Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:43:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549005.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_SRR1549005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549005.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:43:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549005.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,051,335
Mapped reads	9,522,912 / 86.17%
Unmapped reads	1,528,423 / 13.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	885,298 / 8.01%
Duplication rate	8.51%
Clipped reads	482,940 / 4.37%

2.2. ACGT Content

Number/percentage of A's	114,386,412 / 30.26%
Number/percentage of C's	74,051,311 / 19.59%
Number/percentage of T's	114,611,601 / 30.32%
Number/percentage of G's	74,970,639 / 19.83%
Number/percentage of N's	3,764 / 0%
GC Percentage	39.42%

2.3. Coverage

Mean	0.1221
Standard Deviation	1.1109

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

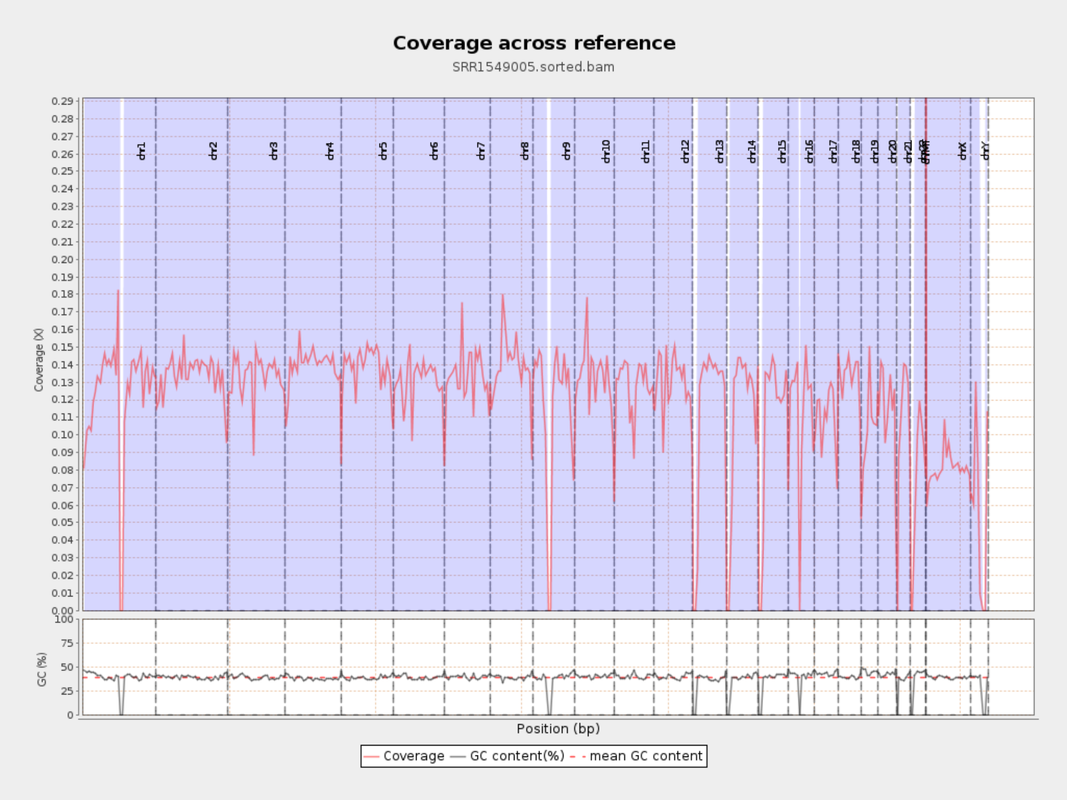
General error rate	0.29%
Mismatches	1,090,723
Insertions	11,919
Mapped reads with at least one insertion	0.13%
Deletions	32,793
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.19%

2.6. Chromosome stats

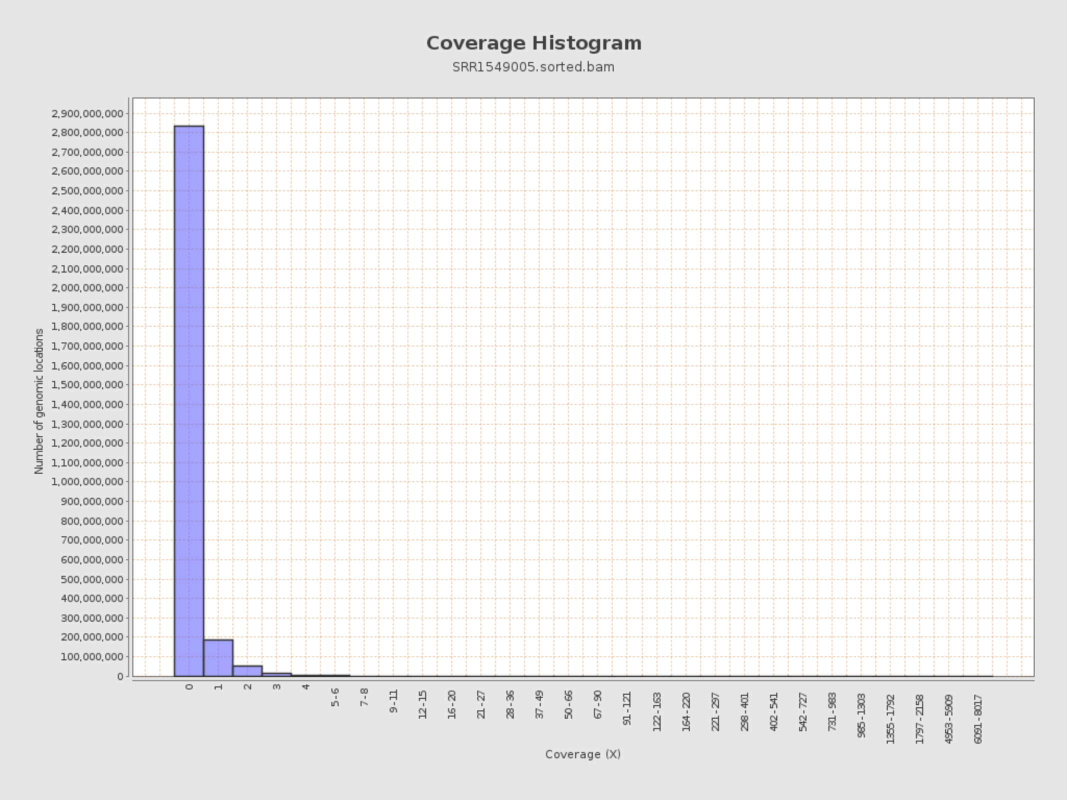
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30648466	0.123	1.434
chr2	243199373	32658409	0.1343	0.6561
chr3	198022430	26460105	0.1336	0.4903
chr4	191154276	26750821	0.1399	0.5445
chr5	180915260	25034493	0.1384	0.5072
chr6	171115067	22460117	0.1313	0.55
chr7	159138663	21155165	0.1329	0.9111
chr8	146364022	20384014	0.1393	3.9379

chr9	141213431	16231597	0.1149	0.6113
chr10	135534747	18079681	0.1334	0.6984
chr11	135006516	17175910	0.1272	0.6112
chr12	133851895	17447707	0.1304	0.508
chr13	115169878	13035191	0.1132	0.4502
chr14	107349540	11769887	0.1096	0.5343
chr15	102531392	10782378	0.1052	0.4293
chr16	90354753	9990976	0.1106	0.4854
chr17	81195210	9016433	0.111	0.4776
chr18	78077248	10508638	0.1346	1.2069
chr19	59128983	6183080	0.1046	1.1078
chr20	63025520	7432677	0.1179	0.4903
chr21	48129895	5097628	0.1059	0.5307
chr22	51304566	3737112	0.0728	0.4027
chrMT	16571	7064	0.4263	0.8528
chrX	155270560	12593349	0.0811	0.4826
chrY	59373566	3425043	0.0577	0.607

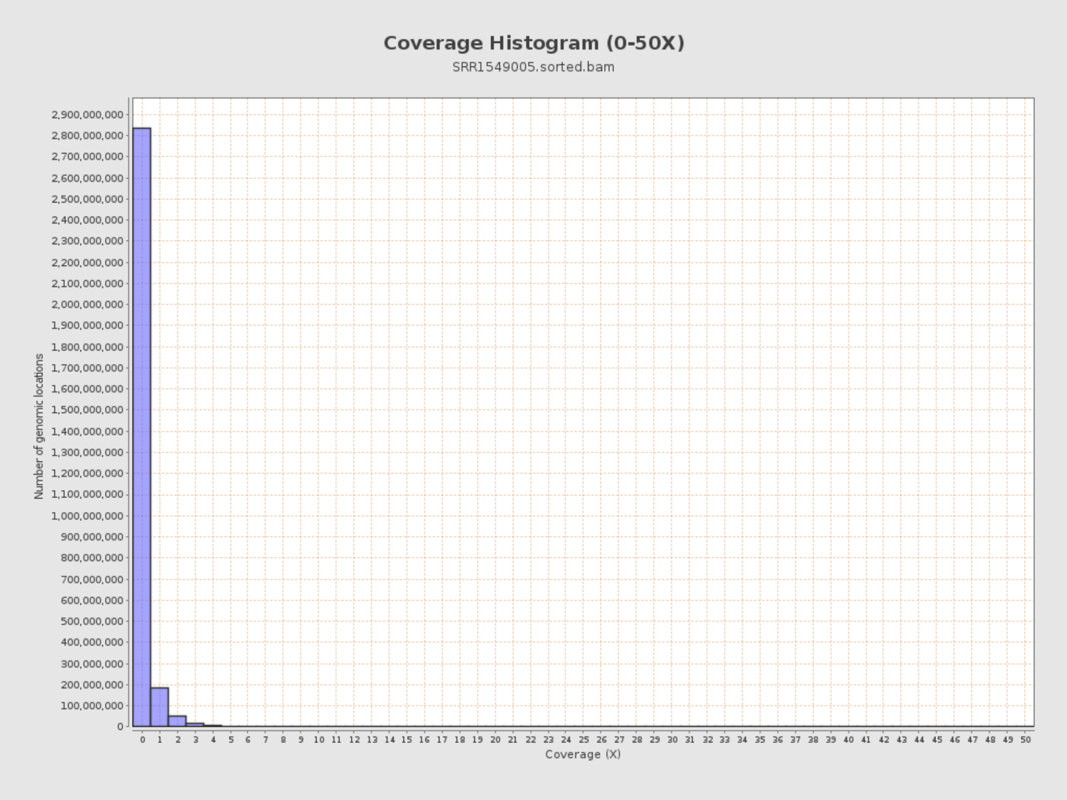
3. Results : Coverage across reference



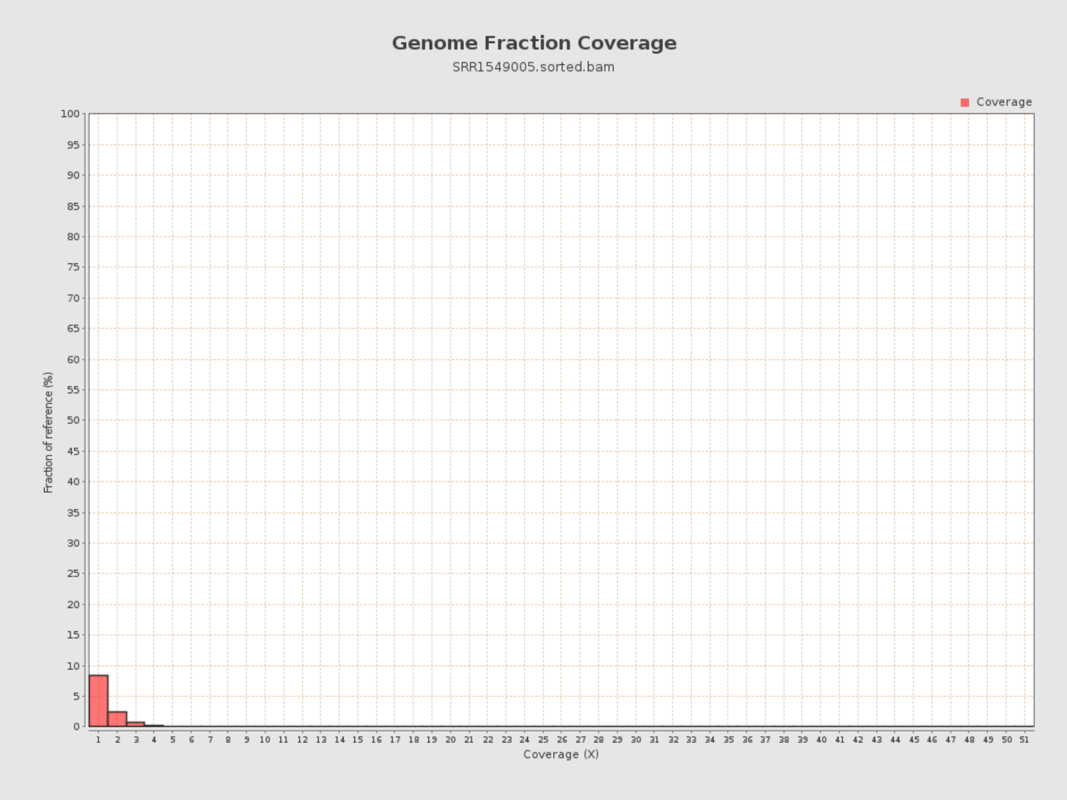
4. Results : Coverage Histogram



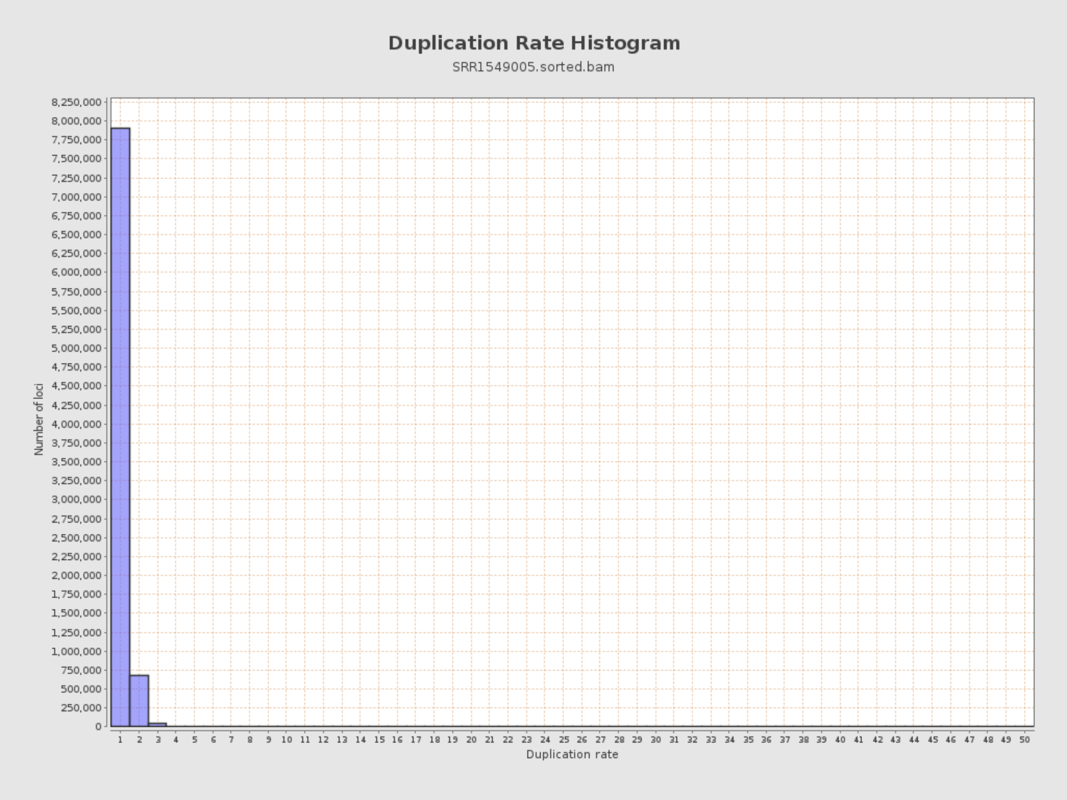
5. Results : Coverage Histogram (0-50X)



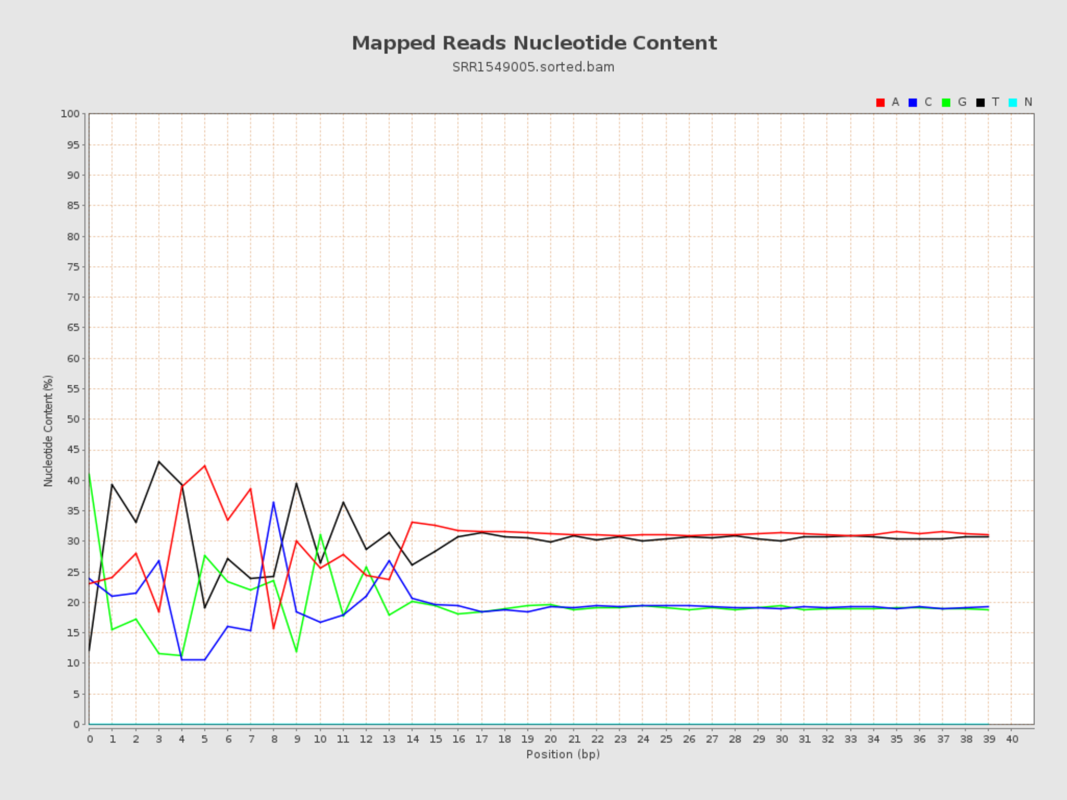
6. Results : Genome Fraction Coverage



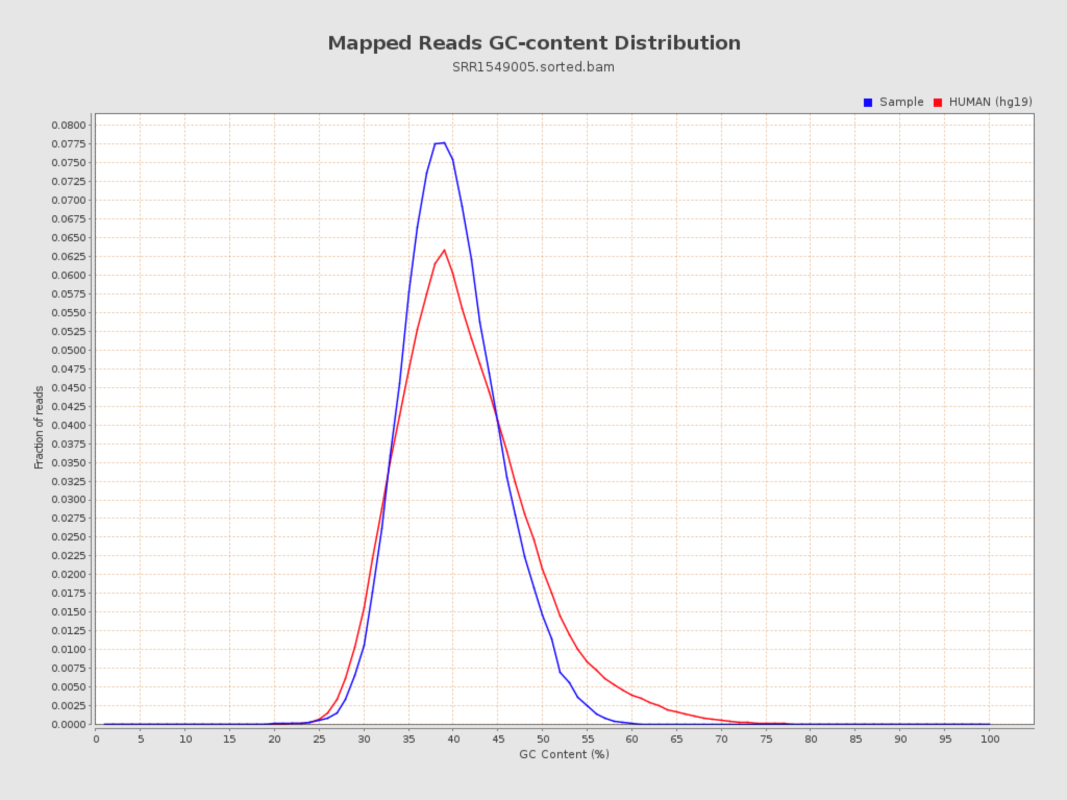
7. Results : Duplication Rate Histogram



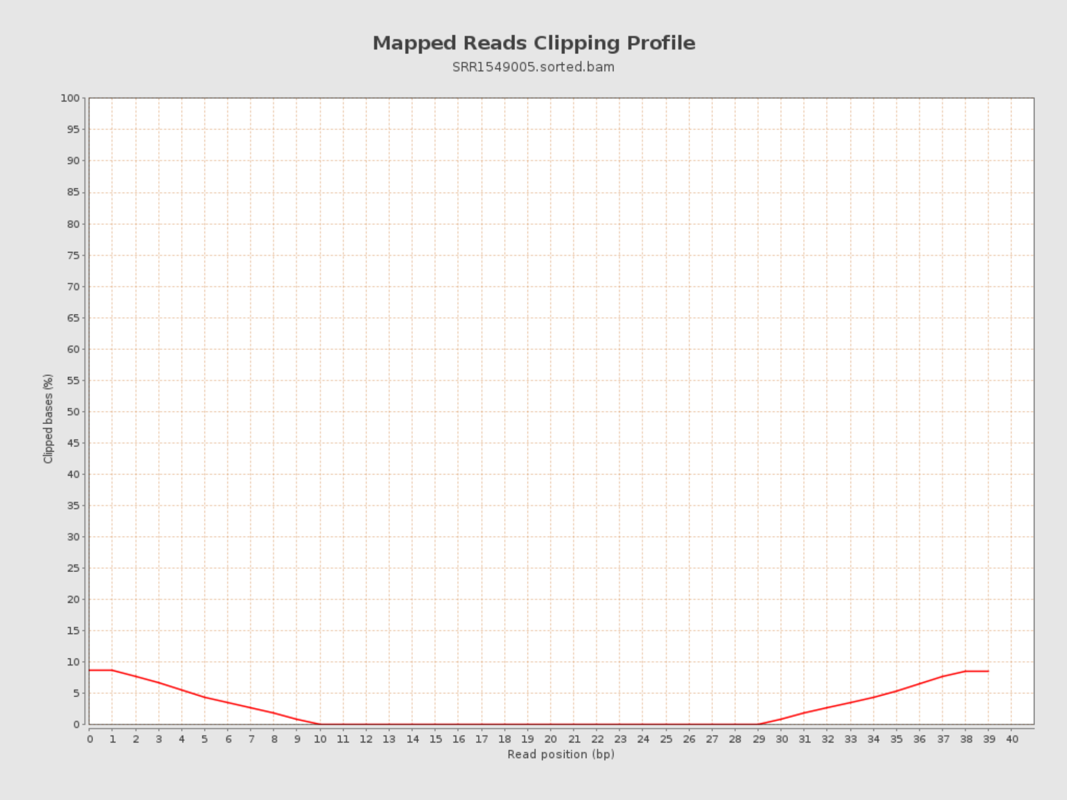
8. Results : Mapped Reads Nucleotide Content



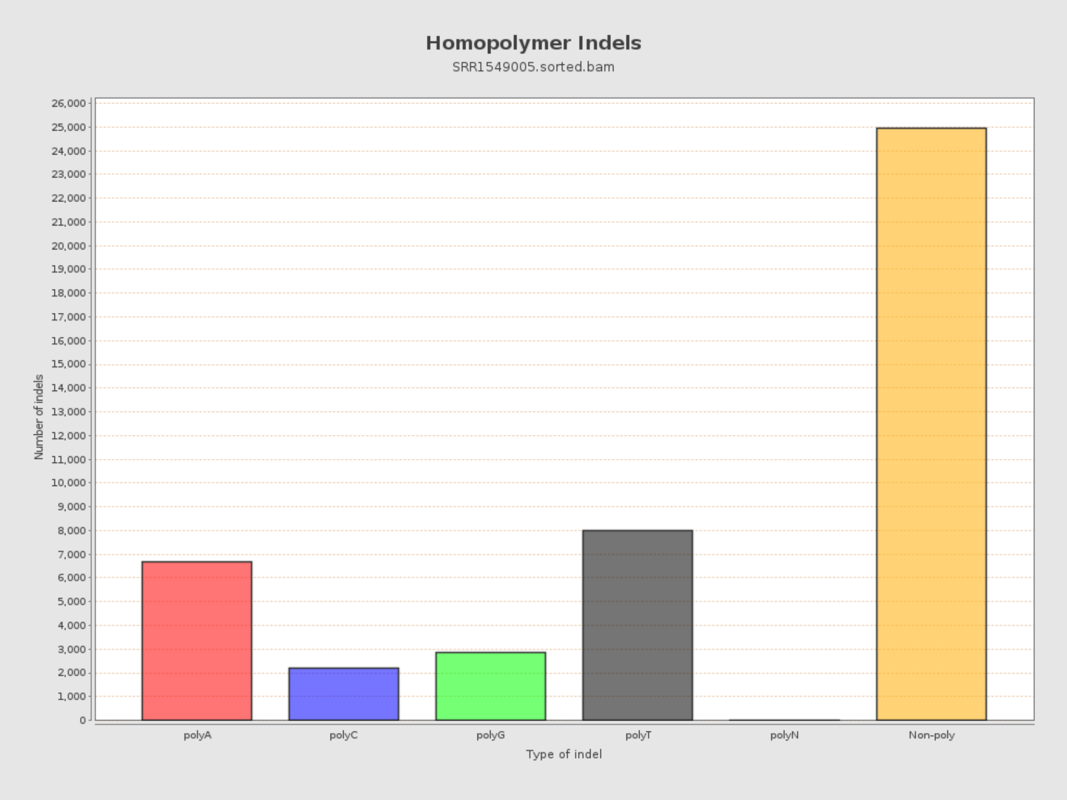
9. Results : Mapped Reads GC-content Distribution



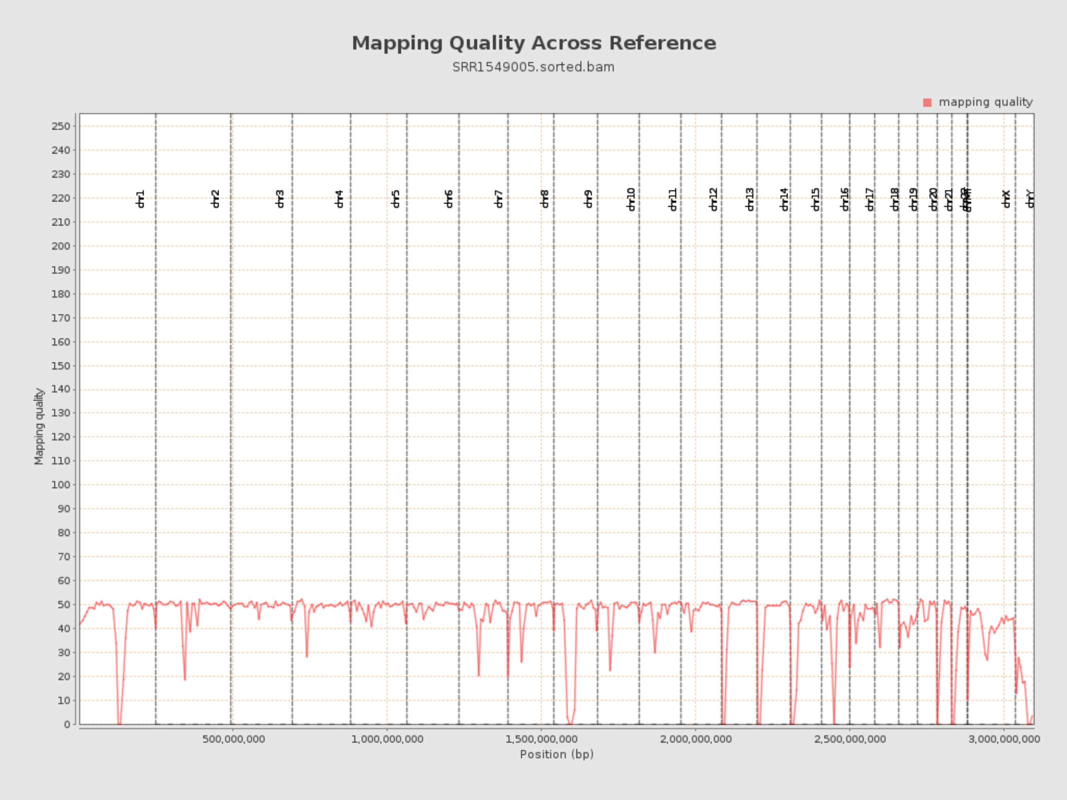
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram