Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 01:40:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504603.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_SRR504603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504603_1.fastq.gz SRR504603_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 01:40:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	443,087,182
Mapped reads	381,054,852 / 86%
Unmapped reads	62,032,330 / 14%
Mapped paired reads	381,054,852 / 86%
Mapped reads, first in pair	190,902,481 / 43.08%
Mapped reads, second in pair	190,152,371 / 42.92%
Mapped reads, both in pair	378,641,932 / 85.46%
Mapped reads, singletons	2,412,920 / 0.54%
Secondary alignments	0
Supplementary alignments	2,068,903 / 0.47%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	95,968,764 / 21.66%
Duplication rate	22.45%
Clipped reads	18,208,665 / 4.11%

2.2. ACGT Content

Number/percentage of A's	9,975,242,268 / 26.37%
Number/percentage of C's	8,834,050,722 / 23.35%
Number/percentage of T's	9,988,088,690 / 26.4%
Number/percentage of G's	8,997,755,411 / 23.79%
Number/percentage of N's	32,505,199 / 0.09%

GC Percentage	47.14%

2.3. Coverage

Mean	12.2226
Standard Deviation	25.3704

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	29,830.42
Standard Deviation	1,680,382.59
P25/Median/P75	180 / 213 / 267

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	247,554,208
Insertions	2,857,357
Mapped reads with at least one insertion	0.73%
Deletions	3,836,708
Mapped reads with at least one deletion	0.98%
Homopolymer indels	40.36%

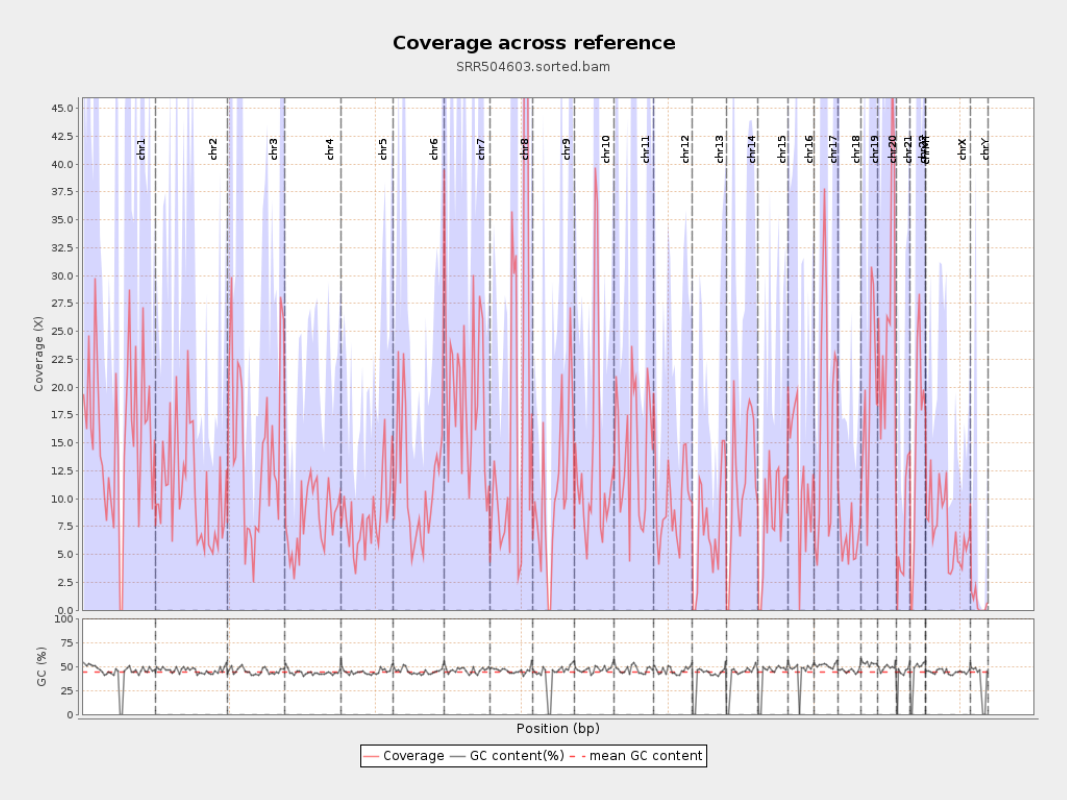
2.7. Chromosome stats

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

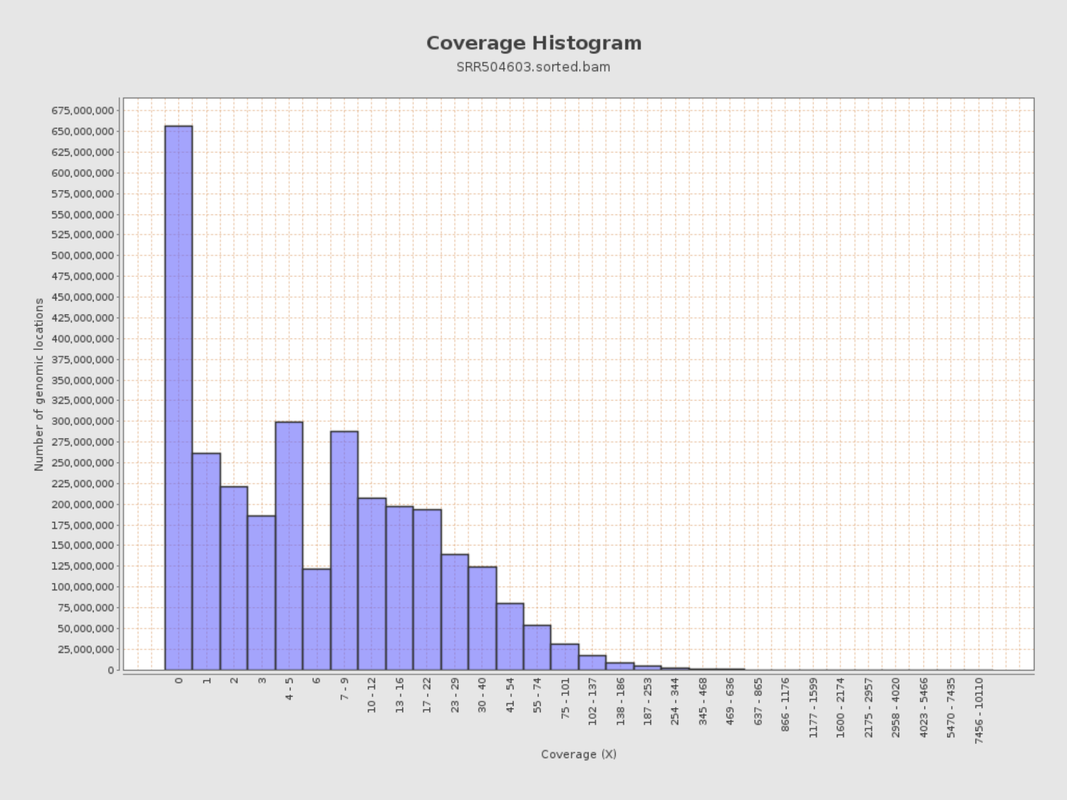
		bases	coverage	deviation
chr1	249250621	3889175550	15.6035	26.4004
chr2	243199373	2595502177	10.6723	19.3937
chr3	198022430	2799280218	14.1362	23.4653
chr4	191154276	1581892958	8.2755	13.1917
chr5	180915260	1538665962	8.5049	14.342
chr6	171115067	1933609343	11.3001	18.4974
chr7	159138663	3077585008	19.339	28.8603
chr8	146364022	2884749513	19.7094	48.5733
chr9	141213431	1487371437	10.5328	20.6096
chr10	135534747	1780322405	13.1355	24.9008
chr11	135006516	1930123703	14.2965	24.3058
chr12	133851895	1290822649	9.6437	16.3679
chr13	115169878	858662080	7.4556	14.0177
chr14	107349540	1263481820	11.7698	20.552
chr15	102531392	843500820	8.2268	15.3764
chr16	90354753	1105034645	12.23	21.0451
chr17	81195210	1374048783	16.9228	52.2565
chr18	78077248	494243960	6.3302	29.305
chr19	59128983	1116549117	18.8833	32.9081
chr20	63025520	1704728083	27.0482	40.4459
chr21	48129895	358238556	7.4432	18.9814
chr22	51304566	778659577	15.1772	28.2569
chrMT	16571	276215	16.6686	13.157
chrX	155270560	1113009632	7.1682	12.6987

chrY	59373566	37975818	0.6396	15.1148

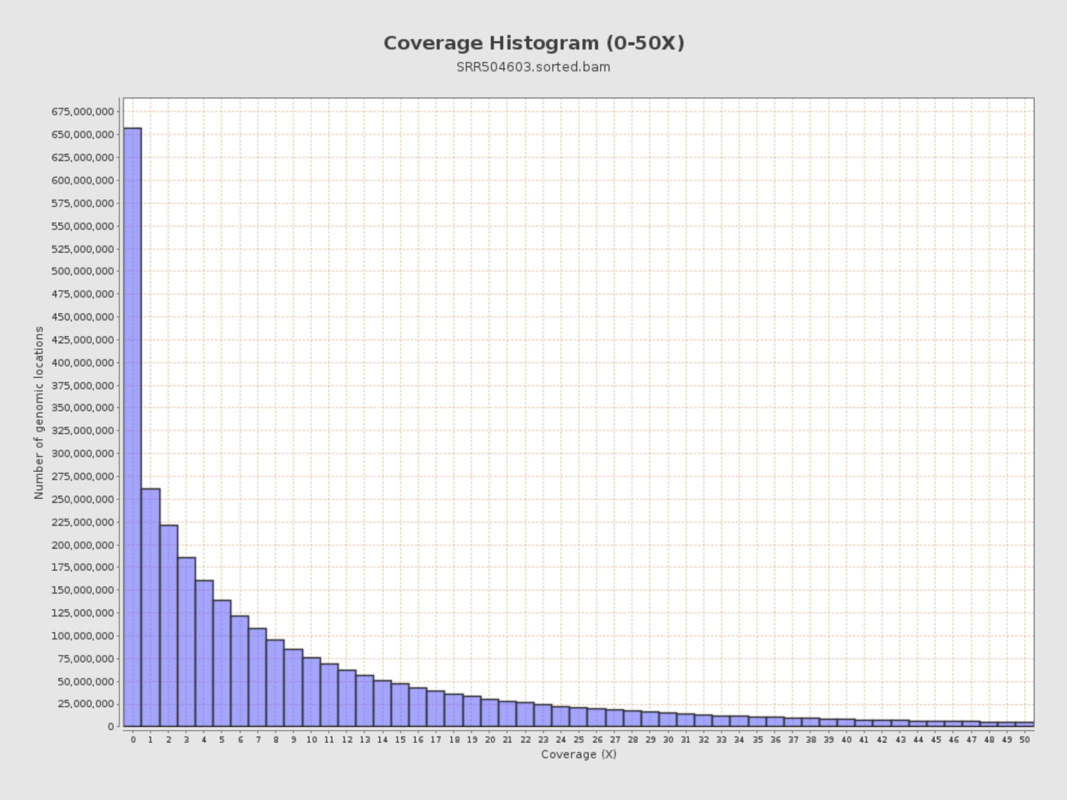
3. Results : Coverage across reference



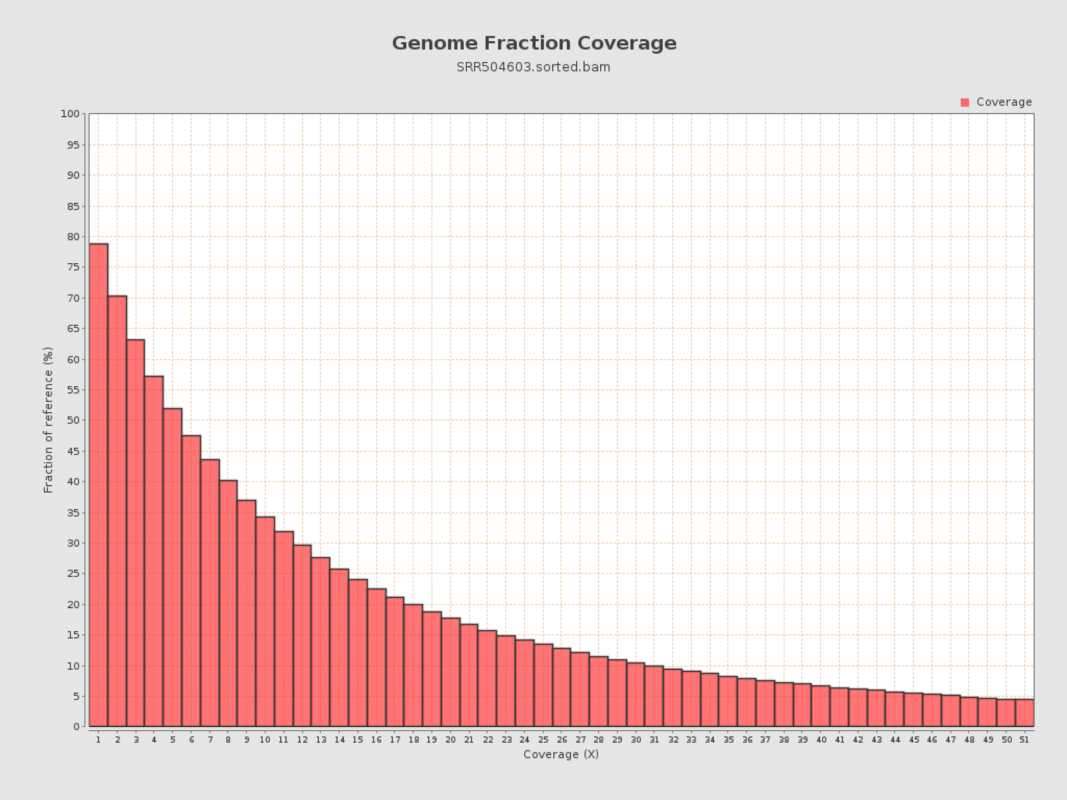
4. Results : Coverage Histogram



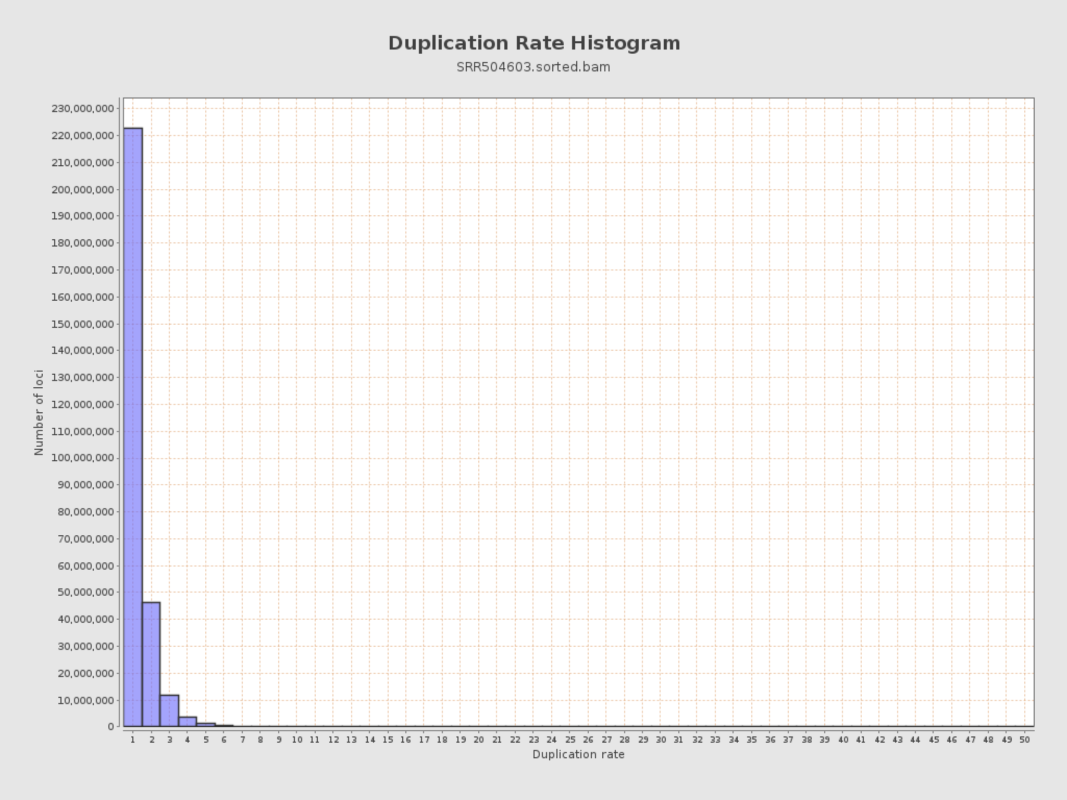
5. Results : Coverage Histogram (0-50X)



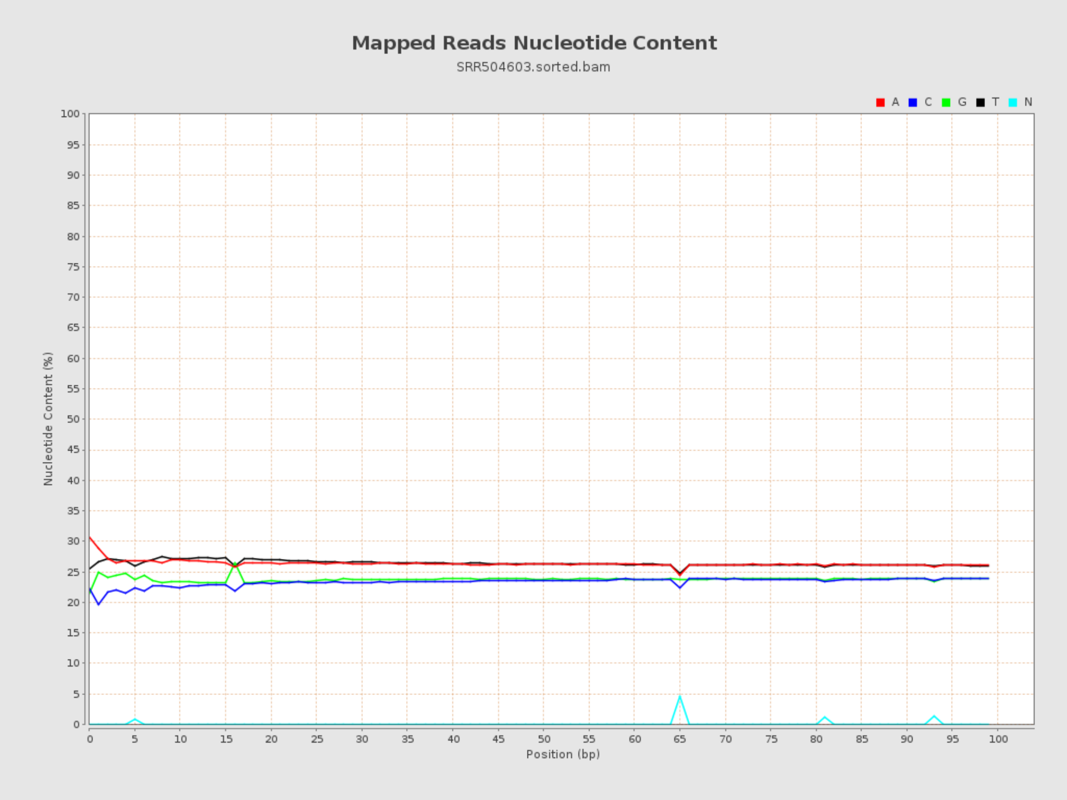
6. Results : Genome Fraction Coverage



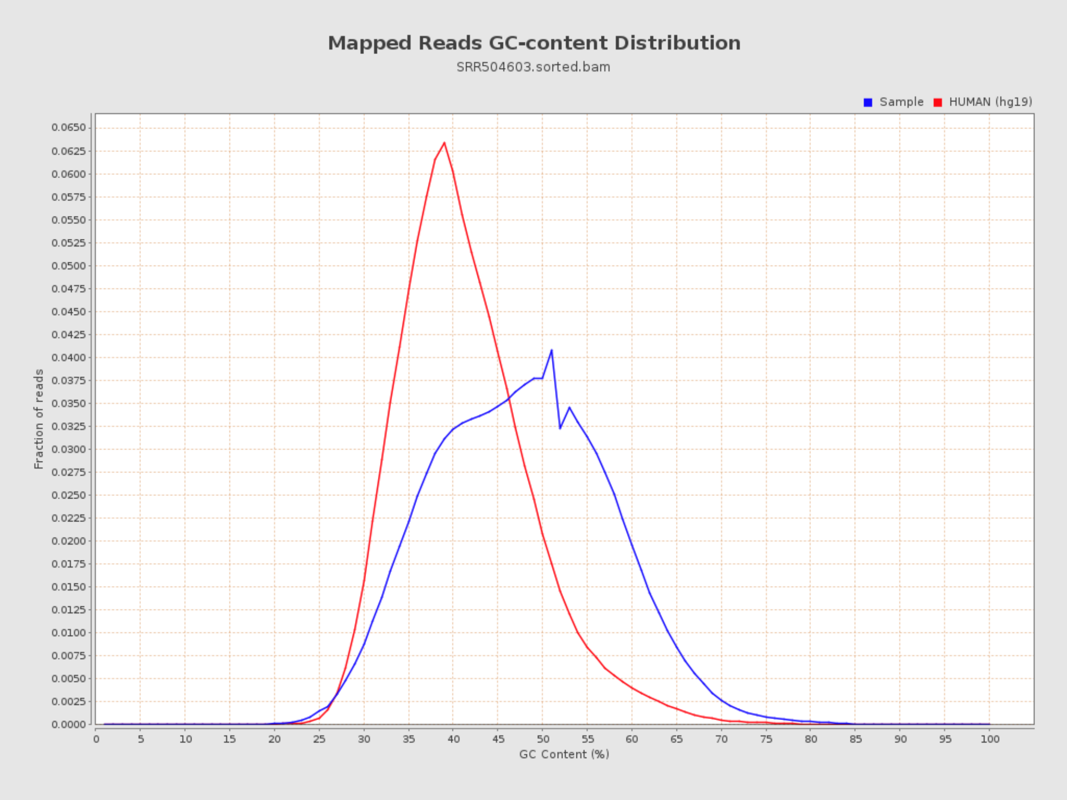
7. Results : Duplication Rate Histogram



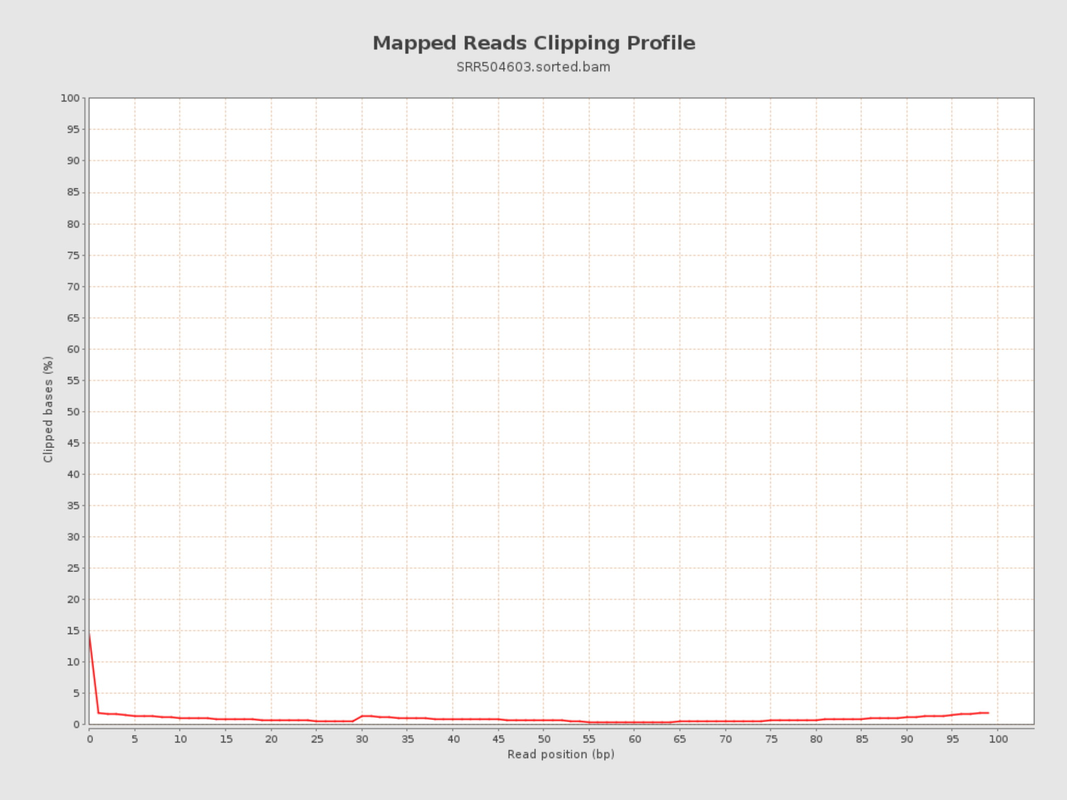
8. Results : Mapped Reads Nucleotide Content



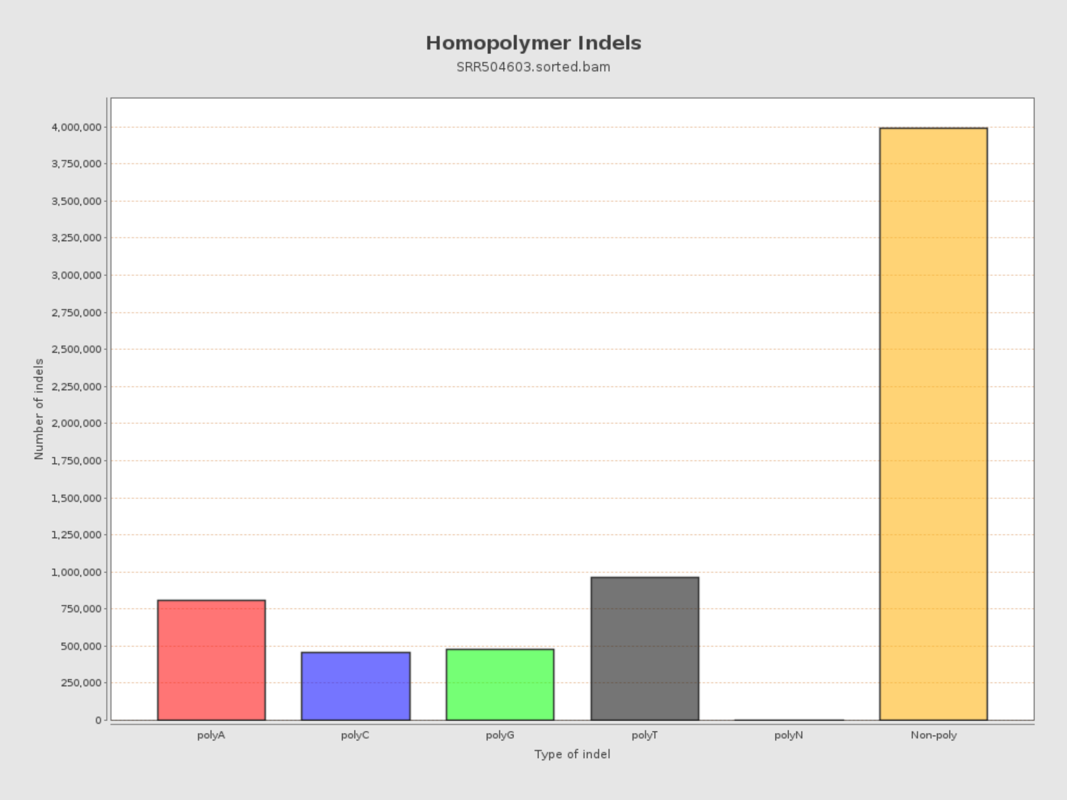
9. Results : Mapped Reads GC-content Distribution



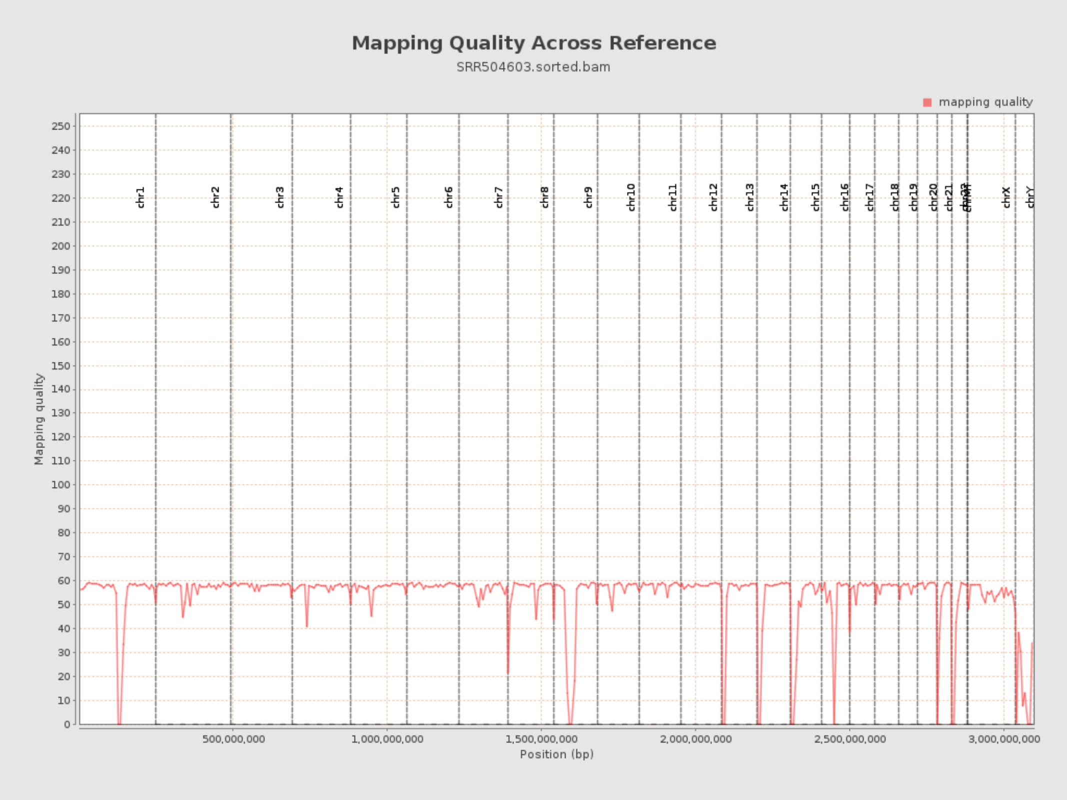
10. Results : Mapped Reads Clipping Profile



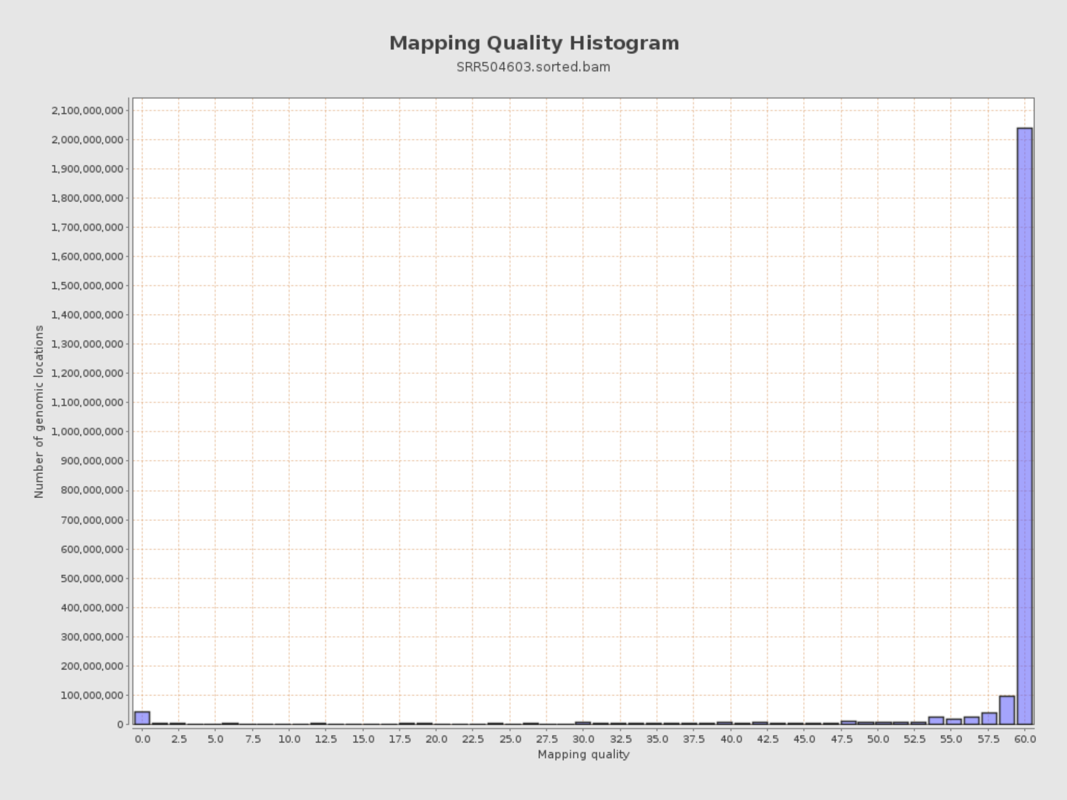
11. Results : Homopolymer Indels



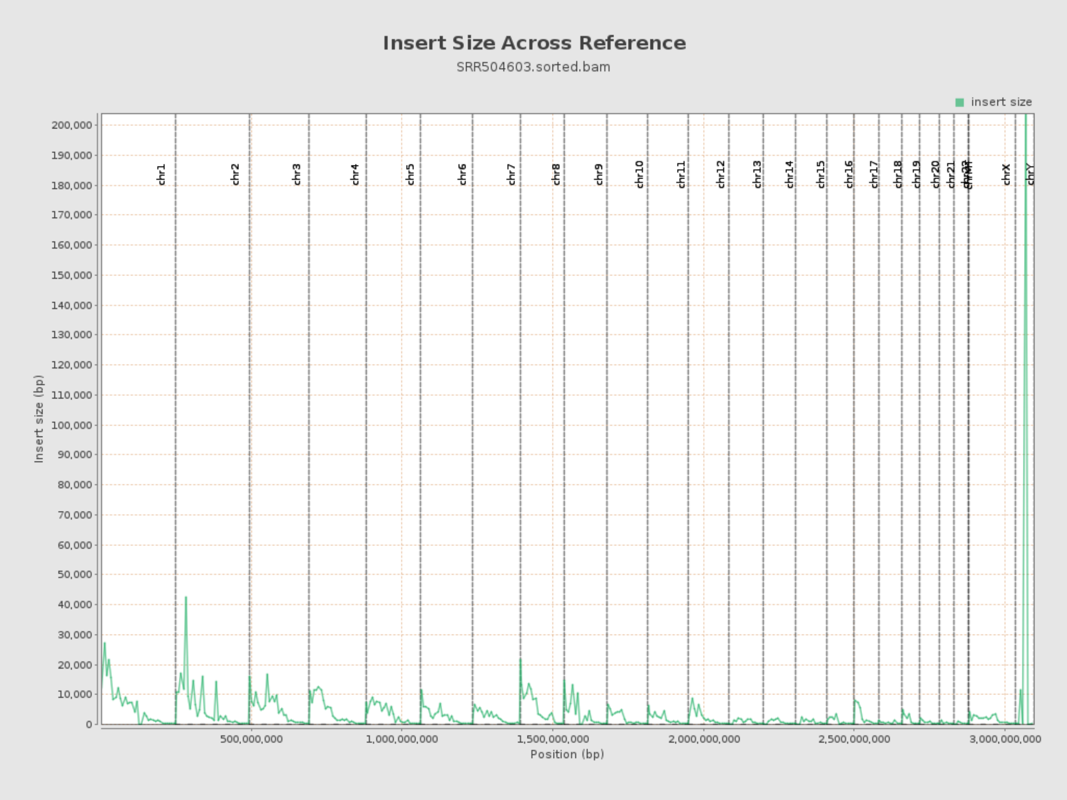
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram