Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 09:02:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504608.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_SRR504608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504608_1.fastq.gz SRR504608_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 09:02:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	424,362,244
Mapped reads	283,163,794 / 66.73%
Unmapped reads	141,198,450 / 33.27%
Mapped paired reads	283,163,794 / 66.73%
Mapped reads, first in pair	141,720,346 / 33.4%
Mapped reads, second in pair	141,443,448 / 33.33%
Mapped reads, both in pair	281,438,970 / 66.32%
Mapped reads, singletons	1,724,824 / 0.41%
Secondary alignments	0
Supplementary alignments	1,793,426 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	72,025,806 / 16.97%
Duplication rate	22.17%
Clipped reads	14,009,139 / 3.3%

2.2. ACGT Content

Number/percentage of A's	7,260,767,699 / 25.83%
Number/percentage of C's	6,735,146,360 / 23.96%
Number/percentage of T's	7,309,151,490 / 26%
Number/percentage of G's	6,804,147,423 / 24.2%
Number/percentage of N's	5,728,286 / 0.02%

GC Percentage	48.16%

2.3. Coverage

Mean	9.0843
Standard Deviation	23.3378

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	24,246.39
Standard Deviation	1,501,934.07
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	139,205,069
Insertions	2,096,186
Mapped reads with at least one insertion	0.72%
Deletions	2,767,158
Mapped reads with at least one deletion	0.95%
Homopolymer indels	39.93%

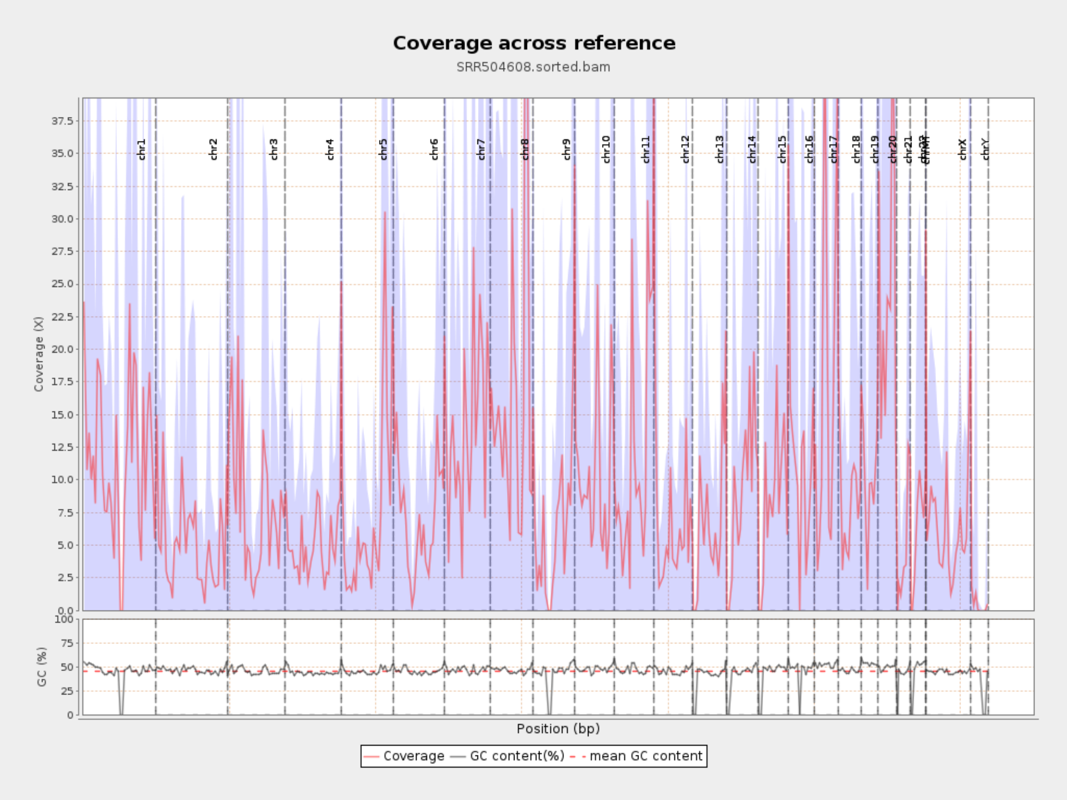
2.7. Chromosome stats

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

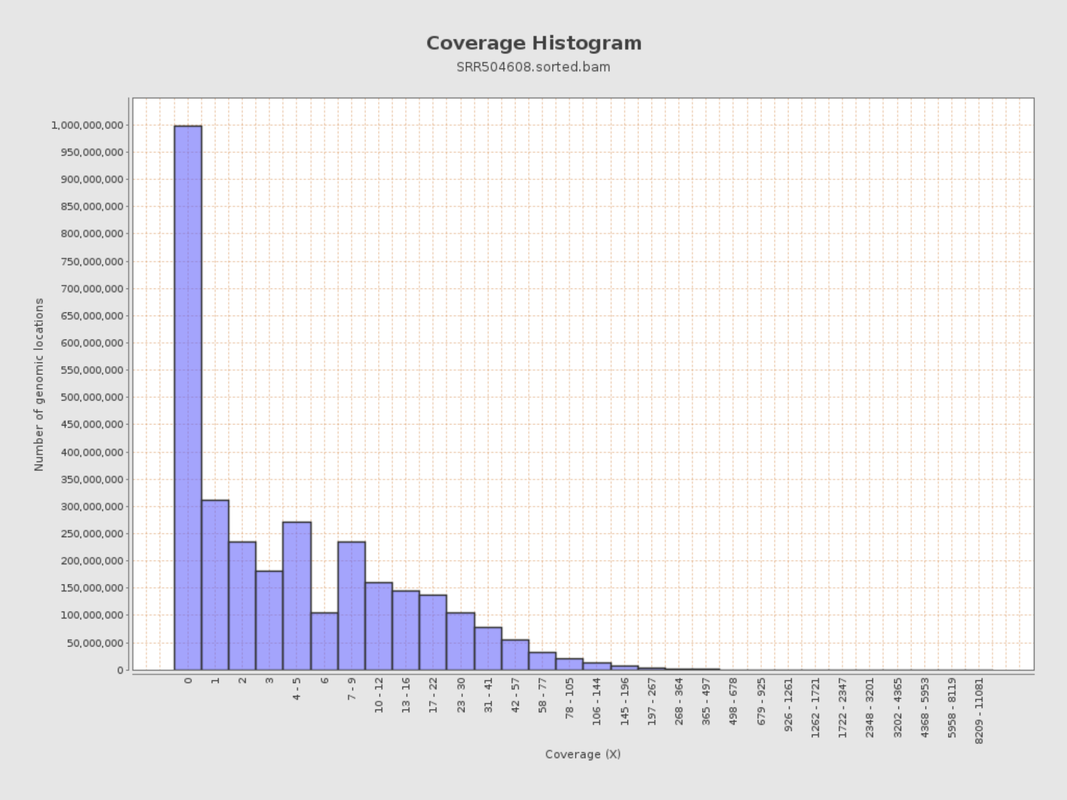
		bases	coverage	deviation
chr1	249250621	2849695616	11.4331	22.7802
chr2	243199373	1255333196	5.1617	12.91
chr3	198022430	1588475520	8.0217	21.7029
chr4	191154276	949940104	4.9695	9.4462
chr5	180915260	1371219673	7.5793	21.6349
chr6	171115067	1192573473	6.9694	13.5346
chr7	159138663	2249662323	14.1365	26.0735
chr8	146364022	2535728840	17.3248	41.3962
chr9	141213431	858691203	6.0808	16.9978
chr10	135534747	1382079463	10.1972	21.0895
chr11	135006516	1583926089	11.7322	26.9458
chr12	133851895	847757560	6.3335	15.6051
chr13	115169878	769601285	6.6823	14.8866
chr14	107349540	997047713	9.2879	18.558
chr15	102531392	857581099	8.3641	17.4027
chr16	90354753	1049905842	11.6198	26.2109
chr17	81195210	1364377891	16.8037	54.082
chr18	78077248	643250406	8.2386	23.6073
chr19	59128983	590782898	9.9914	21.4209
chr20	63025520	1595097069	25.3087	45.1863
chr21	48129895	234497899	4.8722	12.5885
chr22	51304566	308867361	6.0203	15.5599
chrMT	16571	483272	29.1637	13.529
chrX	155270560	1018499072	6.5595	12.2595

chrY	59373566	27030832	0.4553	10.5474

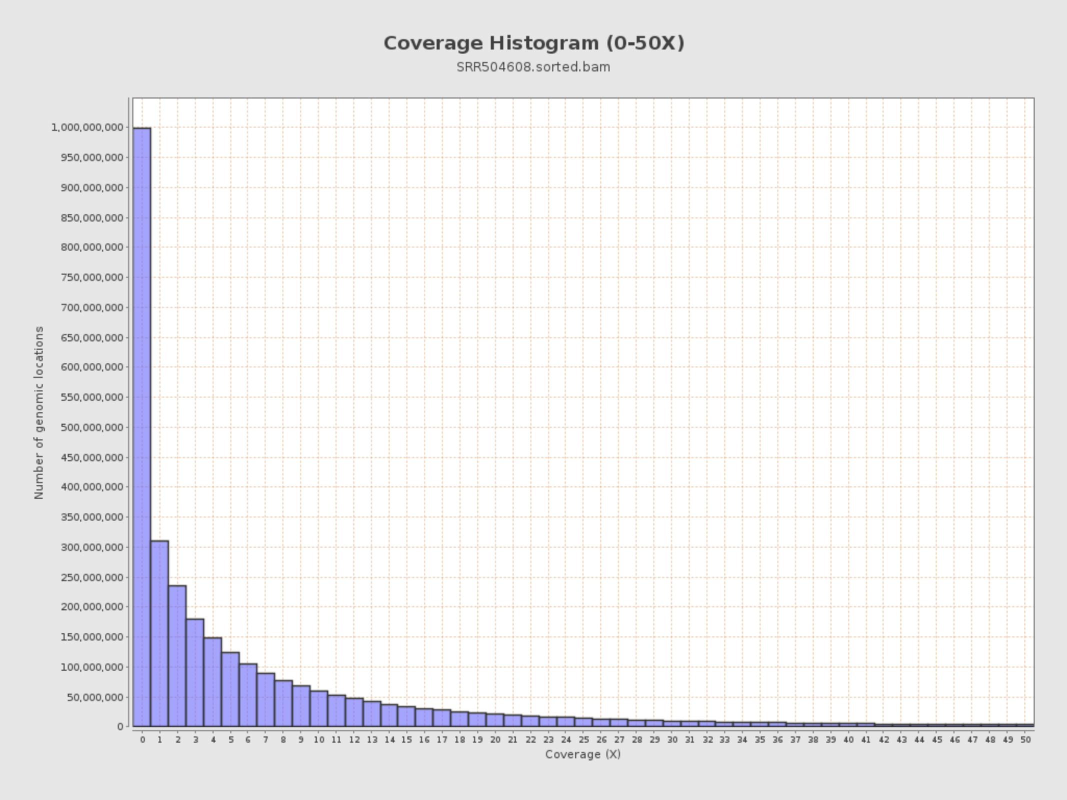
3. Results : Coverage across reference



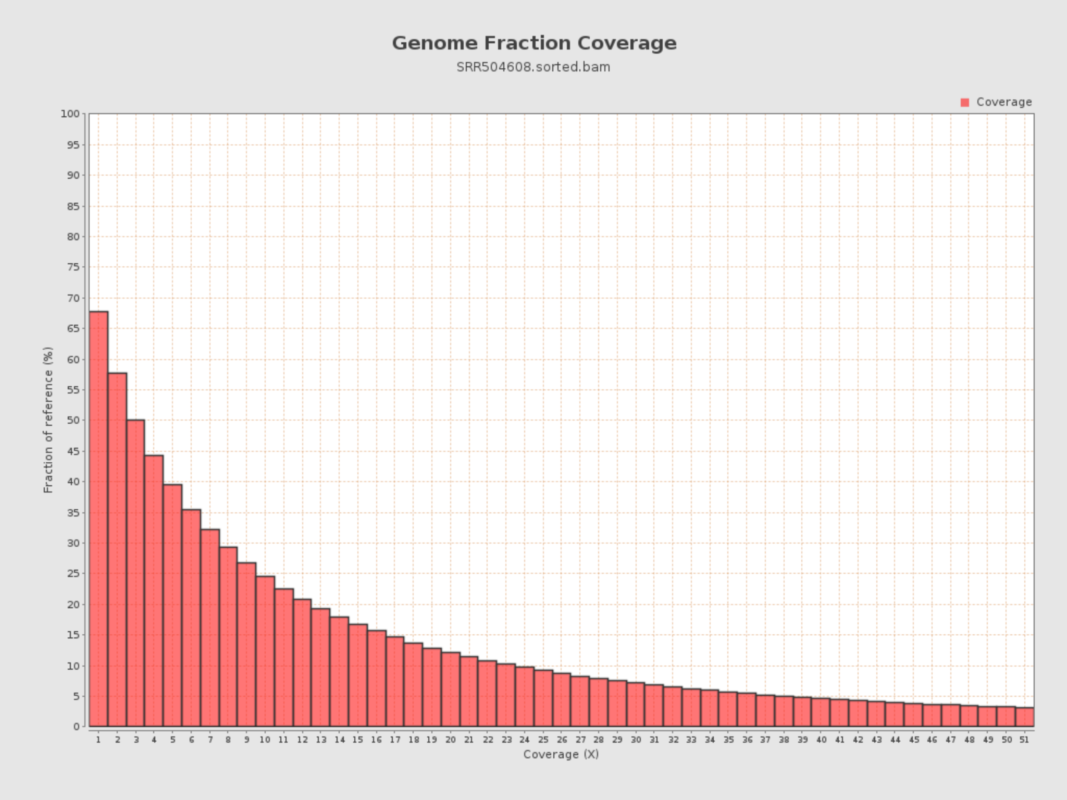
4. Results : Coverage Histogram



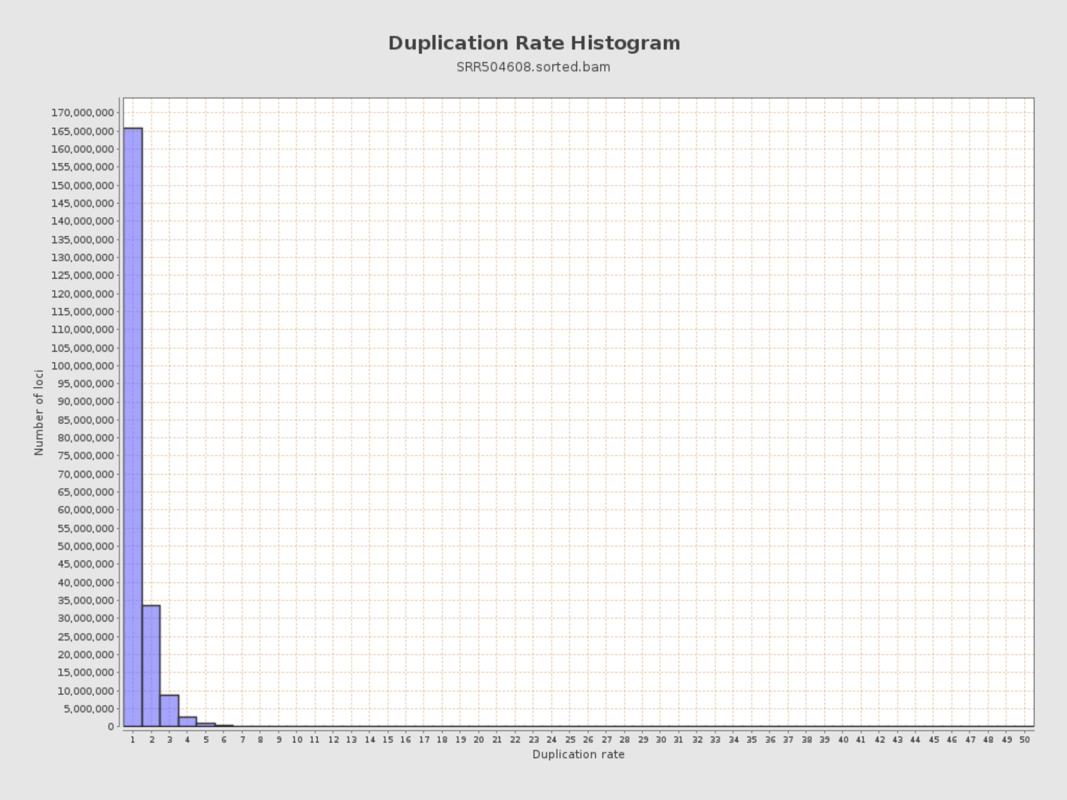
5. Results : Coverage Histogram (0-50X)



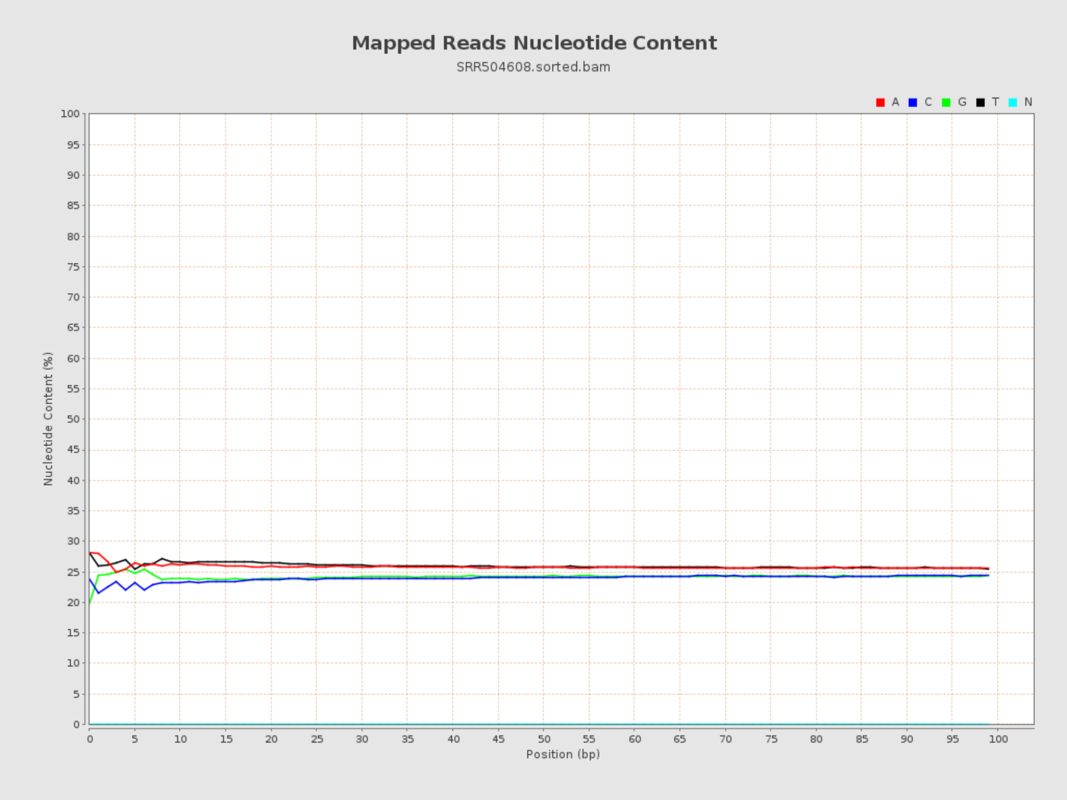
6. Results : Genome Fraction Coverage



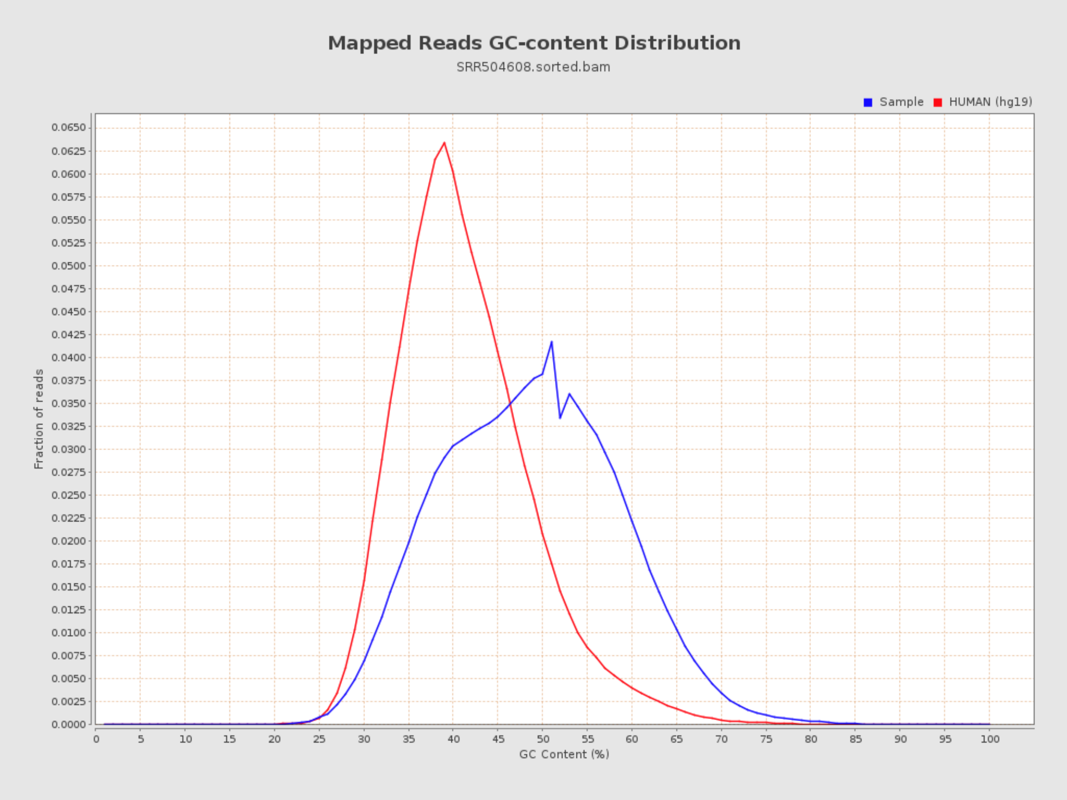
7. Results : Duplication Rate Histogram



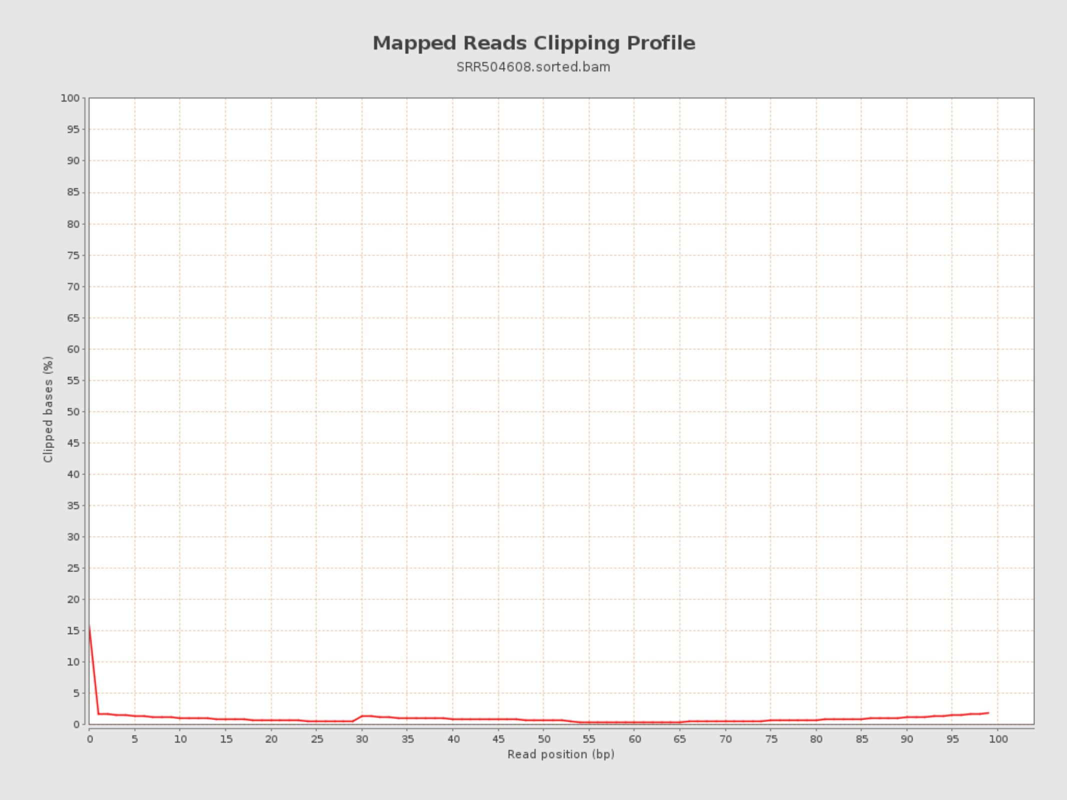
8. Results : Mapped Reads Nucleotide Content



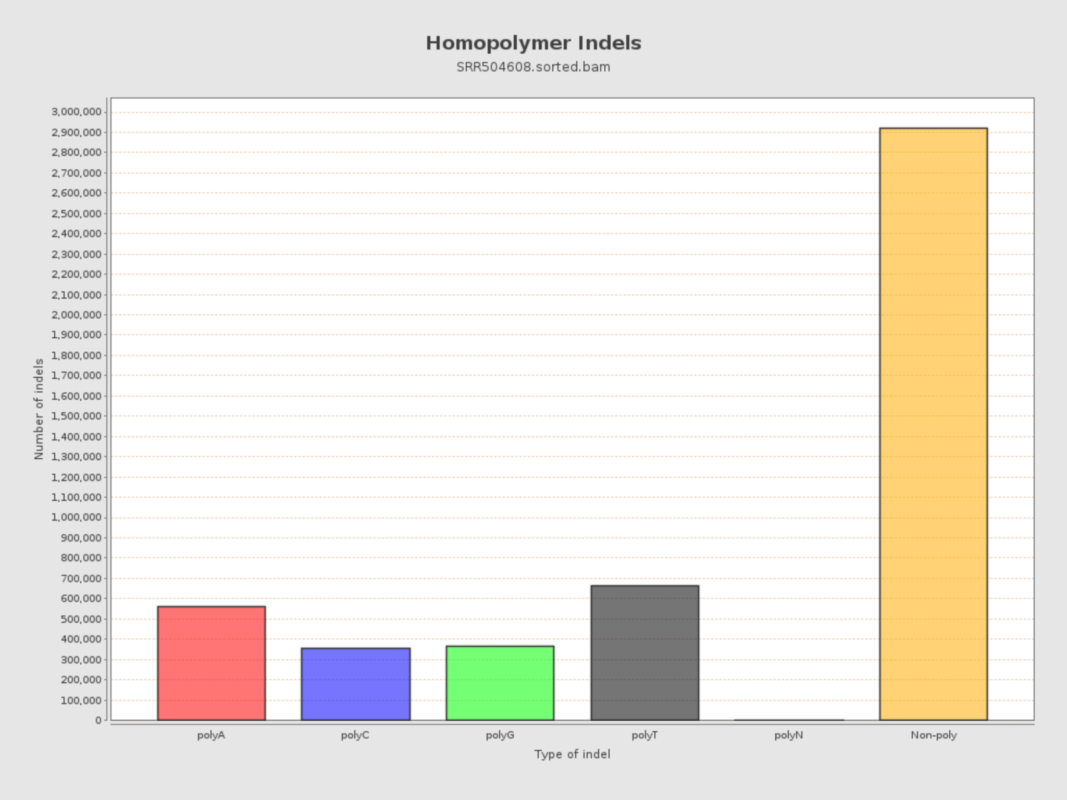
9. Results : Mapped Reads GC-content Distribution



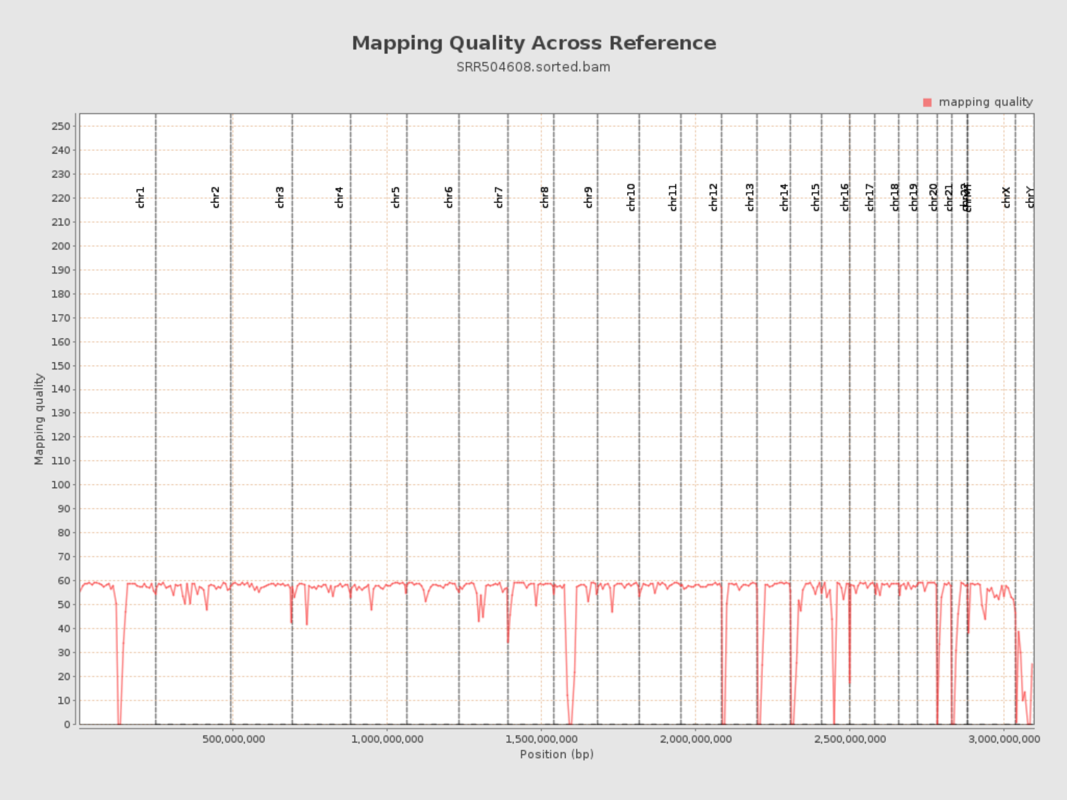
10. Results : Mapped Reads Clipping Profile



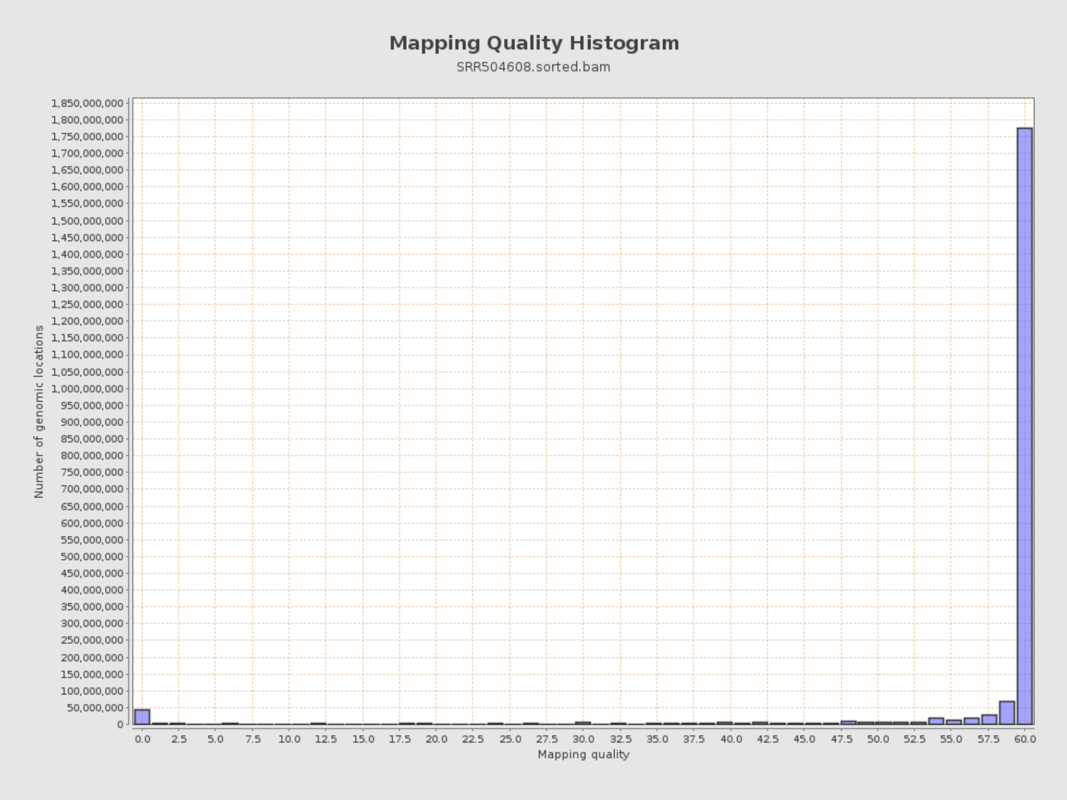
11. Results : Homopolymer Indels



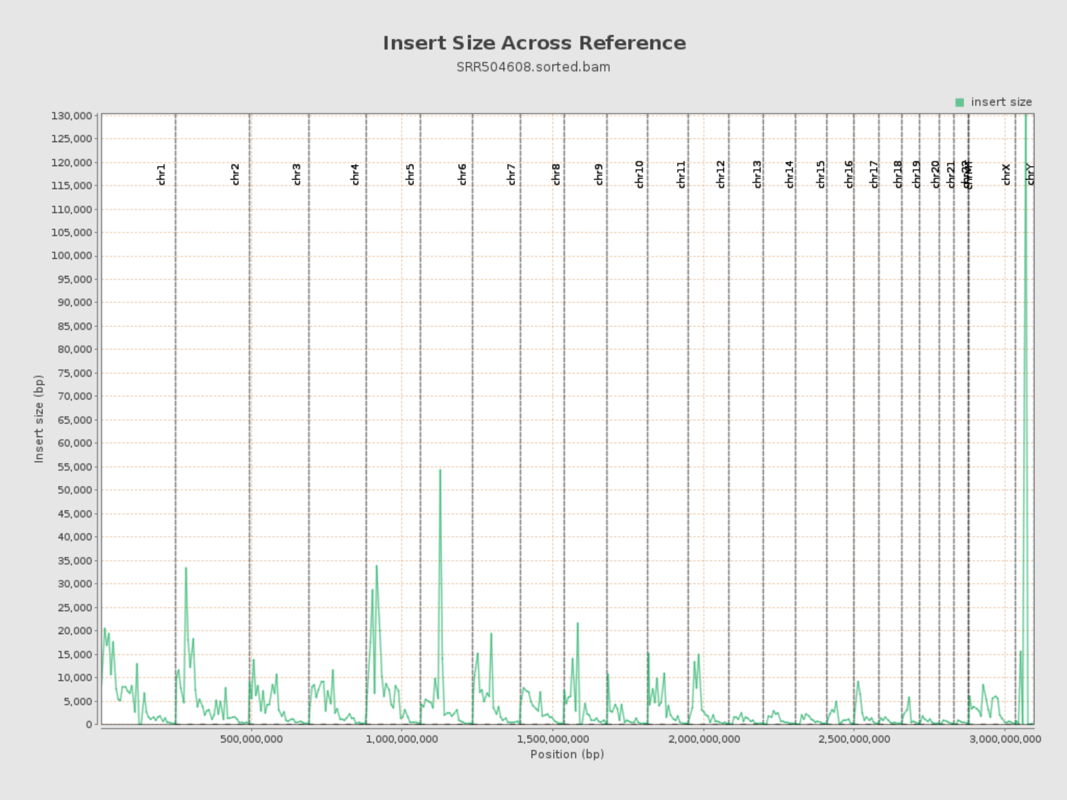
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram