Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:16:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085122.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_SRR3085122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:16:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,009,173
Mapped reads	1,825,486 / 90.86%
Unmapped reads	183,687 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,601 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	60,097 / 2.99%
Duplication rate	2.41%
Clipped reads	729,970 / 36.33%

2.2. ACGT Content

Number/percentage of A's	35,358,936 / 28.45%
Number/percentage of C's	23,067,616 / 18.56%
Number/percentage of T's	39,014,665 / 31.39%
Number/percentage of G's	26,831,333 / 21.59%
Number/percentage of N's	20,311 / 0.02%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.3687

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

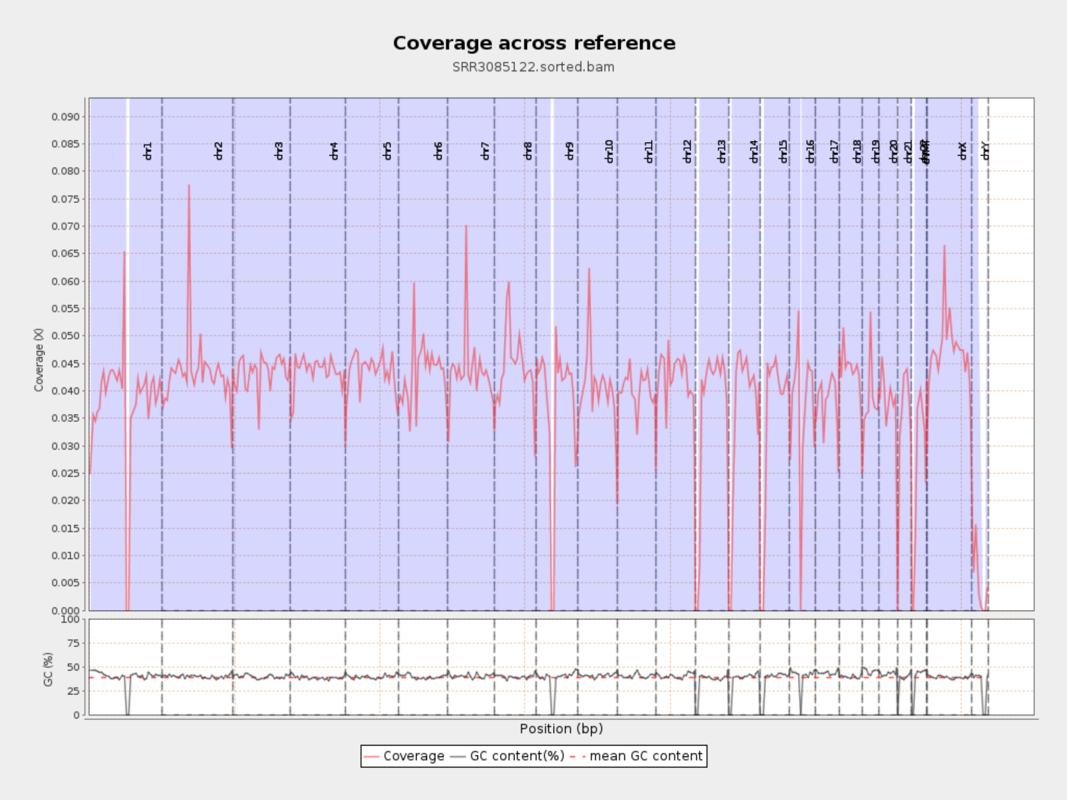
General error rate	0.89%
Mismatches	1,092,550
Insertions	10,083
Mapped reads with at least one insertion	0.55%
Deletions	28,909
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.13%

2.6. Chromosome stats

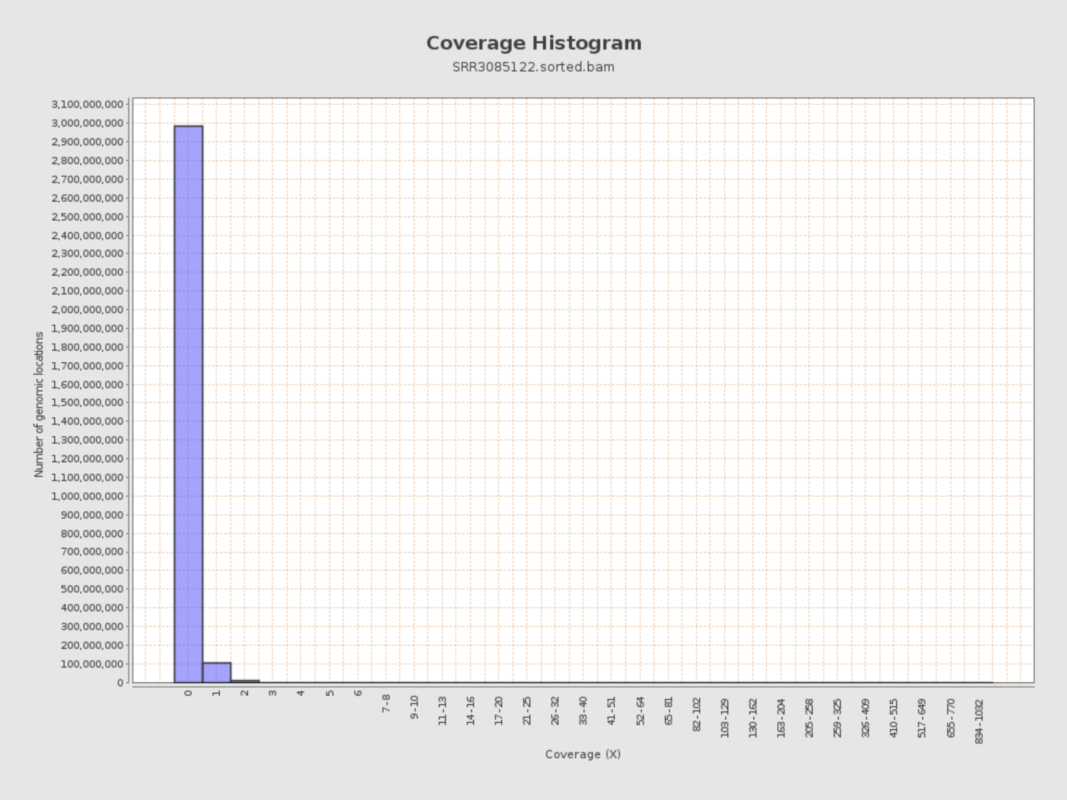
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9425061	0.0378	0.6413
chr2	243199373	10599938	0.0436	0.4233
chr3	198022430	8618245	0.0435	0.2248
chr4	191154276	8341666	0.0436	0.2339
chr5	180915260	7920101	0.0438	0.2271
chr6	171115067	7411651	0.0433	0.2789
chr7	159138663	7014840	0.0441	0.4814

chr8	146364022	6461005	0.0441	0.6545
chr9	141213431	5267180	0.0373	0.3376
chr10	135534747	5568909	0.0411	0.3207
chr11	135006516	5393861	0.04	0.2813
chr12	133851895	5692784	0.0425	0.2269
chr13	115169878	4121416	0.0358	0.2052
chr14	107349540	3831910	0.0357	0.2195
chr15	102531392	3546985	0.0346	0.2034
chr16	90354753	3346833	0.037	0.2336
chr17	81195210	3067106	0.0378	0.2258
chr18	78077248	3457929	0.0443	0.6044
chr19	59128983	2275167	0.0385	0.4893
chr20	63025520	2416957	0.0383	0.2201
chr21	48129895	1648483	0.0343	0.2128
chr22	51304566	1274127	0.0248	0.1688
chrMT	16571	700	0.0422	0.2011
chrX	155270560	7331078	0.0472	0.2651
chrY	59373566	306130	0.0052	0.1139

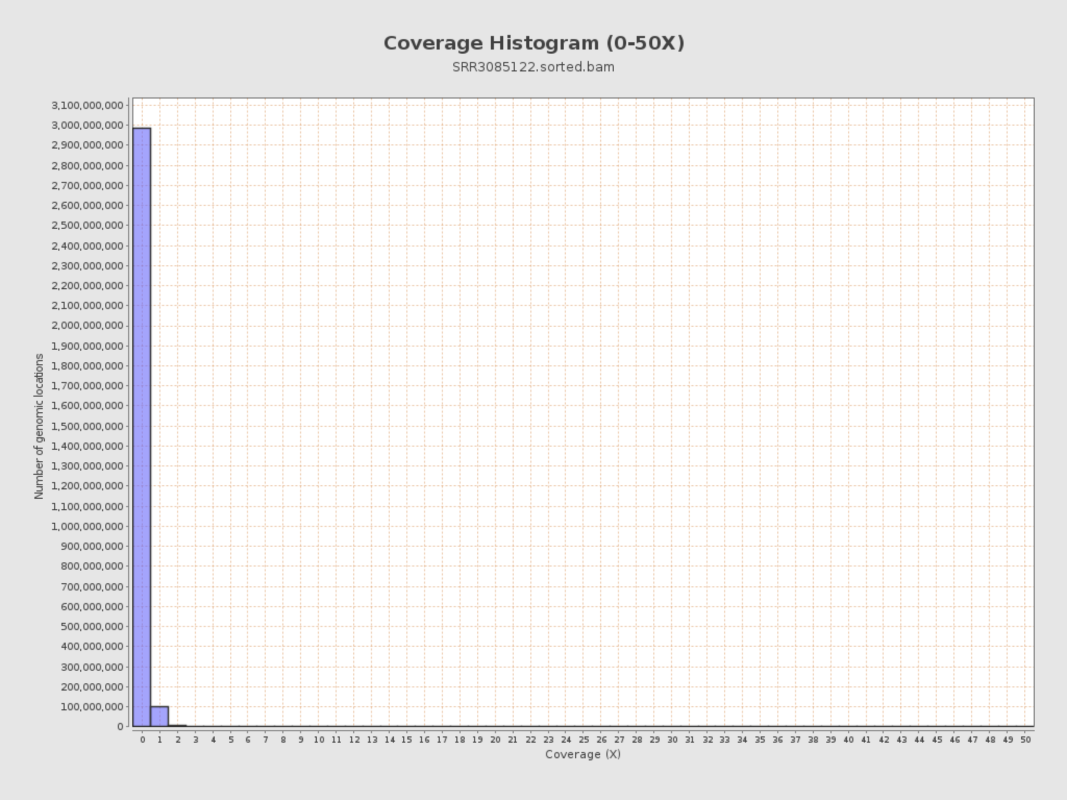
3. Results : Coverage across reference



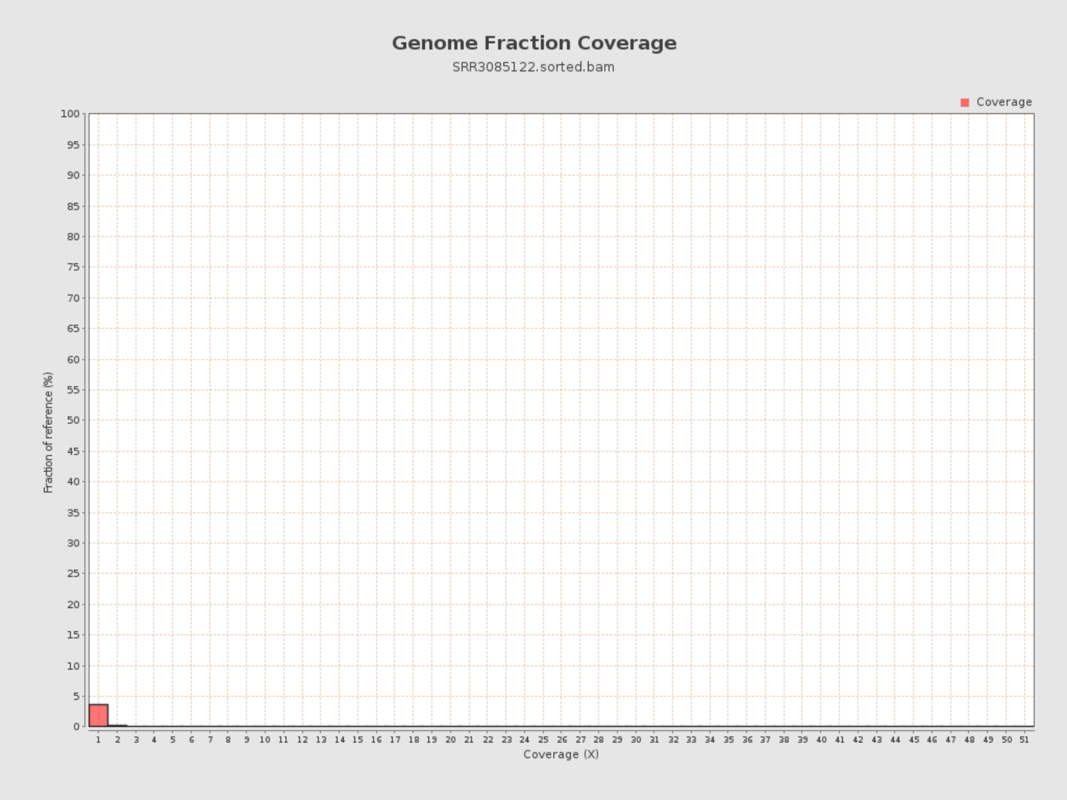
4. Results : Coverage Histogram



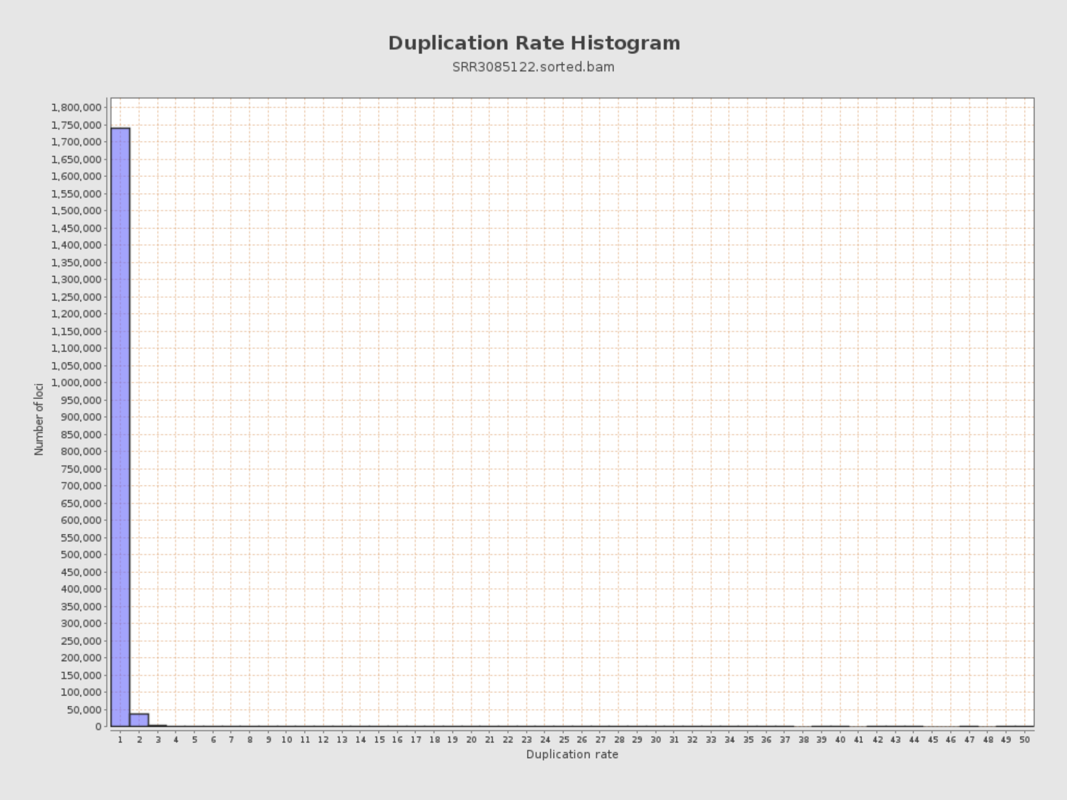
5. Results : Coverage Histogram (0-50X)



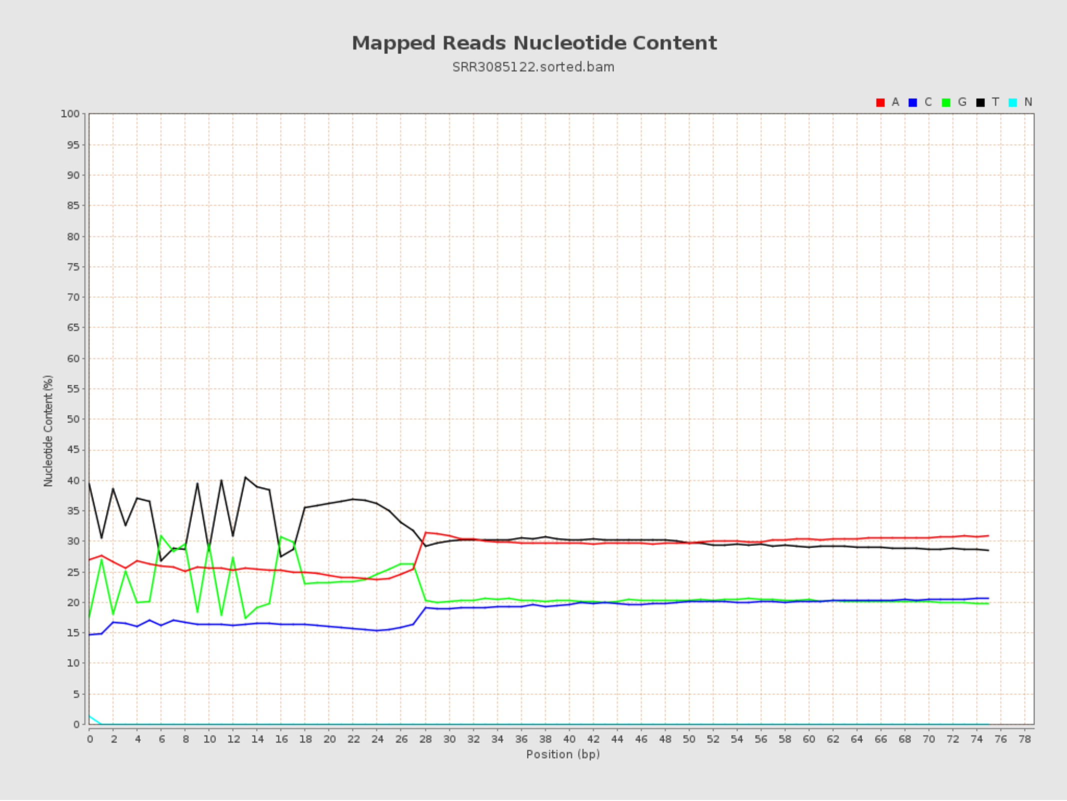
6. Results : Genome Fraction Coverage



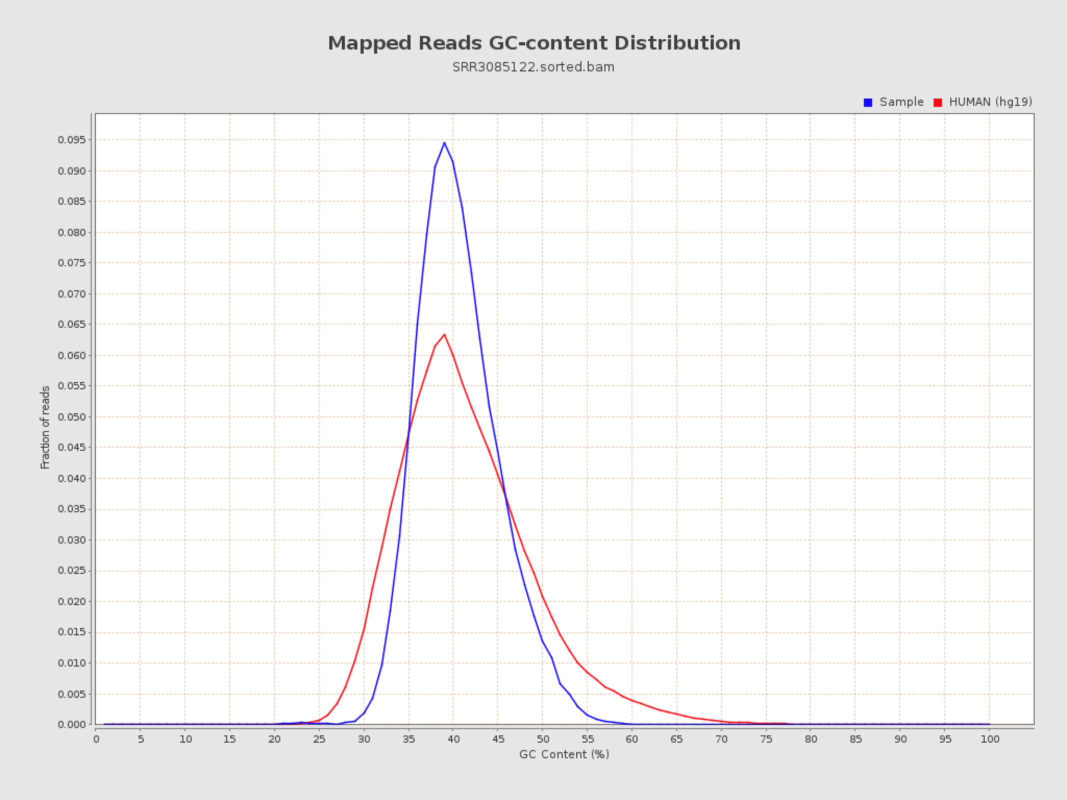
7. Results : Duplication Rate Histogram



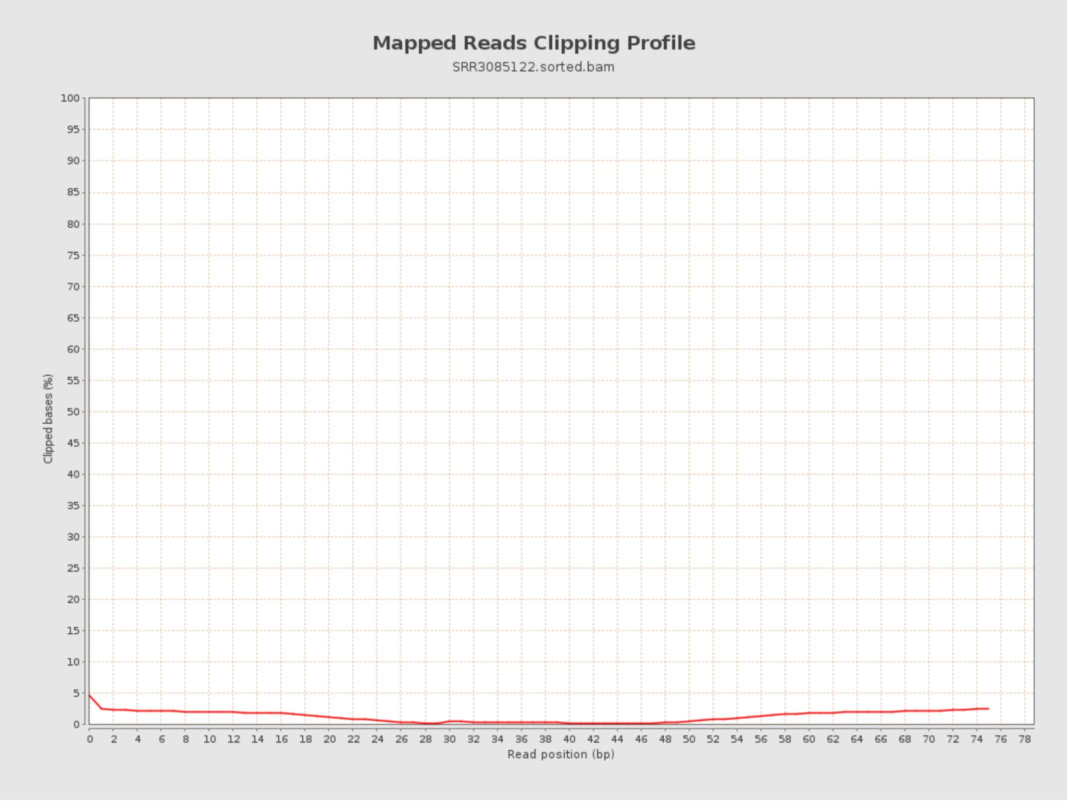
8. Results : Mapped Reads Nucleotide Content



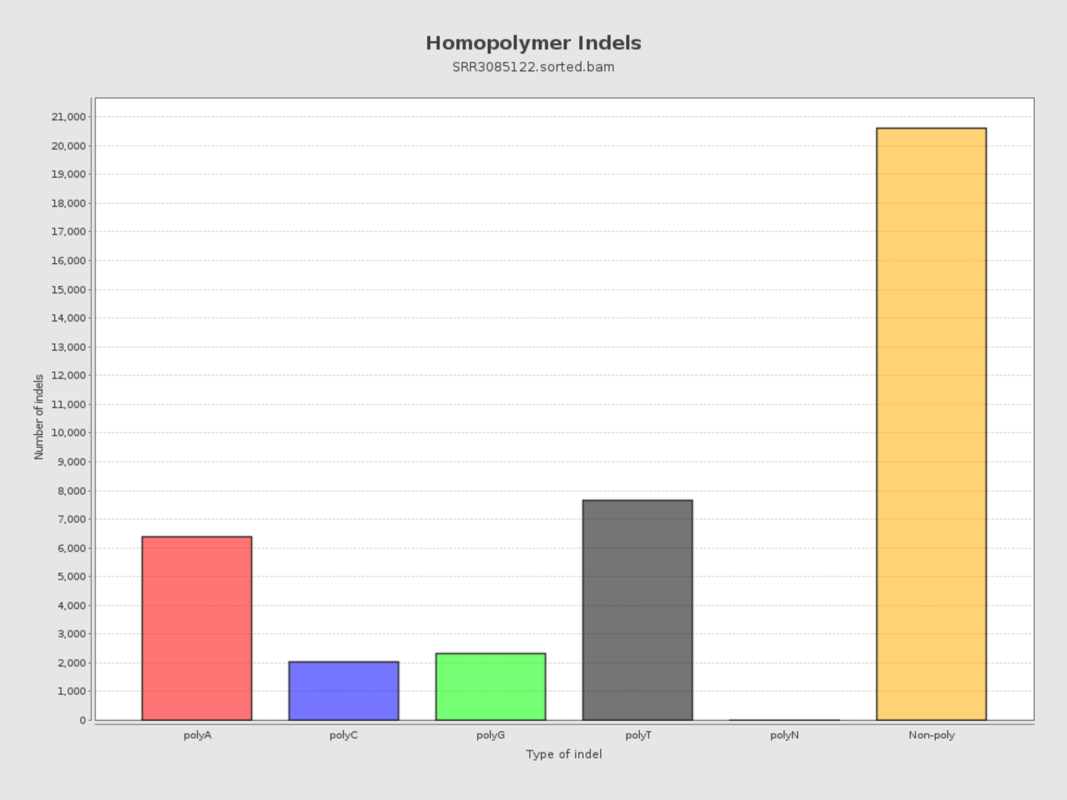
9. Results : Mapped Reads GC-content Distribution



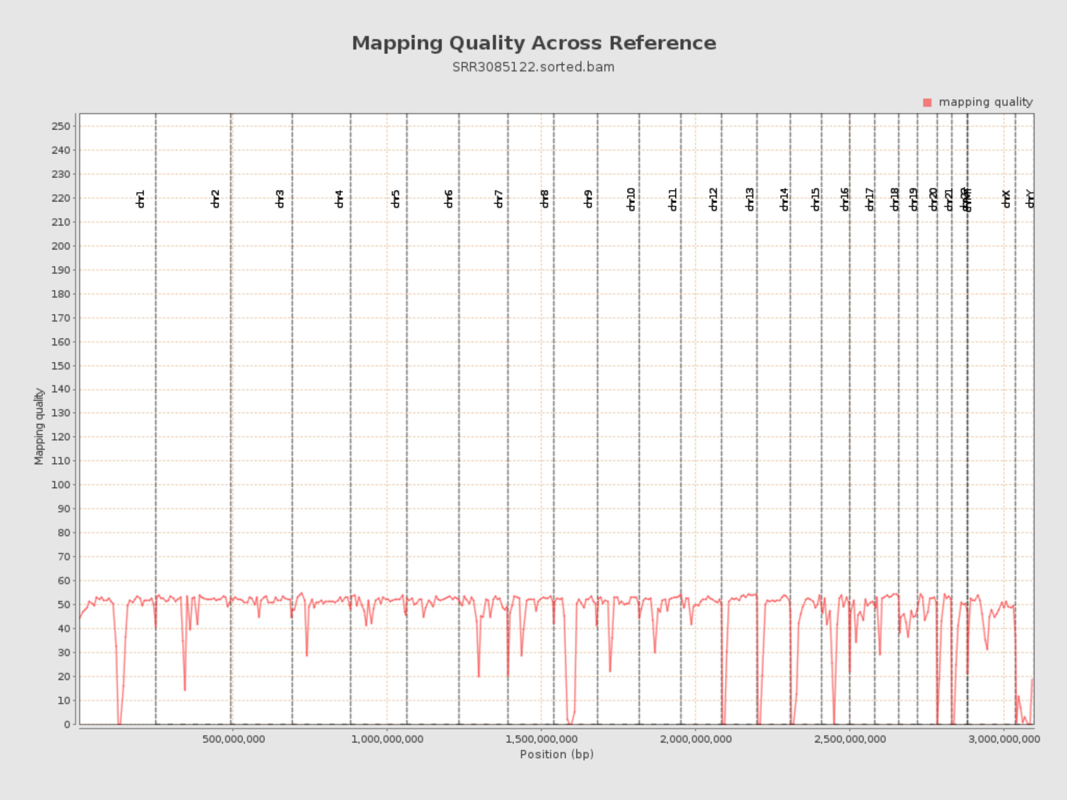
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram