Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/30 01:52:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504627.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_SRR504627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504627_1.fastq.gz SRR504627_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 30 01:52:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	304,888,020
Mapped reads	283,941,383 / 93.13%
Unmapped reads	20,946,637 / 6.87%
Mapped paired reads	283,941,383 / 93.13%
Mapped reads, first in pair	143,840,963 / 47.18%
Mapped reads, second in pair	140,100,420 / 45.95%
Mapped reads, both in pair	276,327,398 / 90.63%
Mapped reads, singletons	7,613,985 / 2.5%
Secondary alignments	0
Supplementary alignments	2,814,021 / 0.92%
Read min/max/mean length	30 / 100 / 100.37
Duplicated reads (estimated)	81,770,343 / 26.82%
Duplication rate	16.06%
Clipped reads	50,983,599 / 16.72%

2.2. ACGT Content

Number/percentage of A's	7,257,438,215 / 26.79%
Number/percentage of C's	6,228,049,267 / 22.99%
Number/percentage of T's	7,315,484,483 / 27.01%
Number/percentage of G's	6,282,595,957 / 23.19%
Number/percentage of N's	4,539,300 / 0.02%

GC Percentage	46.19%

2.3. Coverage

Mean	8.7586
Standard Deviation	206.6161

2.4. Mapping Quality

Mean Mapping Quality	52.05

2.5. Insert size

Mean	113,612.96
Standard Deviation	3,143,701.73
P25/Median/P75	319 / 366 / 423

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	336,956,689
Insertions	8,003,994
Mapped reads with at least one insertion	2.61%
Deletions	7,730,623
Mapped reads with at least one deletion	2.53%
Homopolymer indels	33.59%

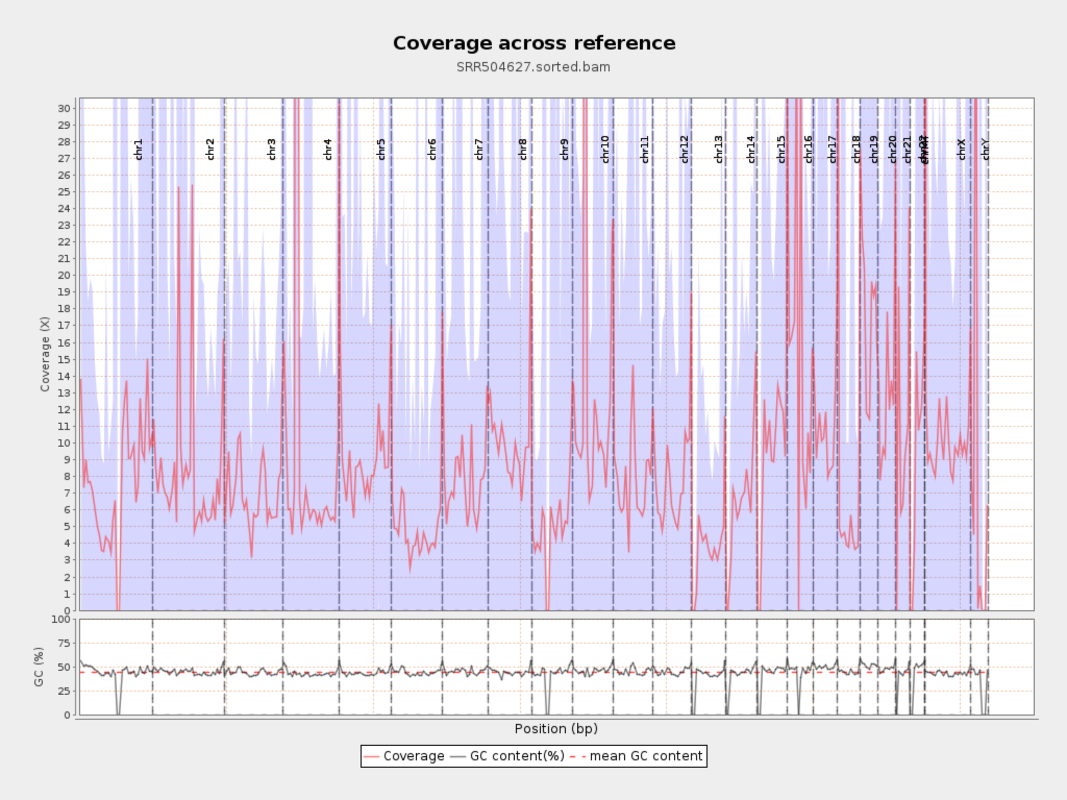
2.7. Chromosome stats

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

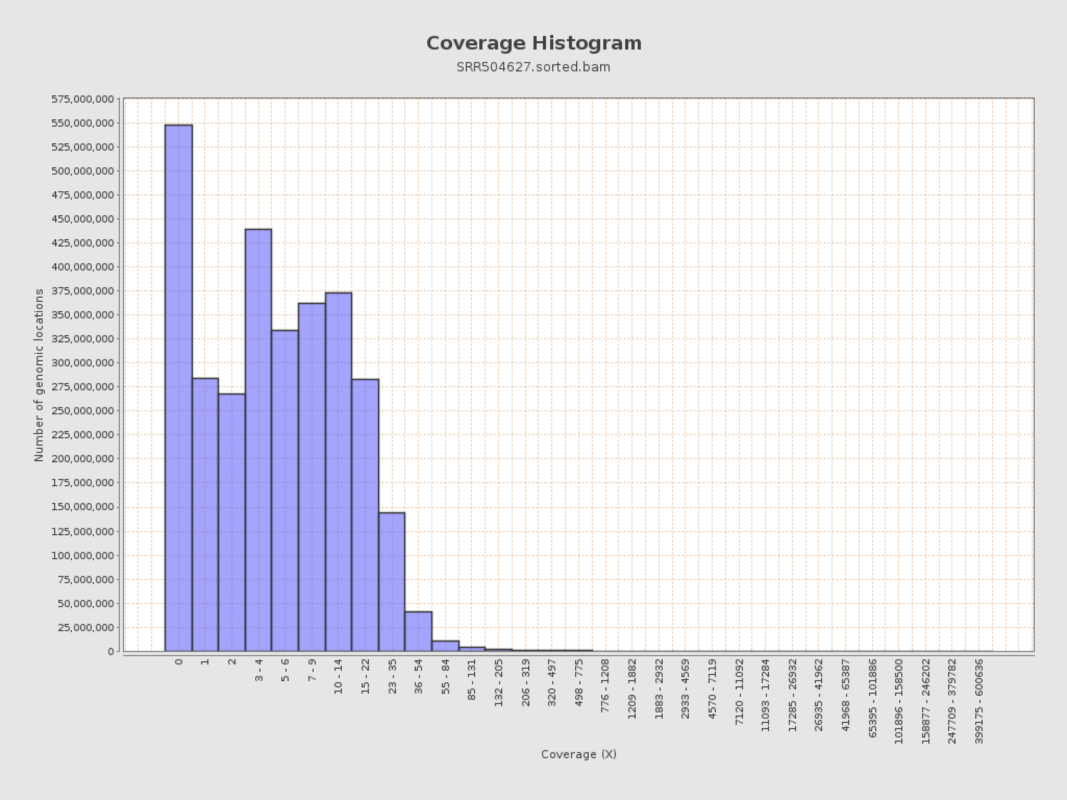
		bases	coverage	deviation
chr1	249250621	1908110515	7.6554	60.3213
chr2	243199373	2066541914	8.4973	238.4375
chr3	198022430	1373007078	6.9336	23.373
chr4	191154276	1957472727	10.2403	531.9002
chr5	180915260	1656057648	9.1538	33.8651
chr6	171115067	793512438	4.6373	25.9549
chr7	159138663	1269642769	7.9782	34.4127
chr8	146364022	1491661312	10.1914	139.003
chr9	141213431	707175136	5.0078	75.0011
chr10	135534747	2026797932	14.9541	475.9649
chr11	135006516	1098469892	8.1364	25.3603
chr12	133851895	1019705919	7.6182	19.9482
chr13	115169878	411405729	3.5722	11.4178
chr14	107349540	694353232	6.4682	30.0096
chr15	102531392	927679100	9.0478	16.8639
chr16	90354753	1453579286	16.0875	202.5924
chr17	81195210	885272297	10.903	72.4754
chr18	78077248	458628693	5.874	278.155
chr19	59128983	1069406287	18.086	40.9245
chr20	63025520	800899358	12.7075	130.0937
chr21	48129895	519199941	10.7875	169.7638
chr22	51304566	484011192	9.4341	30.3015
chrMT	16571	9415047	568.1641	255.8789
chrX	155270560	1545450905	9.9533	21.3727

chrY	59373566	486370681	8.1917	506.5231

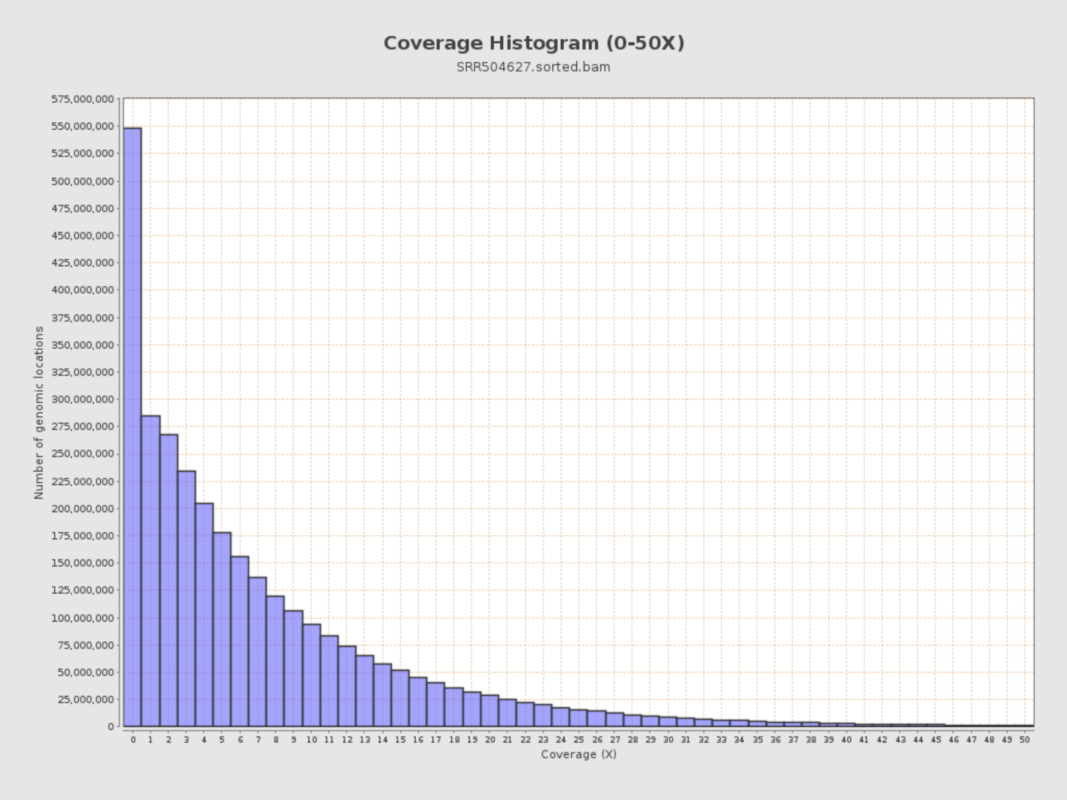
3. Results : Coverage across reference



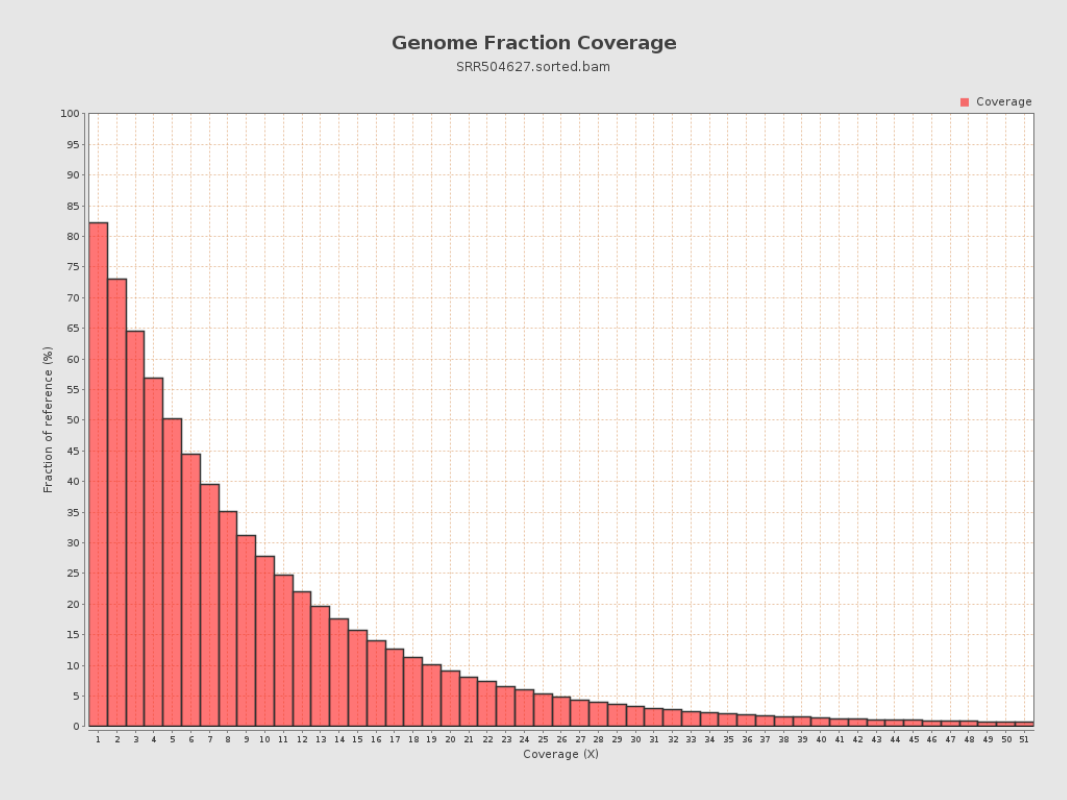
4. Results : Coverage Histogram



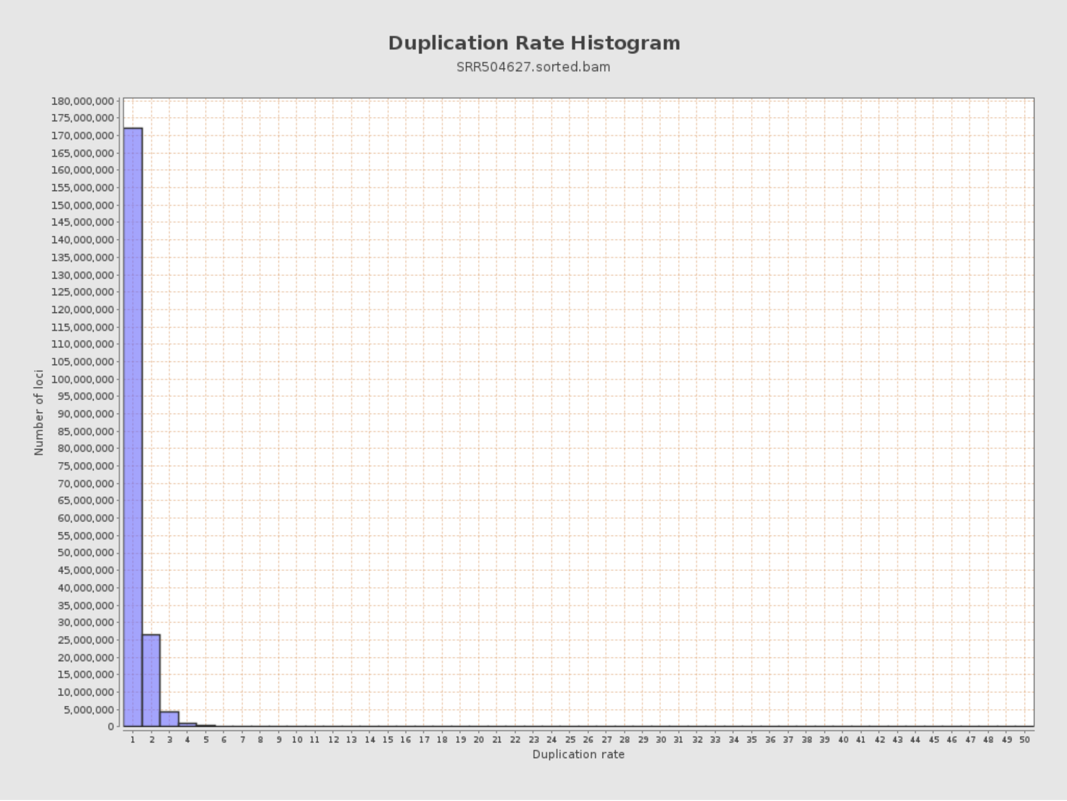
5. Results : Coverage Histogram (0-50X)



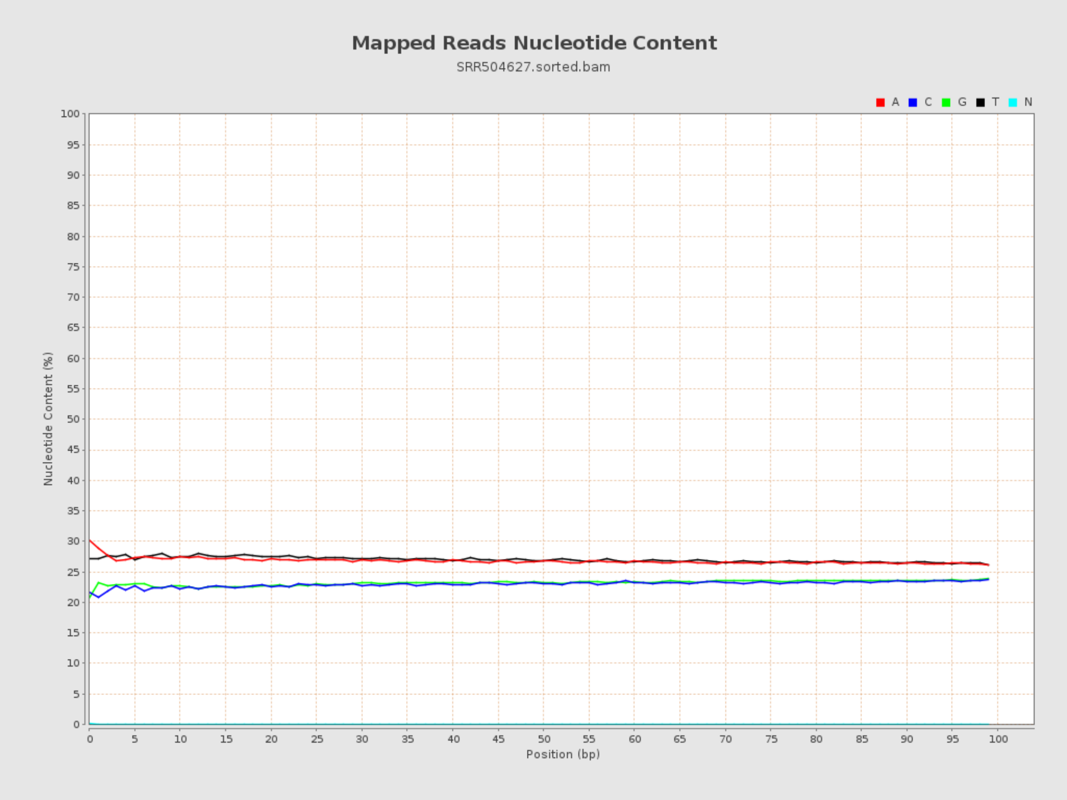
6. Results : Genome Fraction Coverage



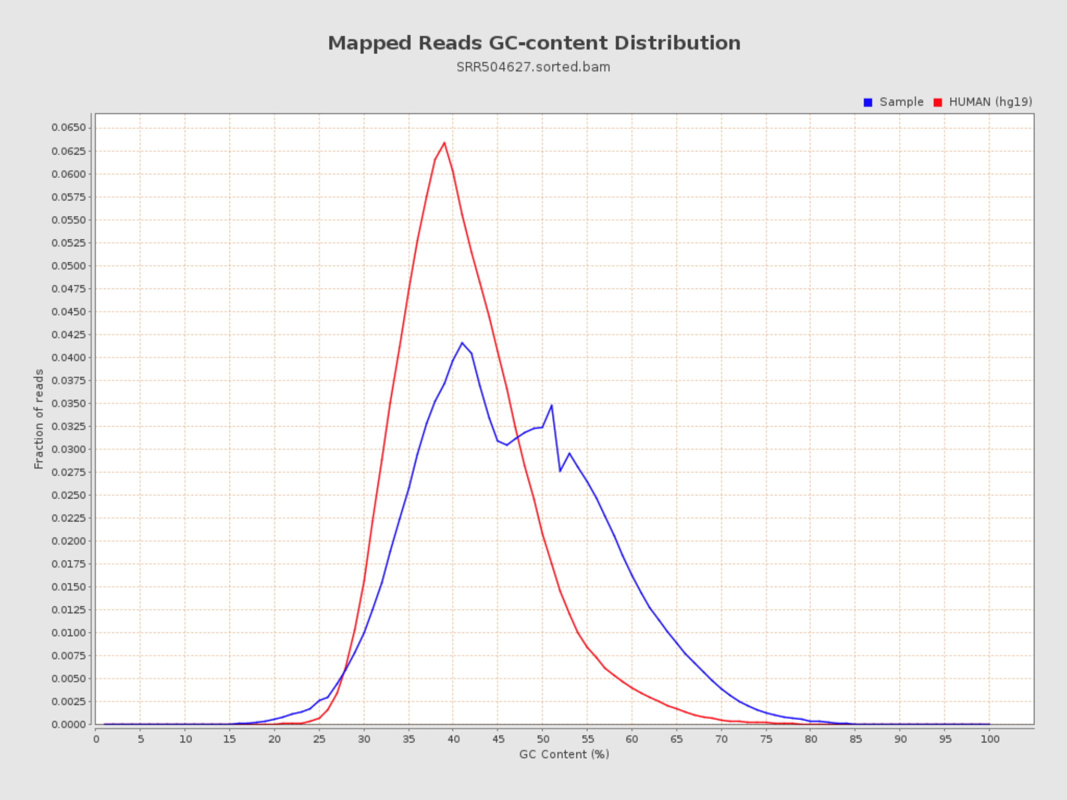
7. Results : Duplication Rate Histogram



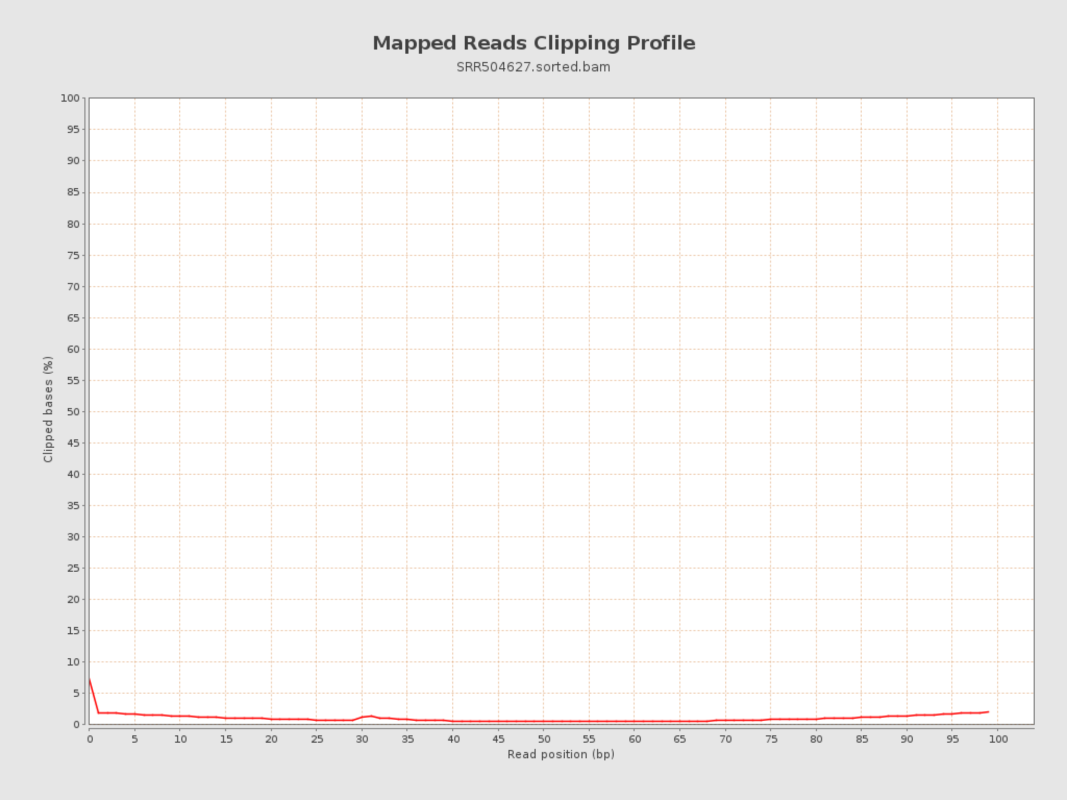
8. Results : Mapped Reads Nucleotide Content



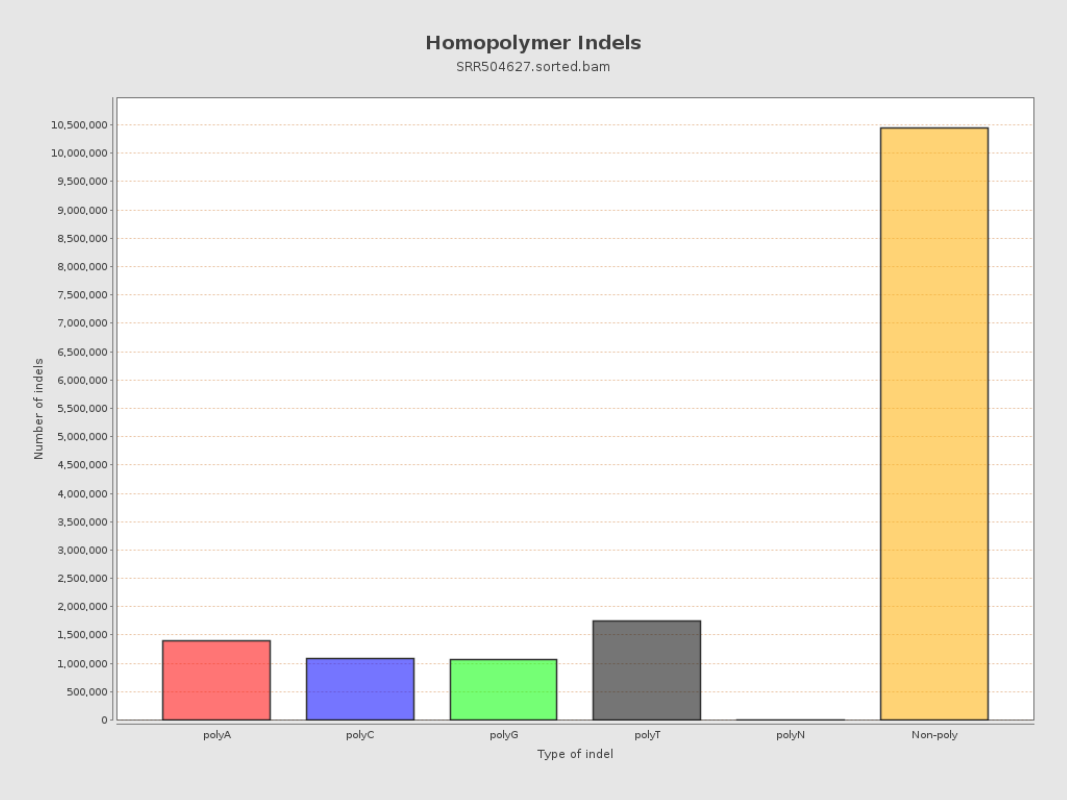
9. Results : Mapped Reads GC-content Distribution



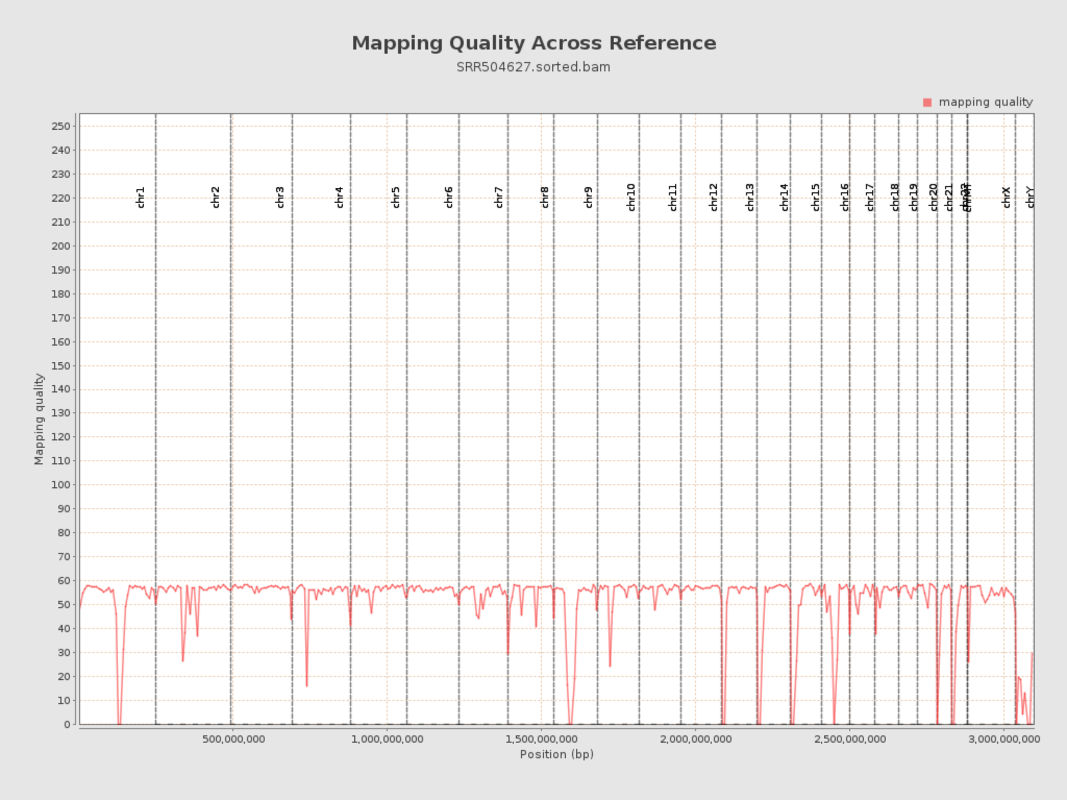
10. Results : Mapped Reads Clipping Profile



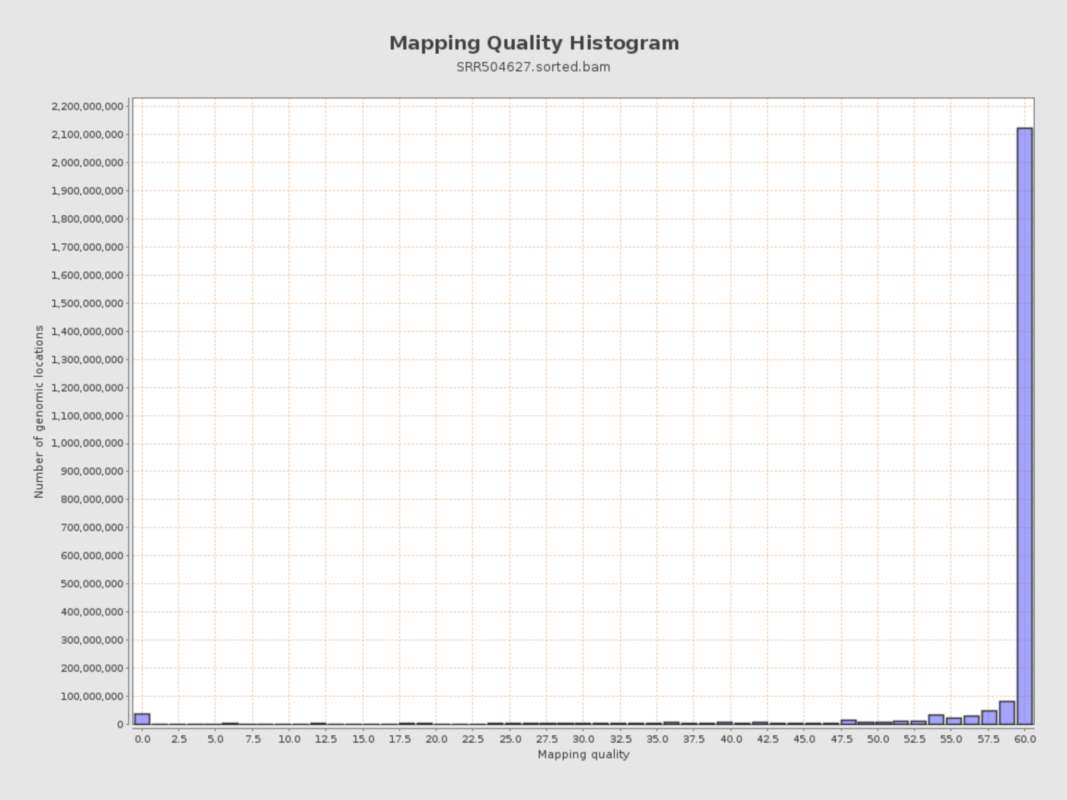
11. Results : Homopolymer Indels



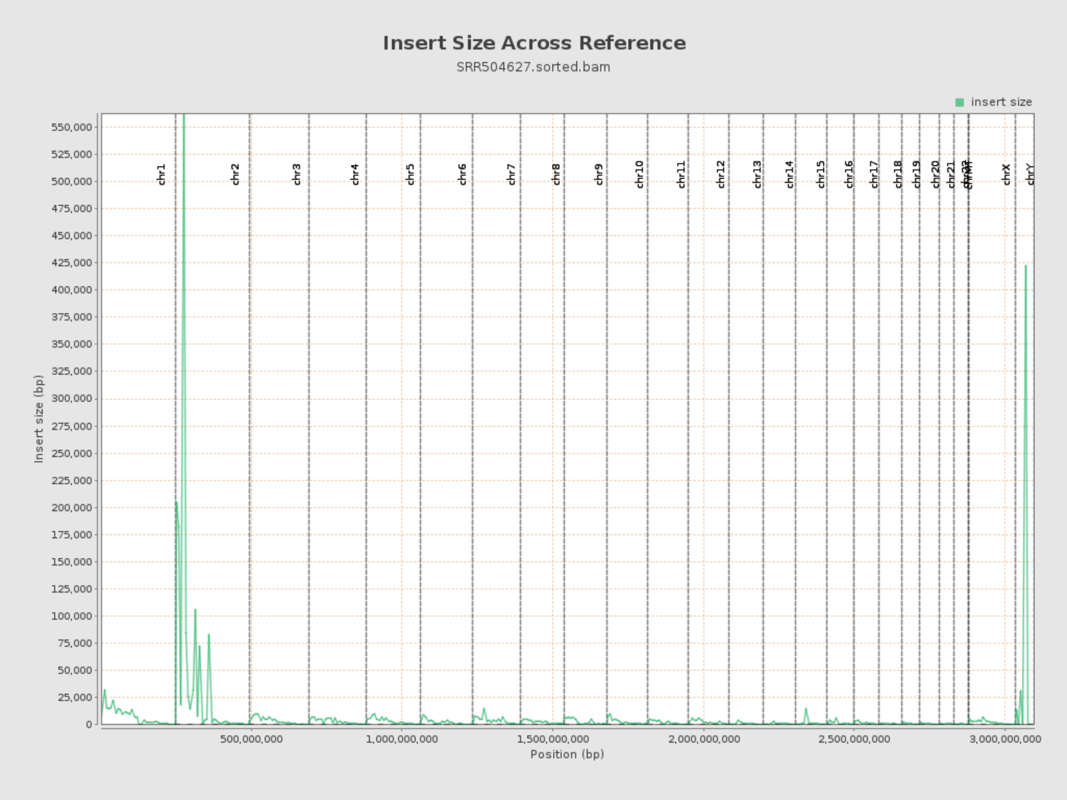
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram