Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/26 10:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504617.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_SRR504617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504617_1.fastq.gz SRR504617_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 26 10:13:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	296,464,732
Mapped reads	281,303,115 / 94.89%
Unmapped reads	15,161,617 / 5.11%
Mapped paired reads	281,303,115 / 94.89%
Mapped reads, first in pair	141,097,767 / 47.59%
Mapped reads, second in pair	140,205,348 / 47.29%
Mapped reads, both in pair	277,130,178 / 93.48%
Mapped reads, singletons	4,172,937 / 1.41%
Secondary alignments	0
Supplementary alignments	3,056,532 / 1.03%
Read min/max/mean length	30 / 100 / 100.42
Duplicated reads (estimated)	83,264,341 / 28.09%
Duplication rate	18.13%
Clipped reads	41,202,536 / 13.9%

2.2. ACGT Content

Number/percentage of A's	7,222,822,796 / 26.66%
Number/percentage of C's	6,279,493,800 / 23.18%
Number/percentage of T's	7,299,121,706 / 26.94%
Number/percentage of G's	6,287,536,427 / 23.21%
Number/percentage of N's	4,119,540 / 0.02%

GC Percentage	46.38%

2.3. Coverage

Mean	8.7601
Standard Deviation	216.1613

2.4. Mapping Quality

Mean Mapping Quality	52.34

2.5. Insert size

Mean	115,612.17
Standard Deviation	3,204,011.85
P25/Median/P75	283 / 337 / 395

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	271,016,325
Insertions	8,255,629
Mapped reads with at least one insertion	2.71%
Deletions	7,702,597
Mapped reads with at least one deletion	2.55%
Homopolymer indels	34.56%

2.7. Chromosome stats

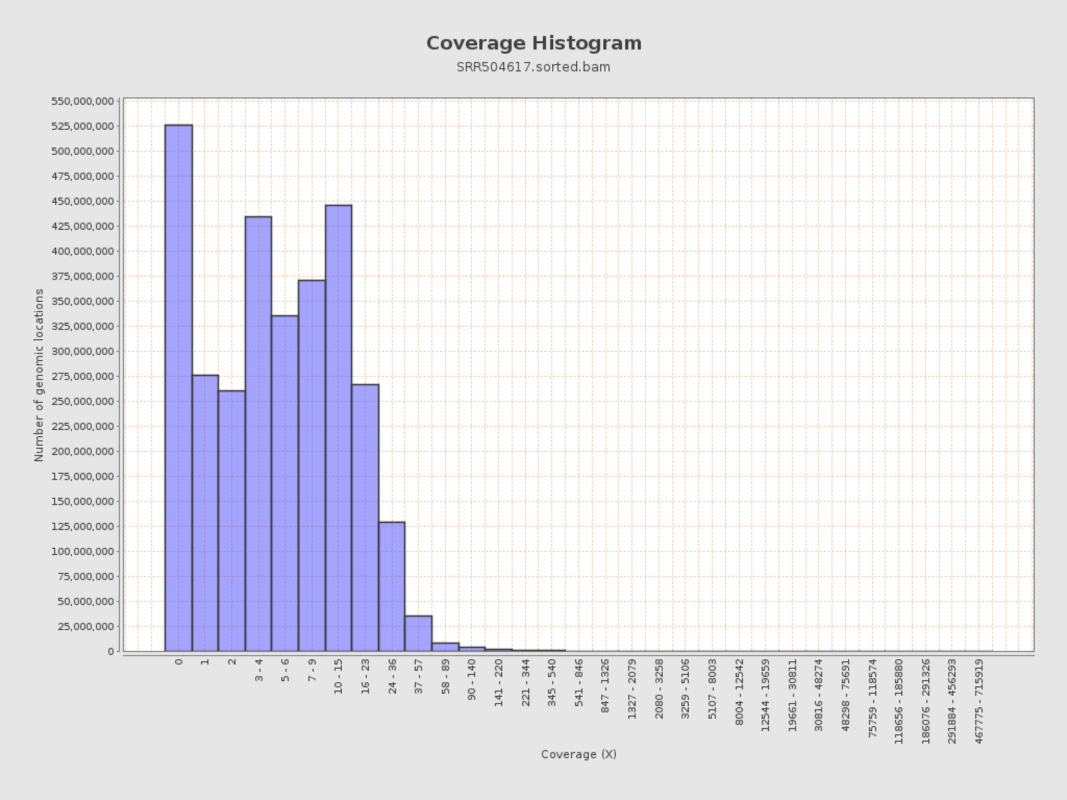
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	2091277191	8.3903	61.4726
chr2	243199373	2149760560	8.8395	229.5676
chr3	198022430	1439299506	7.2684	19.6706
chr4	191154276	2027767661	10.608	606.7651
chr5	180915260	1403435176	7.7574	32.6868
chr6	171115067	1155141293	6.7507	30.2773
chr7	159138663	1333089500	8.3769	32.5858
chr8	146364022	1266907513	8.6559	151.1121
chr9	141213431	990610175	7.015	64.7607
chr10	135534747	1777356389	13.1137	459.8472
chr11	135006516	1163359703	8.6171	27.2709
chr12	133851895	1082243605	8.0854	16.5893
chr13	115169878	600415541	5.2133	13.3018
chr14	107349540	723374092	6.7385	29.3762
chr15	102531392	792448911	7.7288	14.1204
chr16	90354753	1226135561	13.5702	177.6682
chr17	81195210	940412275	11.5821	64.2778
chr18	78077248	616157683	7.8916	250.1263
chr19	59128983	919135190	15.5446	37.3037
chr20	63025520	696924018	11.0578	143.6317
chr21	48129895	452530036	9.4023	192.3272
chr22	51304566	507834780	9.8984	29.022
chrMT	16571	10525596	635.1817	281.6236
chrX	155270560	1318249805	8.49	18.662

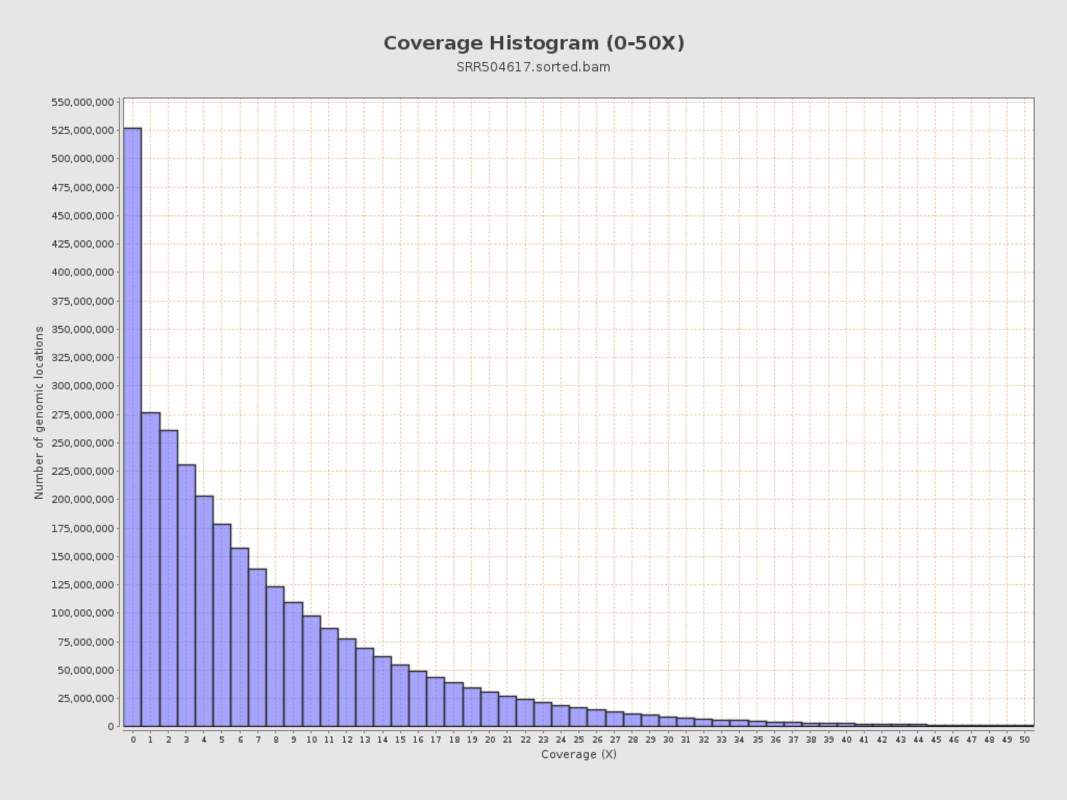
chrY	59373566	434079700	7.311	514.2109

3. Results : Coverage across reference

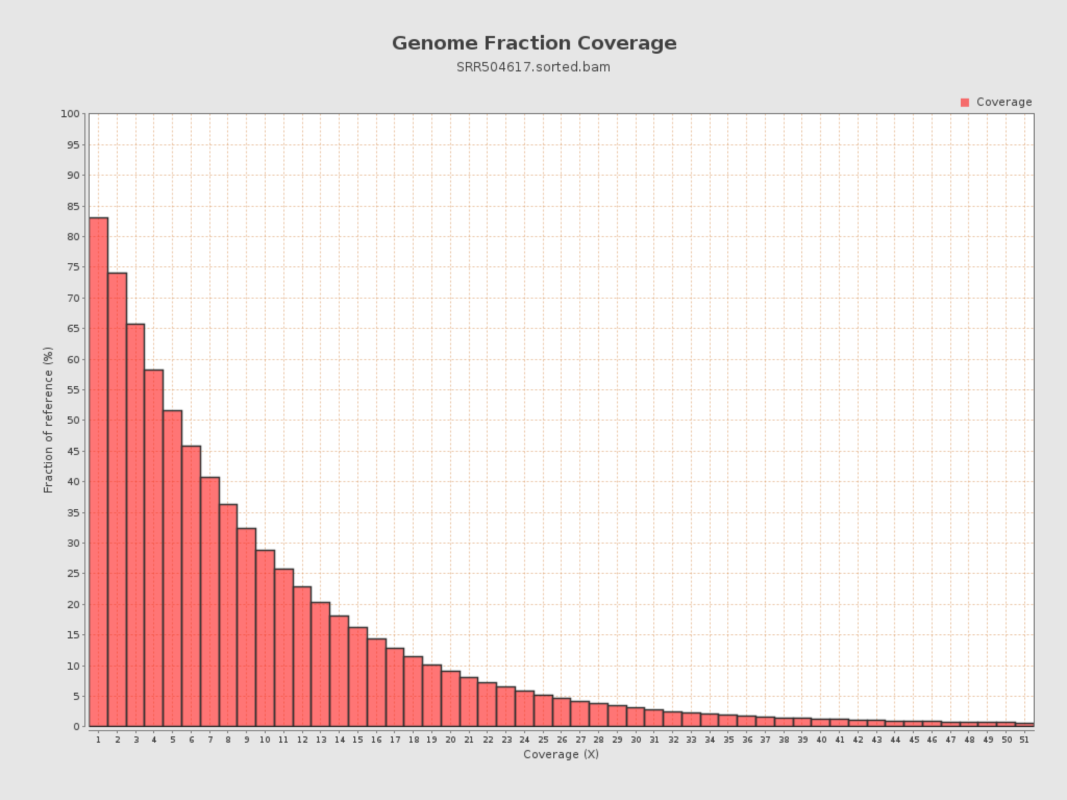
4. Results : Coverage Histogram



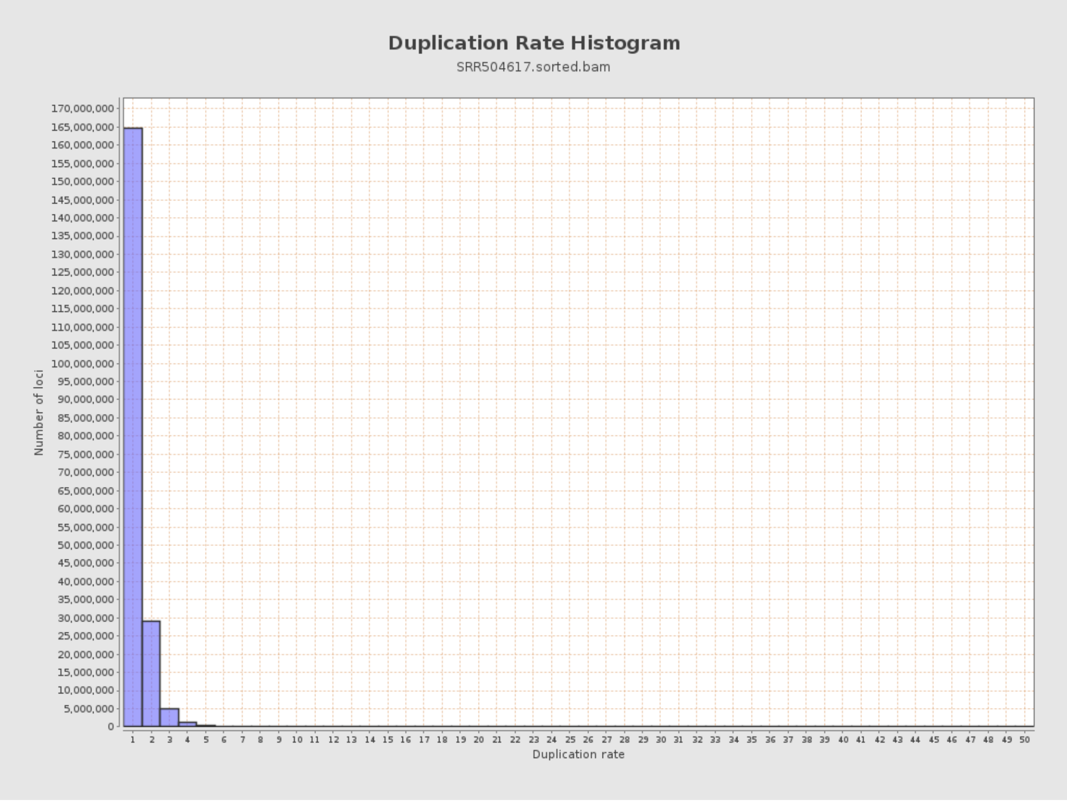
5. Results : Coverage Histogram (0-50X)



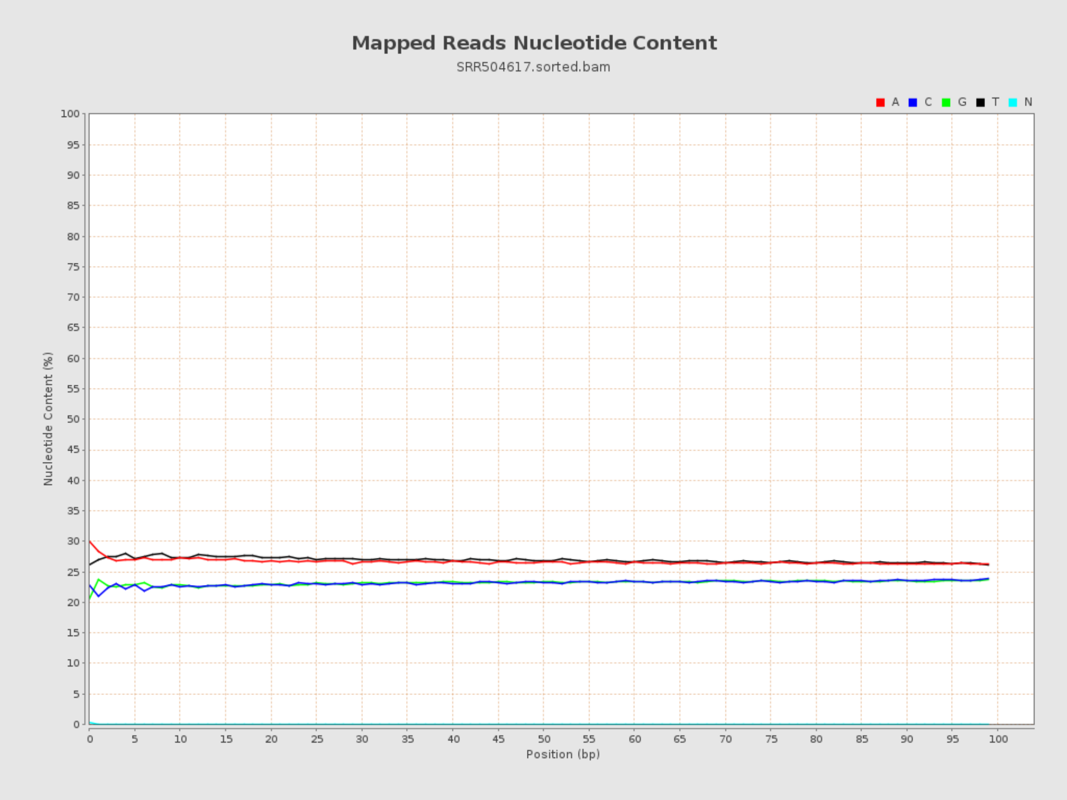
6. Results : Genome Fraction Coverage



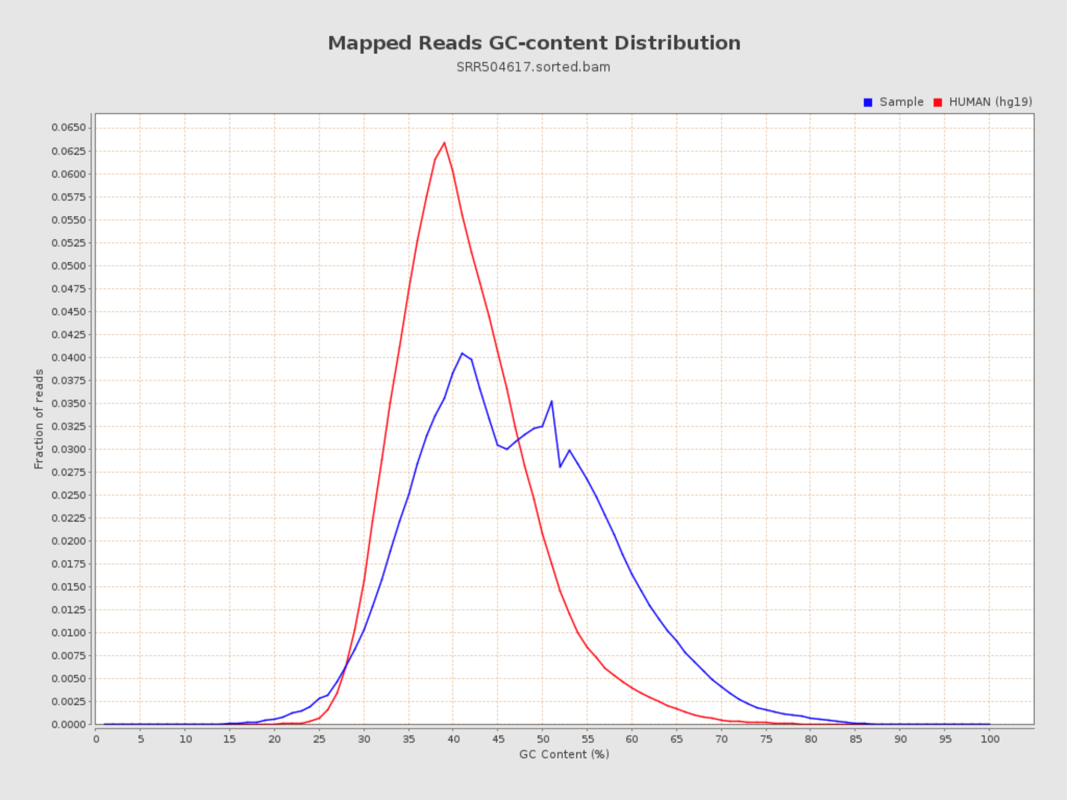
7. Results : Duplication Rate Histogram



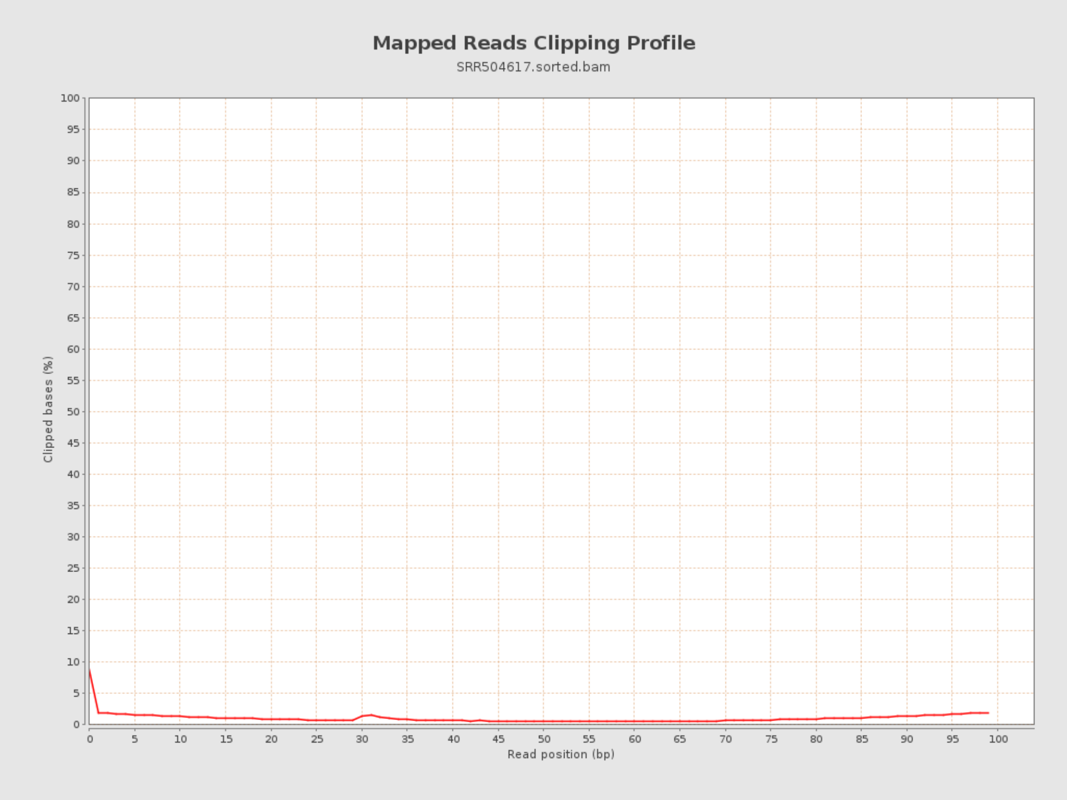
8. Results : Mapped Reads Nucleotide Content



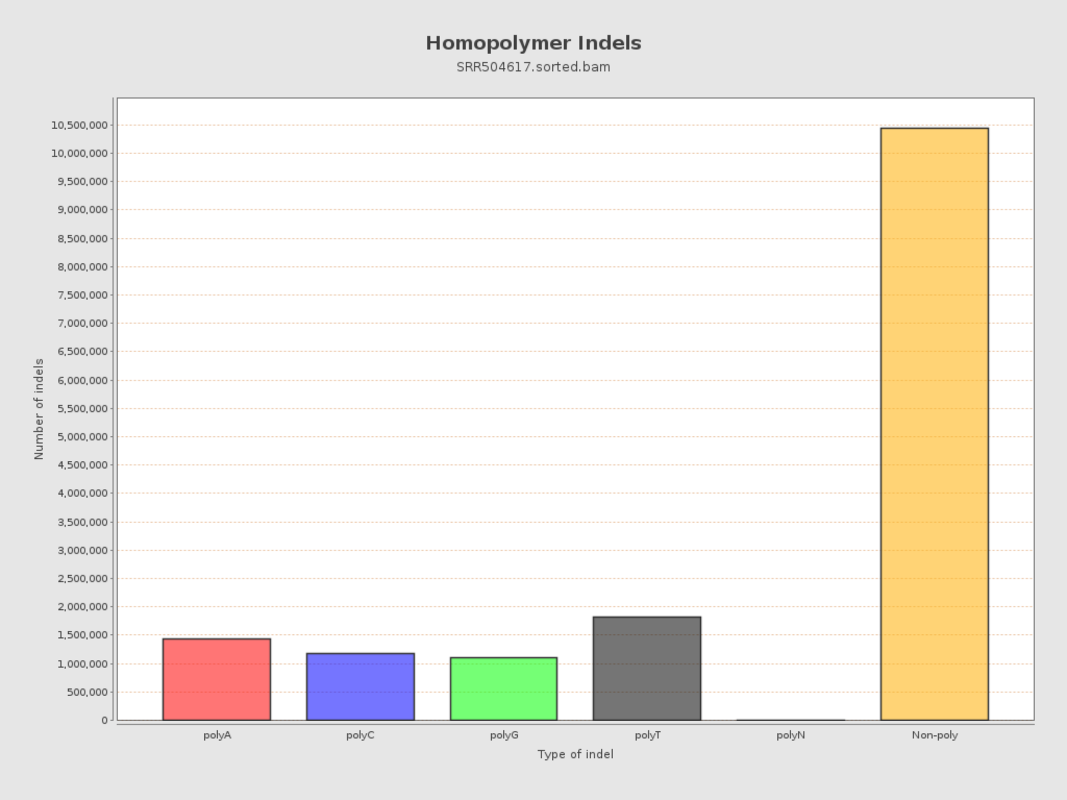
9. Results : Mapped Reads GC-content Distribution



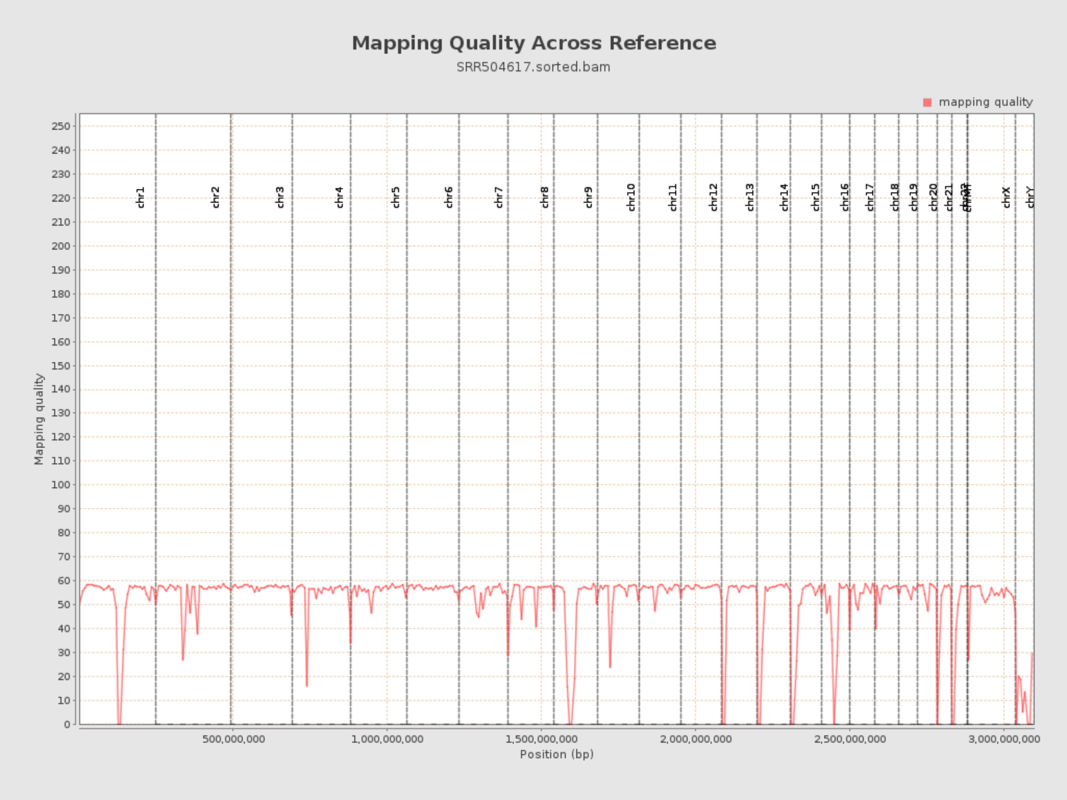
10. Results : Mapped Reads Clipping Profile



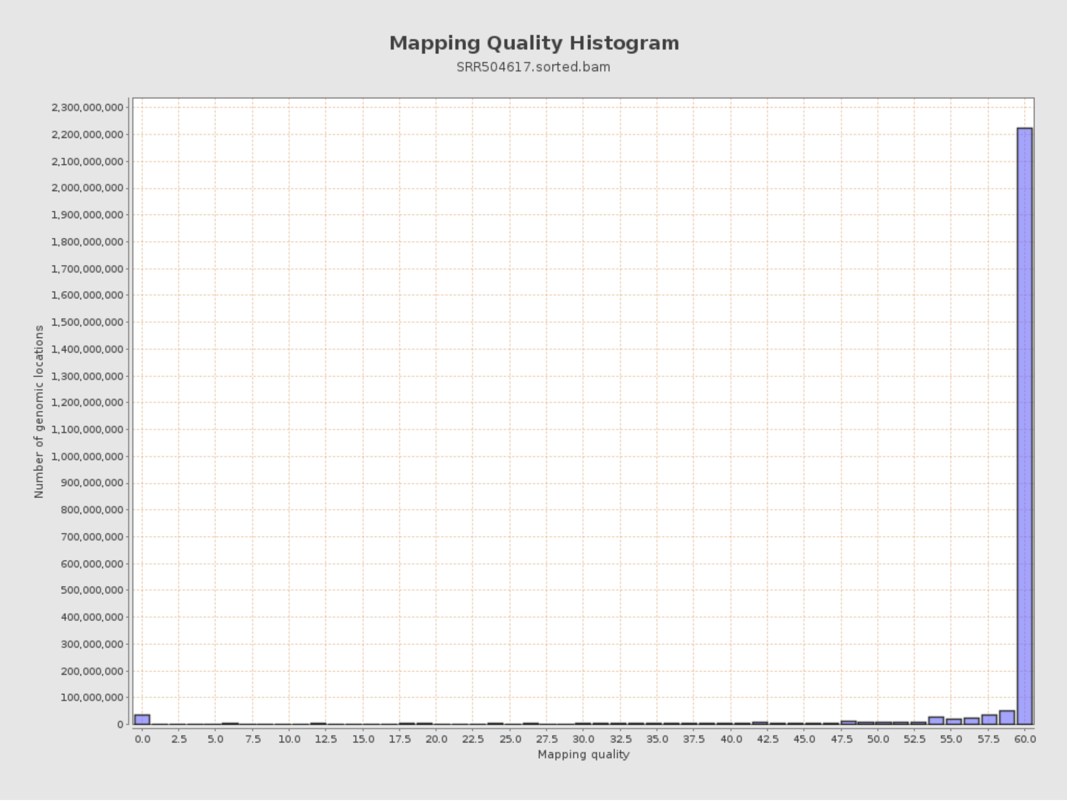
11. Results : Homopolymer Indels



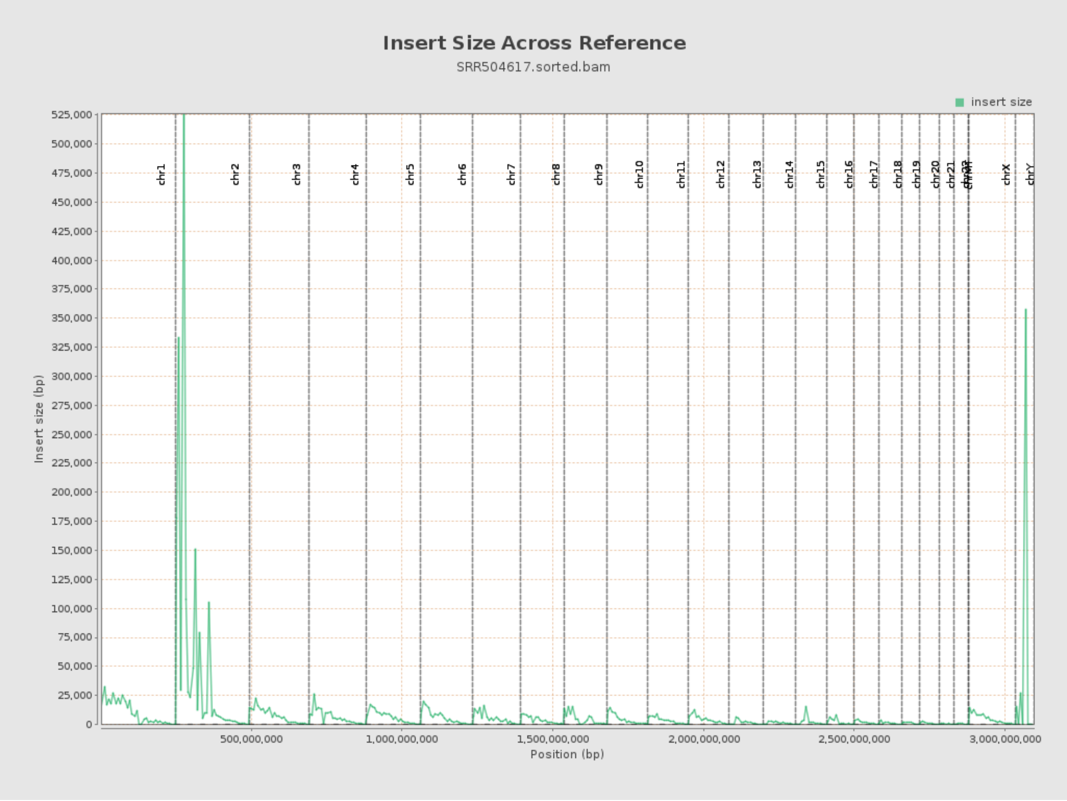
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram