Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 03:29:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504611.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_SRR504611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504611_1.fastq.gz SRR504611_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 03:29:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	483,831,634
Mapped reads	321,606,140 / 66.47%
Unmapped reads	162,225,494 / 33.53%
Mapped paired reads	321,606,140 / 66.47%
Mapped reads, first in pair	161,080,532 / 33.29%
Mapped reads, second in pair	160,525,608 / 33.18%
Mapped reads, both in pair	319,527,030 / 66.04%
Mapped reads, singletons	2,079,110 / 0.43%
Secondary alignments	0
Supplementary alignments	2,061,529 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	89,055,408 / 18.41%
Duplication rate	24.05%
Clipped reads	15,503,810 / 3.2%

2.2. ACGT Content

Number/percentage of A's	8,254,040,512 / 25.85%
Number/percentage of C's	7,643,098,691 / 23.93%
Number/percentage of T's	8,294,048,264 / 25.97%
Number/percentage of G's	7,740,153,499 / 24.24%
Number/percentage of N's	5,286,821 / 0.02%

GC Percentage	48.17%

2.3. Coverage

Mean	10.3191
Standard Deviation	26.6484

2.4. Mapping Quality

Mean Mapping Quality	53.76

2.5. Insert size

Mean	25,183.81
Standard Deviation	1,531,329.49
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	161,267,906
Insertions	2,376,366
Mapped reads with at least one insertion	0.72%
Deletions	3,124,361
Mapped reads with at least one deletion	0.94%
Homopolymer indels	40.05%

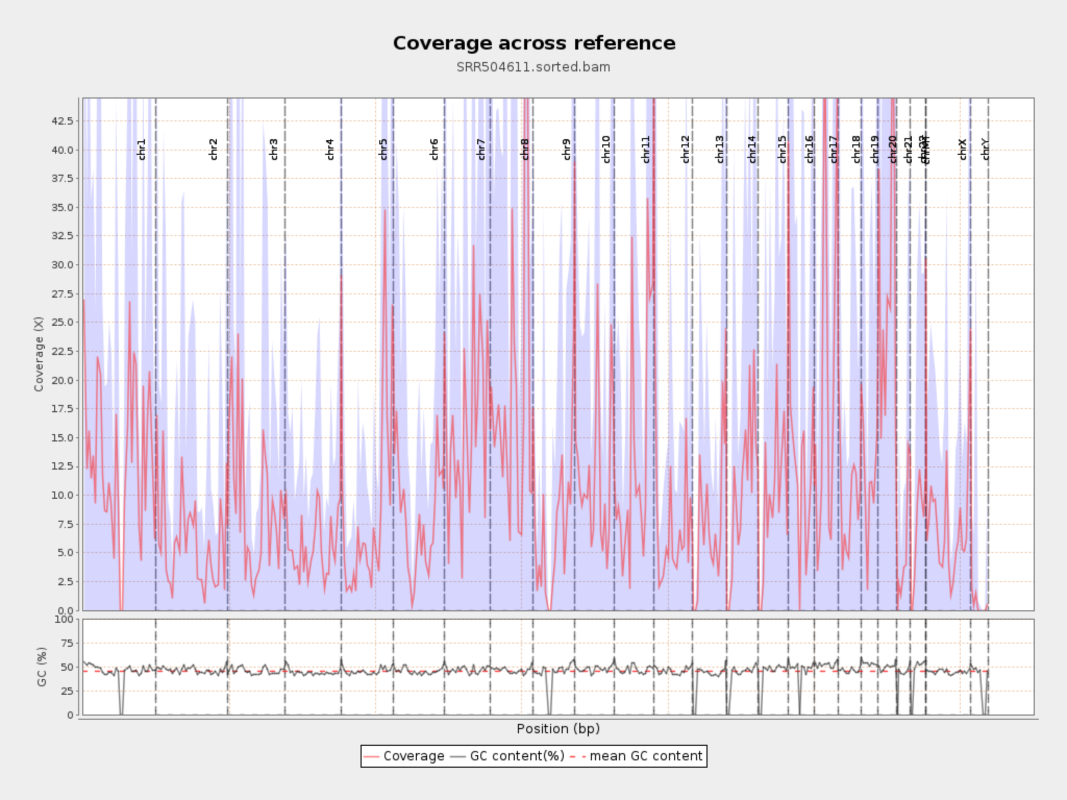
2.7. Chromosome stats

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

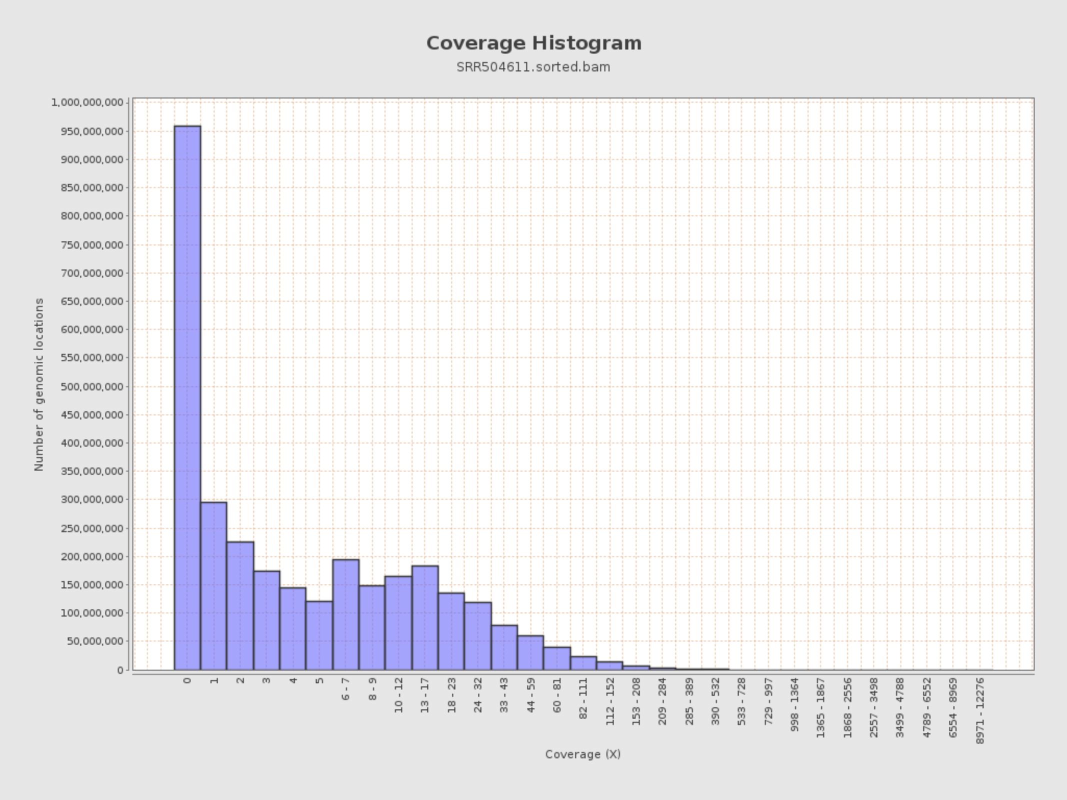
		bases	coverage	deviation
chr1	249250621	3240238669	12.9999	25.9801
chr2	243199373	1426600168	5.866	15.4419
chr3	198022430	1803061962	9.1053	24.7832
chr4	191154276	1075350186	5.6256	10.6772
chr5	180915260	1557287543	8.6078	24.7563
chr6	171115067	1353426560	7.9095	15.383
chr7	159138663	2554607733	16.0527	29.7562
chr8	146364022	2875459310	19.6459	47.1965
chr9	141213431	975112335	6.9052	19.2456
chr10	135534747	1569862305	11.5827	24.0068
chr11	135006516	1801087570	13.3407	30.7271
chr12	133851895	963893680	7.2012	17.974
chr13	115169878	872710117	7.5776	16.9488
chr14	107349540	1132370955	10.5484	21.1169
chr15	102531392	974195520	9.5014	19.8299
chr16	90354753	1194169974	13.2165	29.8992
chr17	81195210	1553988700	19.1389	61.8687
chr18	78077248	729471493	9.3429	26.78
chr19	59128983	672763080	11.3779	24.3742
chr20	63025520	1814982679	28.7976	51.5561
chr21	48129895	266006991	5.5269	14.2741
chr22	51304566	352199650	6.8649	17.7052
chrMT	16571	506253	30.5505	14.2677
chrX	155270560	1154704049	7.4367	13.9605

chrY	59373566	30714612	0.5173	11.8185

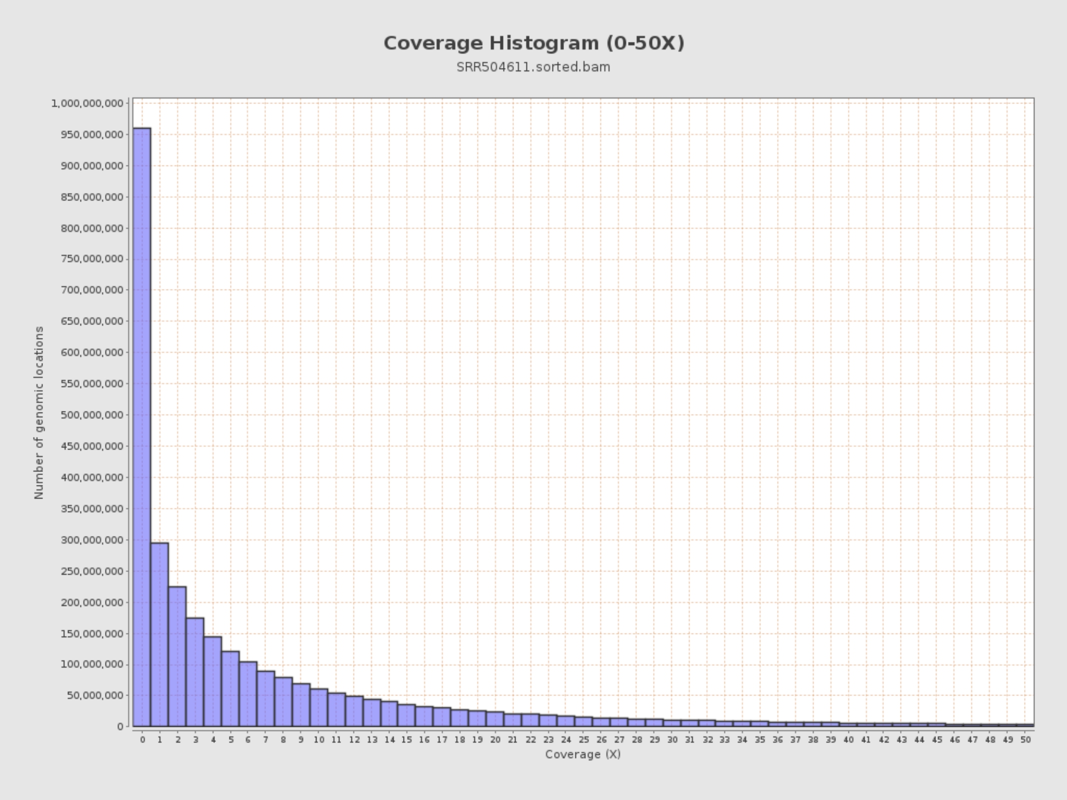
3. Results : Coverage across reference



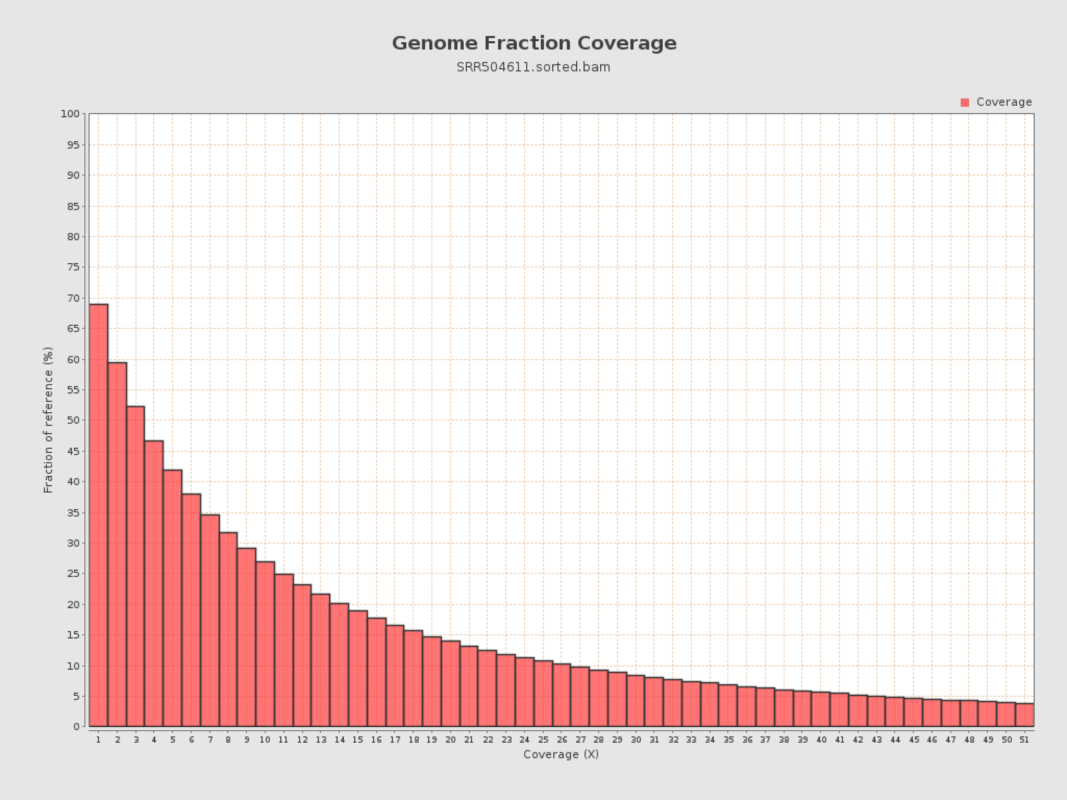
4. Results : Coverage Histogram



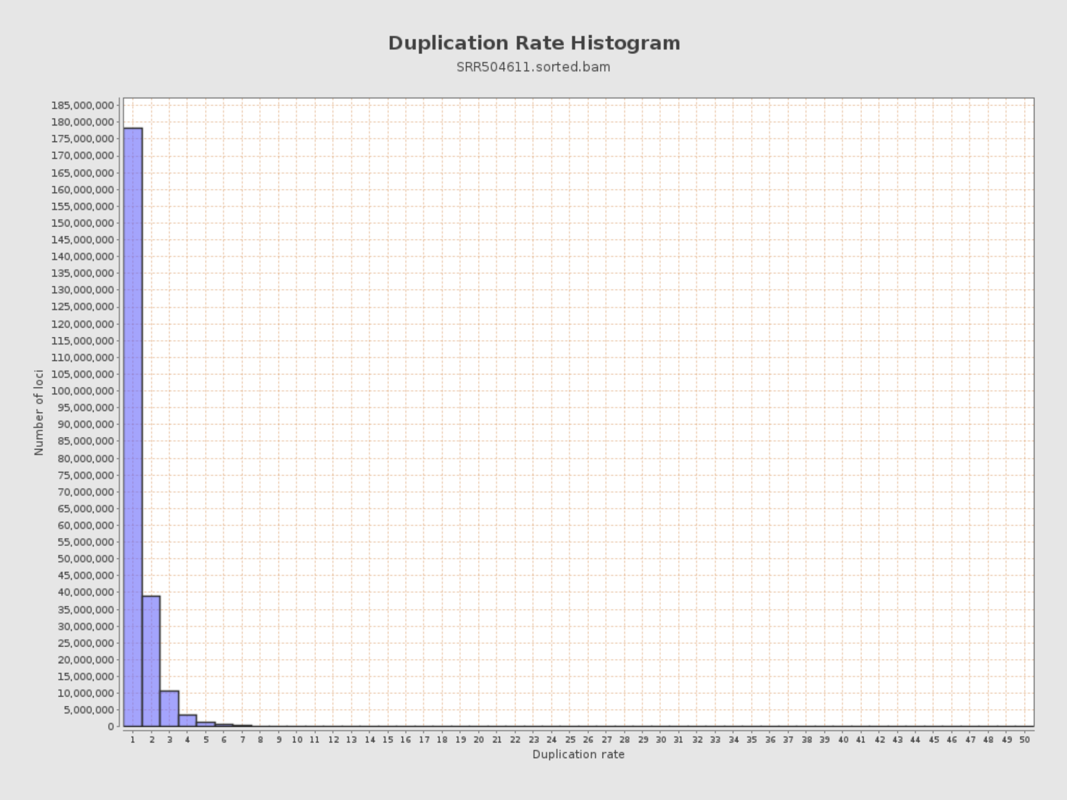
5. Results : Coverage Histogram (0-50X)



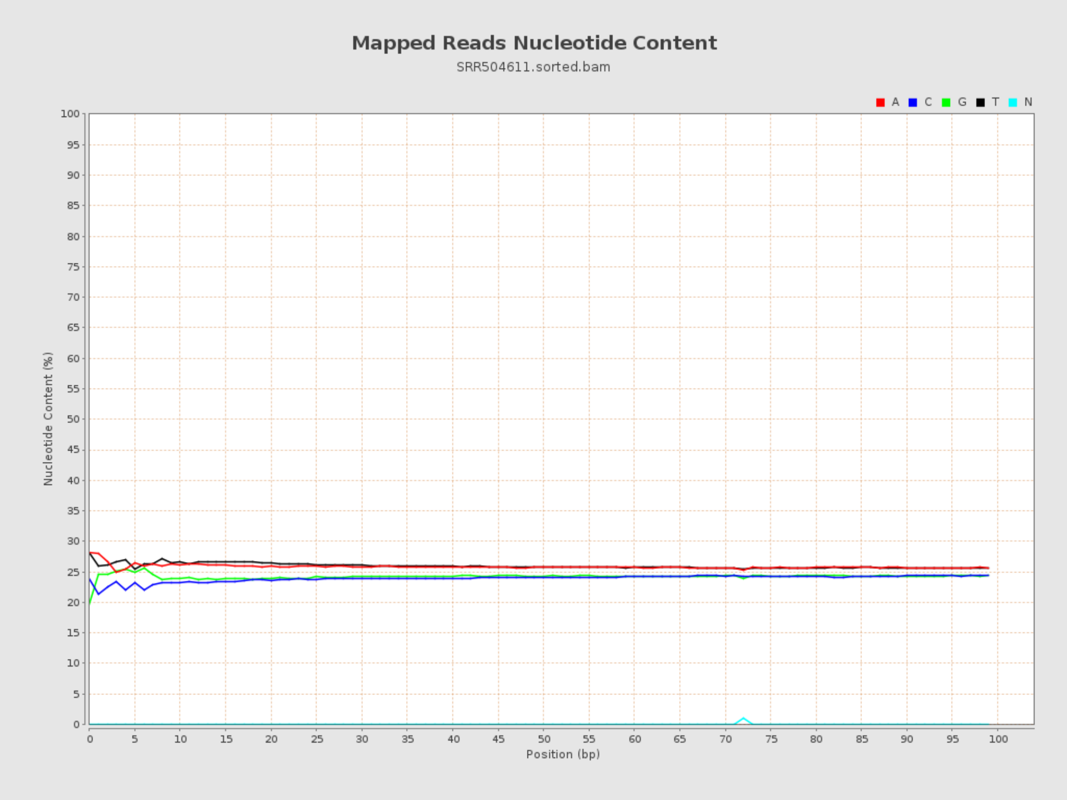
6. Results : Genome Fraction Coverage



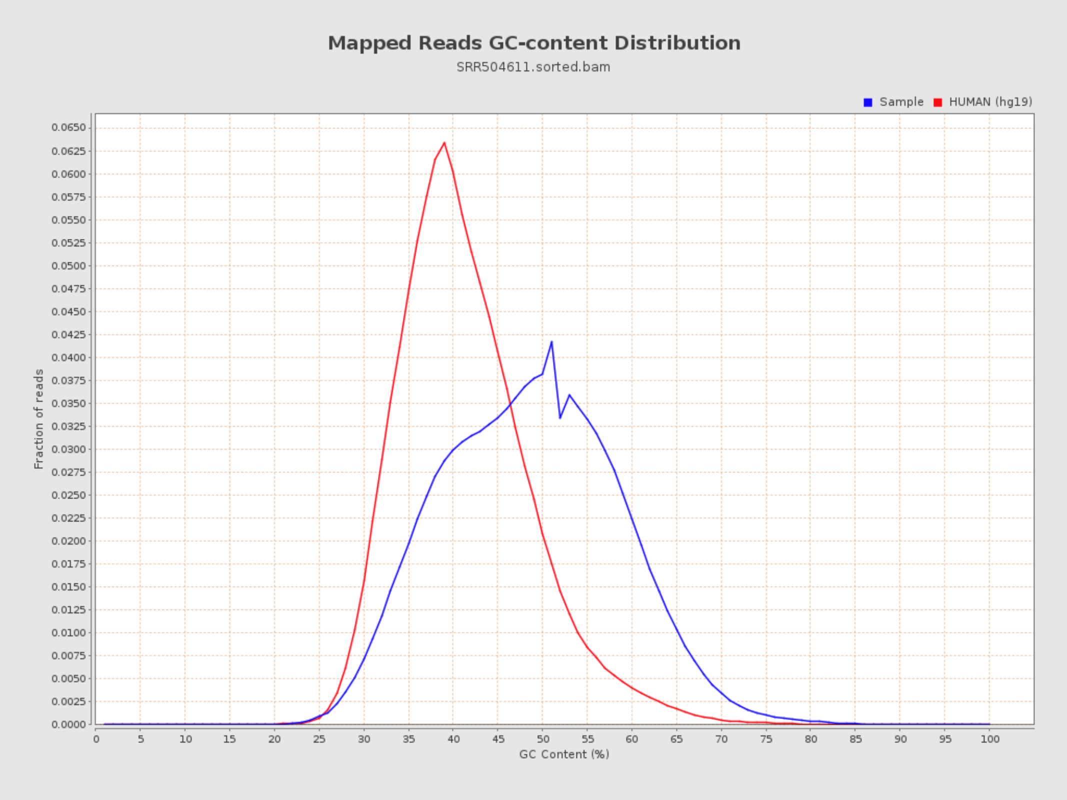
7. Results : Duplication Rate Histogram



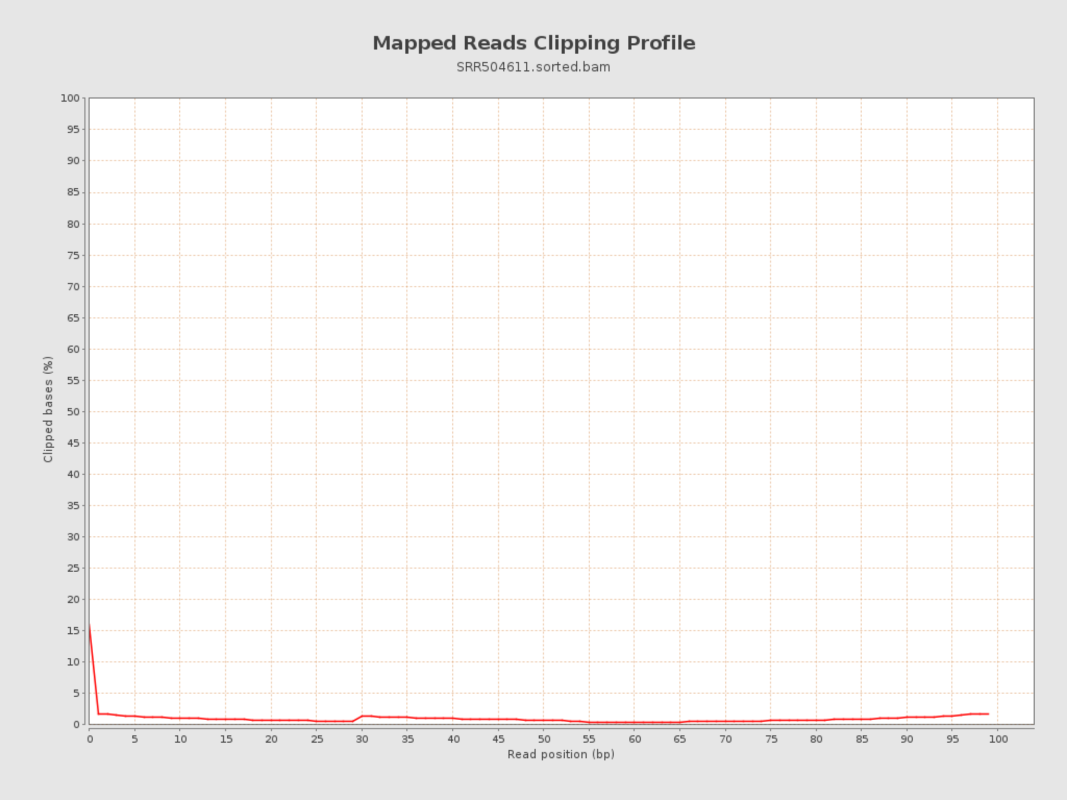
8. Results : Mapped Reads Nucleotide Content



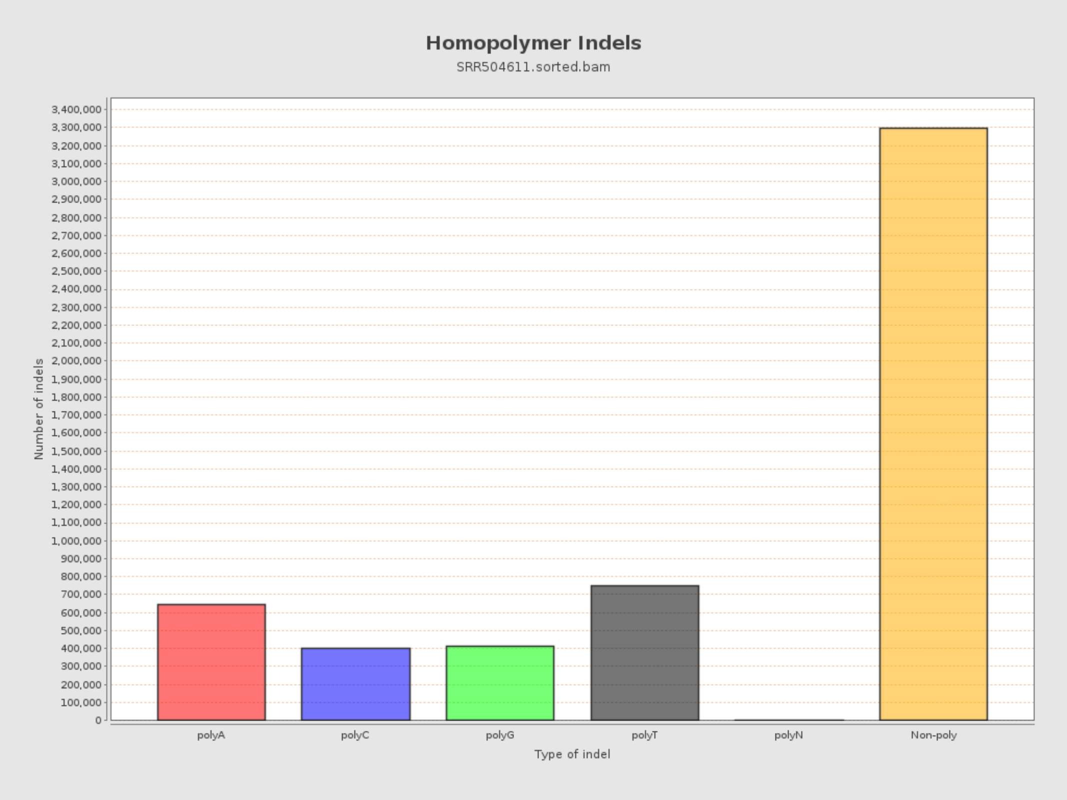
9. Results : Mapped Reads GC-content Distribution



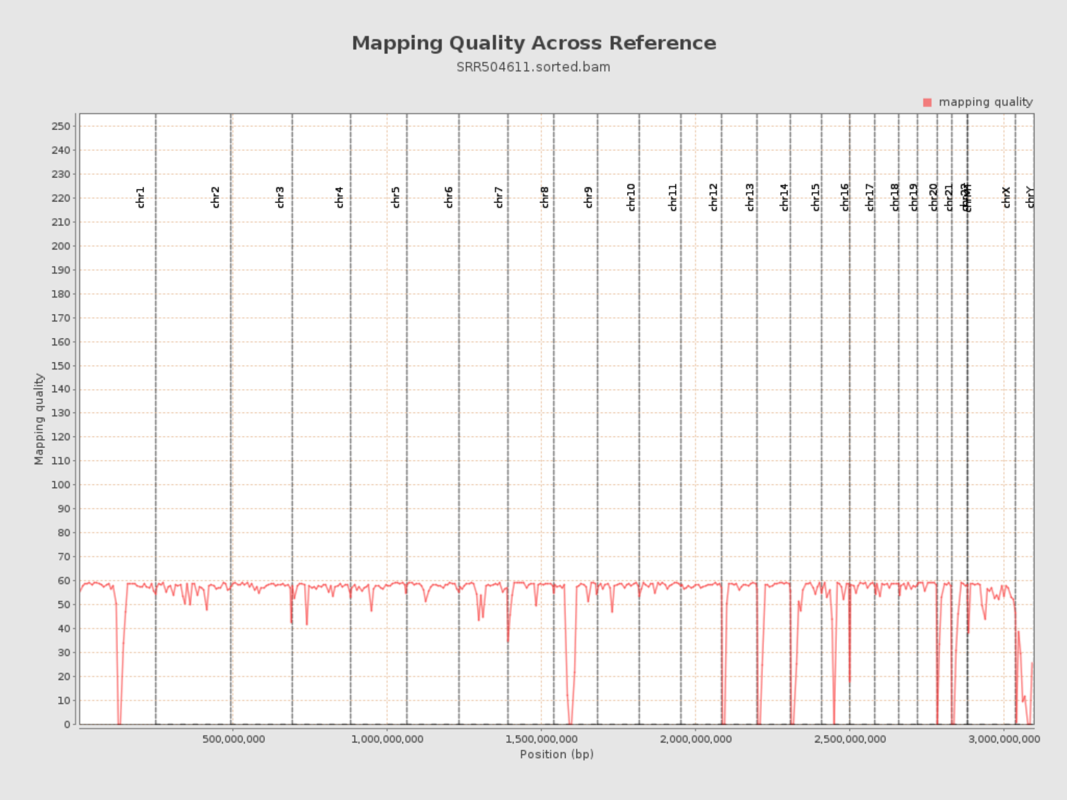
10. Results : Mapped Reads Clipping Profile



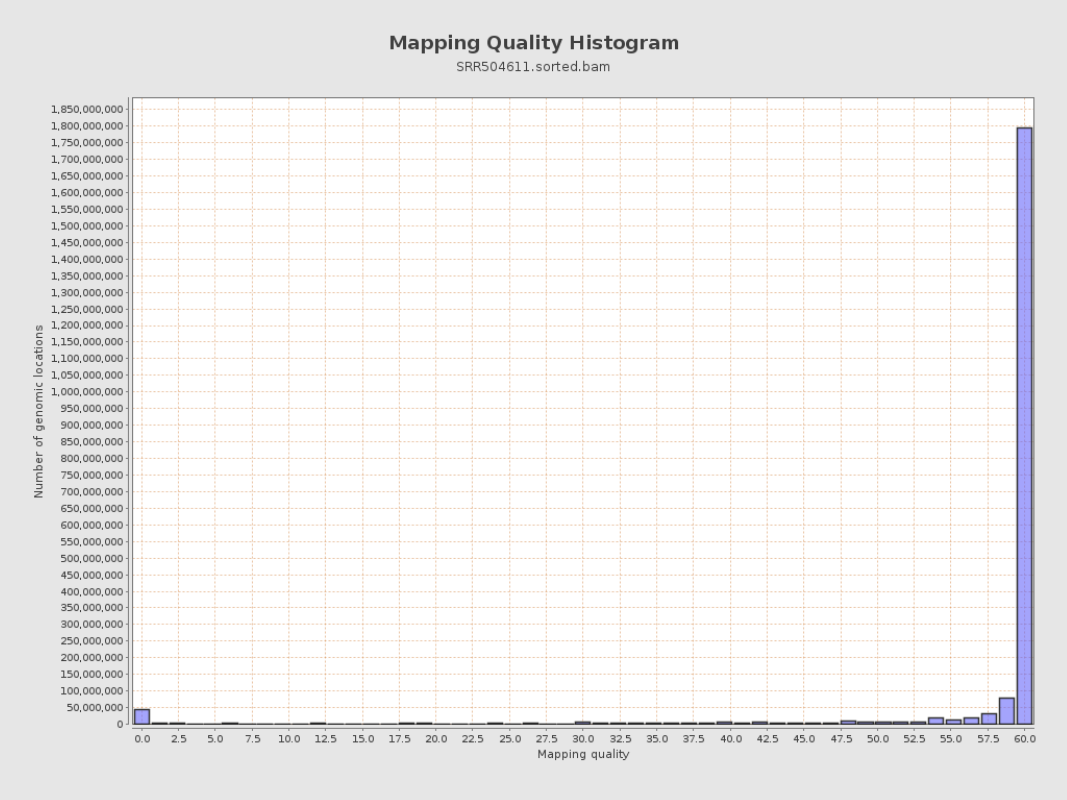
11. Results : Homopolymer Indels



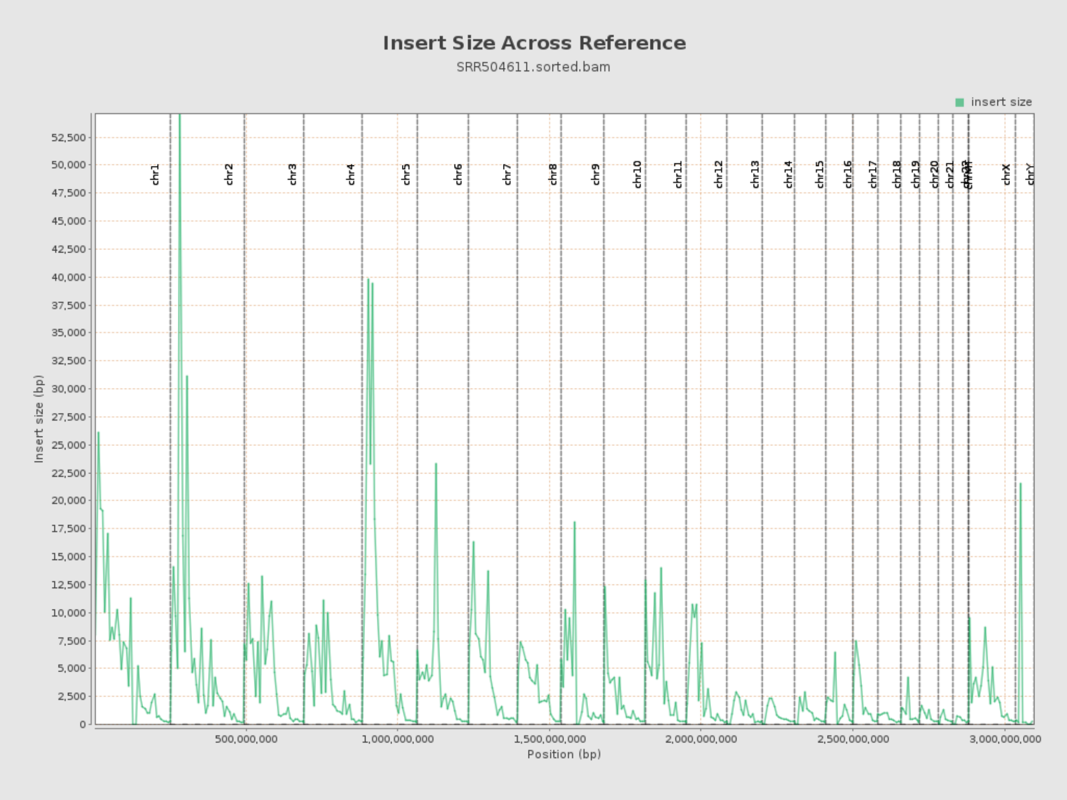
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram