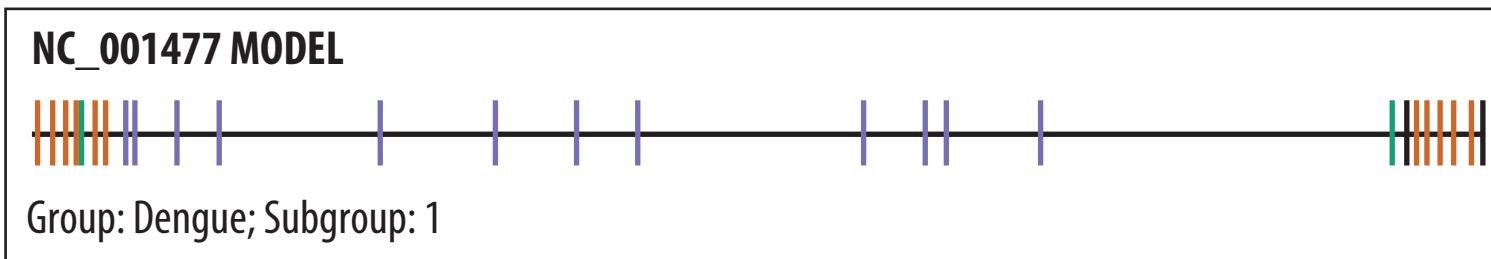


Stage 2: Coverage determination

Search each sequence with best-matching model (HMMER3 full pipeline)

input sequences that match best to NC_001477:



no significant similarity at ends
(unexpected: lowsim5s, lowsim3s, lowcovrg alerts)



no significant similarity in internal region
(unexpected: lowsimis alert)