Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 09:35:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504589.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_SRR504589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504589_1.fastq.gz SRR504589_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 09:35:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504589.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	351,856,500
Mapped reads	336,815,366 / 95.73%
Unmapped reads	15,041,134 / 4.27%
Mapped paired reads	336,815,366 / 95.73%
Mapped reads, first in pair	168,614,898 / 47.92%
Mapped reads, second in pair	168,200,468 / 47.8%
Mapped reads, both in pair	334,117,234 / 94.96%
Mapped reads, singletons	2,698,132 / 0.77%
Secondary alignments	0
Supplementary alignments	967,230 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	72,611,268 / 20.64%
Duplication rate	17.6%
Clipped reads	52,850,970 / 15.02%

2.2. ACGT Content

Number/percentage of A's	9,190,938,049 / 28.41%
Number/percentage of C's	6,937,659,860 / 21.45%
Number/percentage of T's	9,098,664,279 / 28.13%
Number/percentage of G's	7,109,566,283 / 21.98%
Number/percentage of N's	10,782,840 / 0.03%

GC Percentage	43.43%

2.3. Coverage

Mean	10.4526
Standard Deviation	92.1399

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	33,847.01
Standard Deviation	1,744,286.55
P25/Median/P75	133 / 189 / 246

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	187,003,383
Insertions	3,279,145
Mapped reads with at least one insertion	0.94%
Deletions	4,023,347
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.4%

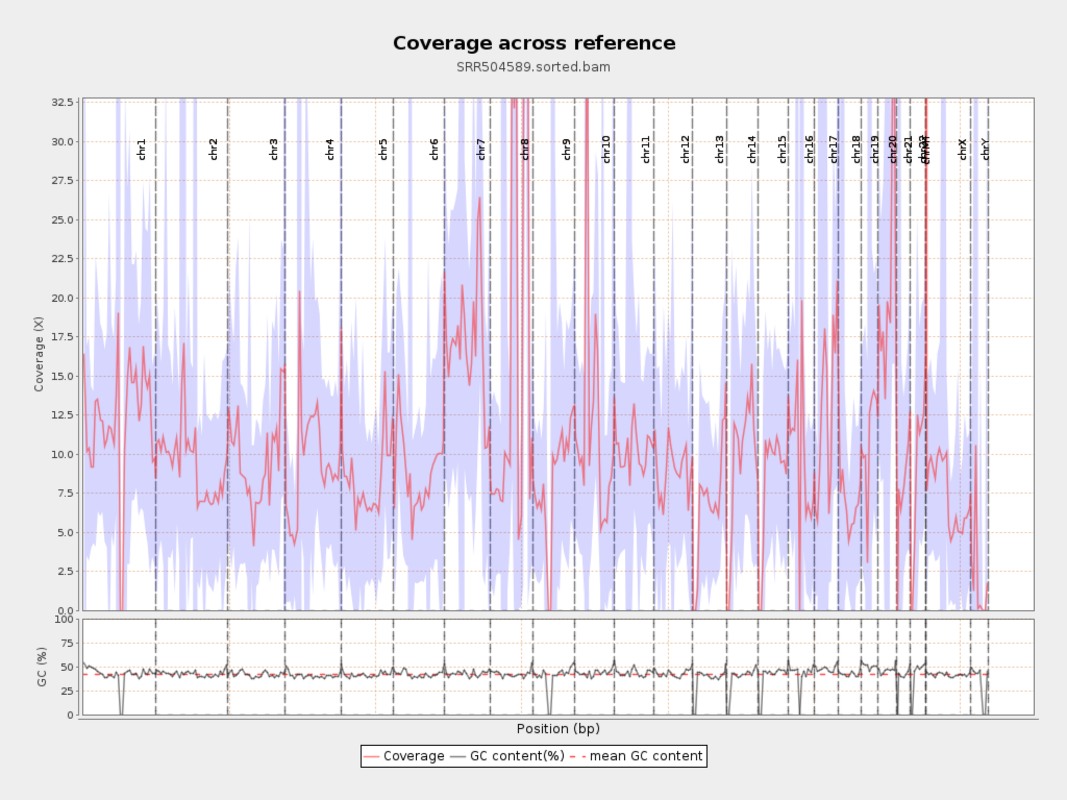
2.7. Chromosome stats

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

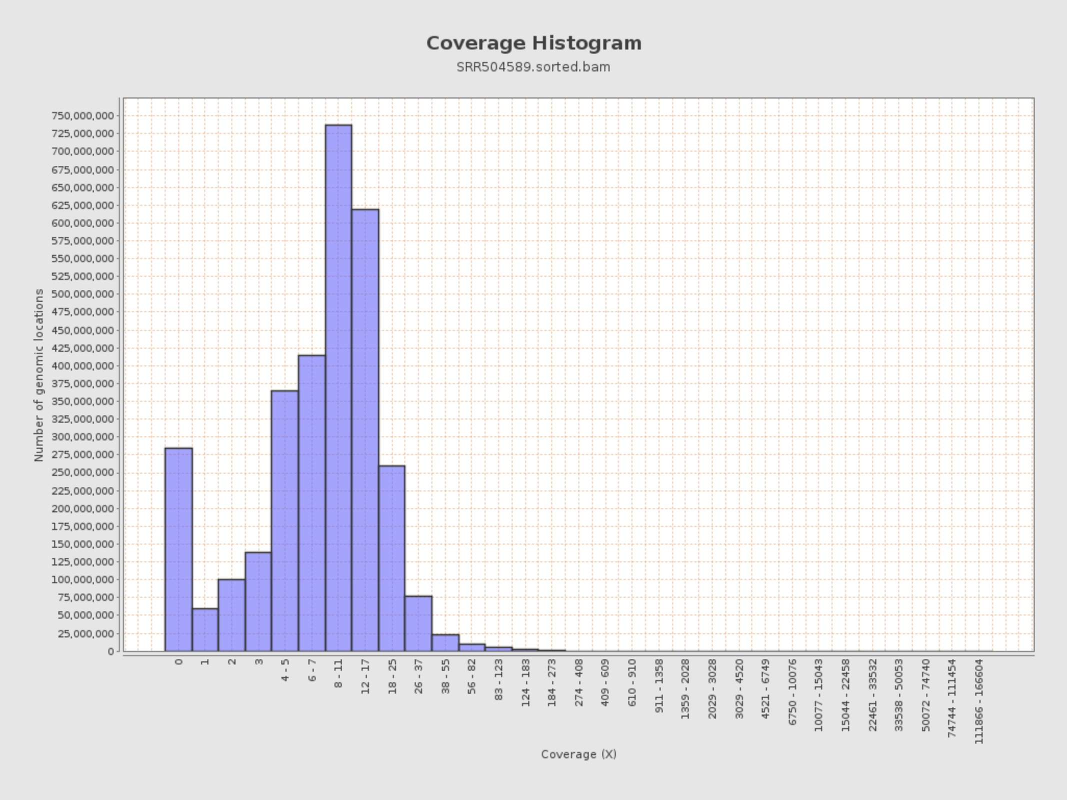
		bases	coverage	deviation
chr1	249250621	3009141232	12.0728	167.2582
chr2	243199373	2285408150	9.3973	55.4522
chr3	198022430	1914574952	9.6685	16.0548
chr4	191154276	1834971154	9.5994	110.1701
chr5	180915260	1527994658	8.4459	10.0021
chr6	171115067	1516115777	8.8602	21.6923
chr7	159138663	2729632642	17.1525	132.5298
chr8	146364022	2844952026	19.4375	64.746
chr9	141213431	1166941149	8.2637	58.3594
chr10	135534747	1576291456	11.6302	249.9807
chr11	135006516	1389319416	10.2908	37.2675
chr12	133851895	1208937390	9.0319	8.3679
chr13	115169878	785404495	6.8195	6.2166
chr14	107349540	1049620282	9.7776	9.2008
chr15	102531392	844344426	8.235	7.0174
chr16	90354753	898985234	9.9495	71.2162
chr17	81195210	1002500489	12.3468	43.4596
chr18	78077248	551616953	7.065	91.3864
chr19	59128983	646795529	10.9387	86.5162
chr20	63025520	1360012578	21.5788	28.1257
chr21	48129895	388055948	8.0627	38.7246
chr22	51304566	436265979	8.5035	9.1435
chrMT	16571	115959182	6,997.7178	1,483.2244
chrX	155270560	1149832766	7.4053	18.1276

chrY	59373566	124338302	2.0942	112.2403

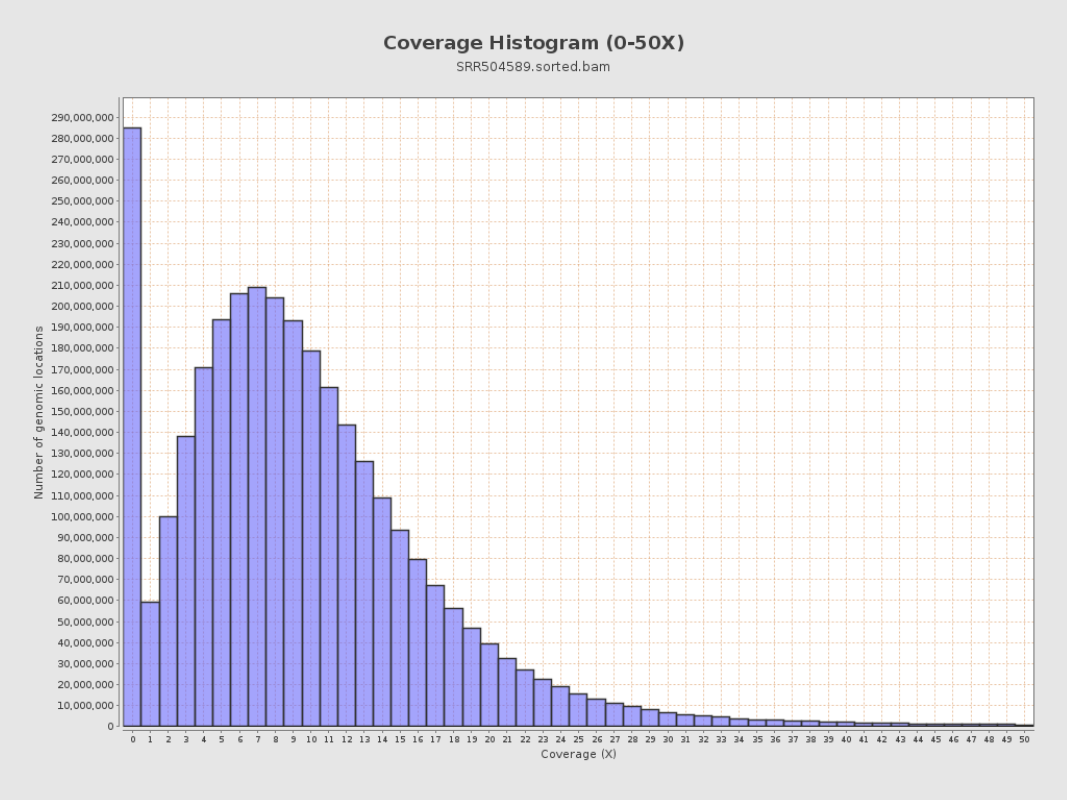
3. Results : Coverage across reference



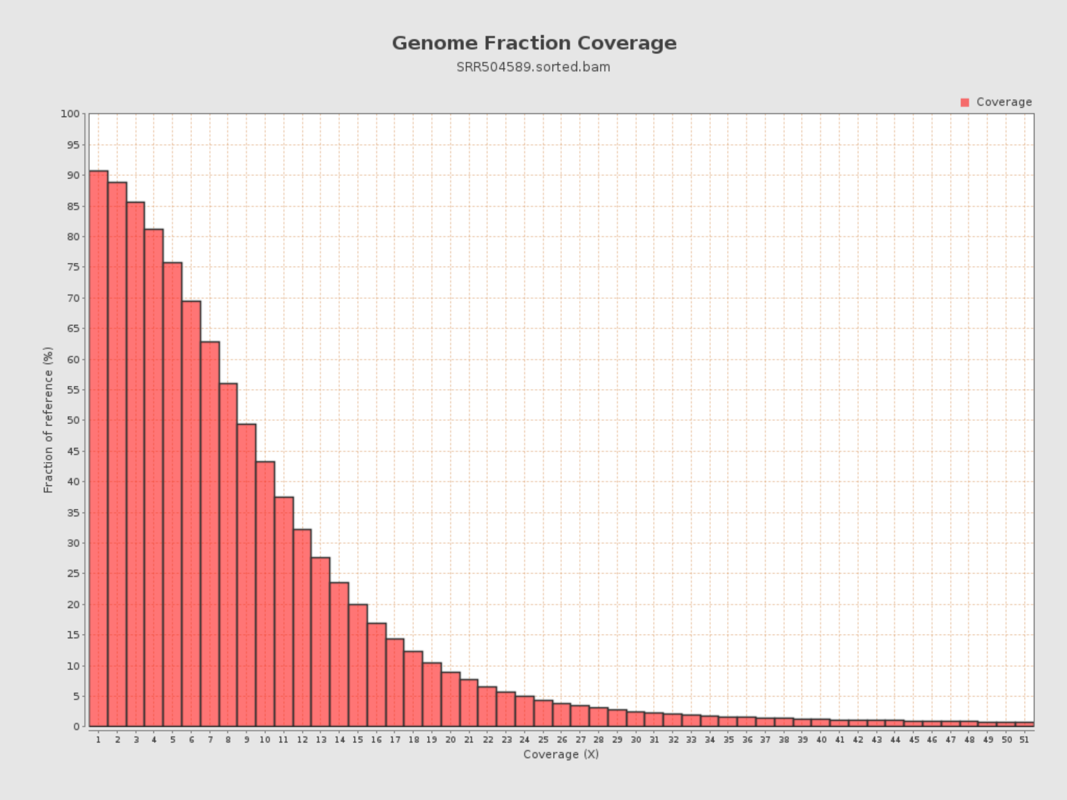
4. Results : Coverage Histogram



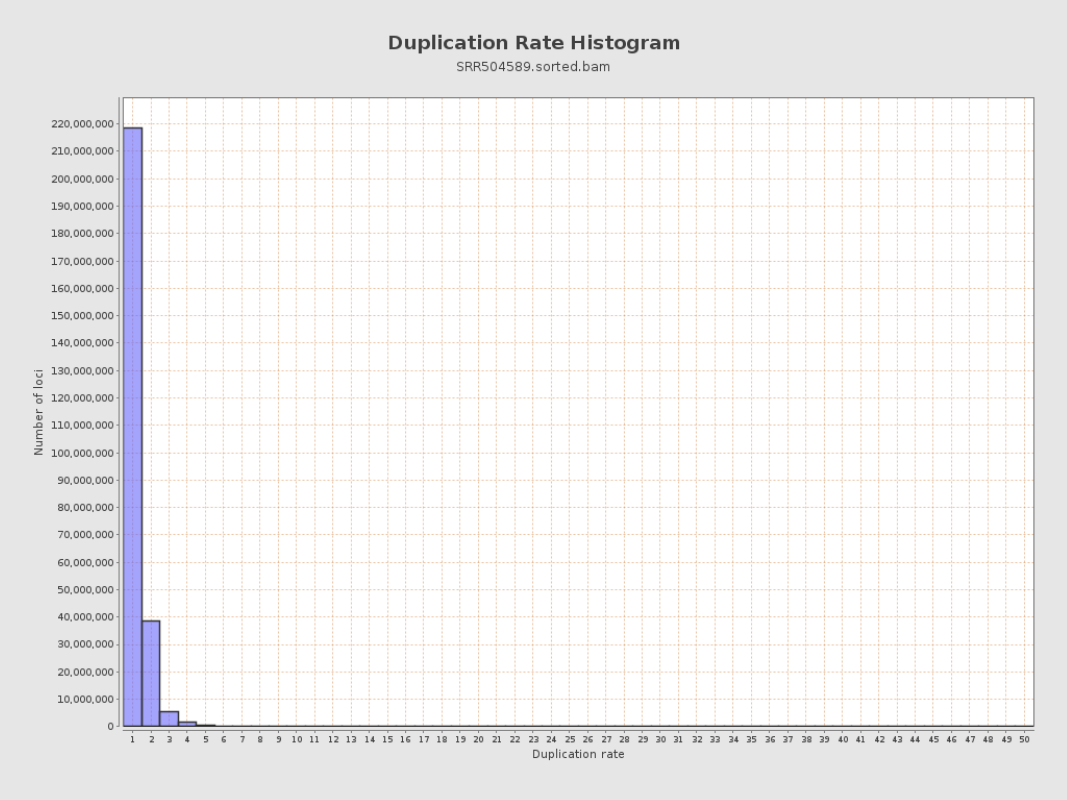
5. Results : Coverage Histogram (0-50X)



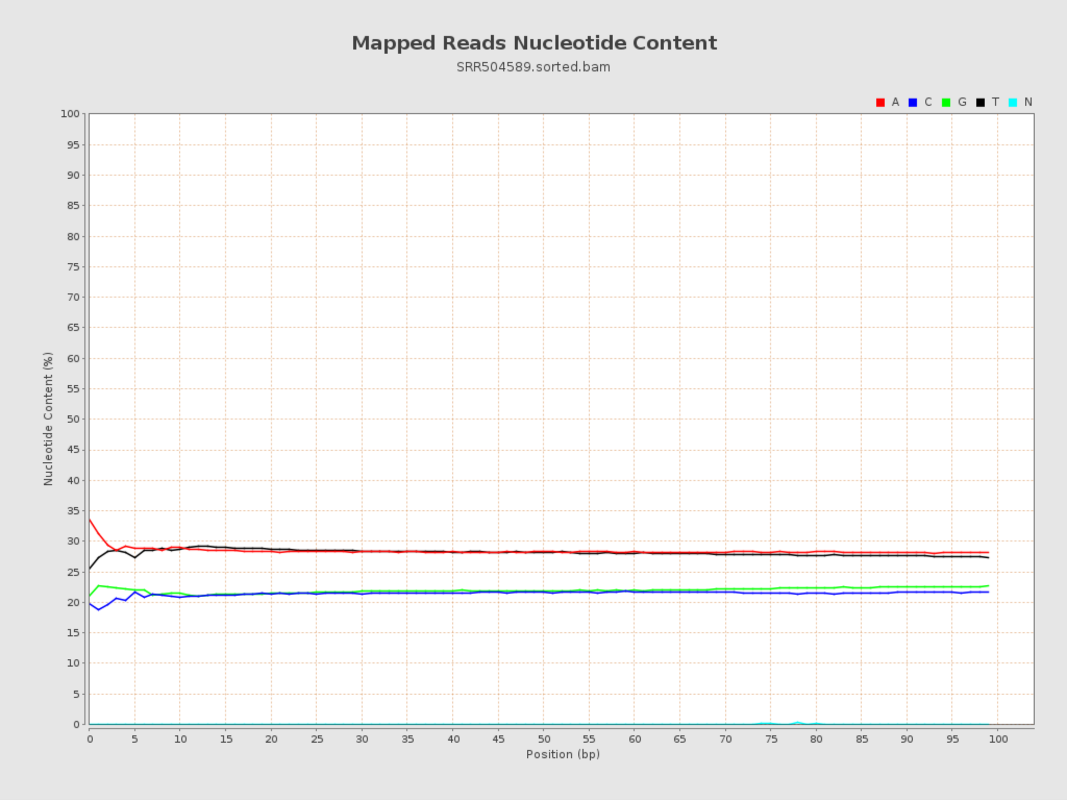
6. Results : Genome Fraction Coverage



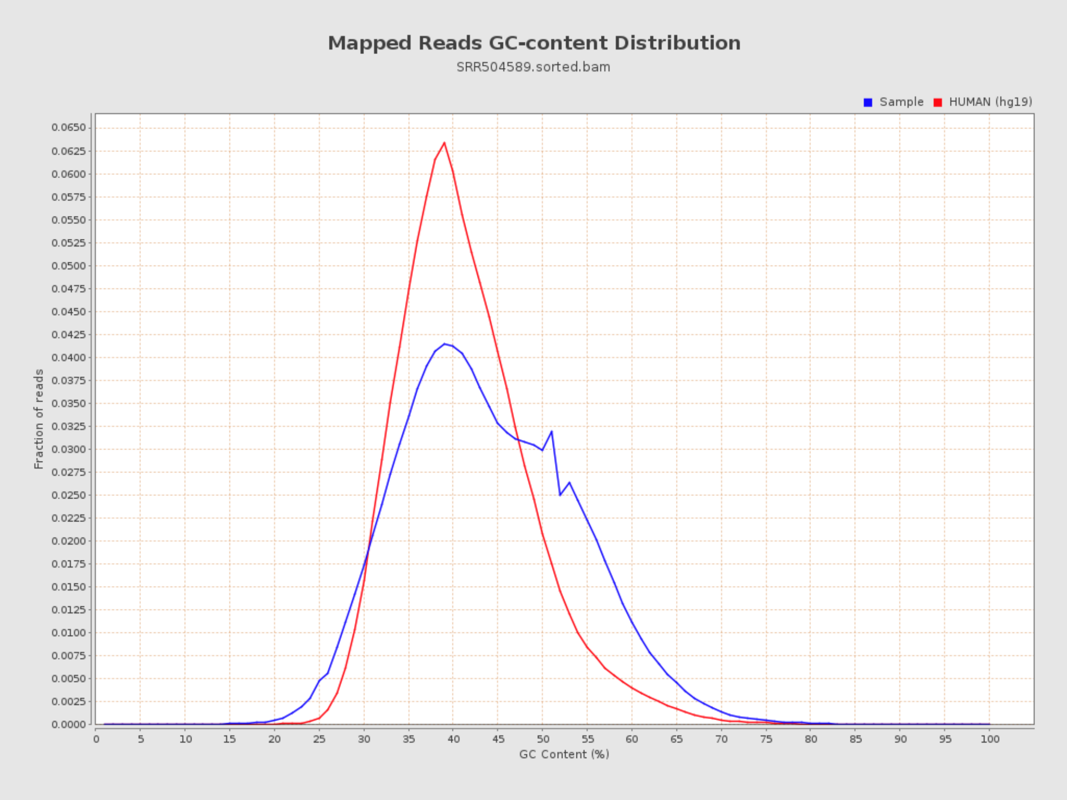
7. Results : Duplication Rate Histogram



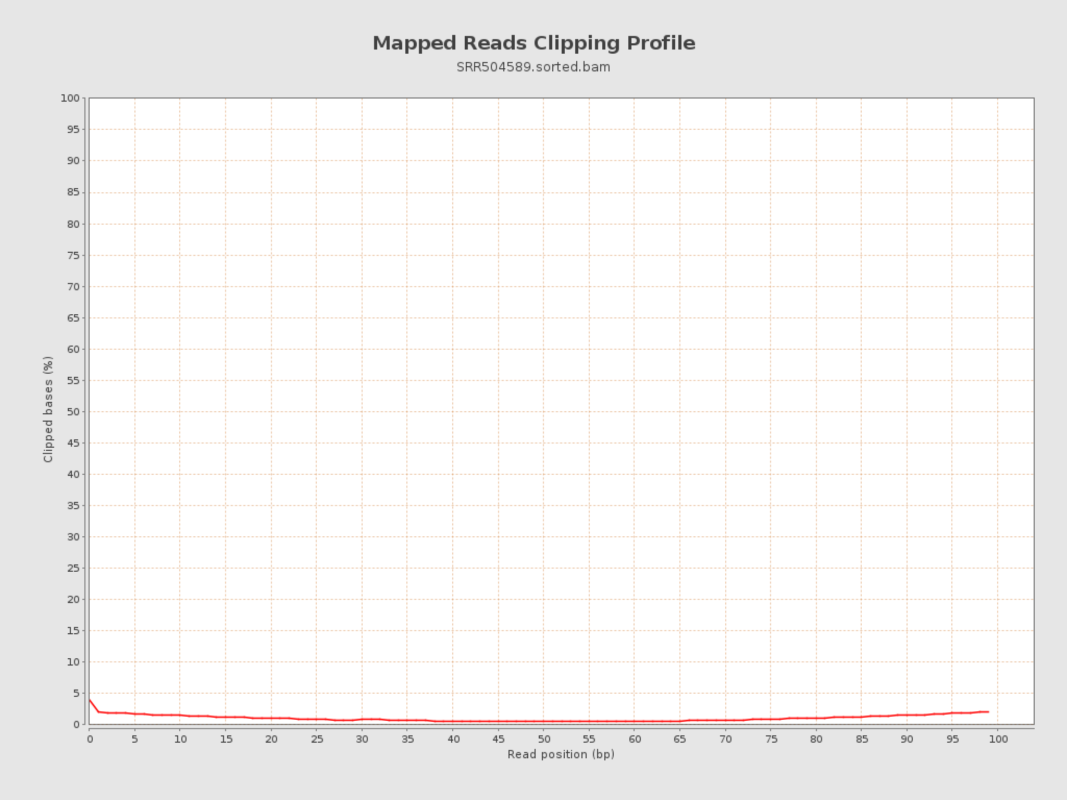
8. Results : Mapped Reads Nucleotide Content



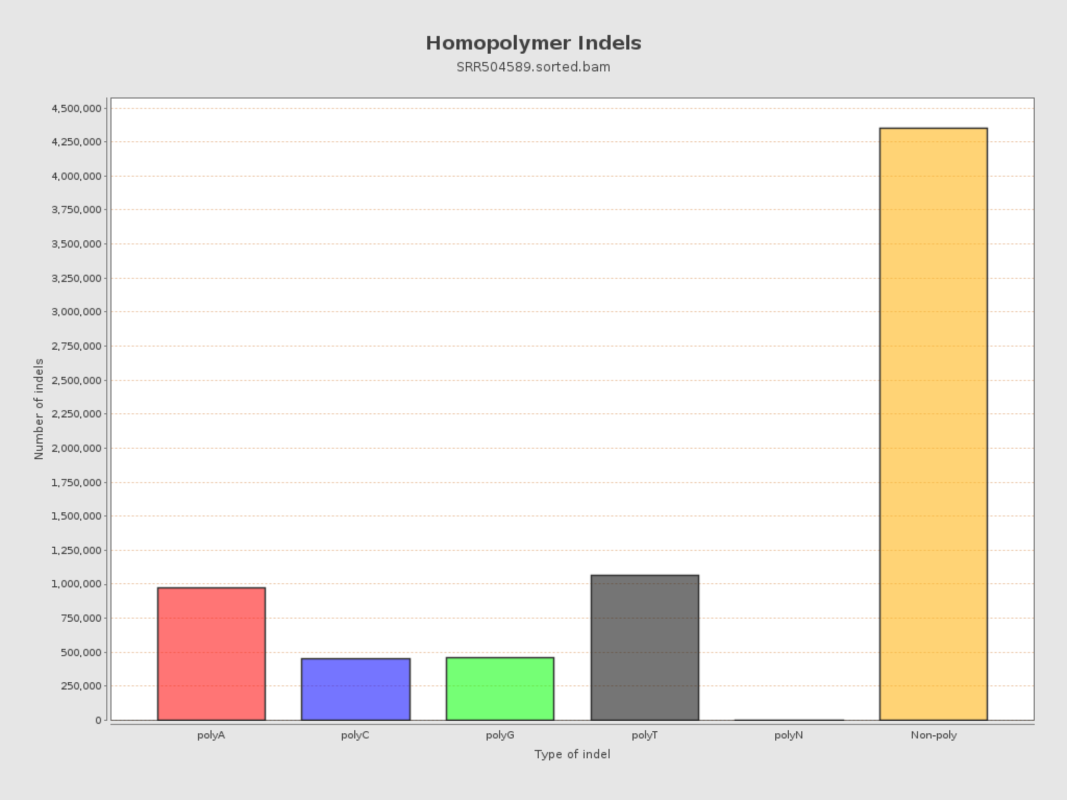
9. Results : Mapped Reads GC-content Distribution



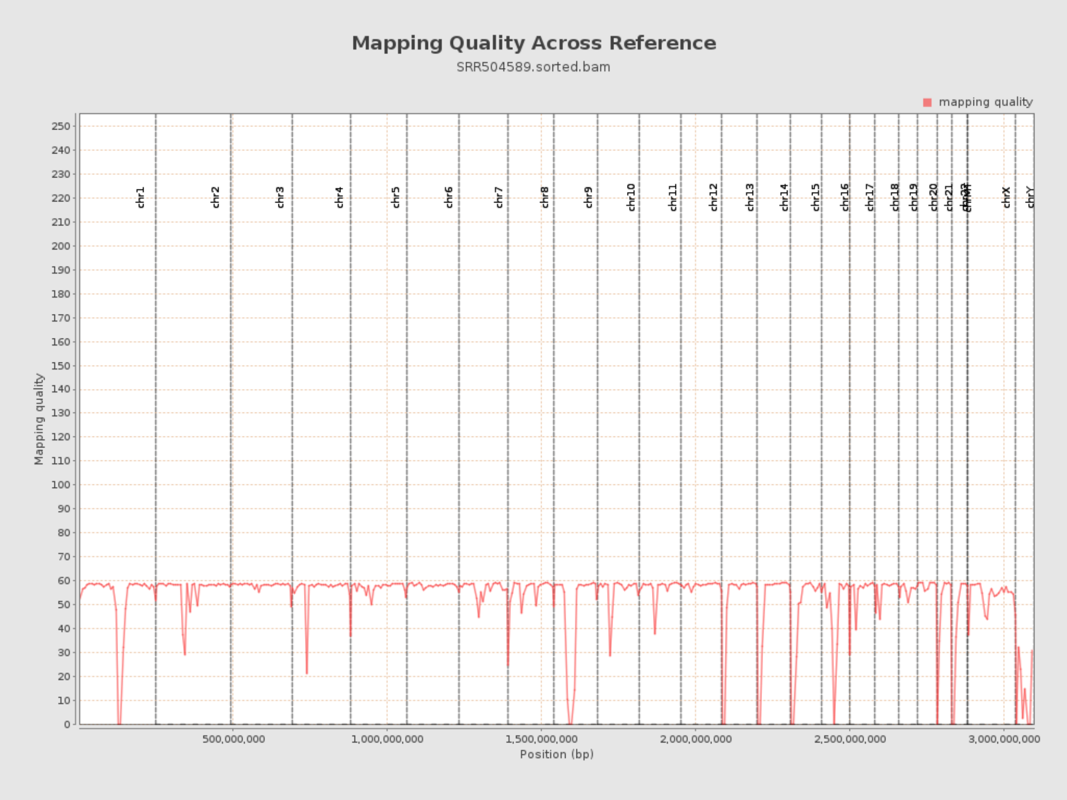
10. Results : Mapped Reads Clipping Profile



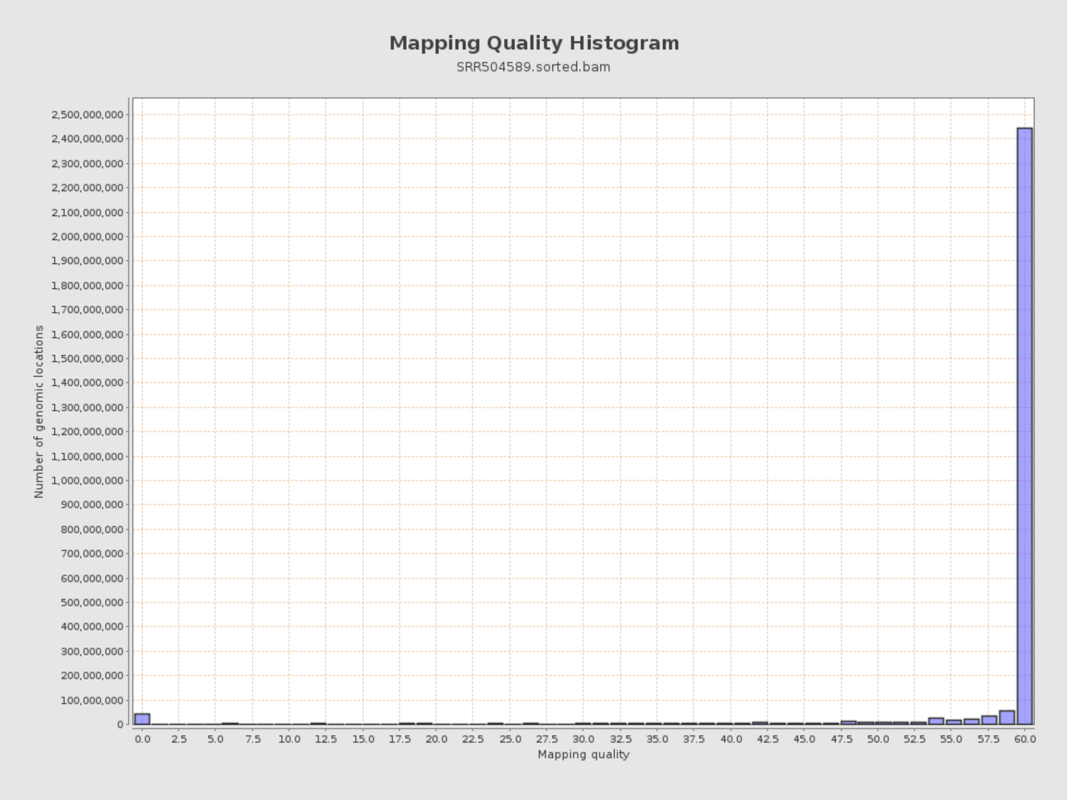
11. Results : Homopolymer Indels



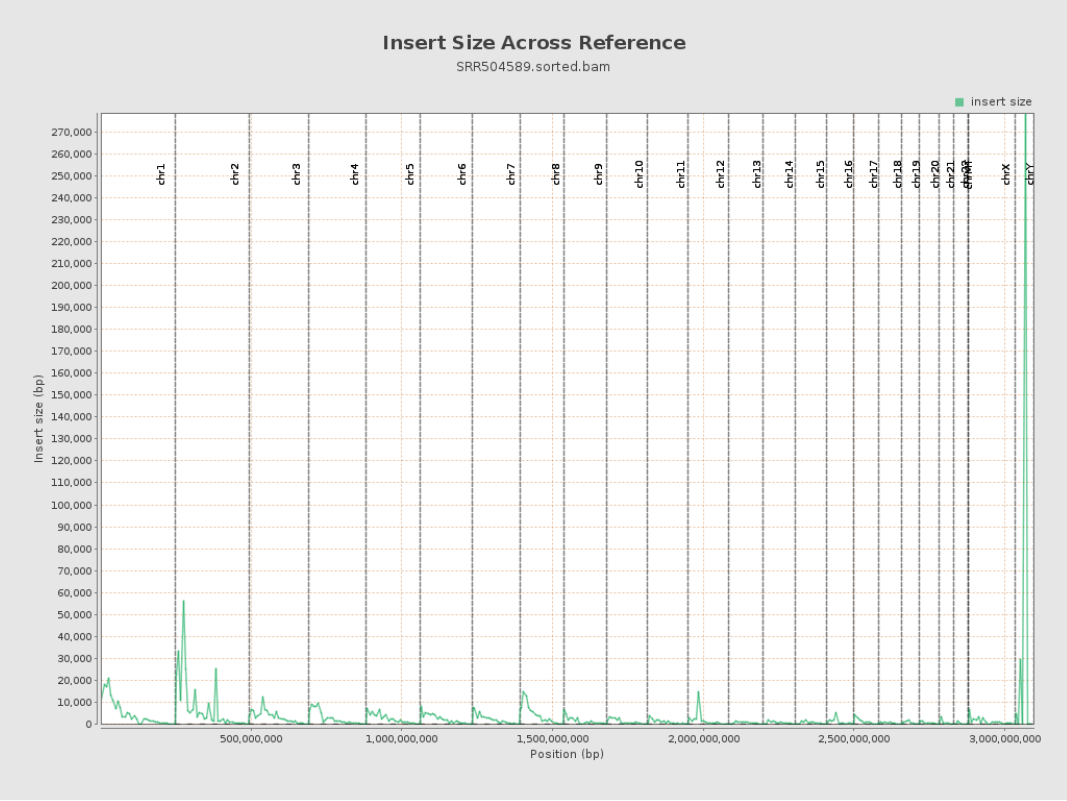
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram