Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/31 19:07:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504632.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_SRR504632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504632_1.fastq.gz SRR504632_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 31 19:07:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	581,613,740
Mapped reads	483,581,890 / 83.14%
Unmapped reads	98,031,850 / 16.86%
Mapped paired reads	483,581,890 / 83.14%
Mapped reads, first in pair	245,815,731 / 42.26%
Mapped reads, second in pair	237,766,159 / 40.88%
Mapped reads, both in pair	460,102,776 / 79.11%
Mapped reads, singletons	23,479,114 / 4.04%
Secondary alignments	0
Supplementary alignments	4,159,930 / 0.72%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	166,545,809 / 28.64%
Duplication rate	22.86%
Clipped reads	117,772,804 / 20.25%

2.2. ACGT Content

Number/percentage of A's	12,313,189,241 / 27.18%
Number/percentage of C's	10,285,277,516 / 22.7%
Number/percentage of T's	12,460,136,294 / 27.5%
Number/percentage of G's	10,192,901,932 / 22.5%
Number/percentage of N's	51,359,336 / 0.11%

GC Percentage	45.2%

2.3. Coverage

Mean	14.6459
Standard Deviation	303.3744

2.4. Mapping Quality

Mean Mapping Quality	51.46

2.5. Insert size

Mean	103,120.02
Standard Deviation	2,987,785.76
P25/Median/P75	308 / 353 / 406

2.6. Mismatches and indels

General error rate	2.69%
Mismatches	1,172,078,239
Insertions	12,343,258
Mapped reads with at least one insertion	2.38%
Deletions	11,308,582
Mapped reads with at least one deletion	2.18%
Homopolymer indels	33.12%

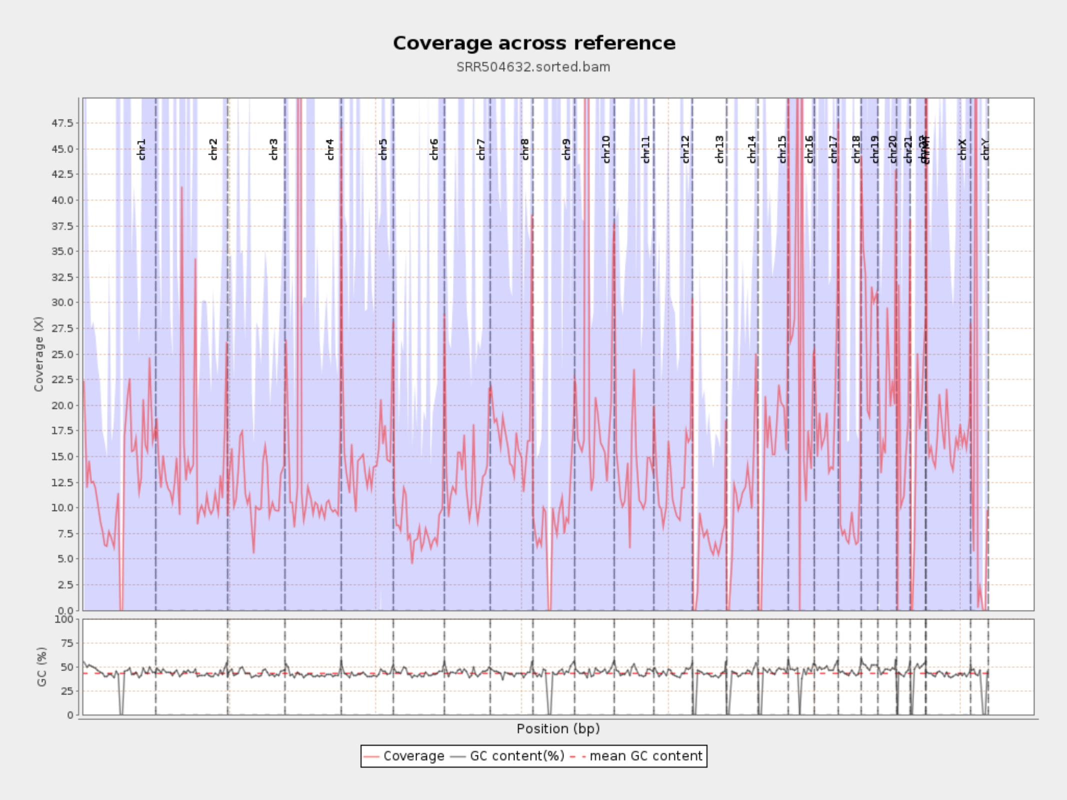
2.7. Chromosome stats

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

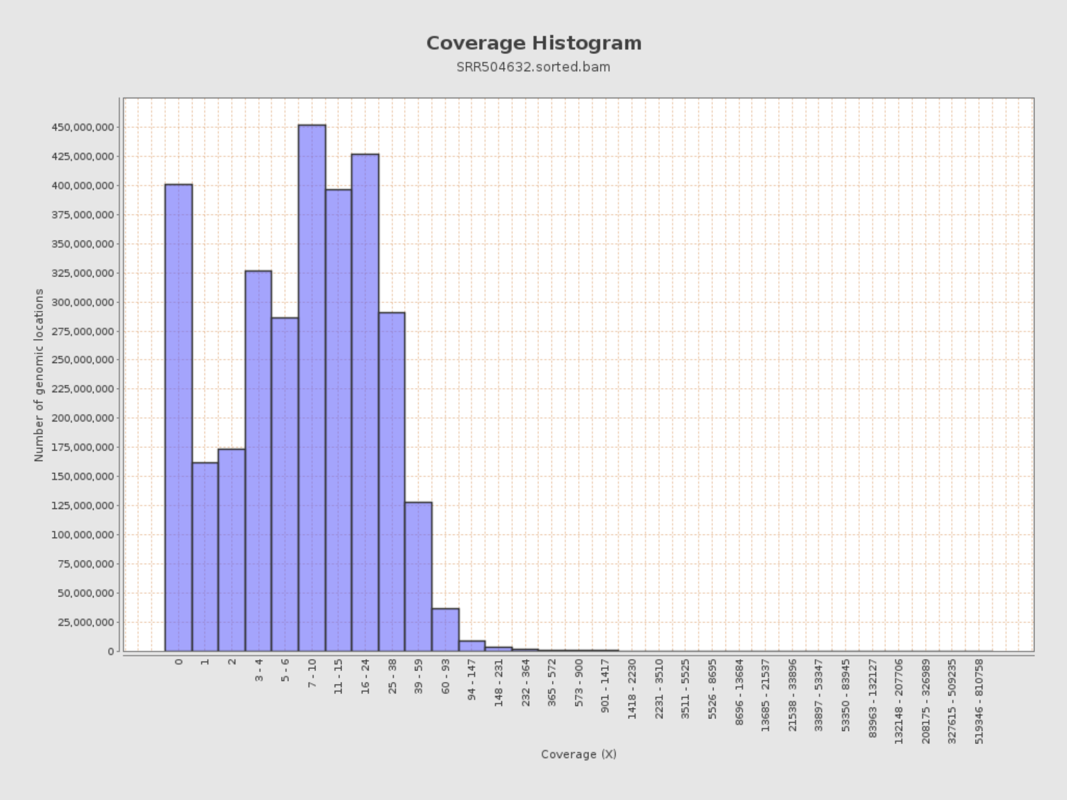
		bases	coverage	deviation
chr1	249250621	3207410434	12.8682	103.3021
chr2	243199373	3425593942	14.0855	312.0345
chr3	198022430	2348086965	11.8577	35.6943
chr4	191154276	3273017291	17.1224	764.1887
chr5	180915260	2821688251	15.5967	43.6809
chr6	171115067	1359924518	7.9474	31.3783
chr7	159138663	2139481079	13.4441	49.4157
chr8	146364022	2533136188	17.3071	229.7378
chr9	141213431	1190165304	8.4281	146.6118
chr10	135534747	3374434921	24.8972	750.0013
chr11	135006516	1846758192	13.679	35.8275
chr12	133851895	1723757086	12.8781	31.6484
chr13	115169878	709798165	6.1631	15.2699
chr14	107349540	1170380910	10.9025	36.9487
chr15	102531392	1546742178	15.0855	25.1637
chr16	90354753	2388526939	26.435	307.8807
chr17	81195210	1440951416	17.7468	98.1698
chr18	78077248	753673744	9.6529	388.9258
chr19	59128983	1722760973	29.1356	62.6465
chr20	63025520	1324784324	21.0198	208.5253
chr21	48129895	859472032	17.8573	277.7743
chr22	51304566	784263820	15.2864	40.3455
chrMT	16571	15134013	913.283	425.865
chrX	155270560	2645200938	17.0361	34.3005

chrY	59373566	734180346	12.3654	711.3607

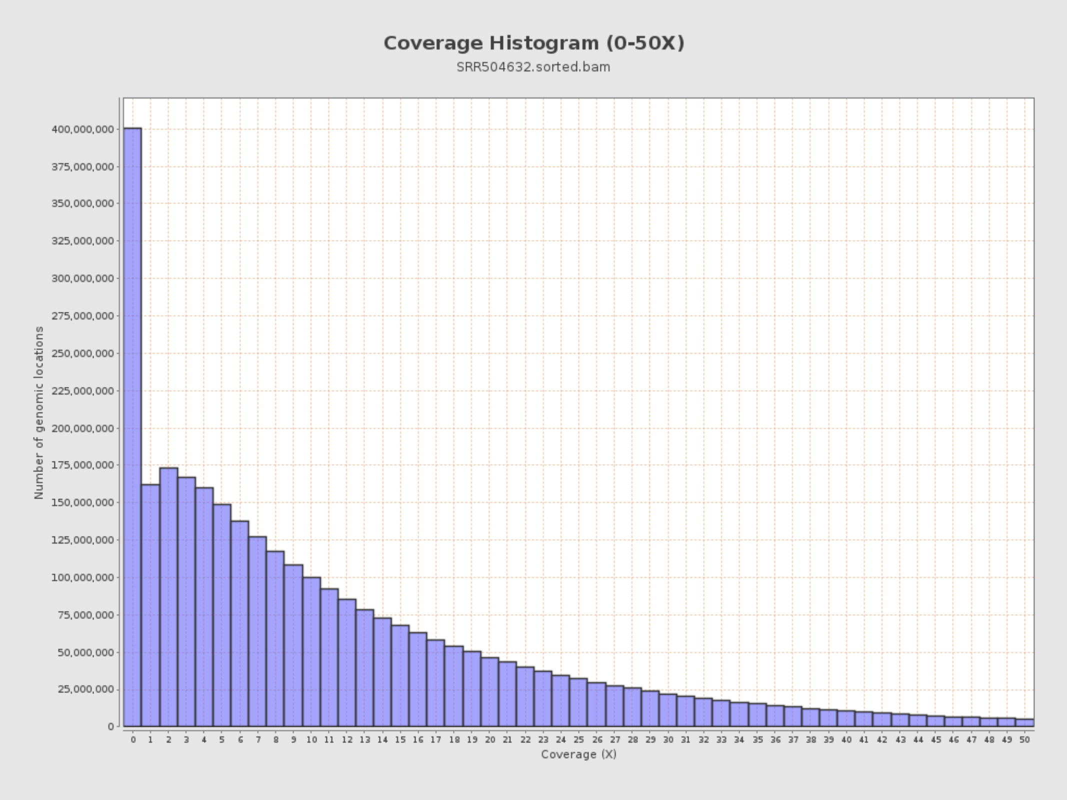
3. Results : Coverage across reference



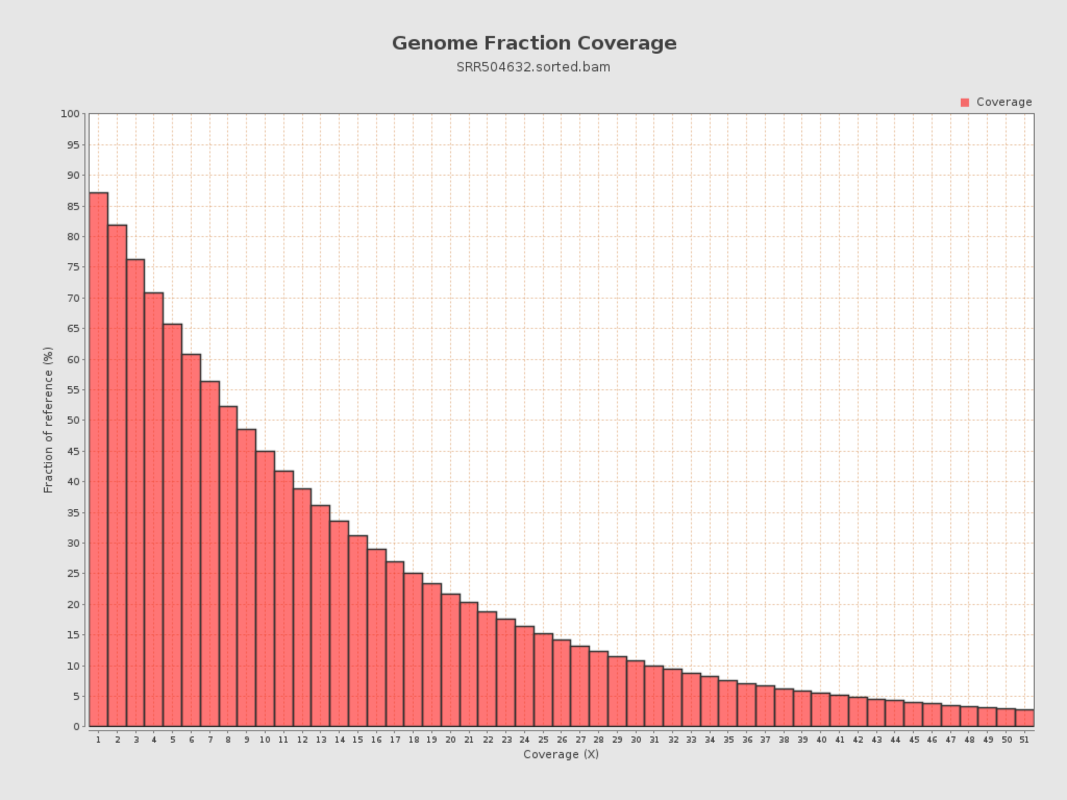
4. Results : Coverage Histogram



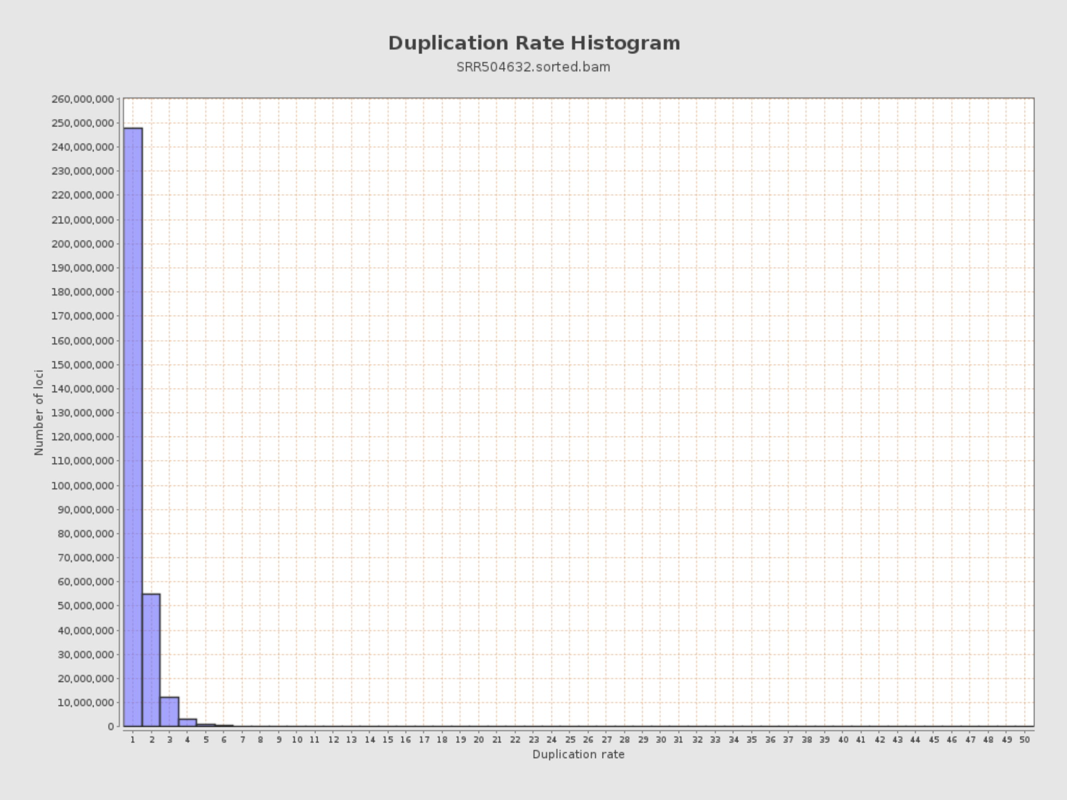
5. Results : Coverage Histogram (0-50X)



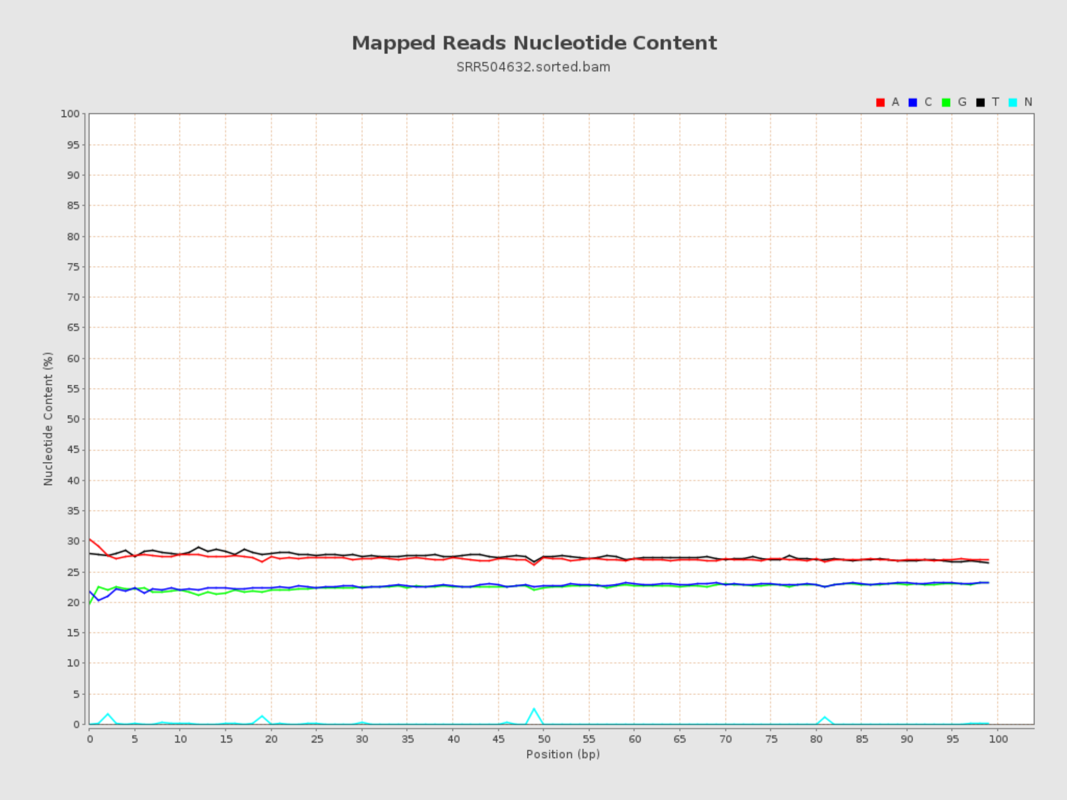
6. Results : Genome Fraction Coverage



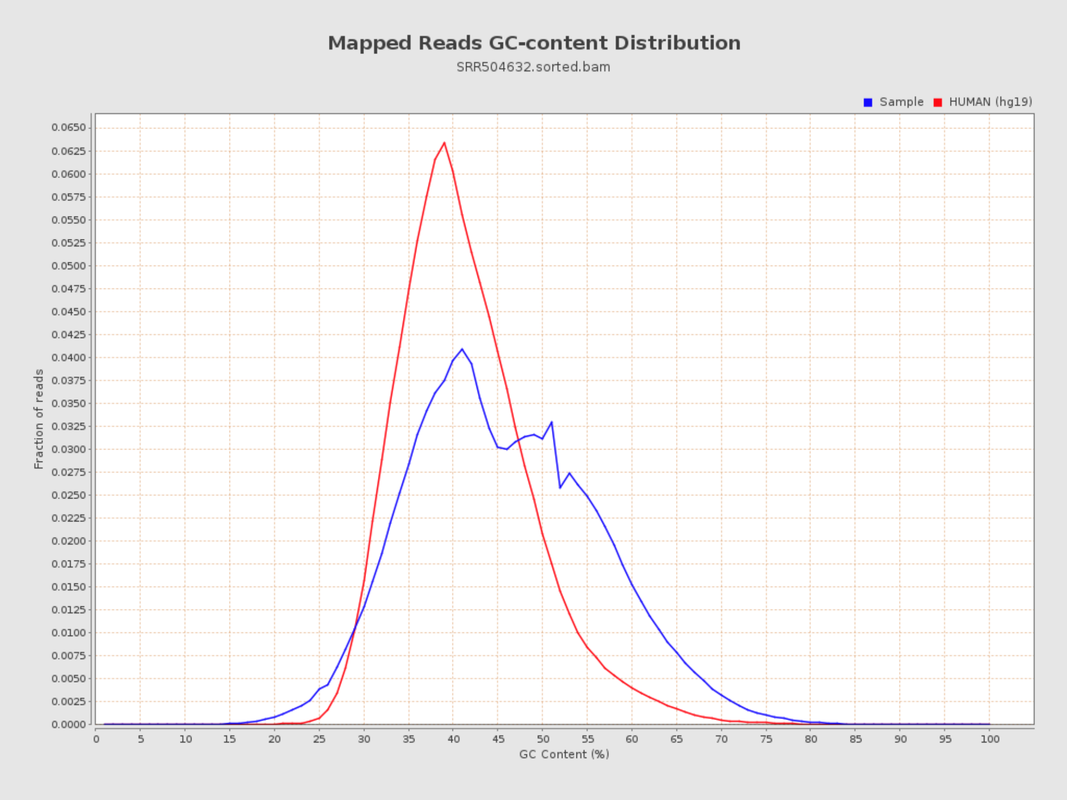
7. Results : Duplication Rate Histogram



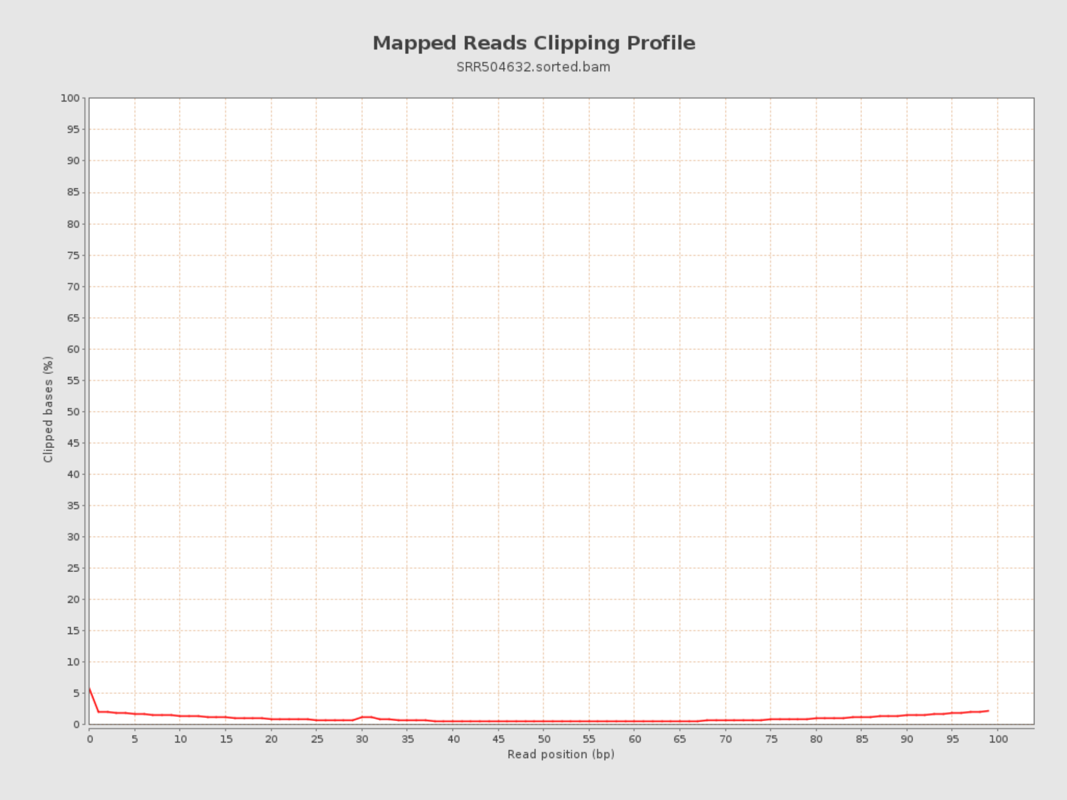
8. Results : Mapped Reads Nucleotide Content



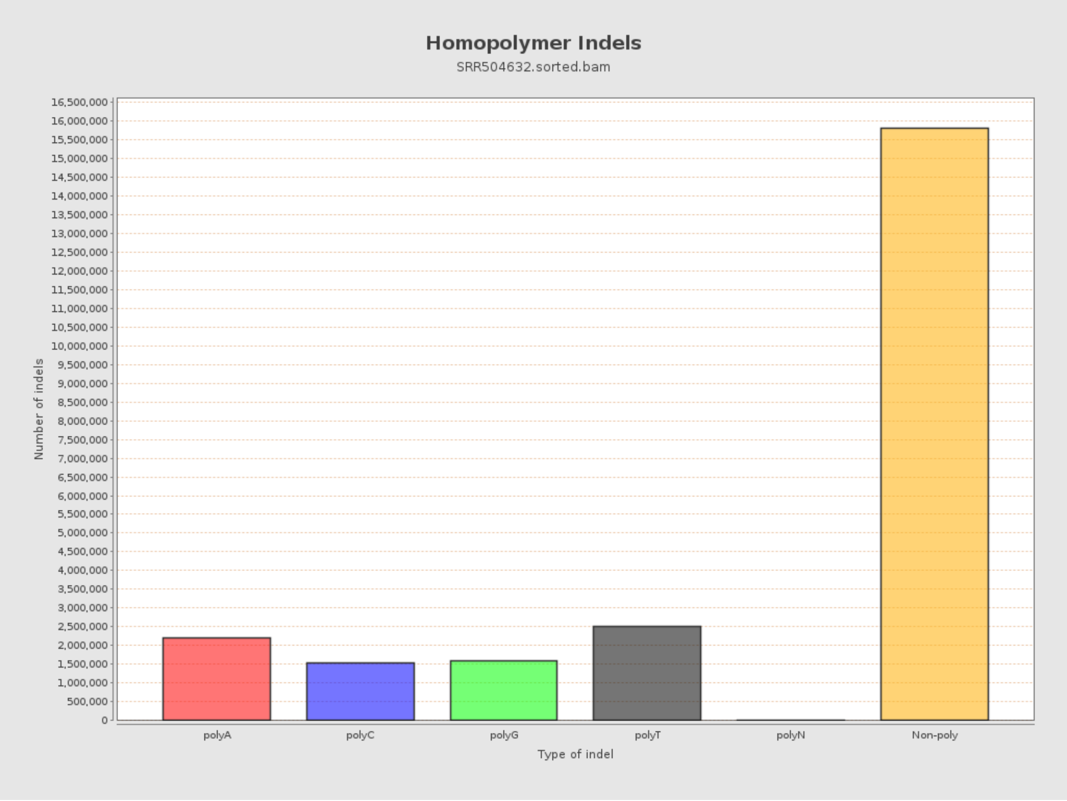
9. Results : Mapped Reads GC-content Distribution



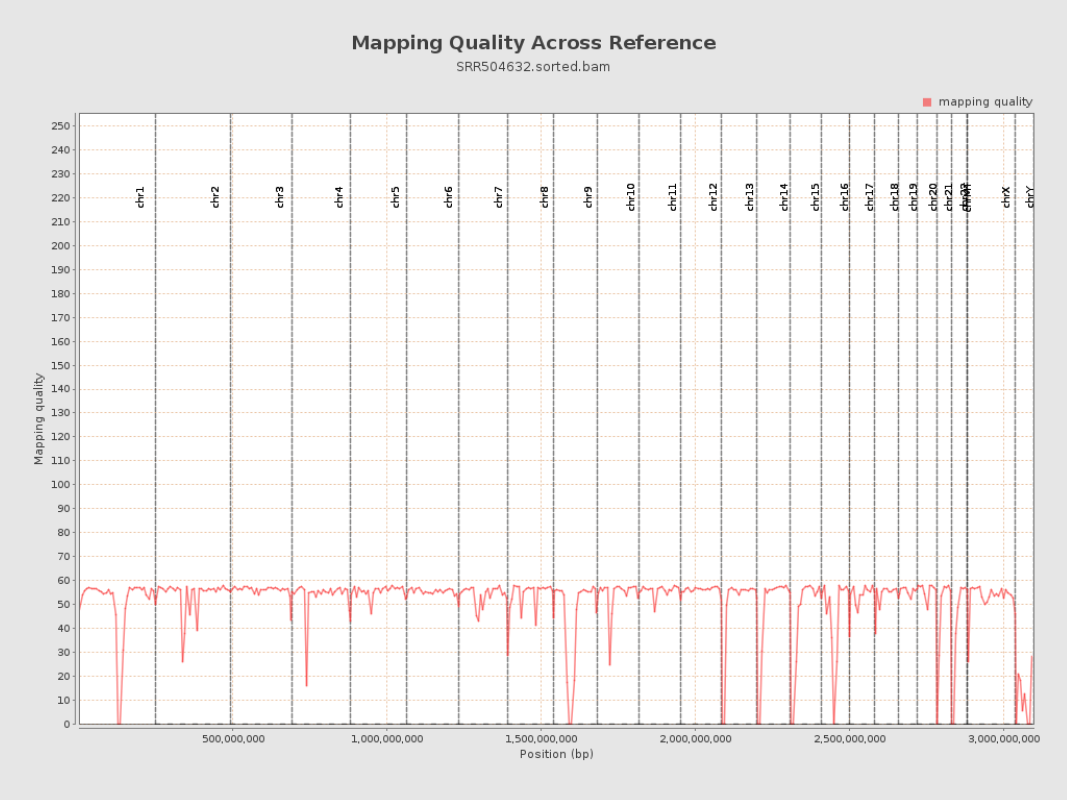
10. Results : Mapped Reads Clipping Profile



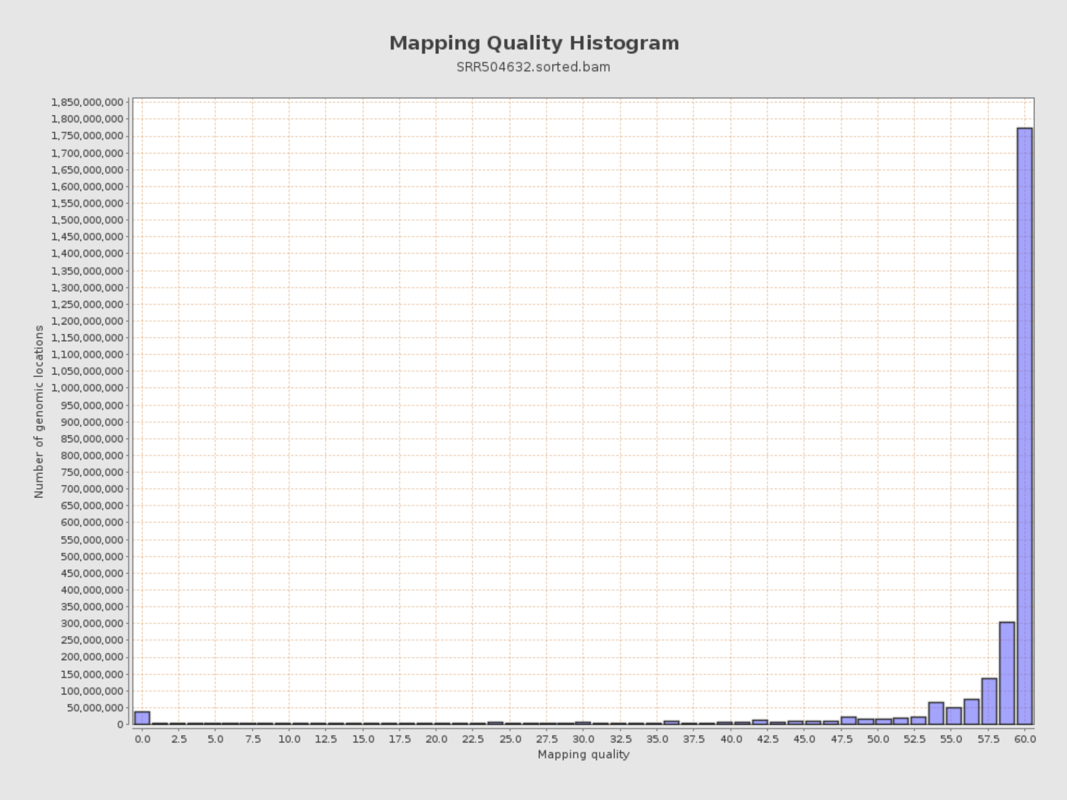
11. Results : Homopolymer Indels



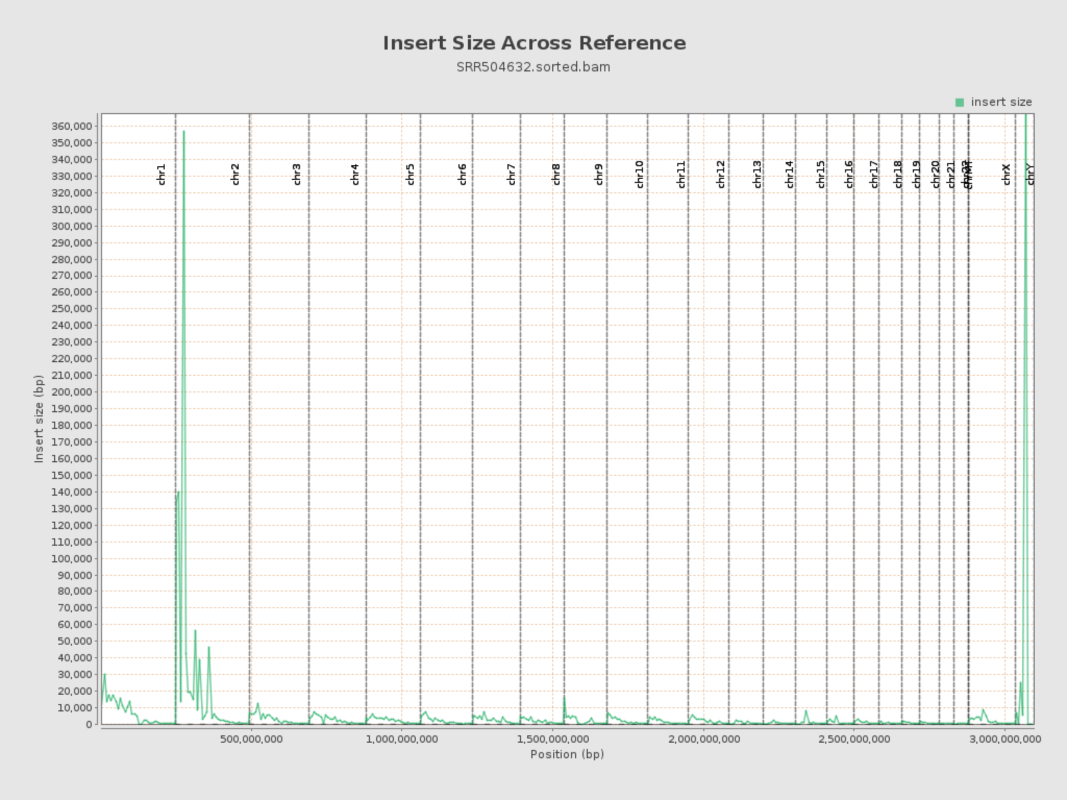
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram