Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 14:19:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617553.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR8617553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617553_1.fastq.gz SRR8617553_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 14:19:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,483,258
Mapped reads	56,499,645 / 98.29%
Unmapped reads	983,613 / 1.71%
Mapped paired reads	56,499,645 / 98.29%
Mapped reads, first in pair	28,523,677 / 49.62%
Mapped reads, second in pair	27,975,968 / 48.67%
Mapped reads, both in pair	55,837,688 / 97.14%
Mapped reads, singletons	661,957 / 1.15%
Secondary alignments	0
Supplementary alignments	1,815,416 / 3.16%
Read min/max/mean length	30 / 150 / 151.55
Duplicated reads (estimated)	21,771,239 / 37.87%
Duplication rate	24.9%
Clipped reads	31,490,030 / 54.78%

2.2. ACGT Content

Number/percentage of A's	2,170,386,634 / 28.82%
Number/percentage of C's	1,438,201,718 / 19.09%
Number/percentage of T's	2,248,110,421 / 29.85%
Number/percentage of G's	1,674,984,920 / 22.24%
Number/percentage of N's	294,934 / 0%

GC Percentage	41.33%

2.3. Coverage

Mean	2.4348
Standard Deviation	23.7208

2.4. Mapping Quality

Mean Mapping Quality	53.36

2.5. Insert size

Mean	233,672.67
Standard Deviation	4,689,383.96
P25/Median/P75	209 / 259 / 324

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	84,176,273
Insertions	1,280,566
Mapped reads with at least one insertion	2.13%
Deletions	2,769,403
Mapped reads with at least one deletion	4.71%
Homopolymer indels	46.53%

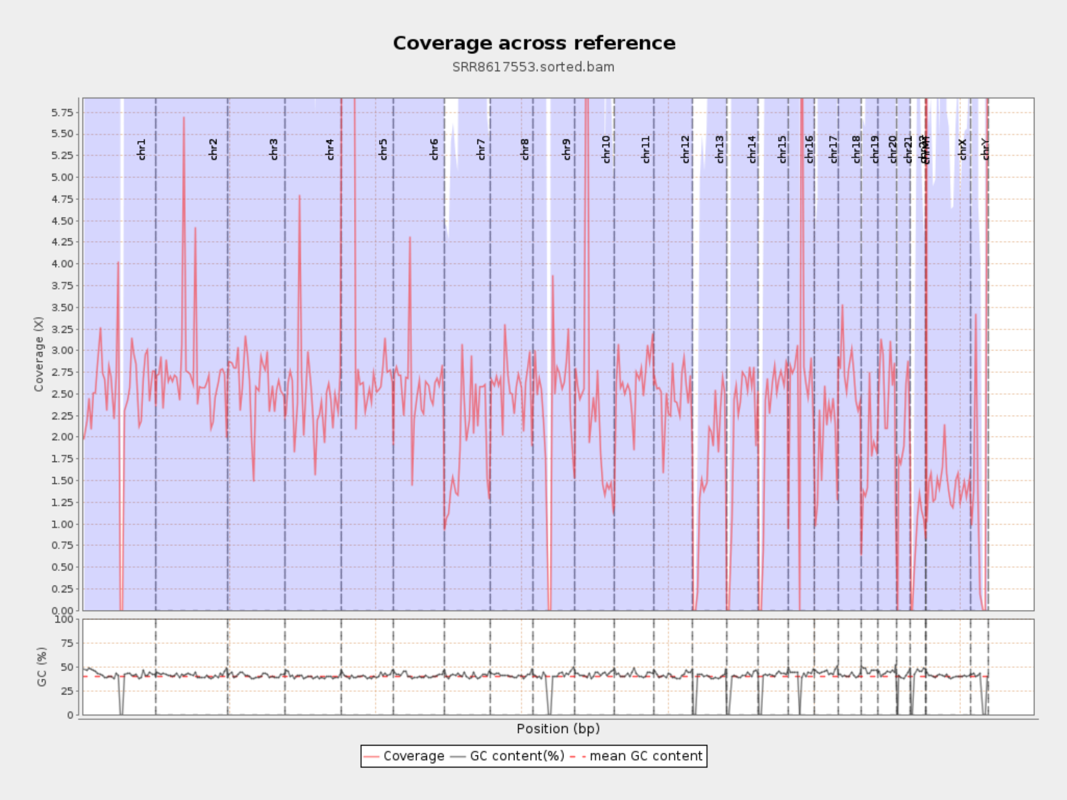
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

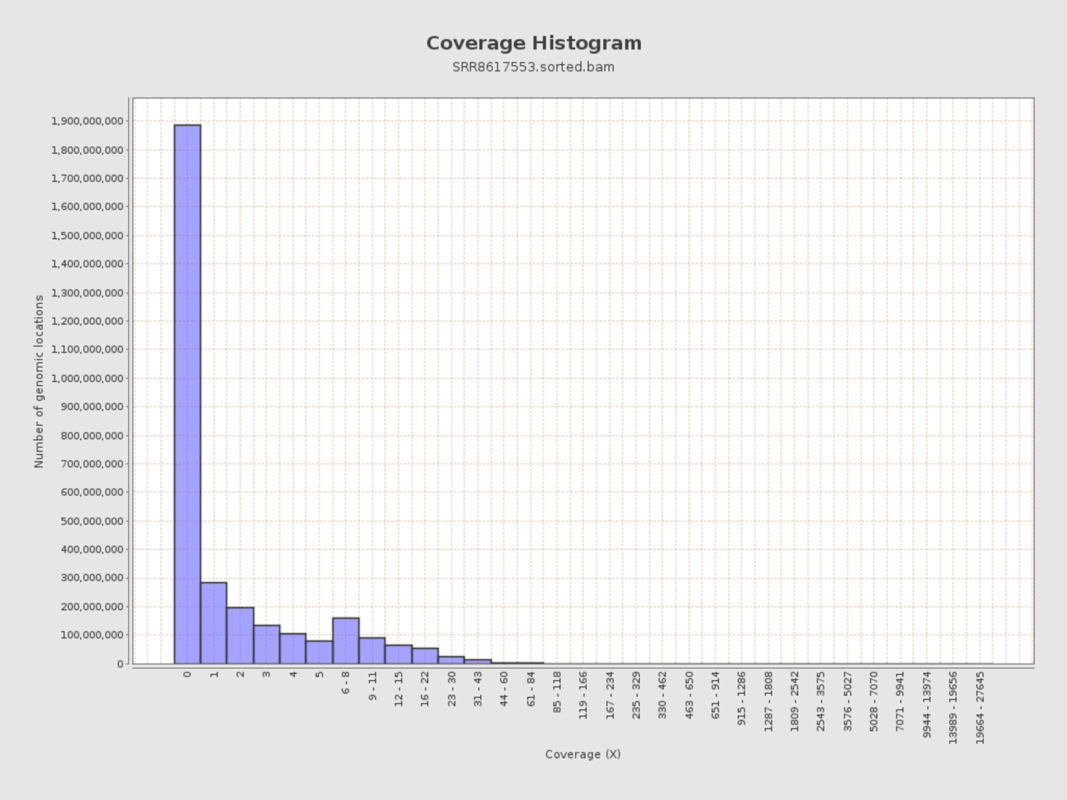
		bases	coverage	deviation
chr1	249250621	616276582	2.4725	27.4009
chr2	243199373	675129096	2.776	27.1914
chr3	198022430	518719868	2.6195	5.7147
chr4	191154276	473567172	2.4774	19.7117
chr5	180915260	788457835	4.3582	9.5422
chr6	171115067	442788159	2.5877	21.153
chr7	159138663	310564297	1.9515	22.4128
chr8	146364022	376379320	2.5715	9.63
chr9	141213431	327422328	2.3186	40.2296
chr10	135534747	329876351	2.4339	54.0046
chr11	135006516	354914563	2.6289	16.8429
chr12	133851895	330532149	2.4694	10.9752
chr13	115169878	187766180	1.6303	4.2751
chr14	107349540	225627669	2.1018	5.4623
chr15	102531392	216927490	2.1157	6.6753
chr16	90354753	258473619	2.8607	42.5825
chr17	81195210	159552930	1.9651	18.8679
chr18	78077248	214208472	2.7435	34.8066
chr19	59128983	102181453	1.7281	15.1612
chr20	63025520	164160917	2.6047	8.0244
chr21	48129895	92815439	1.9284	10.2974
chr22	51304566	41271013	0.8044	3.6474
chrMT	16571	2764667	166.8377	82.7488
chrX	155270560	223703589	1.4407	6.8796

chrY	59373566	103336363	1.7404	40.9487

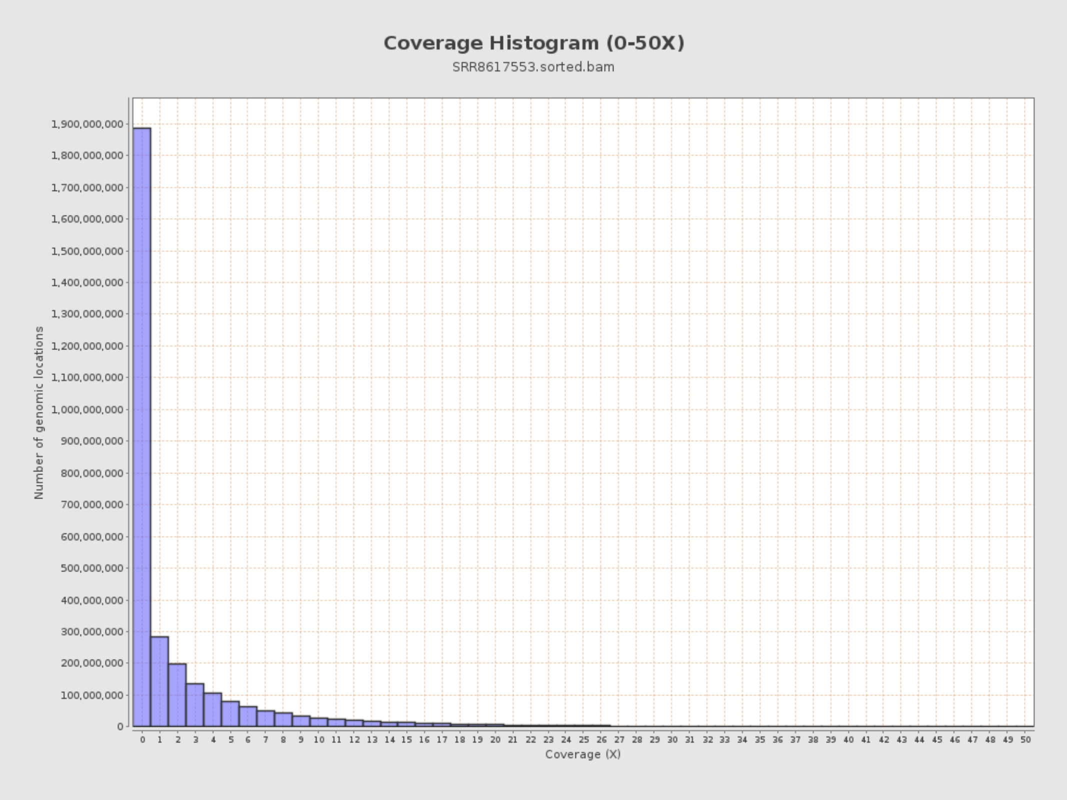
3. Results : Coverage across reference



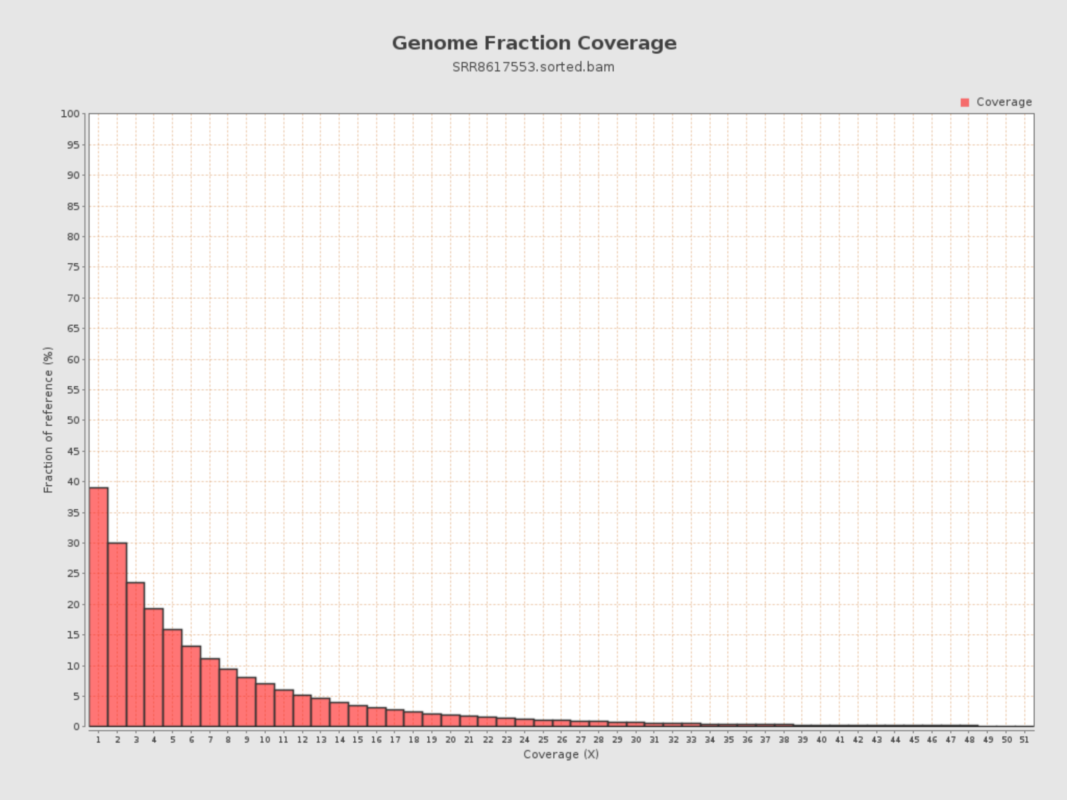
4. Results : Coverage Histogram



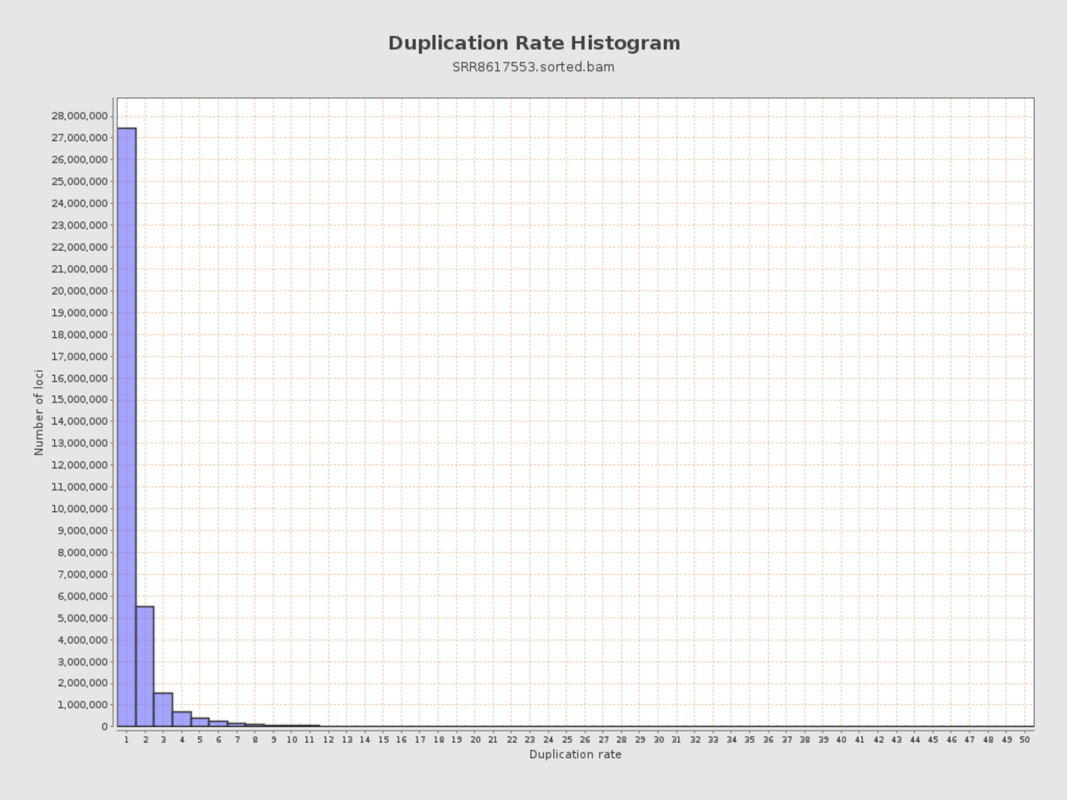
5. Results : Coverage Histogram (0-50X)



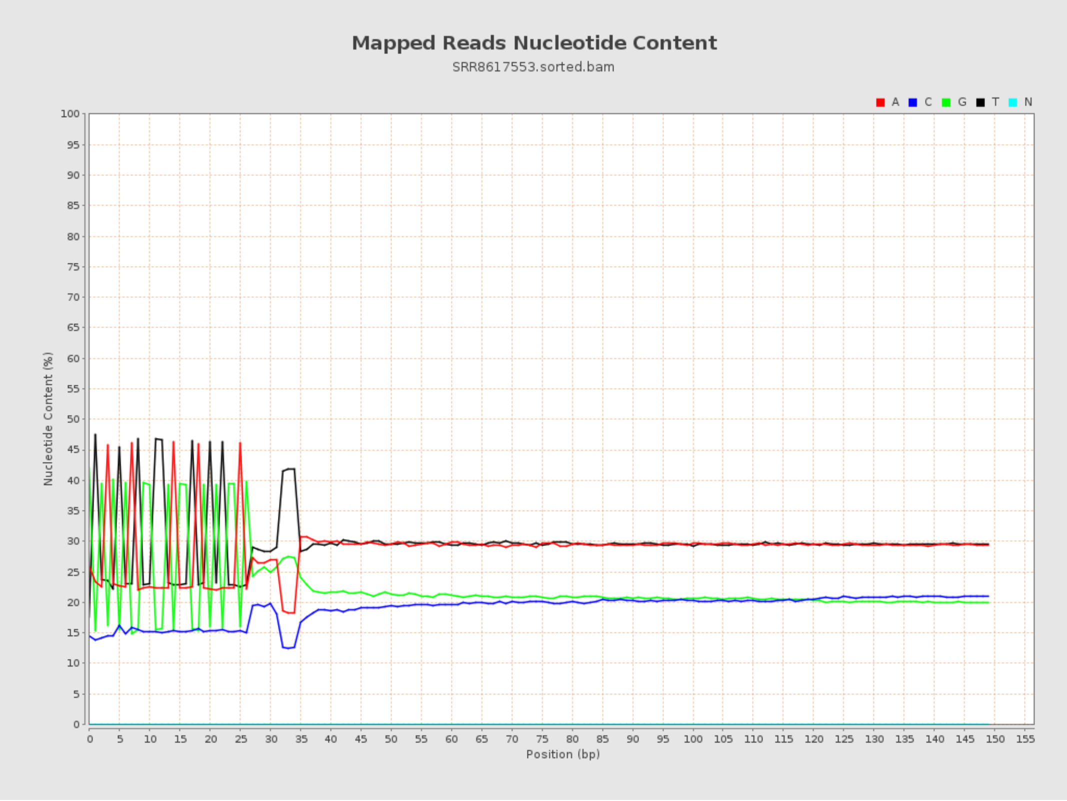
6. Results : Genome Fraction Coverage



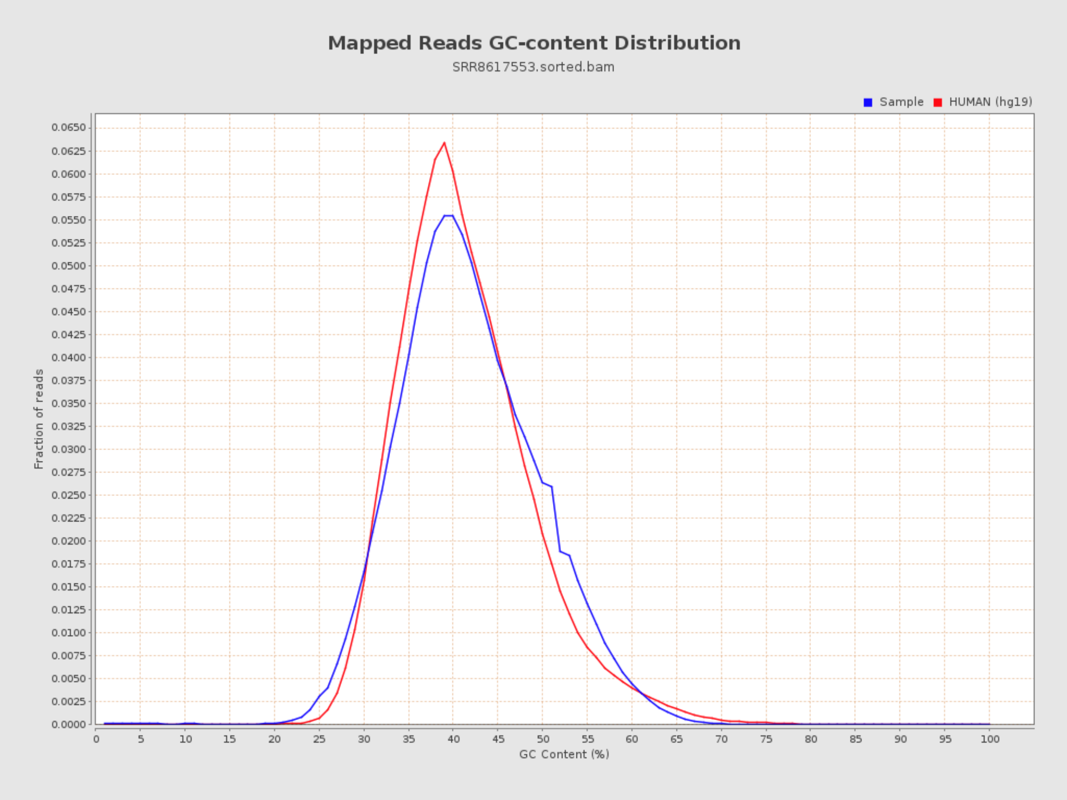
7. Results : Duplication Rate Histogram



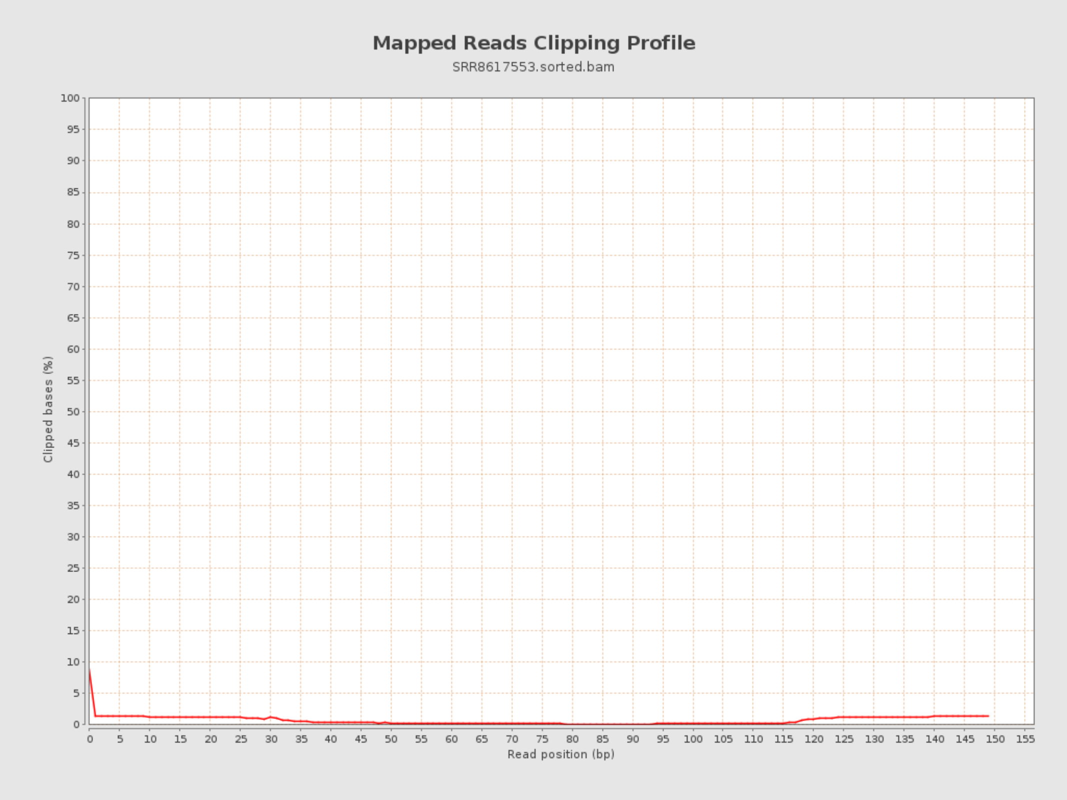
8. Results : Mapped Reads Nucleotide Content



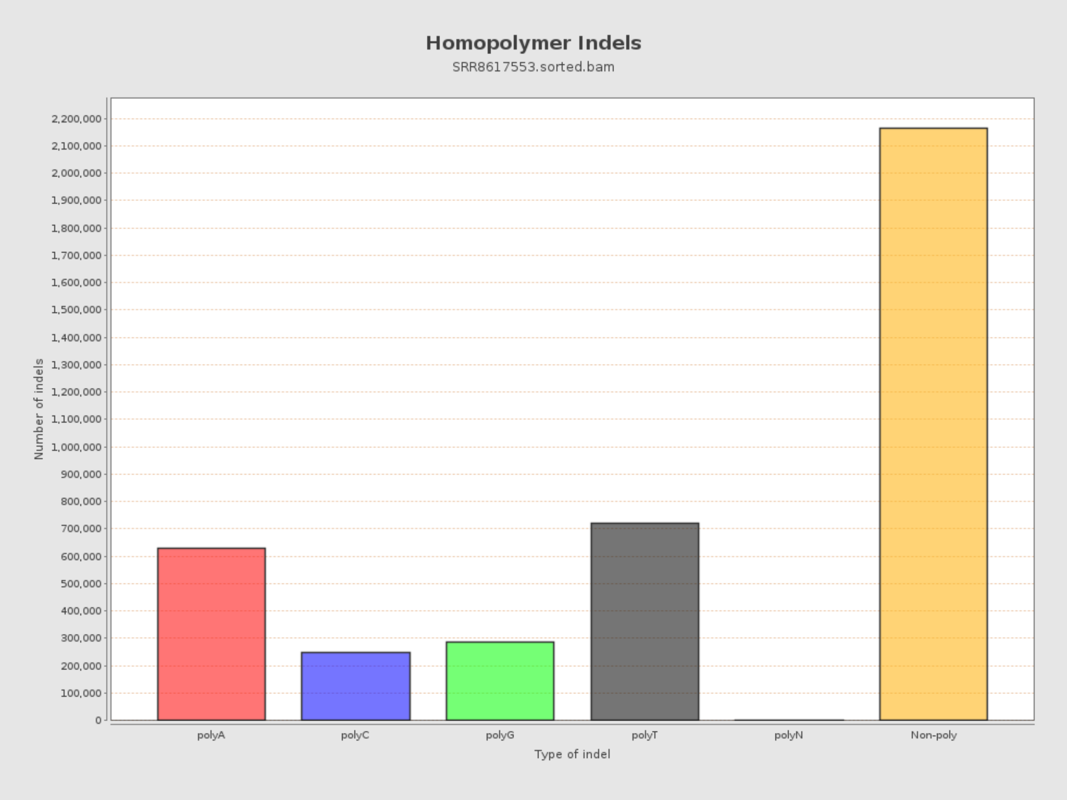
9. Results : Mapped Reads GC-content Distribution



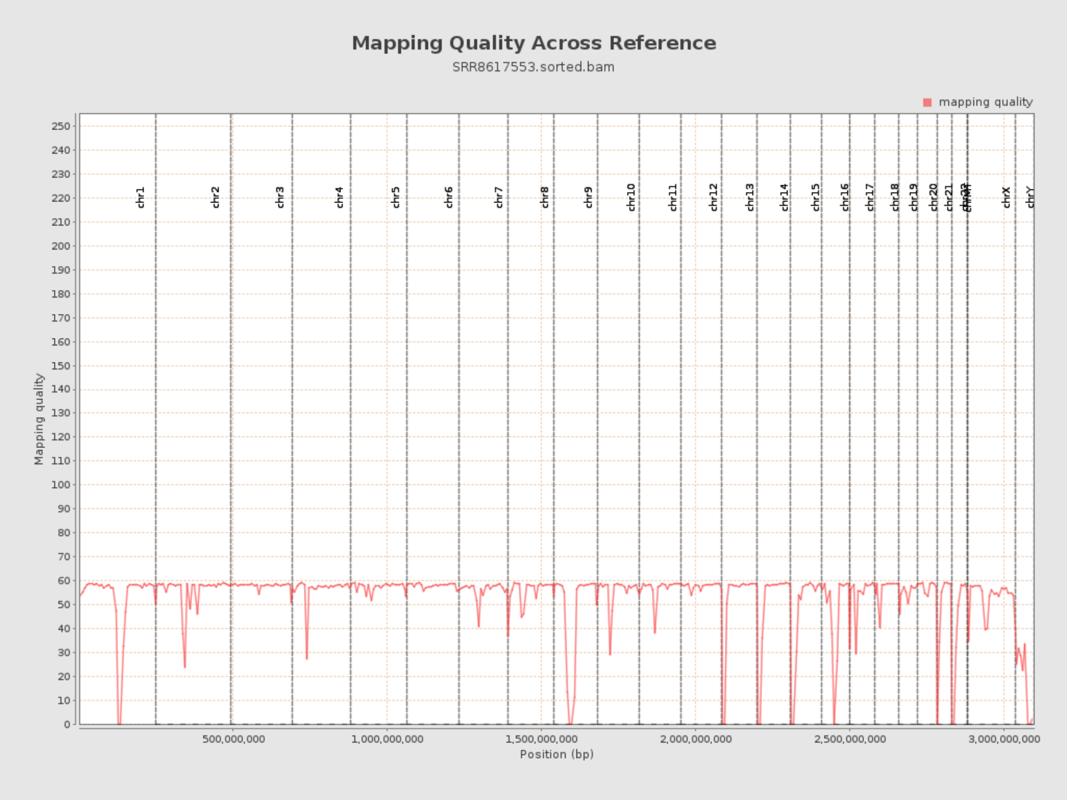
10. Results : Mapped Reads Clipping Profile



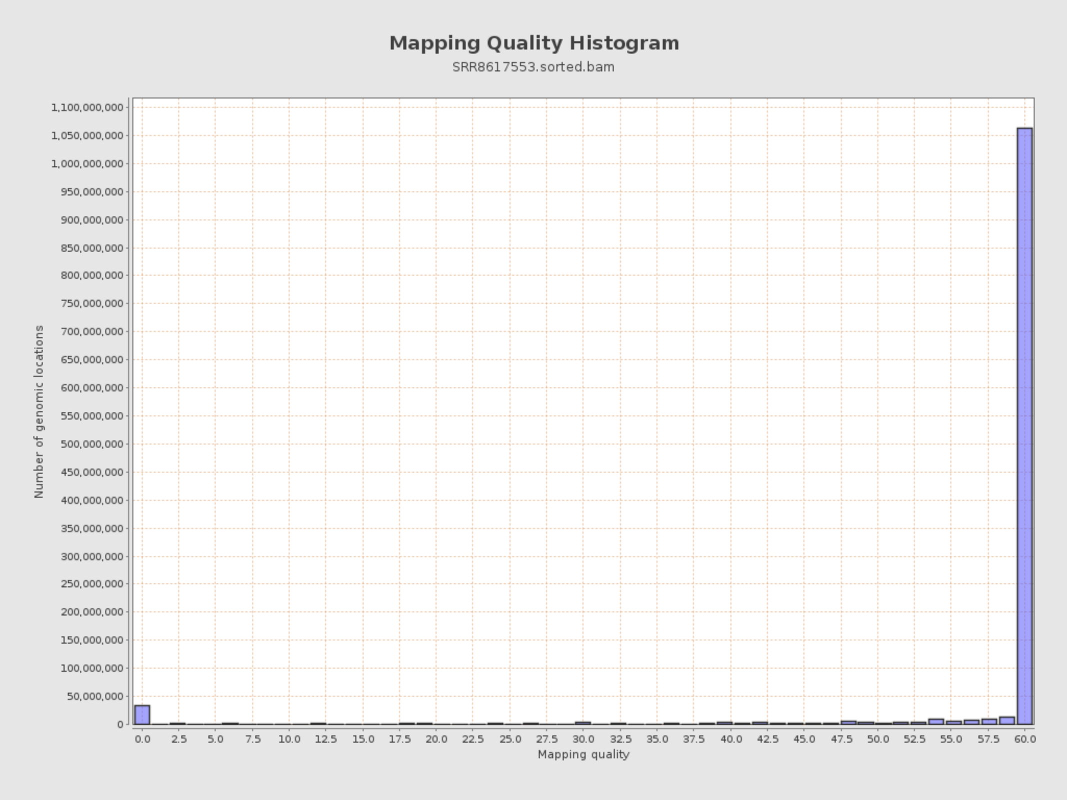
11. Results : Homopolymer Indels



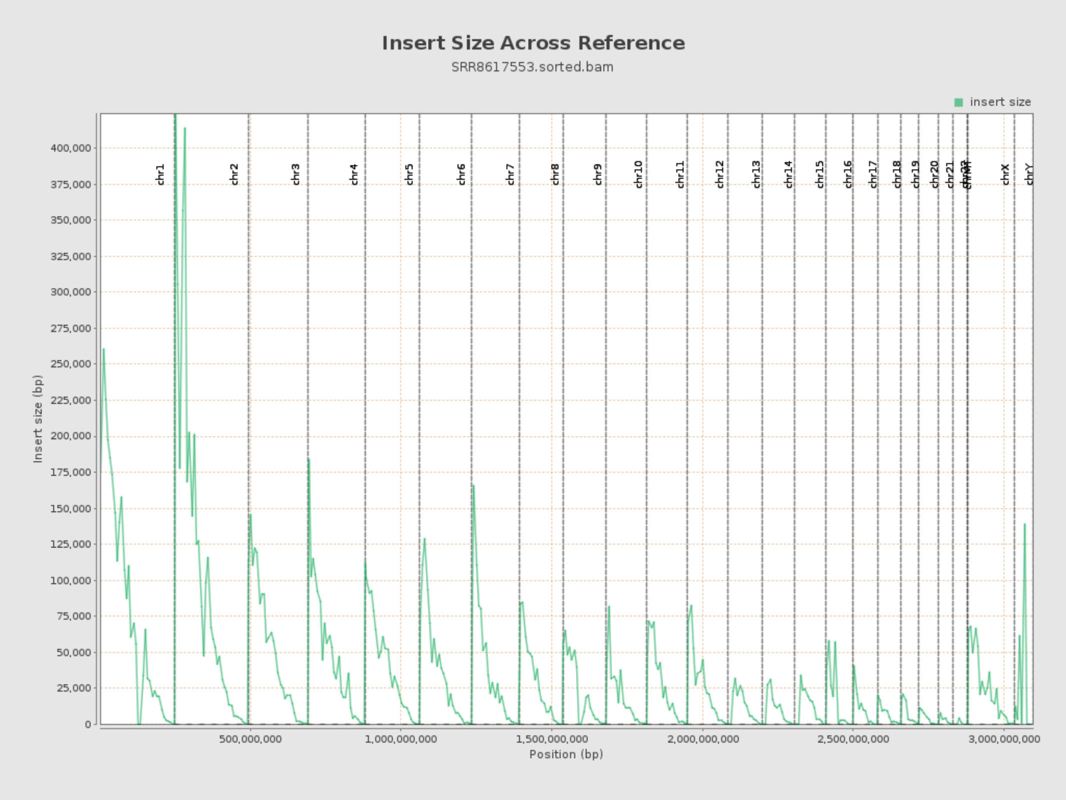
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram