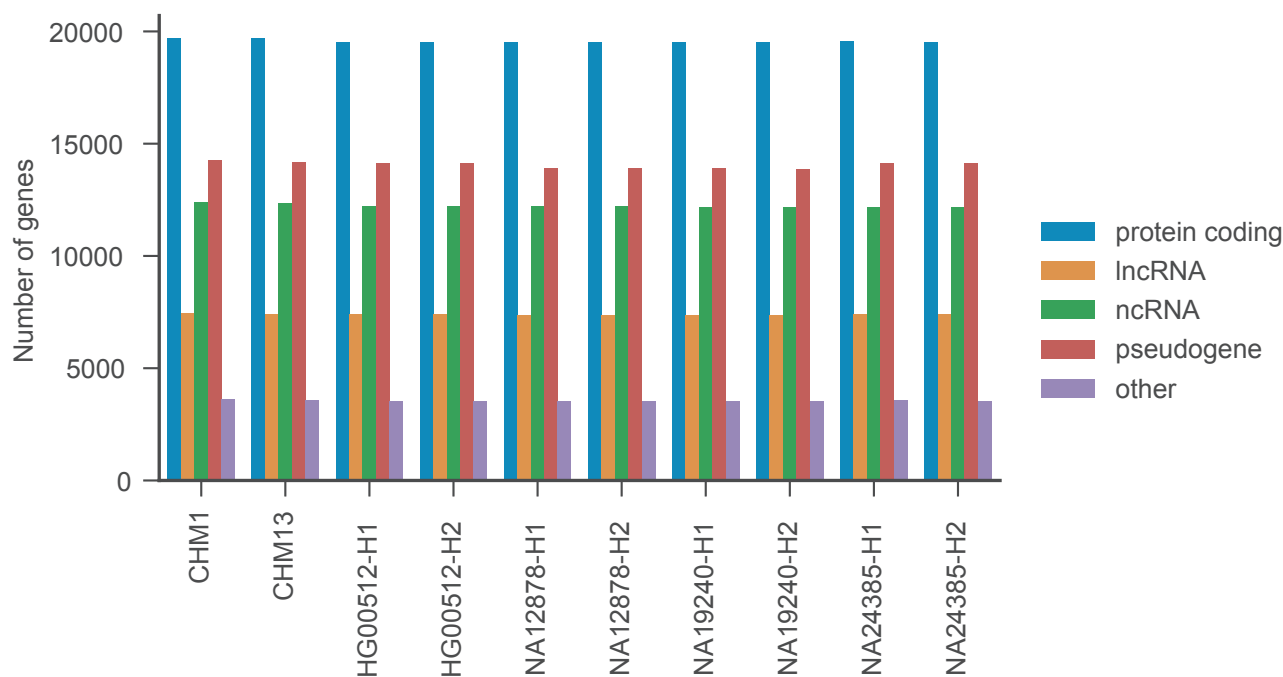
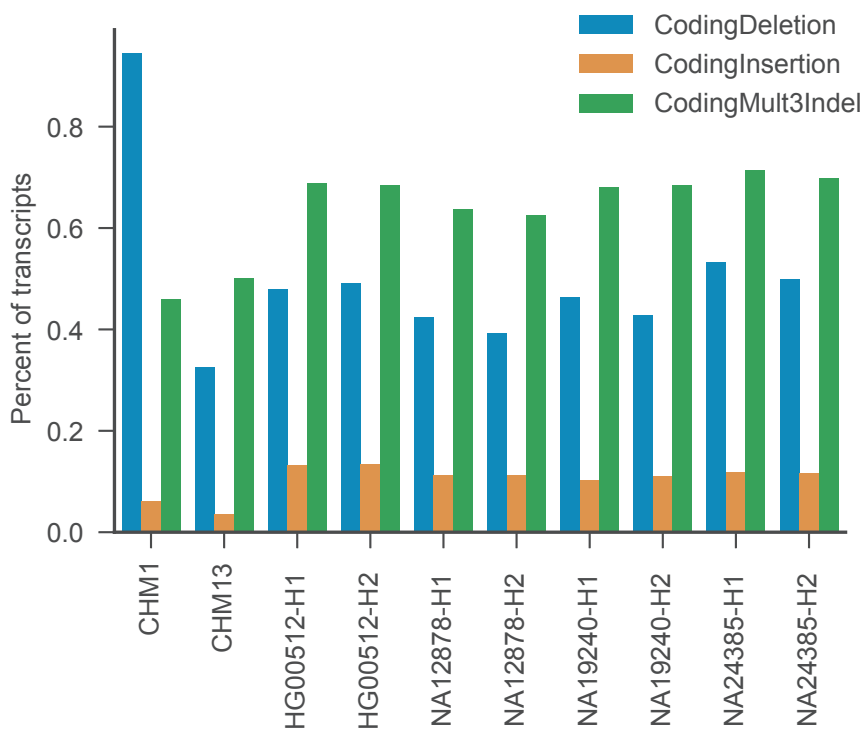


A) Completeness of comparative annotation



B) Coding indel rates



C) Contig split genes

