

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:31:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085042.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_SRR3085042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:31:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,701,068
Mapped reads	2,475,088 / 91.63%
Unmapped reads	225,980 / 8.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,788 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	89,084 / 3.3%
Duplication rate	2.89%
Clipped reads	1,115,574 / 41.3%

2.2. ACGT Content

Number/percentage of A's	47,591,248 / 28.7%
Number/percentage of C's	31,460,866 / 18.97%
Number/percentage of T's	51,391,401 / 30.99%
Number/percentage of G's	35,365,004 / 21.33%
Number/percentage of N's	17,856 / 0.01%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.3893
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.12
----------------------	-------

2.5. Mismatches and indels

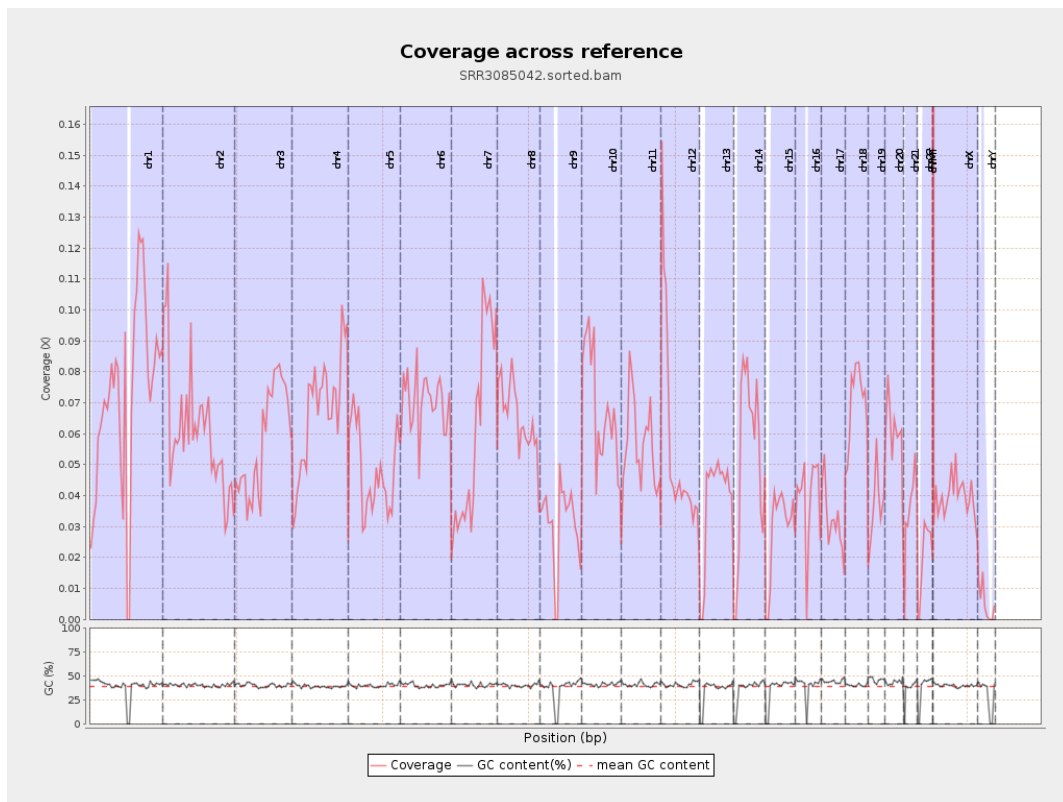
General error rate	0.89%
Mismatches	1,453,362
Insertions	12,085
Mapped reads with at least one insertion	0.48%
Deletions	34,925
Mapped reads with at least one deletion	1.4%
Homopolymer indels	46.63%

2.6. Chromosome stats

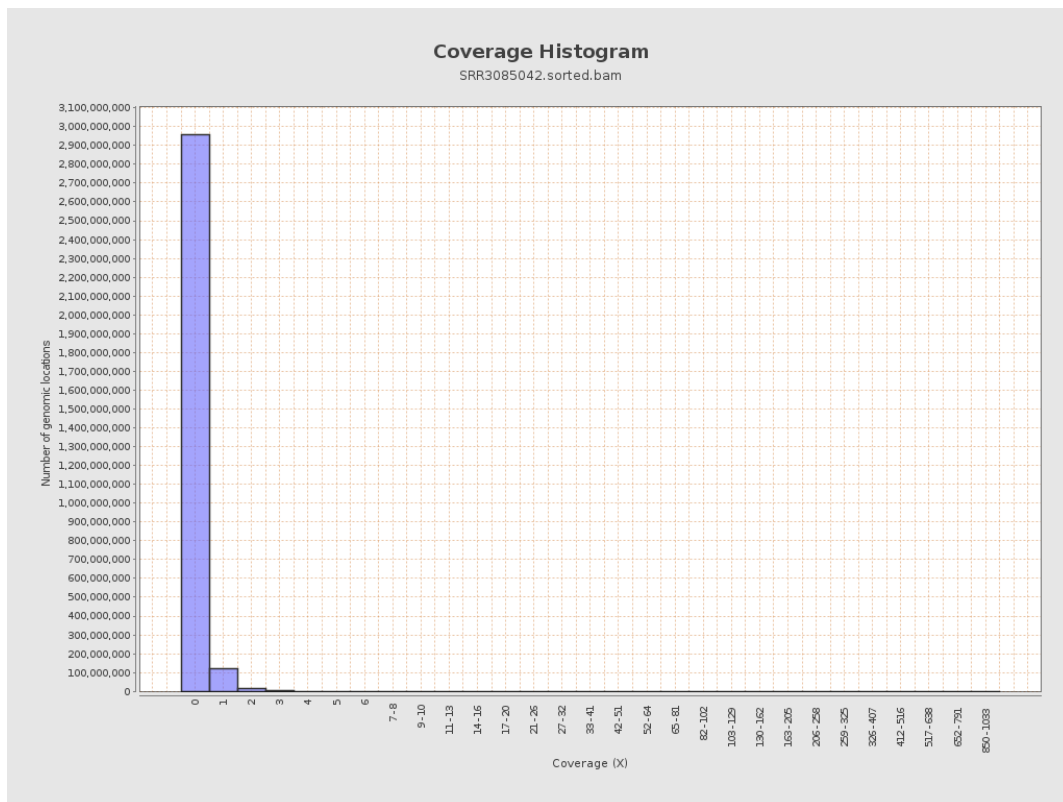
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17928146	0.0719	0.62
chr2	243199373	14711023	0.0605	0.487
chr3	198022430	11468642	0.0579	0.2812
chr4	191154276	12924498	0.0676	0.3036
chr5	180915260	8662766	0.0479	0.2515
chr6	171115067	12072531	0.0706	0.3585
chr7	159138663	9717537	0.0611	0.3254

chr8	146364022	9485366	0.0648	0.6905
chr9	141213431	4416209	0.0313	0.3187
chr10	135534747	9245318	0.0682	0.4961
chr11	135006516	7609831	0.0564	0.3793
chr12	133851895	7486149	0.0559	0.2768
chr13	115169878	4426252	0.0384	0.2248
chr14	107349540	5800043	0.054	0.28
chr15	102531392	2974996	0.029	0.2023
chr16	90354753	3415882	0.0378	0.2379
chr17	81195210	2654025	0.0327	0.2328
chr18	78077248	5492238	0.0703	0.5533
chr19	59128983	2221421	0.0376	0.4378
chr20	63025520	3880645	0.0616	0.2905
chr21	48129895	1713788	0.0356	0.2252
chr22	51304566	1046201	0.0204	0.1605
chrMT	16571	114189	6.8909	5.4131
chrX	155270560	6114268	0.0394	0.2554
chrY	59373566	303506	0.0051	0.1033

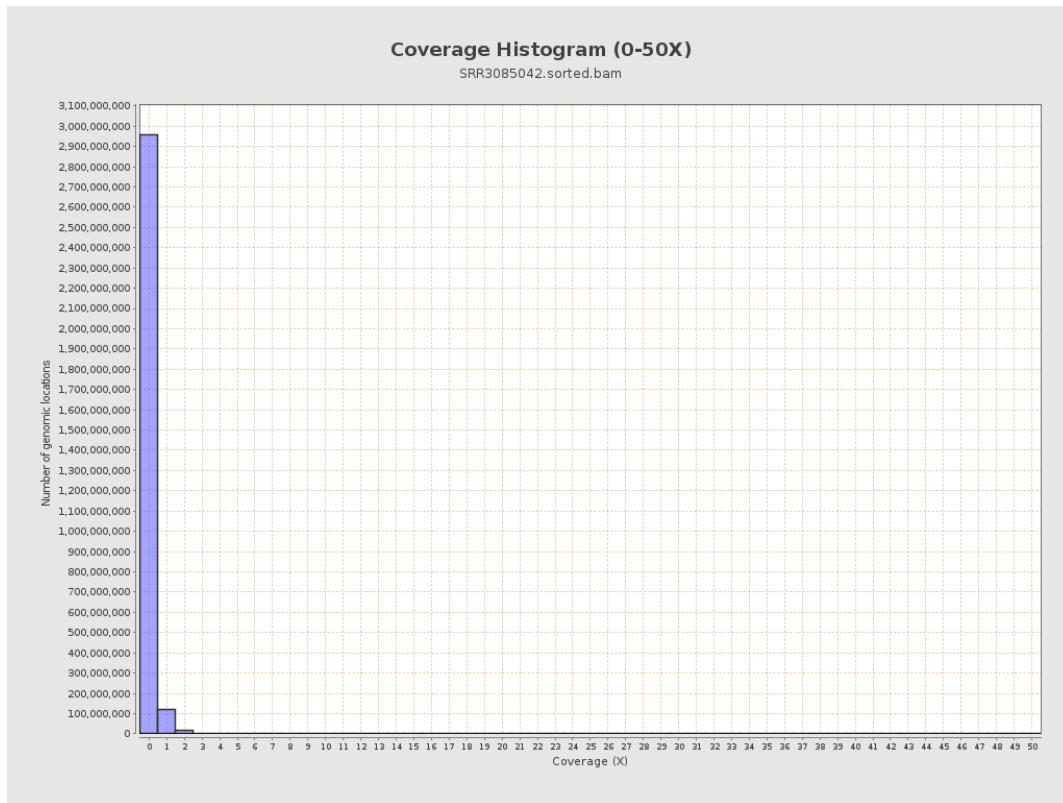
3. Results : Coverage across reference



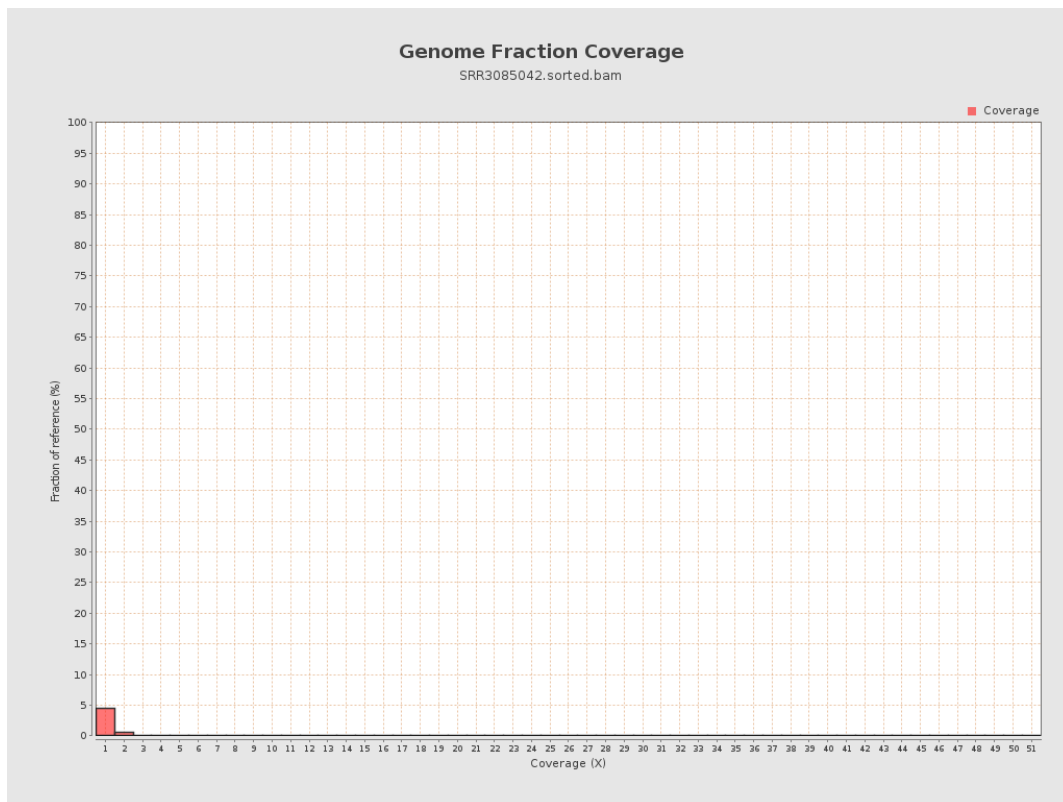
4. Results : Coverage Histogram



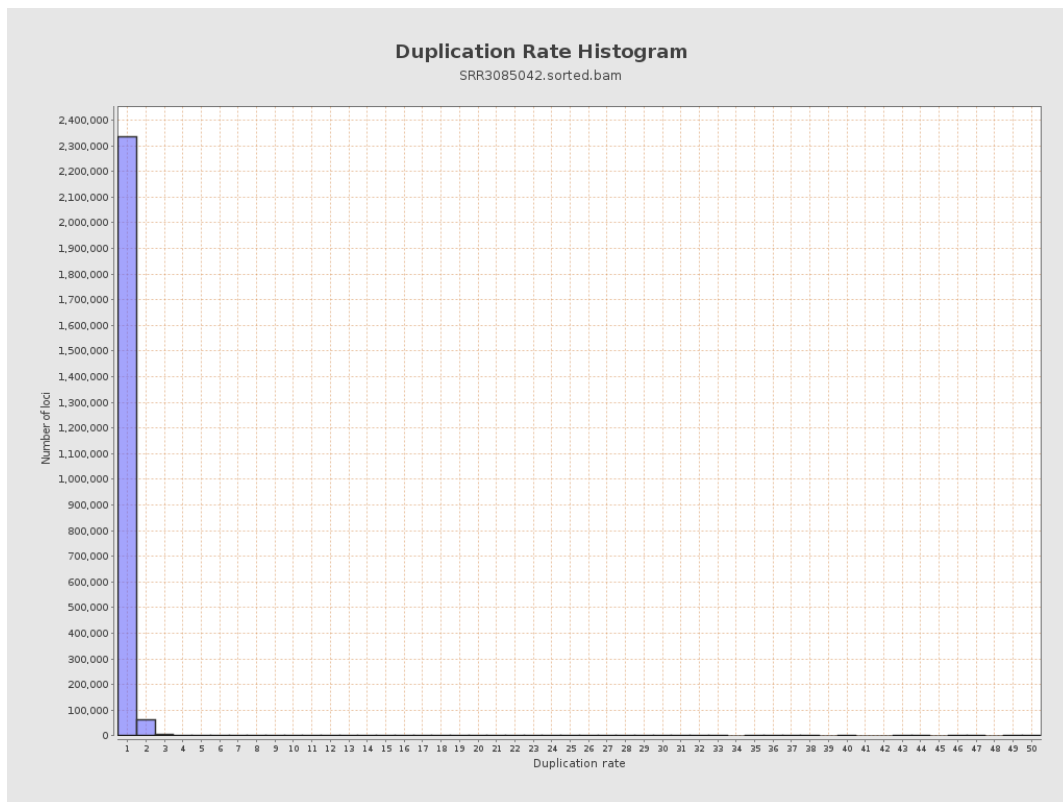
5. Results : Coverage Histogram (0-50X)



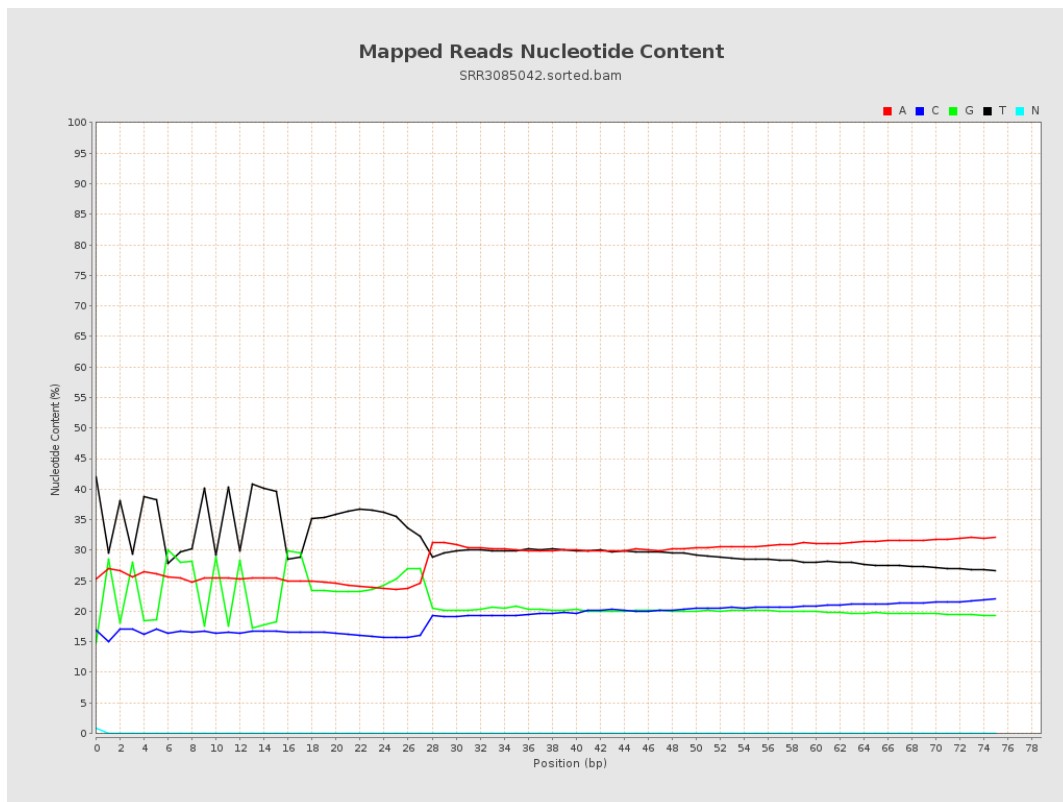
6. Results : Genome Fraction Coverage



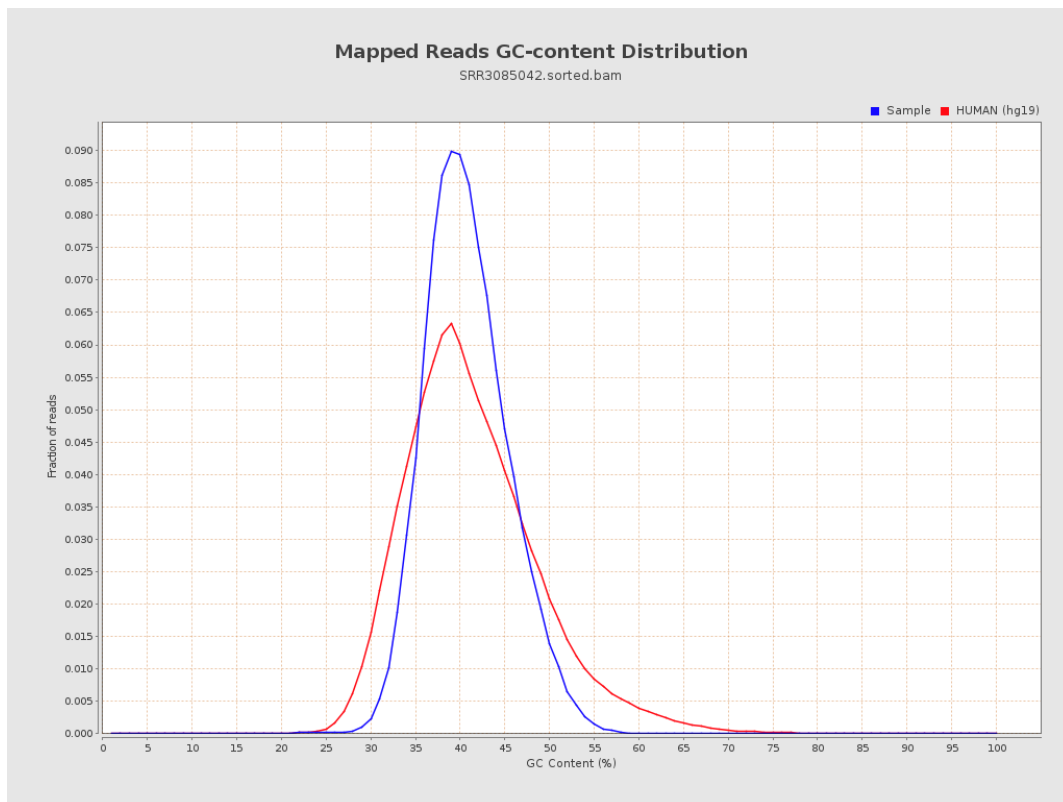
7. Results : Duplication Rate Histogram



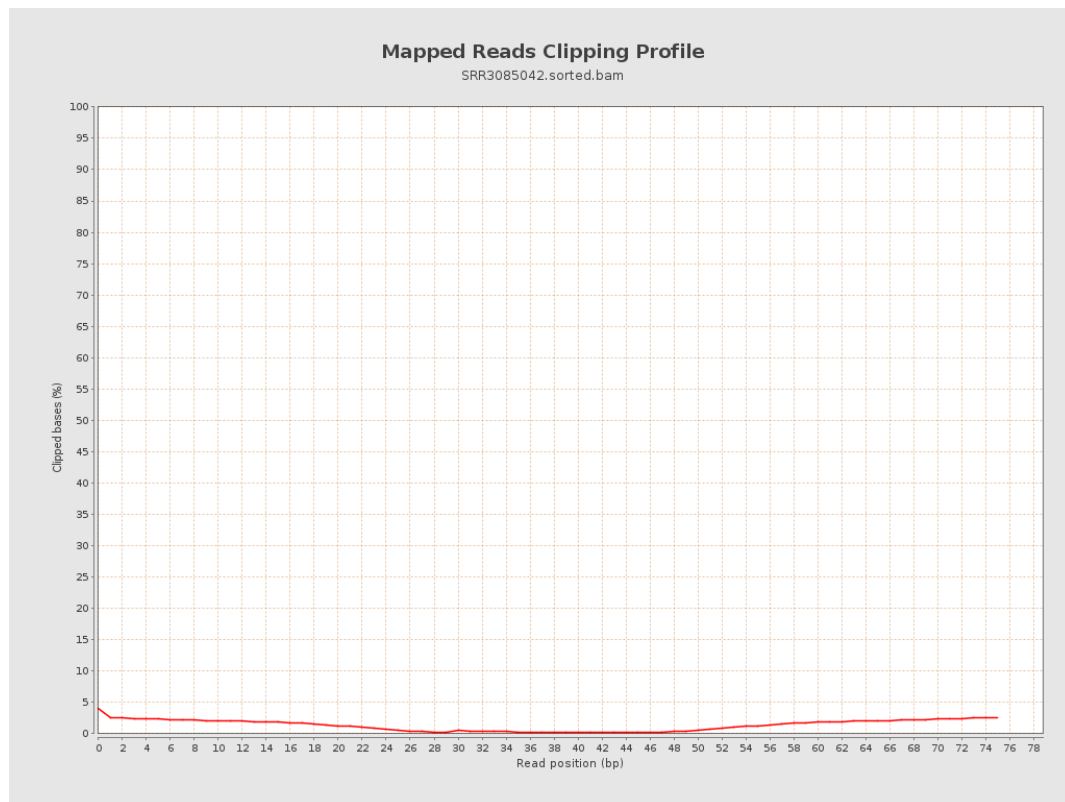
8. Results : Mapped Reads Nucleotide Content



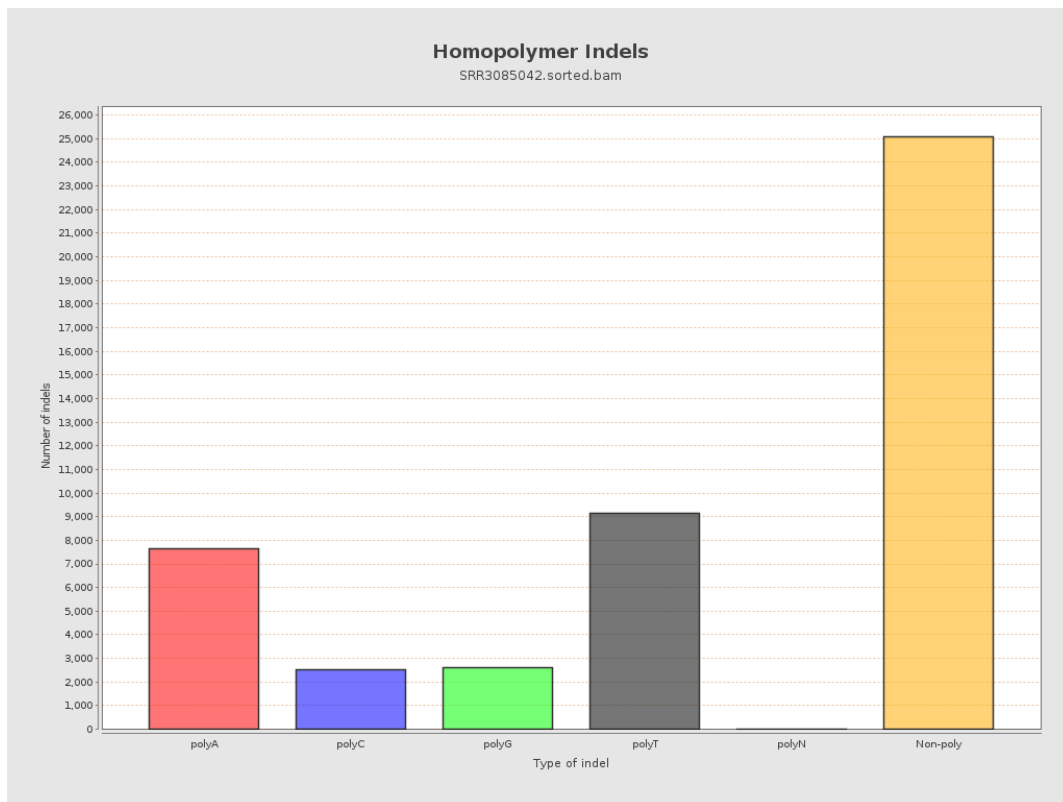
9. Results : Mapped Reads GC-content Distribution



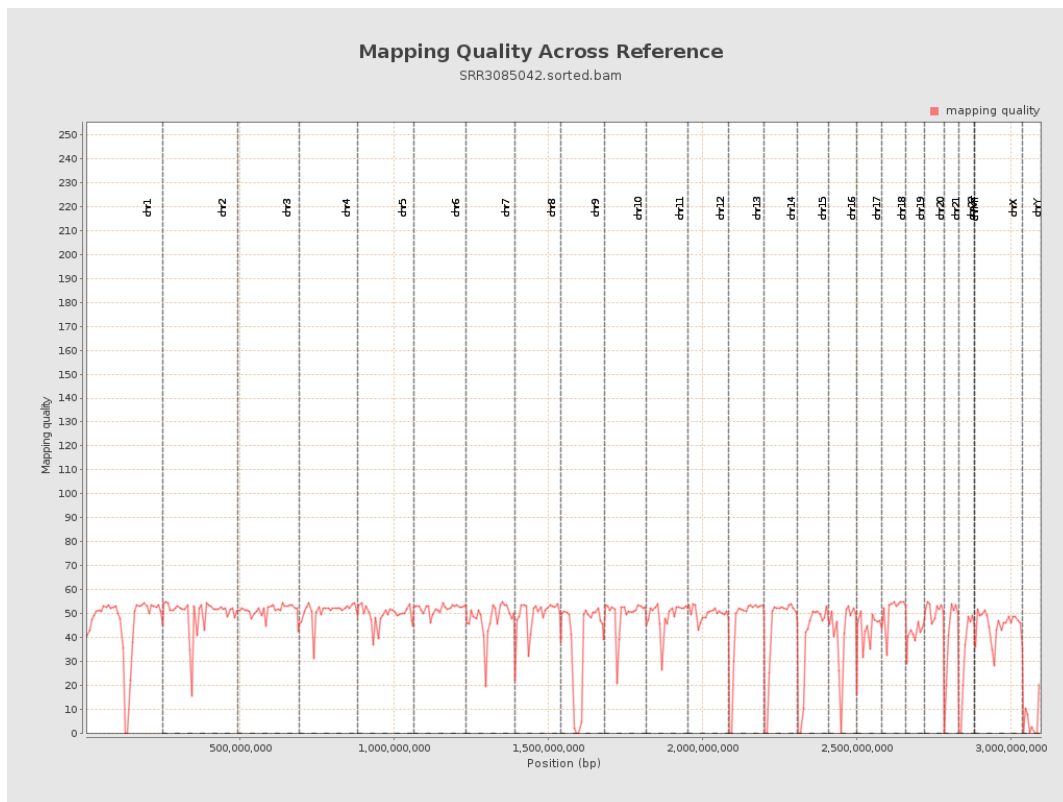
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

