Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:46:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234041.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_SRR6234041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:46:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,633,666
Mapped reads	2,450,712 / 93.05%
Unmapped reads	182,954 / 6.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,954 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	145,411 / 5.52%
Duplication rate	4.27%
Clipped reads	1,070,616 / 40.65%

2.2. ACGT Content

Number/percentage of A's	44,783,724 / 27.28%
Number/percentage of C's	31,447,130 / 19.15%
Number/percentage of T's	50,481,214 / 30.75%
Number/percentage of G's	37,414,665 / 22.79%
Number/percentage of N's	62,382 / 0.04%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0531

Standard Deviation	0.7042

2.4. Mapping Quality

Mean Mapping Quality	41.16

2.5. Mismatches and indels

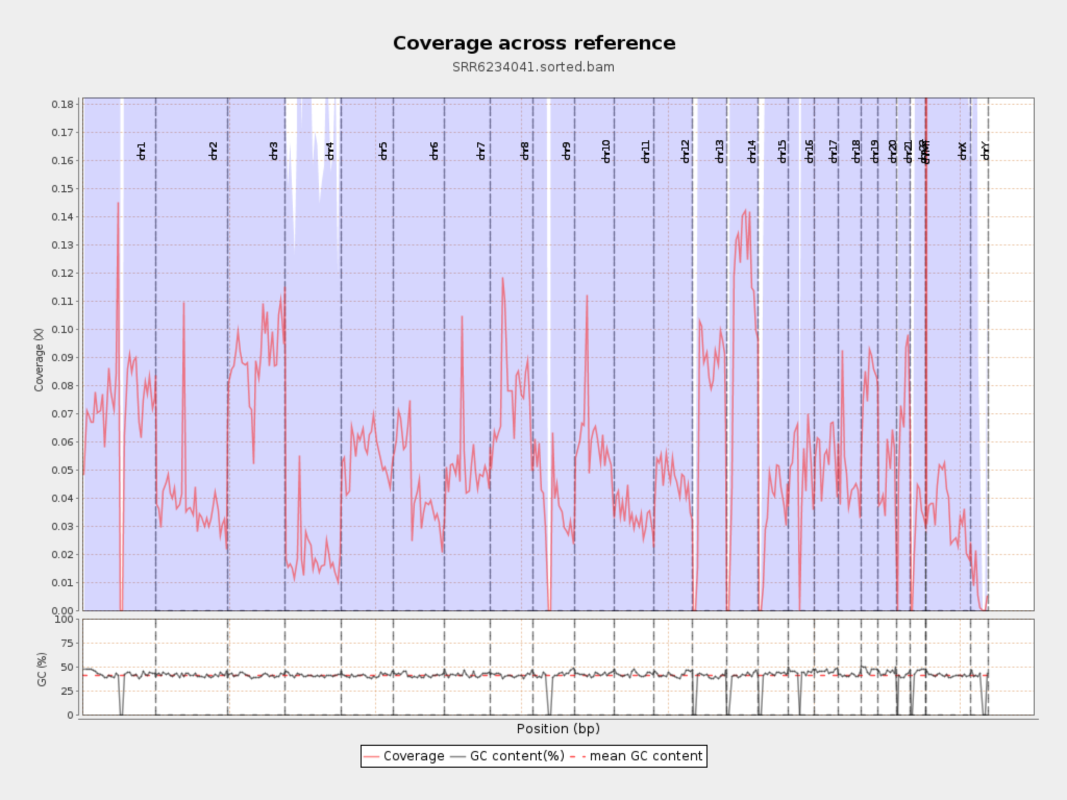
General error rate	0.77%
Mismatches	1,240,052
Insertions	12,713
Mapped reads with at least one insertion	0.51%
Deletions	41,493
Mapped reads with at least one deletion	1.67%
Homopolymer indels	44.46%

2.6. Chromosome stats

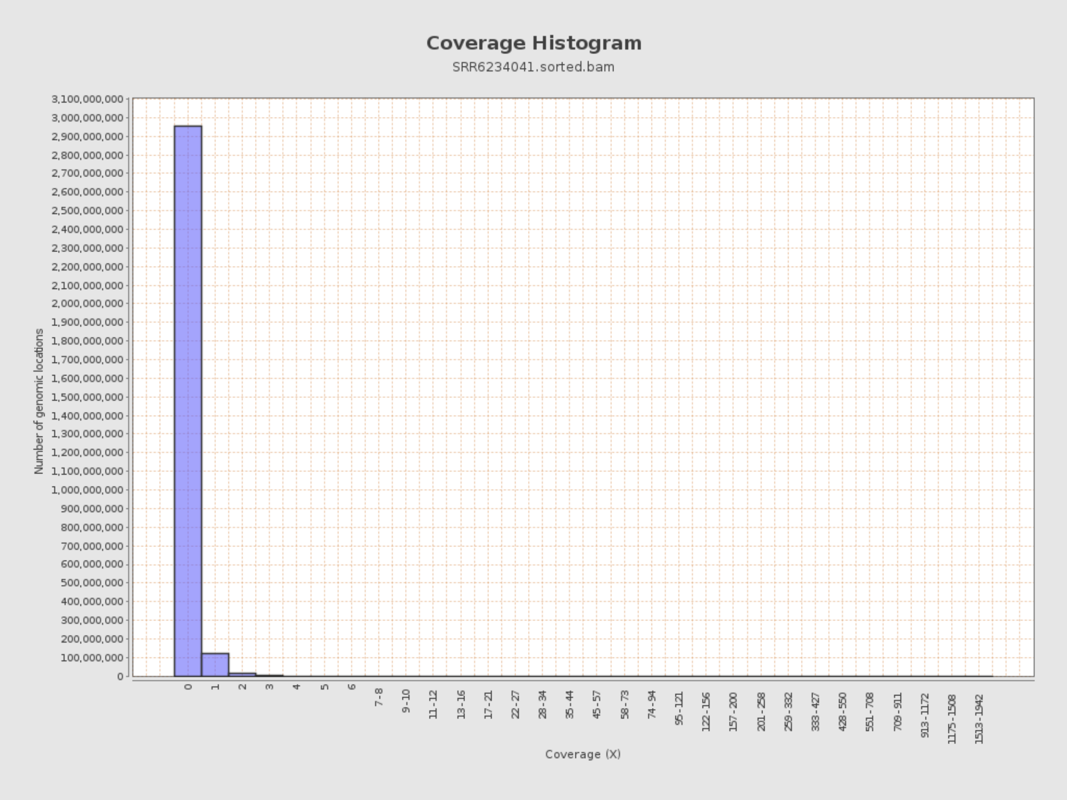
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17986725	0.0722	1.6812
chr2	243199373	9341325	0.0384	0.702
chr3	198022430	17745120	0.0896	0.3388
chr4	191154276	3629269	0.019	0.2033
chr5	180915260	10106917	0.0559	0.2699
chr6	171115067	7686101	0.0449	0.3094
chr7	159138663	8143699	0.0512	0.7551

chr8	146364022	11168811	0.0763	0.994
chr9	141213431	5088762	0.036	0.5089
chr10	135534747	8239059	0.0608	0.6382
chr11	135006516	4562496	0.0338	0.3811
chr12	133851895	6274254	0.0469	0.2498
chr13	115169878	8717637	0.0757	0.3141
chr14	107349540	11153331	0.1039	0.4153
chr15	102531392	3360060	0.0328	0.2252
chr16	90354753	4281401	0.0474	0.3534
chr17	81195210	4542782	0.0559	0.2824
chr18	78077248	3816088	0.0489	1.3838
chr19	59128983	4861951	0.0822	1.0474
chr20	63025520	3002099	0.0476	0.2894
chr21	48129895	3246403	0.0675	0.3139
chr22	51304566	1430089	0.0279	0.1845
chrMT	16571	114945	6.9365	4.4092
chrX	155270560	5354105	0.0345	0.284
chrY	59373566	410432	0.0069	0.1501

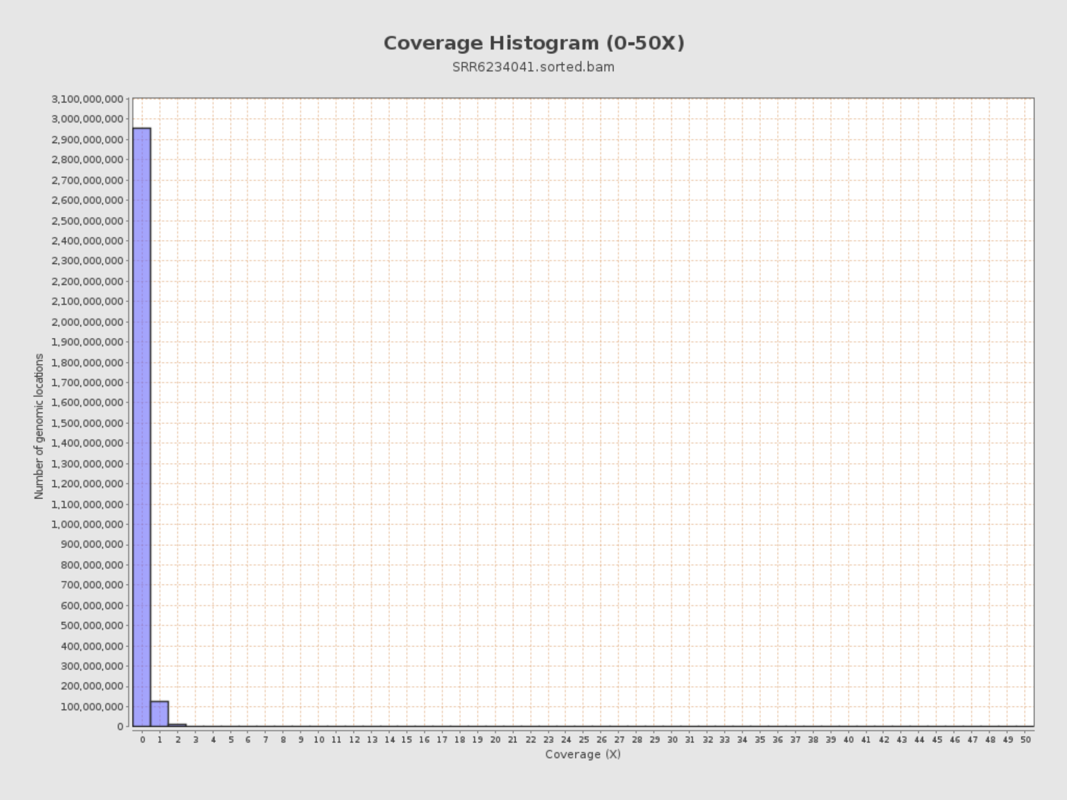
3. Results : Coverage across reference



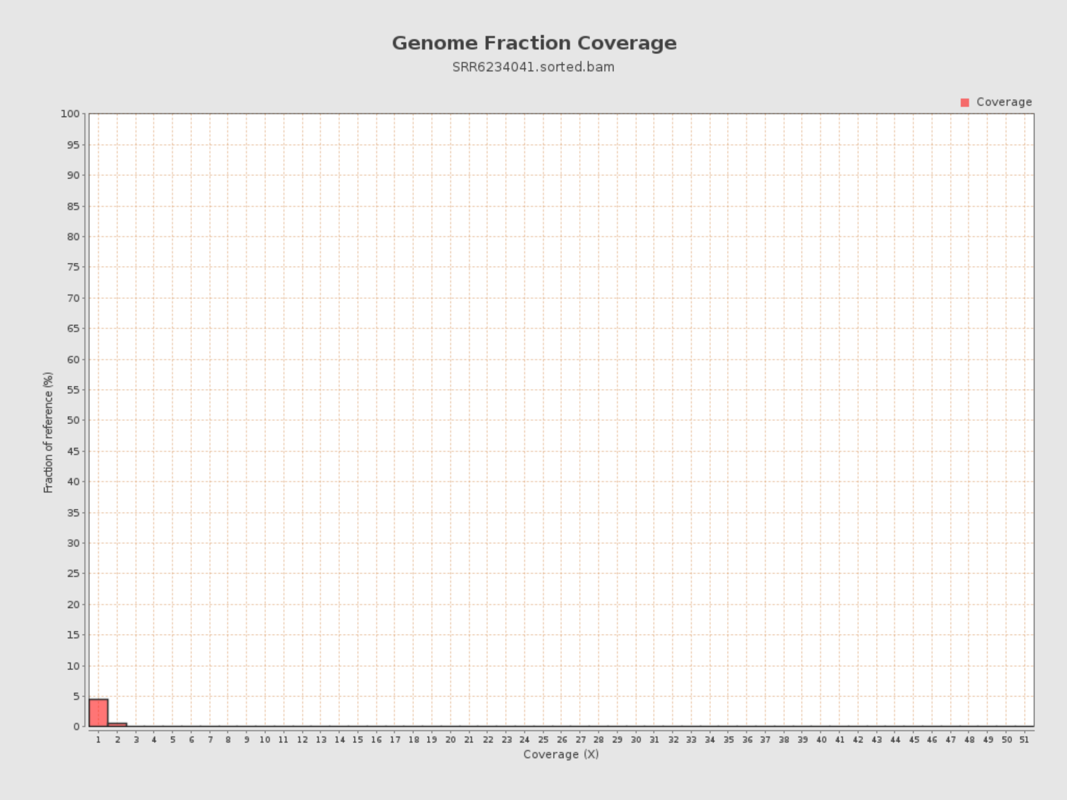
4. Results : Coverage Histogram



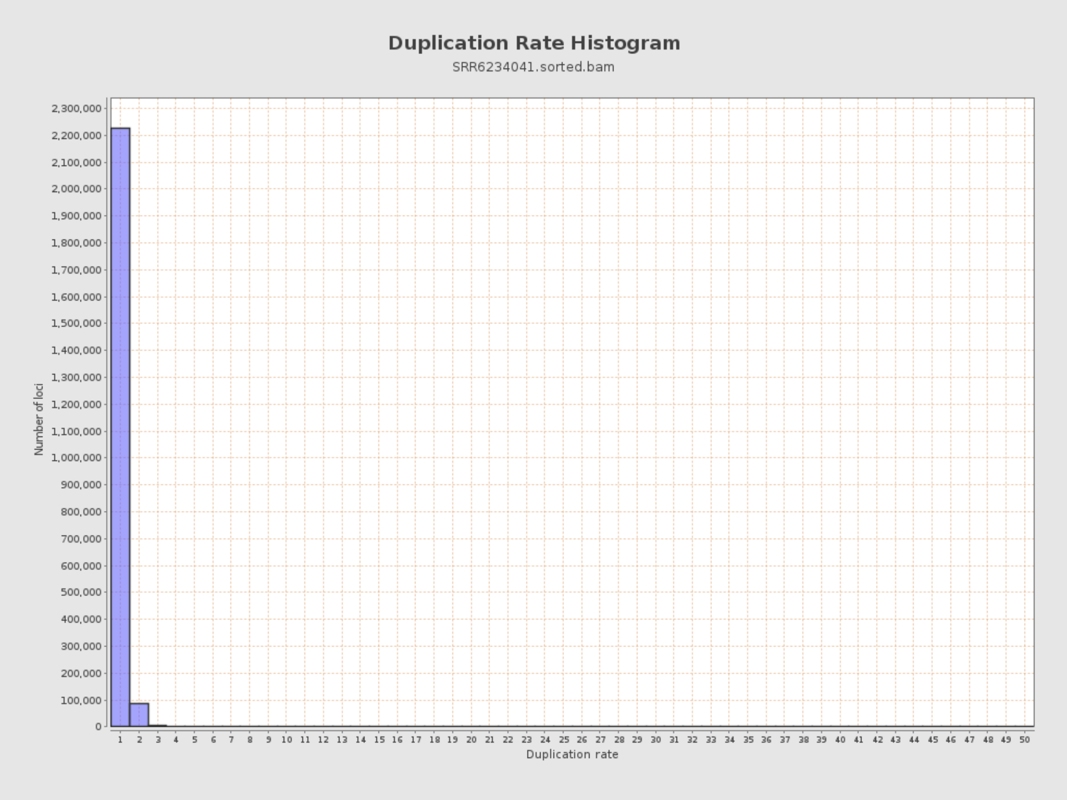
5. Results : Coverage Histogram (0-50X)



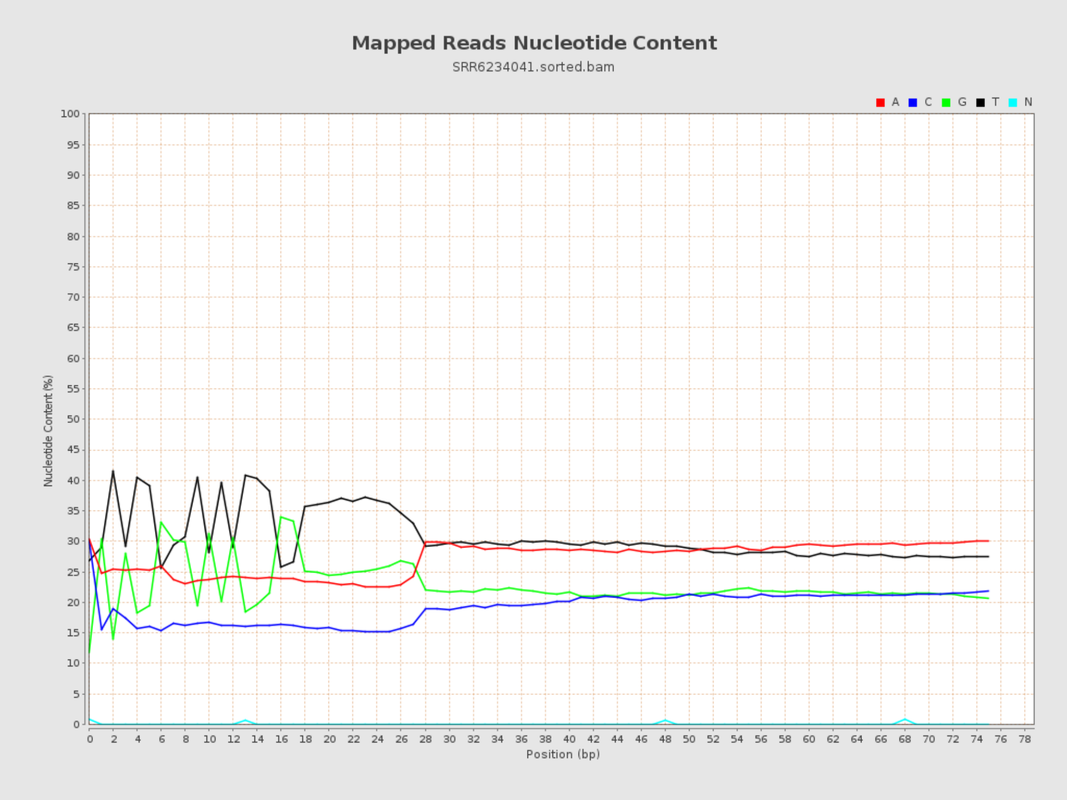
6. Results : Genome Fraction Coverage



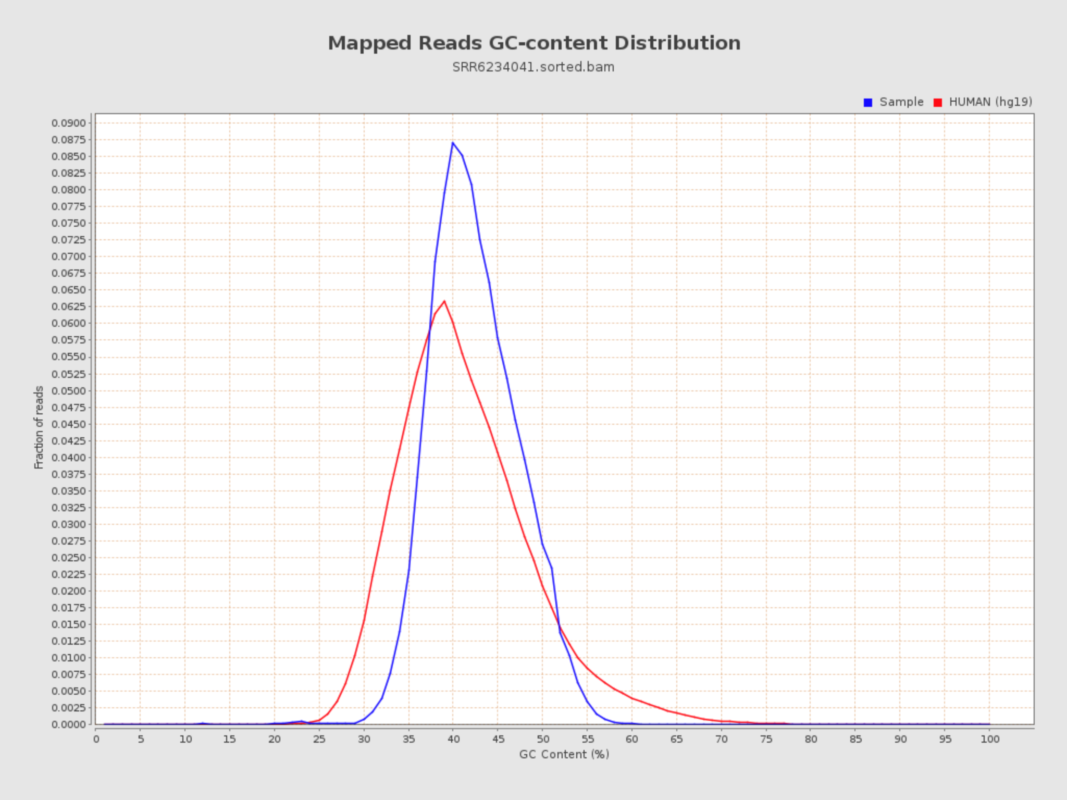
7. Results : Duplication Rate Histogram



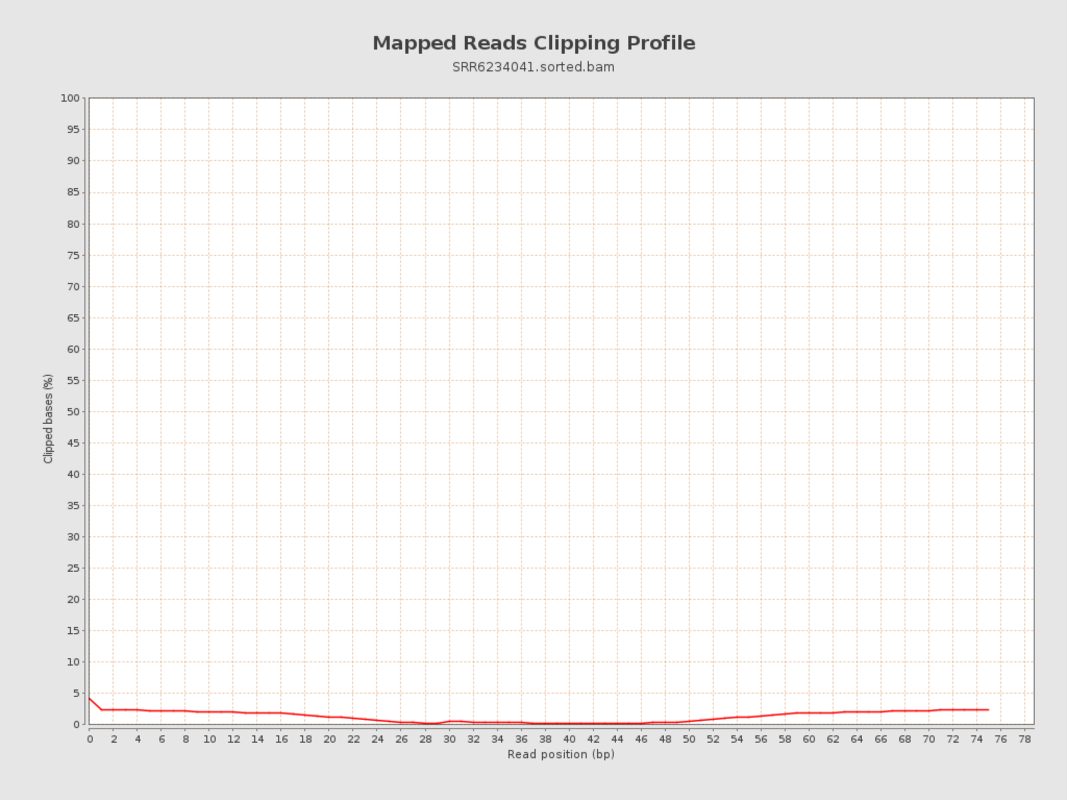
8. Results : Mapped Reads Nucleotide Content



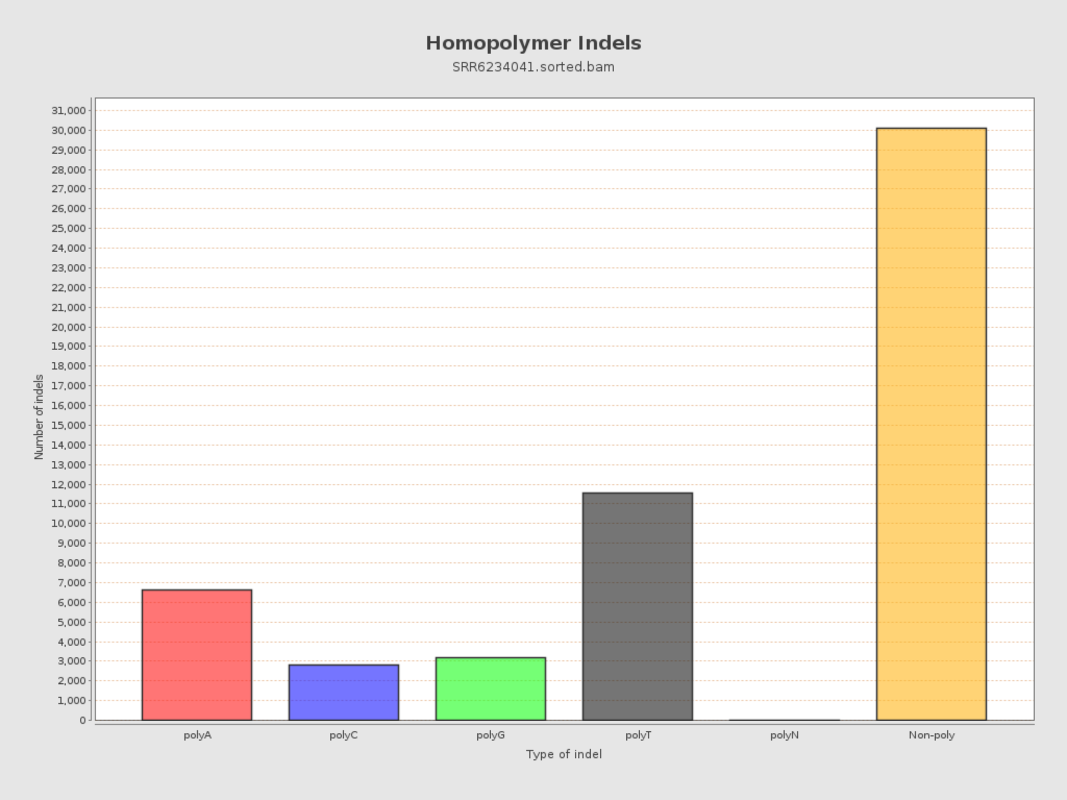
9. Results : Mapped Reads GC-content Distribution



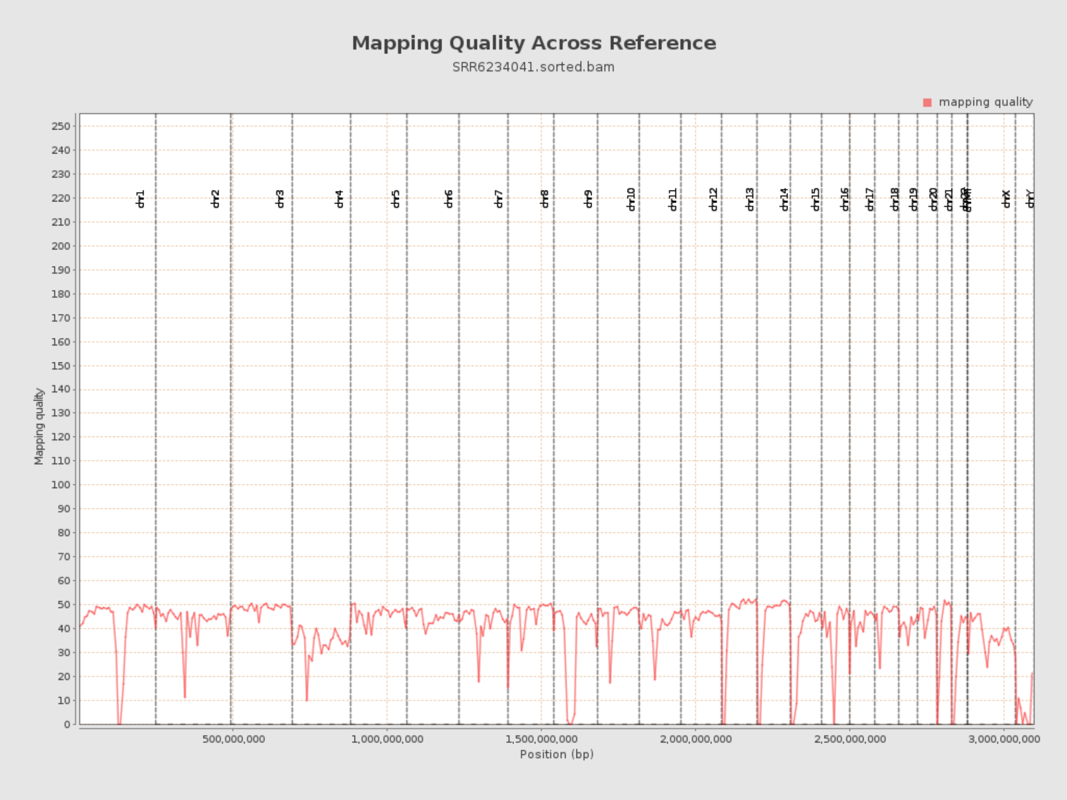
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram