Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 19:21:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504602.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_SRR504602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504602_1.fastq.gz SRR504602_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 19:21:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	399,979,832
Mapped reads	344,313,098 / 86.08%
Unmapped reads	55,666,734 / 13.92%
Mapped paired reads	344,313,098 / 86.08%
Mapped reads, first in pair	172,493,575 / 43.13%
Mapped reads, second in pair	171,819,523 / 42.96%
Mapped reads, both in pair	342,249,944 / 85.57%
Mapped reads, singletons	2,063,154 / 0.52%
Secondary alignments	0
Supplementary alignments	1,893,890 / 0.47%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	80,804,887 / 20.2%
Duplication rate	20.98%
Clipped reads	17,334,259 / 4.33%

2.2. ACGT Content

Number/percentage of A's	9,016,738,739 / 26.39%
Number/percentage of C's	7,993,995,010 / 23.39%
Number/percentage of T's	9,044,550,708 / 26.47%
Number/percentage of G's	8,105,977,235 / 23.72%
Number/percentage of N's	8,949,743 / 0.03%

GC Percentage	47.12%

2.3. Coverage

Mean	11.0408
Standard Deviation	22.8236

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	29,608.93
Standard Deviation	1,669,709.49
P25/Median/P75	180 / 212 / 265

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	179,791,828
Insertions	2,568,327
Mapped reads with at least one insertion	0.73%
Deletions	3,449,965
Mapped reads with at least one deletion	0.97%
Homopolymer indels	40.48%

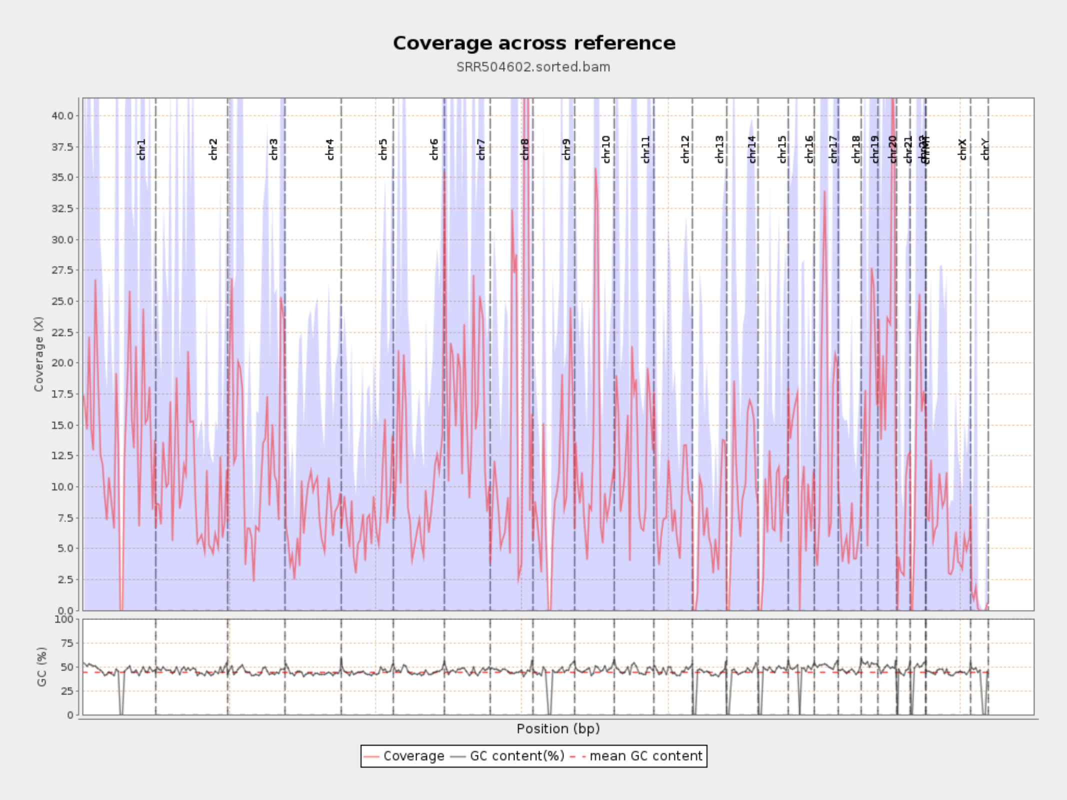
2.7. Chromosome stats

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

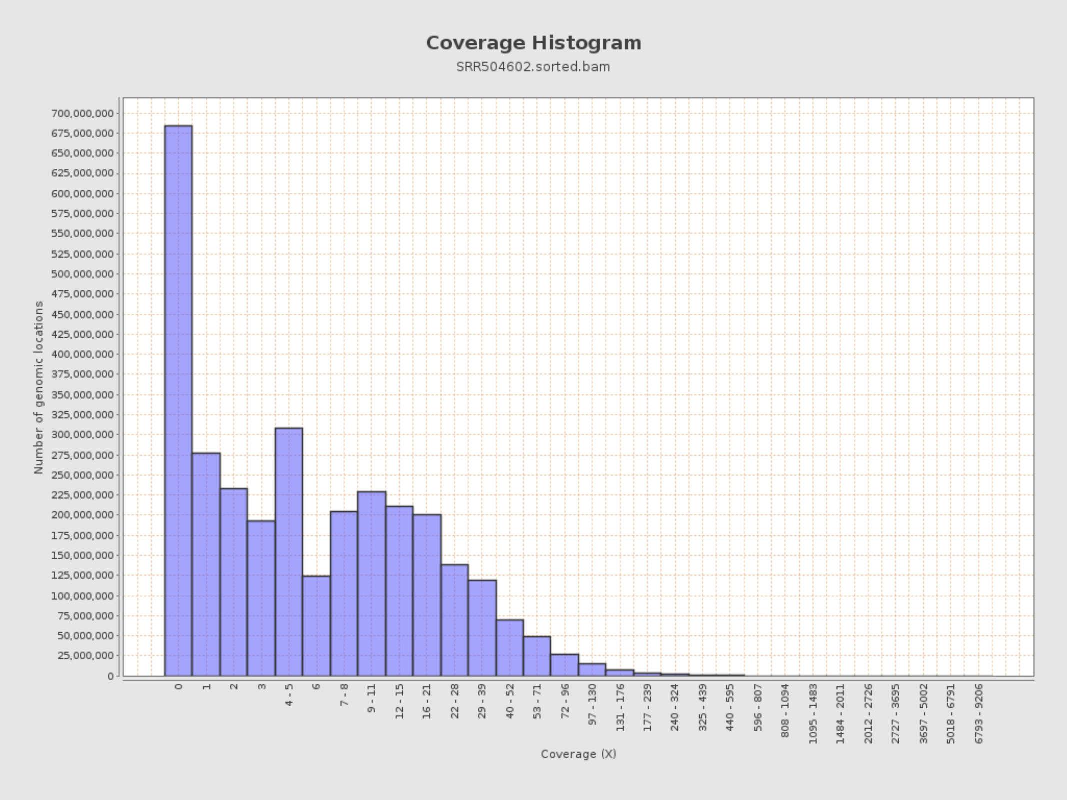
		bases	coverage	deviation
chr1	249250621	3507490200	14.0721	23.7369
chr2	243199373	2344744009	9.6412	17.202
chr3	198022430	2532109522	12.787	21.1283
chr4	191154276	1433796053	7.5007	11.894
chr5	180915260	1391441659	7.6911	12.9262
chr6	171115067	1747876360	10.2146	16.644
chr7	159138663	2782116908	17.4823	25.9503
chr8	146364022	2611218178	17.8406	43.8318
chr9	141213431	1344086648	9.5181	18.5608
chr10	135534747	1609908340	11.8782	22.434
chr11	135006516	1741685322	12.9008	21.8463
chr12	133851895	1165170516	8.7049	14.6475
chr13	115169878	777535386	6.7512	12.6736
chr14	107349540	1140705579	10.6261	18.4594
chr15	102531392	761386534	7.4259	13.862
chr16	90354753	996194868	11.0254	18.9588
chr17	81195210	1237480403	15.2408	46.7972
chr18	78077248	447650525	5.7334	26.7804
chr19	59128983	1004118481	16.9818	29.4389
chr20	63025520	1535514065	24.3634	36.3105
chr21	48129895	324013720	6.7321	17.0189
chr22	51304566	701516839	13.6736	25.502
chrMT	16571	237835	14.3525	11.5299
chrX	155270560	1006513001	6.4823	11.4309

chrY	59373566	34551888	0.5819	13.9222

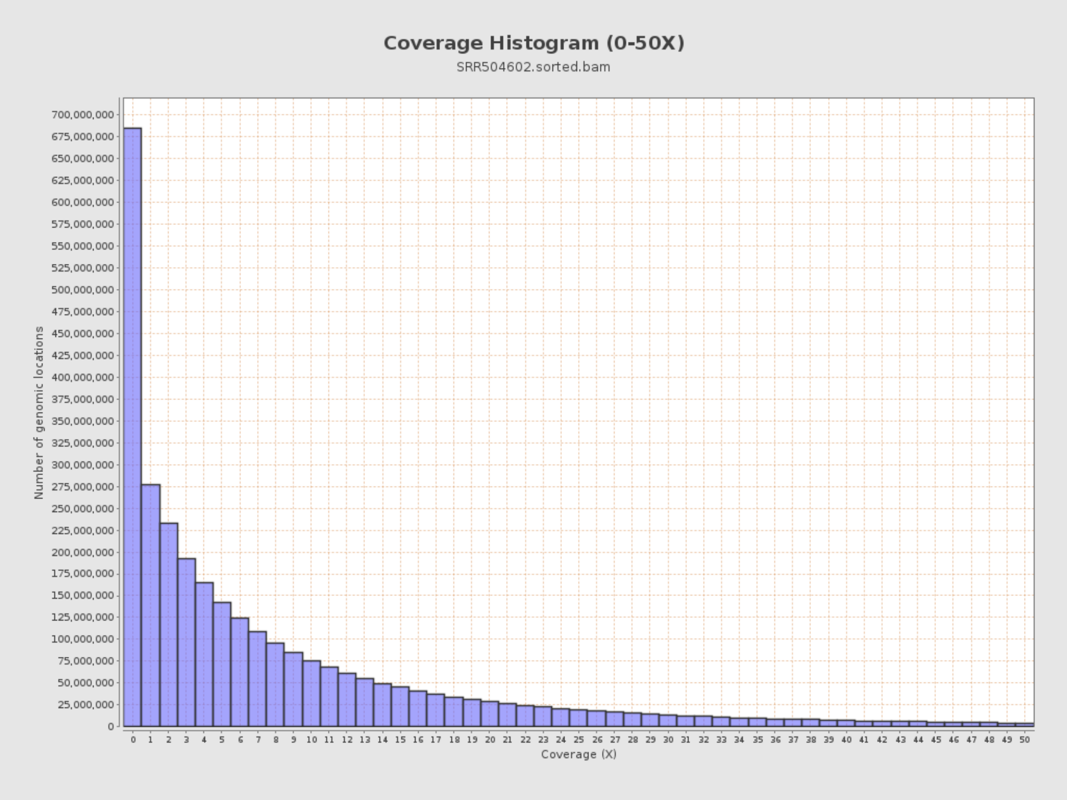
3. Results : Coverage across reference



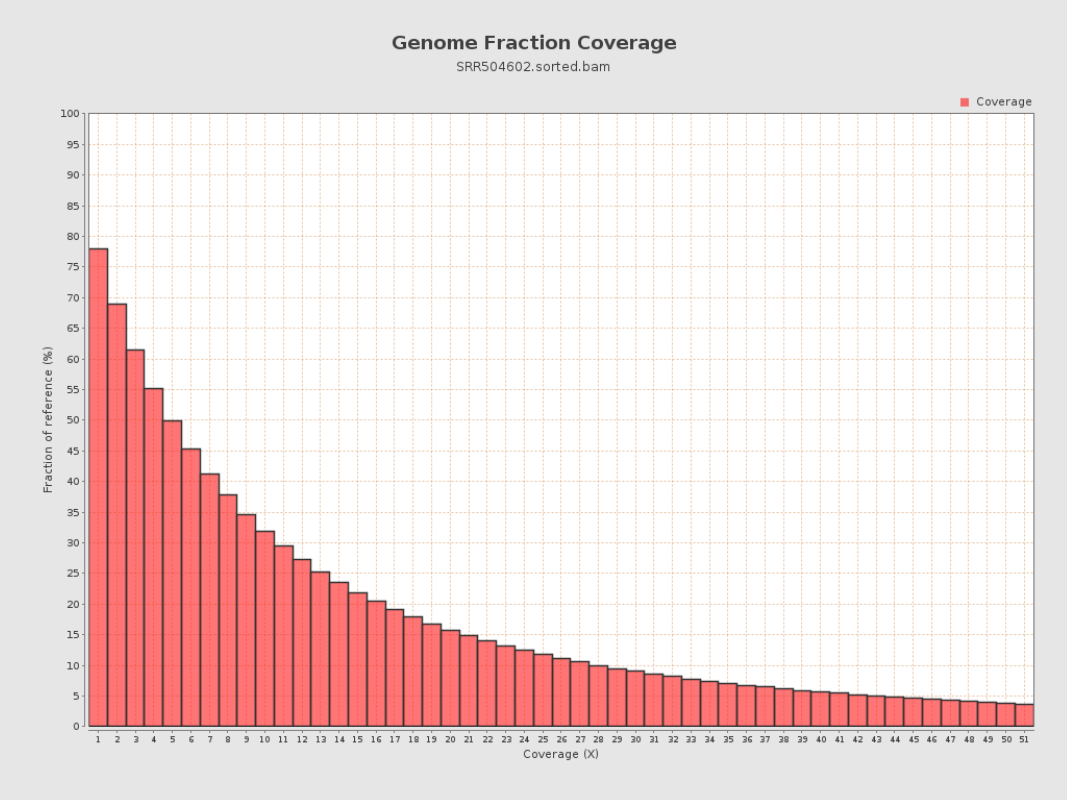
4. Results : Coverage Histogram



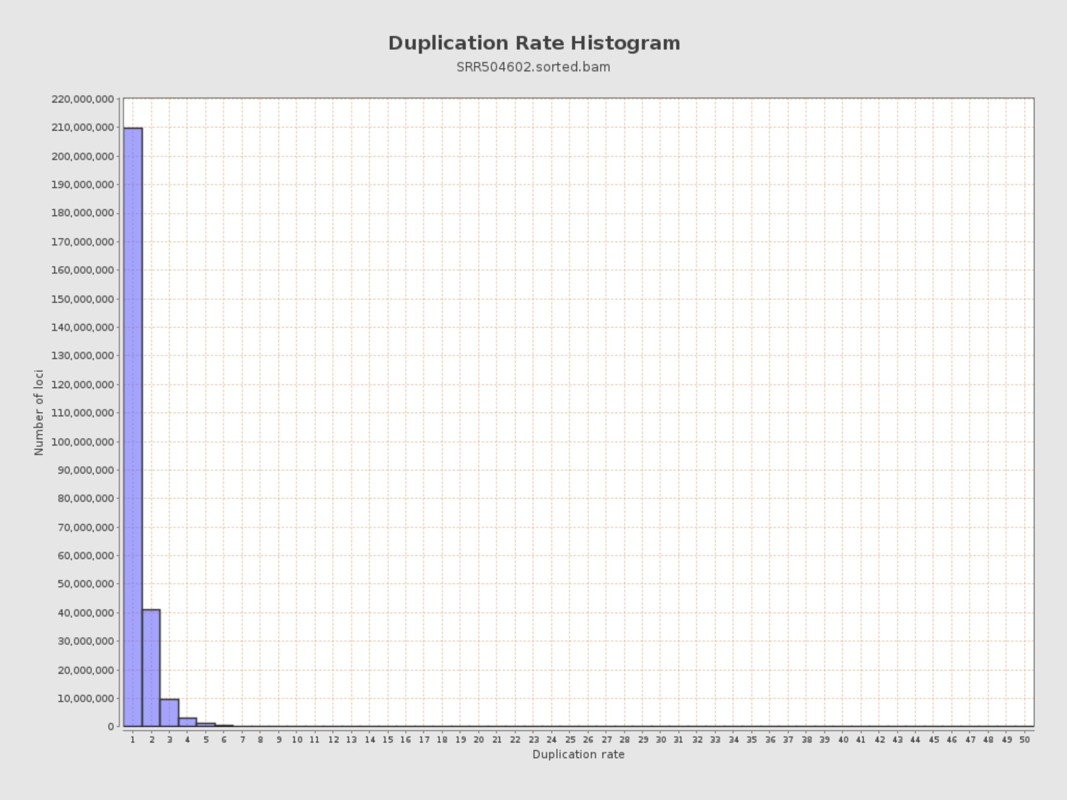
5. Results : Coverage Histogram (0-50X)



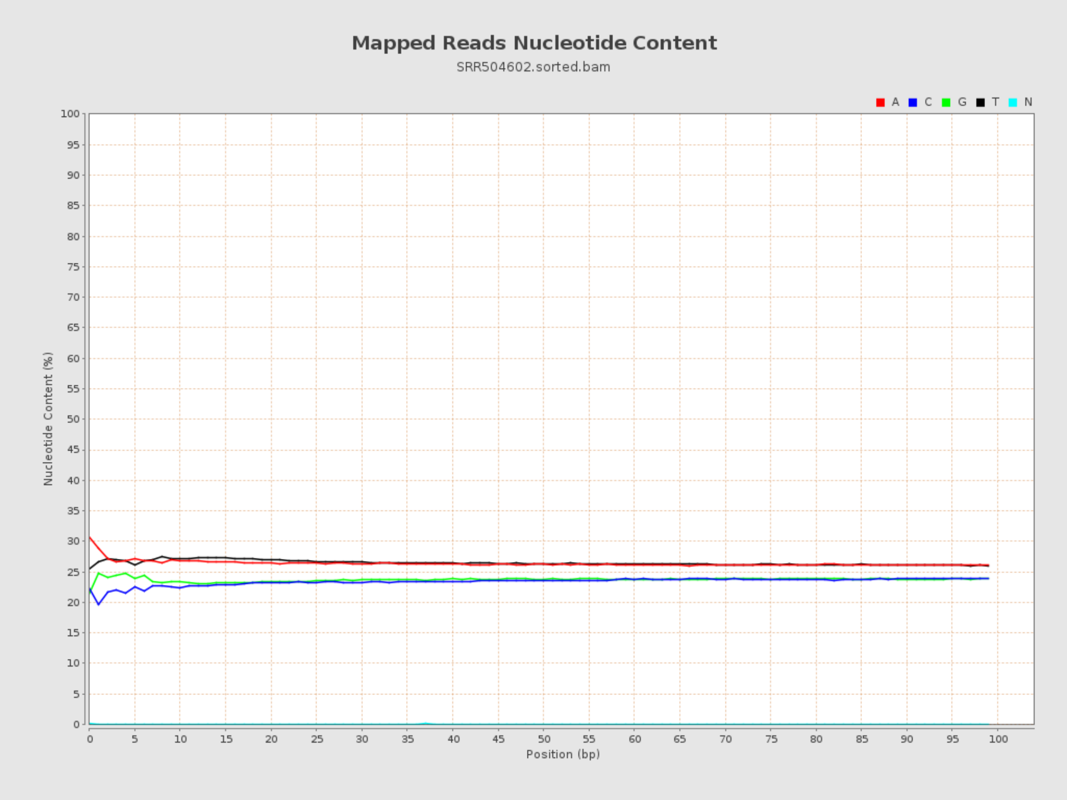
6. Results : Genome Fraction Coverage



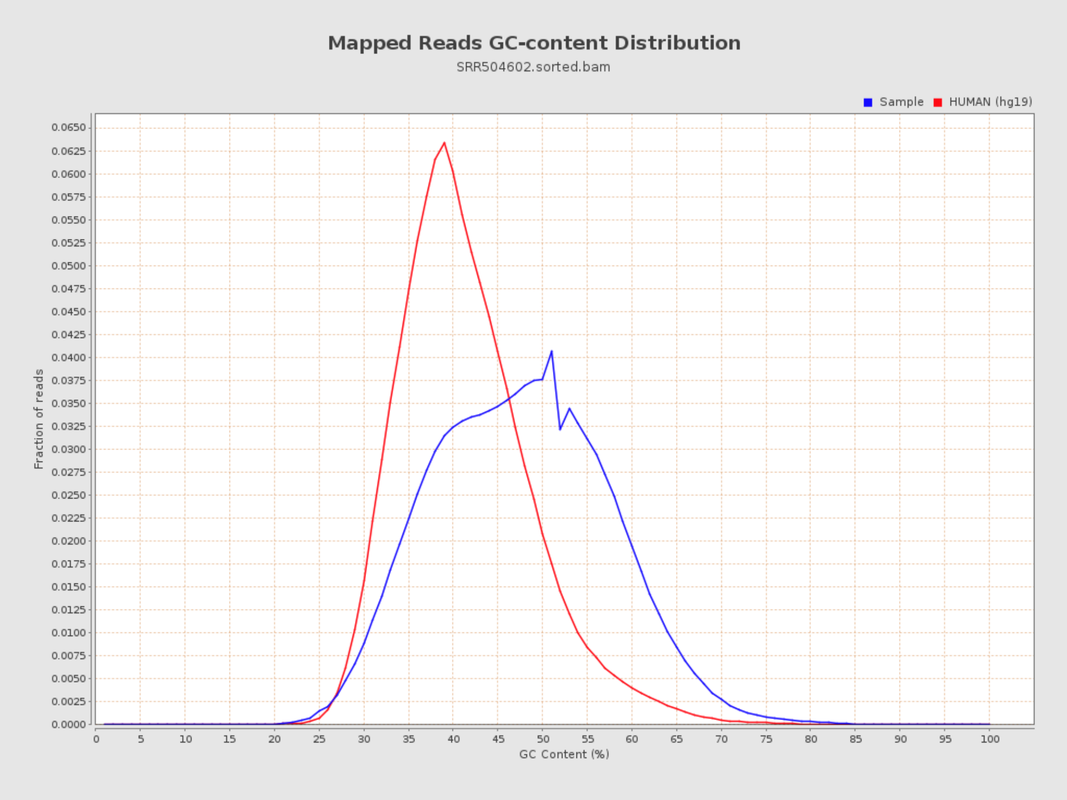
7. Results : Duplication Rate Histogram



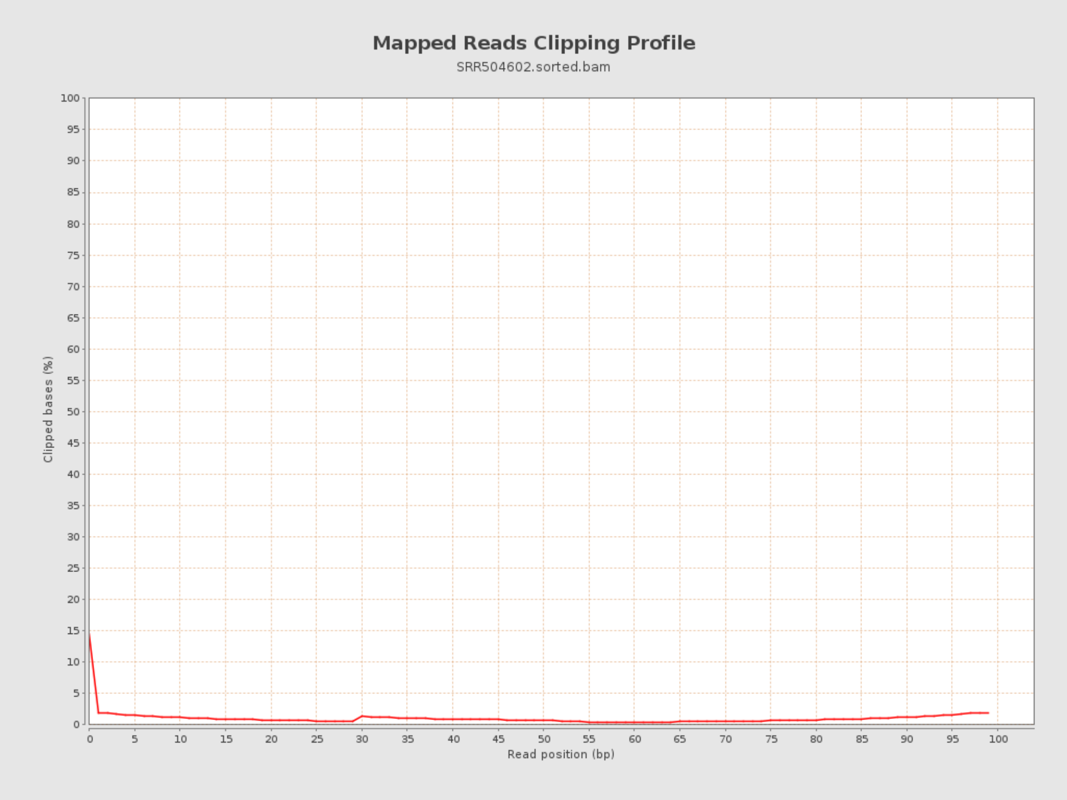
8. Results : Mapped Reads Nucleotide Content



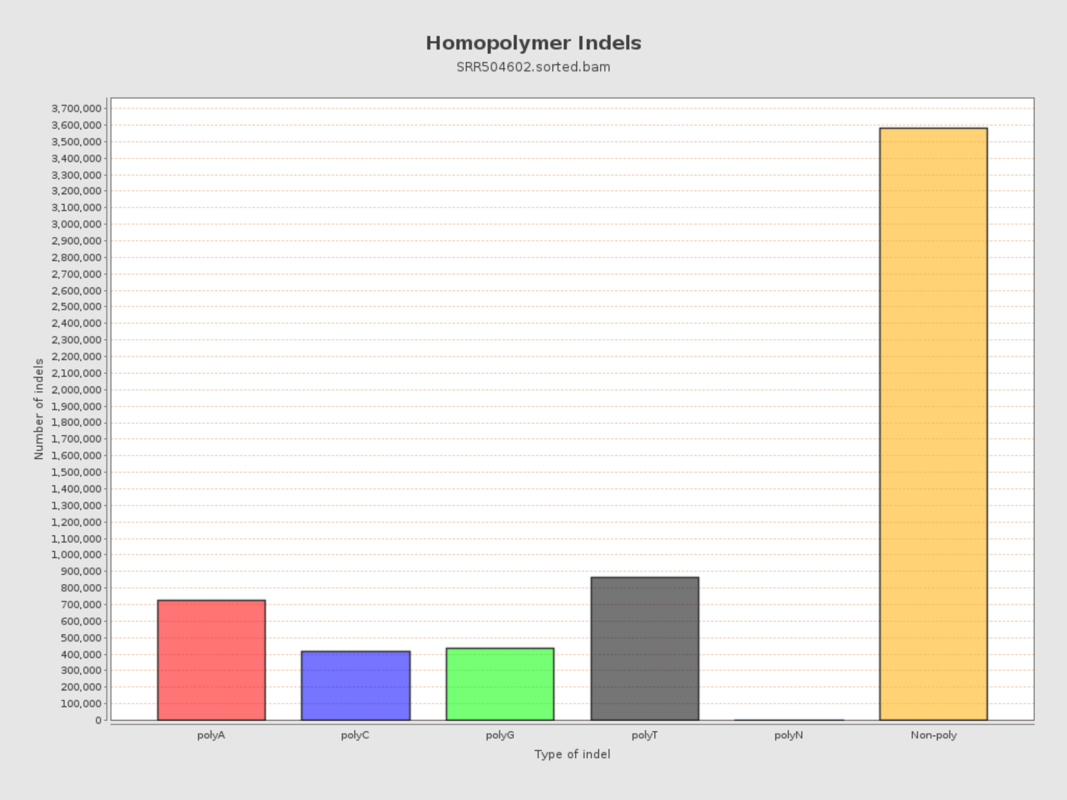
9. Results : Mapped Reads GC-content Distribution



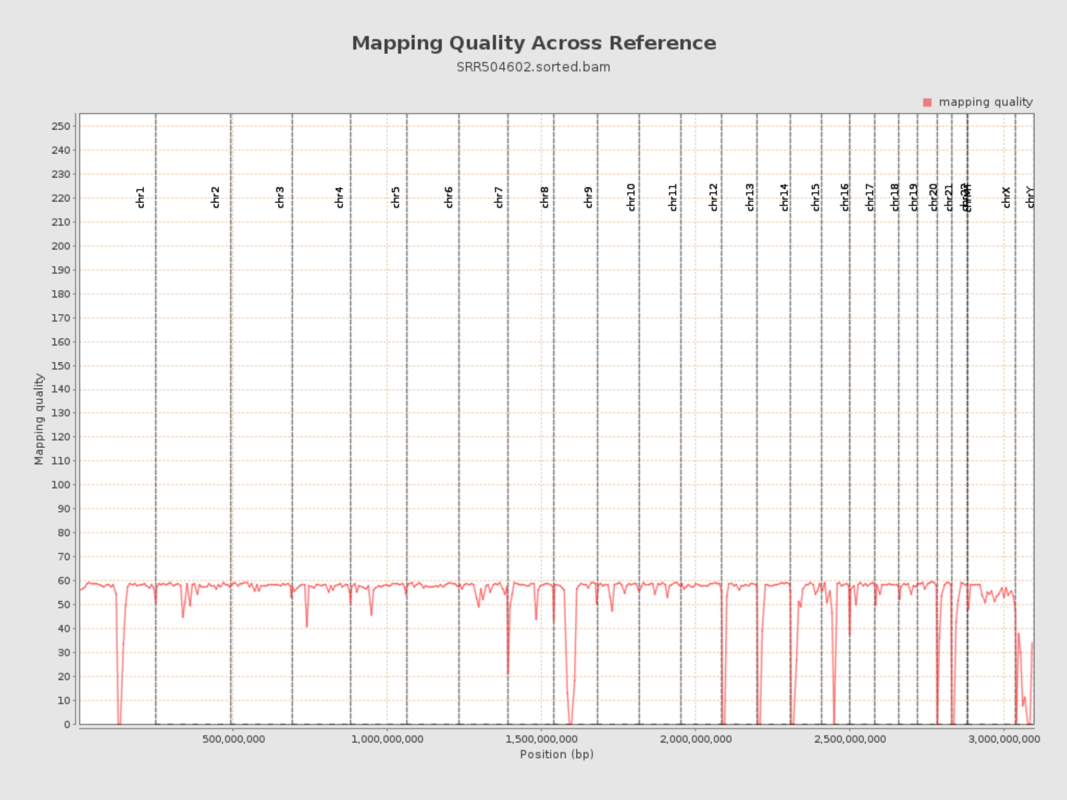
10. Results : Mapped Reads Clipping Profile



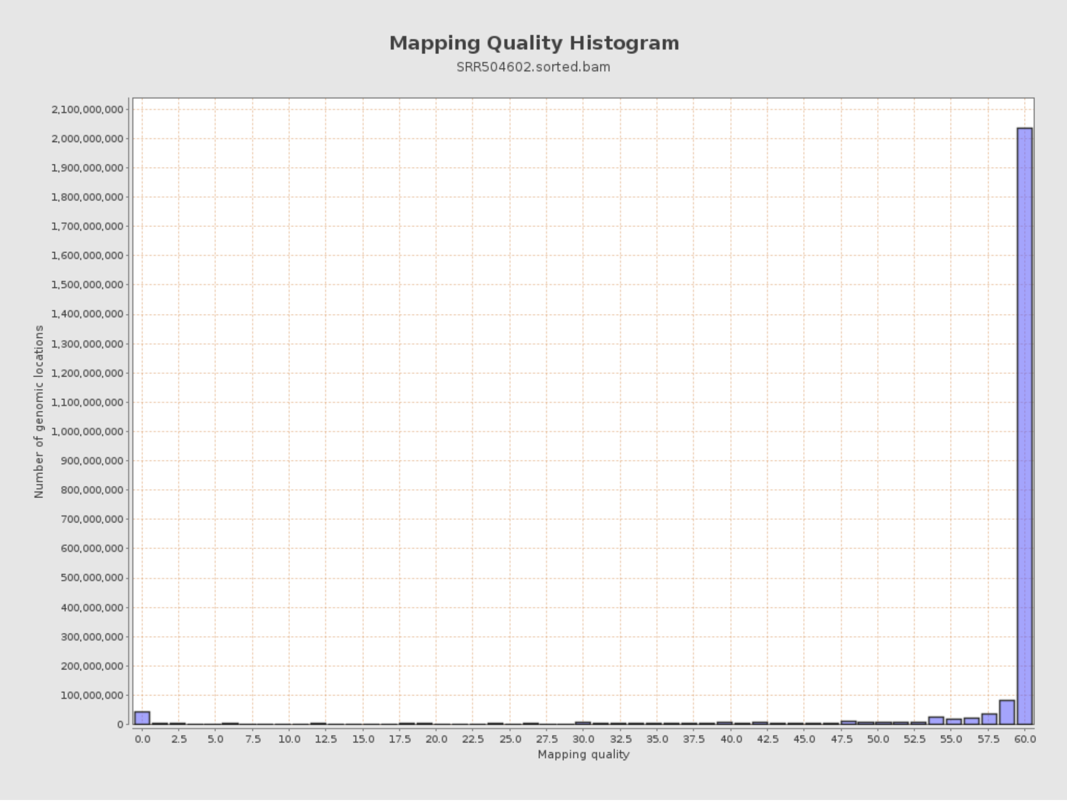
11. Results : Homopolymer Indels



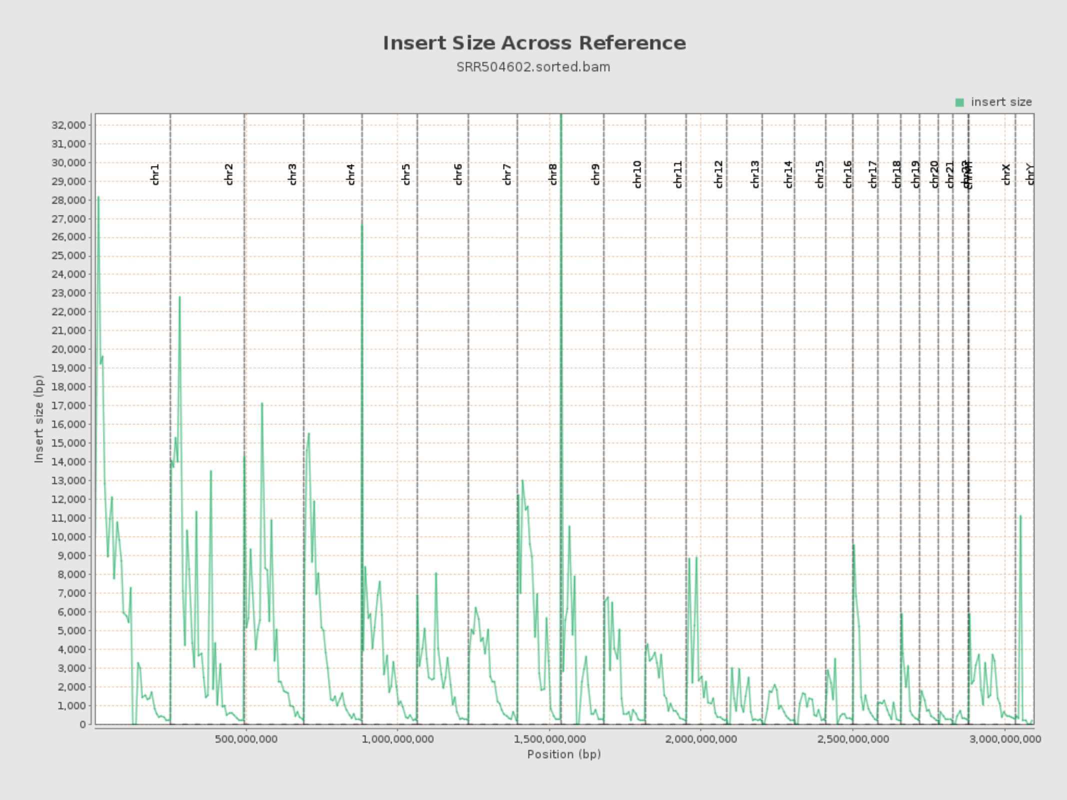
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram