Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:43:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004102.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_SRR6004102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:43:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,940,746
Mapped reads	3,499,915 / 88.81%
Unmapped reads	440,831 / 11.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,616 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	150,455 / 3.82%
Duplication rate	2.51%
Clipped reads	1,775,054 / 45.04%

2.2. ACGT Content

Number/percentage of A's	66,384,567 / 28.92%
Number/percentage of C's	43,715,253 / 19.05%
Number/percentage of T's	70,669,912 / 30.79%
Number/percentage of G's	48,703,147 / 21.22%
Number/percentage of N's	48,443 / 0.02%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0742

Standard Deviation	0.8503

2.4. Mapping Quality

Mean Mapping Quality	43.41

2.5. Mismatches and indels

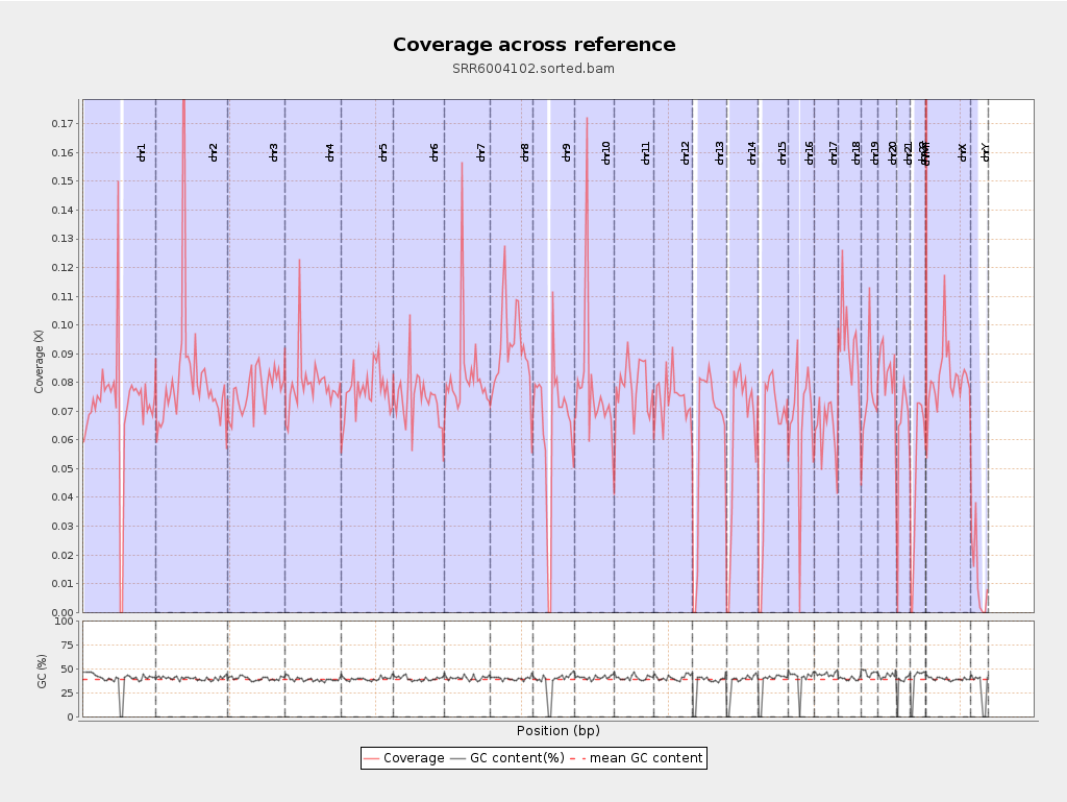
General error rate	1%
Mismatches	2,245,389
Insertions	21,488
Mapped reads with at least one insertion	0.61%
Deletions	60,379
Mapped reads with at least one deletion	1.7%
Homopolymer indels	45%

2.6. Chromosome stats

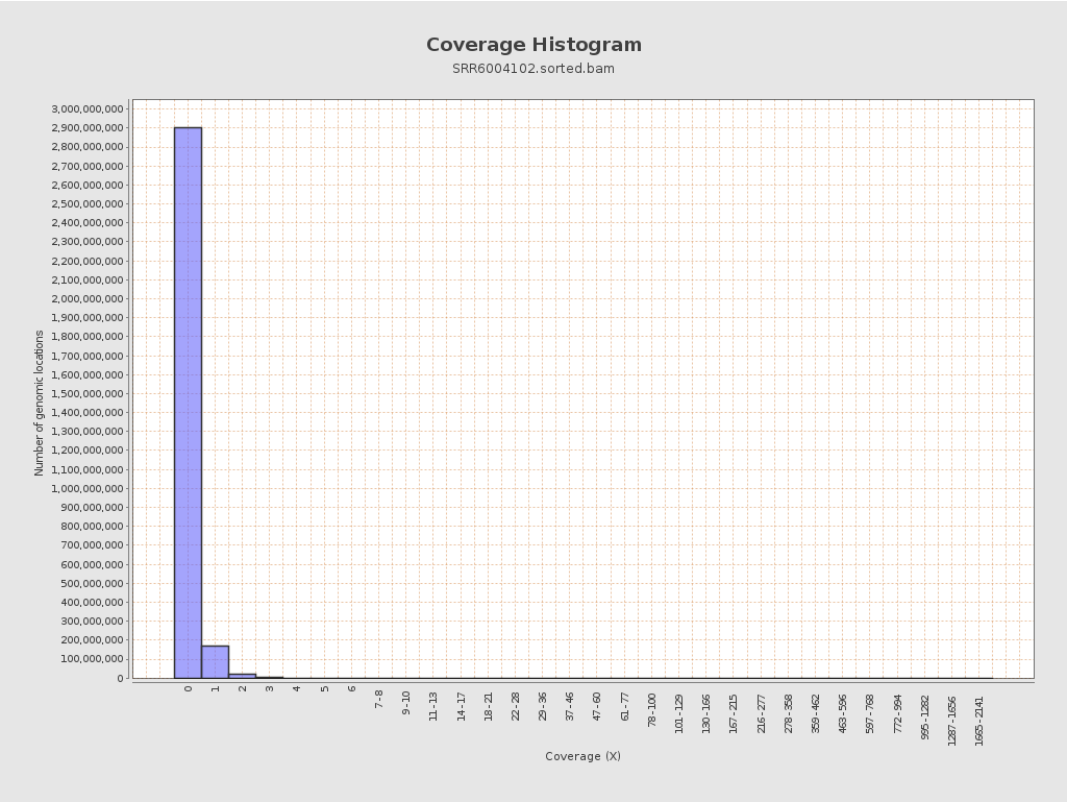
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17848767	0.0716	1.8528
chr2	243199373	19868299	0.0817	1.1264
chr3	198022430	15321980	0.0774	0.3408
chr4	191154276	15183373	0.0794	0.3916
chr5	180915260	13966318	0.0772	0.3227
chr6	171115067	12710445	0.0743	0.453
chr7	159138663	13130016	0.0825	1.1257

chr8	146364022	13367593	0.0913	0.9948
chr9	141213431	9275284	0.0657	0.7619
chr10	135534747	10556504	0.0779	0.8235
chr11	135006516	10610277	0.0786	0.5651
chr12	133851895	9978530	0.0745	0.3269
chr13	115169878	7226302	0.0627	0.2865
chr14	107349540	6781872	0.0632	0.4042
chr15	102531392	6132275	0.0598	0.3023
chr16	90354753	5909321	0.0654	0.401
chr17	81195210	5254488	0.0647	0.3588
chr18	78077248	7351071	0.0942	1.5298
chr19	59128983	4464280	0.0755	1.1197
chr20	63025520	5312240	0.0843	0.3777
chr21	48129895	3002763	0.0624	0.3613
chr22	51304566	2507403	0.0489	0.2502
chrMT	16571	522902	31.5552	19.1106
chrX	155270560	12645883	0.0814	0.4085
chrY	59373566	692858	0.0117	0.2729

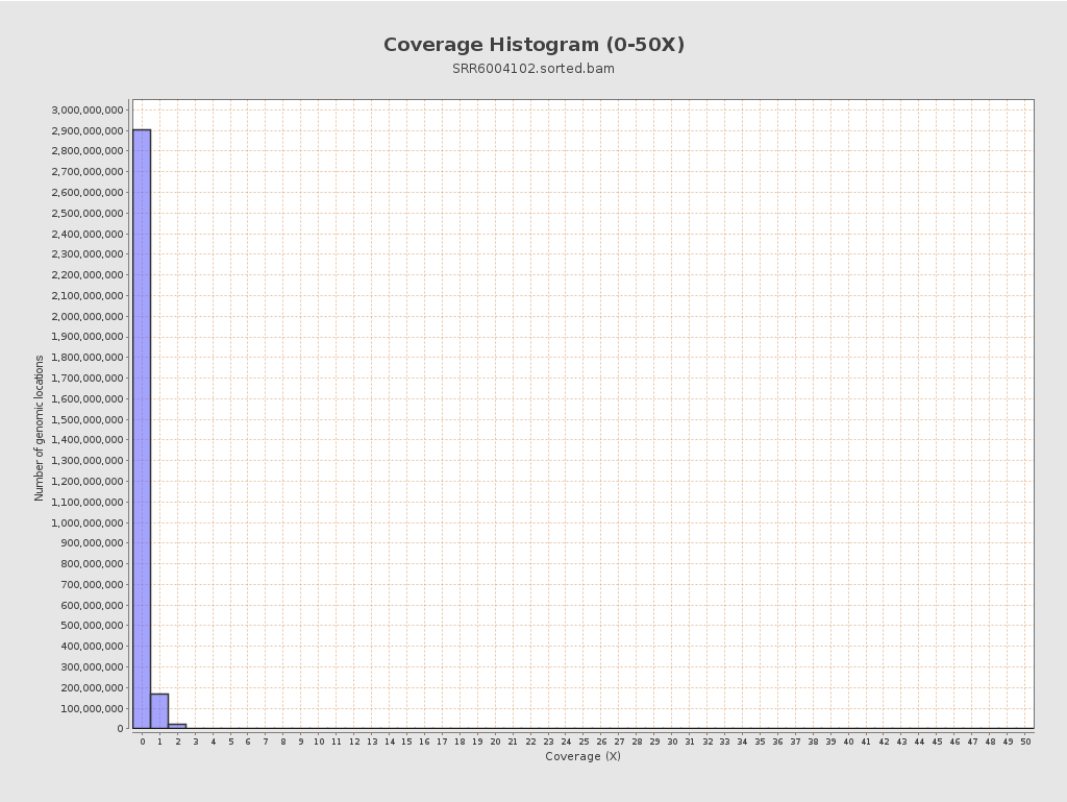
3. Results : Coverage across reference



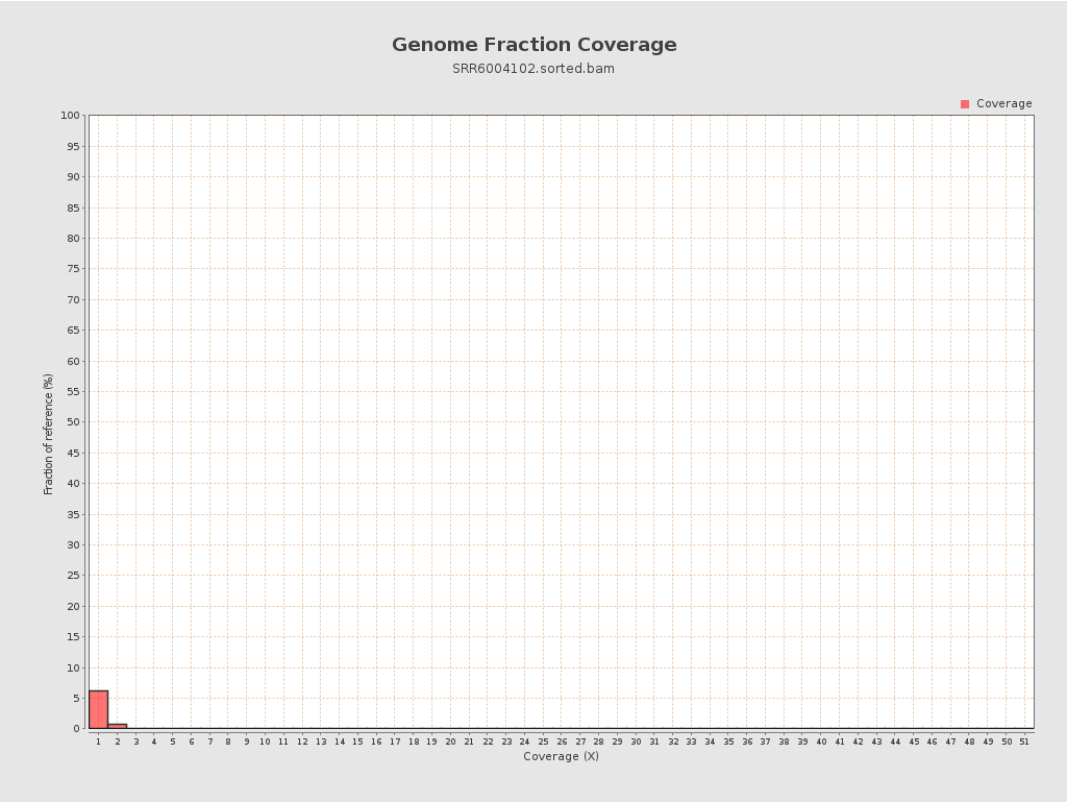
4. Results : Coverage Histogram



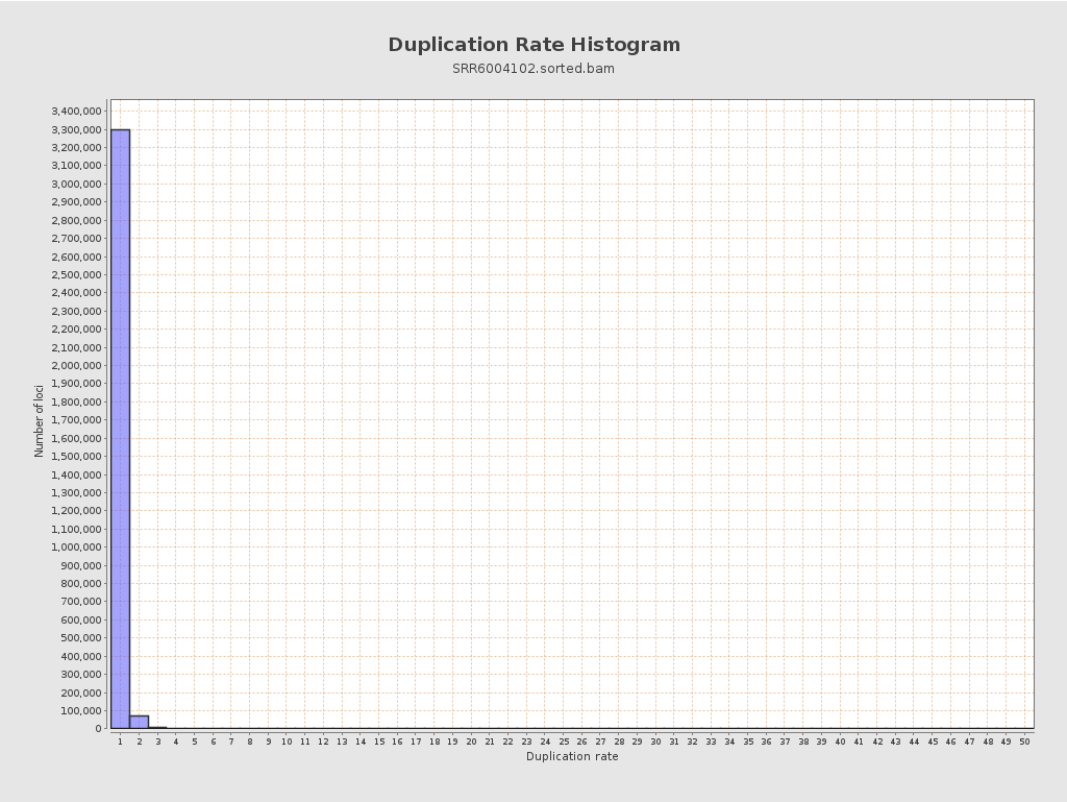
5. Results : Coverage Histogram (0-50X)



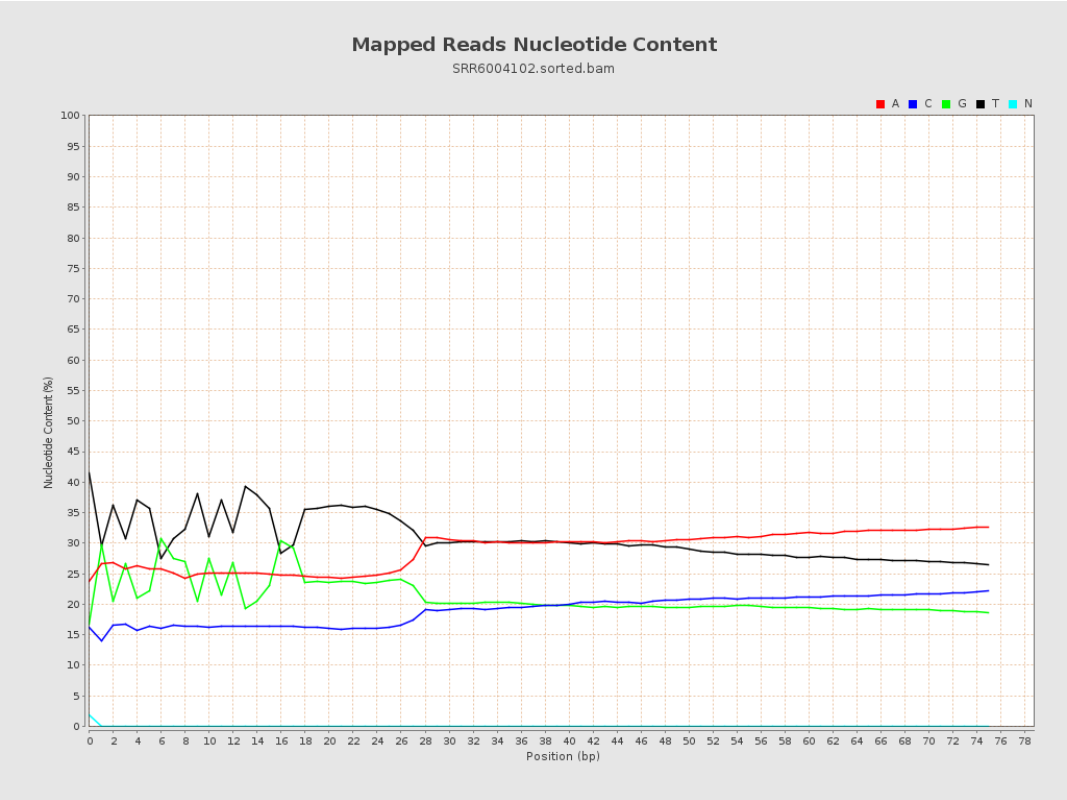
6. Results : Genome Fraction Coverage



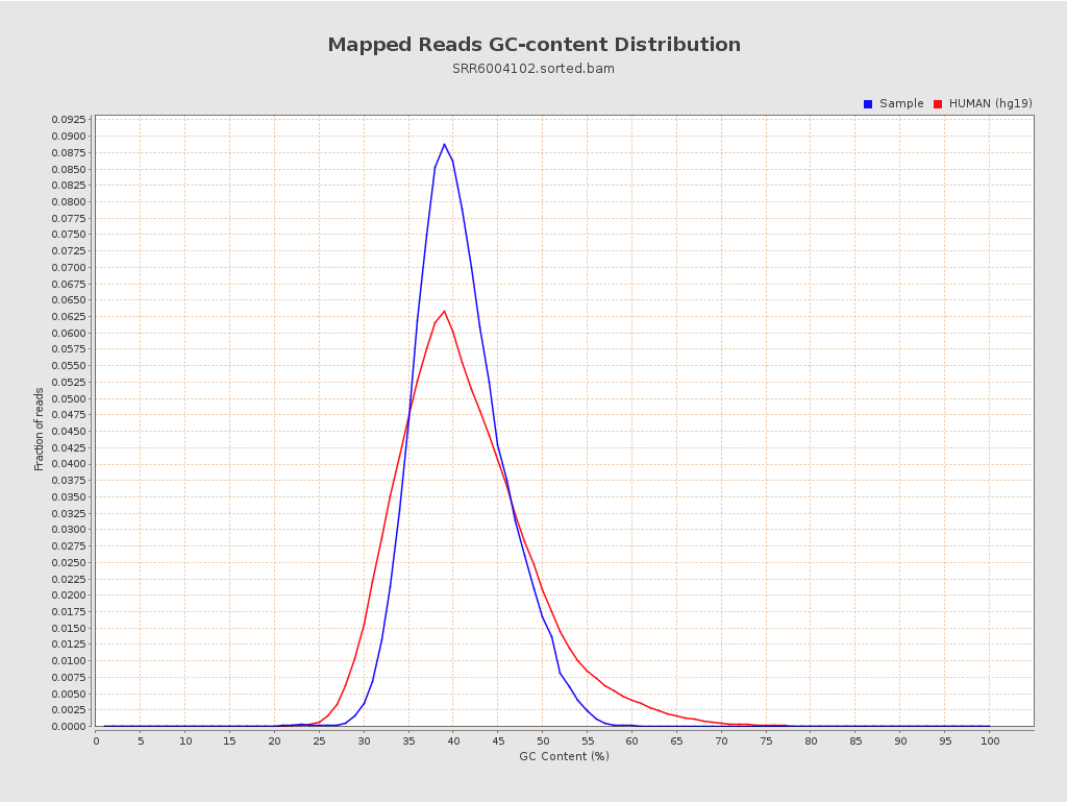
7. Results : Duplication Rate Histogram



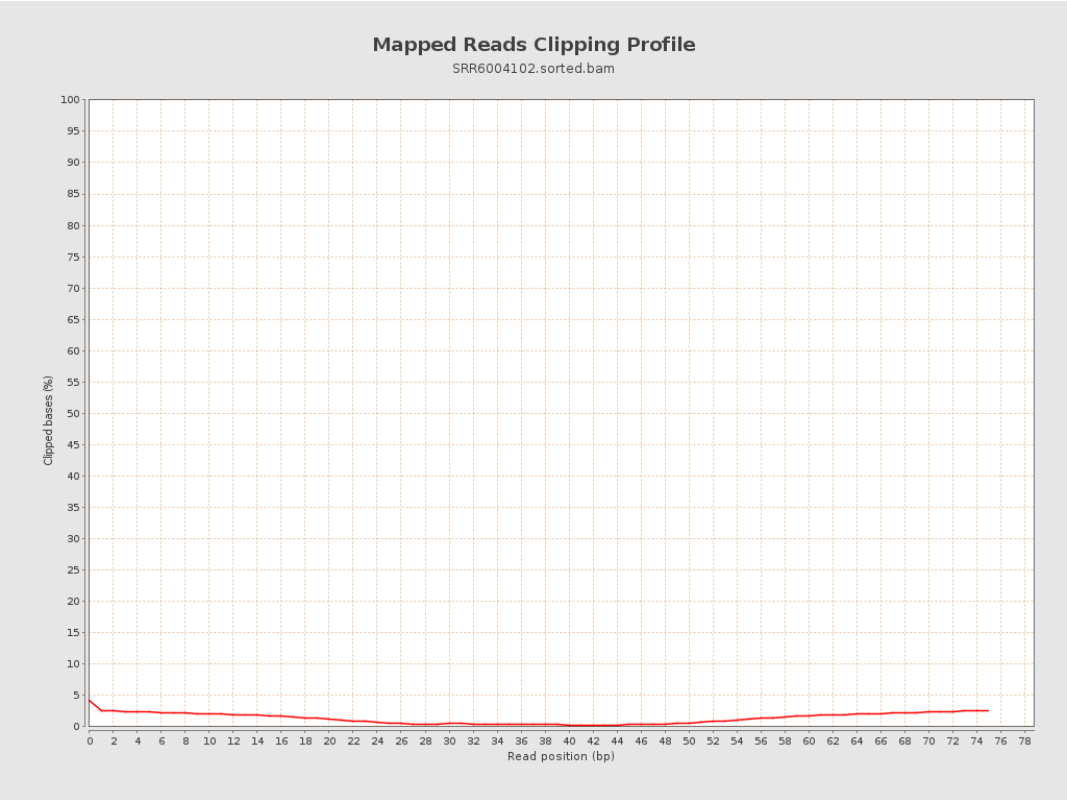
8. Results : Mapped Reads Nucleotide Content



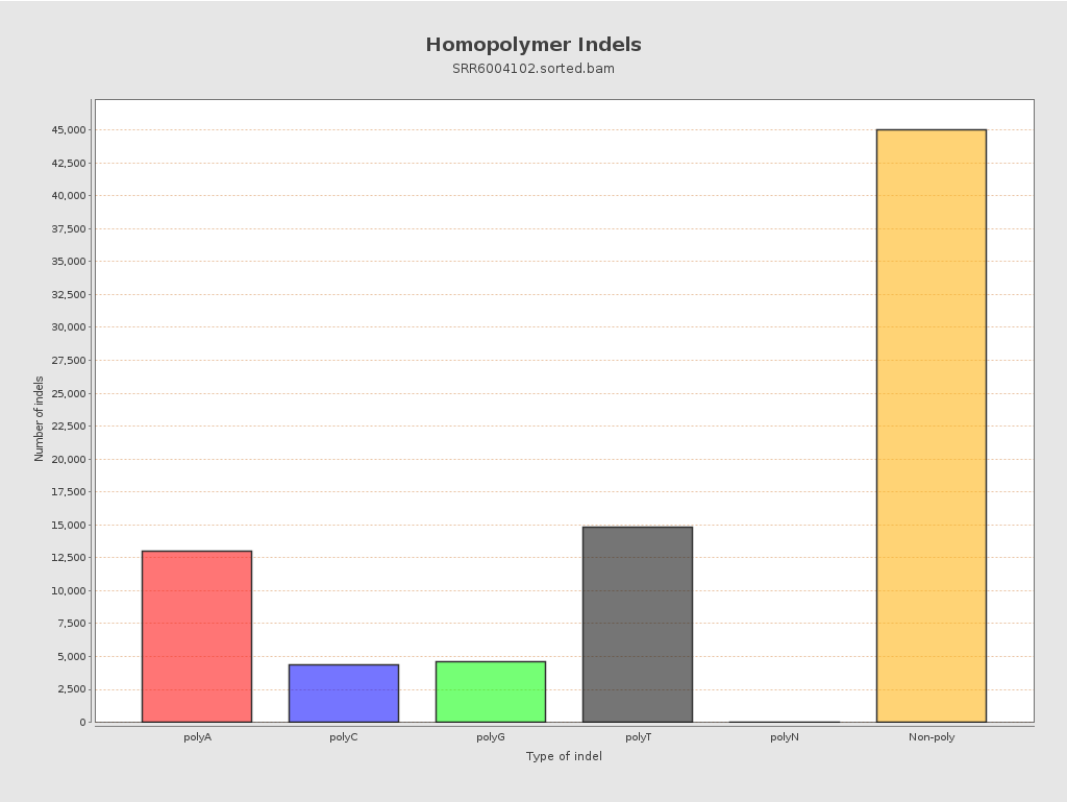
9. Results : Mapped Reads GC-content Distribution



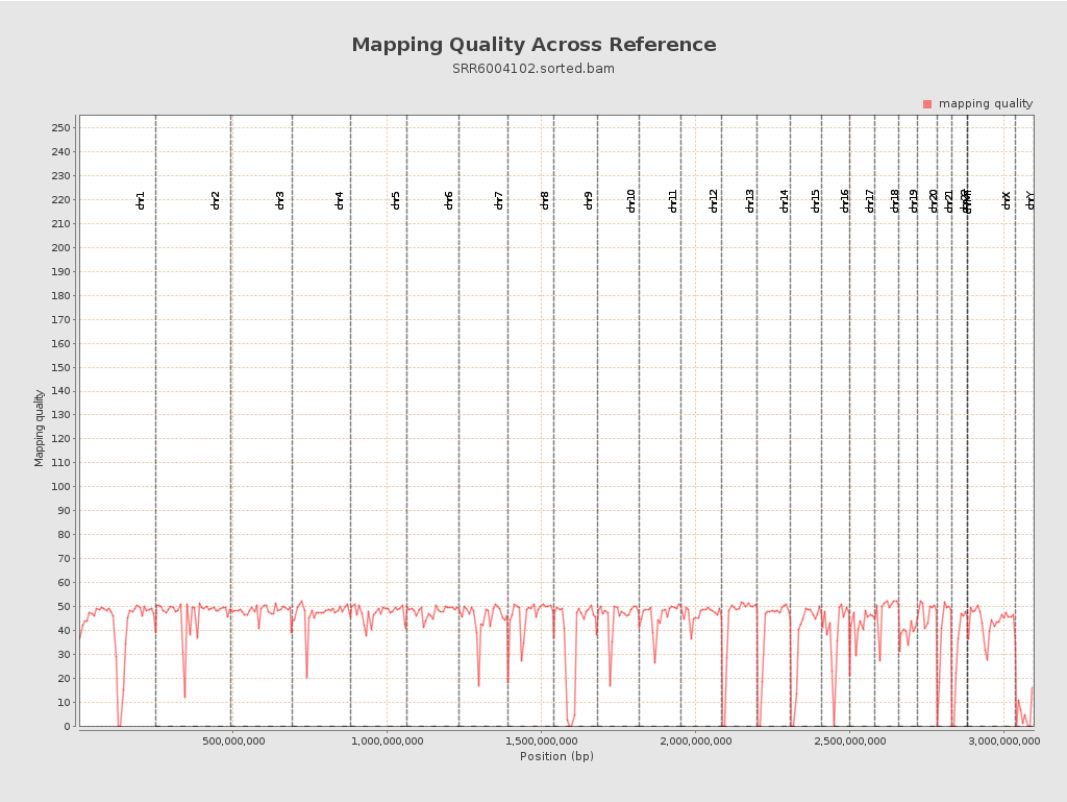
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram