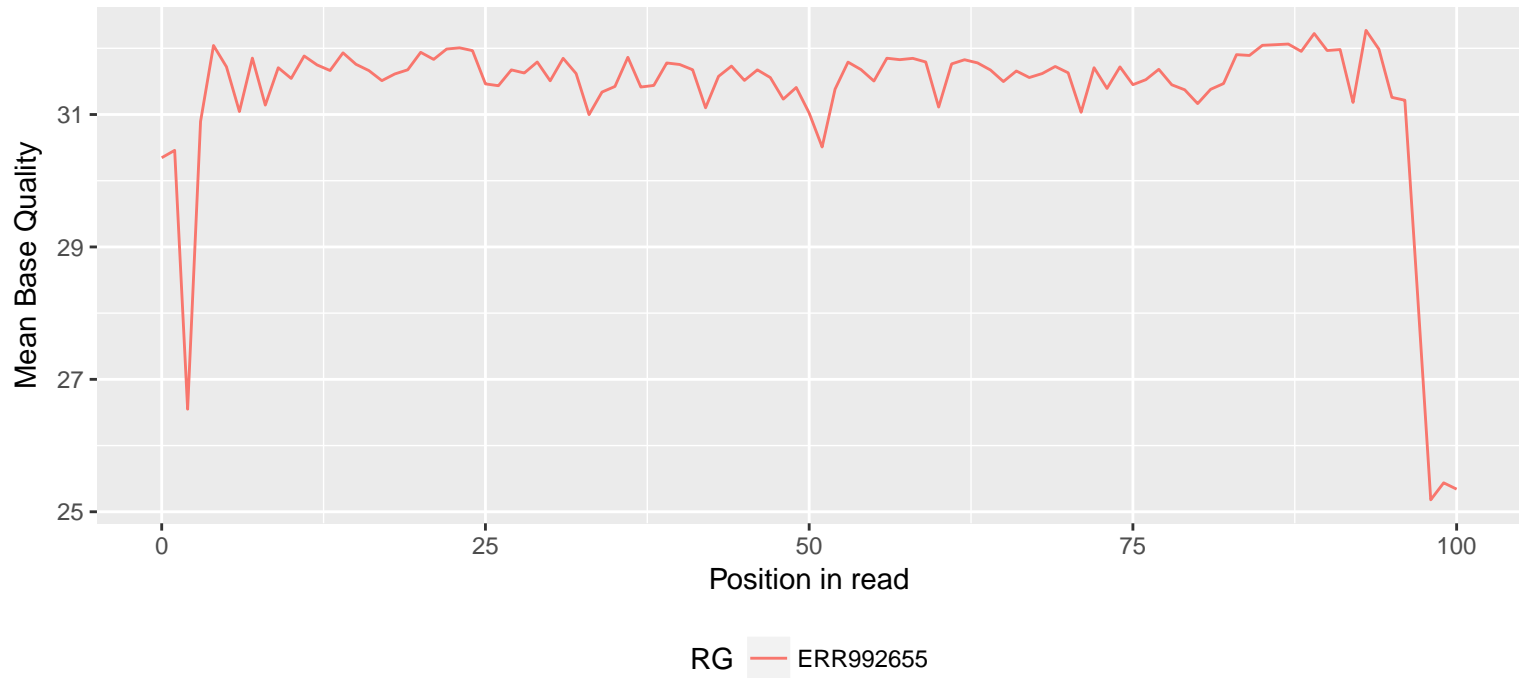
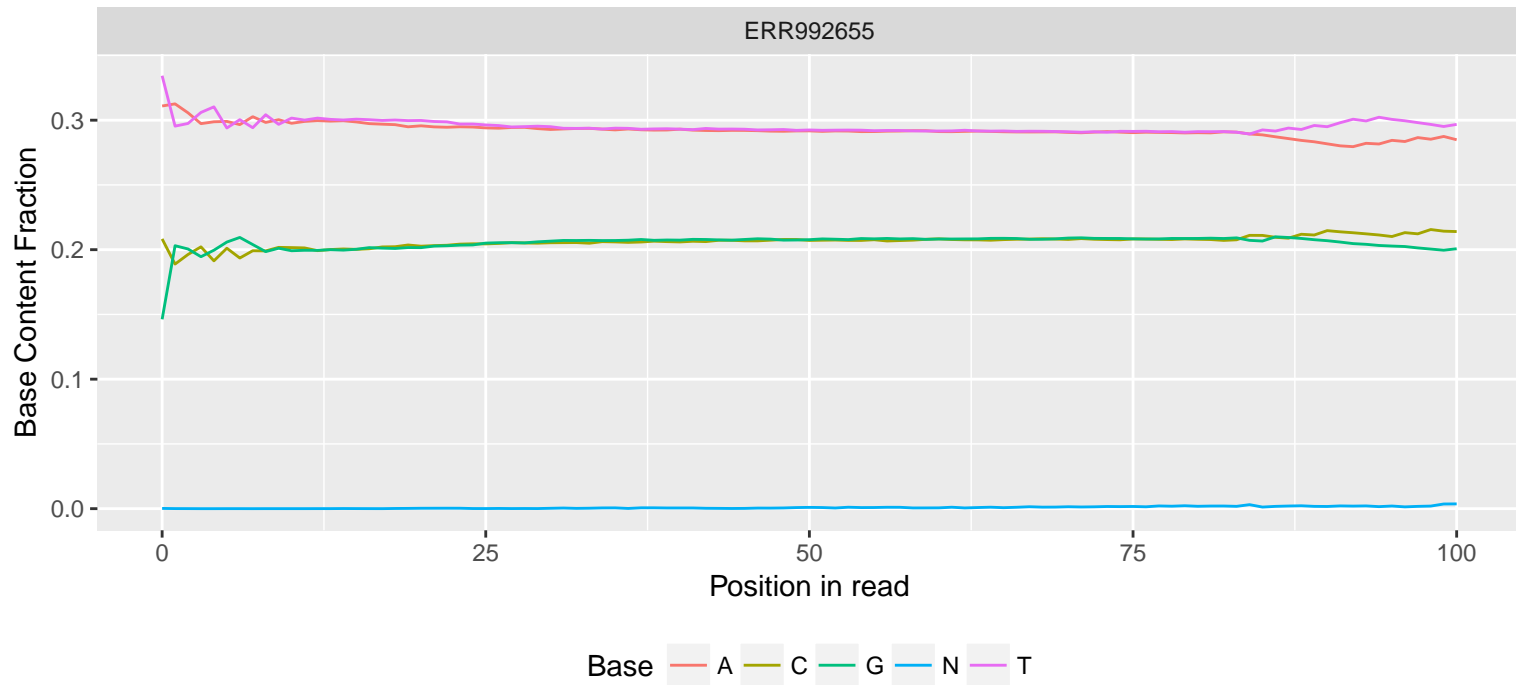


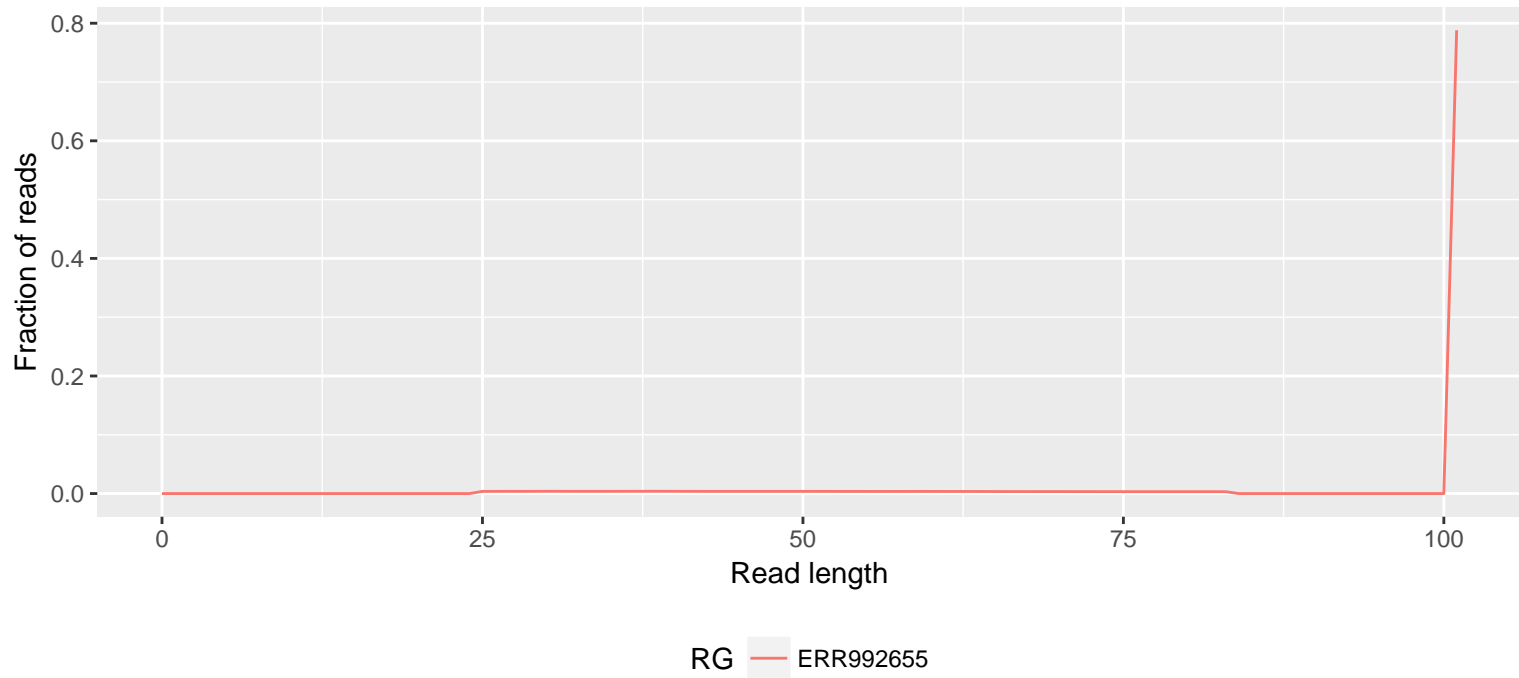
Base Quality Distribution



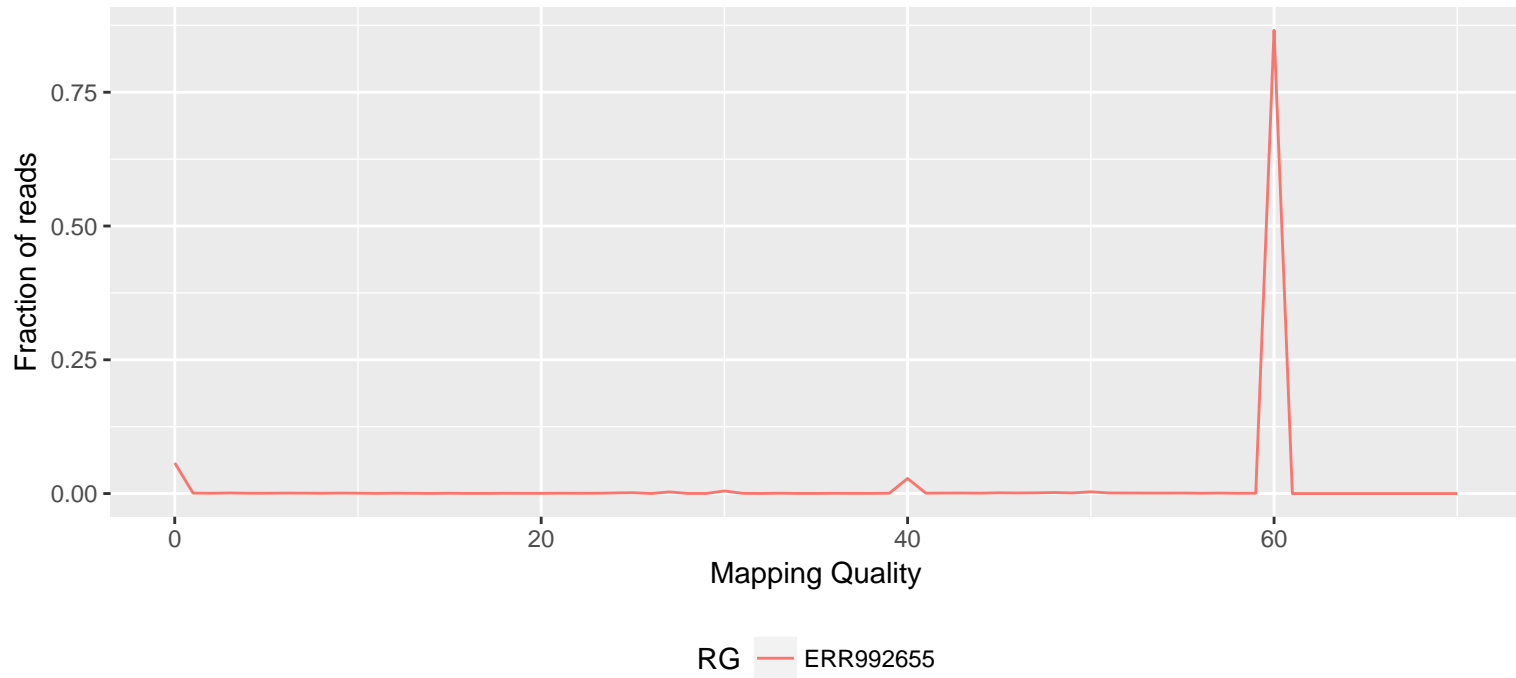
Base Content Distribution



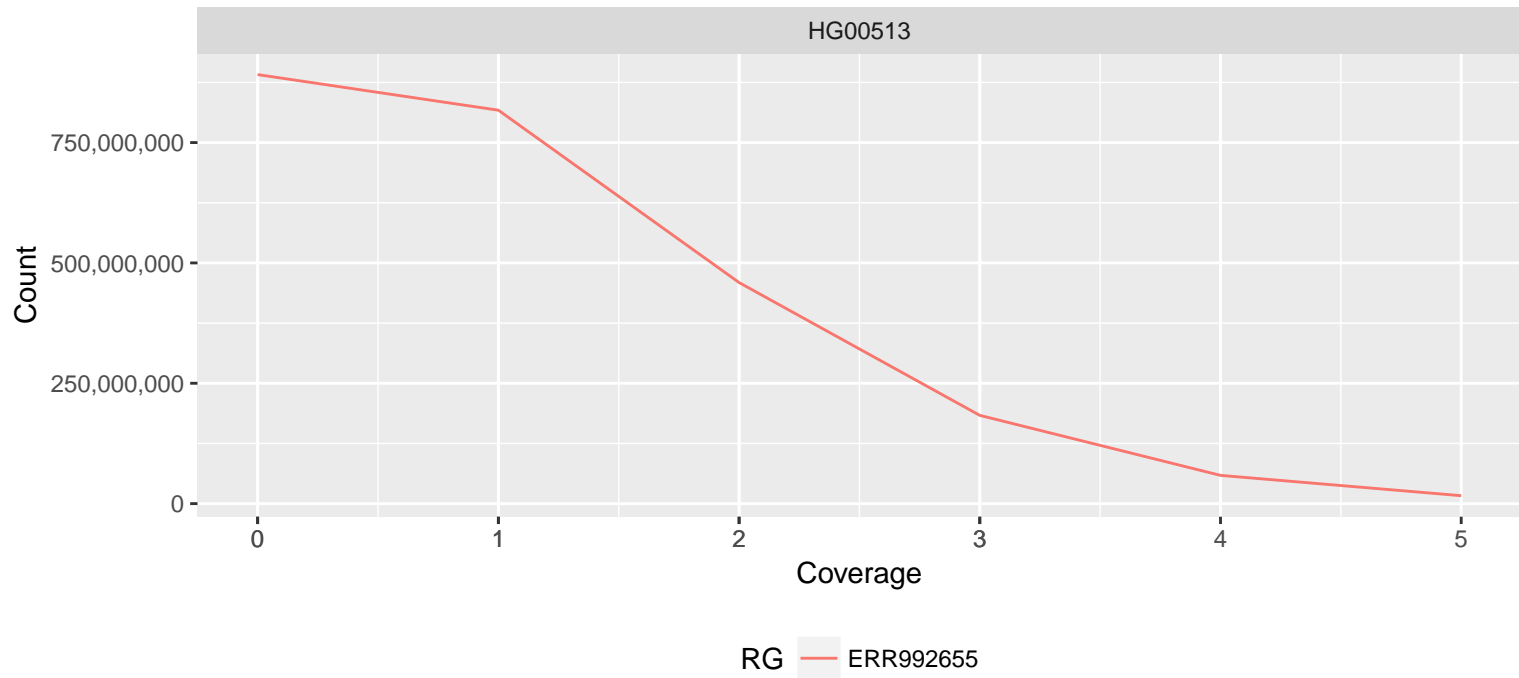
Read Length Distribution



Mapping Quality Distribution



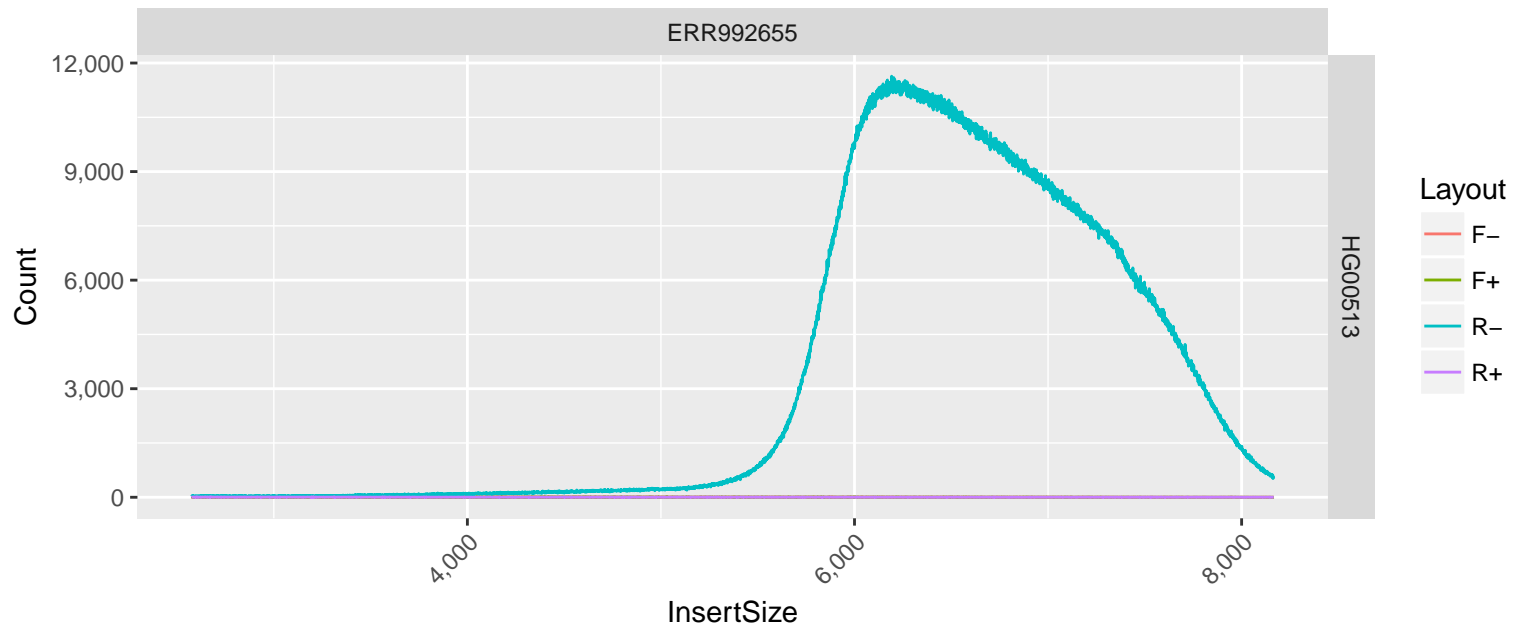
Coverage Distribution



Insert Size Distribution

Insert size > 8166 (4.33%)

Insert size < 2575 (0.97%)



Sample	HG00513
Library	ERR992655
#QCFail	0
QCFailFraction	0
#DuplicateMarked	565499
DuplicateFraction	0.0144855
#Unmapped	155603
UnmappedFraction	0.00398584
#Mapped	38317868
MappedFraction	0.981529
#MappedRead1	19207951
#MappedRead2	19109917
RatioMapped2vsMapped1	0.994896
#SecondaryAlignments	175564
SecondaryAlignmentFraction	0.00458178
#SupplementaryAlignments	1445051
SupplementaryAlignmentFraction	0.0377122
#Pairs	20326703
#MappedPairs	20166855
MappedFraction	0.992136
#MappedSameChr	18920808
MappedSameChrFraction	0.930835
#ReferenceBp	3216011937
#ReferenceNs	173893355
#AlignedBases	3420663700
#MatchedBases	3405602459
MatchRate	0.995597
#MismatchedBases	15061241
MismatchRate	0.00440302
#DeletionsCigarD	362844
DeletionRate	0.000106074
#InsertionsCigarI	311083
InsertionRate	9.09423e-05
#SoftClippedBases	3564155
SoftClipRate	0.00104195
#HardClippedBases	0
HardClipRate	0
ErrorRate	0.00564198
MedianReadLength	101
DefaultLibraryLayout	3
MedianInsertSize	6624
MedianCoverage	1
SDCoverage	0.306449
MedianMAPQ	60