Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:12:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549008.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_SRR1549008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549008.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:12:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,226,955
Mapped reads	9,766,445 / 86.99%
Unmapped reads	1,460,510 / 13.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	928,832 / 8.27%
Duplication rate	8.81%
Clipped reads	535,261 / 4.77%

2.2. ACGT Content

Number/percentage of A's	115,109,111 / 29.71%
Number/percentage of C's	77,456,307 / 19.99%
Number/percentage of T's	116,054,297 / 29.95%
Number/percentage of G's	78,812,837 / 20.34%
Number/percentage of N's	3,862 / 0%
GC Percentage	40.33%

2.3. Coverage

Mean	0.1252
Standard Deviation	0.8685

2.4. Mapping Quality

Mean Mapping Quality	43.43

2.5. Mismatches and indels

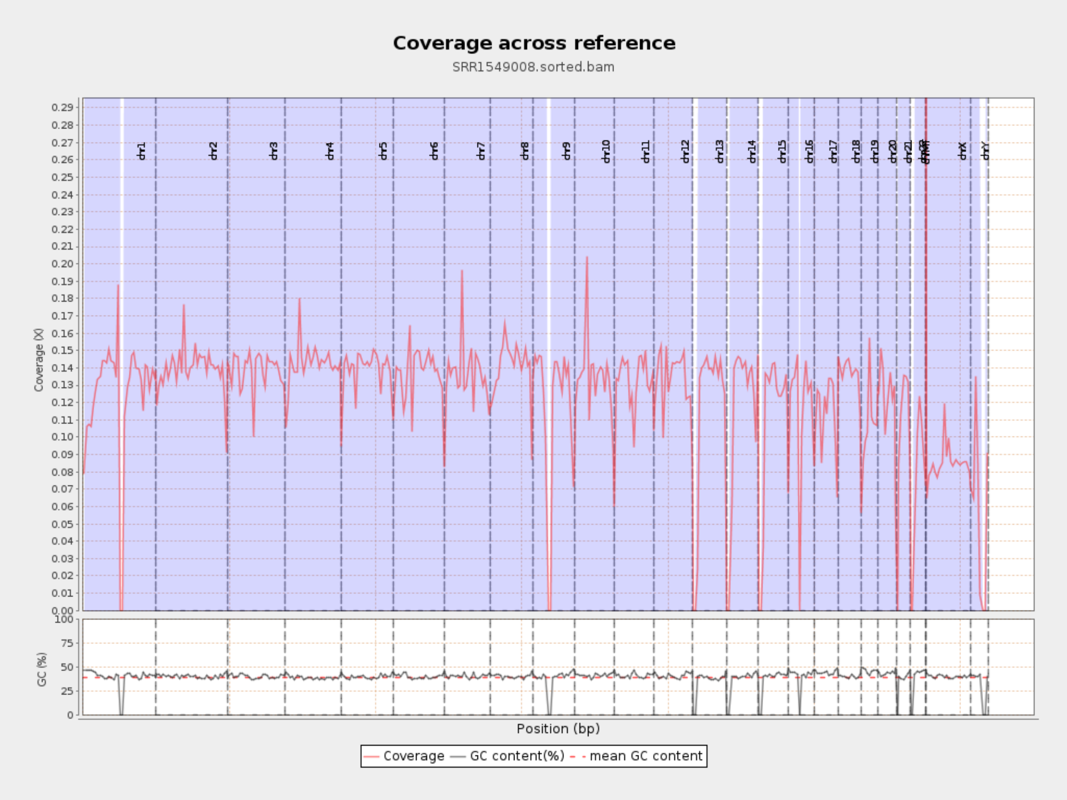
General error rate	0.3%
Mismatches	1,146,546
Insertions	12,088
Mapped reads with at least one insertion	0.12%
Deletions	32,745
Mapped reads with at least one deletion	0.34%
Homopolymer indels	42.77%

2.6. Chromosome stats

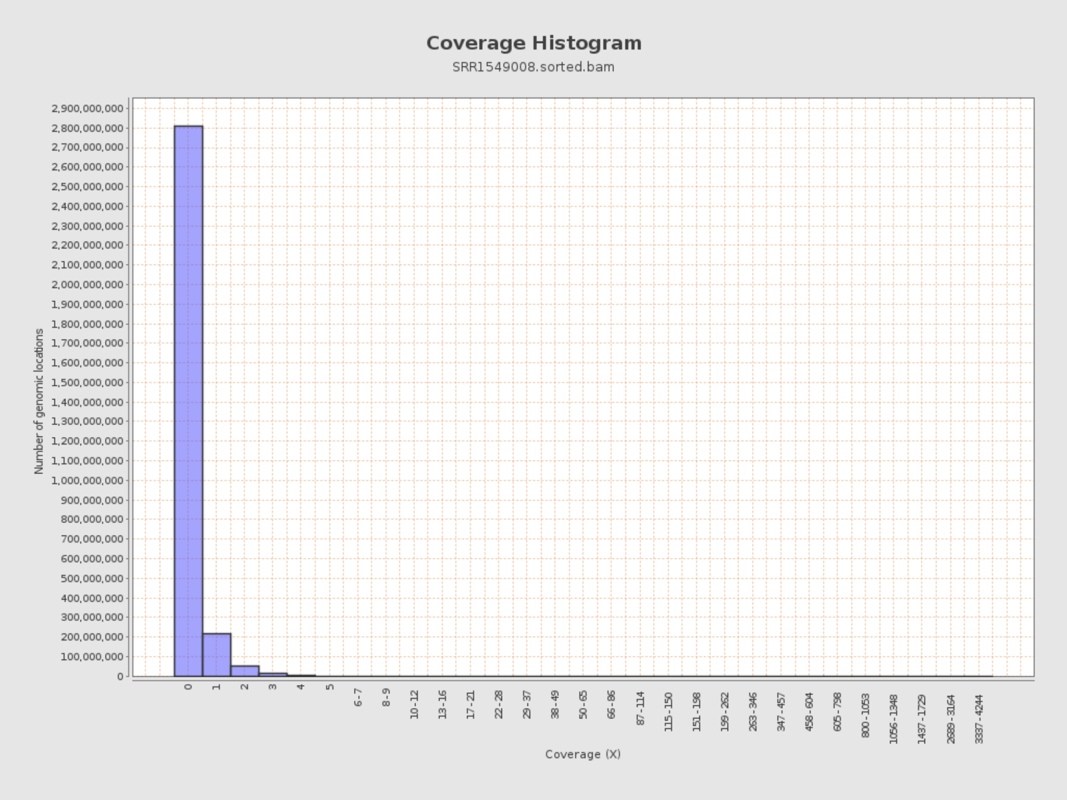
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31082862	0.1247	1.3994
chr2	243199373	33943478	0.1396	0.7207
chr3	198022430	27466615	0.1387	0.4753
chr4	191154276	27278478	0.1427	0.5446
chr5	180915260	25077516	0.1386	0.4841
chr6	171115067	23550967	0.1376	0.5701
chr7	159138663	21621451	0.1359	1.0448
chr8	146364022	20601600	0.1408	2.1441

chr9	141213431	16491268	0.1168	0.6875
chr10	135534747	18336750	0.1353	0.7874
chr11	135006516	17847619	0.1322	0.6425
chr12	133851895	17986615	0.1344	0.4896
chr13	115169878	13185933	0.1145	0.4263
chr14	107349540	12153125	0.1132	0.529
chr15	102531392	10911347	0.1064	0.4105
chr16	90354753	10201553	0.1129	0.4928
chr17	81195210	9365938	0.1154	0.4876
chr18	78077248	10772301	0.138	1.4196
chr19	59128983	6394797	0.1081	1.1216
chr20	63025520	7841299	0.1244	0.4839
chr21	48129895	5044075	0.1048	0.5406
chr22	51304566	3760462	0.0733	0.369
chrMT	16571	9479	0.572	0.9751
chrX	155270560	13211804	0.0851	0.5051
chrY	59373566	3341496	0.0563	0.5501

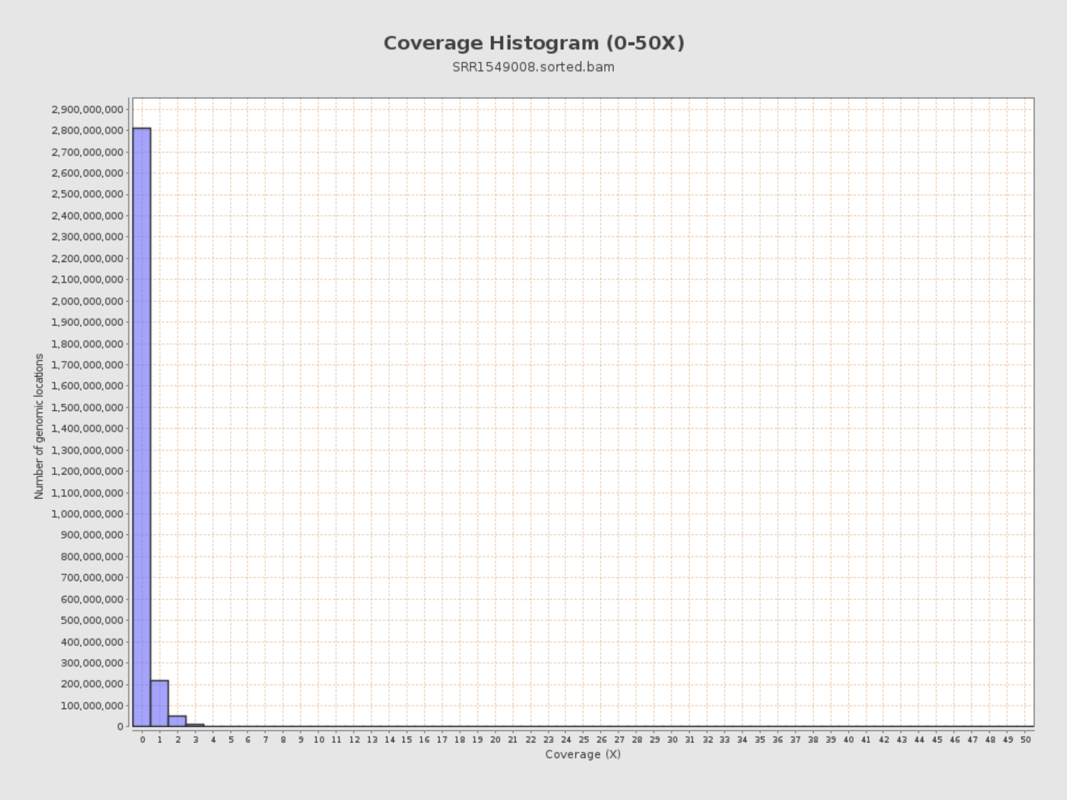
3. Results : Coverage across reference



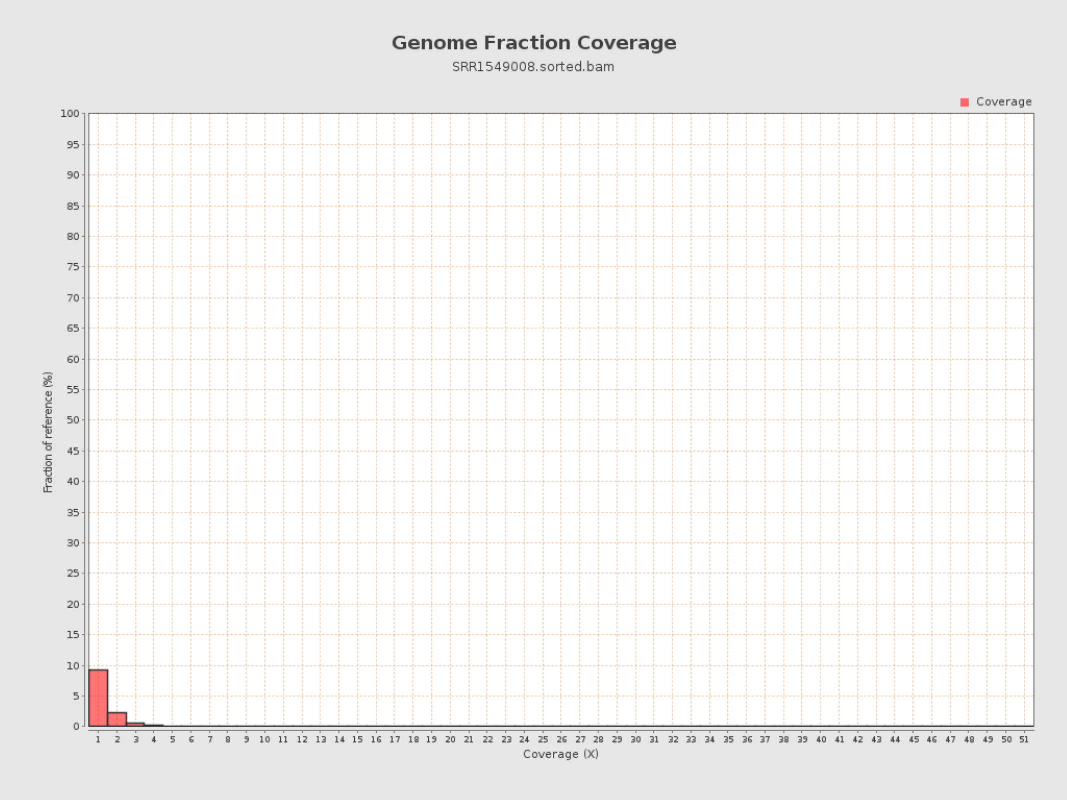
4. Results : Coverage Histogram



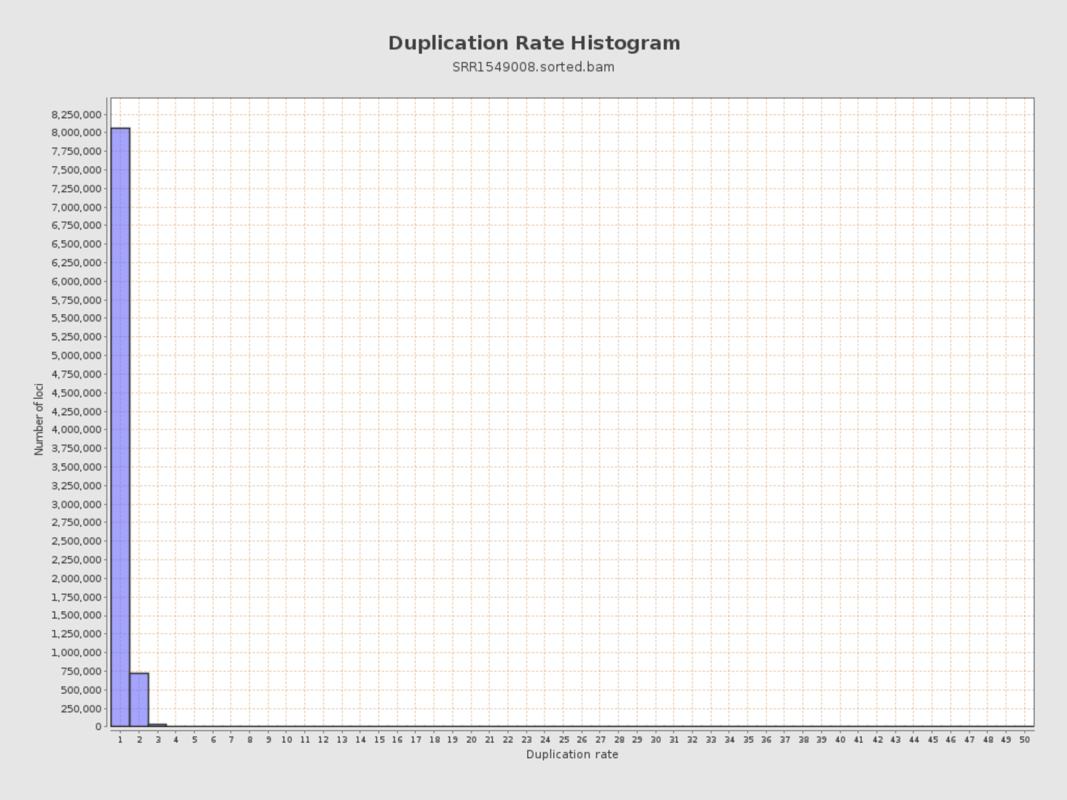
5. Results : Coverage Histogram (0-50X)



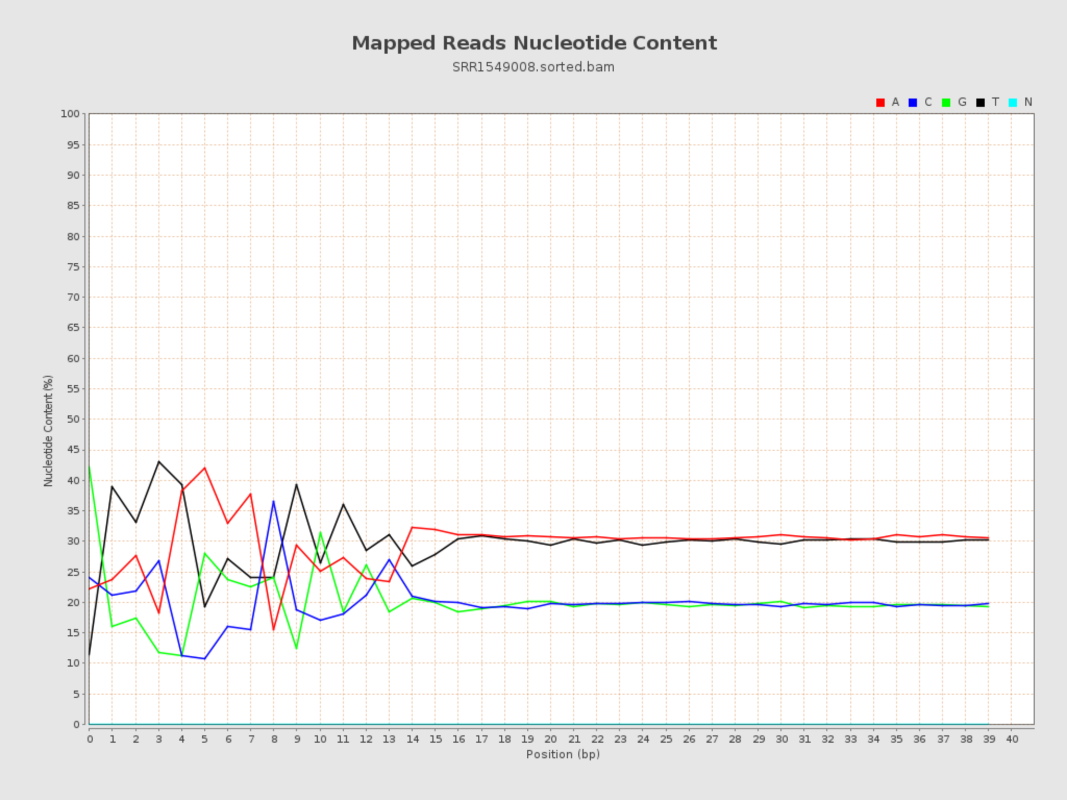
6. Results : Genome Fraction Coverage



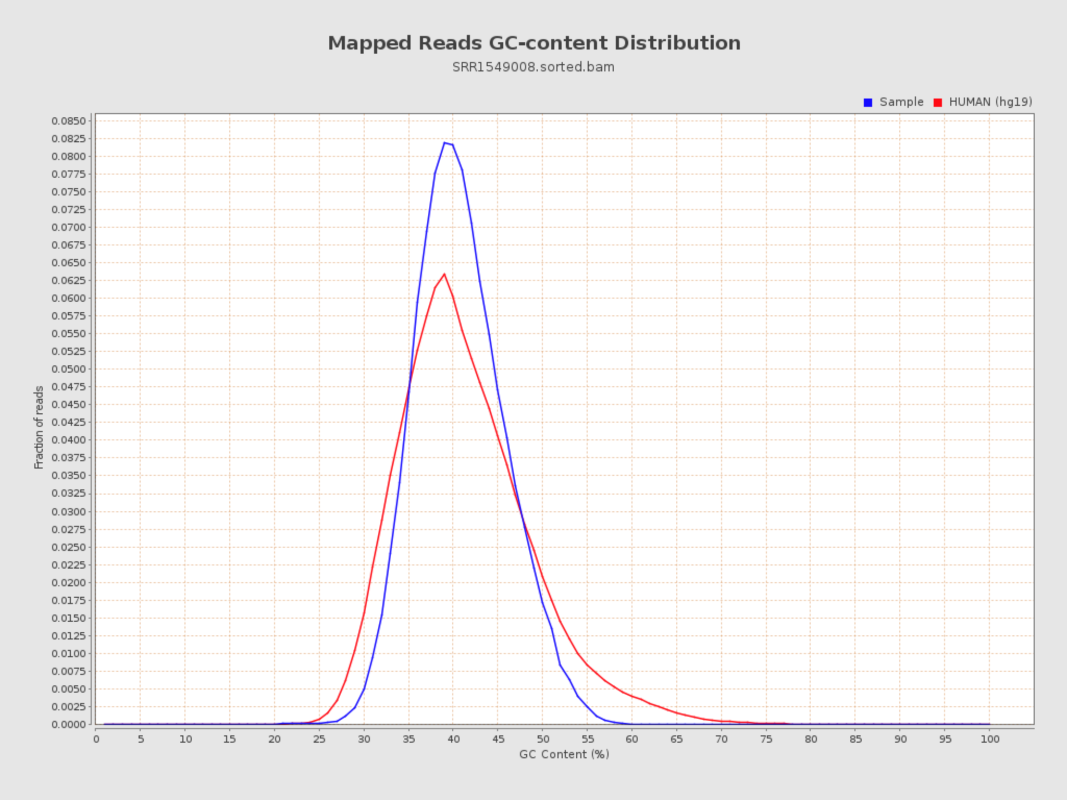
7. Results : Duplication Rate Histogram



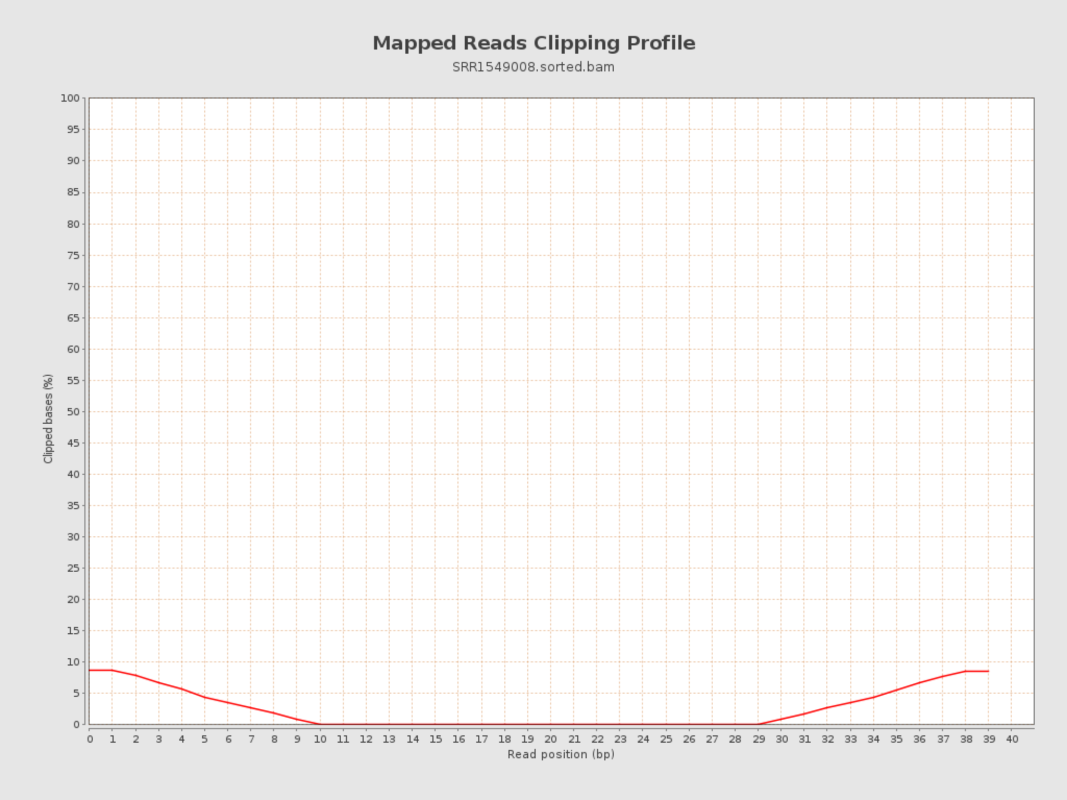
8. Results : Mapped Reads Nucleotide Content



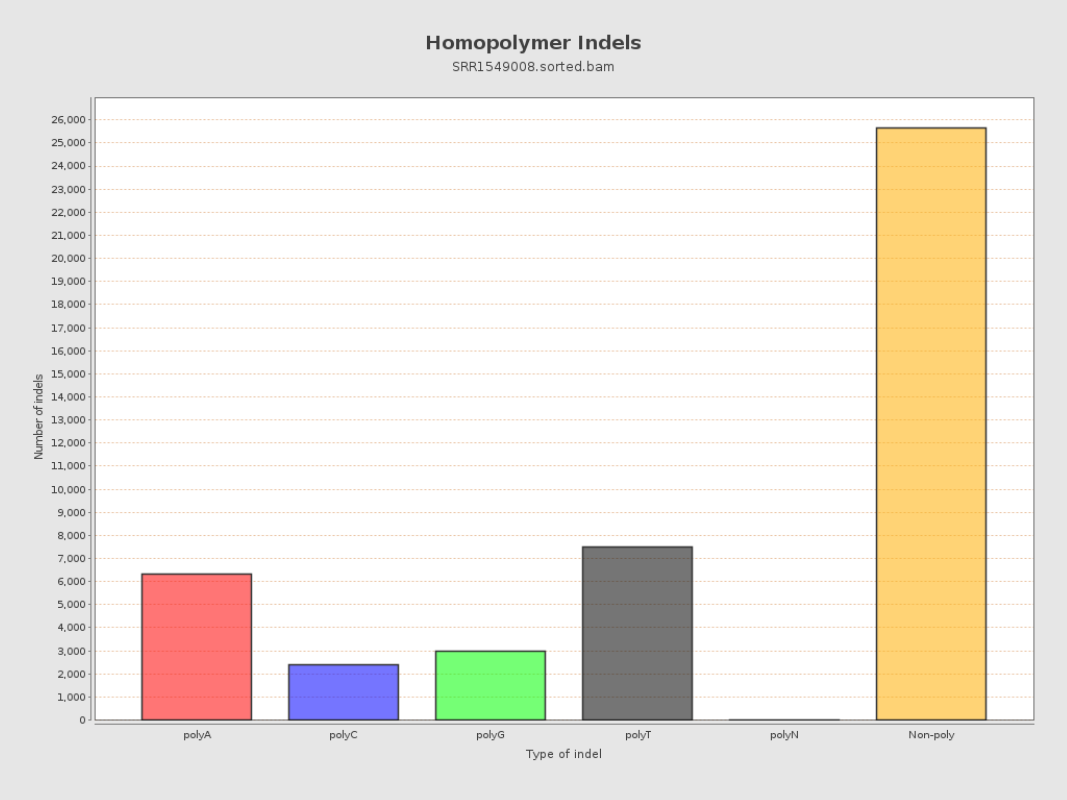
9. Results : Mapped Reads GC-content Distribution



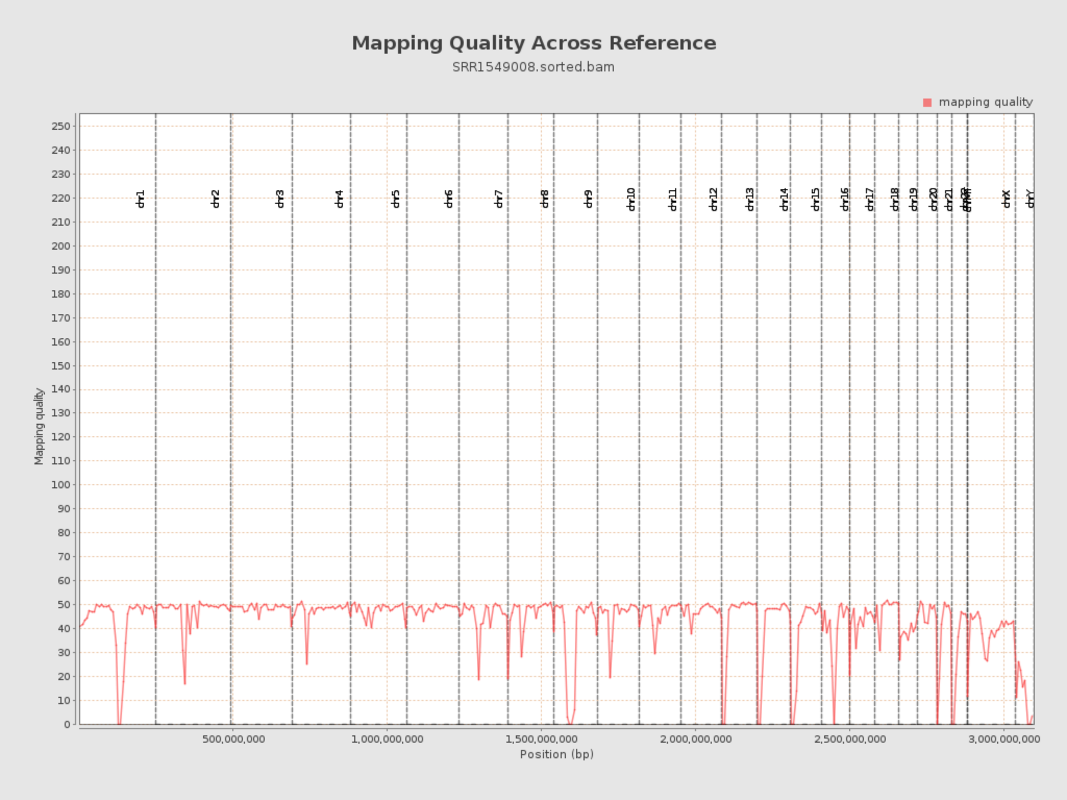
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram