



Figure S1. Neighbour Joining Tree (K2P distances; pairwise deletion) of *Strongylocentrous COI* sequences from the current study (ASU_depth_individual; n = 104; 399bp), the unique haplotypes from Addison and Hart (2005; Hap1-31; n = 31; 418bp), and the overlapping sequences from two individuals of S. sp. described by Layton et al 2016 (ECNN008-08, ECNN007-08; 75bp). Major clades are indicated using colour and correspond to those recovered using Likelihood and Bayesian methods (see results above and Addison and Hart, 2005 for more detail). Samples clustering with the cryptic *S. droebachiensis* "deep" lineage include S. sp. from the Canadian Arctic (Layton et al 2016), and Haps 14, 23, 30 and 31 sampled primarily from Norway and Iceland (Addison and Hart 2005).