Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:13:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548941.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_SRR1548941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548941.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:13:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,235,713
Mapped reads	9,091,265 / 88.82%
Unmapped reads	1,144,448 / 11.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	412,334 / 4.03%
Duplication rate	3.02%
Clipped reads	854,056 / 8.34%

2.2. ACGT Content

Number/percentage of A's	103,152,557 / 28.74%
Number/percentage of C's	76,085,188 / 21.2%
Number/percentage of T's	103,955,166 / 28.96%
Number/percentage of G's	75,705,051 / 21.09%
Number/percentage of N's	3,303 / 0%
GC Percentage	42.29%

2.3. Coverage

Mean	0.1159
Standard Deviation	1.0581

2.4. Mapping Quality

Mean Mapping Quality	34.41

2.5. Mismatches and indels

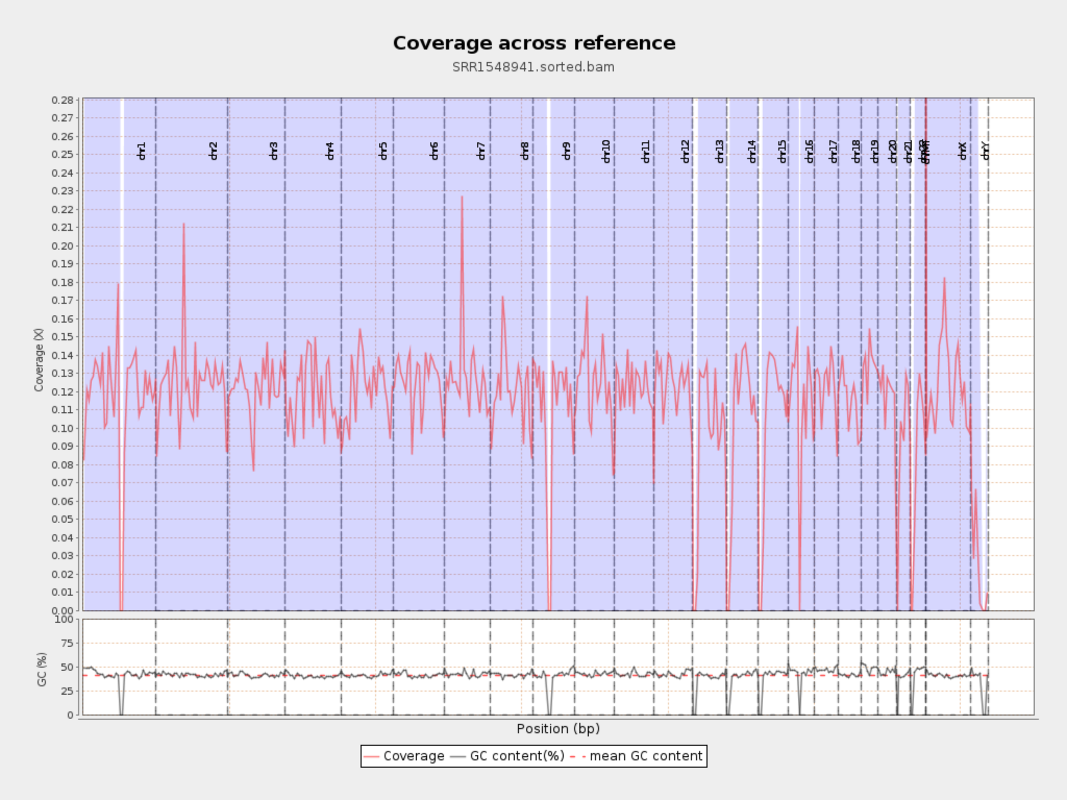
General error rate	0.36%
Mismatches	1,274,531
Insertions	14,012
Mapped reads with at least one insertion	0.15%
Deletions	29,154
Mapped reads with at least one deletion	0.32%
Homopolymer indels	38.15%

2.6. Chromosome stats

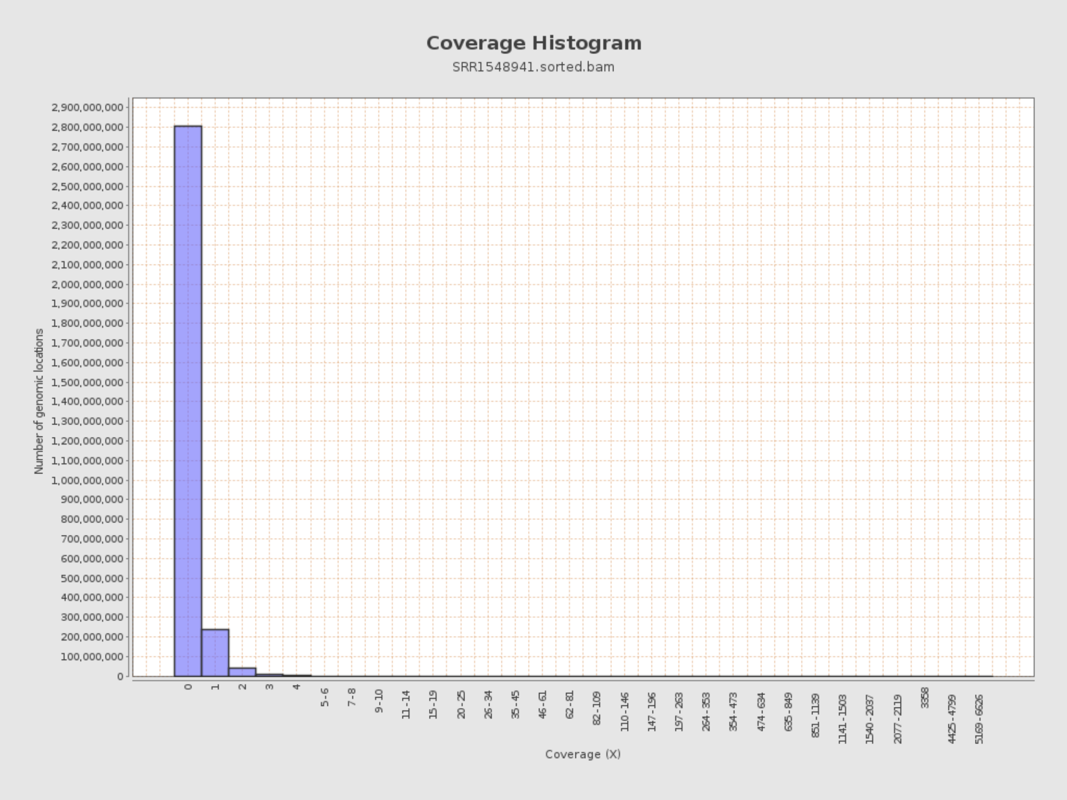
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29019103	0.1164	1.4385
chr2	243199373	30494920	0.1254	0.8726
chr3	198022430	24074904	0.1216	0.4228
chr4	191154276	22515539	0.1178	0.4457
chr5	180915260	21938068	0.1213	0.439
chr6	171115067	21516864	0.1257	0.466
chr7	159138663	20415180	0.1283	1.2039
chr8	146364022	17539575	0.1198	3.2353

chr9	141213431	15196449	0.1076	0.8624
chr10	135534747	16942838	0.125	0.7287
chr11	135006516	16446156	0.1218	0.7705
chr12	133851895	16797401	0.1255	0.4647
chr13	115169878	10780166	0.0936	0.3569
chr14	107349540	11193066	0.1043	0.529
chr15	102531392	10332822	0.1008	0.3851
chr16	90354753	9974796	0.1104	0.4975
chr17	81195210	10113776	0.1246	0.4528
chr18	78077248	9087771	0.1164	1.727
chr19	59128983	7915735	0.1339	1.5531
chr20	63025520	7499690	0.119	0.4614
chr21	48129895	4355978	0.0905	0.4607
chr22	51304566	4124172	0.0804	0.383
chrMT	16571	6284	0.3792	0.7552
chrX	155270560	19223697	0.1238	0.6235
chrY	59373566	1433857	0.0241	0.2632

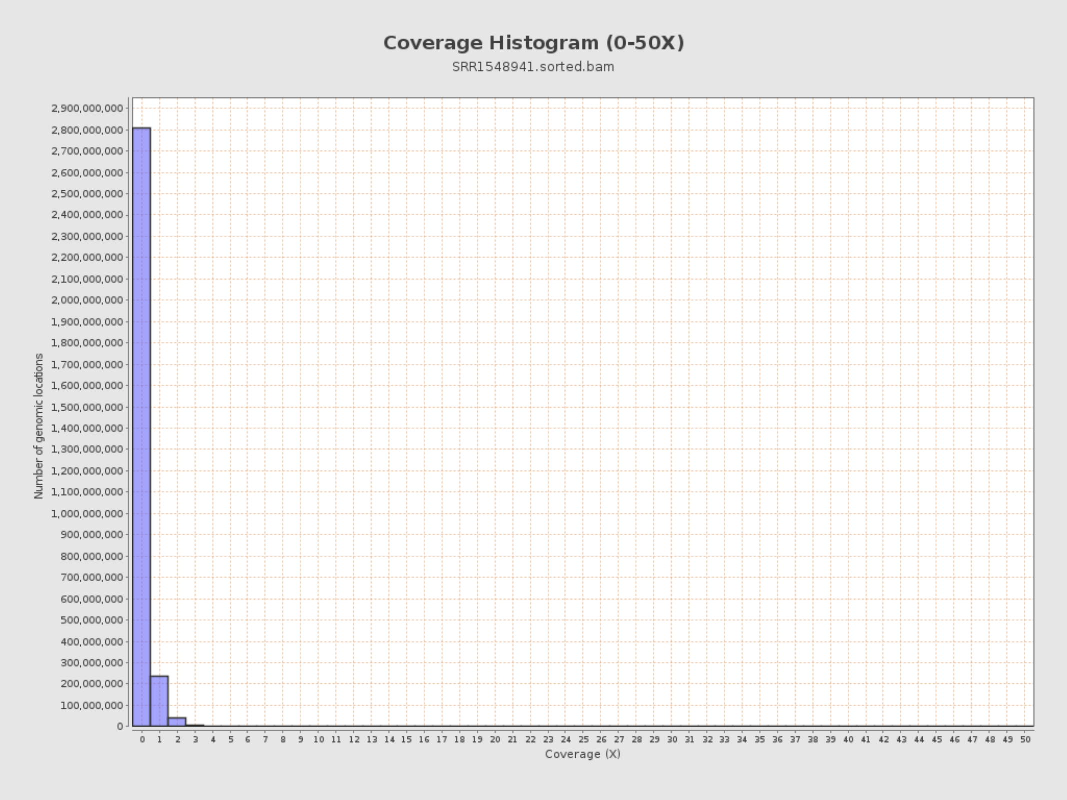
3. Results : Coverage across reference



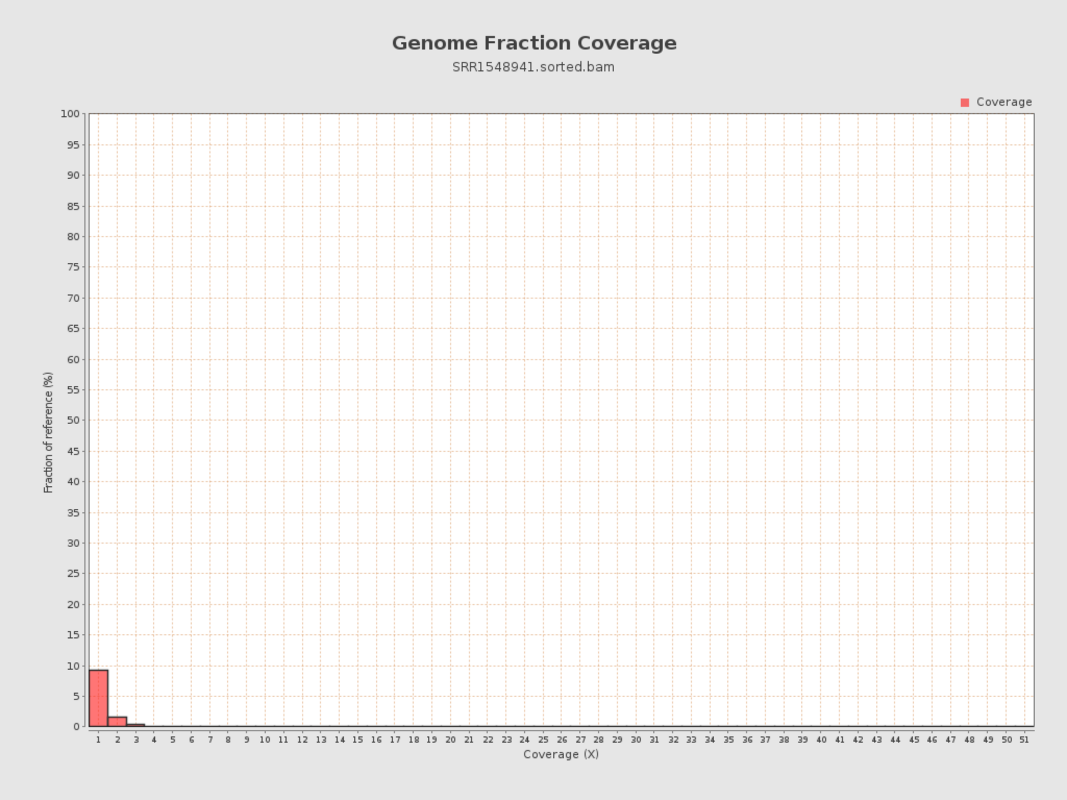
4. Results : Coverage Histogram



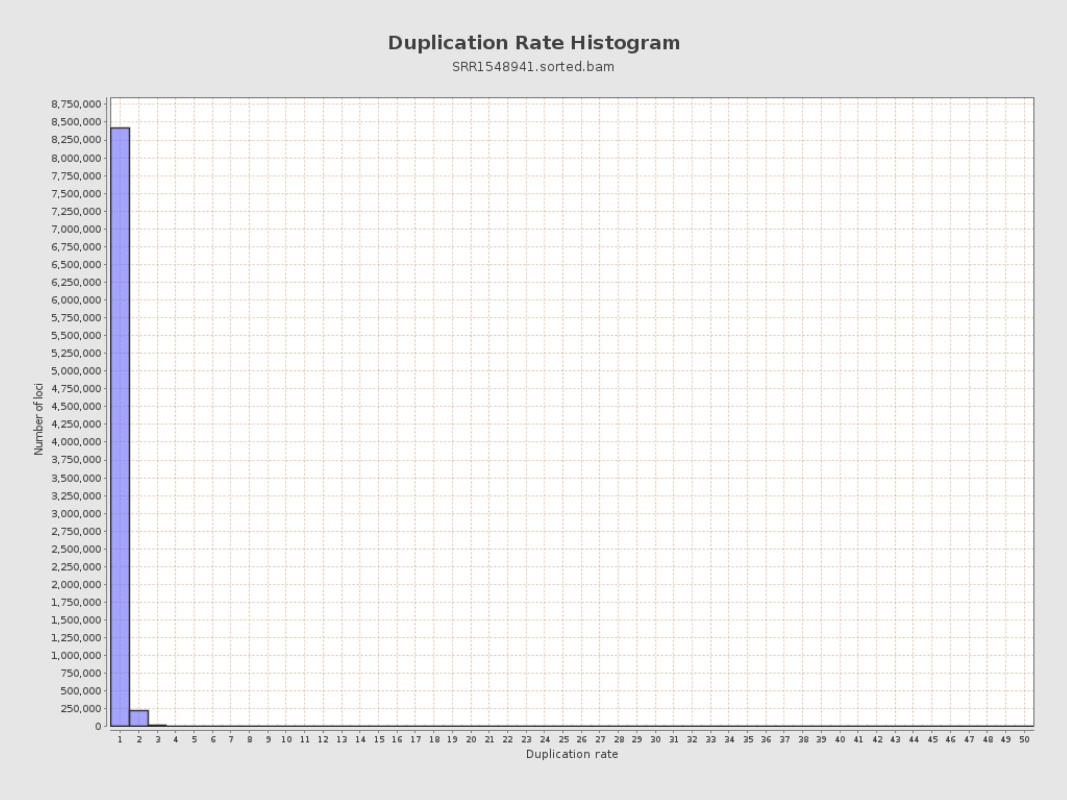
5. Results : Coverage Histogram (0-50X)



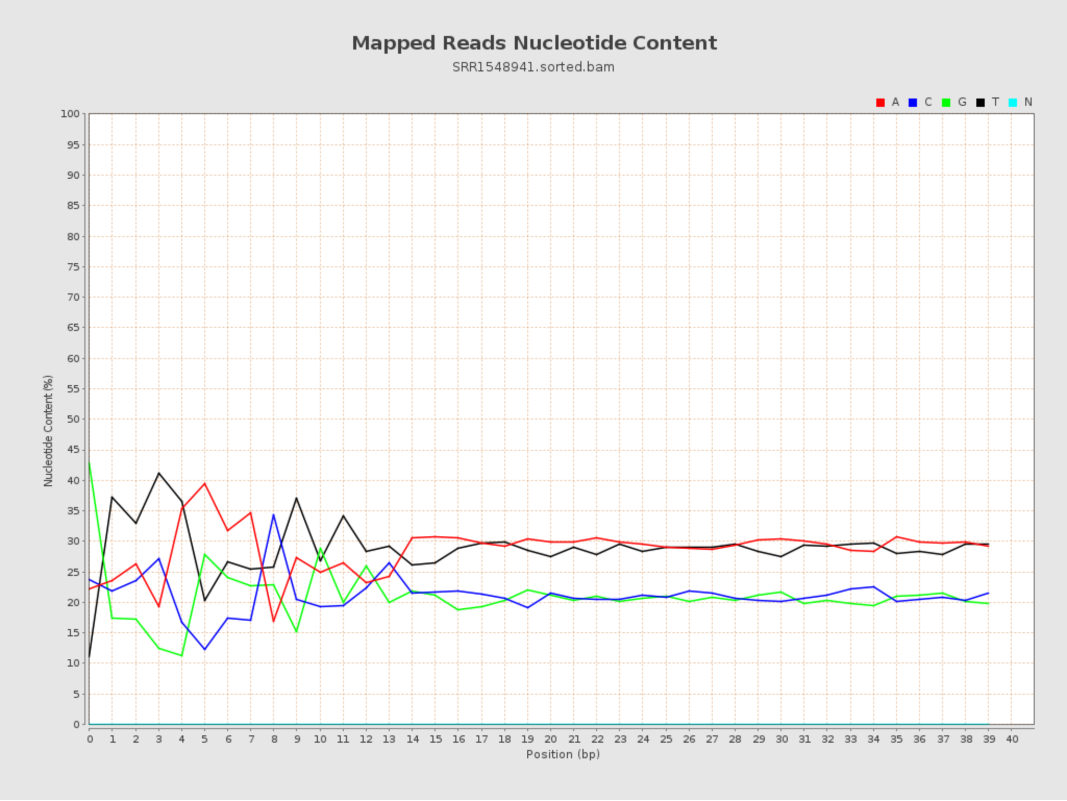
6. Results : Genome Fraction Coverage



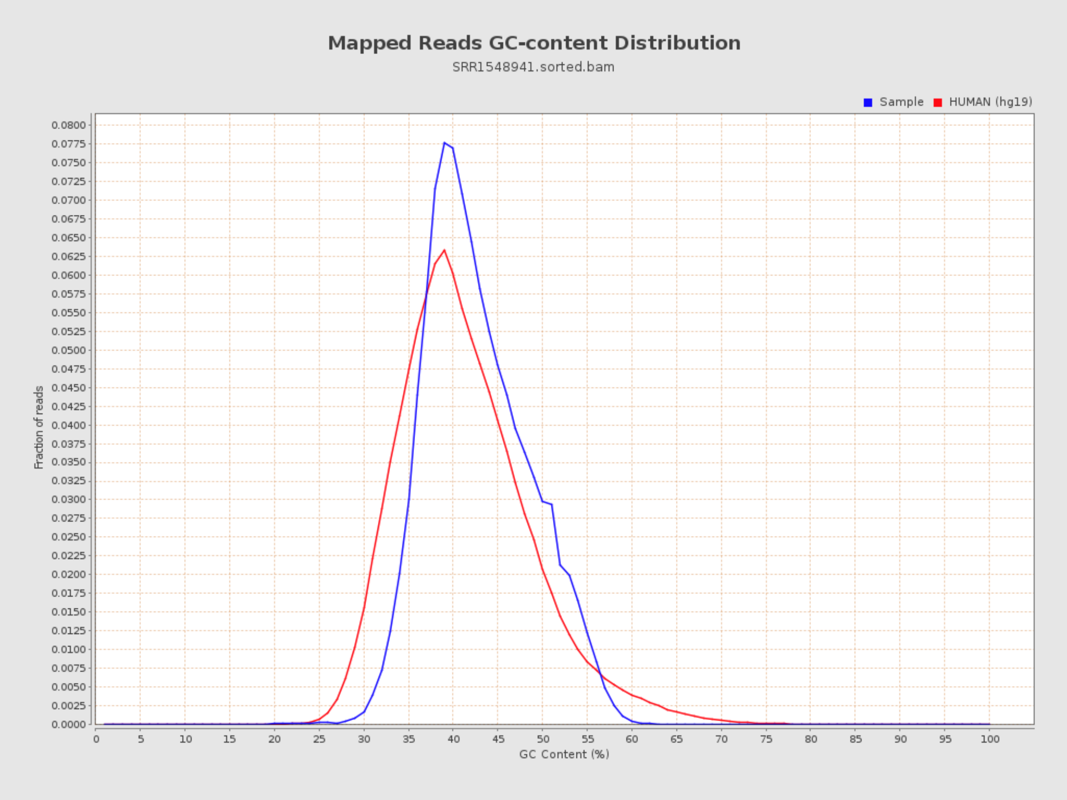
7. Results : Duplication Rate Histogram



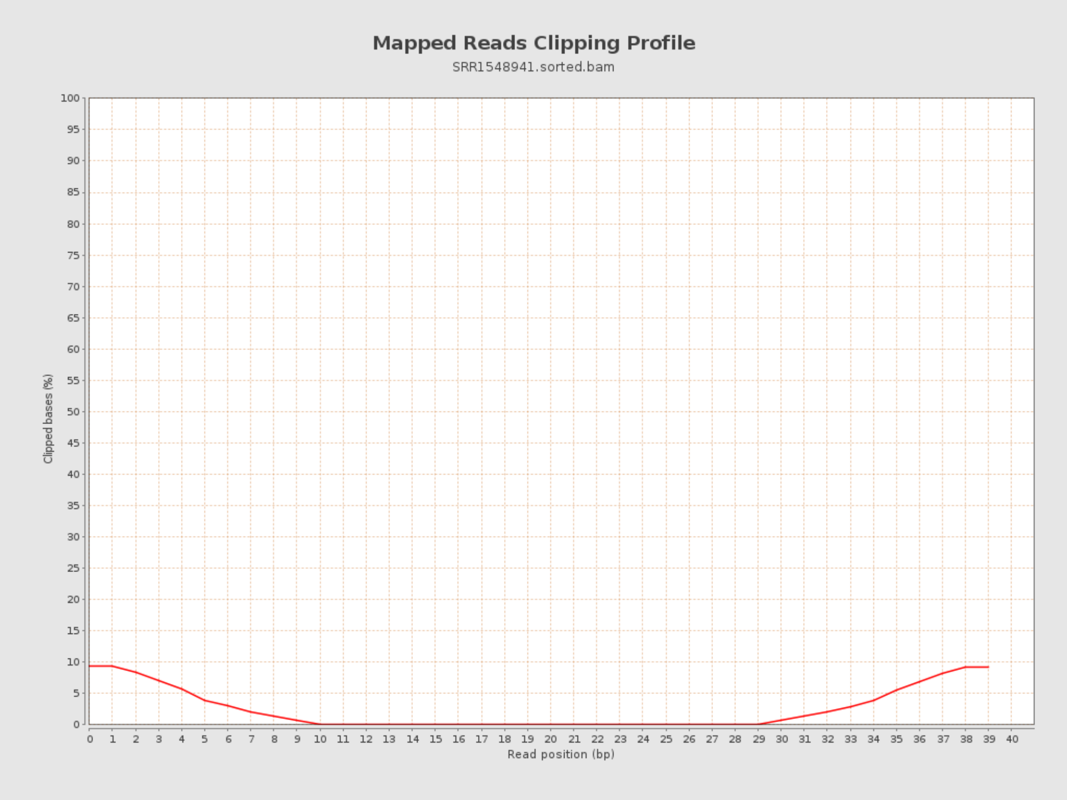
8. Results : Mapped Reads Nucleotide Content



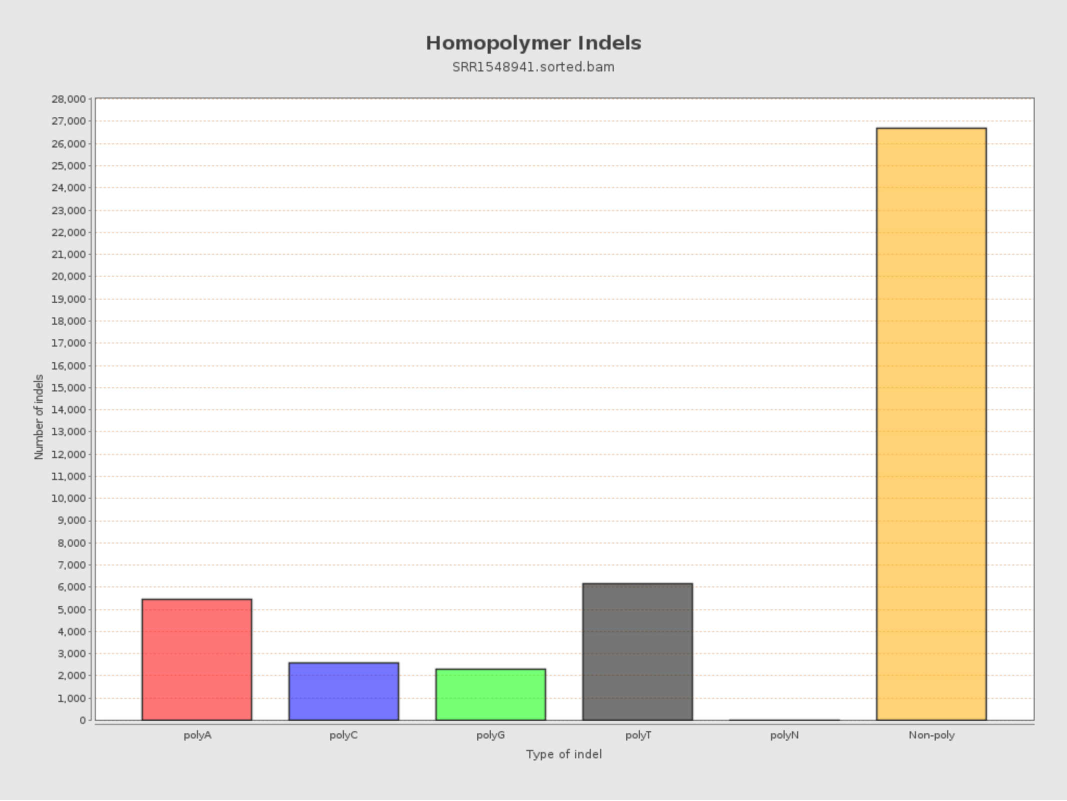
9. Results : Mapped Reads GC-content Distribution



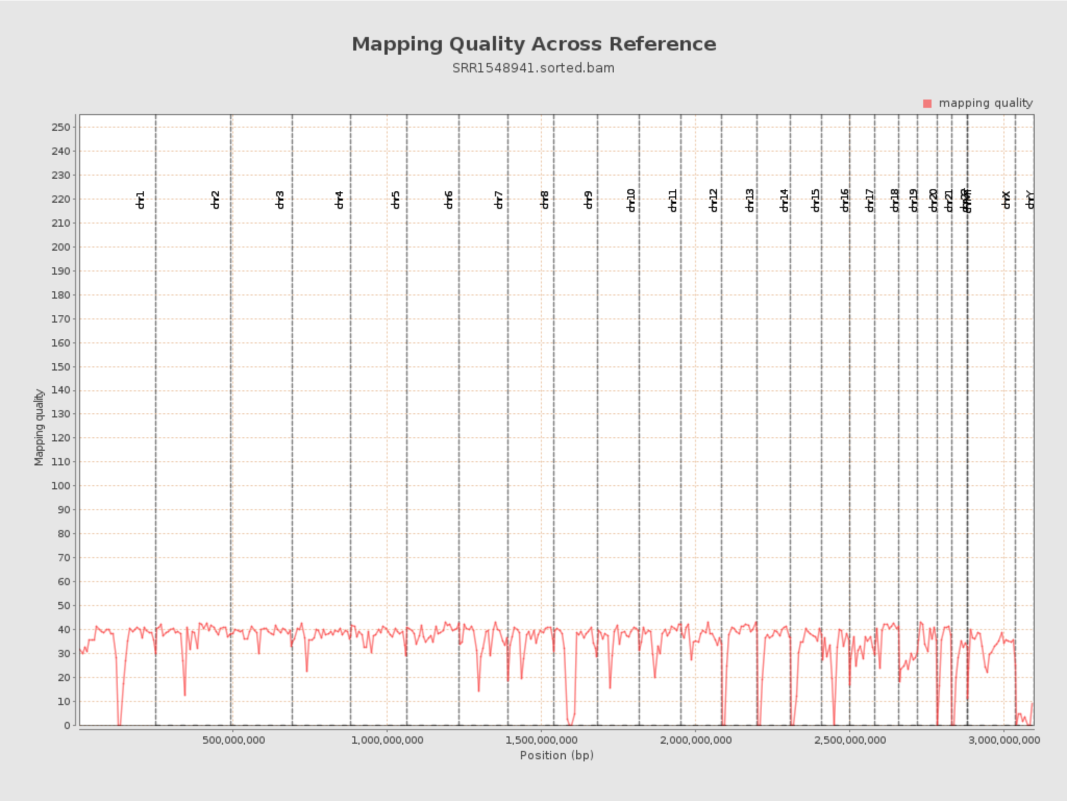
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram