Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:30:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234066.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_SRR6234066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:30:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,286,293
Mapped reads	5,877,517 / 93.5%
Unmapped reads	408,776 / 6.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,025 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	584,294 / 9.29%
Duplication rate	4.62%
Clipped reads	2,482,447 / 39.49%

2.2. ACGT Content

Number/percentage of A's	104,663,095 / 26.42%
Number/percentage of C's	73,285,053 / 18.5%
Number/percentage of T's	114,971,906 / 29.02%
Number/percentage of G's	103,118,846 / 26.03%
Number/percentage of N's	86,332 / 0.02%
GC Percentage	44.53%

2.3. Coverage

Mean	0.128

Standard Deviation	33.667

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

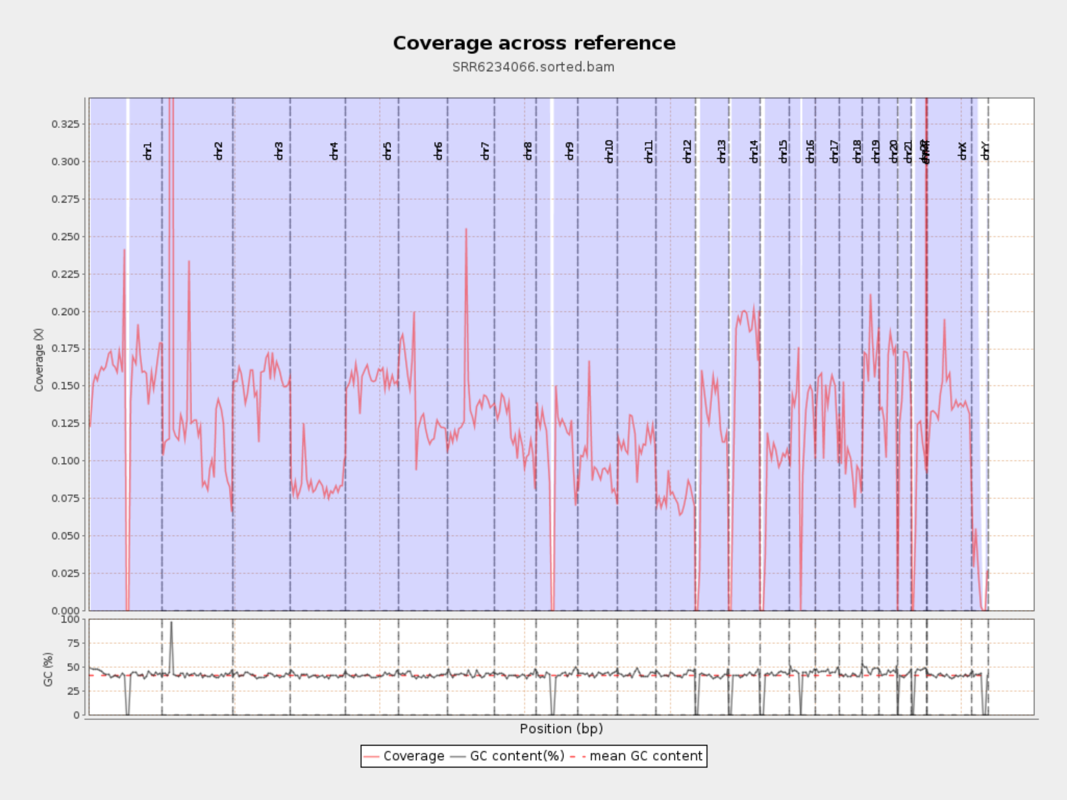
General error rate	0.67%
Mismatches	2,610,298
Insertions	27,412
Mapped reads with at least one insertion	0.46%
Deletions	84,944
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.22%

2.6. Chromosome stats

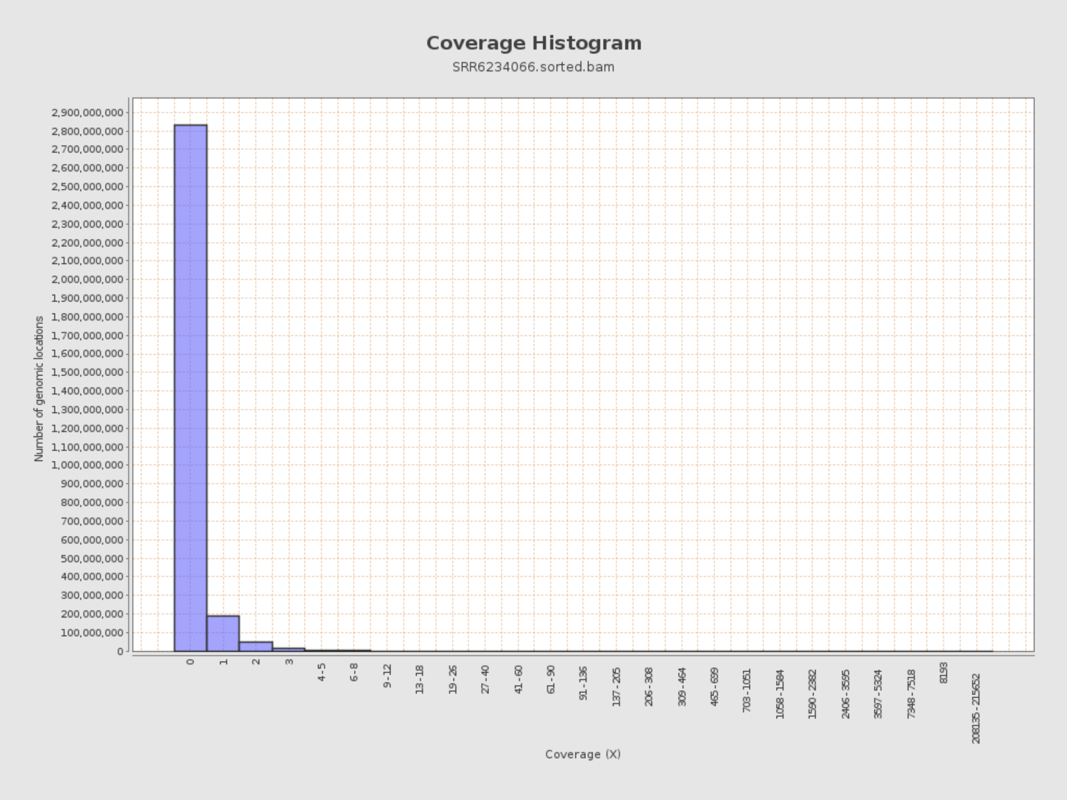
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38222903	0.1534	1.9823
chr2	243199373	45064107	0.1853	120.0637
chr3	198022430	30546673	0.1543	0.5388
chr4	191154276	16098425	0.0842	0.4446
chr5	180915260	28010985	0.1548	0.5485
chr6	171115067	23540290	0.1376	0.6887
chr7	159138663	21725441	0.1365	1.8058

chr8	146364022	17237513	0.1178	1.2126
chr9	141213431	14918387	0.1056	0.9242
chr10	135534747	13179120	0.0972	0.7564
chr11	135006516	15138341	0.1121	1.0698
chr12	133851895	10053699	0.0751	0.4049
chr13	115169878	12980803	0.1127	0.4554
chr14	107349540	17110294	0.1594	0.756
chr15	102531392	8788506	0.0857	0.4048
chr16	90354753	11280257	0.1248	0.6112
chr17	81195210	11320825	0.1394	0.6821
chr18	78077248	7810962	0.1	2.1041
chr19	59128983	10179240	0.1722	1.3677
chr20	63025520	9375162	0.1488	0.5885
chr21	48129895	6689625	0.139	0.5896
chr22	51304566	4169395	0.0813	0.3949
chrMT	16571	27300	1.6475	1.994
chrX	155270560	21478694	0.1383	0.6627
chrY	59373566	1315298	0.0222	0.2848

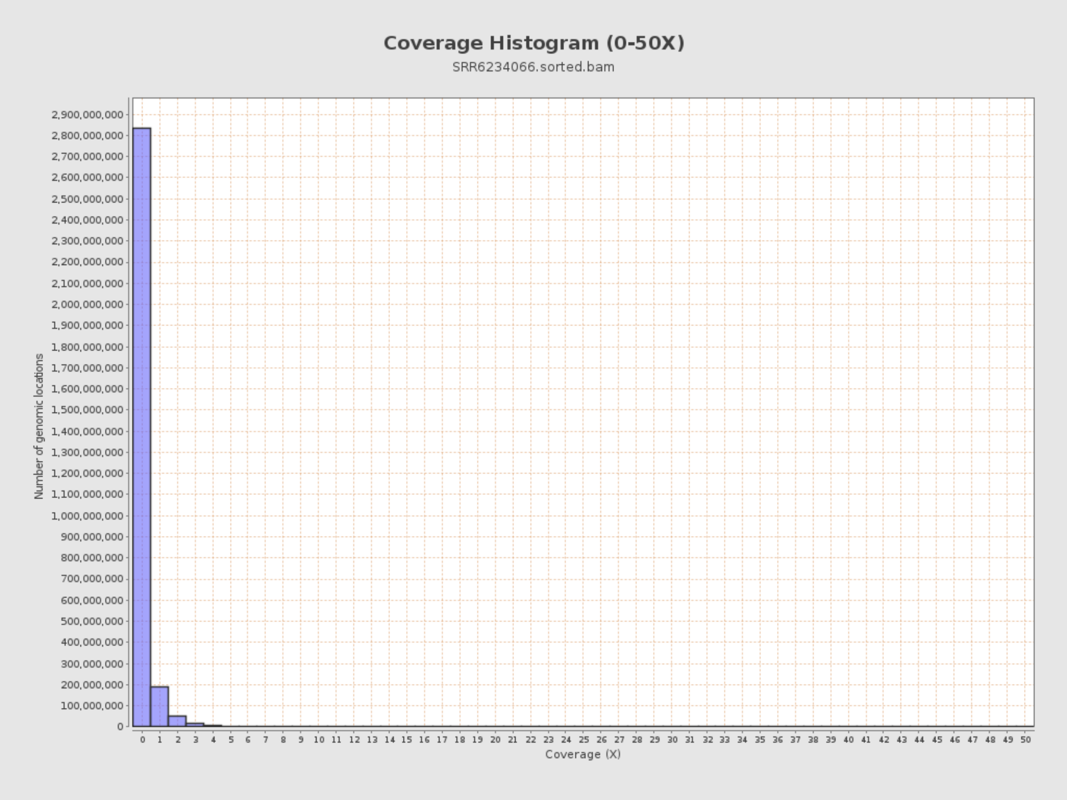
3. Results : Coverage across reference



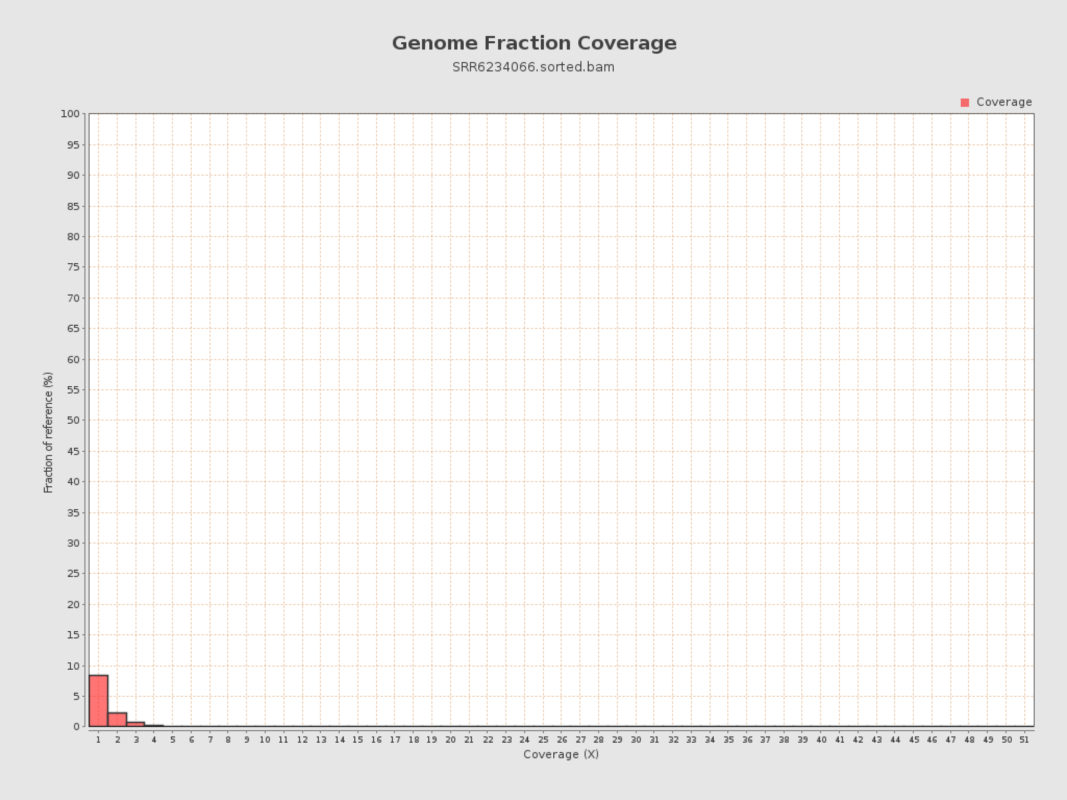
4. Results : Coverage Histogram



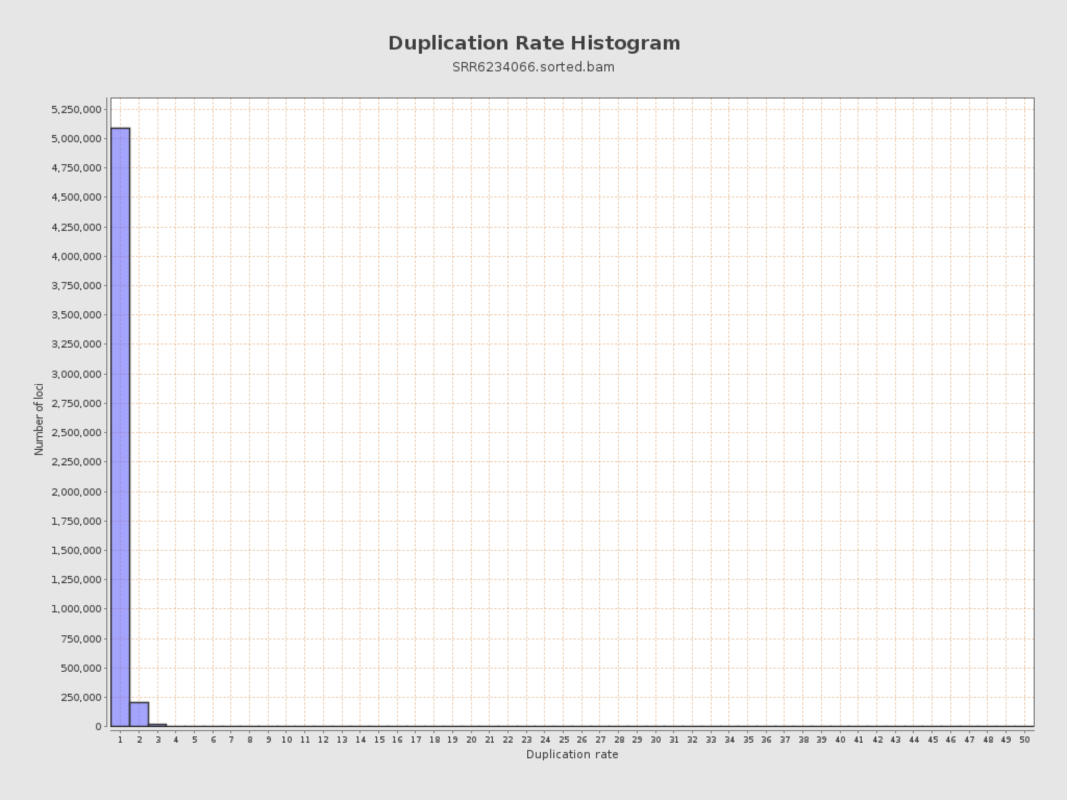
5. Results : Coverage Histogram (0-50X)



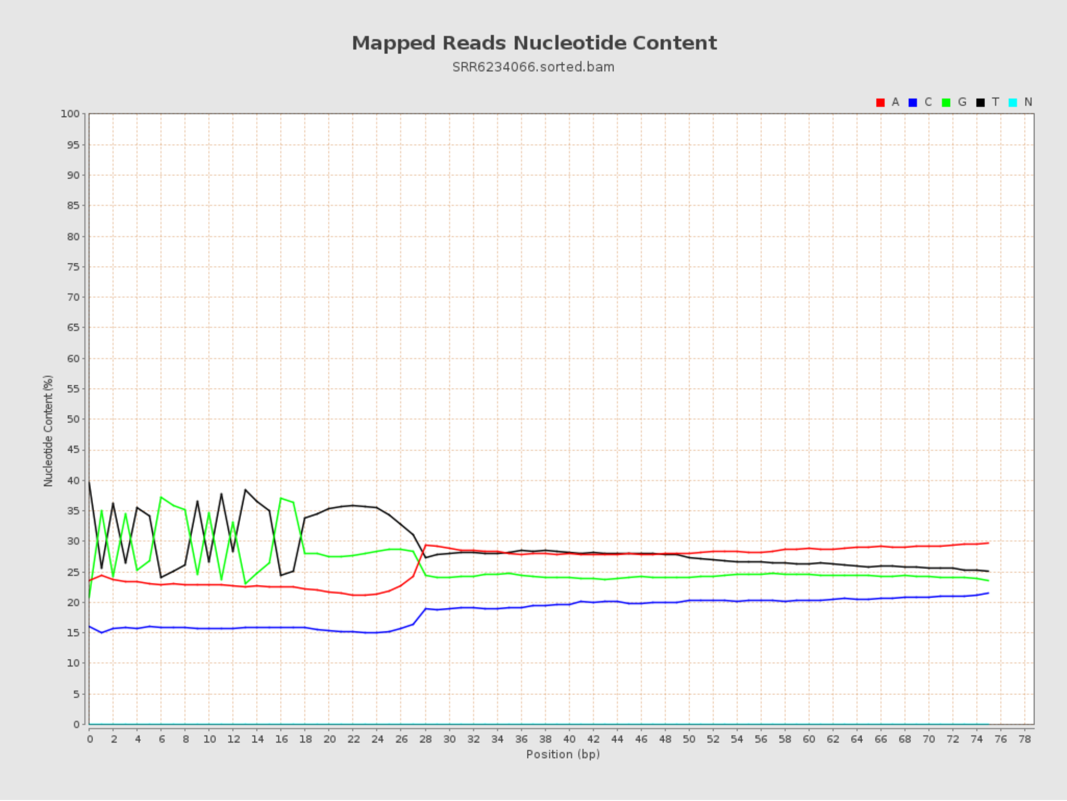
6. Results : Genome Fraction Coverage



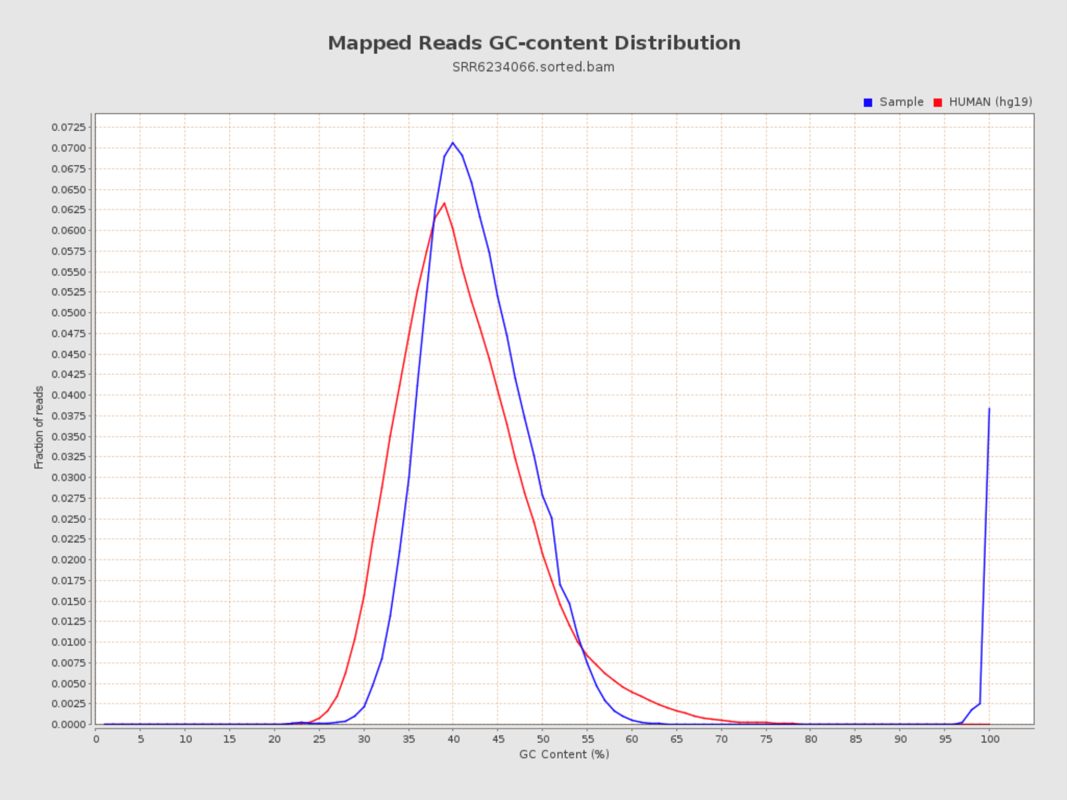
7. Results : Duplication Rate Histogram



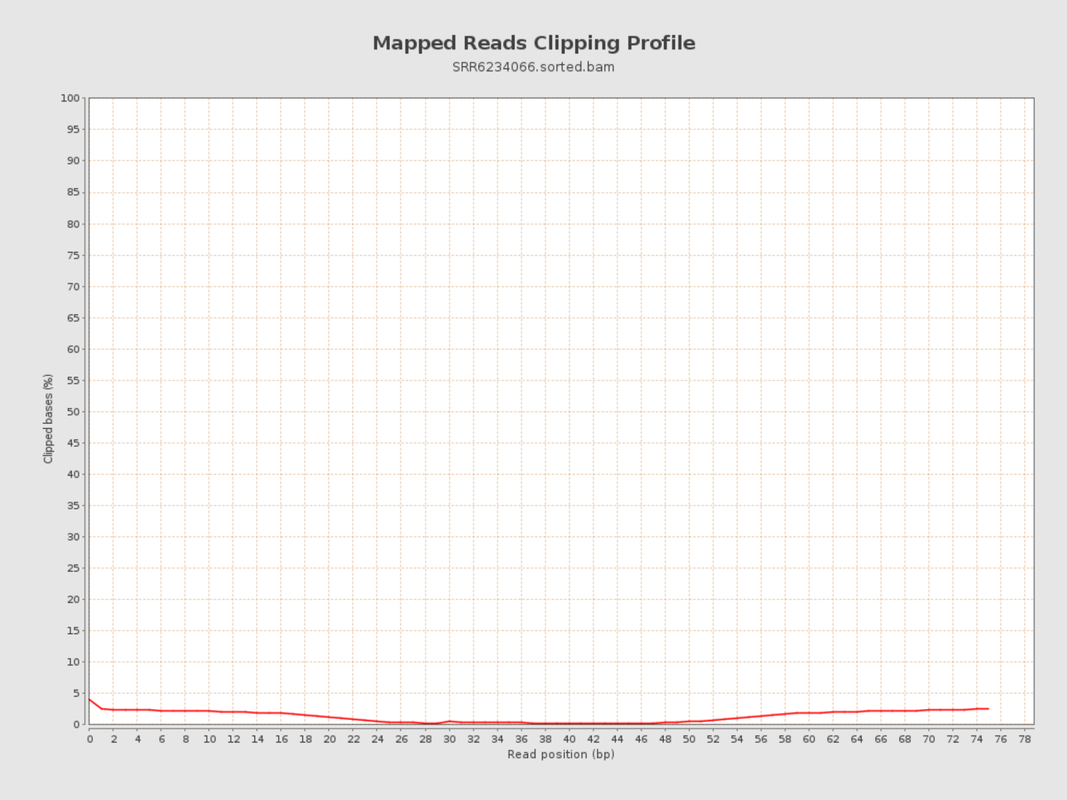
8. Results : Mapped Reads Nucleotide Content



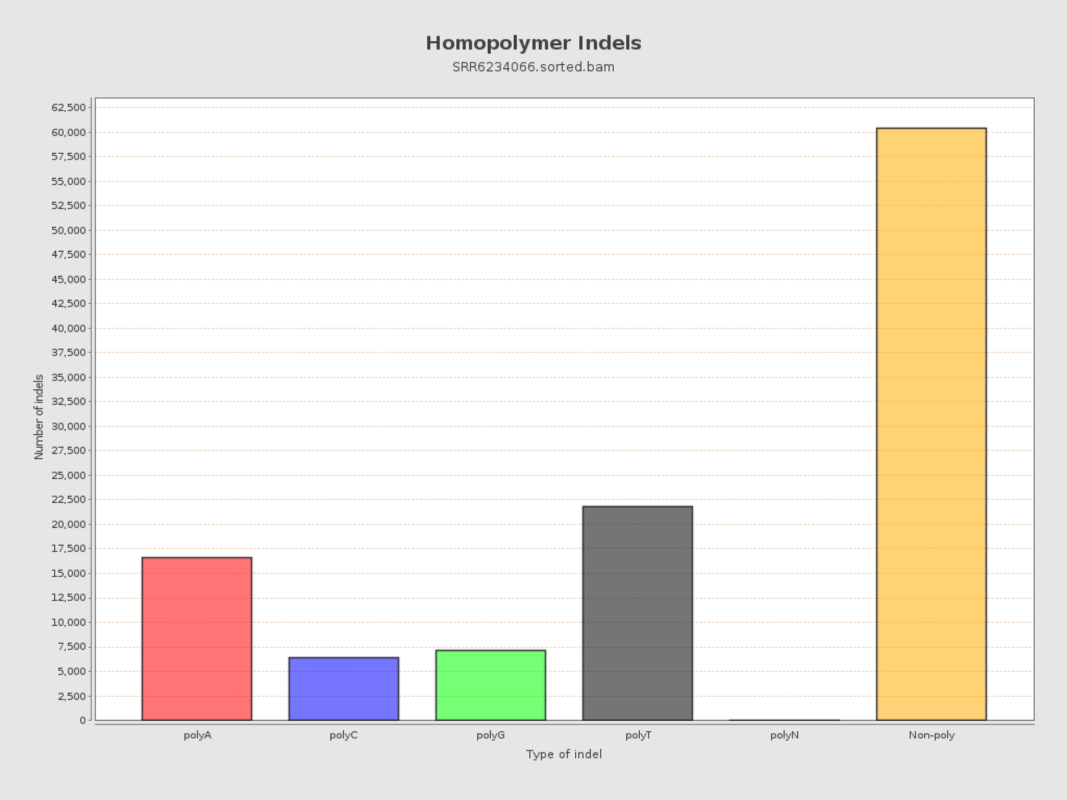
9. Results : Mapped Reads GC-content Distribution



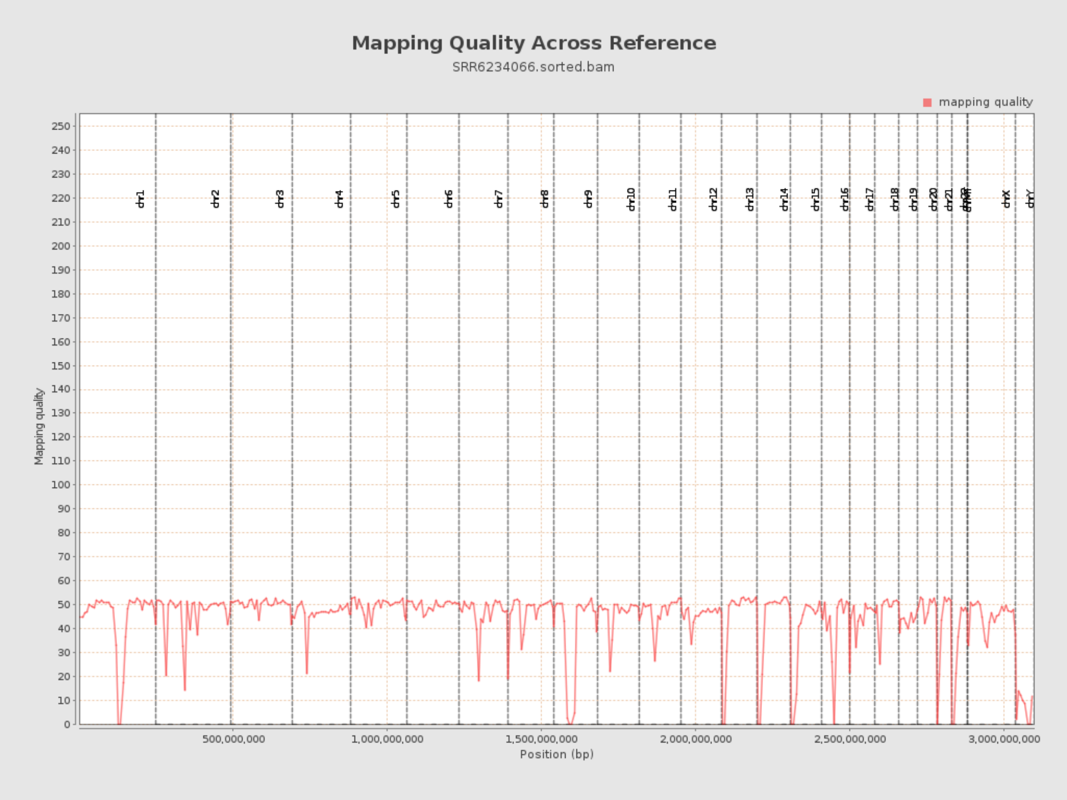
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram