Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:09:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549076.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_SRR1549076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:09:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,529,104
Mapped reads	9,231,374 / 87.67%
Unmapped reads	1,297,730 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	341,459 / 3.24%
Duplication rate	2.53%
Clipped reads	483,637 / 4.59%

2.2. ACGT Content

Number/percentage of A's	108,564,997 / 29.63%
Number/percentage of C's	74,299,065 / 20.28%
Number/percentage of T's	110,514,442 / 30.16%
Number/percentage of G's	72,926,926 / 19.9%
Number/percentage of N's	85,178 / 0.02%
GC Percentage	40.18%

2.3. Coverage

Mean	0.1184
Standard Deviation	0.8068

2.4. Mapping Quality

Mean Mapping Quality	43.54

2.5. Mismatches and indels

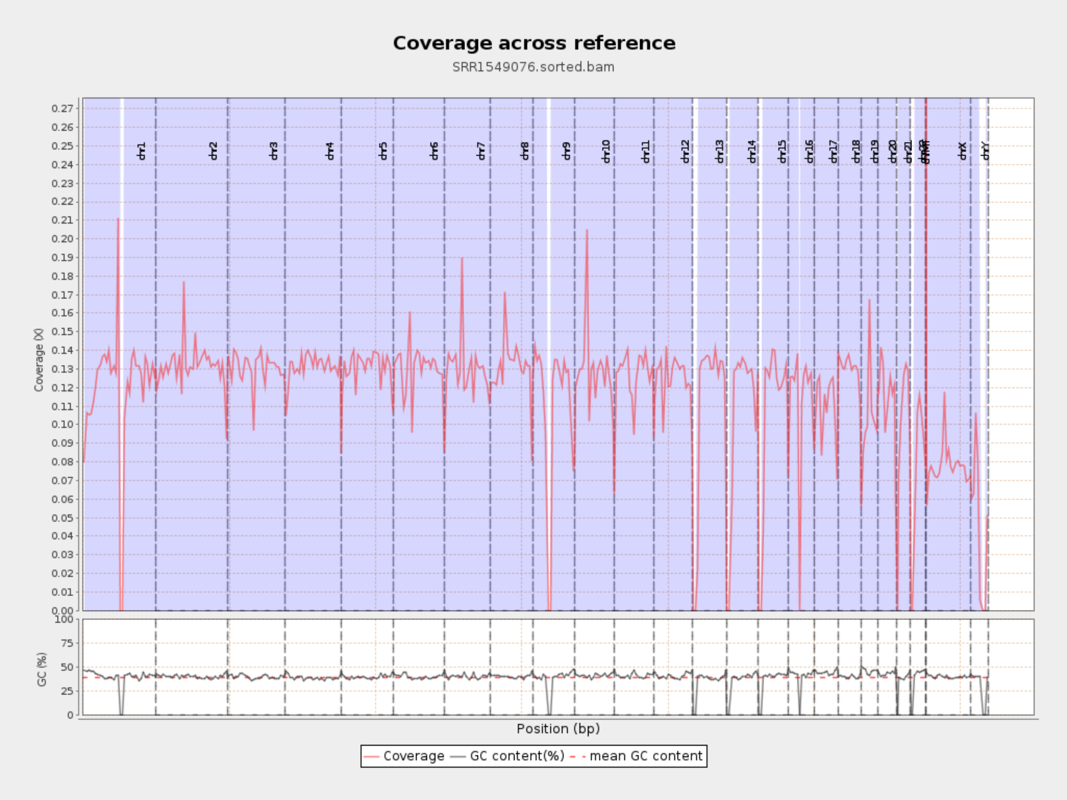
General error rate	0.4%
Mismatches	1,464,881
Insertions	9,167
Mapped reads with at least one insertion	0.1%
Deletions	29,806
Mapped reads with at least one deletion	0.32%
Homopolymer indels	45.89%

2.6. Chromosome stats

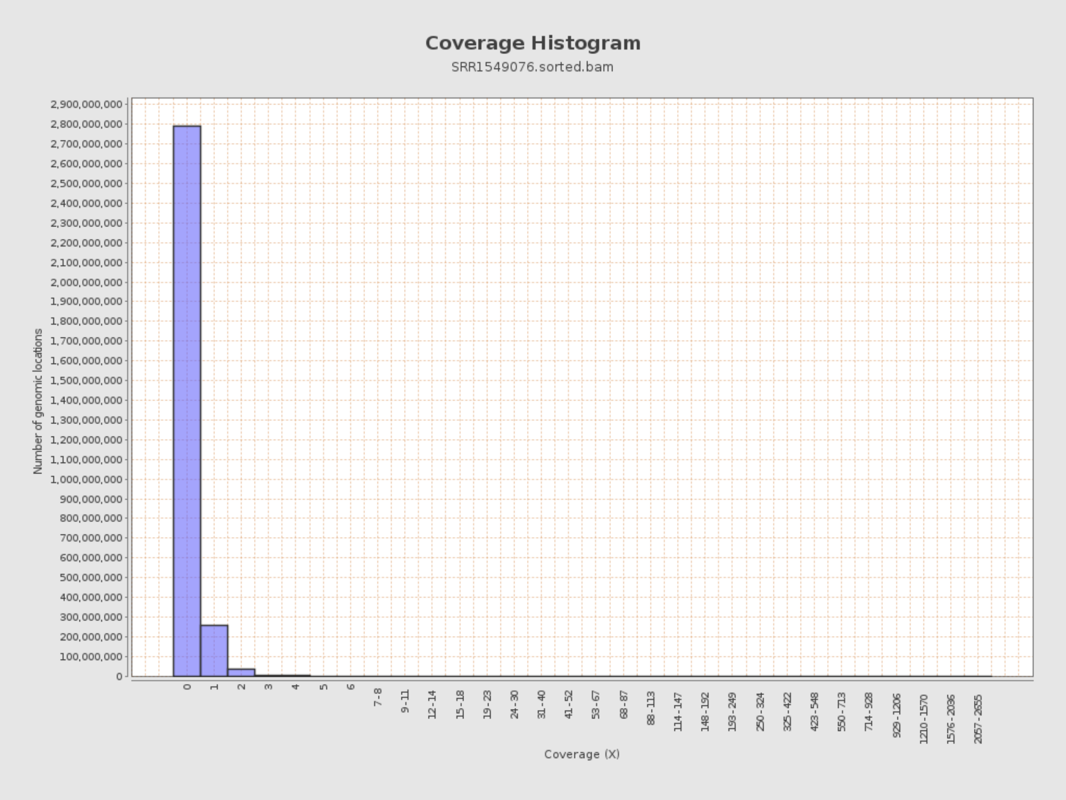
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29689839	0.1191	1.8489
chr2	243199373	32084814	0.1319	0.6795
chr3	198022430	25886044	0.1307	0.4243
chr4	191154276	25125098	0.1314	0.4265
chr5	180915260	23639784	0.1307	0.4284
chr6	171115067	22413399	0.131	0.5569
chr7	159138663	20630093	0.1296	0.9121
chr8	146364022	19165278	0.1309	0.5508

chr9	141213431	15523295	0.1099	0.6598
chr10	135534747	17583916	0.1297	0.9006
chr11	135006516	17108245	0.1267	0.6699
chr12	133851895	16790880	0.1254	0.4403
chr13	115169878	12663341	0.11	0.3743
chr14	107349540	11363651	0.1059	0.4845
chr15	102531392	10639165	0.1038	0.3691
chr16	90354753	9912748	0.1097	0.5137
chr17	81195210	8989477	0.1107	0.4633
chr18	78077248	10254834	0.1313	1.4618
chr19	59128983	6253680	0.1058	1.4829
chr20	63025520	7389710	0.1172	0.4176
chr21	48129895	4783867	0.0994	0.4469
chr22	51304566	3718499	0.0725	0.3613
chrMT	16571	9096	0.5489	1.131
chrX	155270560	12125275	0.0781	0.4466
chrY	59373566	2683988	0.0452	0.3279

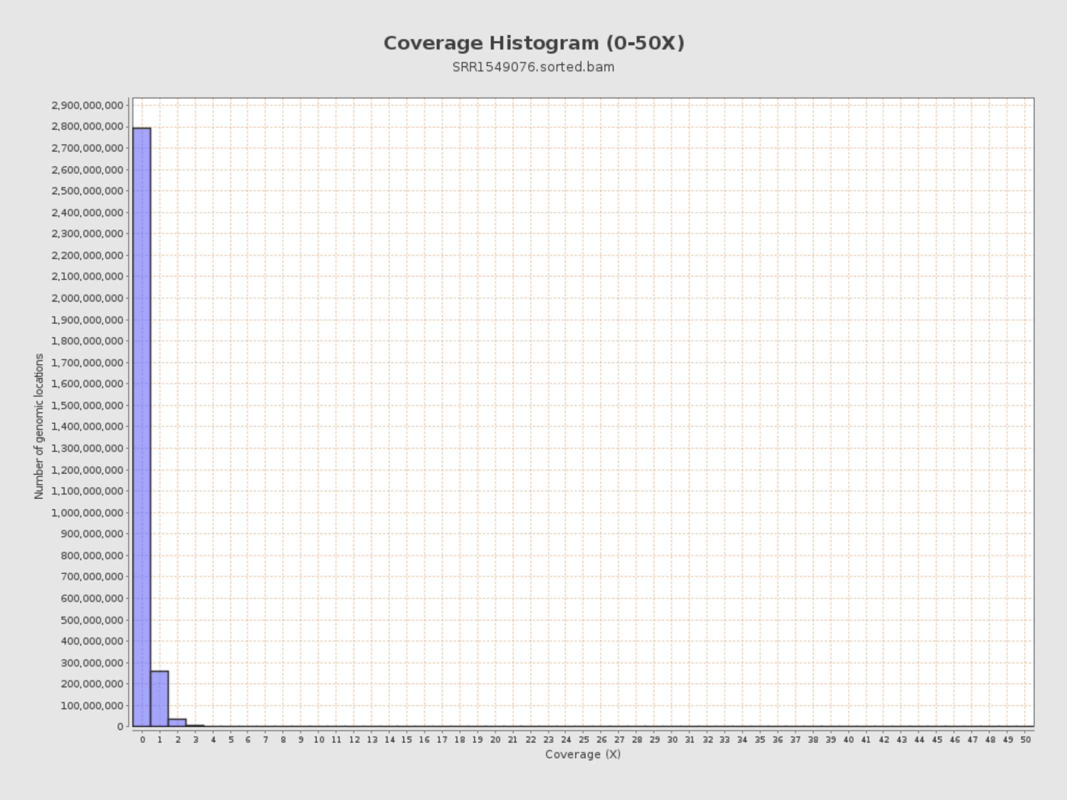
3. Results : Coverage across reference



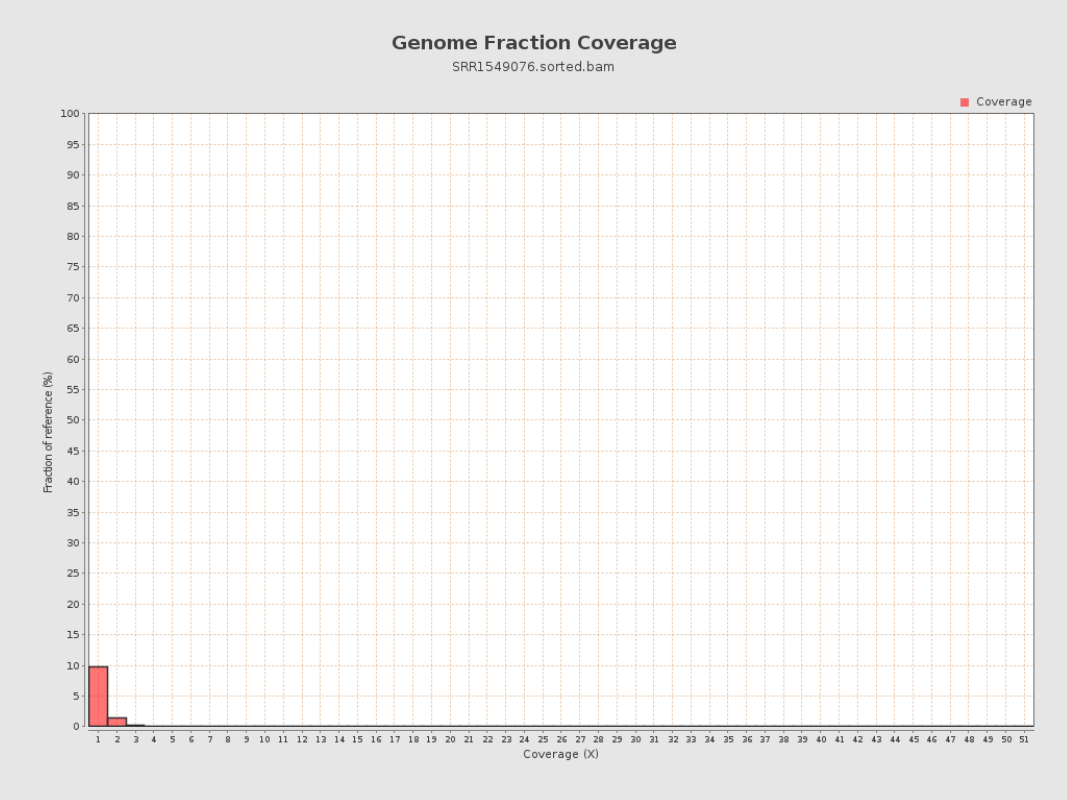
4. Results : Coverage Histogram



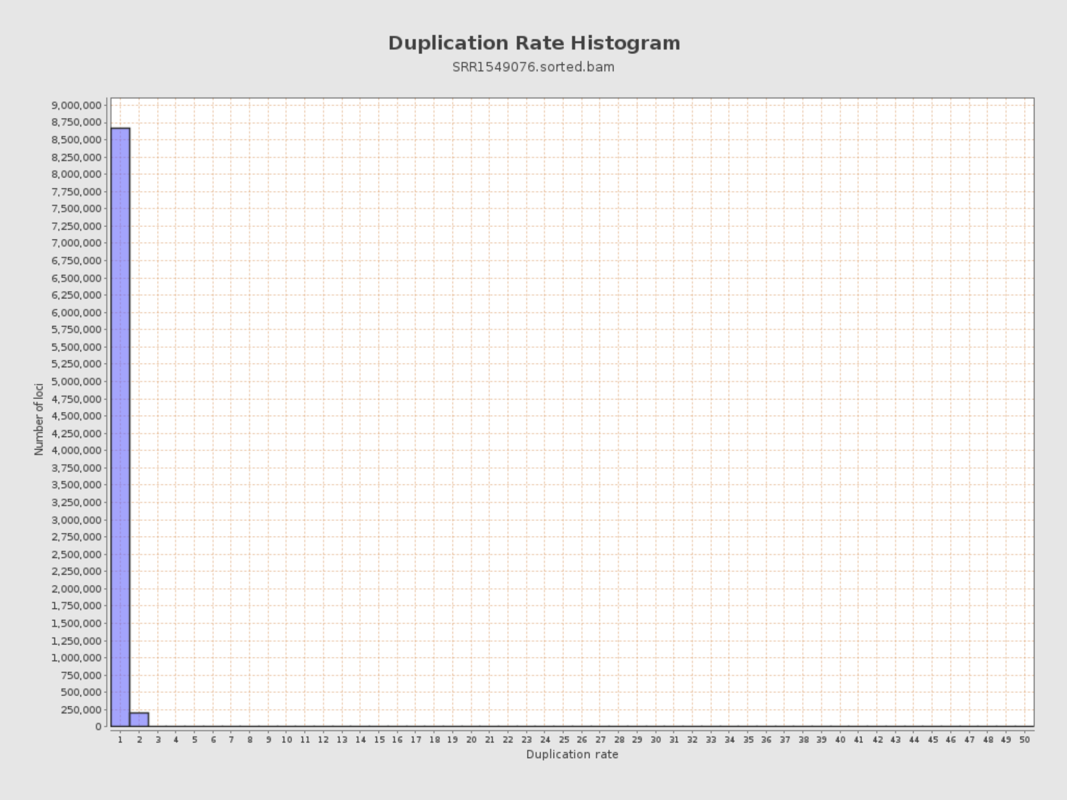
5. Results : Coverage Histogram (0-50X)



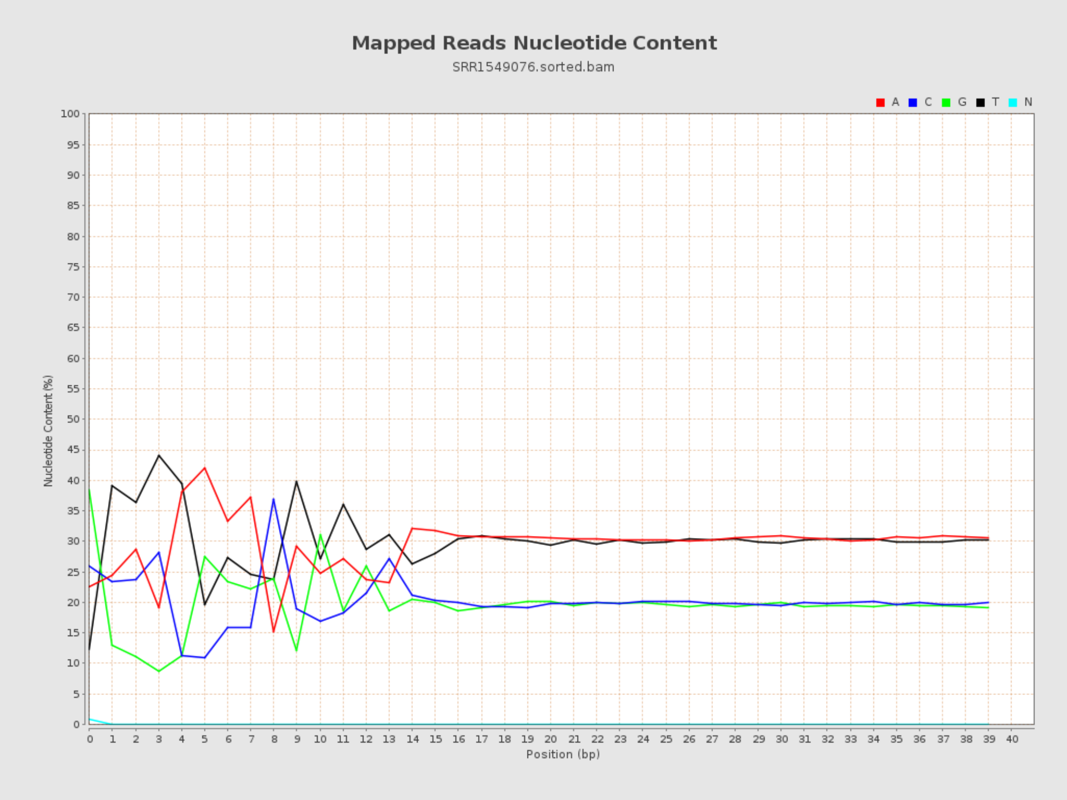
6. Results : Genome Fraction Coverage



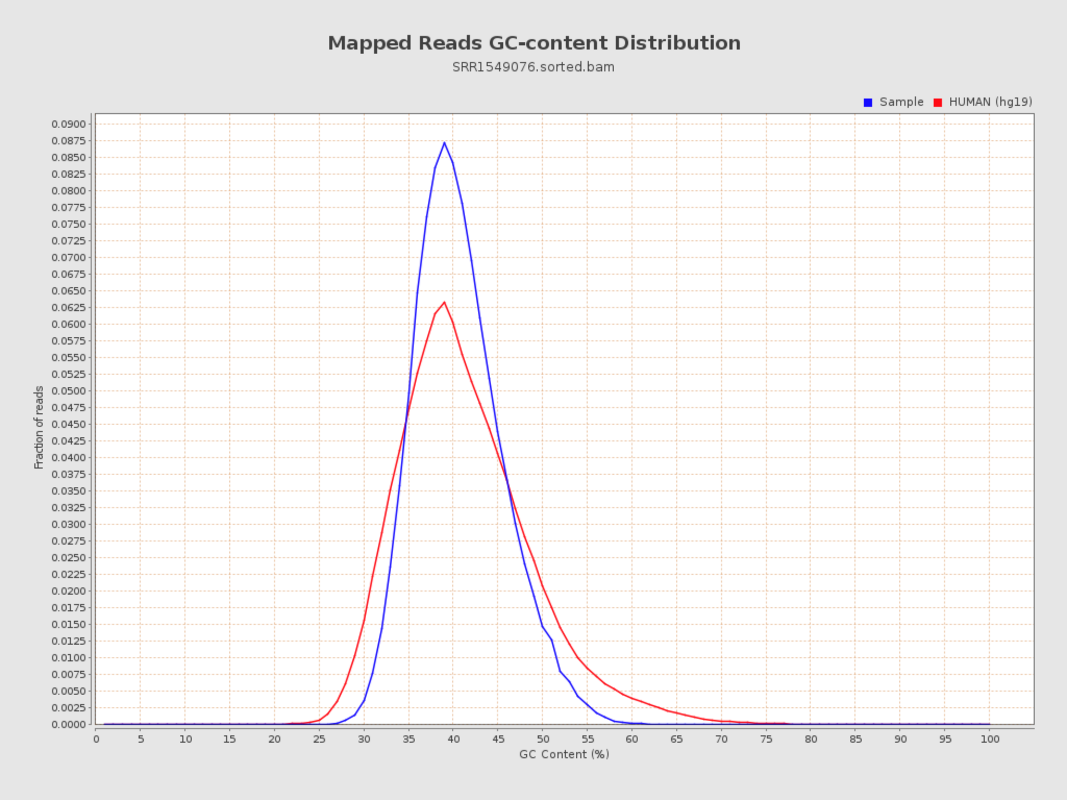
7. Results : Duplication Rate Histogram



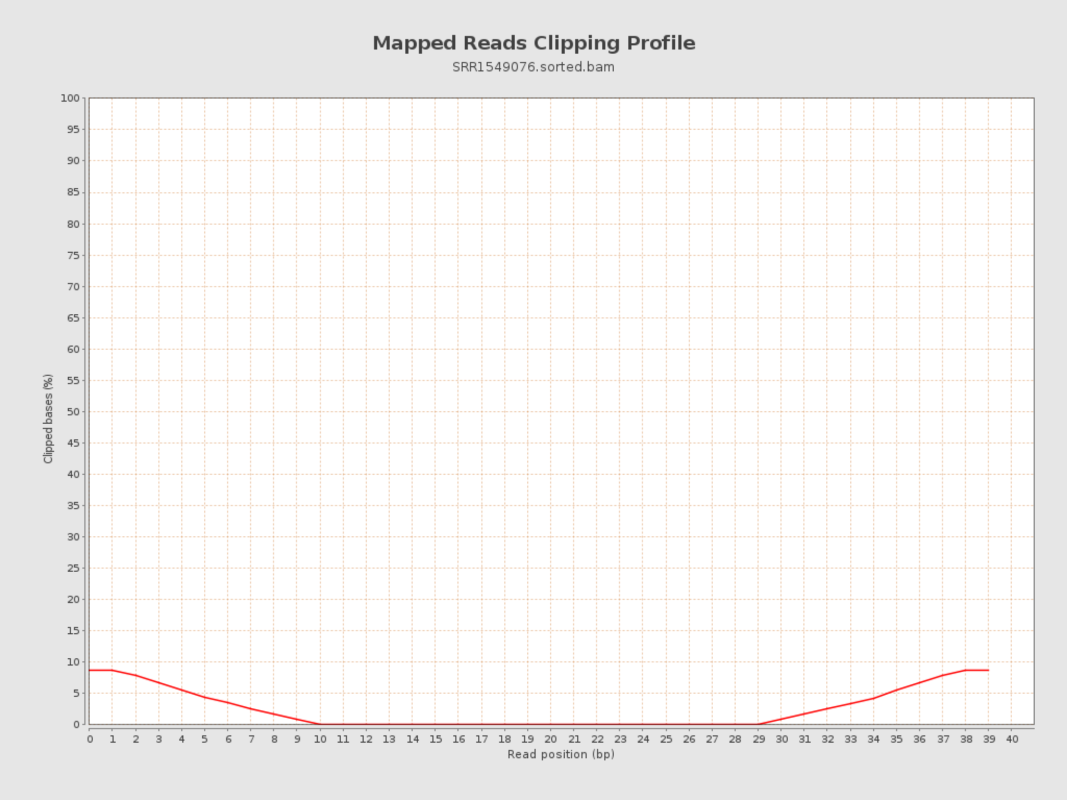
8. Results : Mapped Reads Nucleotide Content



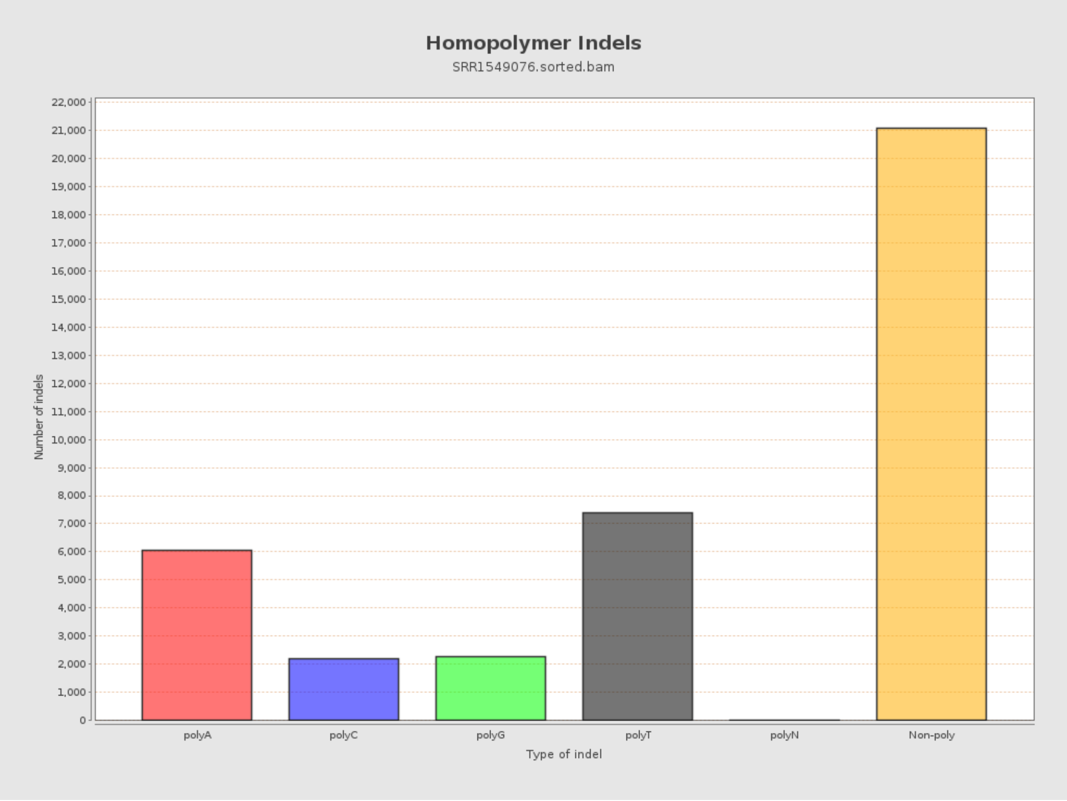
9. Results : Mapped Reads GC-content Distribution



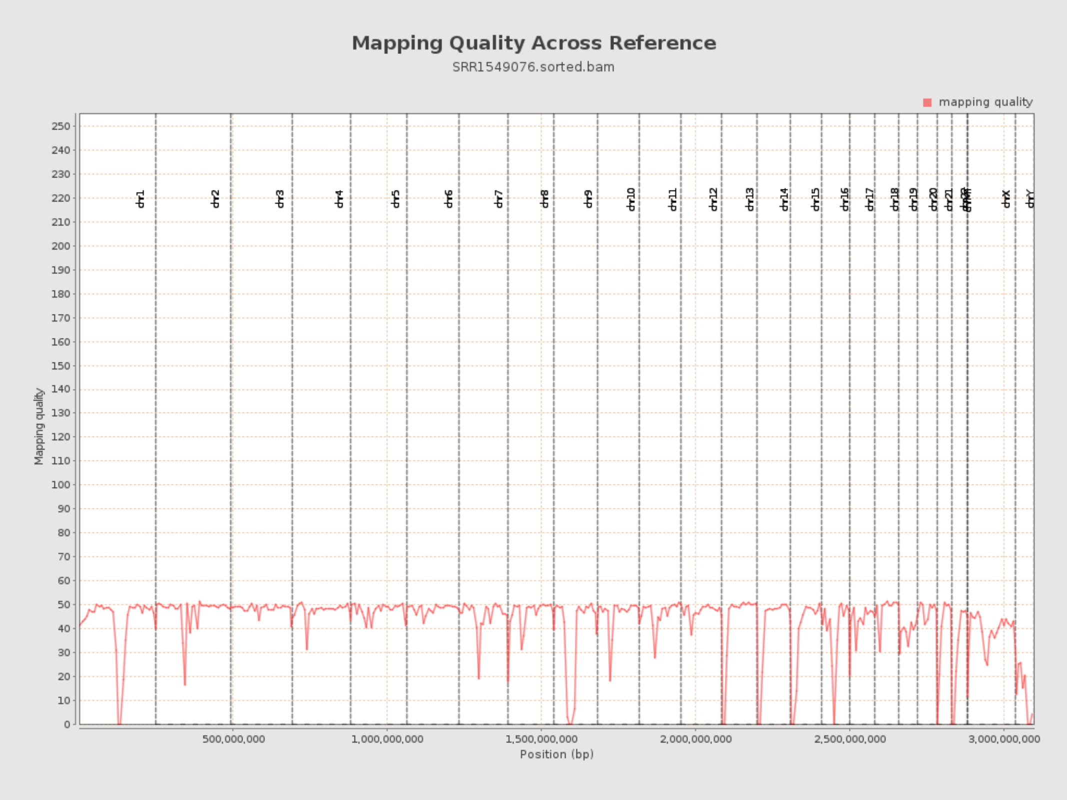
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram