Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:32:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234053.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_SRR6234053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:32:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,671,186
Mapped reads	1,433,693 / 85.79%
Unmapped reads	237,493 / 14.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,233 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	60,510 / 3.62%
Duplication rate	3.33%
Clipped reads	721,136 / 43.15%

2.2. ACGT Content

Number/percentage of A's	26,386,963 / 28.2%
Number/percentage of C's	17,217,728 / 18.4%
Number/percentage of T's	29,535,952 / 31.56%
Number/percentage of G's	20,422,835 / 21.82%
Number/percentage of N's	18,239 / 0.02%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.3246

2.4. Mapping Quality

Mean Mapping Quality	42.89

2.5. Mismatches and indels

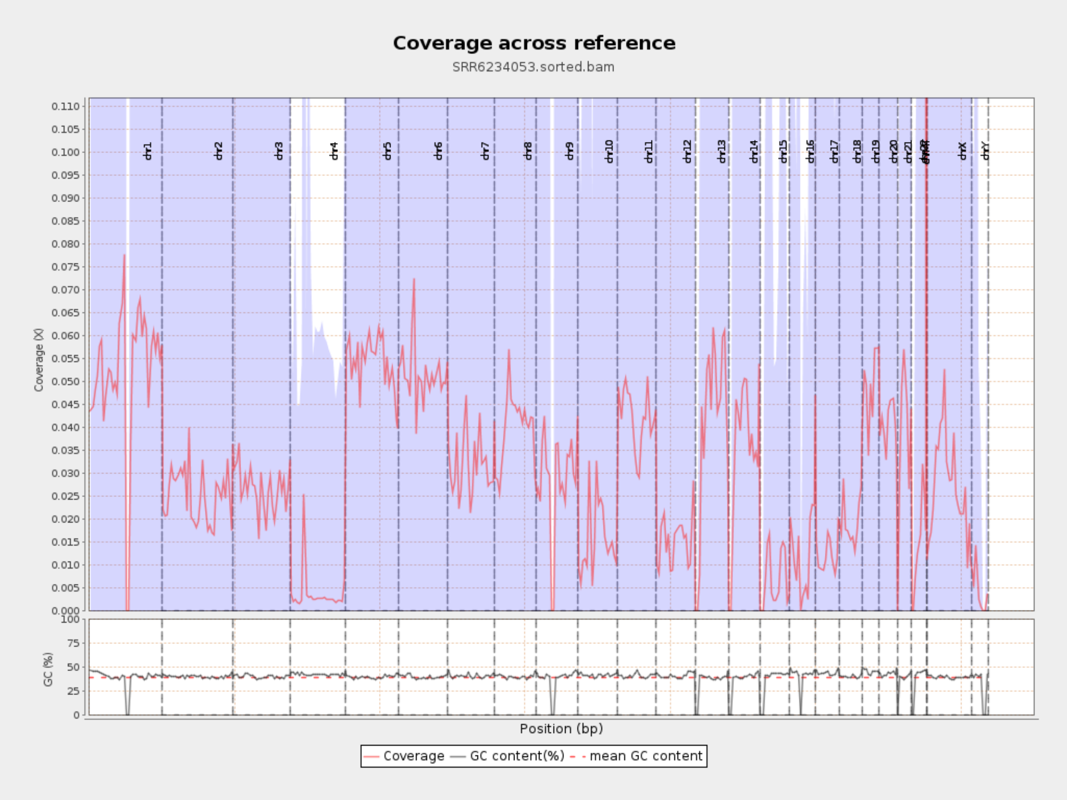
General error rate	0.79%
Mismatches	730,611
Insertions	6,958
Mapped reads with at least one insertion	0.48%
Deletions	29,107
Mapped reads with at least one deletion	2.01%
Homopolymer indels	45.04%

2.6. Chromosome stats

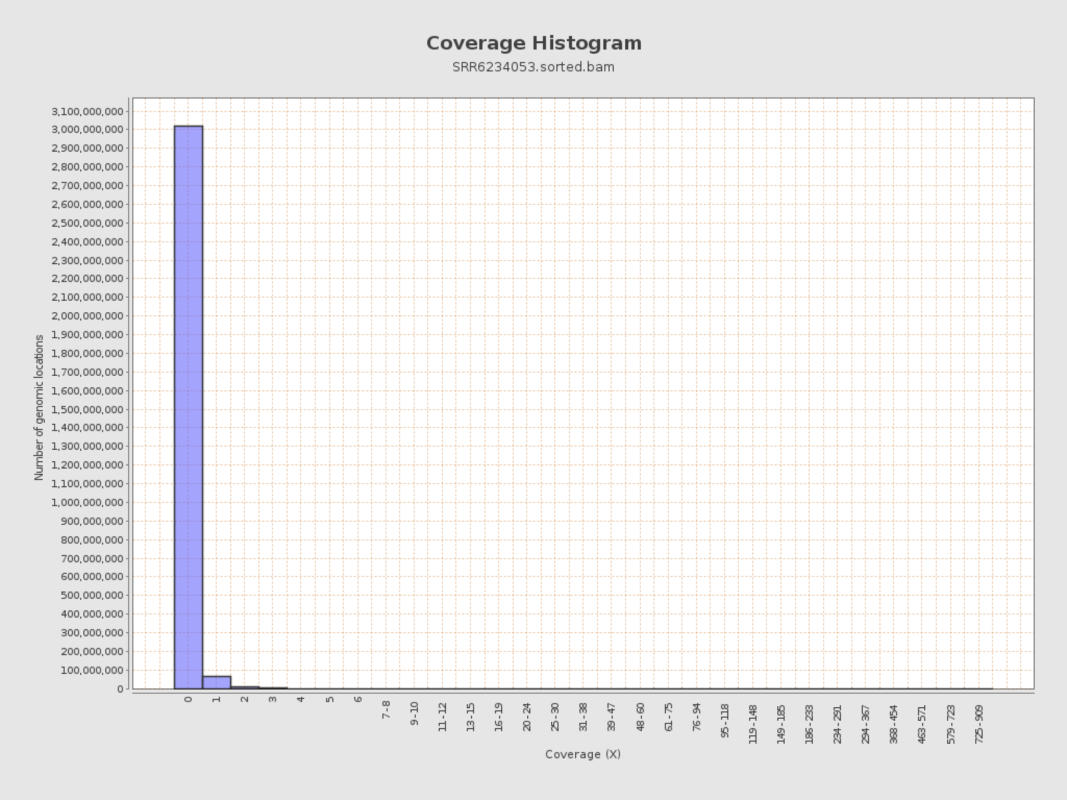
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12956324	0.052	0.7351
chr2	243199373	6124721	0.0252	0.2954
chr3	198022430	5235988	0.0264	0.1865
chr4	191154276	672960	0.0035	0.0975
chr5	180915260	9837455	0.0544	0.2699
chr6	171115067	8860883	0.0518	0.31
chr7	159138663	5019416	0.0315	0.3338

chr8	146364022	5839646	0.0399	0.3984
chr9	141213431	3961902	0.0281	0.2375
chr10	135534747	2144472	0.0158	0.1996
chr11	135006516	5633209	0.0417	0.3481
chr12	133851895	2034975	0.0152	0.1449
chr13	115169878	4768742	0.0414	0.2343
chr14	107349540	3684053	0.0343	0.2216
chr15	102531392	738727	0.0072	0.0985
chr16	90354753	1092512	0.0121	0.1474
chr17	81195210	984698	0.0121	0.1646
chr18	78077248	1480028	0.019	0.4283
chr19	59128983	2884140	0.0488	0.4396
chr20	63025520	2563023	0.0407	0.2391
chr21	48129895	1829704	0.038	0.2332
chr22	51304566	756901	0.0148	0.138
chrMT	16571	50530	3.0493	2.7215
chrX	155270560	4232973	0.0273	0.2142
chrY	59373566	244510	0.0041	0.1052

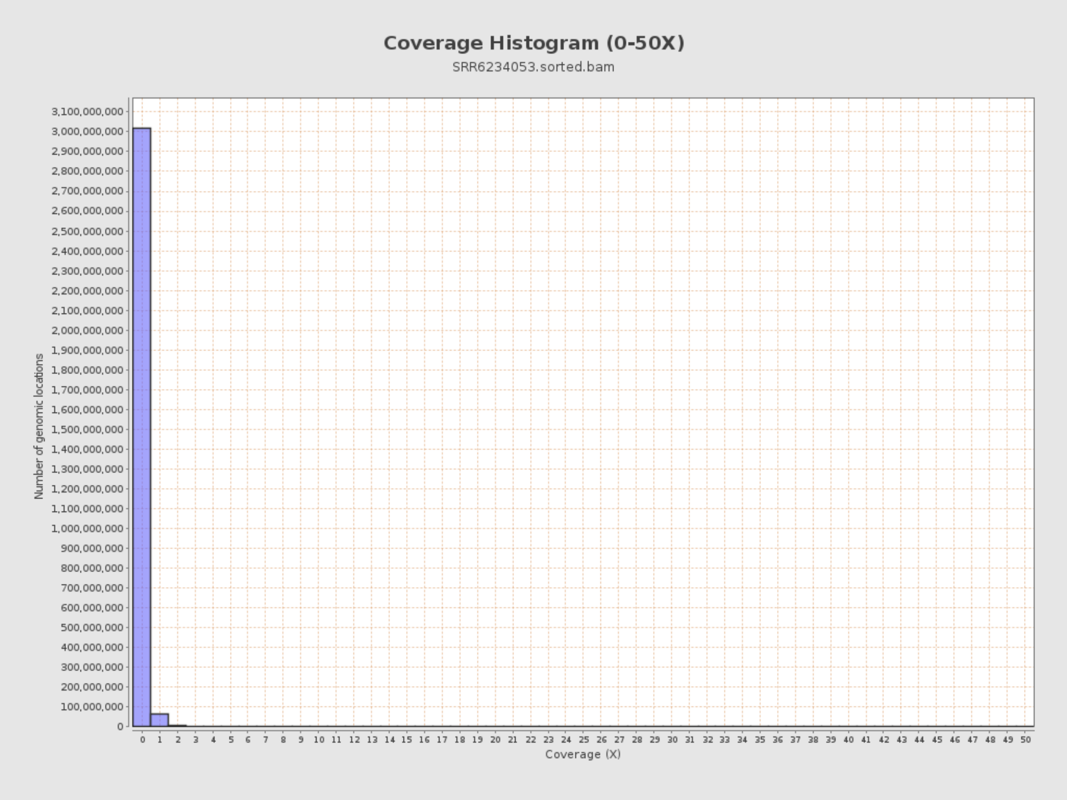
3. Results : Coverage across reference



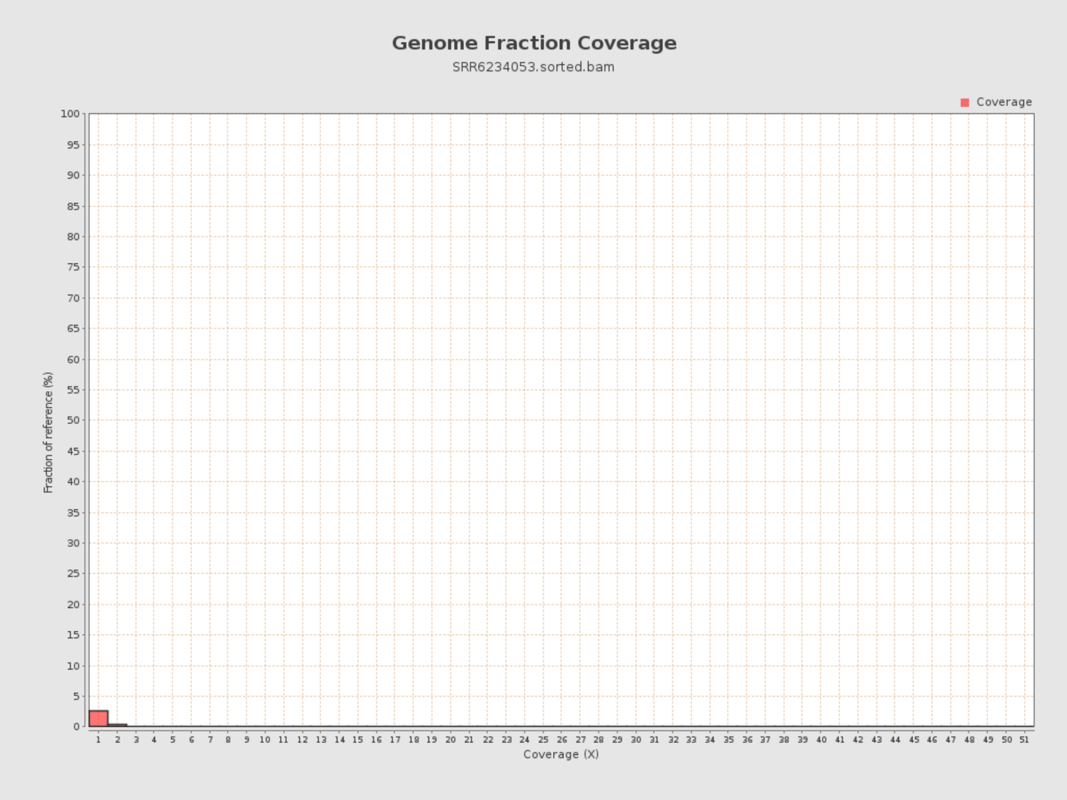
4. Results : Coverage Histogram



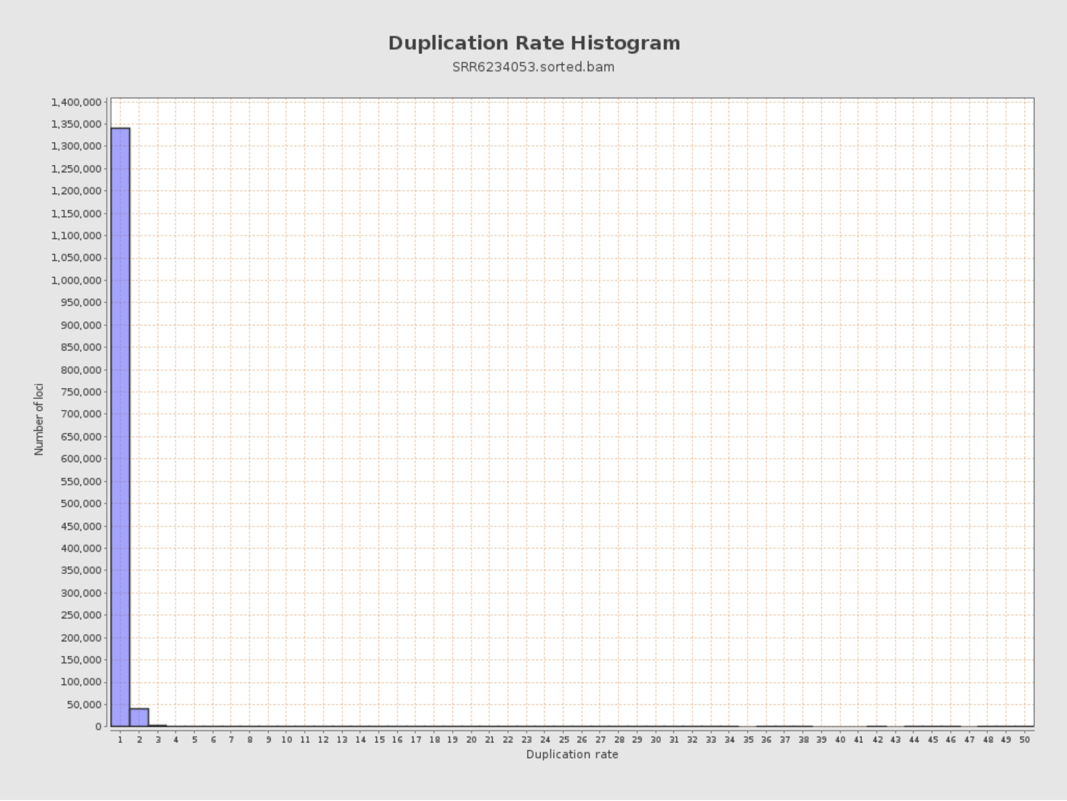
5. Results : Coverage Histogram (0-50X)



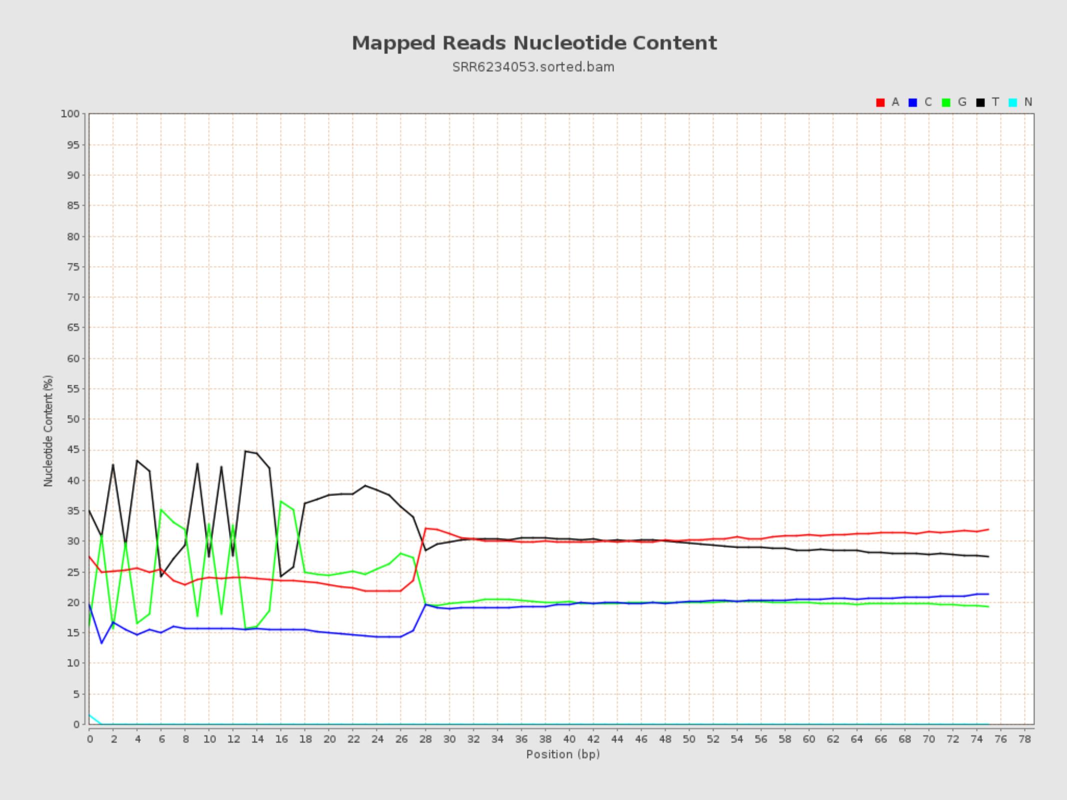
6. Results : Genome Fraction Coverage



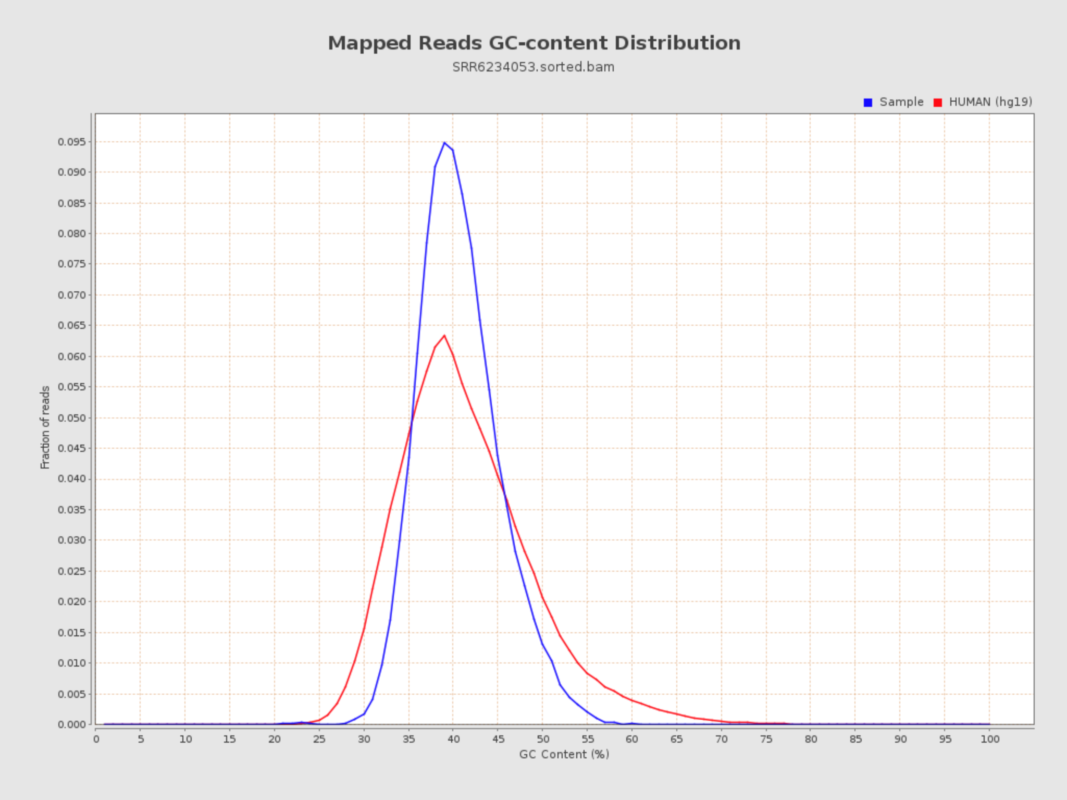
7. Results : Duplication Rate Histogram



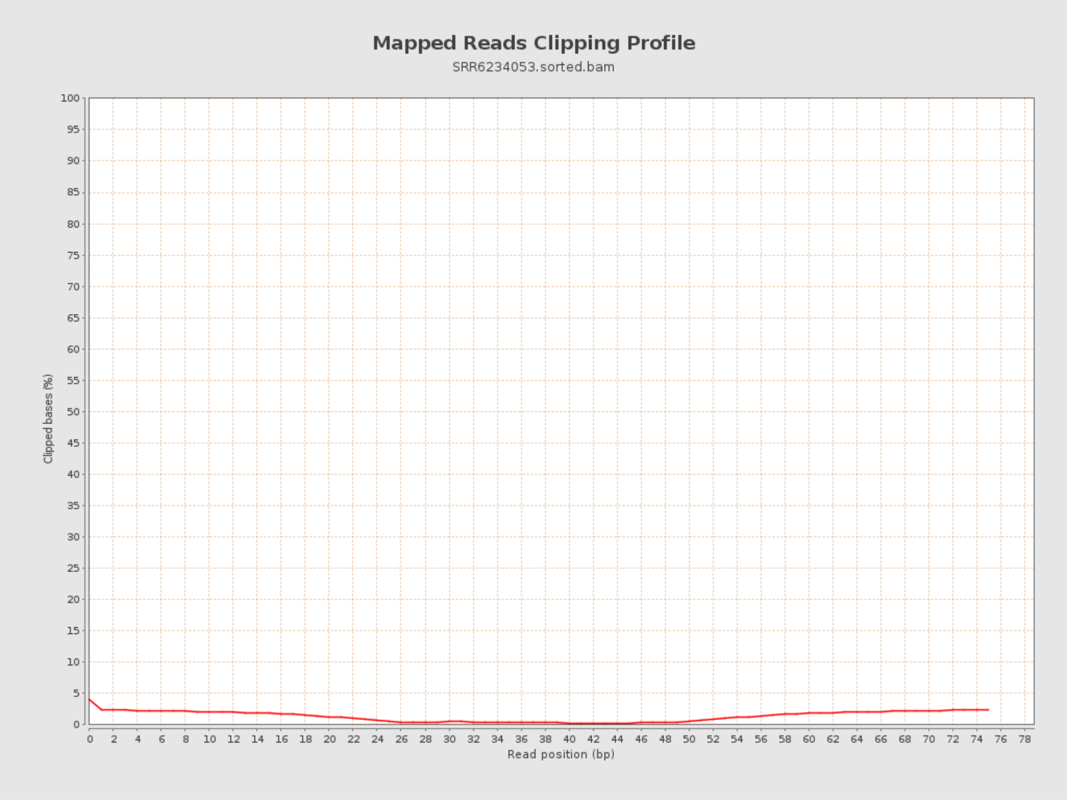
8. Results : Mapped Reads Nucleotide Content



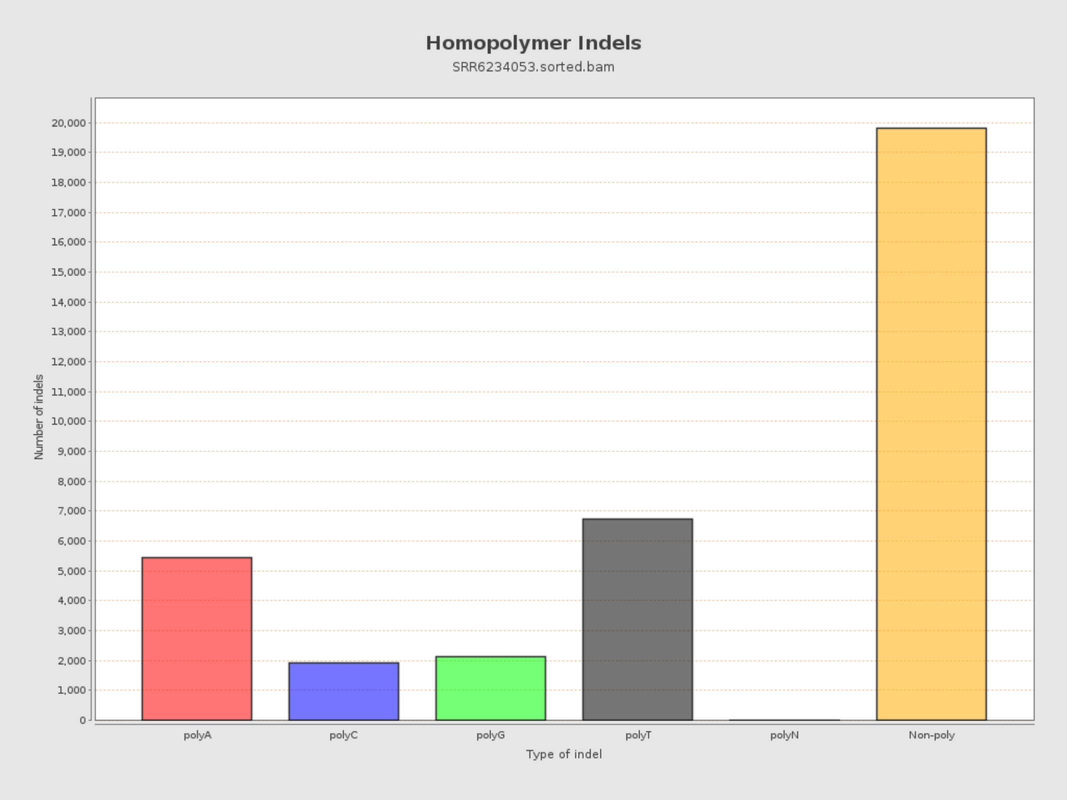
9. Results : Mapped Reads GC-content Distribution



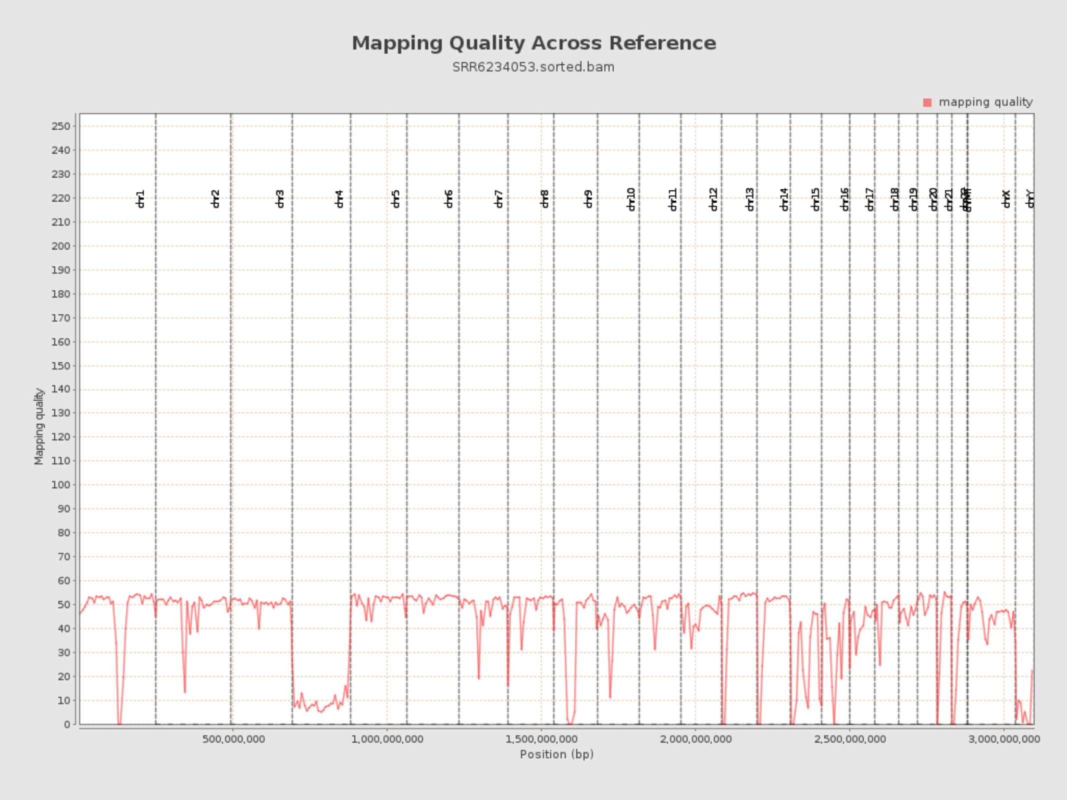
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram