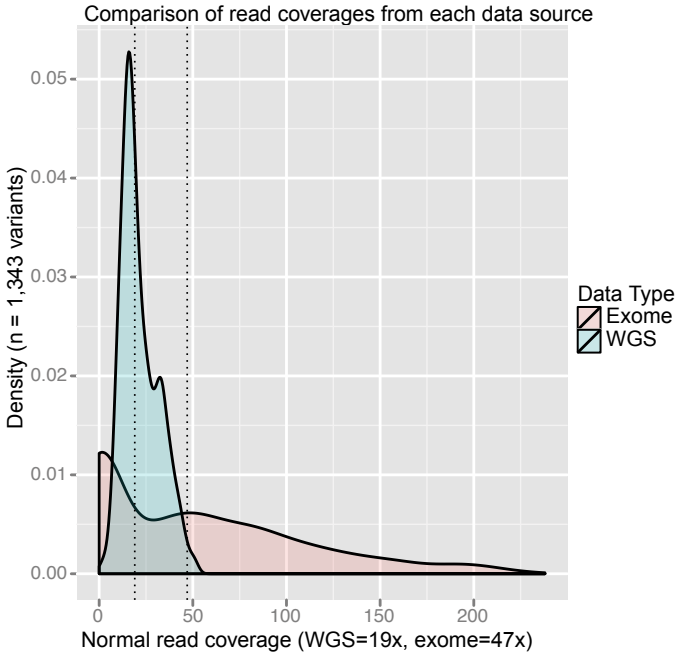
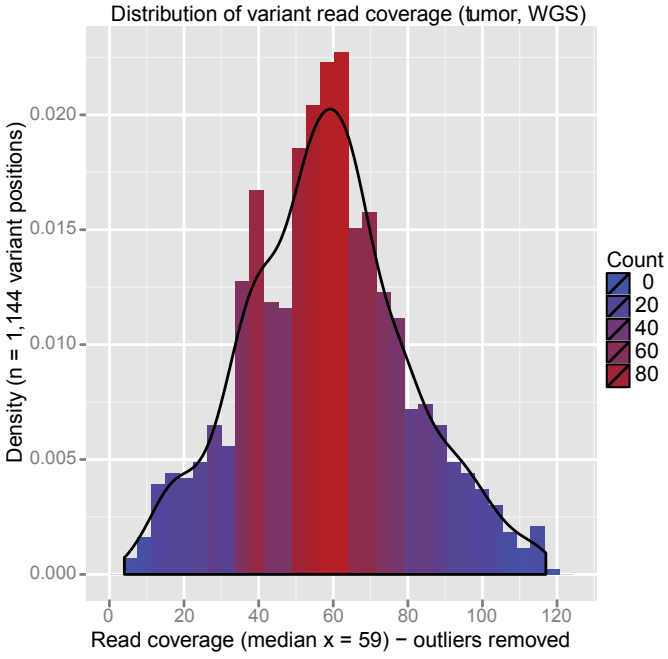
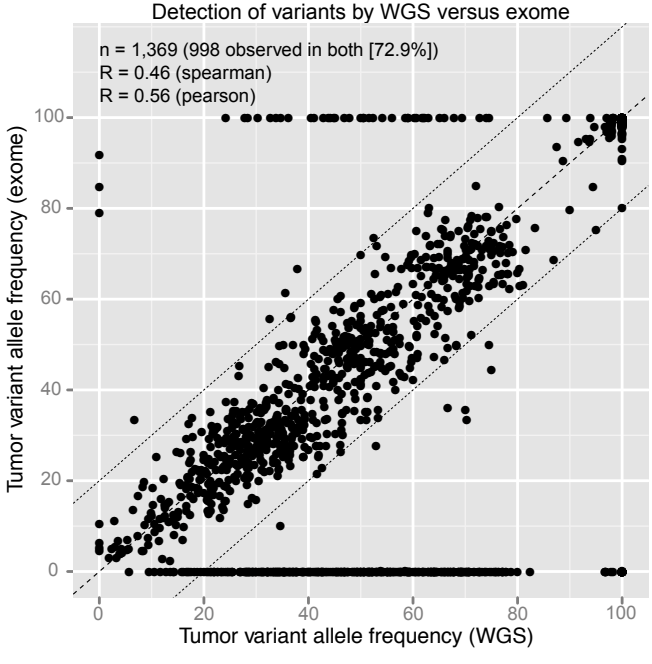
A. Normal sample read coverage (WGS & exome)



B. Tumor WGS coverage over variant positions



C. Tumor variant allele frequency (WGS vs. exome)



D. Tumor variant allele frequeny (exome vs. RNA)