Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:18:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549080.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_SRR1549080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:18:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,703,605
Mapped reads	7,577,654 / 87.06%
Unmapped reads	1,125,951 / 12.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	288,050 / 3.31%
Duplication rate	2.51%
Clipped reads	346,812 / 3.98%

2.2. ACGT Content

Number/percentage of A's	90,217,282 / 29.97%
Number/percentage of C's	60,571,345 / 20.12%
Number/percentage of T's	91,378,526 / 30.36%
Number/percentage of G's	58,788,099 / 19.53%
Number/percentage of N's	72,414 / 0.02%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0972
Standard Deviation	0.8754

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

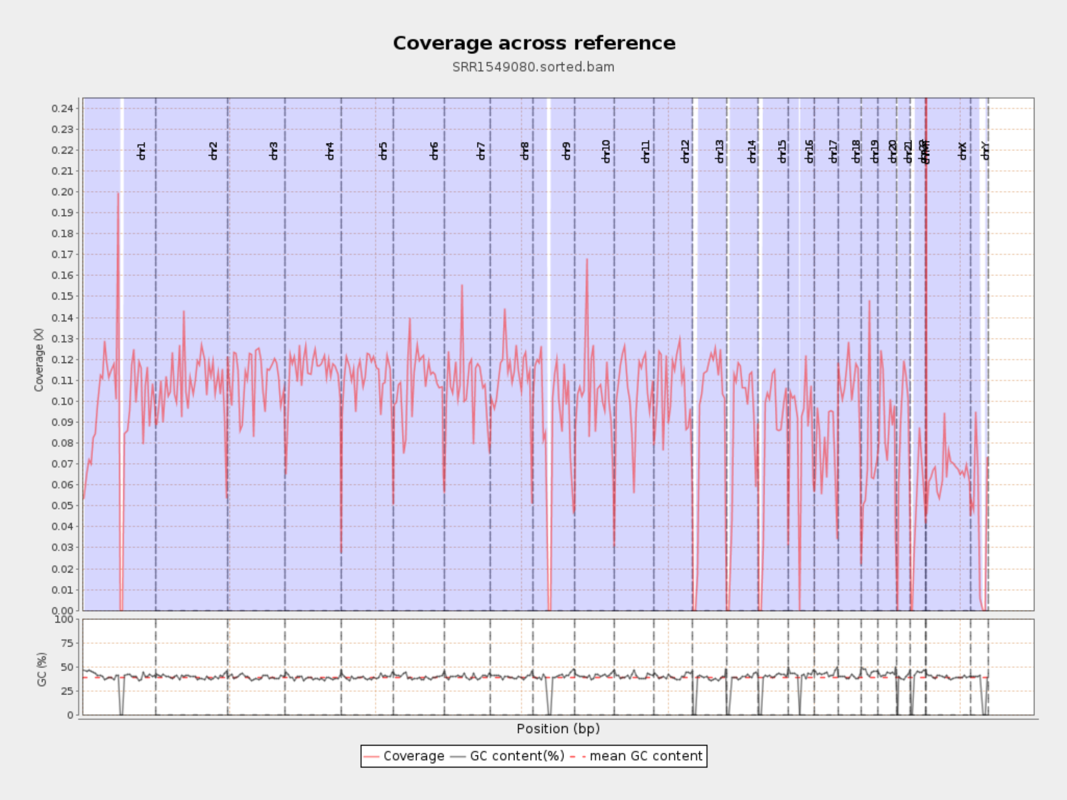
General error rate	0.39%
Mismatches	1,161,679
Insertions	6,692
Mapped reads with at least one insertion	0.09%
Deletions	21,671
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.22%

2.6. Chromosome stats

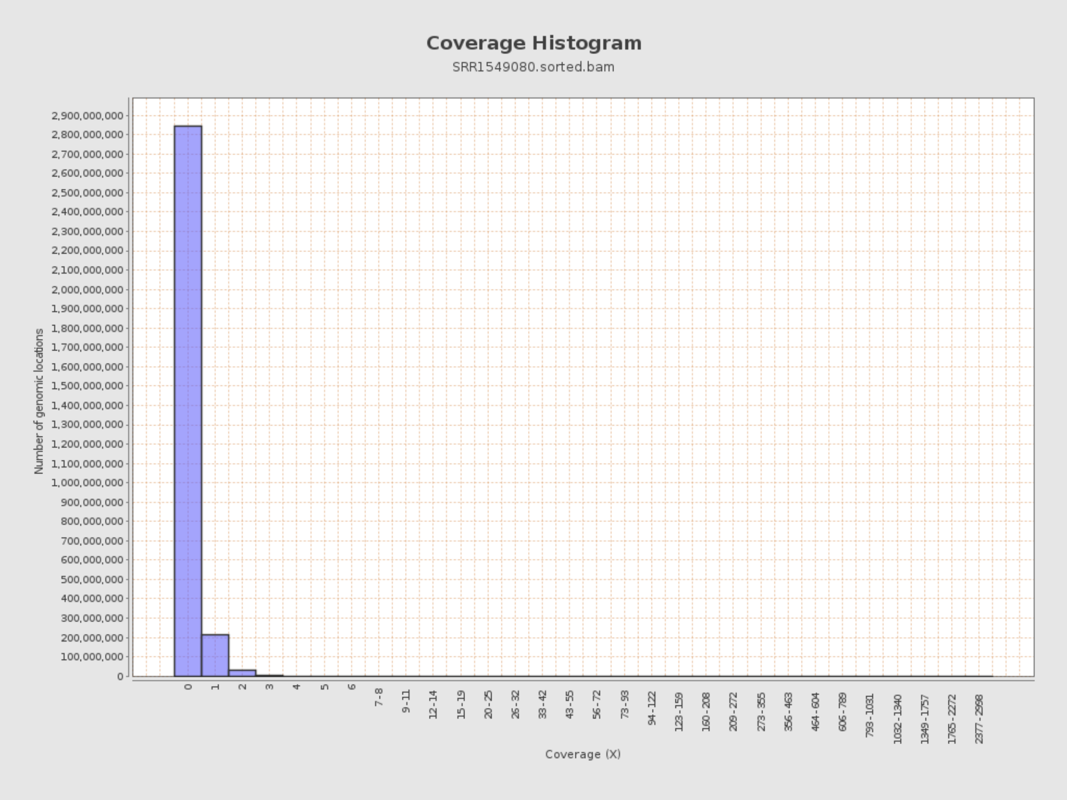
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23996622	0.0963	2.1363
chr2	243199373	26322477	0.1082	0.5892
chr3	198022430	21924419	0.1107	0.3918
chr4	191154276	21876917	0.1144	0.404
chr5	180915260	19978285	0.1104	0.3966
chr6	171115067	18649851	0.109	0.4949
chr7	159138663	17021394	0.107	0.8613
chr8	146364022	16323358	0.1115	1.5014

chr9	141213431	12637579	0.0895	0.5729
chr10	135534747	14211681	0.1049	0.7179
chr11	135006516	14100534	0.1044	0.588
chr12	133851895	13993344	0.1045	0.3976
chr13	115169878	10719120	0.0931	0.3432
chr14	107349540	9307729	0.0867	0.4033
chr15	102531392	8226552	0.0802	0.3212
chr16	90354753	7663545	0.0848	0.4378
chr17	81195210	6319330	0.0778	0.3844
chr18	78077248	8543727	0.1094	1.2002
chr19	59128983	4216373	0.0713	1.5935
chr20	63025520	5810006	0.0922	0.3693
chr21	48129895	3961349	0.0823	0.3912
chr22	51304566	2484764	0.0484	0.2863
chrMT	16571	14517	0.876	1.316
chrX	155270560	10227247	0.0659	0.3857
chrY	59373566	2524131	0.0425	0.3854

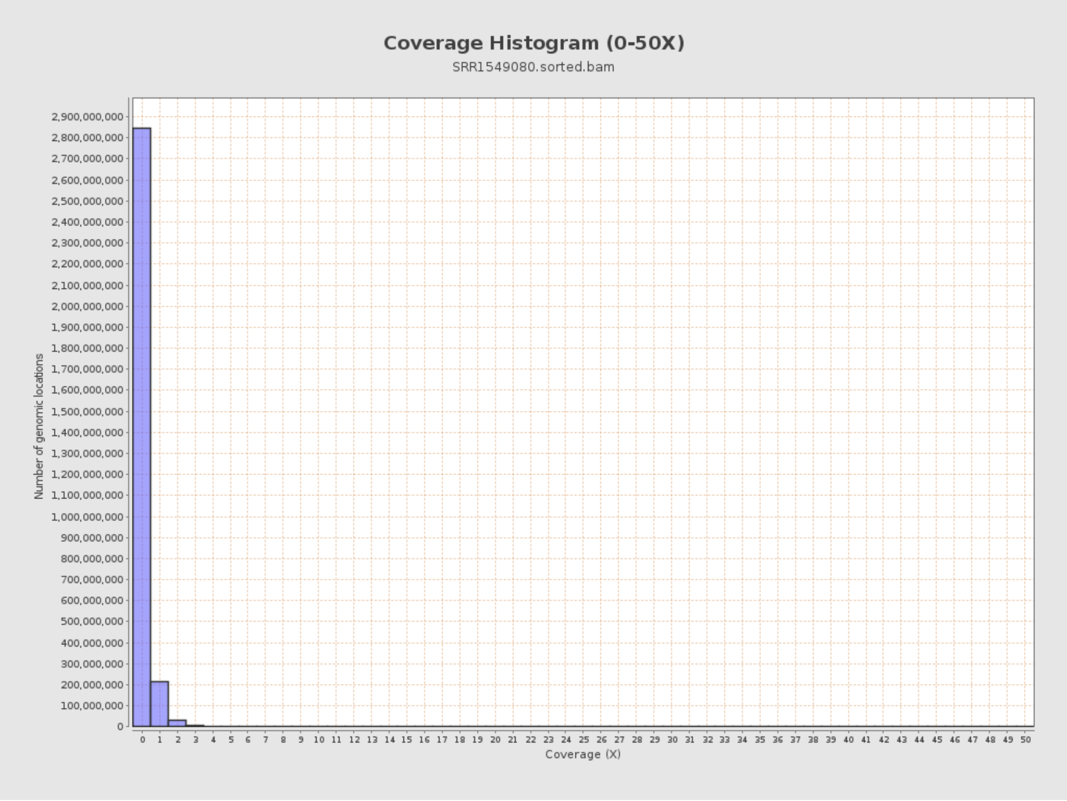
3. Results : Coverage across reference



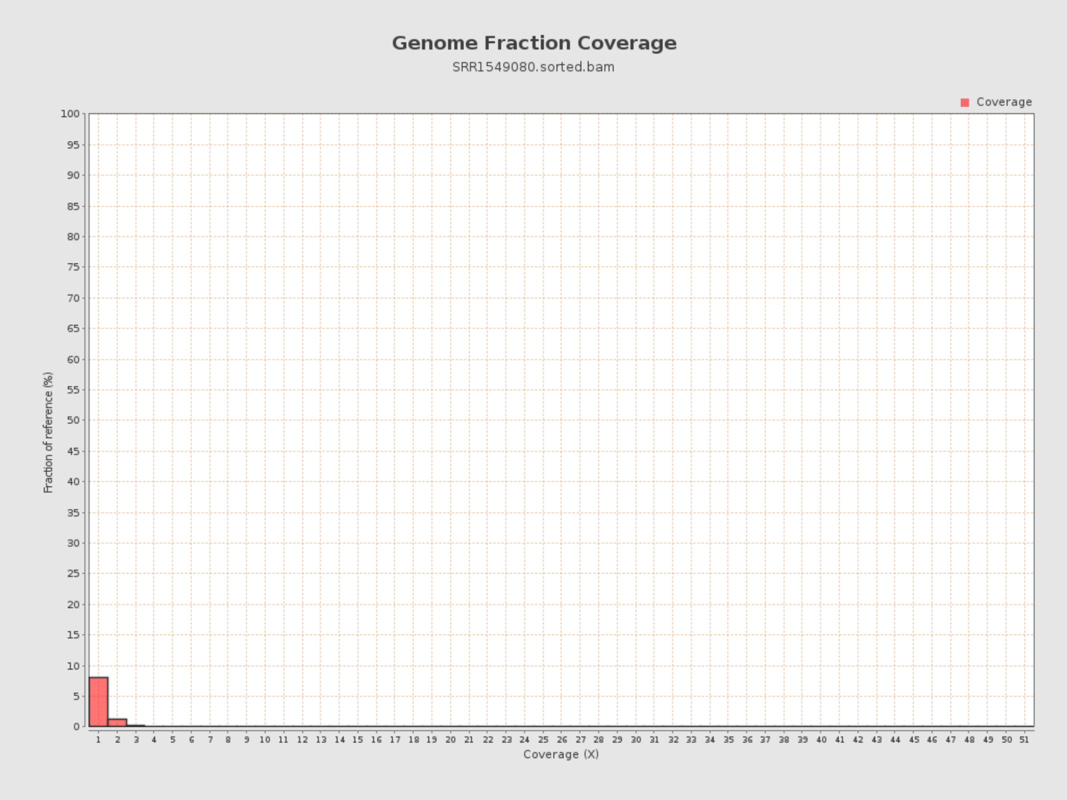
4. Results : Coverage Histogram



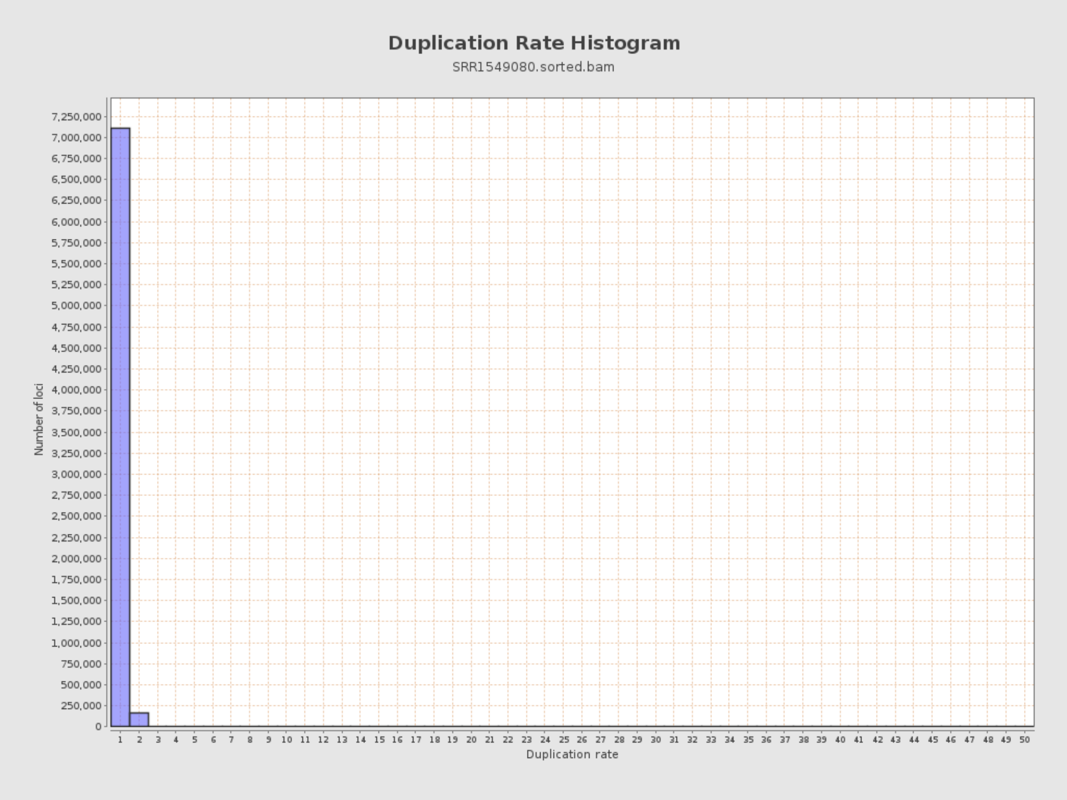
5. Results : Coverage Histogram (0-50X)



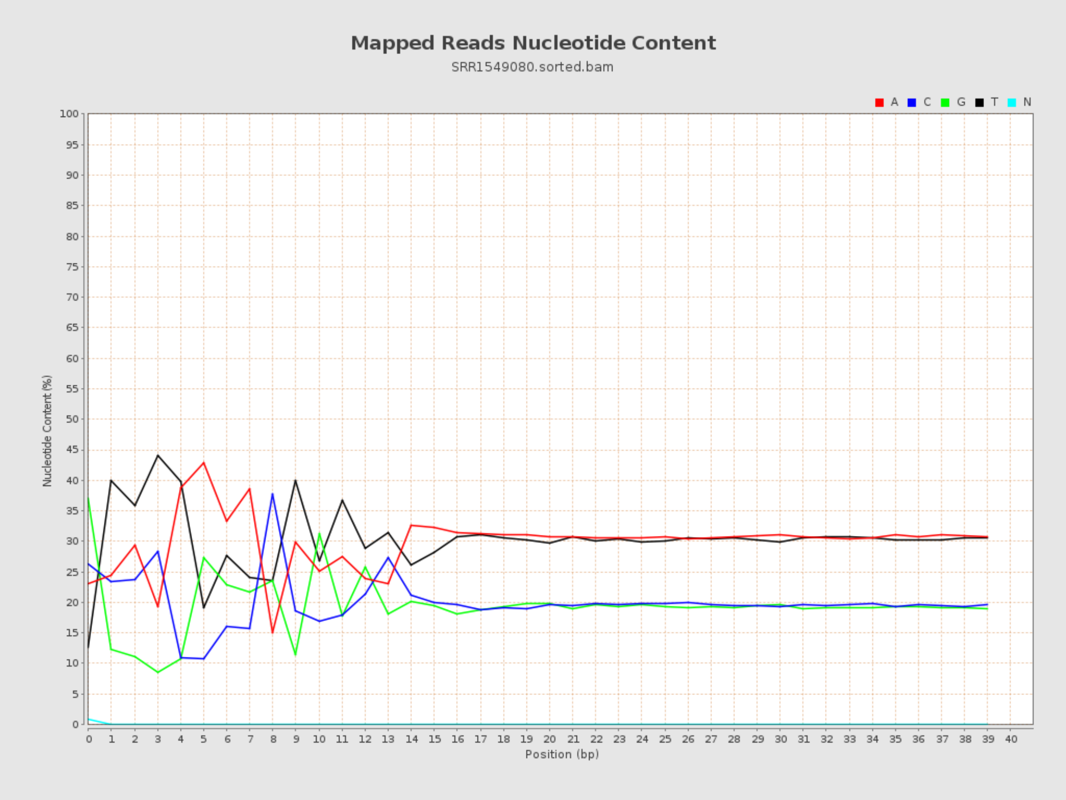
6. Results : Genome Fraction Coverage



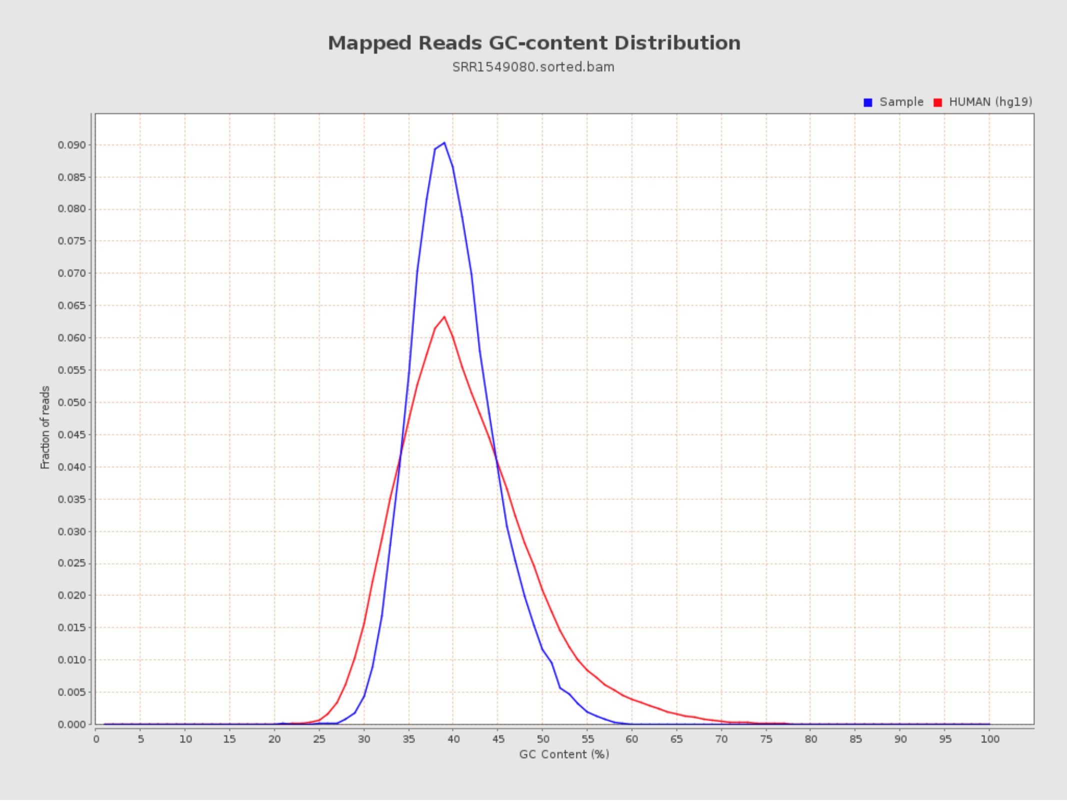
7. Results : Duplication Rate Histogram



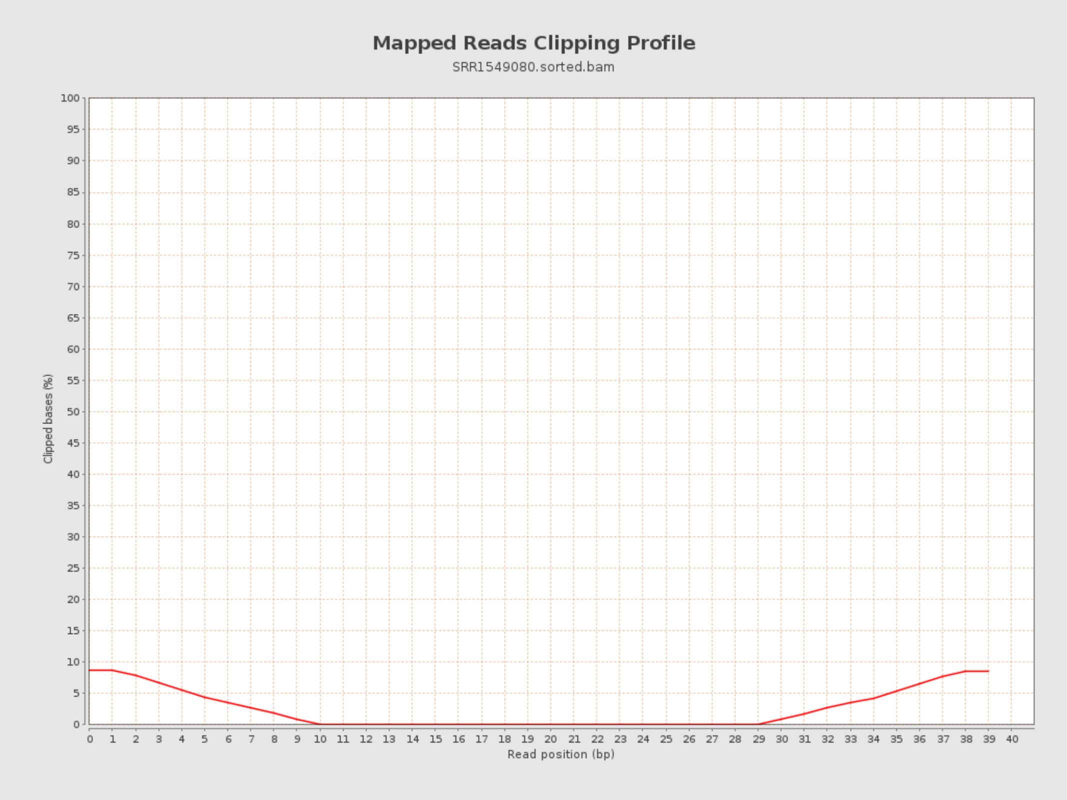
8. Results : Mapped Reads Nucleotide Content



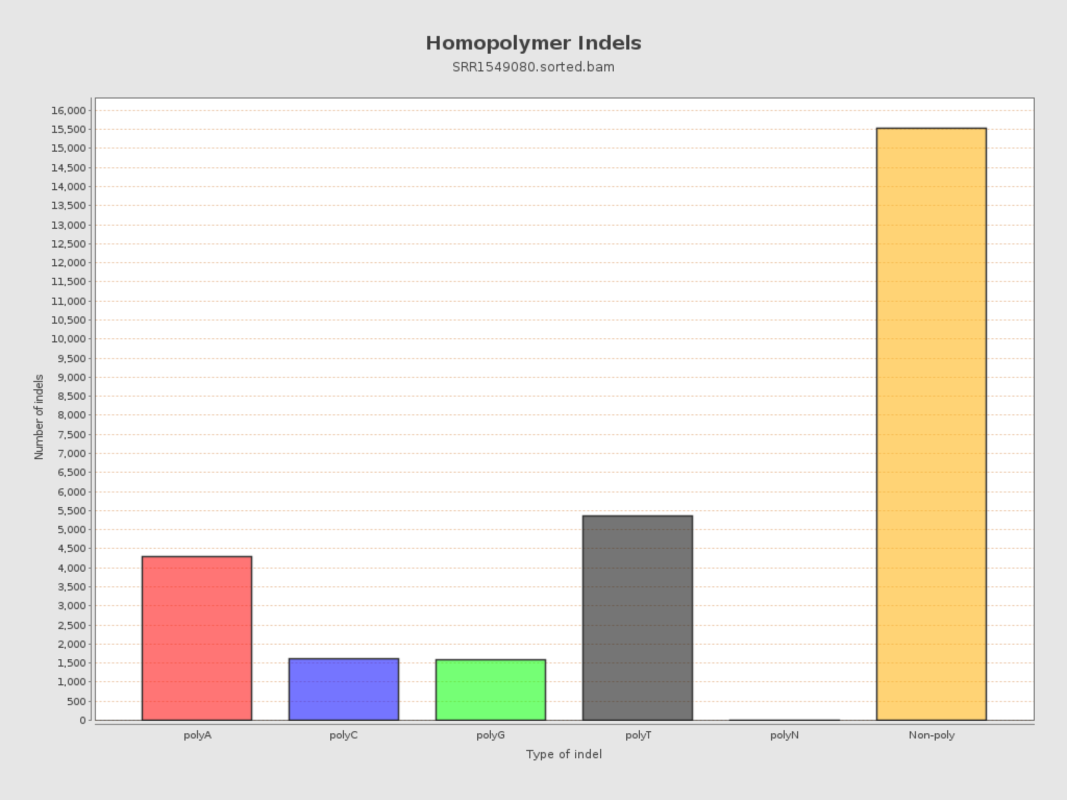
9. Results : Mapped Reads GC-content Distribution



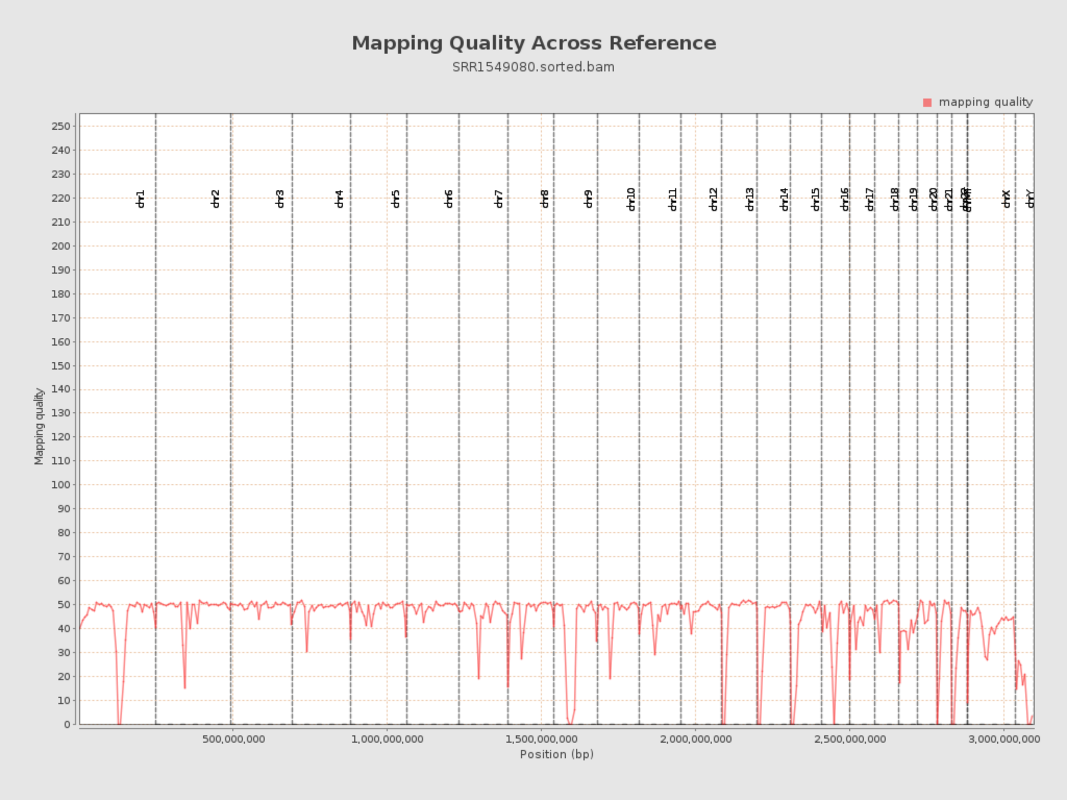
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram