Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 03:27:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504607.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_SRR504607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504607_1.fastq.gz SRR504607_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 03:26:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	441,345,966
Mapped reads	294,225,897 / 66.67%
Unmapped reads	147,120,069 / 33.33%
Mapped paired reads	294,225,897 / 66.67%
Mapped reads, first in pair	147,297,612 / 33.37%
Mapped reads, second in pair	146,928,285 / 33.29%
Mapped reads, both in pair	292,576,654 / 66.29%
Mapped reads, singletons	1,649,243 / 0.37%
Secondary alignments	0
Supplementary alignments	1,863,768 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	76,681,841 / 17.37%
Duplication rate	22.69%
Clipped reads	14,422,210 / 3.27%

2.2. ACGT Content

Number/percentage of A's	7,544,234,770 / 25.82%
Number/percentage of C's	7,000,935,272 / 23.96%
Number/percentage of T's	7,593,958,999 / 25.99%
Number/percentage of G's	7,073,464,428 / 24.21%
Number/percentage of N's	5,053,773 / 0.02%

GC Percentage	48.17%

2.3. Coverage

Mean	9.4406
Standard Deviation	24.2585

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	24,081.55
Standard Deviation	1,497,161.92
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	141,905,609
Insertions	2,173,290
Mapped reads with at least one insertion	0.72%
Deletions	2,866,659
Mapped reads with at least one deletion	0.94%
Homopolymer indels	39.99%

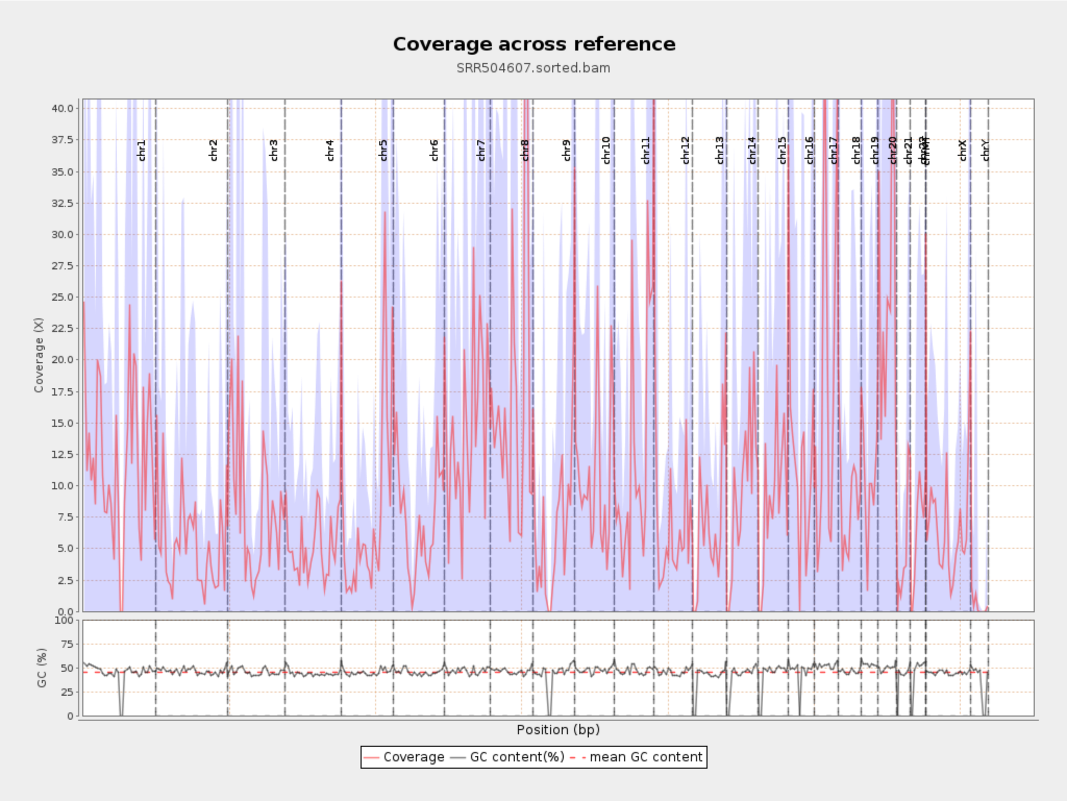
2.7. Chromosome stats

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

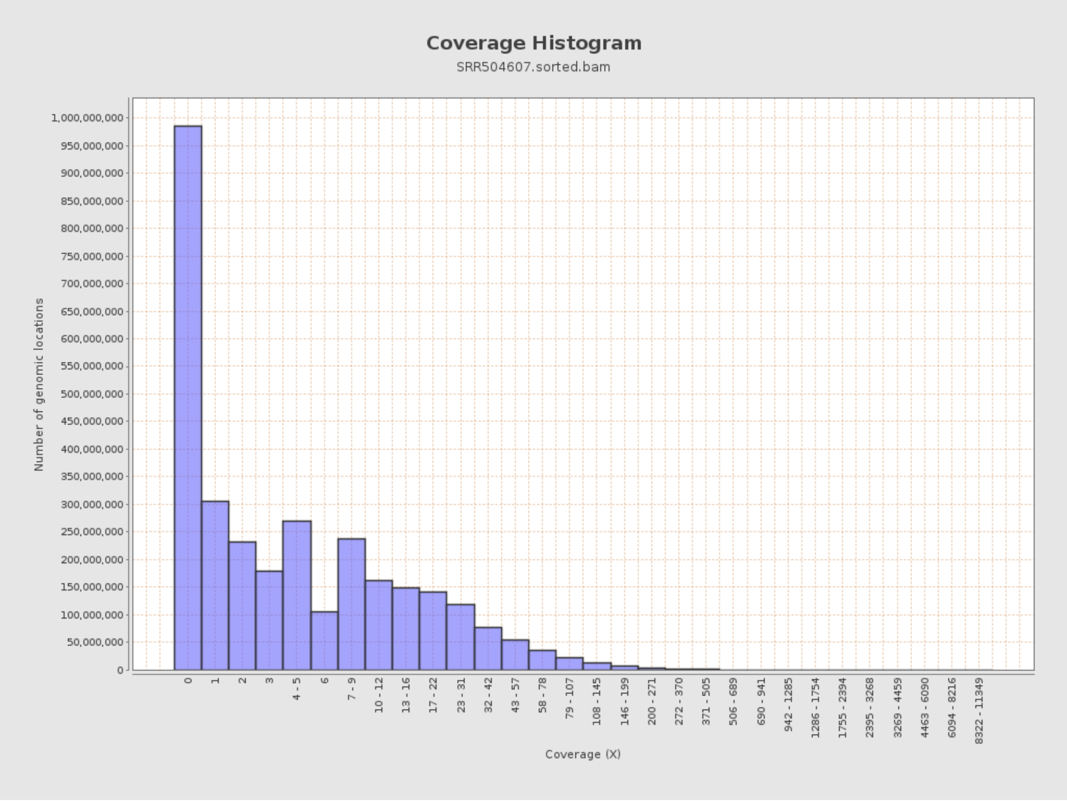
		bases	**coverage**	**deviation**
chr1	249250621	2962180633	11.8843	23.6639
chr2	243199373	1304353755	5.3633	13.4263
chr3	198022430	1650878106	8.3368	22.6132
chr4	191154276	986748068	5.1621	9.8018
chr5	180915260	1424840108	7.8757	22.5125
chr6	171115067	1238353817	7.237	14.0509
chr7	159138663	2337911408	14.691	27.1283
chr8	146364022	2635201510	18.0044	42.9981
chr9	141213431	892993944	6.3237	17.6458
chr10	135534747	1436946211	10.6021	21.9216
chr11	135006516	1646949929	12.199	27.9793
chr12	133851895	880757003	6.5801	16.2381
chr13	115169878	799100481	6.9385	15.4478
chr14	107349540	1036240367	9.653	19.2886
chr15	102531392	891202556	8.692	18.1102
chr16	90354753	1091184296	12.0767	27.2545
chr17	81195210	1417669993	17.46	56.2274
chr18	78077248	668426099	8.5611	24.5959
chr19	59128983	614058495	10.3851	22.2086
chr20	63025520	1658202288	26.31	46.9828
chr21	48129895	243440418	5.058	13.0294
chr22	51304566	320794105	6.2527	16.1875
chrMT	16571	498912	30.1075	14.916
chrX	155270560	1058249531	6.8155	12.7412

chrY	59373566	27892700	0.4698	10.7889

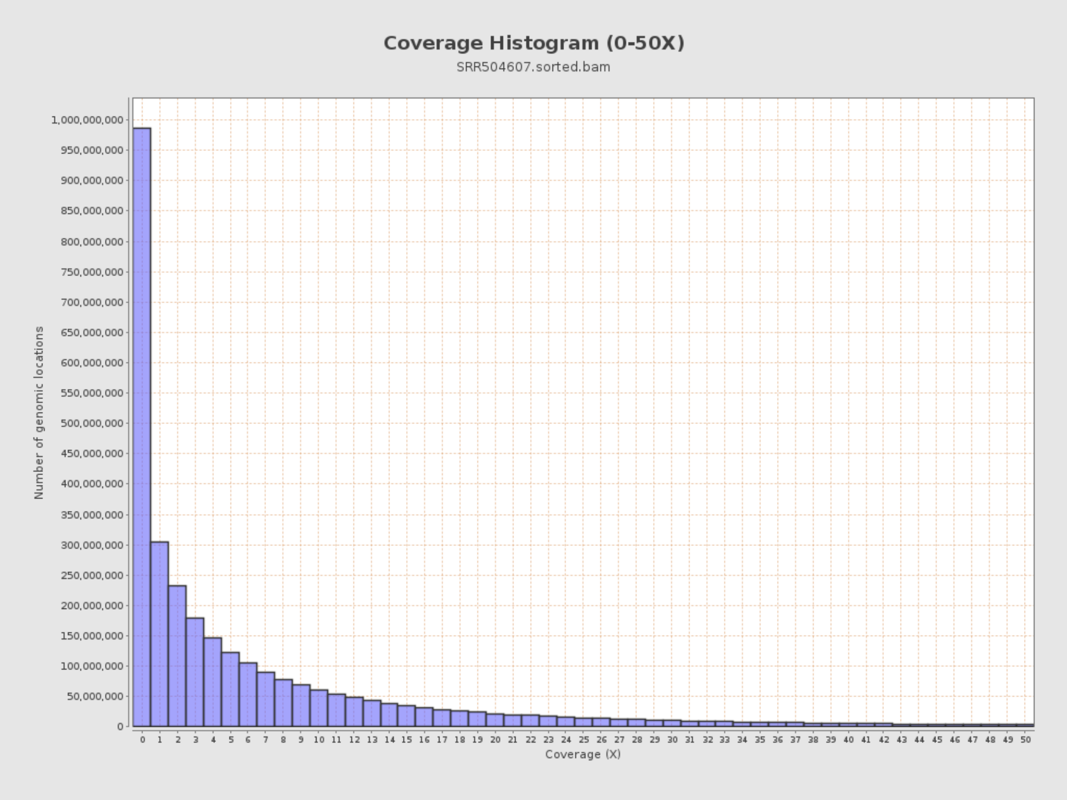
3. Results : Coverage across reference



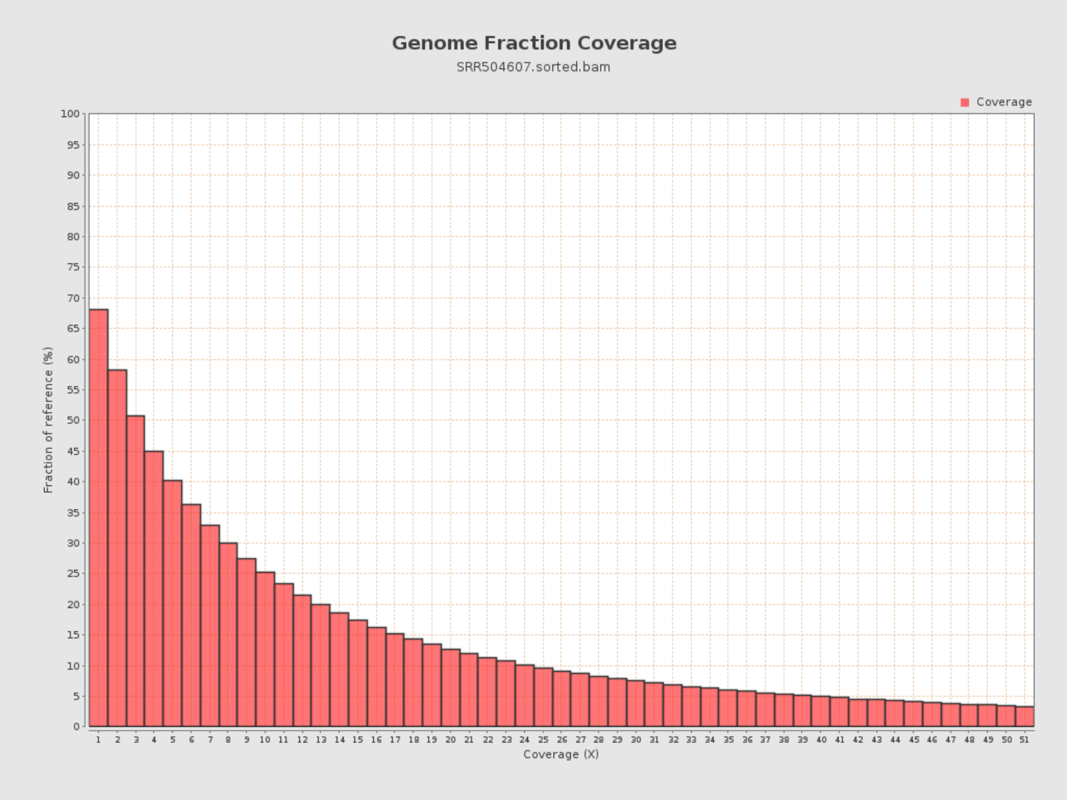
4. Results : Coverage Histogram



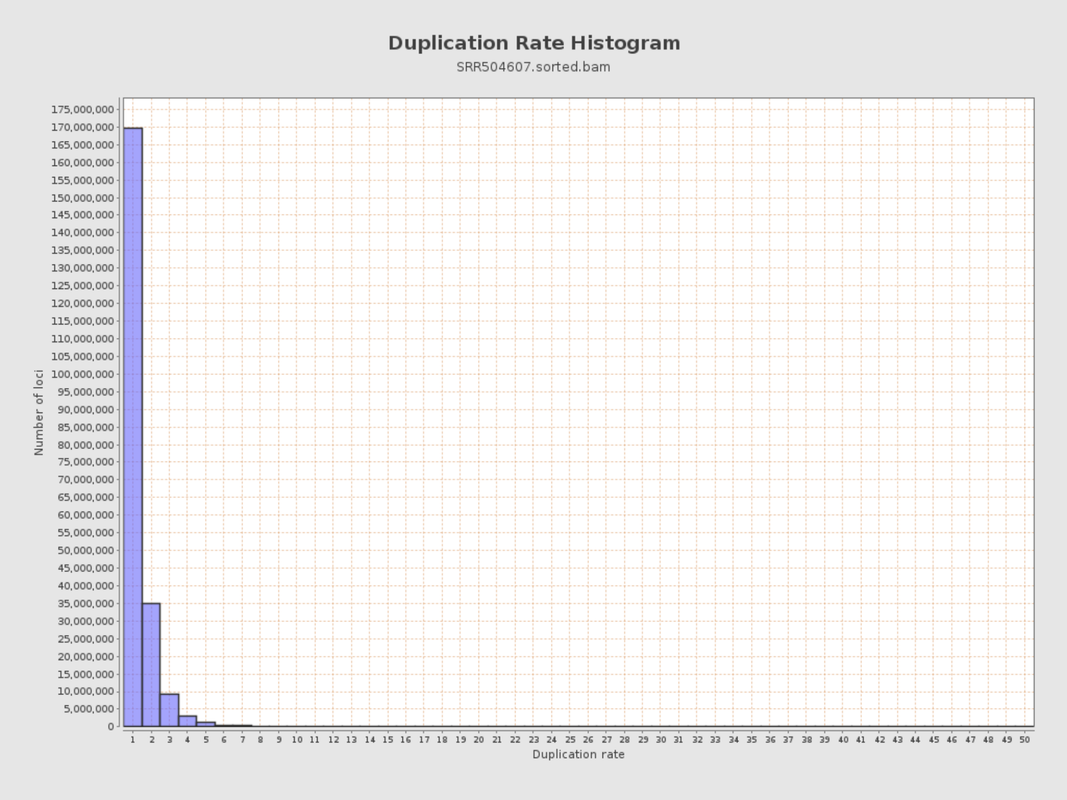
5. Results : Coverage Histogram (0-50X)



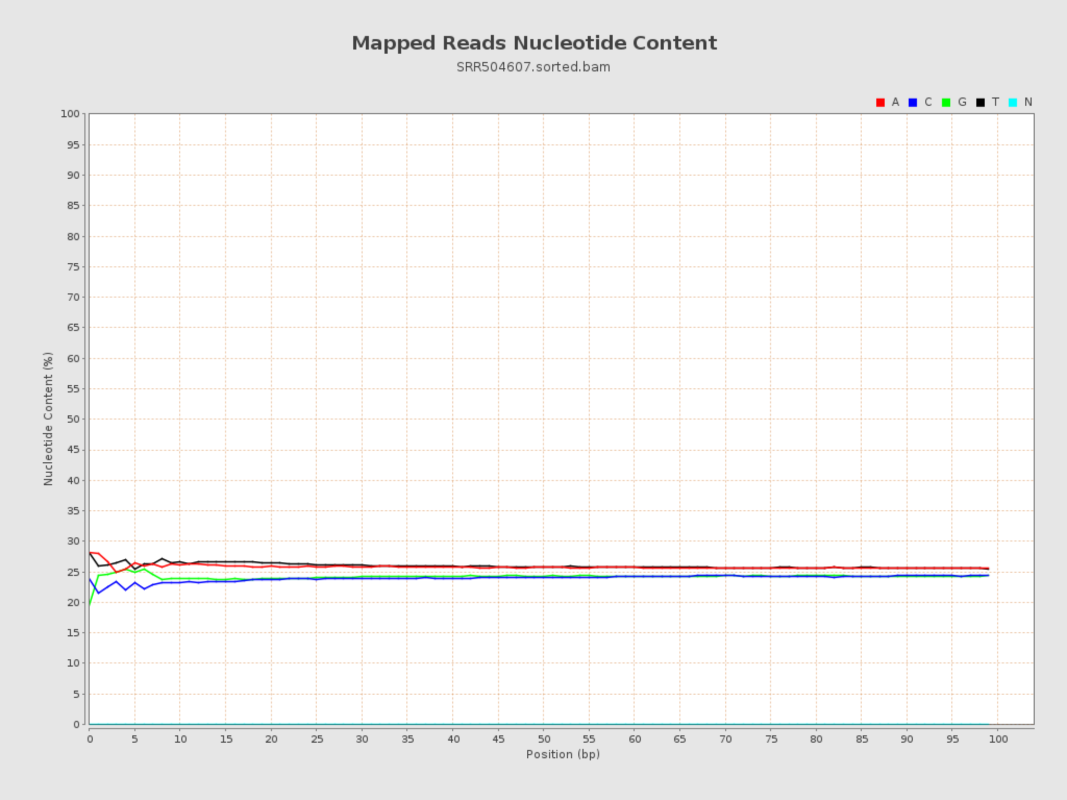
6. Results : Genome Fraction Coverage



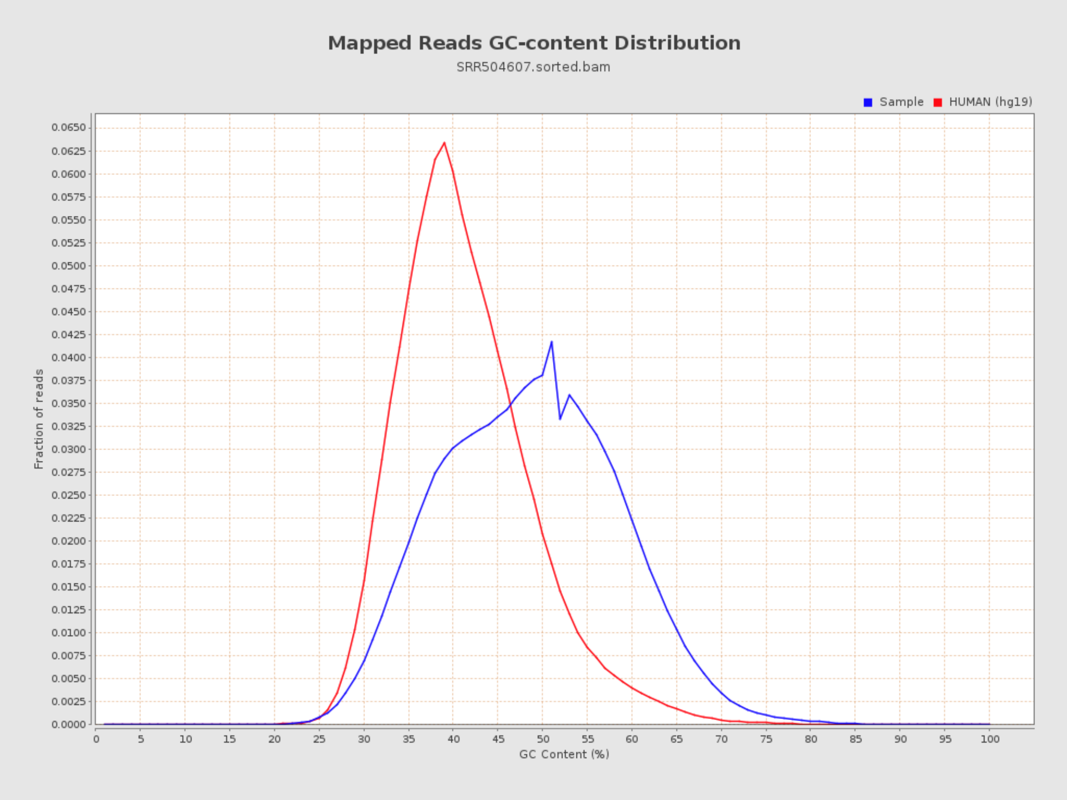
7. Results : Duplication Rate Histogram



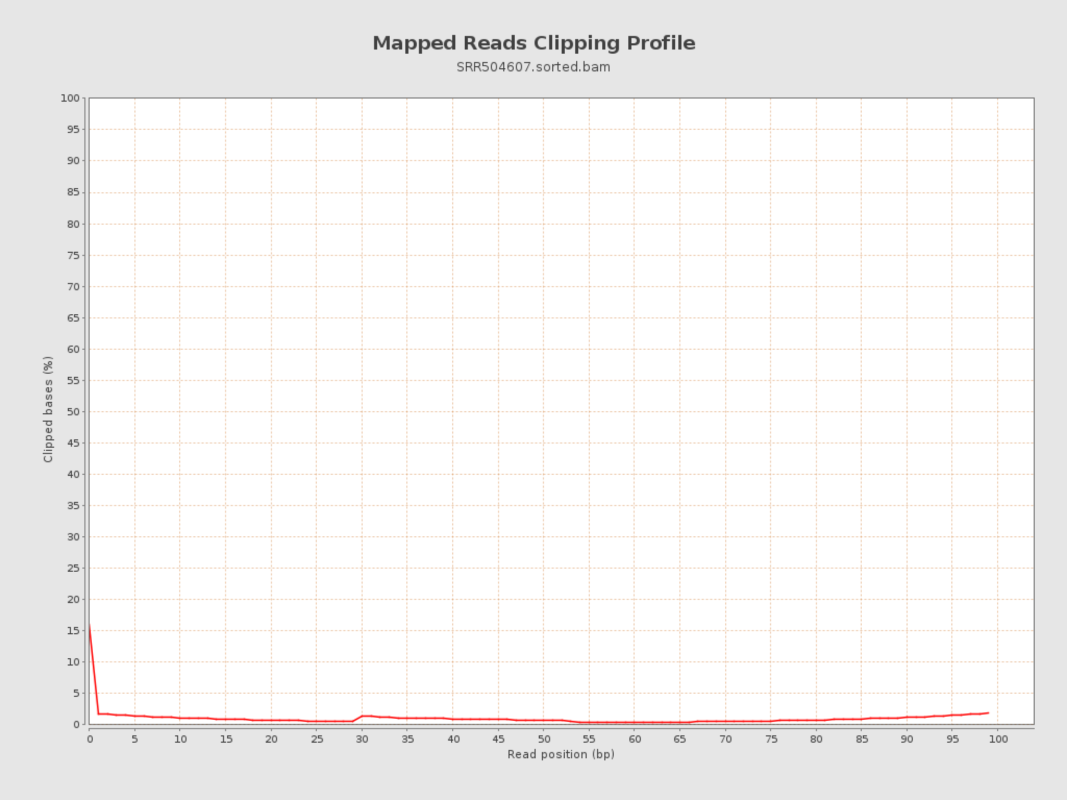
8. Results : Mapped Reads Nucleotide Content



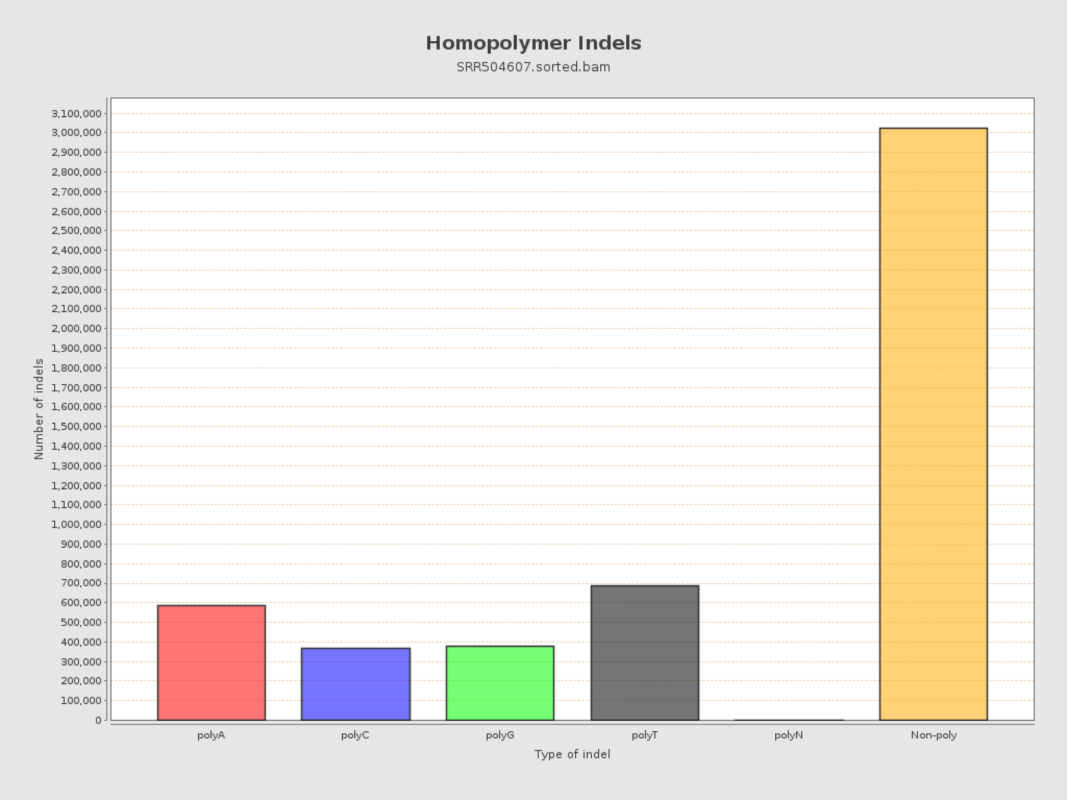
9. Results : Mapped Reads GC-content Distribution



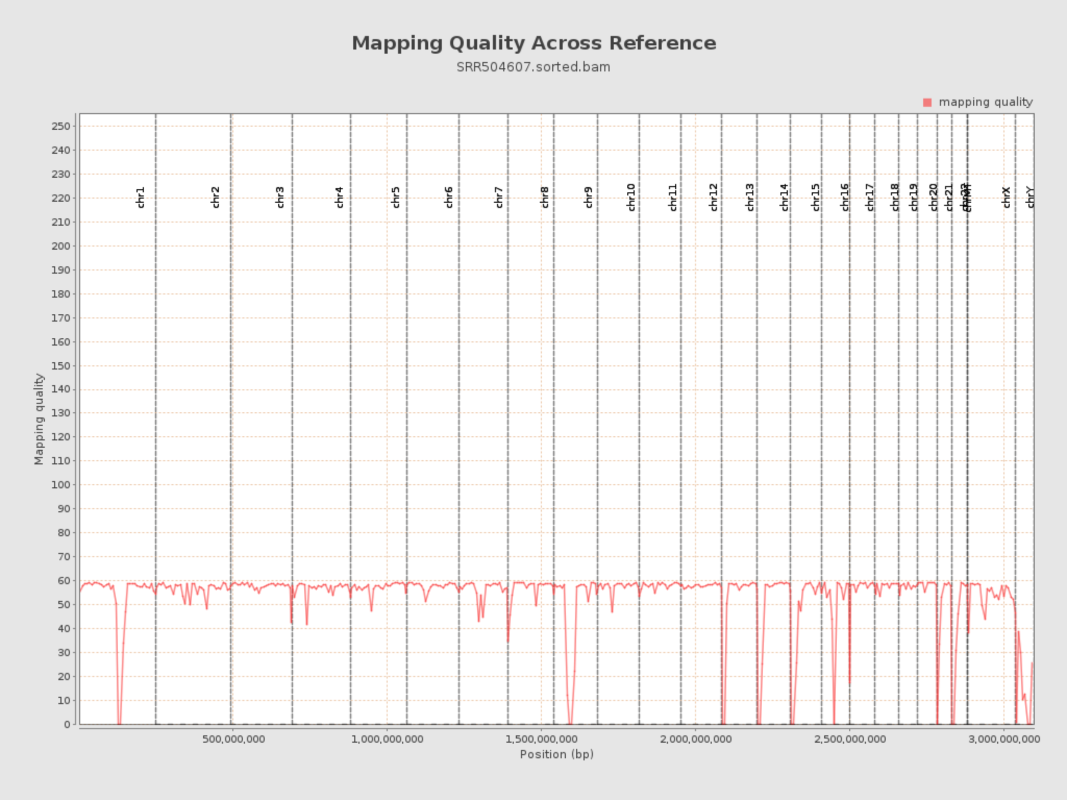
10. Results : Mapped Reads Clipping Profile



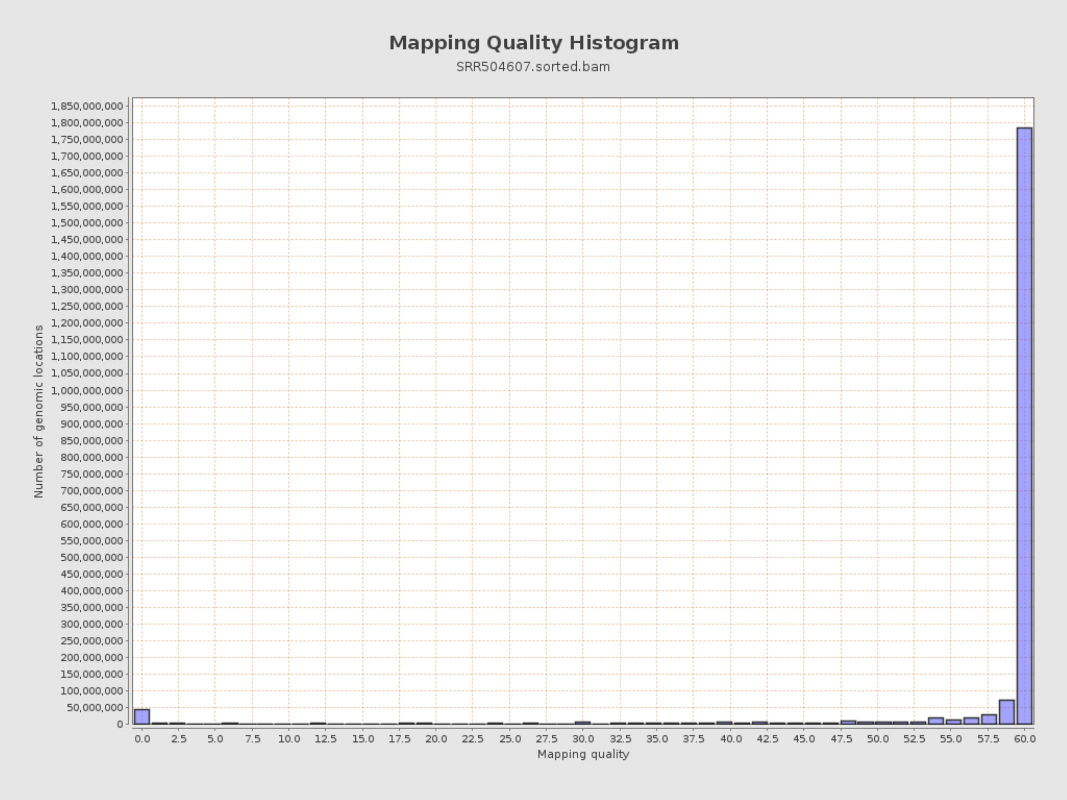
11. Results : Homopolymer Indels



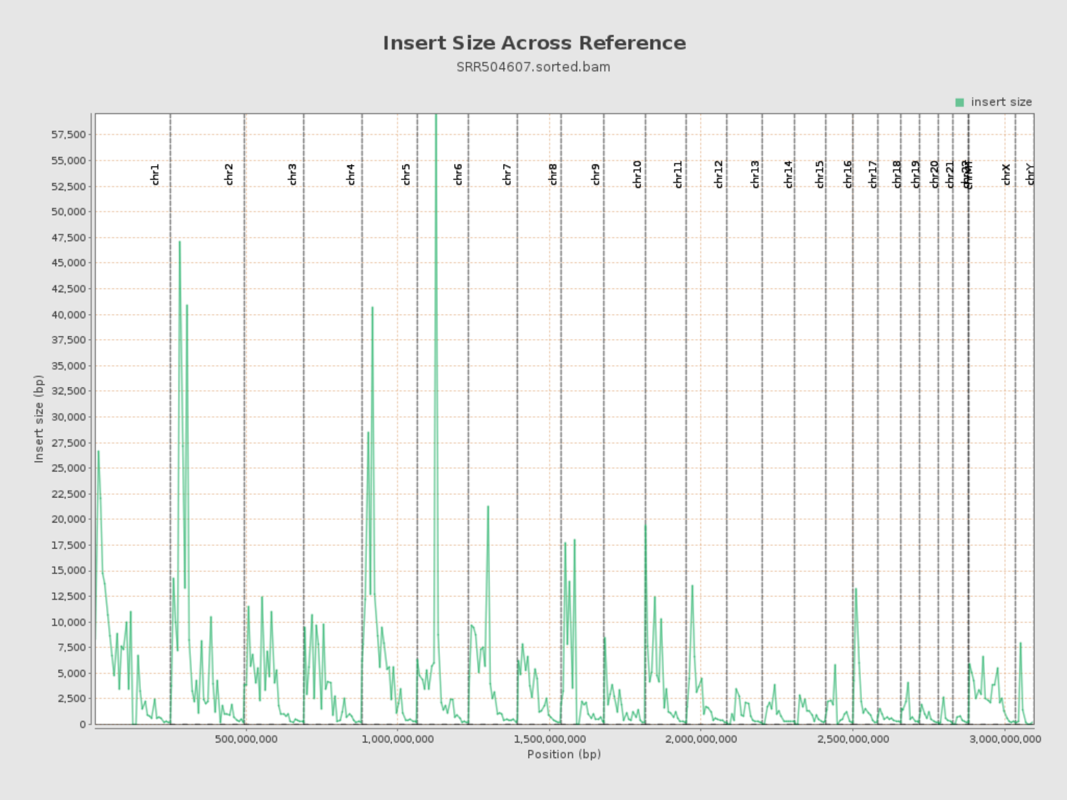
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram