Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:13:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234104.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_SRR6234104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:13:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,233,950
Mapped reads	4,942,295 / 94.43%
Unmapped reads	291,655 / 5.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,953 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	631,158 / 12.06%
Duplication rate	10.83%
Clipped reads	2,621,192 / 50.08%

2.2. ACGT Content

Number/percentage of A's	82,215,189 / 25.87%
Number/percentage of C's	57,463,043 / 18.08%
Number/percentage of T's	103,019,237 / 32.42%
Number/percentage of G's	75,061,914 / 23.62%
Number/percentage of N's	30,765 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.1027

Standard Deviation	1.0207

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

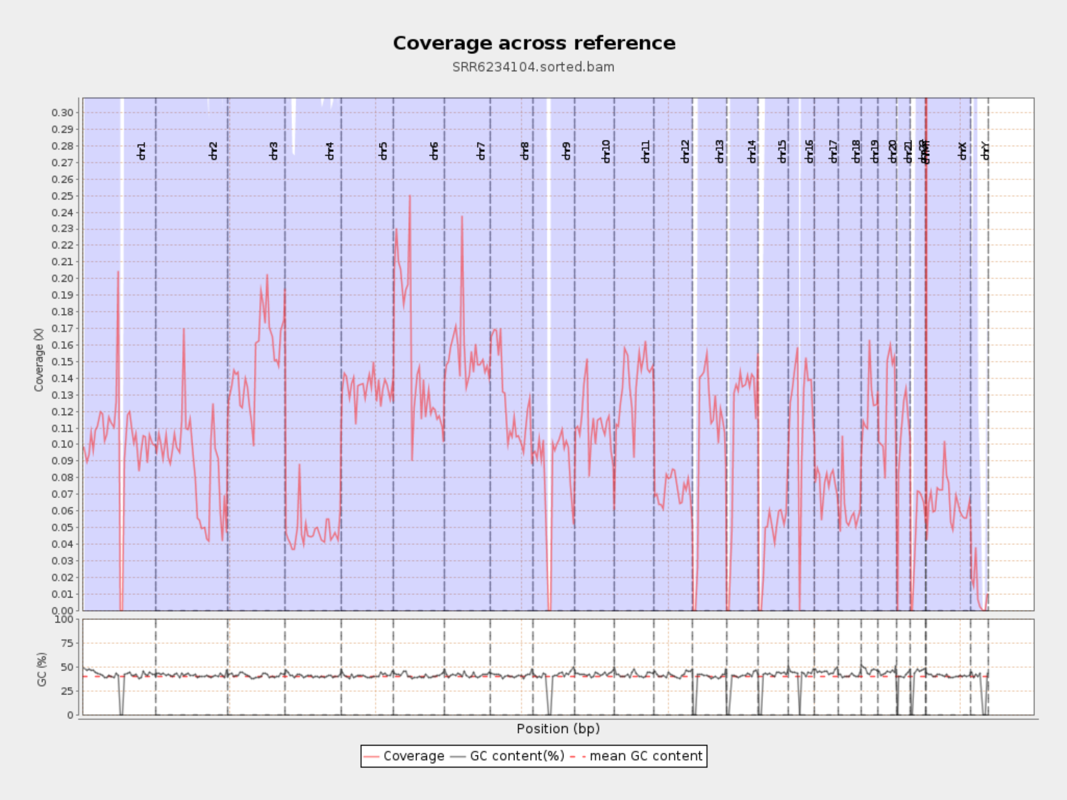
General error rate	0.54%
Mismatches	1,682,851
Insertions	19,932
Mapped reads with at least one insertion	0.4%
Deletions	68,540
Mapped reads with at least one deletion	1.37%
Homopolymer indels	44.06%

2.6. Chromosome stats

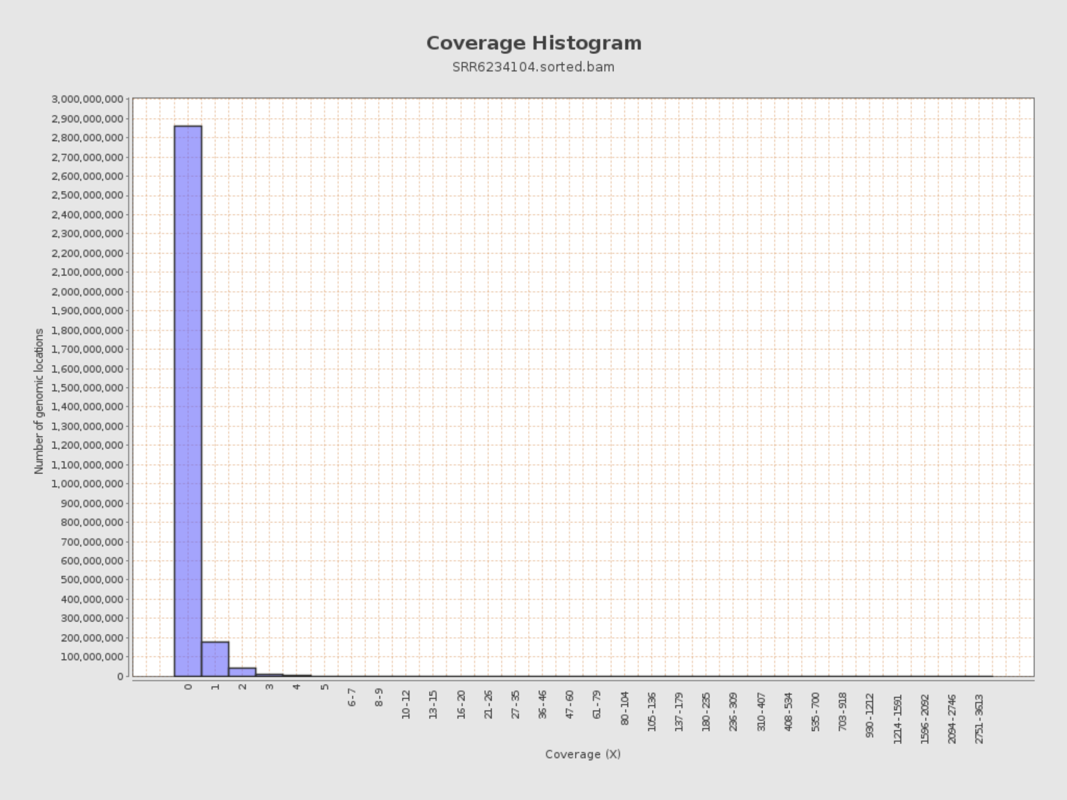
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25340556	0.1017	2.1082
chr2	243199373	21357691	0.0878	1.683
chr3	198022430	29705437	0.15	0.499
chr4	191154276	9101611	0.0476	0.3409
chr5	180915260	24297203	0.1343	0.4779
chr6	171115067	26062657	0.1523	0.871
chr7	159138663	24650578	0.1549	1.4647

chr8	146364022	18315081	0.1251	0.9787
chr9	141213431	11647194	0.0825	0.6021
chr10	135534747	15092438	0.1114	0.7674
chr11	135006516	18275143	0.1354	0.8663
chr12	133851895	9733271	0.0727	0.3689
chr13	115169878	12098798	0.1051	0.4602
chr14	107349540	12060528	0.1123	0.4746
chr15	102531392	4500637	0.0439	0.3209
chr16	90354753	10778228	0.1193	0.5463
chr17	81195210	6276729	0.0773	0.4619
chr18	78077248	4733986	0.0606	1.478
chr19	59128983	7335817	0.1241	1.2292
chr20	63025520	7824637	0.1242	0.511
chr21	48129895	4872931	0.1012	0.4331
chr22	51304566	2455605	0.0479	0.2718
chrMT	16571	549840	33.1809	18.1524
chrX	155270560	10189181	0.0656	0.4424
chrY	59373566	654721	0.011	0.2411

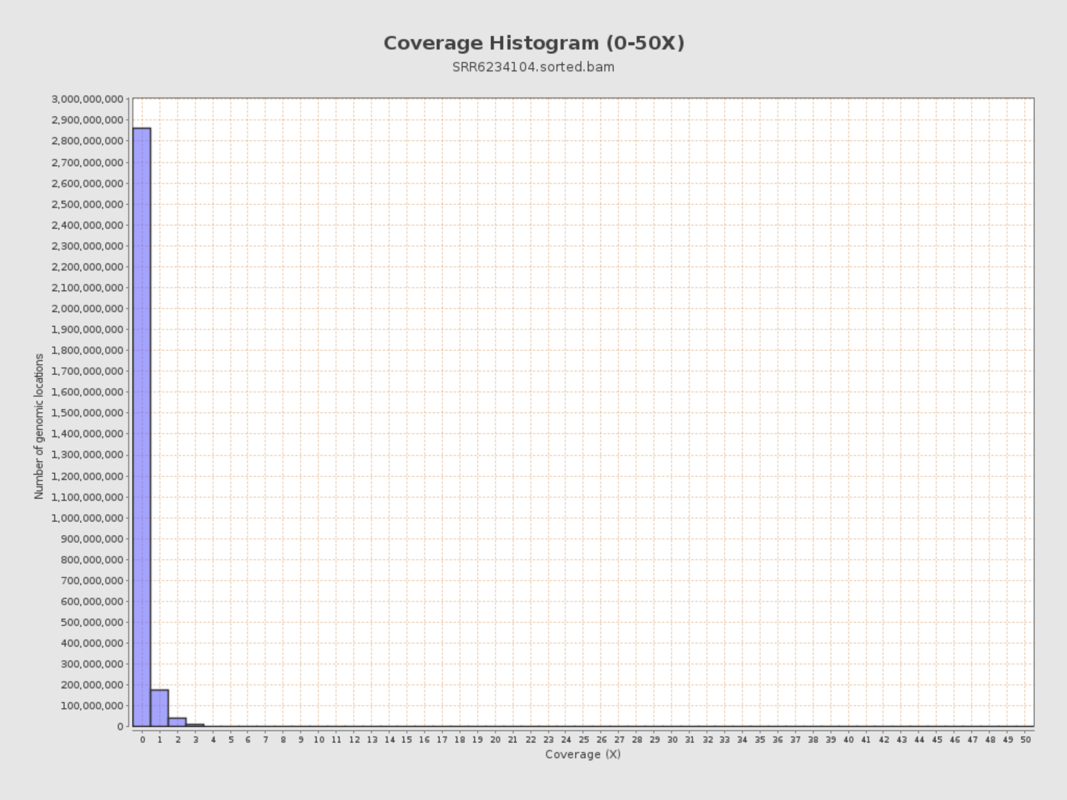
3. Results : Coverage across reference



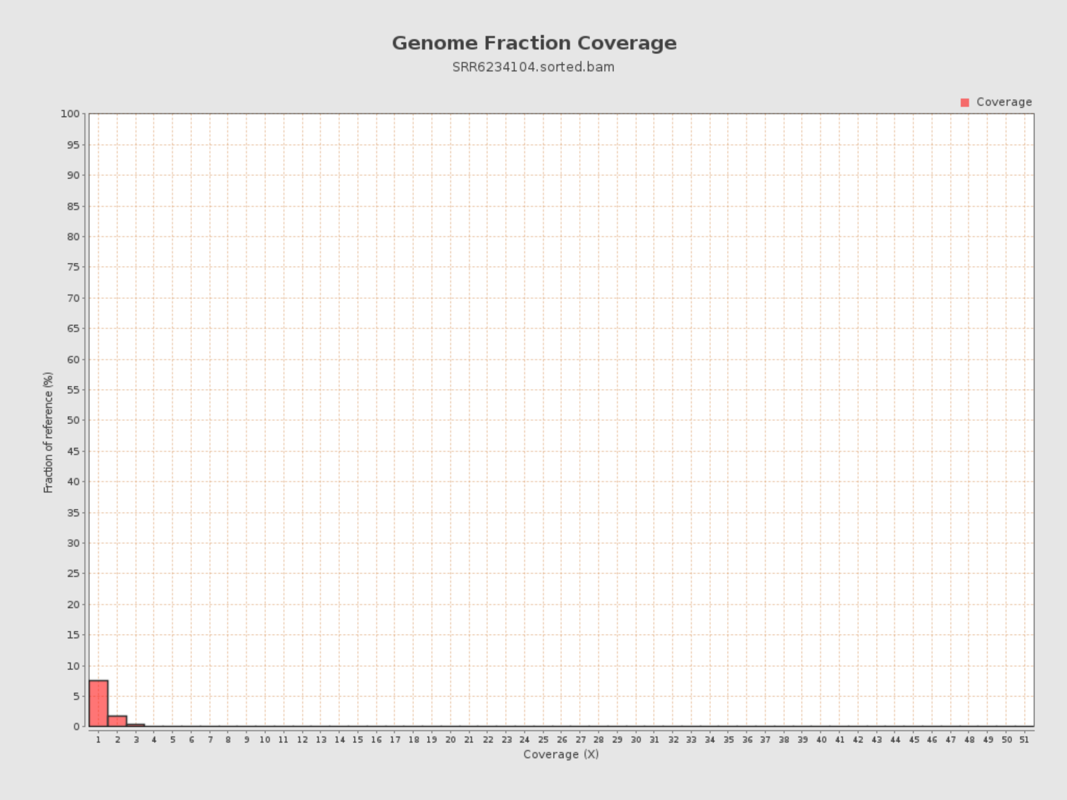
4. Results : Coverage Histogram



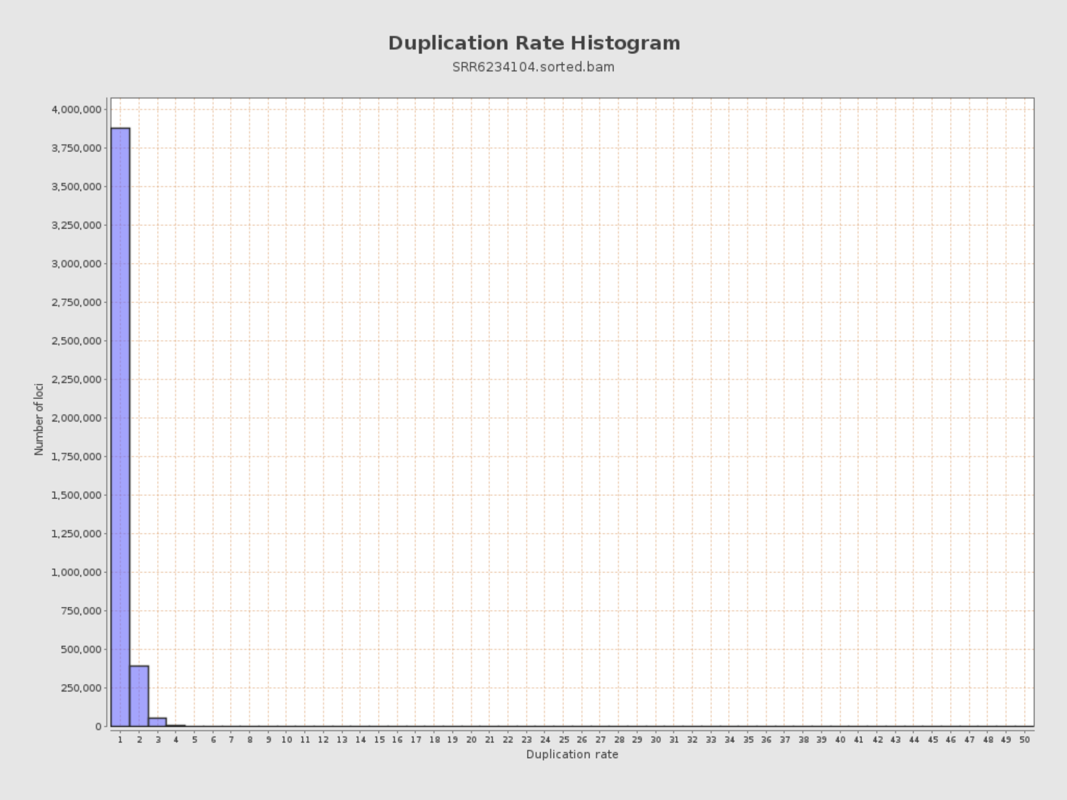
5. Results : Coverage Histogram (0-50X)



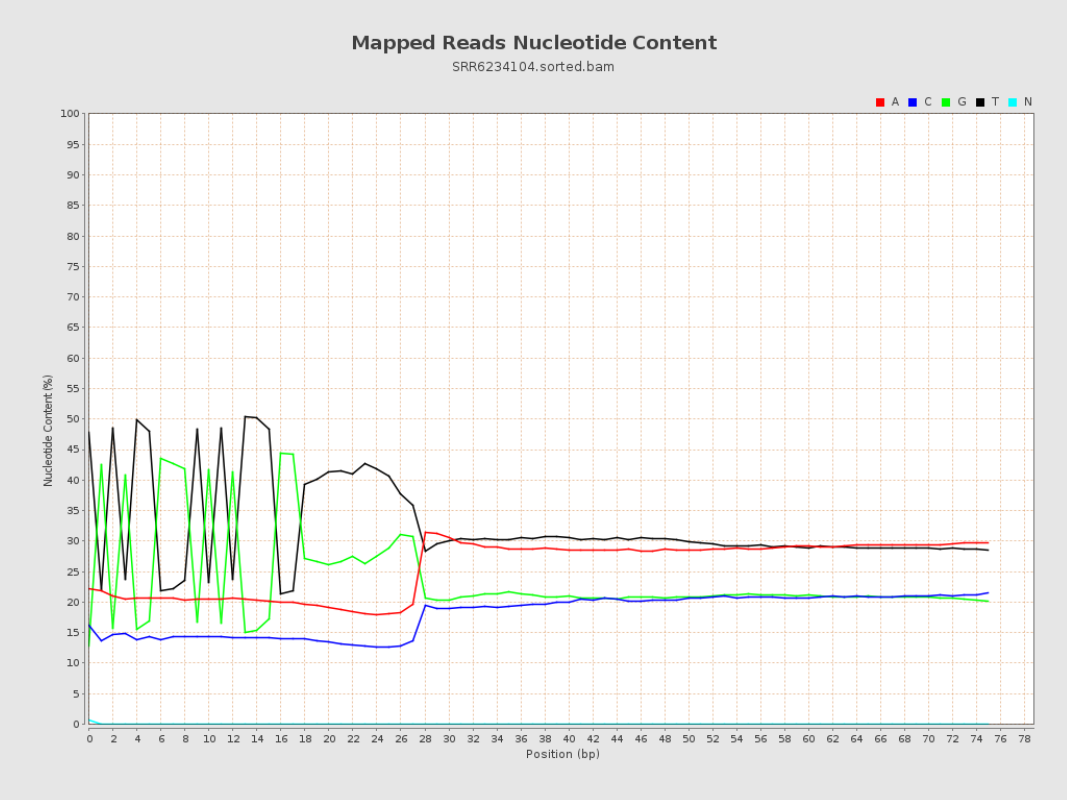
6. Results : Genome Fraction Coverage



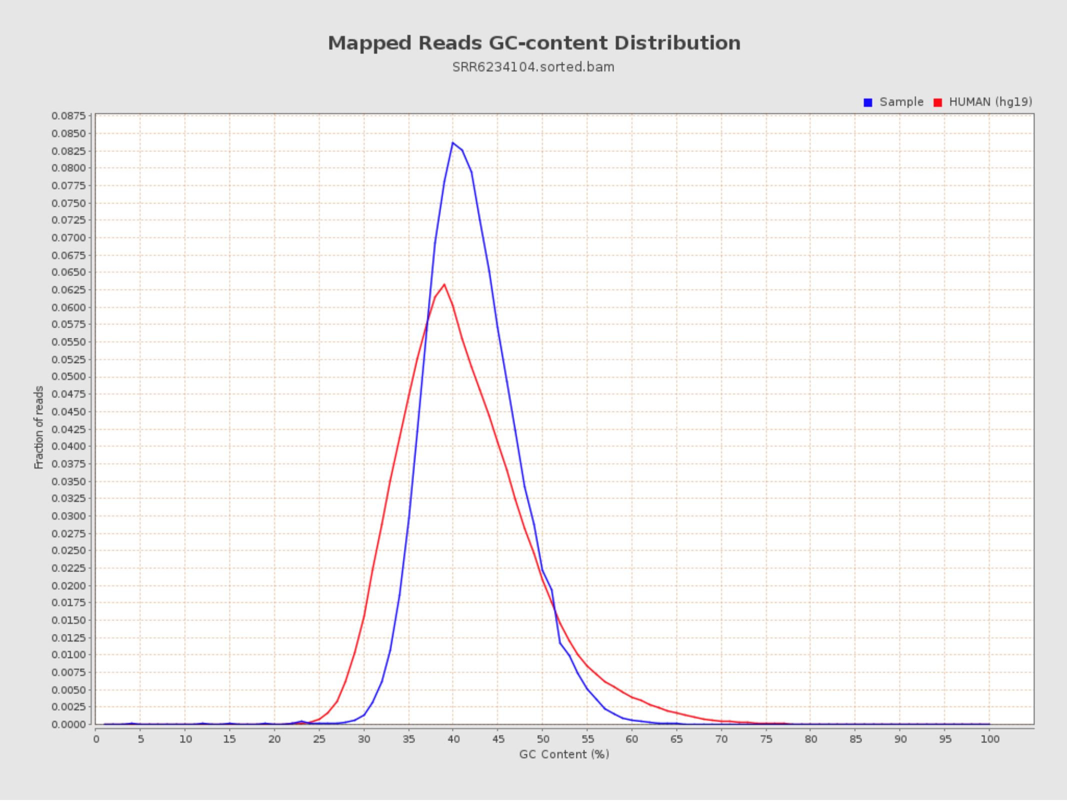
7. Results : Duplication Rate Histogram



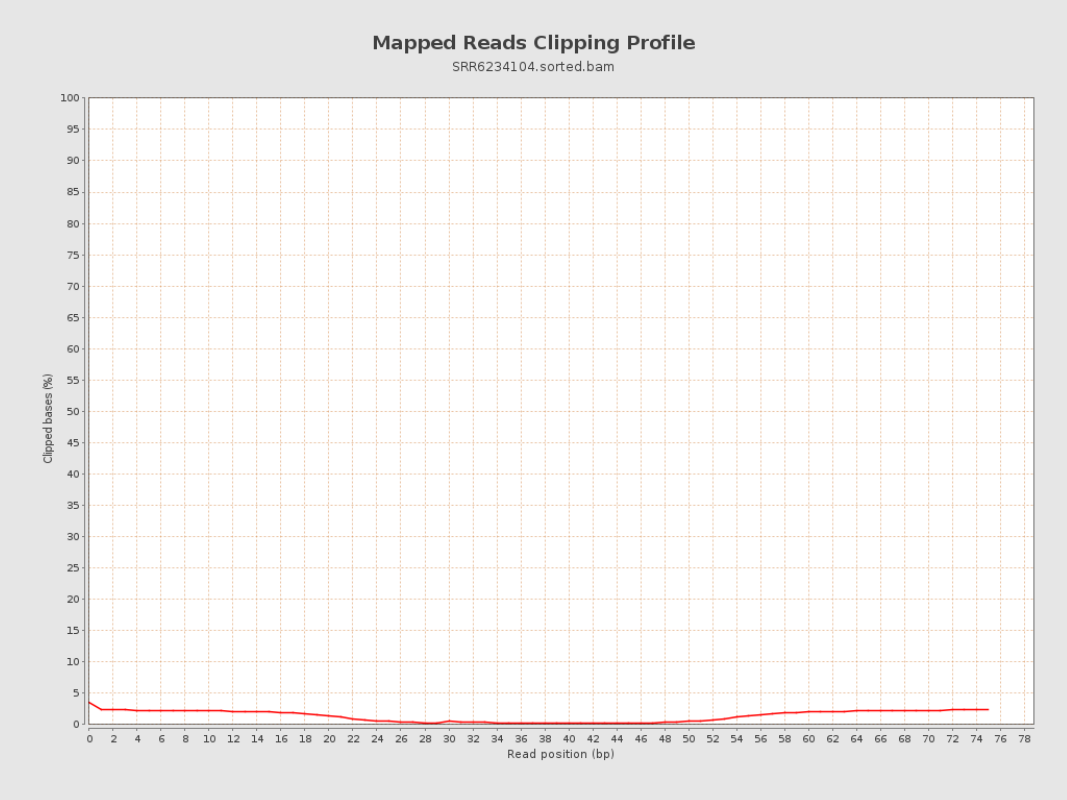
8. Results : Mapped Reads Nucleotide Content



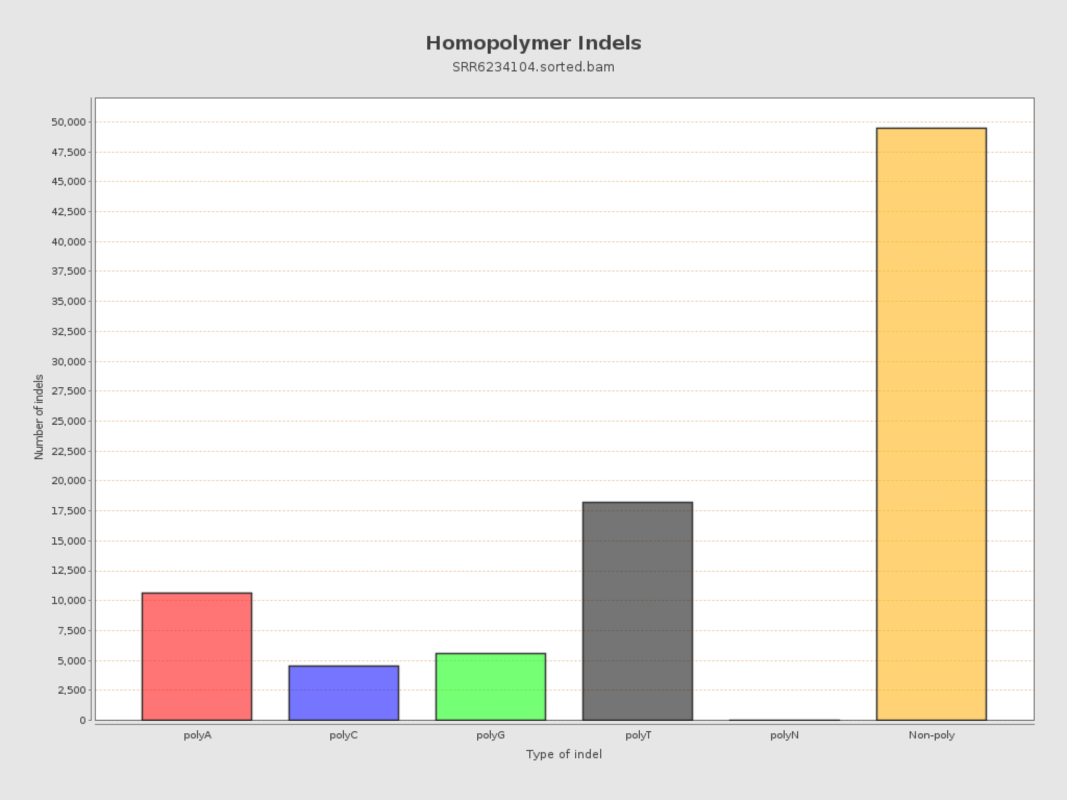
9. Results : Mapped Reads GC-content Distribution



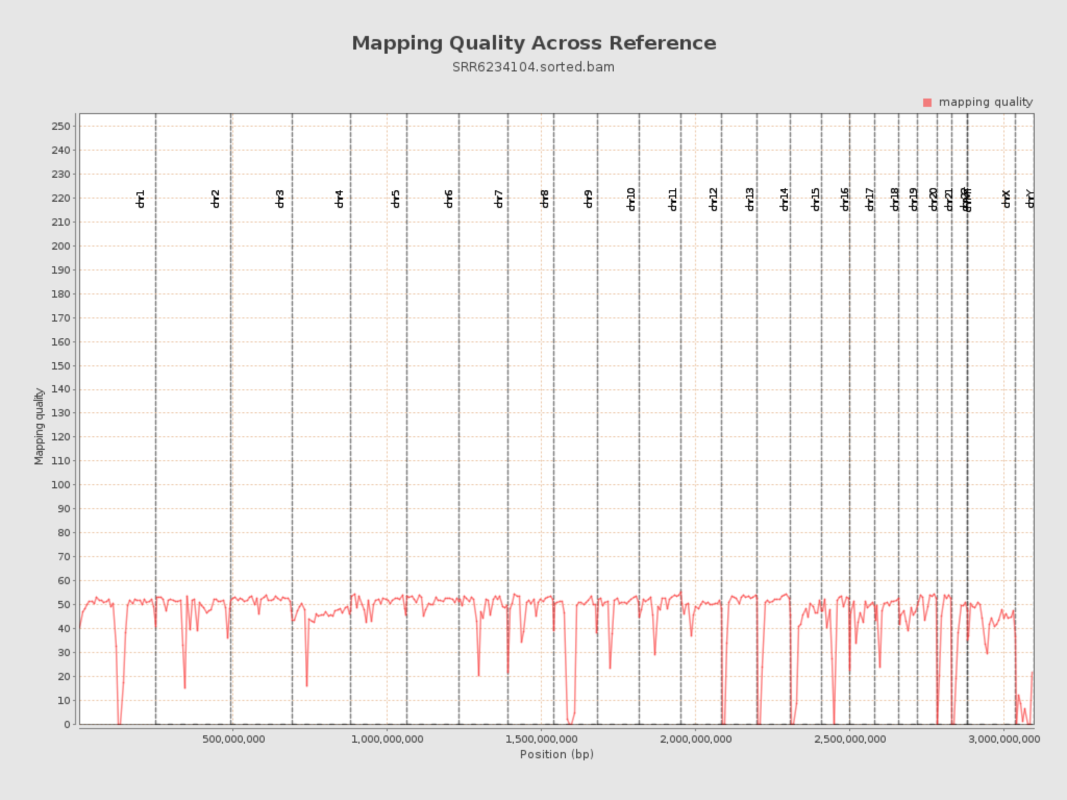
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram