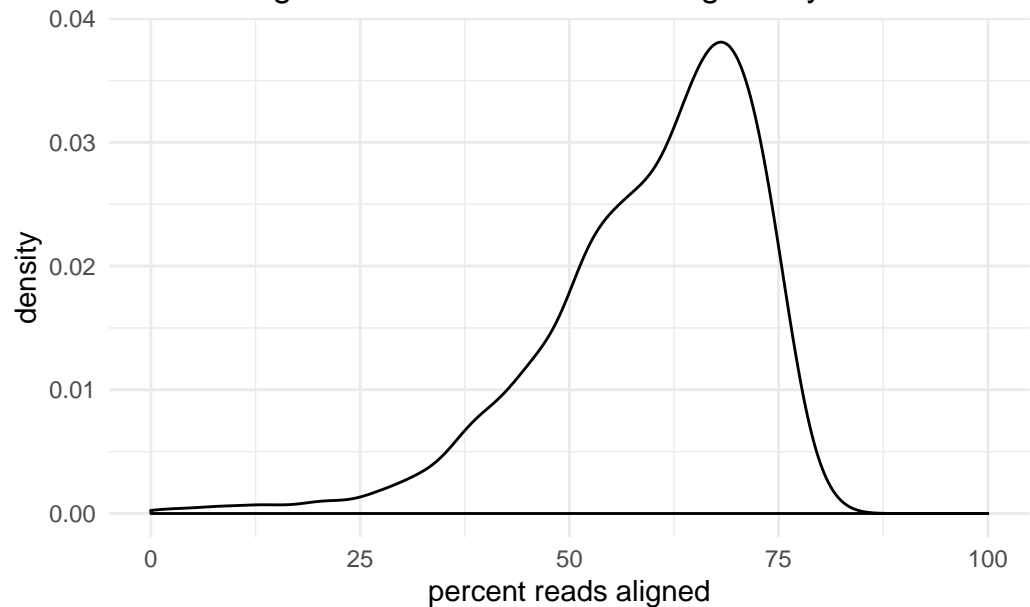


# HMP Metagenomes Percent Reads Aligned by HUMANN2



mean = 59.6

sd = 12.7

1330 metagenome samples from iHMP with HUMANN2 log files