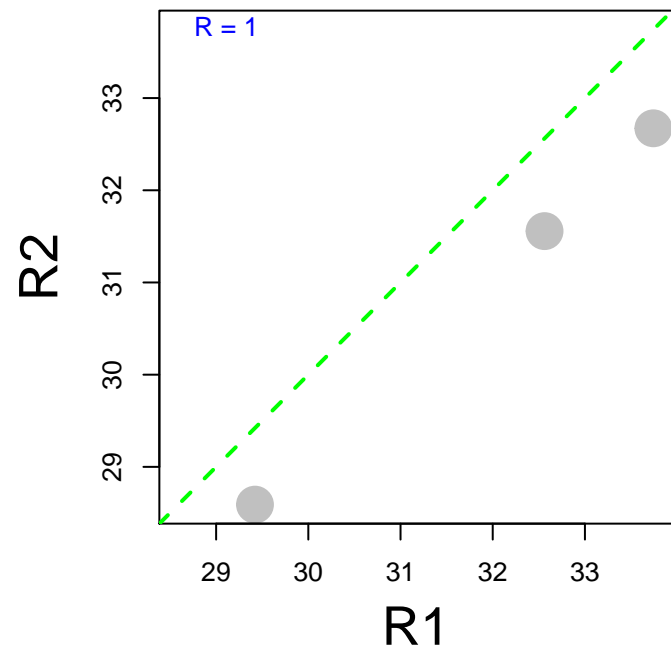
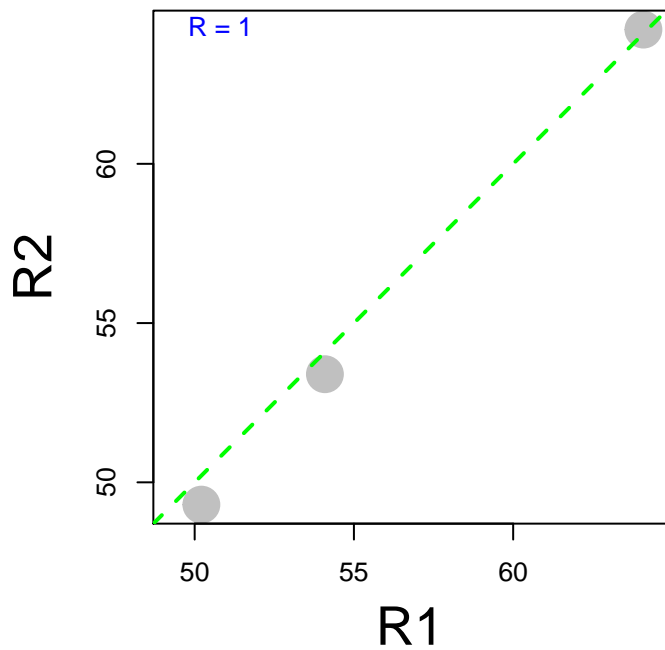


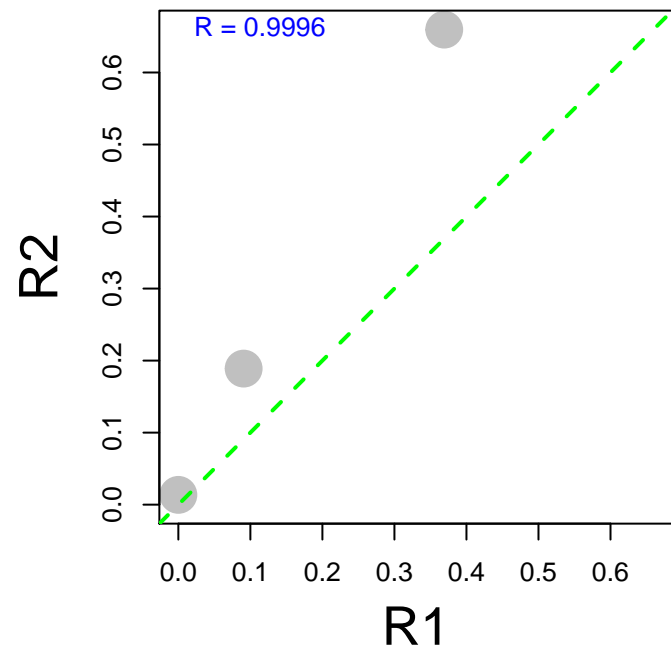
Average score of sequence quality



Overall percentage of GC bases



Average percentage of Ns



Percentage of duplicated reads

