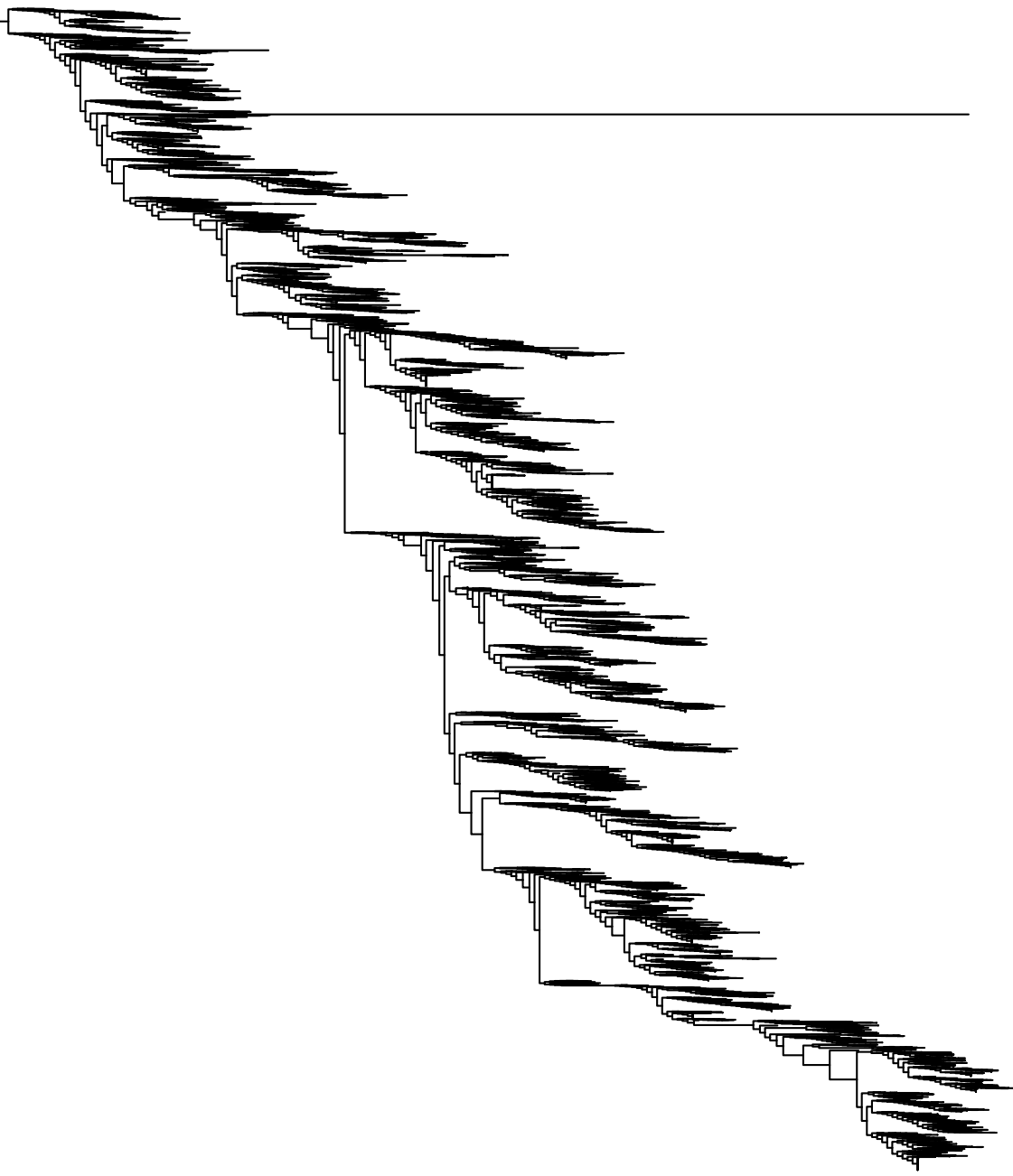


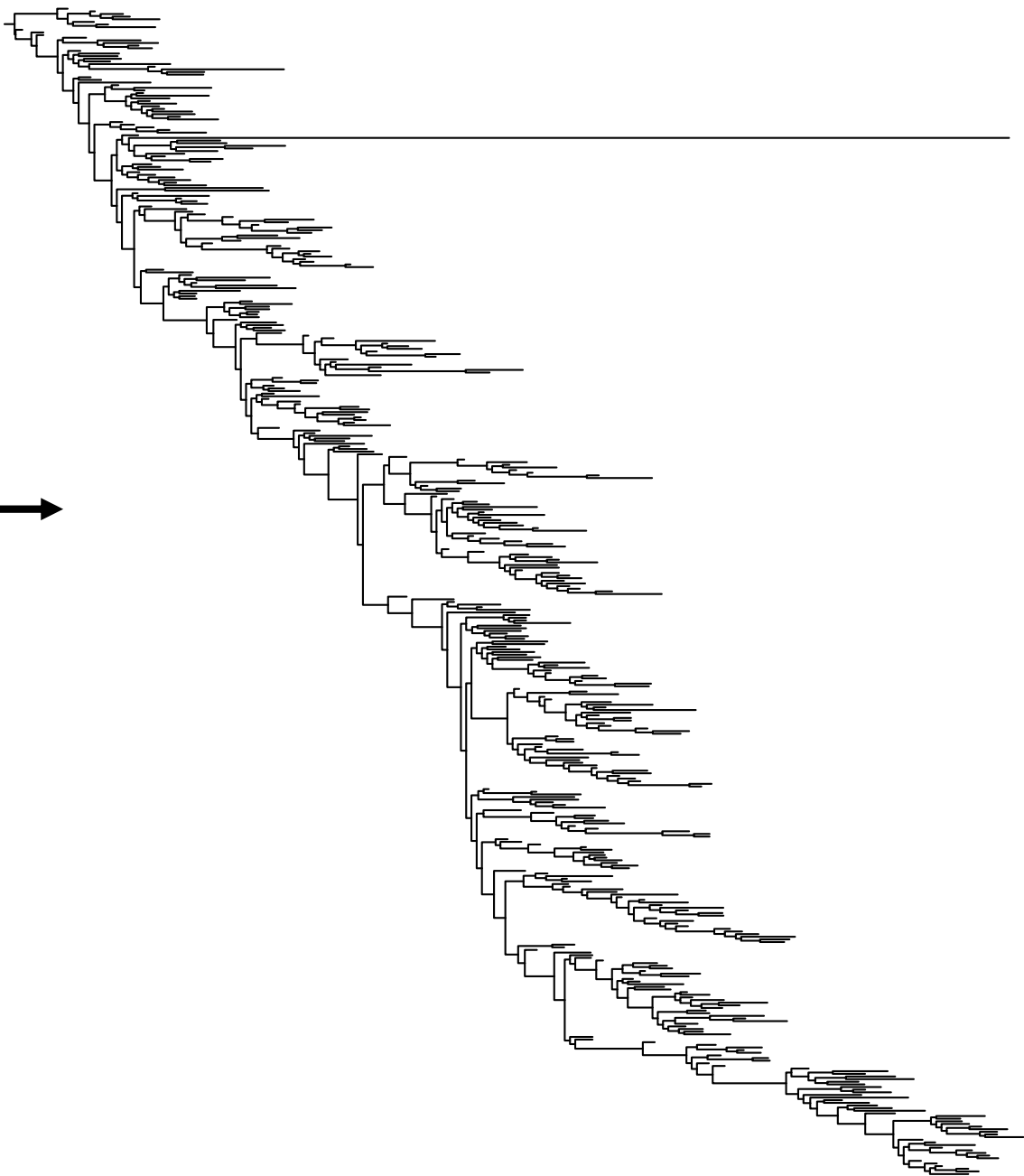
12,000 H1N1pdm HA sequences



0.008

443 sequences after optimal downsampling
(Under 0.5% sequence divergence threshold)

PARNAS
→



0.008