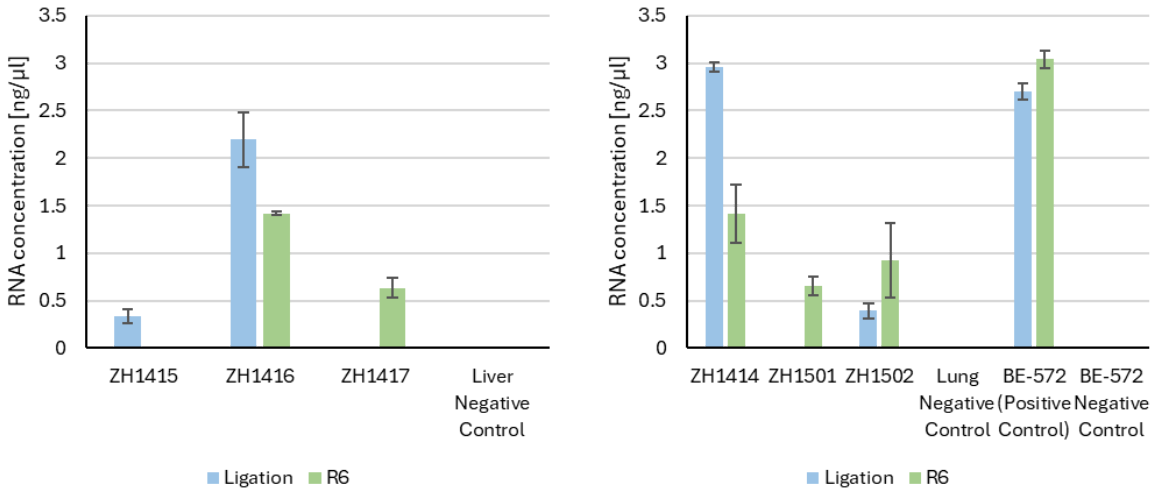

Figure S1: RNA quantification after extraction. Results for Liver samples are displayed on the left and lung samples on the right.

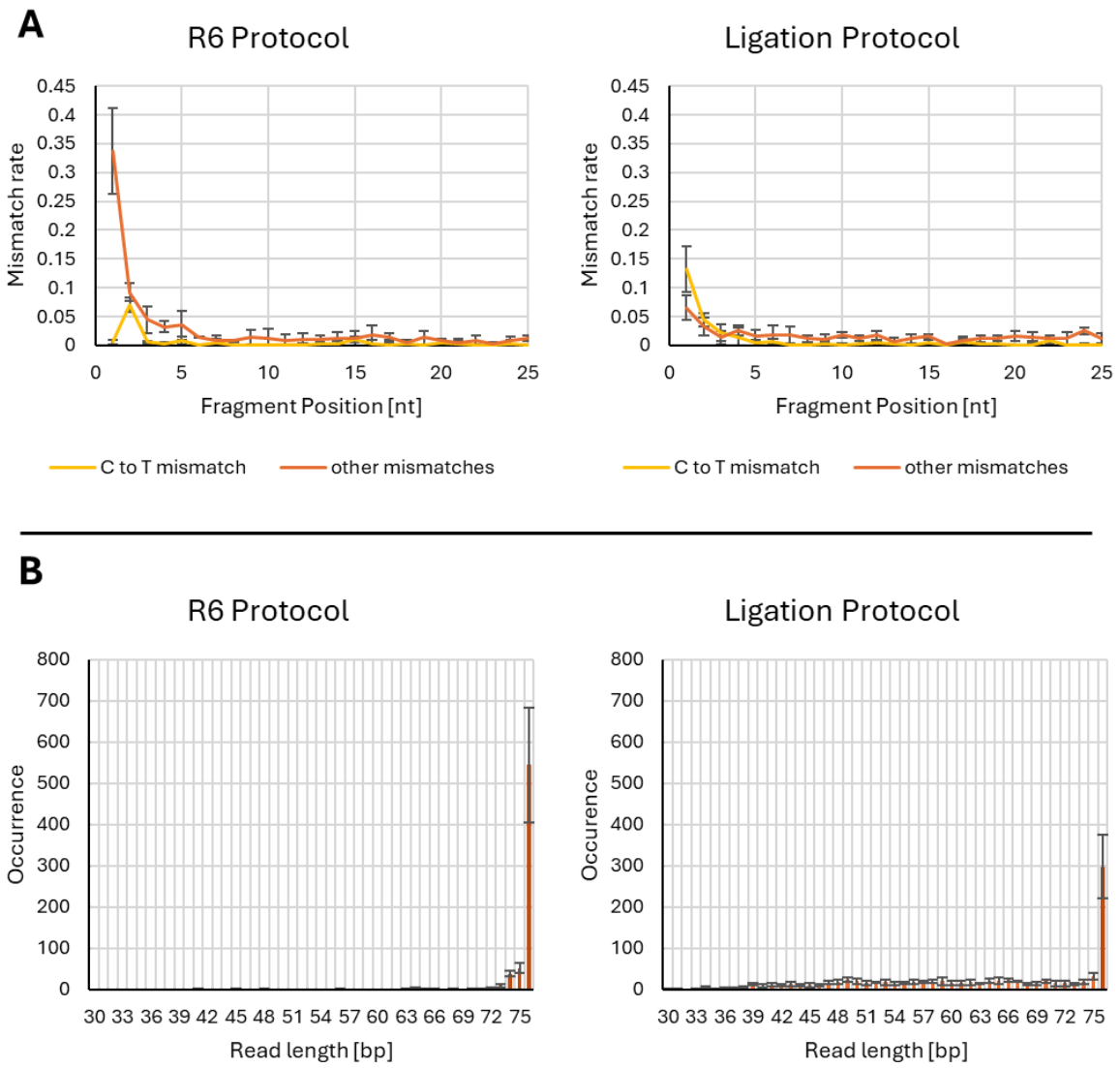

Figure S2: Mismatches A) and read-length B) distribution for mapping of the positive control BE-572 against the influenza A reference MU-162 [12].

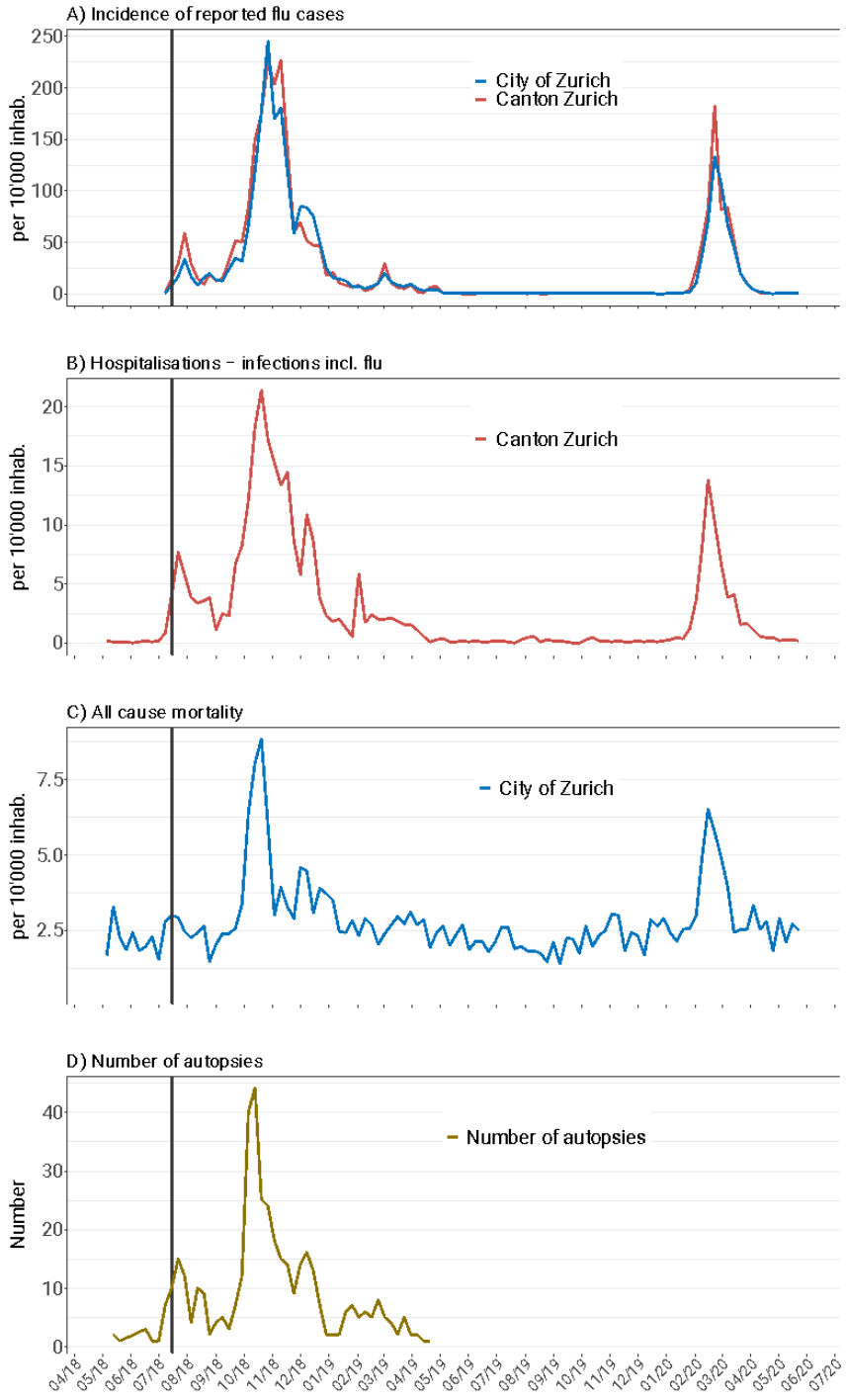

Figure S3: The weekly course of the 1918-1920 pandemic in Zurich. A) Incidence of new cases of influenza reported by physicians (excluding mild cases that did not go to the physician); B) Hospitalisations due to the category "Infections incl. influenza"; C) Deaths (all causes); D) Number of autopsies at Zurich University Hospital in which influenza pneumonia was the main cause of death (data sources: A-C [81], D [36]). The black vertical line represents the week of autopsy of the presented death of the 18-year-old male (sample ZH1502).

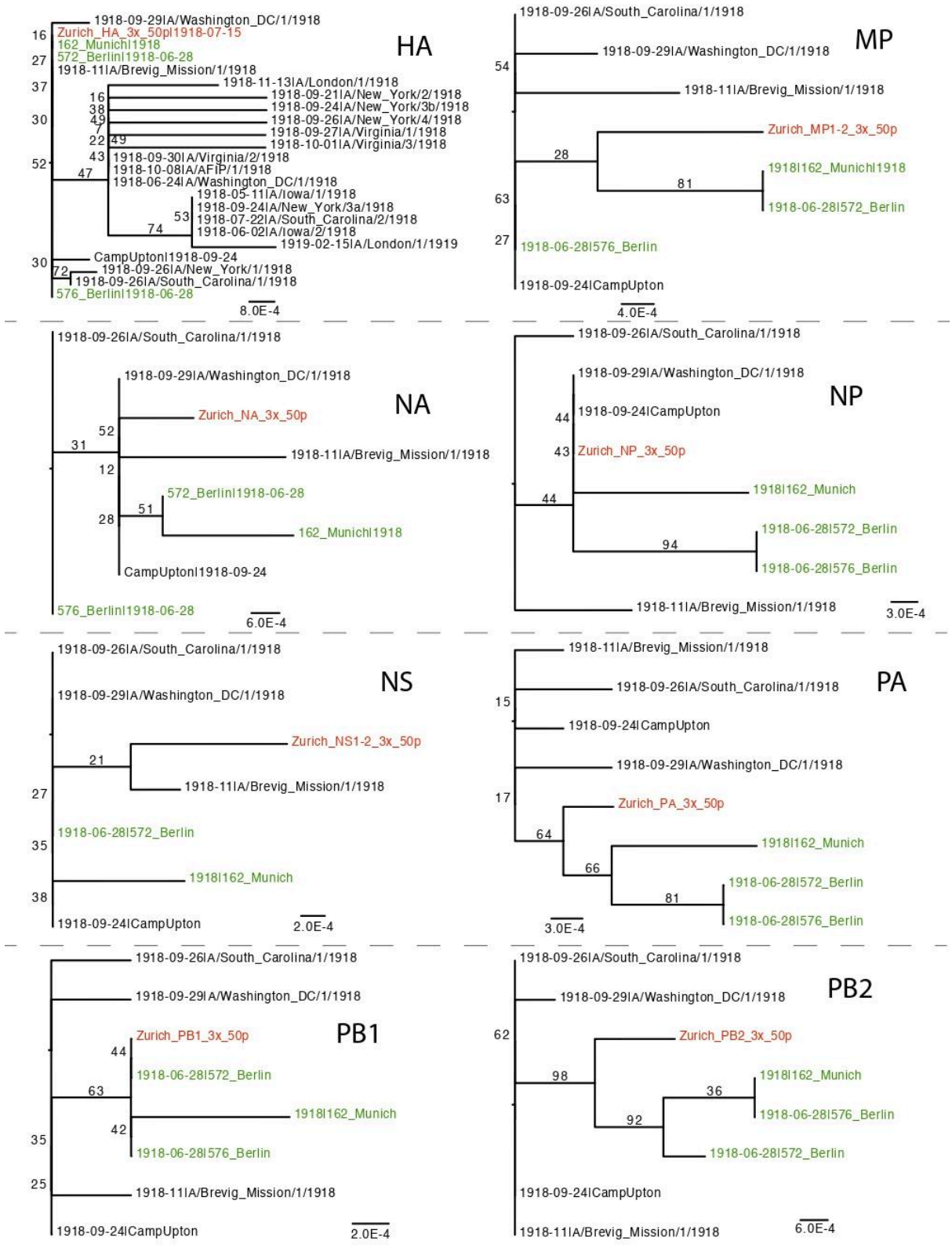

Figure S4: Maximum Likelihood trees for all individual IAV segments.

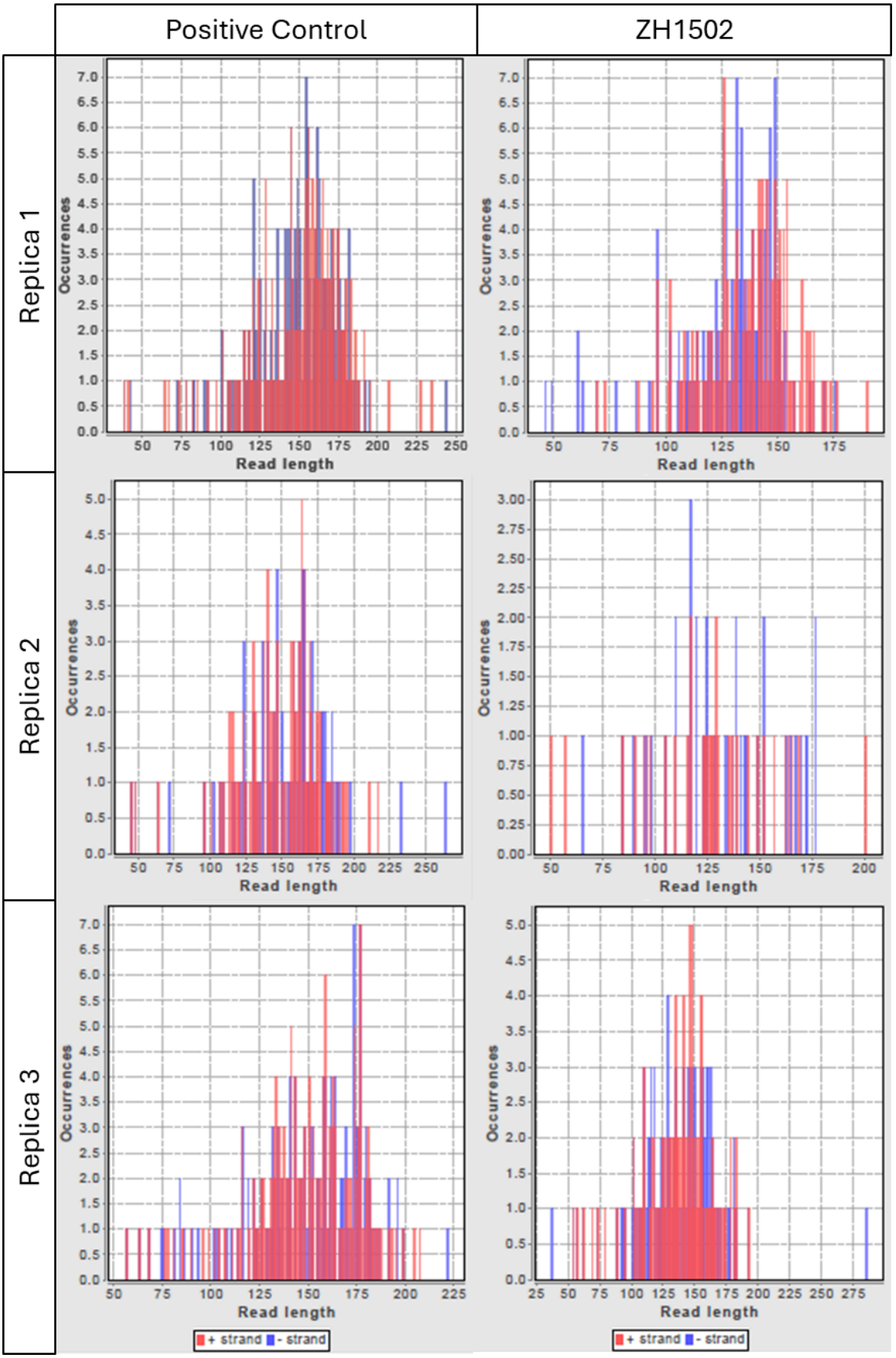

Figure S5: R6 Protocol fragment length distribution from 300 PE sequencing.

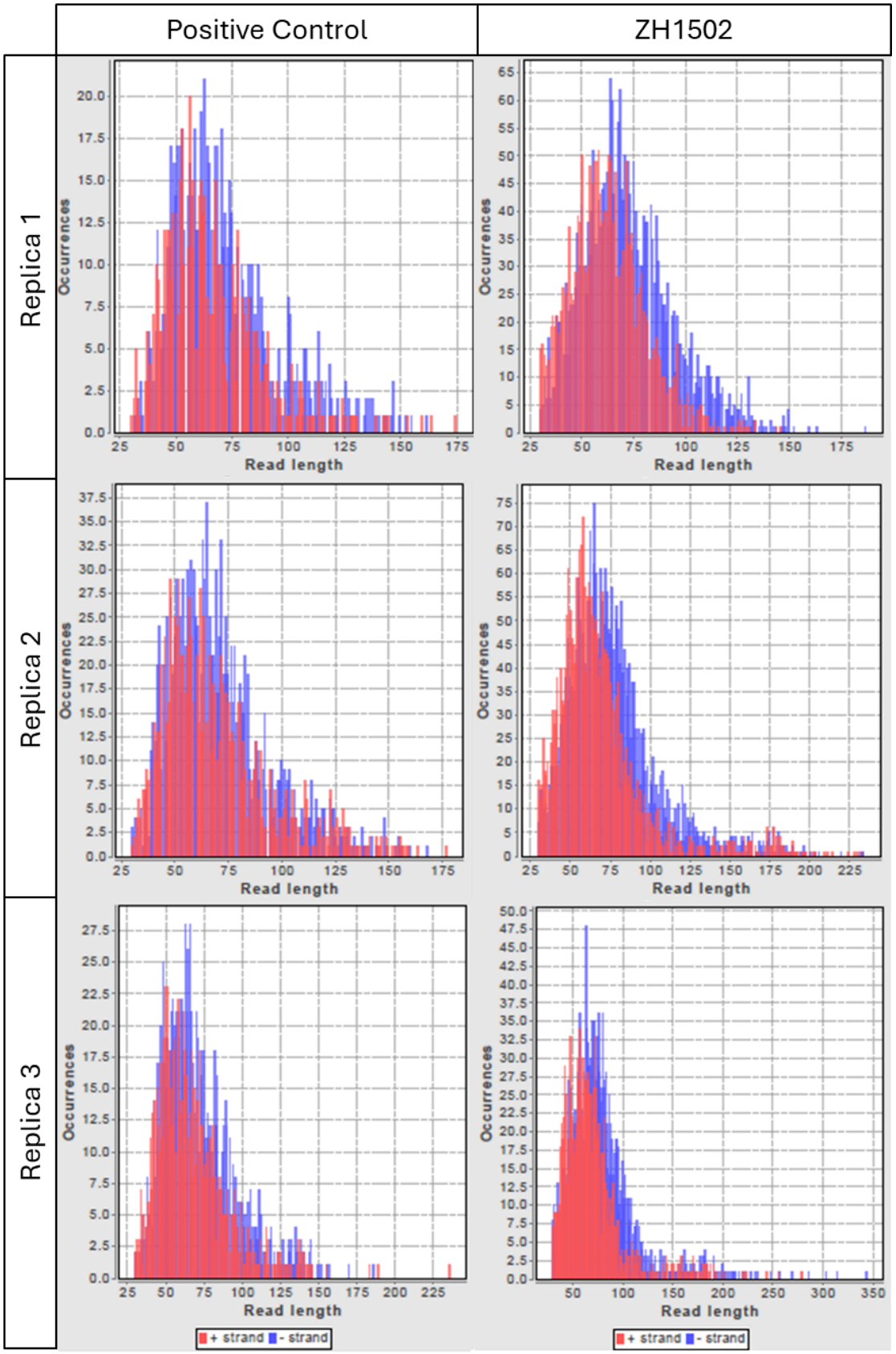

Figure S6: Ligation Protocol fragment length distribution from 300 PE sequencing.

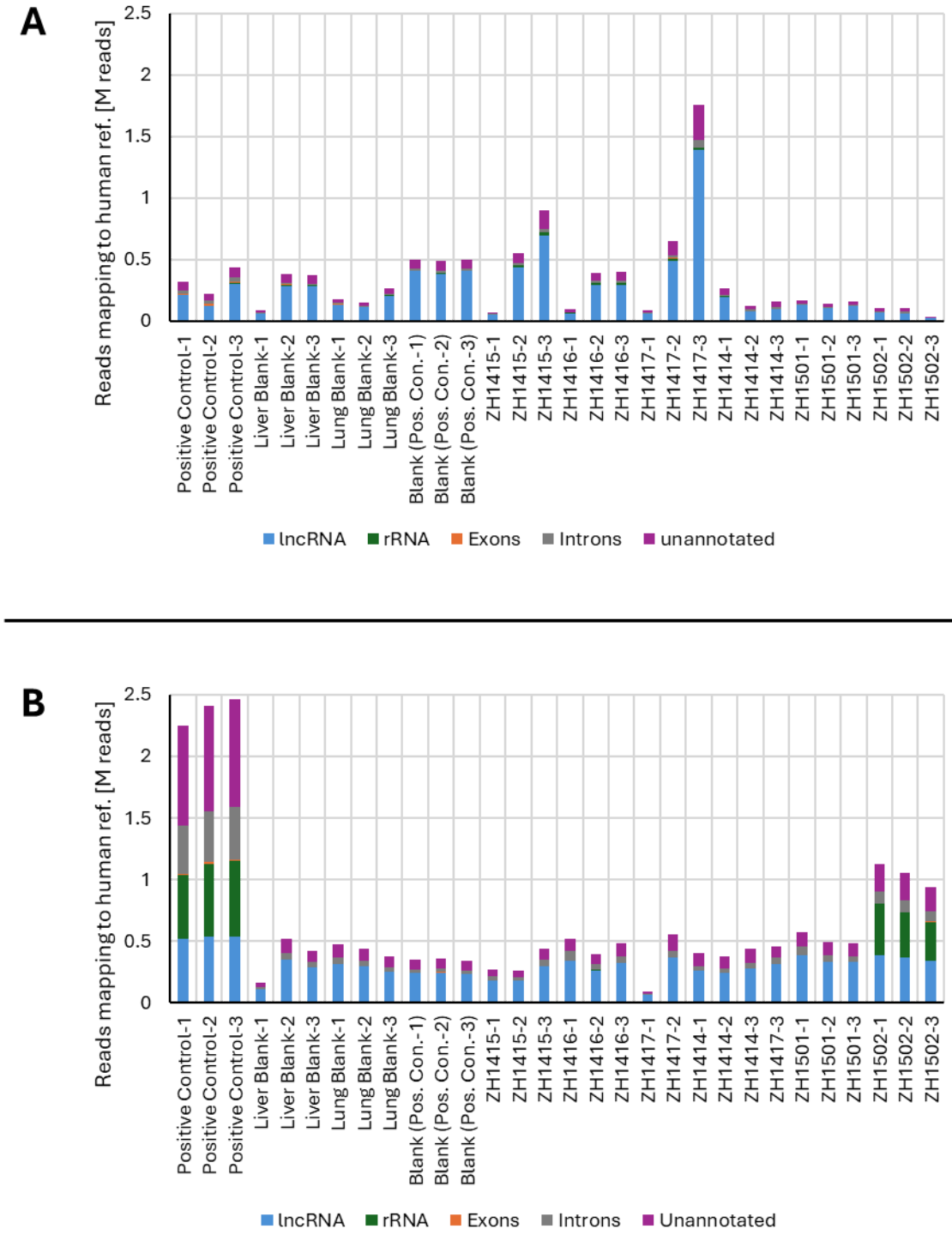

Figure S7: Mapping results against human reference. A) Results for the R6 workflow. B) Results for the Ligation workflow.