Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:40:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549090.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_SRR1549090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549090.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:40:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,279,026
Mapped reads	8,892,905 / 86.52%
Unmapped reads	1,386,121 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	354,124 / 3.45%
Duplication rate	2.61%
Clipped reads	447,627 / 4.35%

2.2. ACGT Content

Number/percentage of A's	105,508,281 / 29.88%
Number/percentage of C's	70,918,633 / 20.09%
Number/percentage of T's	107,021,540 / 30.31%
Number/percentage of G's	69,551,591 / 19.7%
Number/percentage of N's	87,153 / 0.02%
GC Percentage	39.78%

2.3. Coverage

Mean	0.1141
Standard Deviation	0.9401

2.4. Mapping Quality

Mean Mapping Quality	43.82

2.5. Mismatches and indels

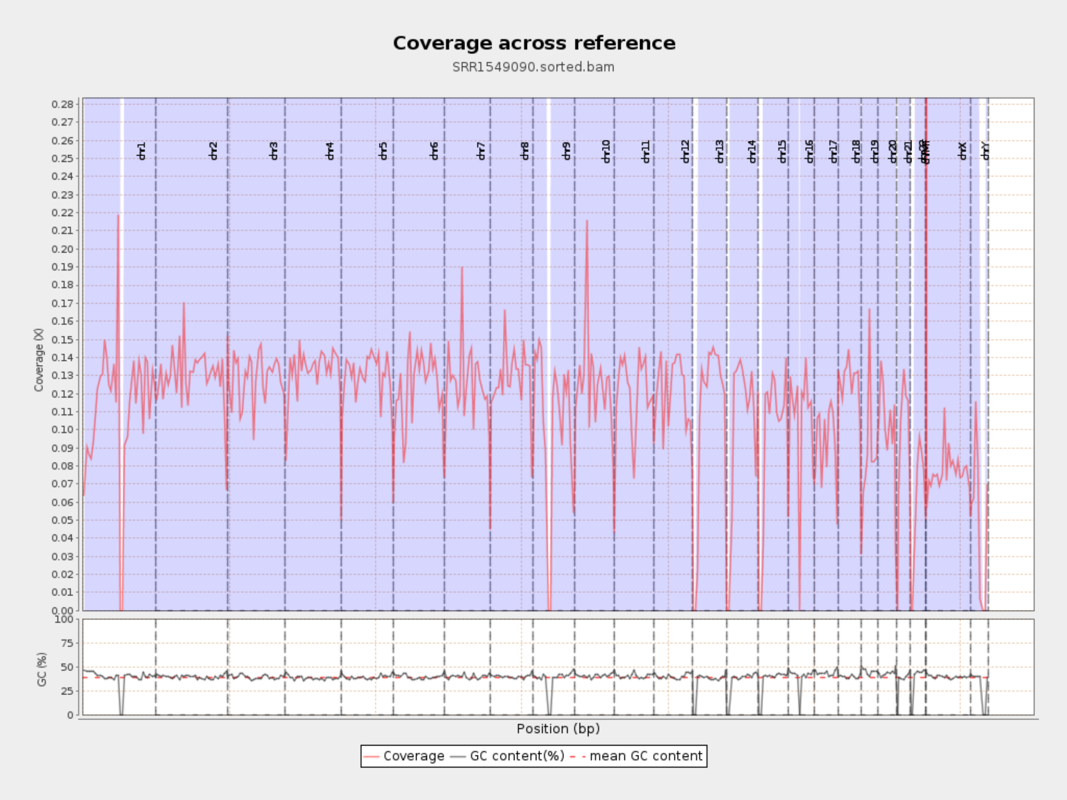
General error rate	0.41%
Mismatches	1,426,740
Insertions	8,418
Mapped reads with at least one insertion	0.09%
Deletions	25,306
Mapped reads with at least one deletion	0.28%
Homopolymer indels	45.64%

2.6. Chromosome stats

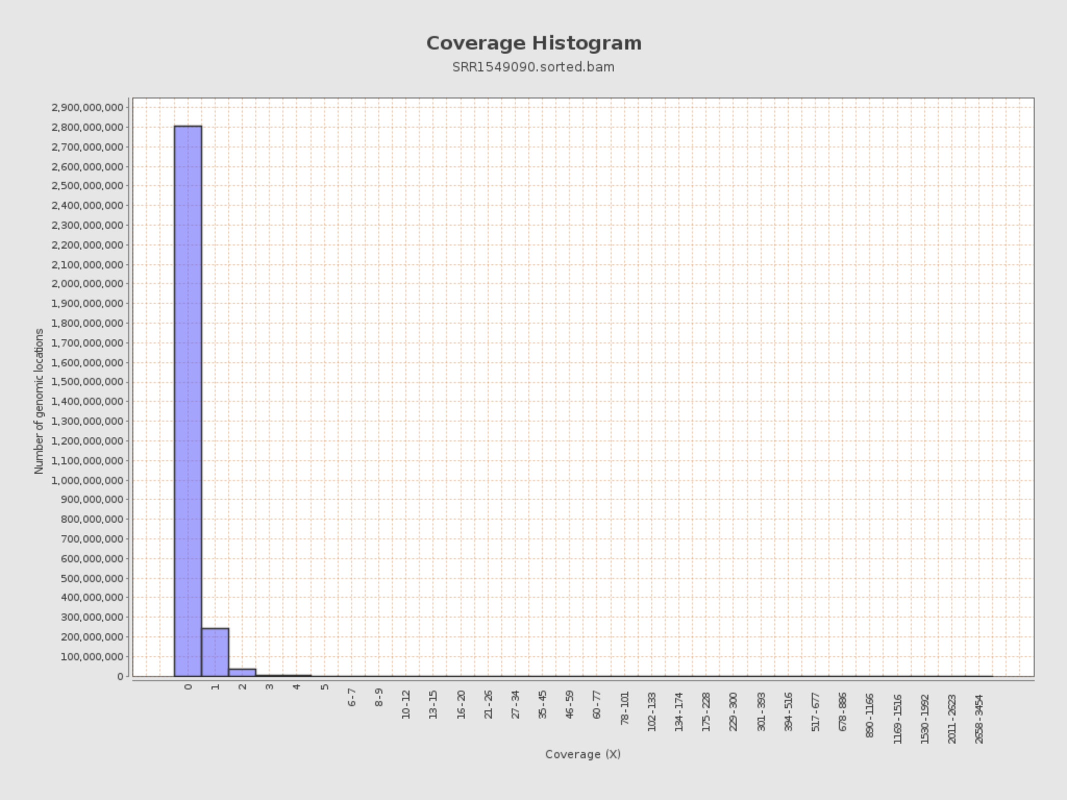
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28087330	0.1127	2.3671
chr2	243199373	31687118	0.1303	0.7057
chr3	198022430	25529980	0.1289	0.4317
chr4	191154276	25451721	0.1331	0.4401
chr5	180915260	23279203	0.1287	0.4356
chr6	171115067	21430179	0.1252	0.5161
chr7	159138663	20019866	0.1258	1.0209
chr8	146364022	18868922	0.1289	0.7793

chr9	141213431	14700456	0.1041	0.672
chr10	135534747	17185771	0.1268	0.9471
chr11	135006516	16268084	0.1205	0.7213
chr12	133851895	16229886	0.1213	0.4452
chr13	115169878	12509723	0.1086	0.3743
chr14	107349540	10887865	0.1014	0.4904
chr15	102531392	9728942	0.0949	0.3549
chr16	90354753	9251478	0.1024	0.5375
chr17	81195210	7690919	0.0947	0.4882
chr18	78077248	10004721	0.1281	1.4313
chr19	59128983	5252278	0.0888	1.8336
chr20	63025520	6666670	0.1058	0.4029
chr21	48129895	4492644	0.0933	0.4531
chr22	51304566	3005051	0.0586	0.3485
chrMT	16571	51497	3.1077	3.8665
chrX	155270560	11928763	0.0768	0.4511
chrY	59373566	2909605	0.049	0.3901

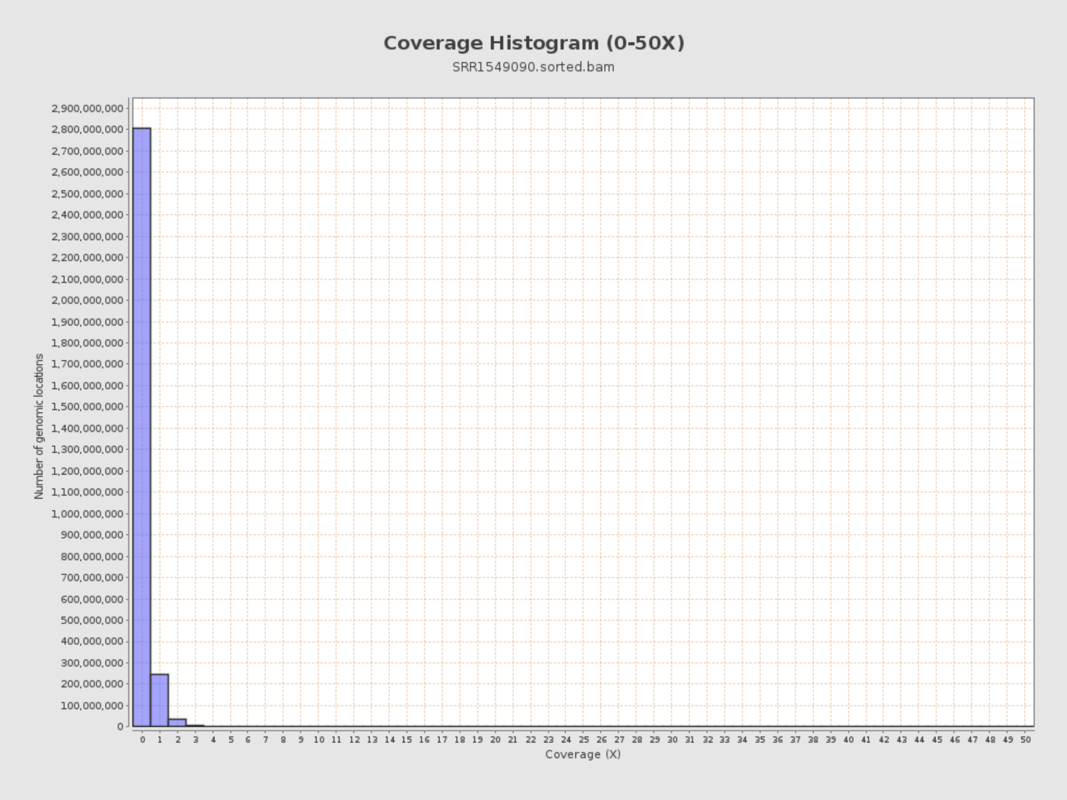
3. Results : Coverage across reference



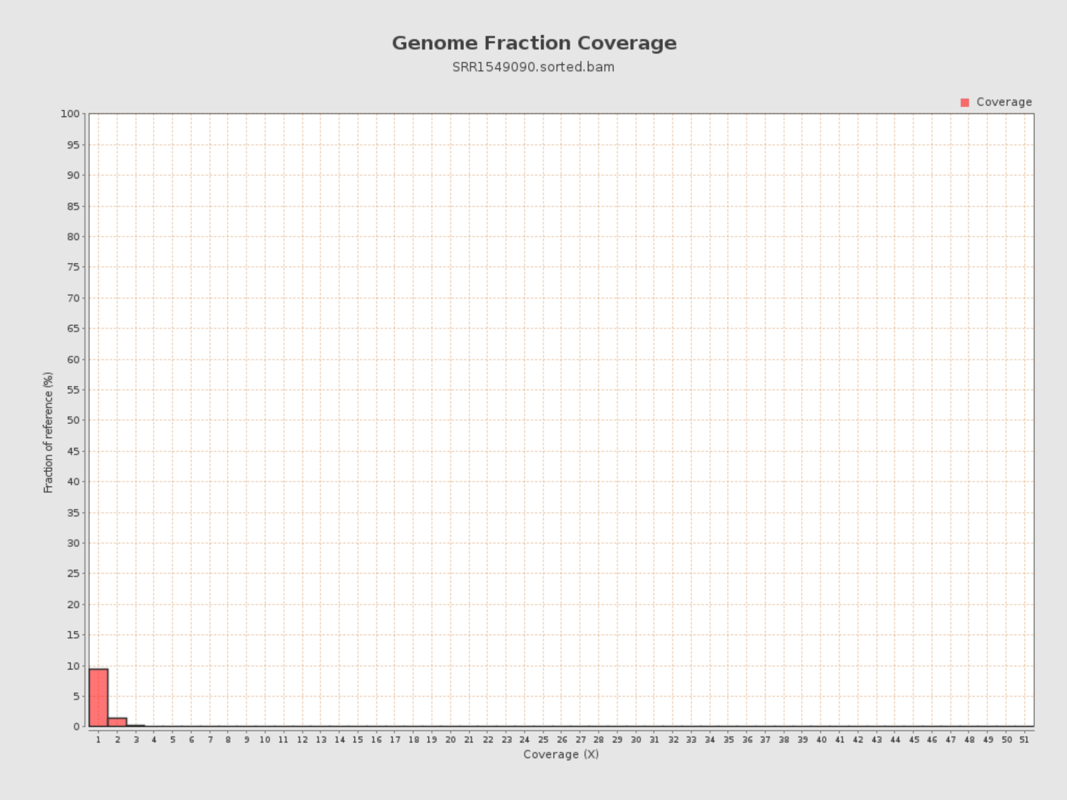
4. Results : Coverage Histogram



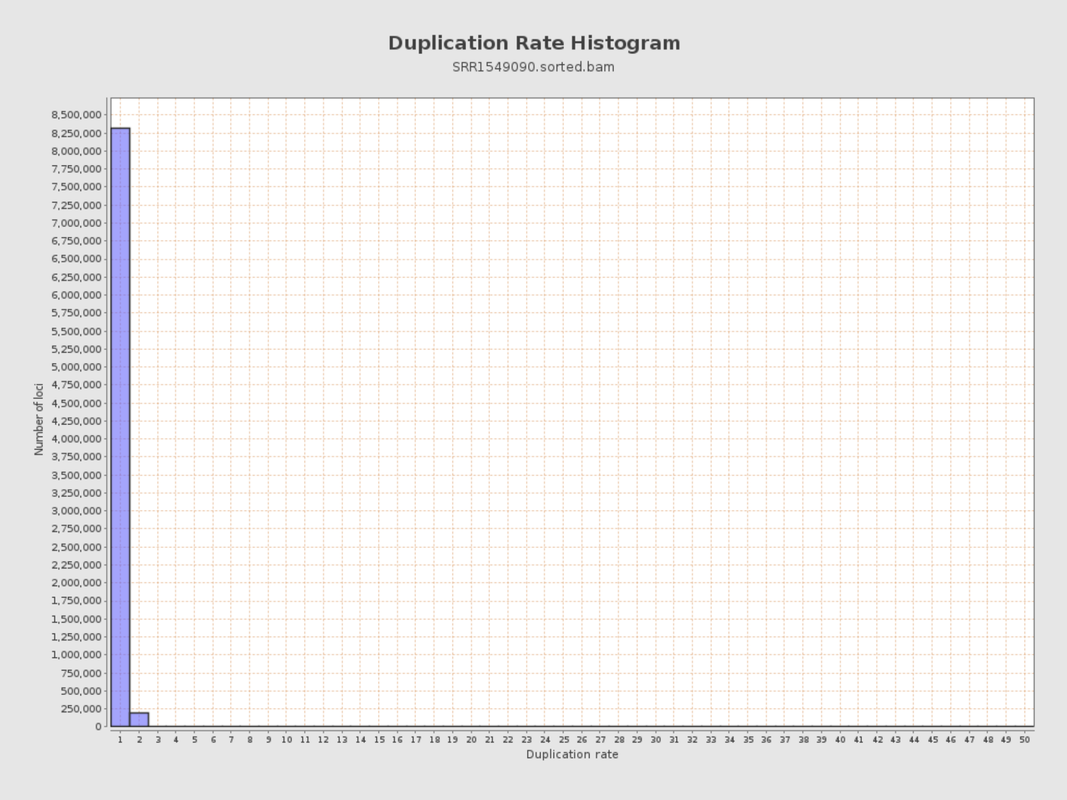
5. Results : Coverage Histogram (0-50X)



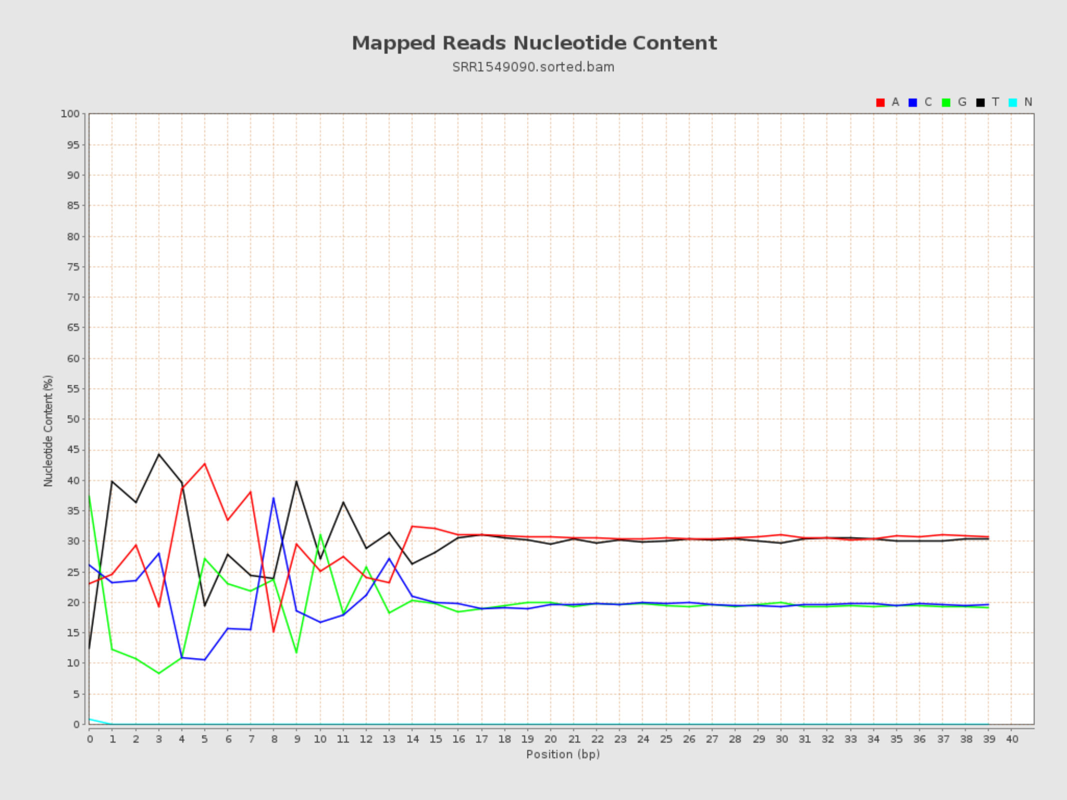
6. Results : Genome Fraction Coverage



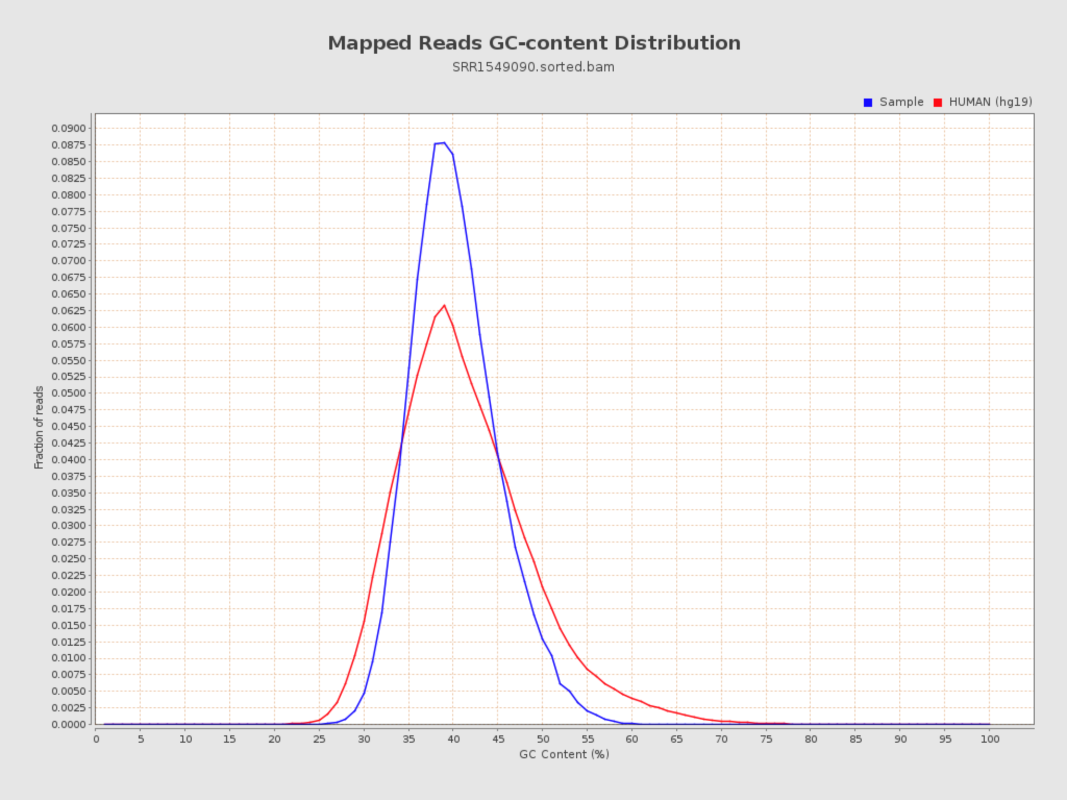
7. Results : Duplication Rate Histogram



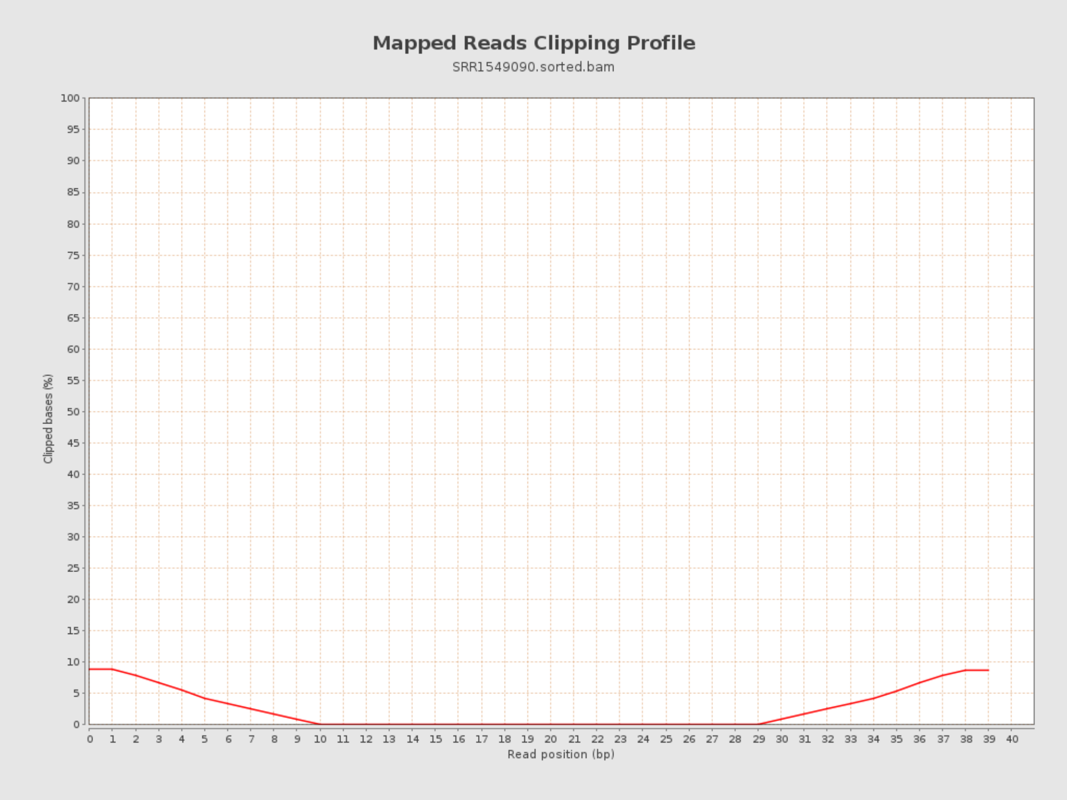
8. Results : Mapped Reads Nucleotide Content



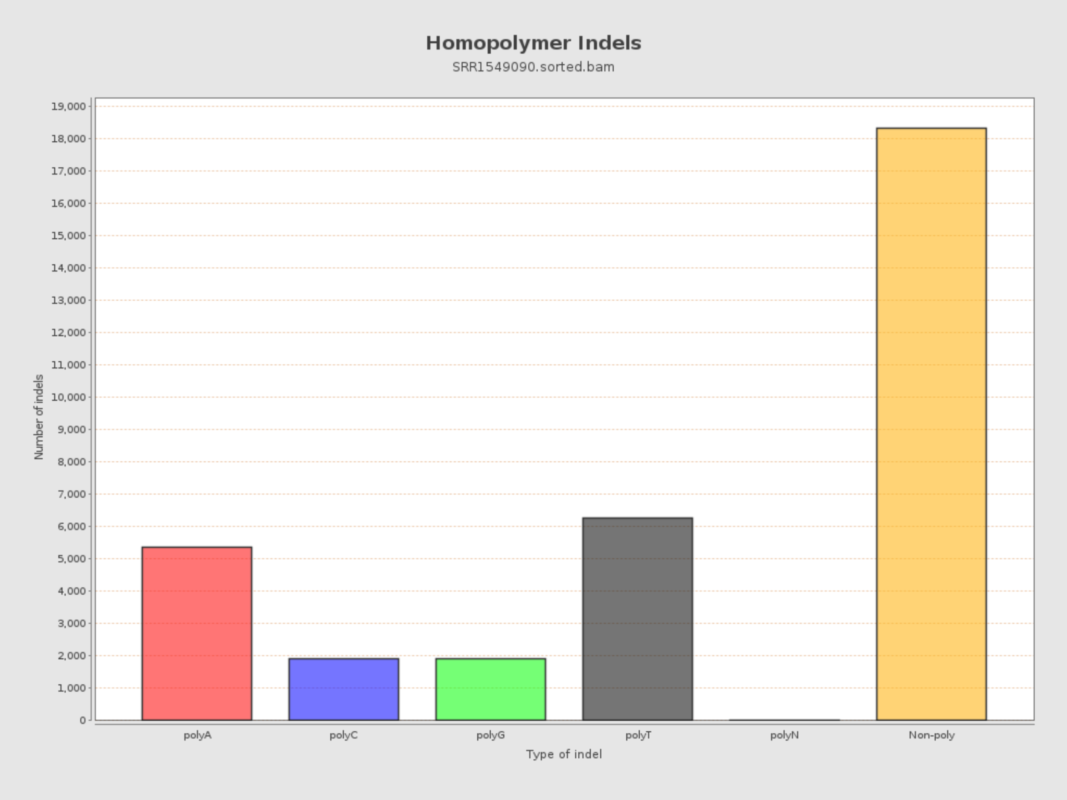
9. Results : Mapped Reads GC-content Distribution



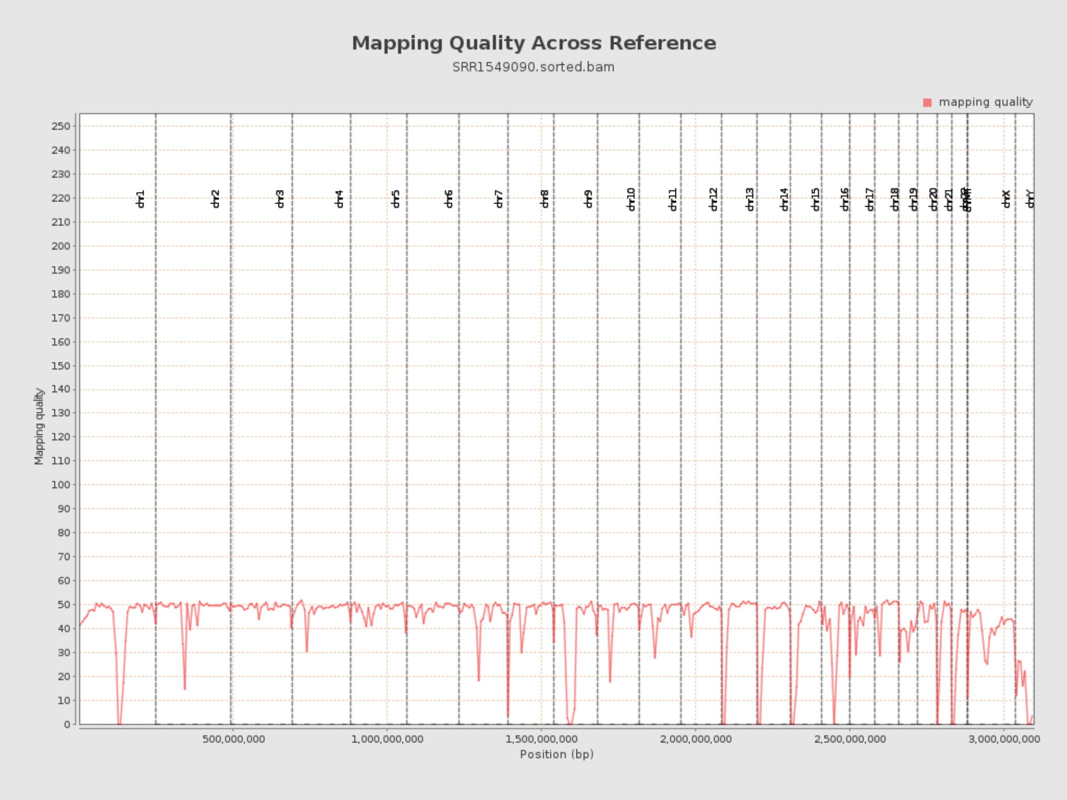
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram