Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 17:09:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617596.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_SRR8617596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617596_1.fastq.gz SRR8617596_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 17:09:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	52,011,210
Mapped reads	50,216,889 / 96.55%
Unmapped reads	1,794,321 / 3.45%
Mapped paired reads	50,216,889 / 96.55%
Mapped reads, first in pair	25,369,951 / 48.78%
Mapped reads, second in pair	24,846,938 / 47.77%
Mapped reads, both in pair	49,466,744 / 95.11%
Mapped reads, singletons	750,145 / 1.44%
Secondary alignments	0
Supplementary alignments	928,006 / 1.78%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	16,075,851 / 30.91%
Duplication rate	24.26%
Clipped reads	25,073,278 / 48.21%

2.2. ACGT Content

Number/percentage of A's	1,951,722,217 / 29.01%
Number/percentage of C's	1,273,087,334 / 18.92%
Number/percentage of T's	2,014,520,084 / 29.94%
Number/percentage of G's	1,488,794,390 / 22.13%
Number/percentage of N's	280,186 / 0%

GC Percentage	41.05%

2.3. Coverage

Mean	2.1749
Standard Deviation	22.5961

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	120,695.12
Standard Deviation	3,332,470.19
P25/Median/P75	226 / 283 / 353

2.6. Mismatches and indels

General error rate	1.13%
Mismatches	73,274,659
Insertions	1,112,765
Mapped reads with at least one insertion	2.07%
Deletions	2,265,759
Mapped reads with at least one deletion	4.33%
Homopolymer indels	45.72%

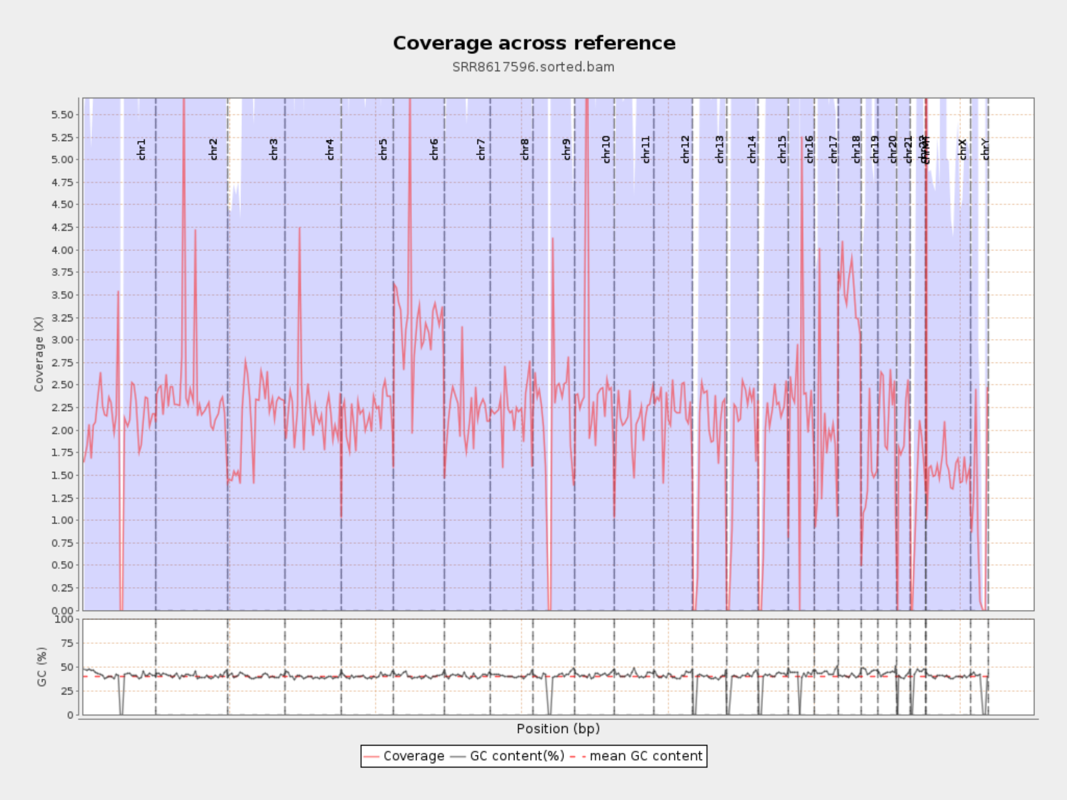
2.7. Chromosome stats

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

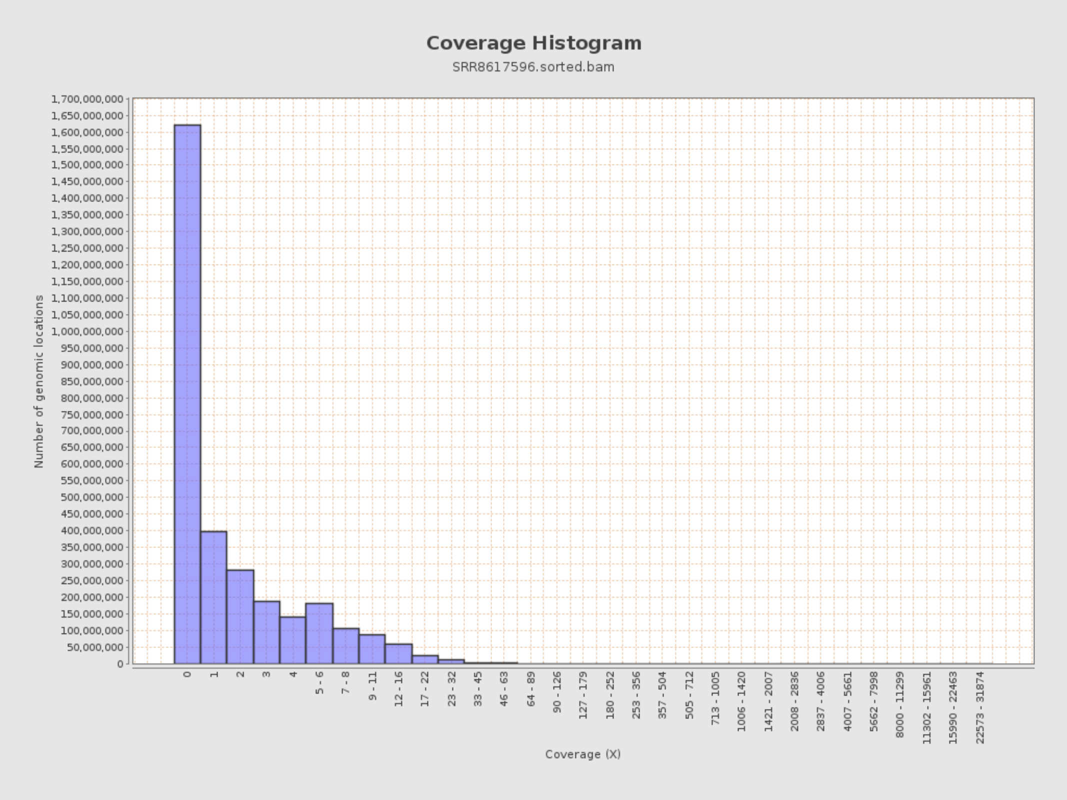
		bases	coverage	deviation
chr1	249250621	512700835	2.057	23.3129
chr2	243199373	603106110	2.4799	29.035
chr3	198022430	419542675	2.1187	3.8603
chr4	191154276	427205582	2.2349	16.5889
chr5	180915260	390940985	2.1609	4.3839
chr6	171115067	557345833	3.2571	31.2177
chr7	159138663	348206282	2.1881	24.3657
chr8	146364022	324448307	2.2167	7.0867
chr9	141213431	299867115	2.1235	46.8413
chr10	135534747	347499869	2.5639	39.602
chr11	135006516	284493988	2.1073	17.6521
chr12	133851895	298535295	2.2303	7.9053
chr13	115169878	206905587	1.7965	3.5632
chr14	107349540	202454093	1.8859	4.4485
chr15	102531392	187001121	1.8238	4.6556
chr16	90354753	210378210	2.3284	26.7025
chr17	81195210	152452677	1.8776	34.2083
chr18	78077248	278105519	3.5619	37.0837
chr19	59128983	87262233	1.4758	13.0779
chr20	63025520	142343105	2.2585	6.1272
chr21	48129895	87212624	1.812	8.8653
chr22	51304566	63852628	1.2446	3.6847
chrMT	16571	1400816	84.5342	51.6153
chrX	155270560	239716901	1.5439	6.6251

chrY	59373566	59937500	1.0095	26.738

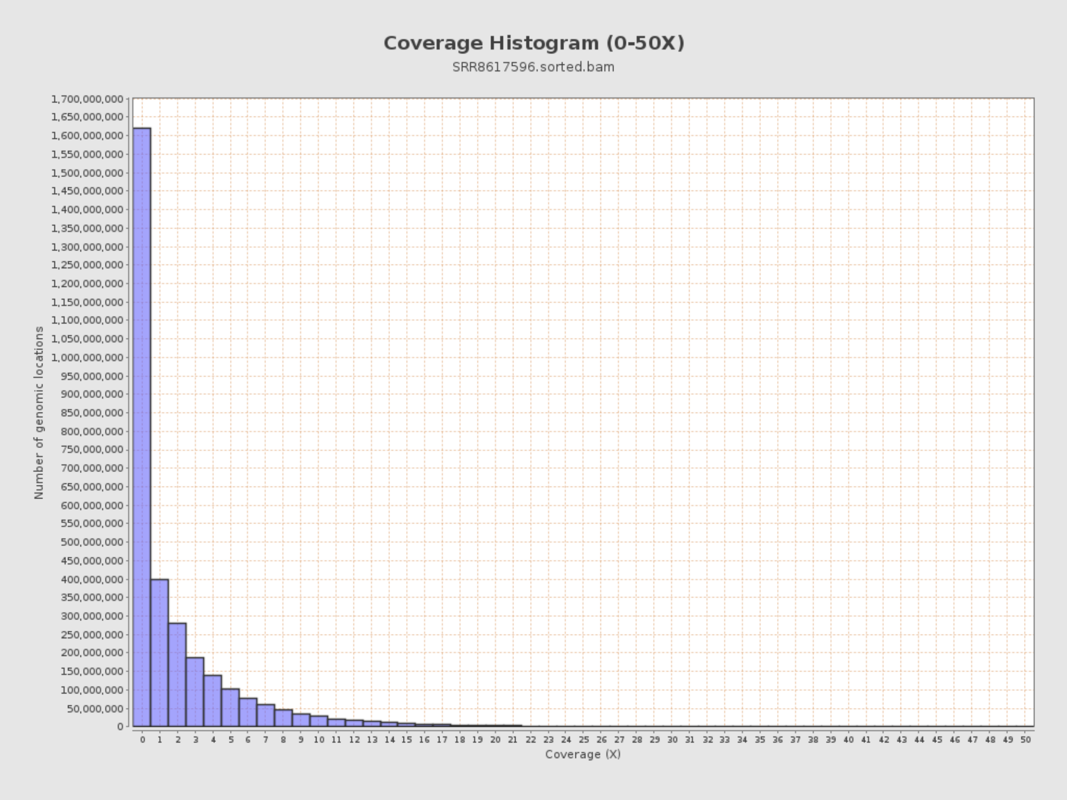
3. Results : Coverage across reference



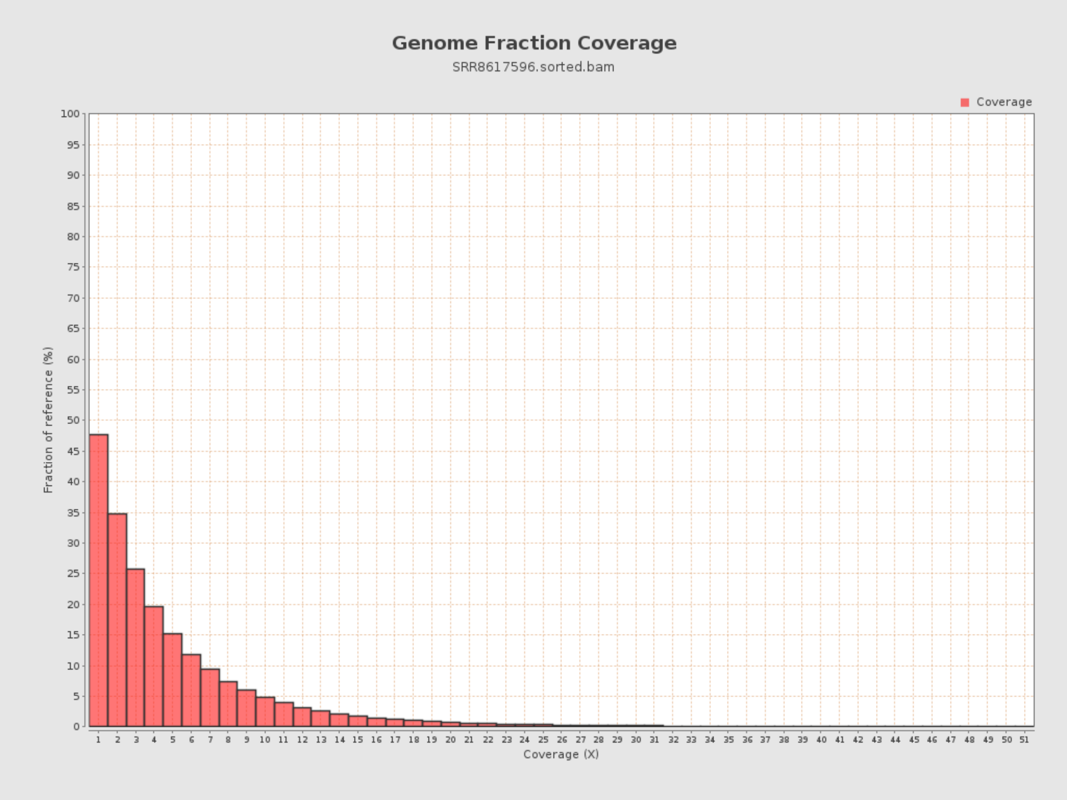
4. Results : Coverage Histogram



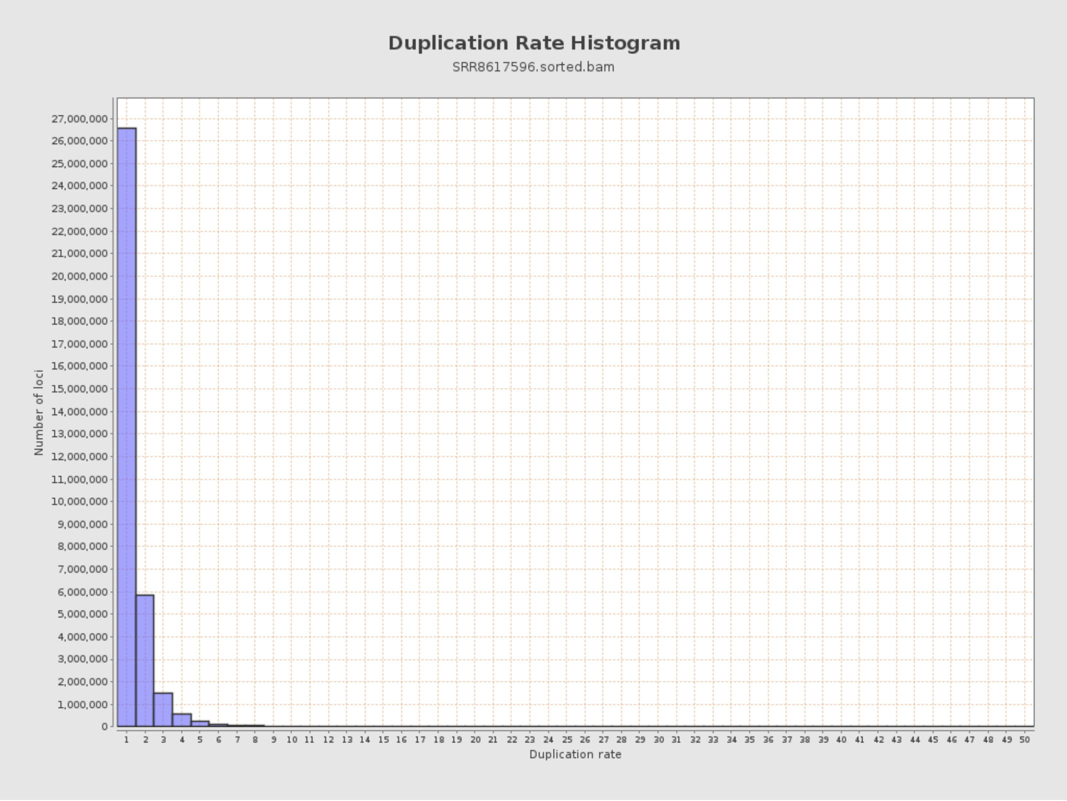
5. Results : Coverage Histogram (0-50X)



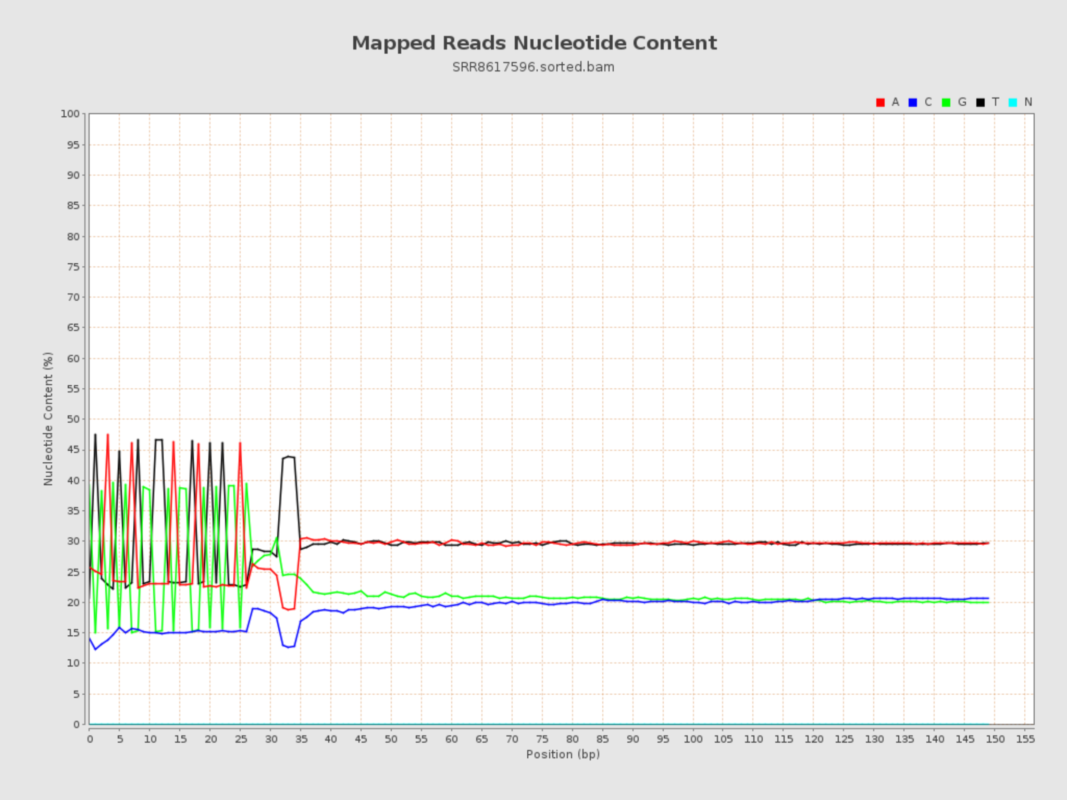
6. Results : Genome Fraction Coverage



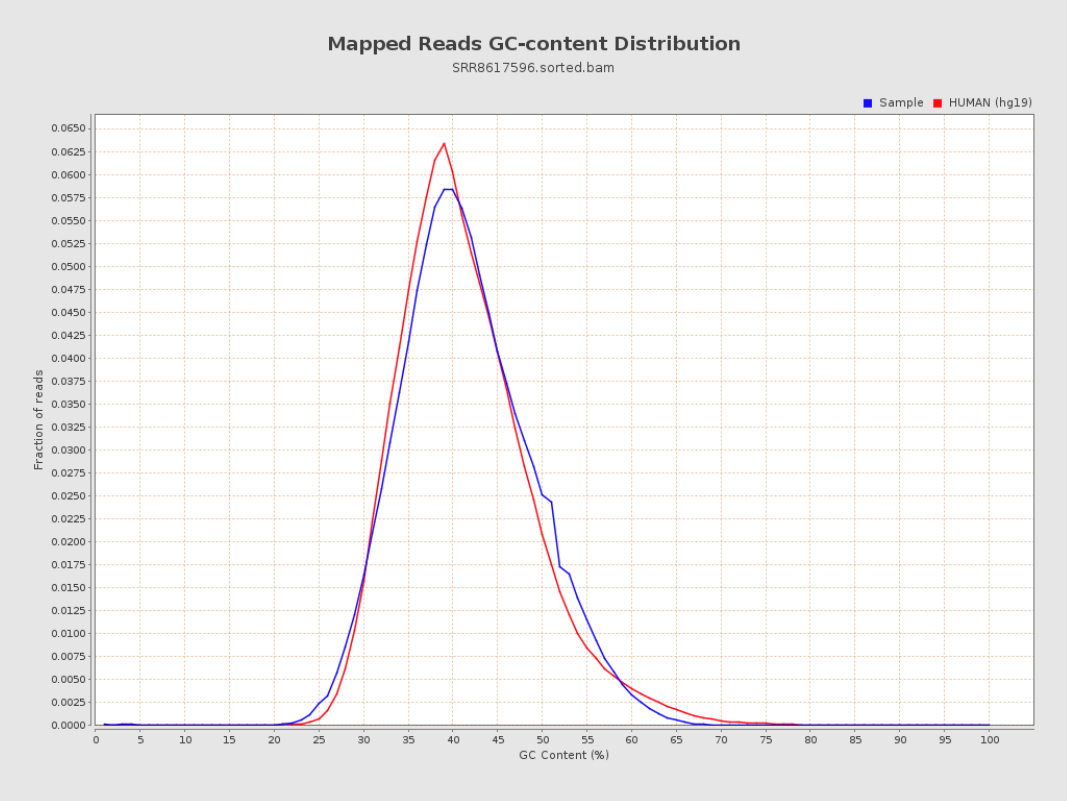
7. Results : Duplication Rate Histogram



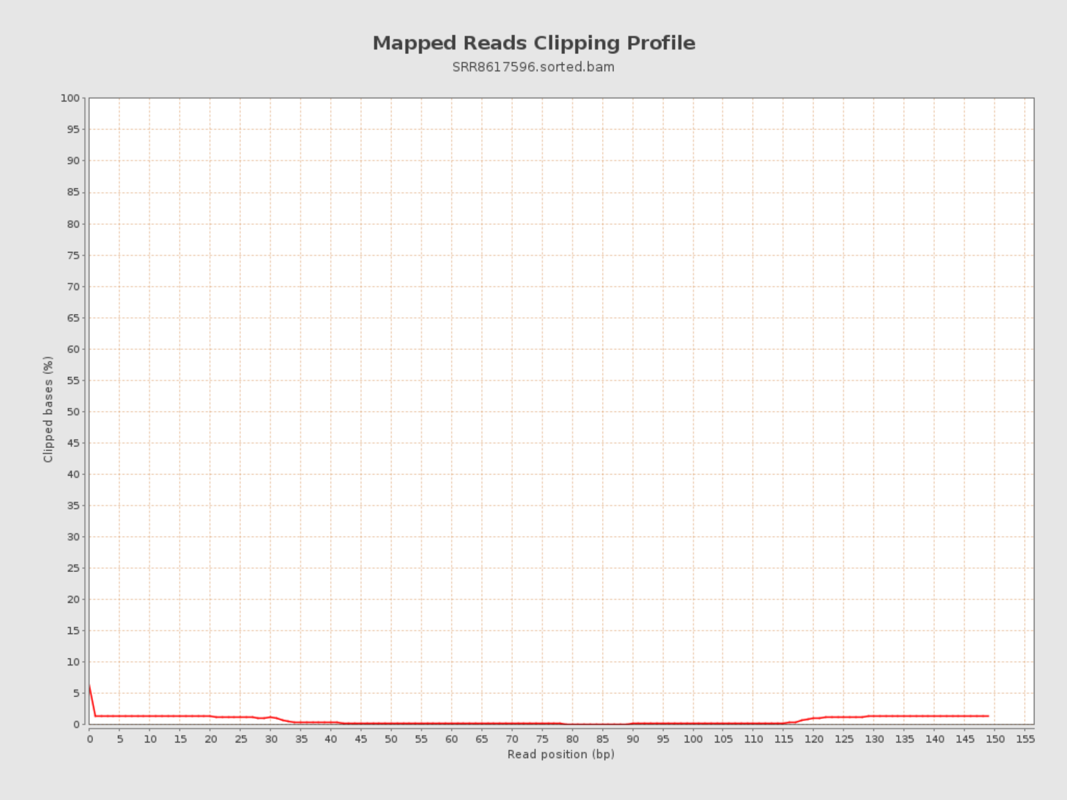
8. Results : Mapped Reads Nucleotide Content



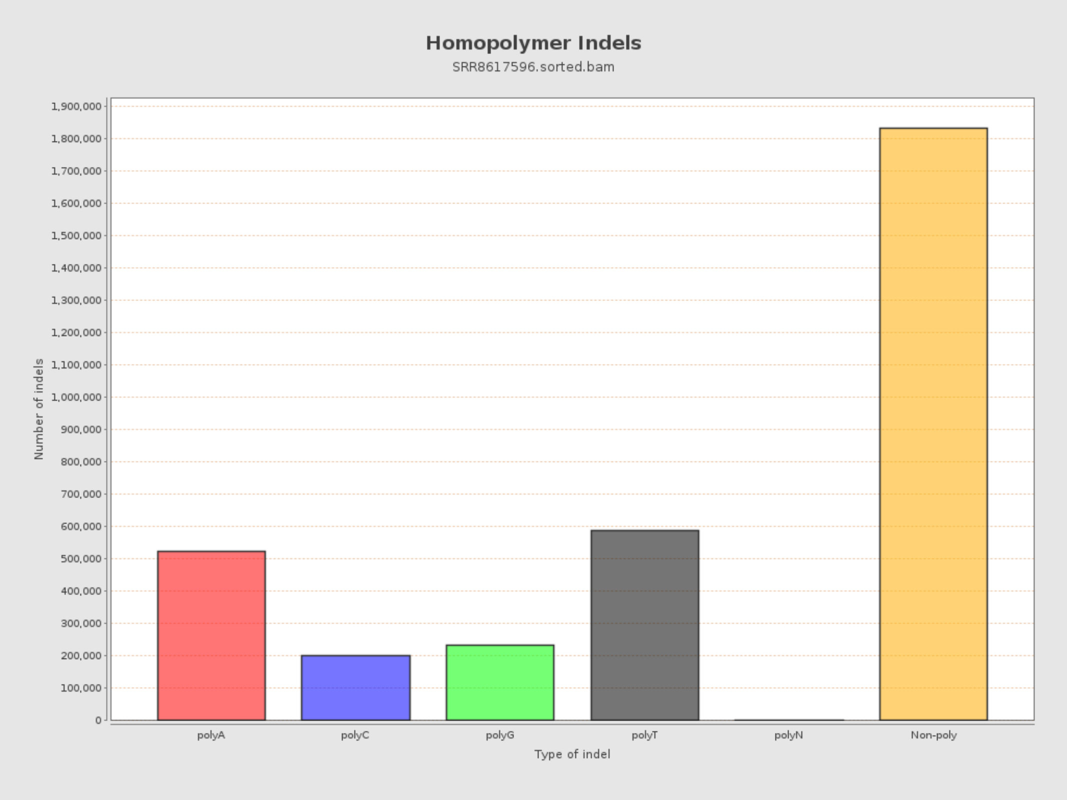
9. Results : Mapped Reads GC-content Distribution



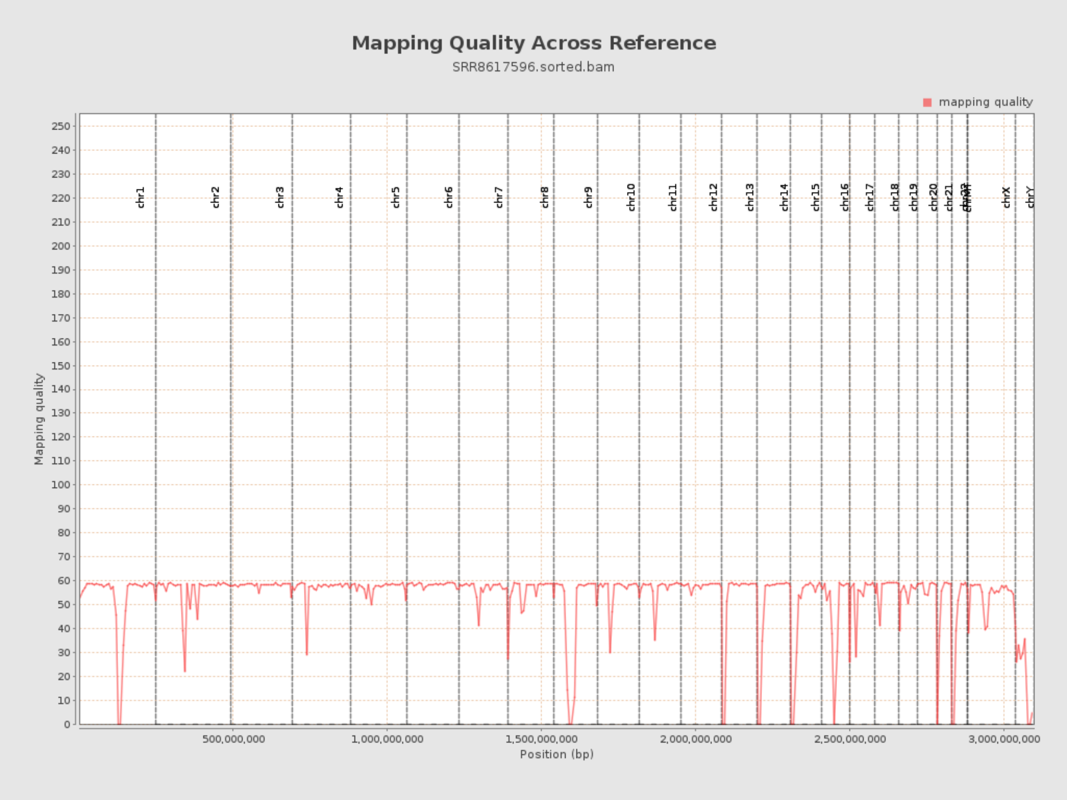
10. Results : Mapped Reads Clipping Profile



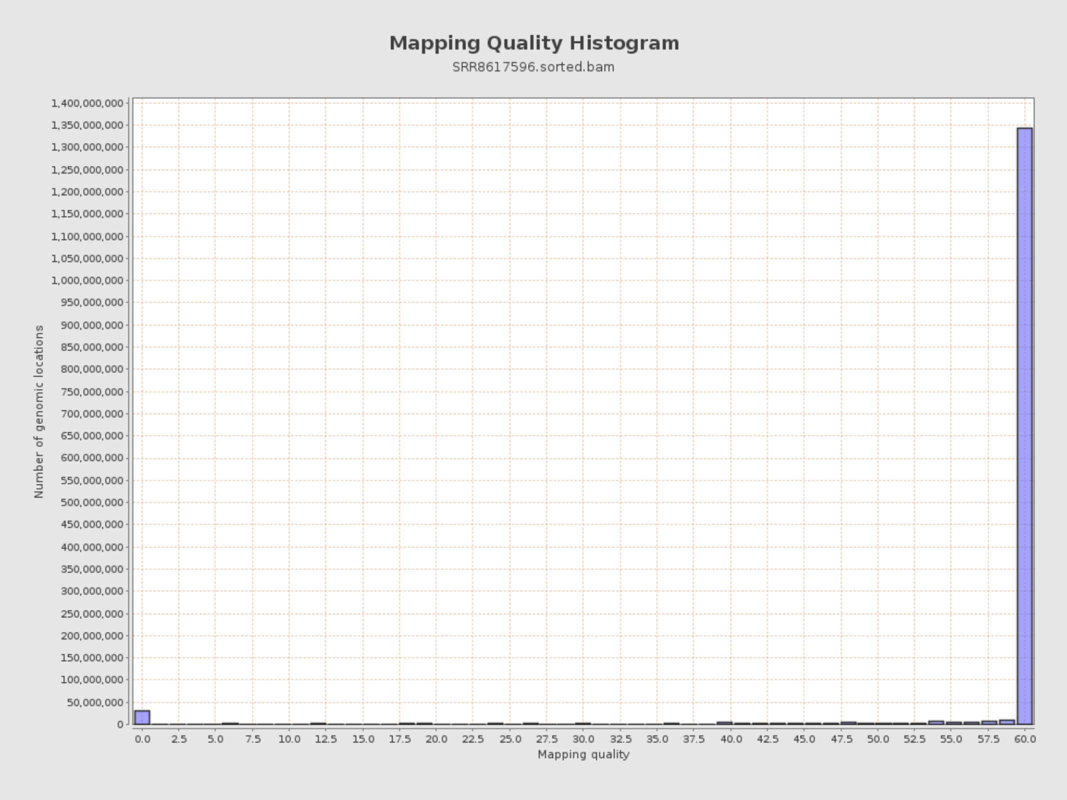
11. Results : Homopolymer Indels



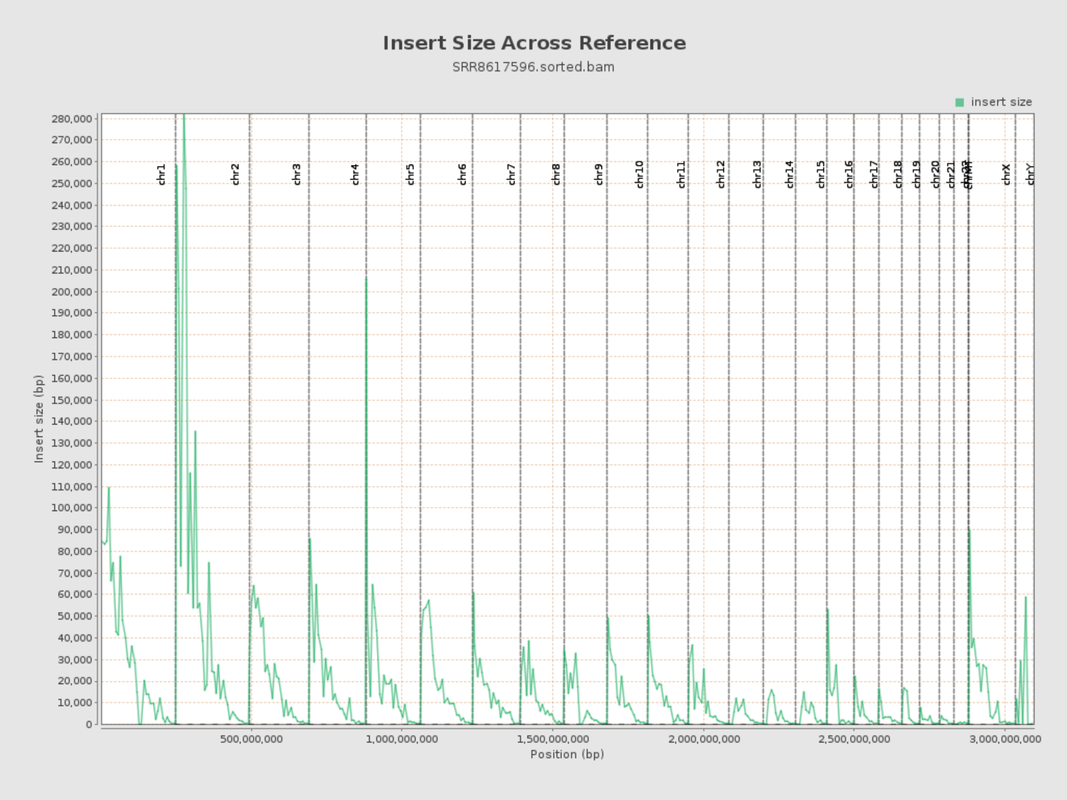
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram