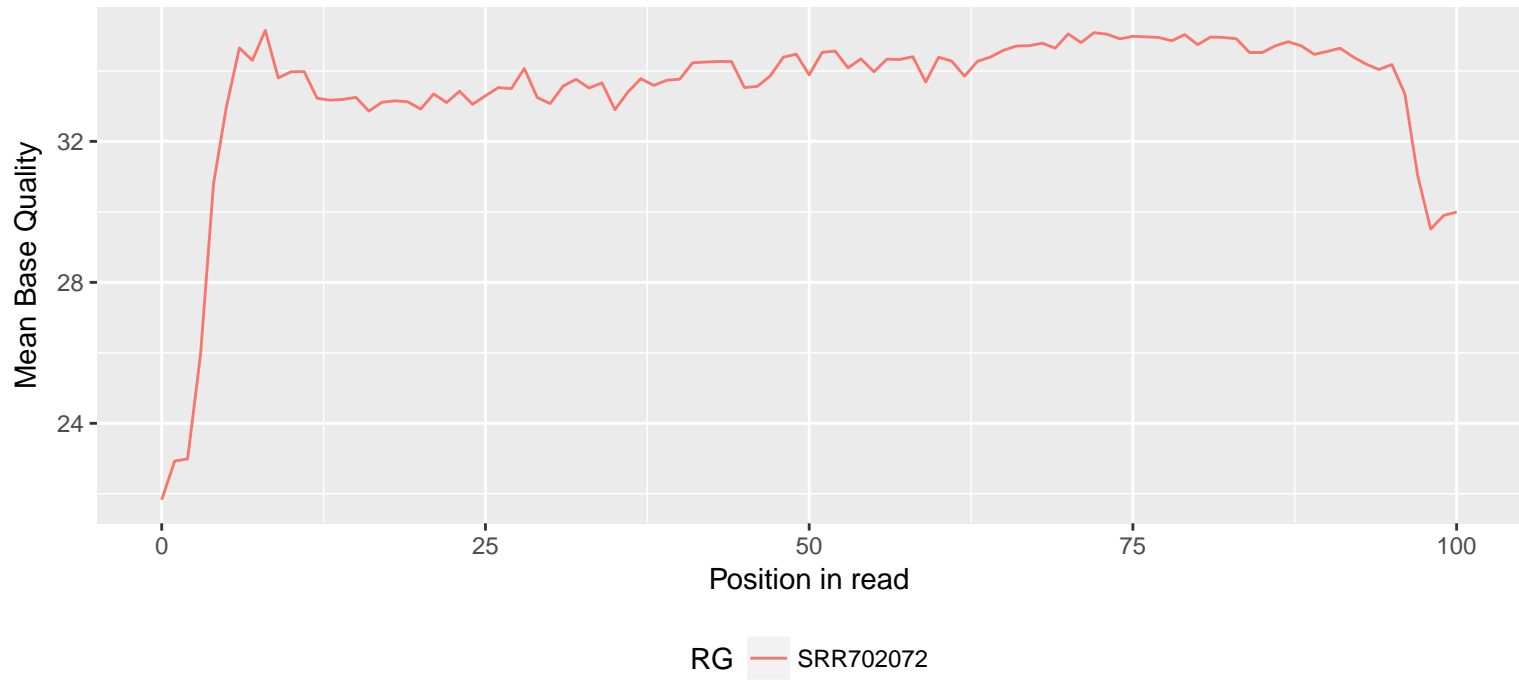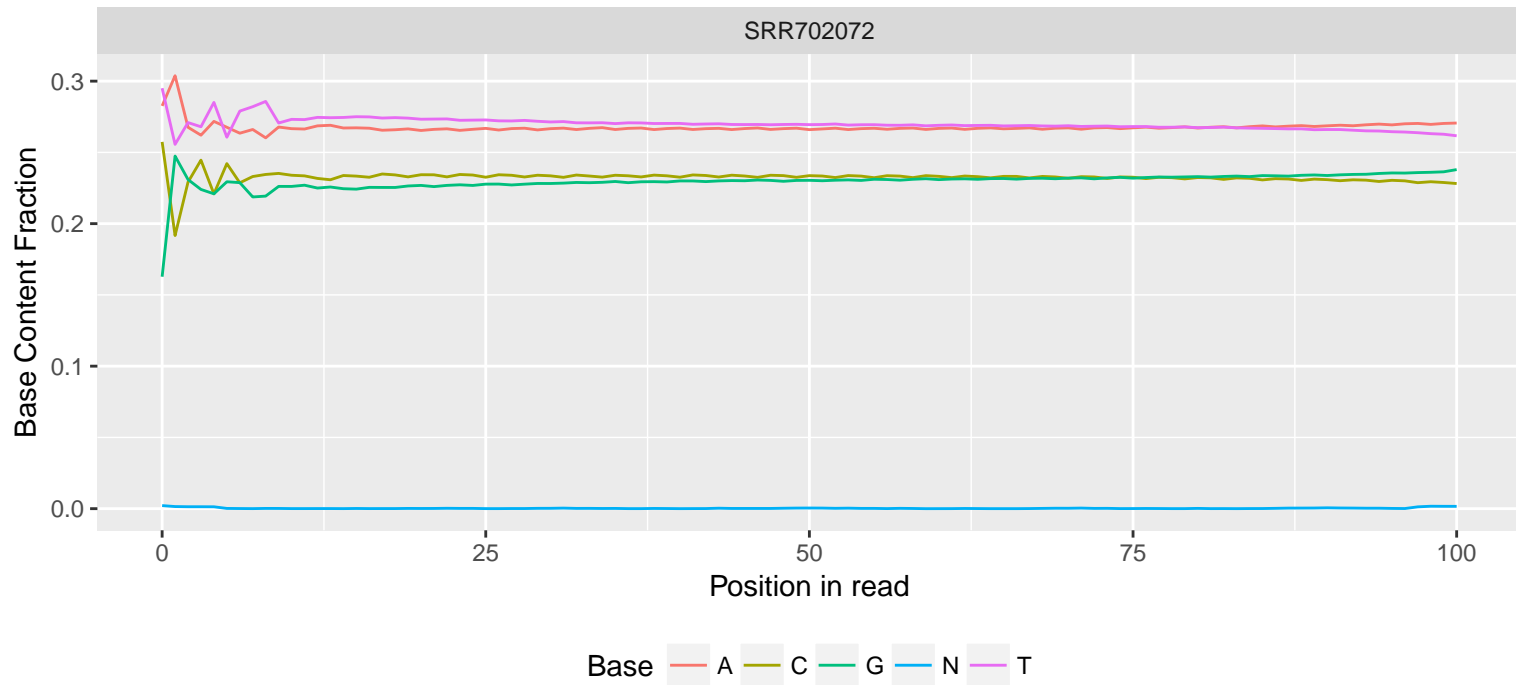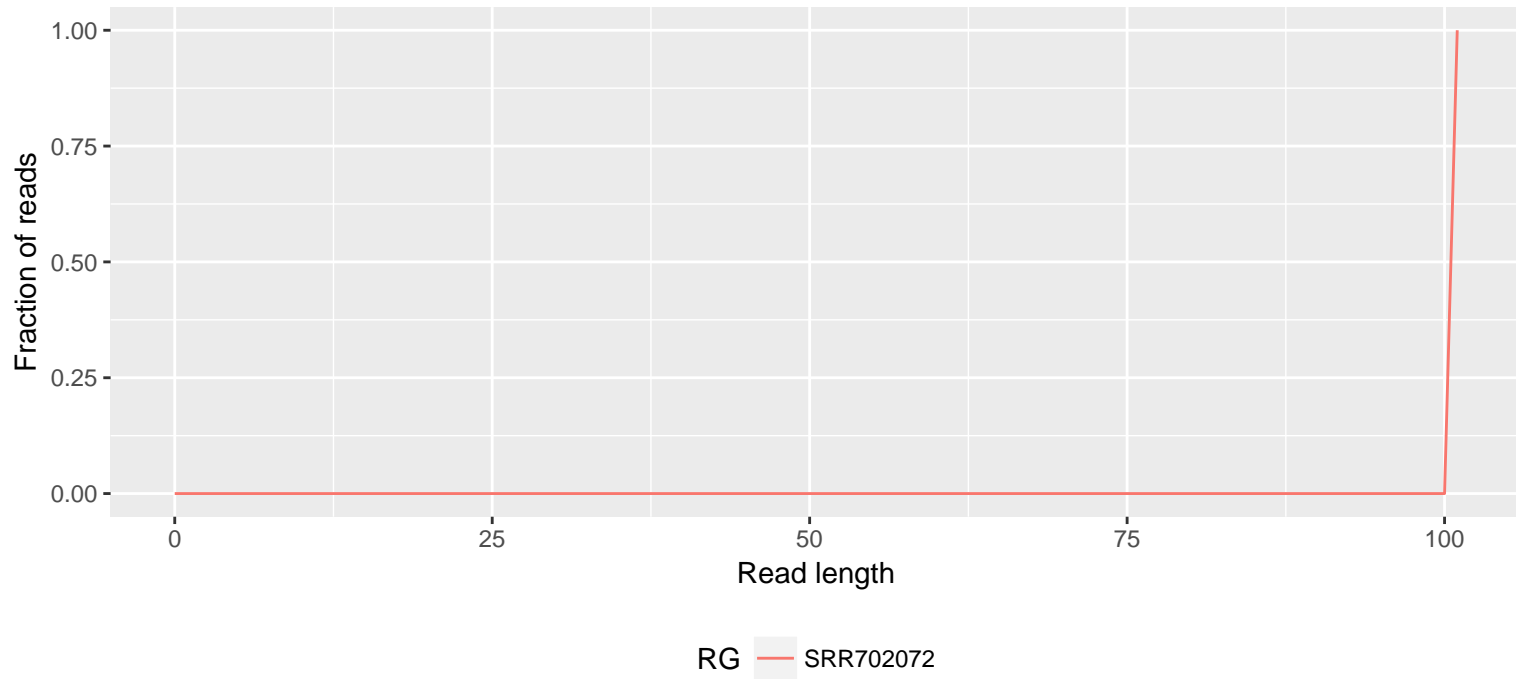Base Quality Distribution
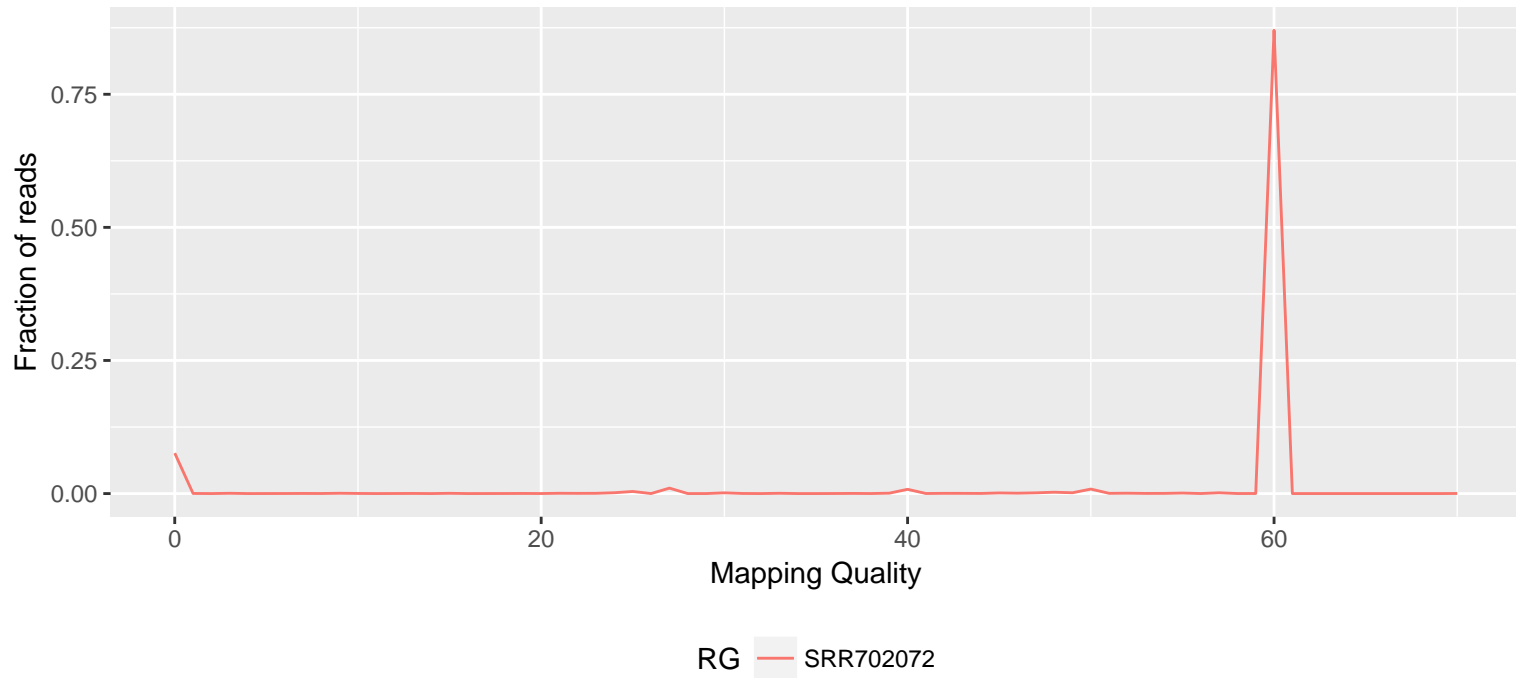
Base Content Distribution

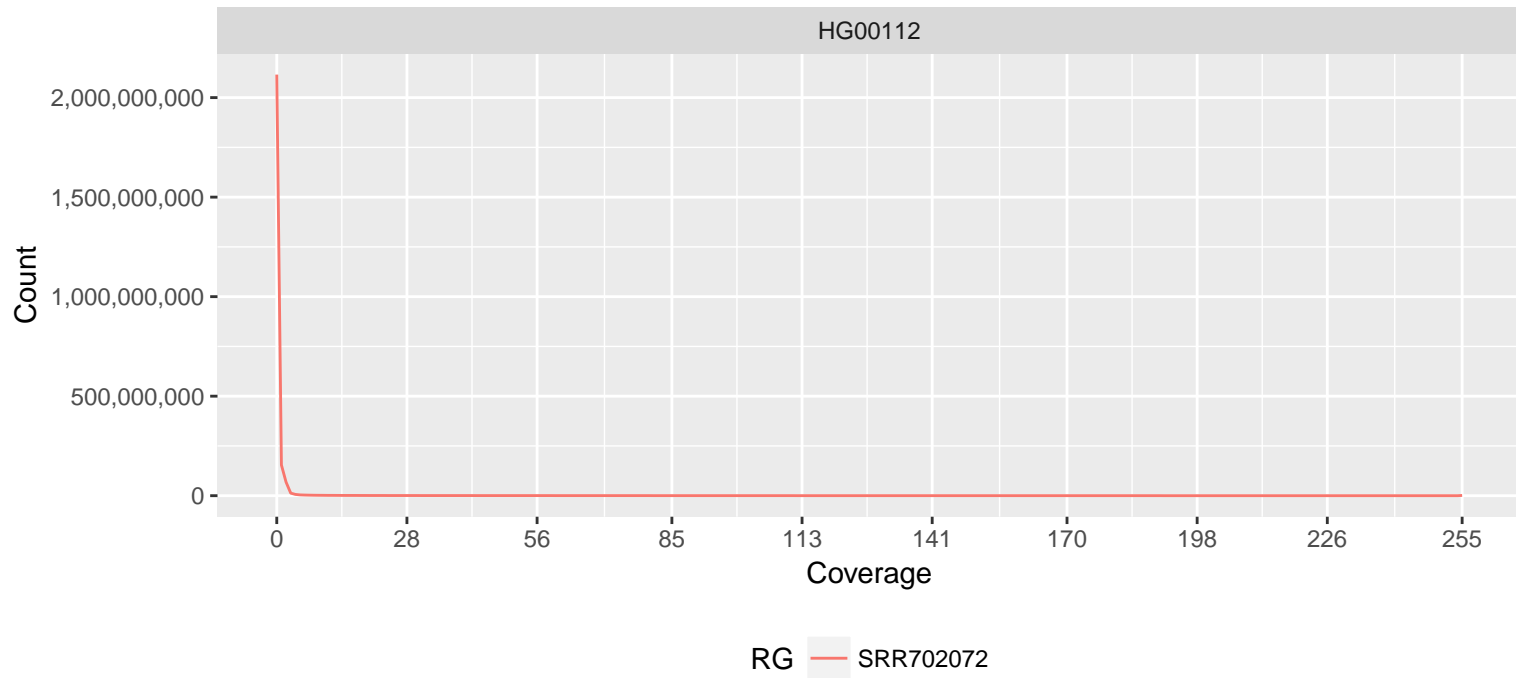# Read Length Distribution
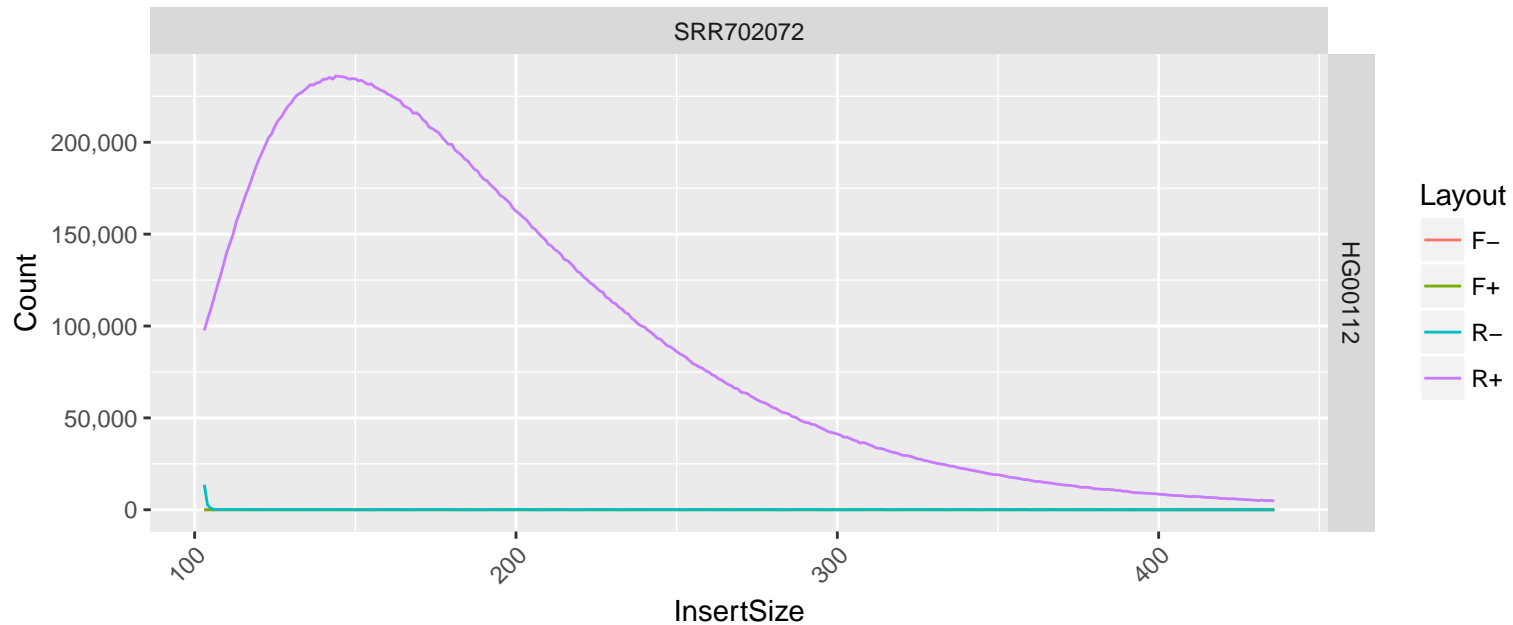
Mapping Quality Distribution

RG — SRR702072

Coverage Distribution
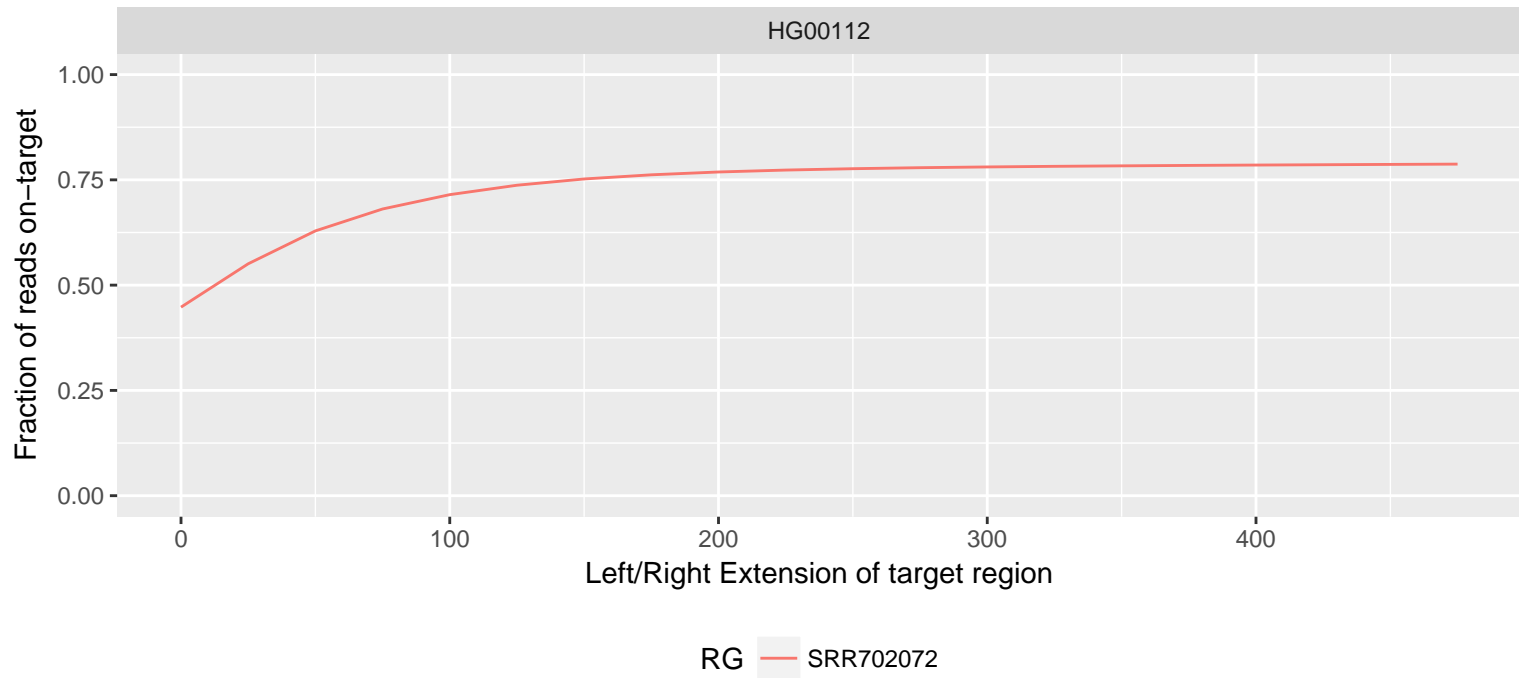
Insert Size Distribution
Insert size > 436 (1.25%)
Insert size < 103 (1.26%)

Target coverage distribution

On−target rate

HG00112

Fraction of reads on−target

Left/Right Extension of target region

RG — SRR702072

Sample	HG00112
Library	SRR702072
#QCFail	0
QCFailFraction	0
#DuplicateMarked	3415496
DuplicateFraction	0.0543994
#Unmapped	241904
UnmappedFraction	0.00385286
#Mapped	59128126
MappedFraction	0.941748
#MappedRead1	29602594
#MappedRead2	29525532
RatioMapped2vsMapped1	0.997397
#SecondaryAlignments	58125
SecondaryAlignmentFraction	0.000983035
#SupplementaryAlignments	5486170
SupplementaryAlignmentFraction	0.0927844
#Pairs	34153083
#MappedPairs	33950345
MappedFraction	0.994064
#MappedSameChr	32153003
MappedSameChrFraction	0.941438
#ReferenceBp	3214818421
#ReferenceNs	173893355
#AlignedBases	5944863566
#MatchedBases	5928103588
MatchRate	0.997181
#MismatchedBases	16759978
MismatchRate	0.00281924
#DeletionsCigarD	227551
DeletionRate	$3.82769\mathrm{e}{-05}$
#InsertionsCigarI	154107
InsertionRate	$2.59227\mathrm{e}{-05}$
#SoftClippedBases	1898775
SoftClipRate	0.000319398
#HardClippedBases	0
HardClipRate	0
ErrorRate	0.00320283
MedianReadLength	101
DefaultLibraryLayout	2
MedianInsertSize	179
MedianCoverage	0
SDCoverage	1.70956
MedianMAPQ	60
#TotalBedBp	32995992
#AlignedBasesInBed	2661629718
EnrichmentOverBed	41.262