Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:22:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085112.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_SRR3085112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:22:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,014,447
Mapped reads	1,663,736 / 82.59%
Unmapped reads	350,711 / 17.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,724 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	47,586 / 2.36%
Duplication rate	2.2%
Clipped reads	1,134,758 / 56.33%

2.2. ACGT Content

Number/percentage of A's	29,727,941 / 29.4%
Number/percentage of C's	19,844,940 / 19.63%
Number/percentage of T's	28,903,354 / 28.59%
Number/percentage of G's	22,624,712 / 22.38%
Number/percentage of N's	2,089 / 0%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.2866

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Mismatches and indels

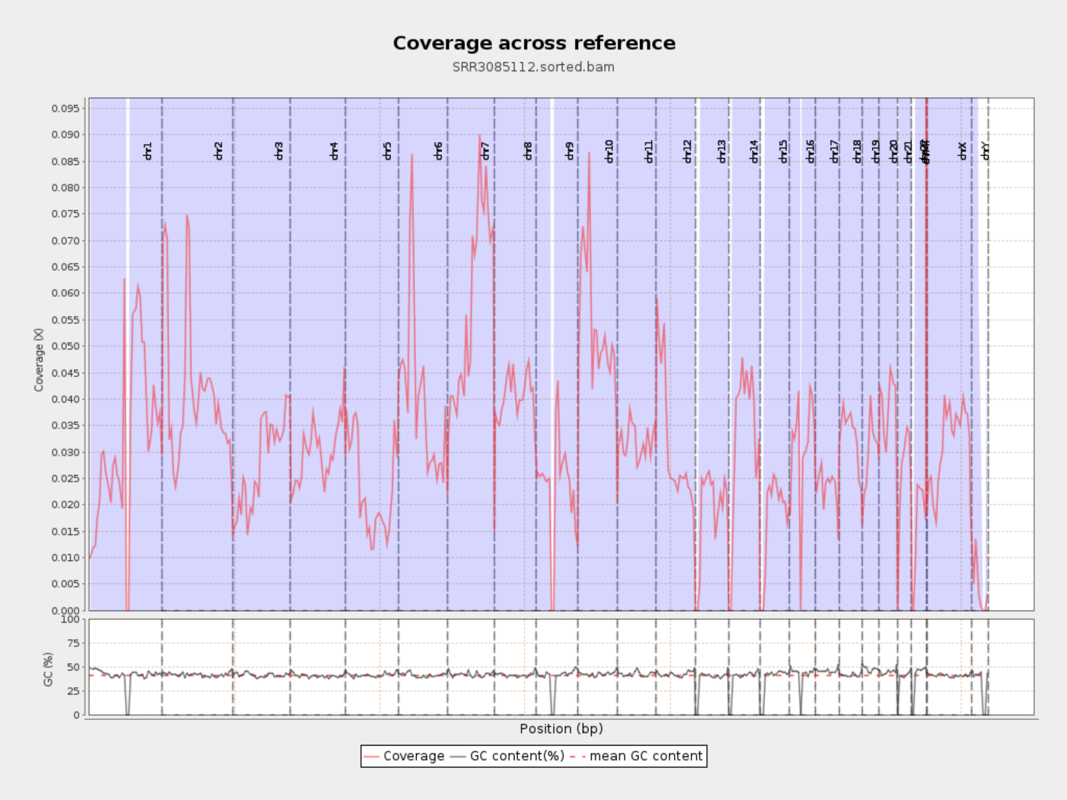
General error rate	0.89%
Mismatches	884,925
Insertions	7,698
Mapped reads with at least one insertion	0.46%
Deletions	20,879
Mapped reads with at least one deletion	1.24%
Homopolymer indels	44.15%

2.6. Chromosome stats

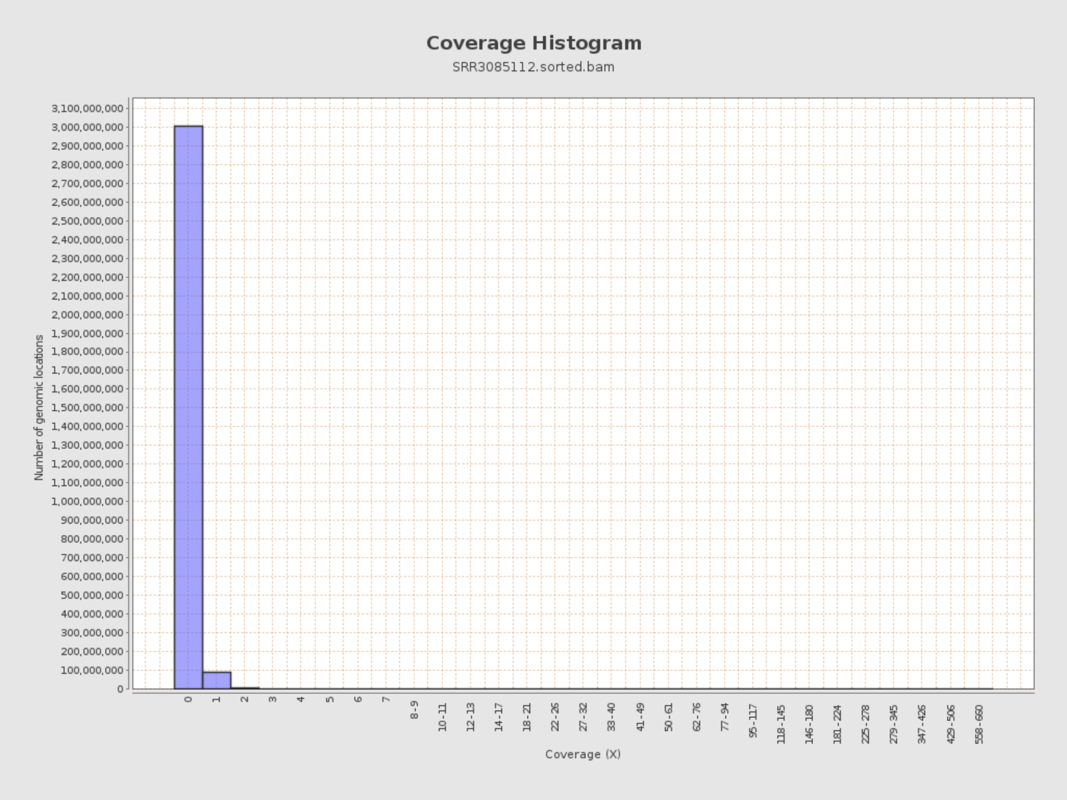
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7972937	0.032	0.4785
chr2	243199373	10173437	0.0418	0.3275
chr3	198022430	5535057	0.028	0.1848
chr4	191154276	5737491	0.03	0.1903
chr5	180915260	4154626	0.023	0.163
chr6	171115067	6890670	0.0403	0.2453
chr7	159138663	9317222	0.0585	0.3295

chr8	146364022	5963412	0.0407	0.4389
chr9	141213431	3313119	0.0235	0.2392
chr10	135534747	7427159	0.0548	0.4213
chr11	135006516	4278971	0.0317	0.2752
chr12	133851895	4180324	0.0312	0.1924
chr13	115169878	2151383	0.0187	0.1442
chr14	107349540	3546671	0.033	0.2034
chr15	102531392	1810948	0.0177	0.1412
chr16	90354753	2824898	0.0313	0.2043
chr17	81195210	1882080	0.0232	0.1879
chr18	78077248	2614710	0.0335	0.4314
chr19	59128983	1772560	0.03	0.33
chr20	63025520	2431902	0.0386	0.2112
chr21	48129895	1240446	0.0258	0.1824
chr22	51304566	791333	0.0154	0.1317
chrMT	16571	7787	0.4699	0.8086
chrX	155270560	4869519	0.0314	0.2103
chrY	59373566	247675	0.0042	0.0898

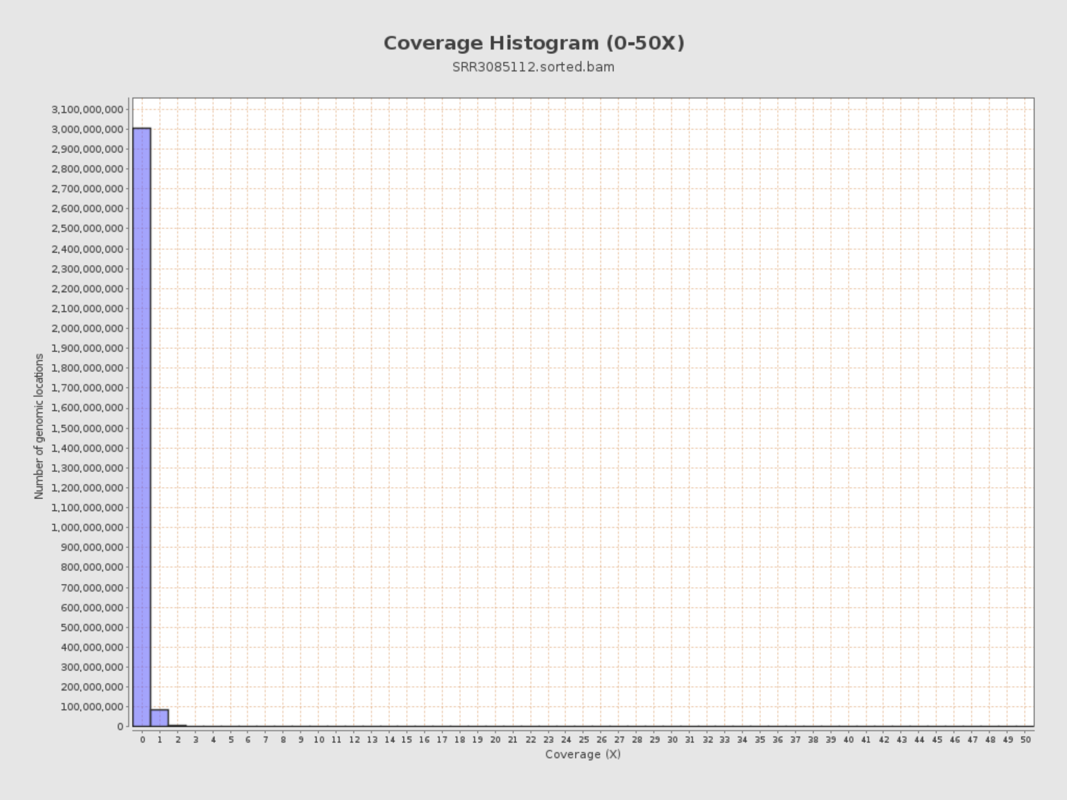
3. Results : Coverage across reference



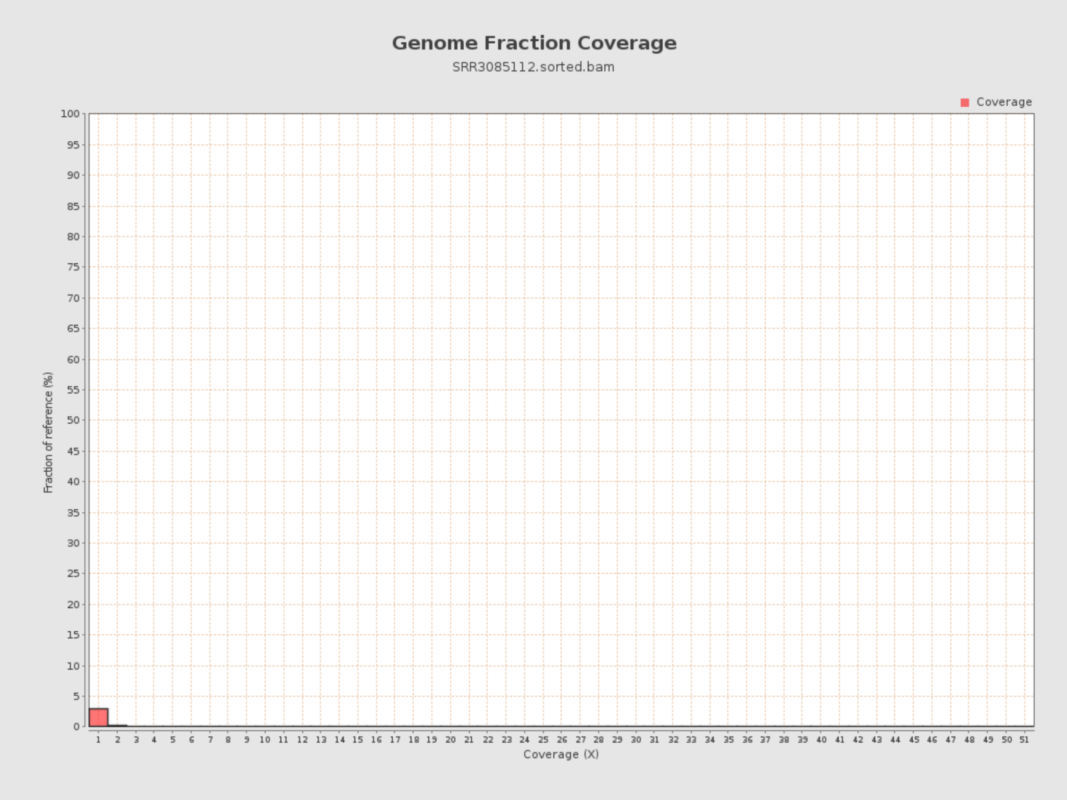
4. Results : Coverage Histogram



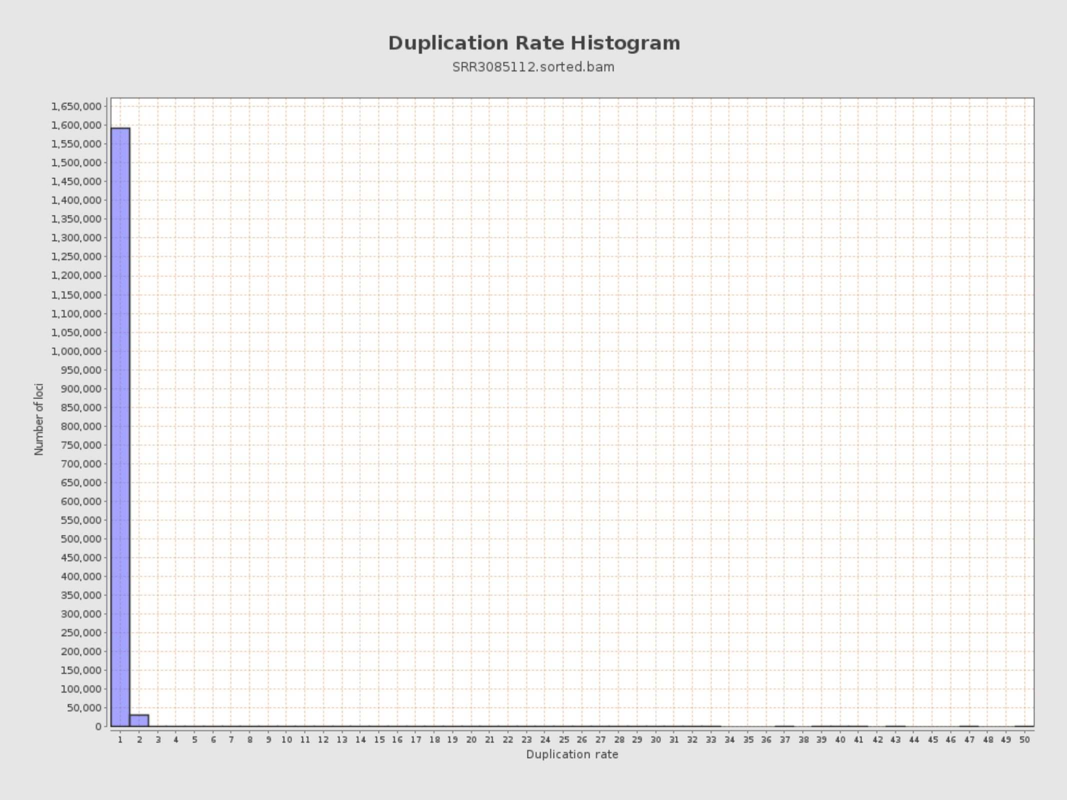
5. Results : Coverage Histogram (0-50X)



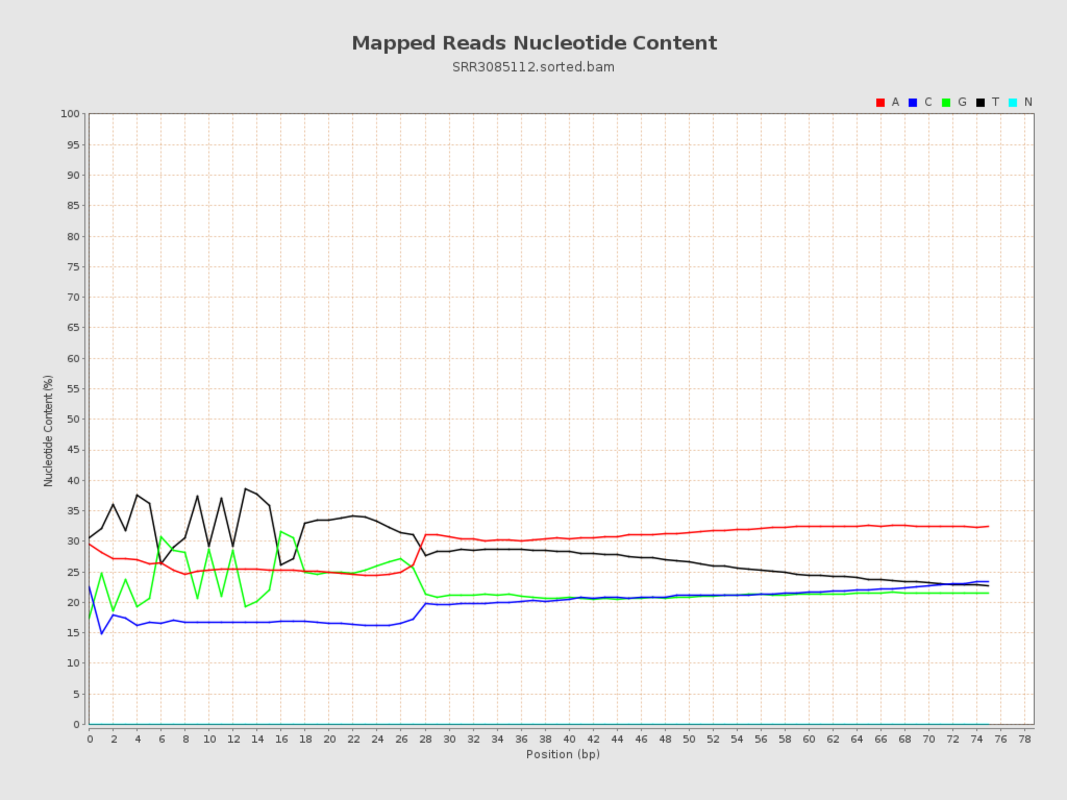
6. Results : Genome Fraction Coverage



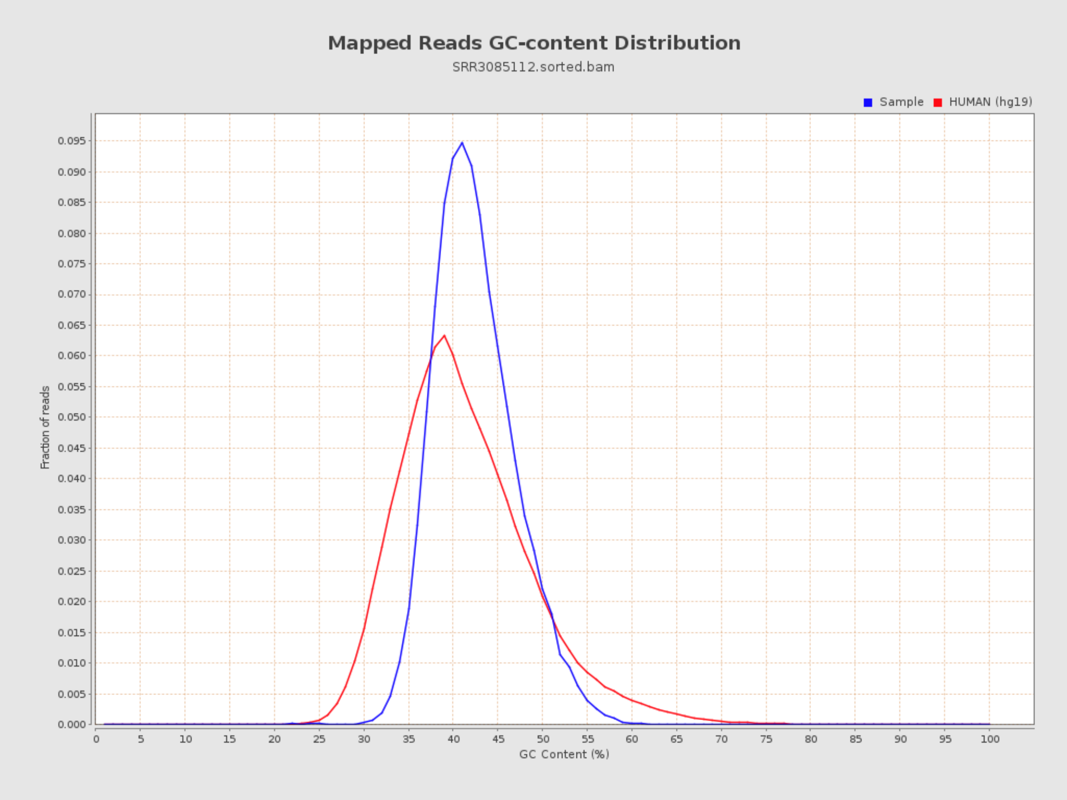
7. Results : Duplication Rate Histogram



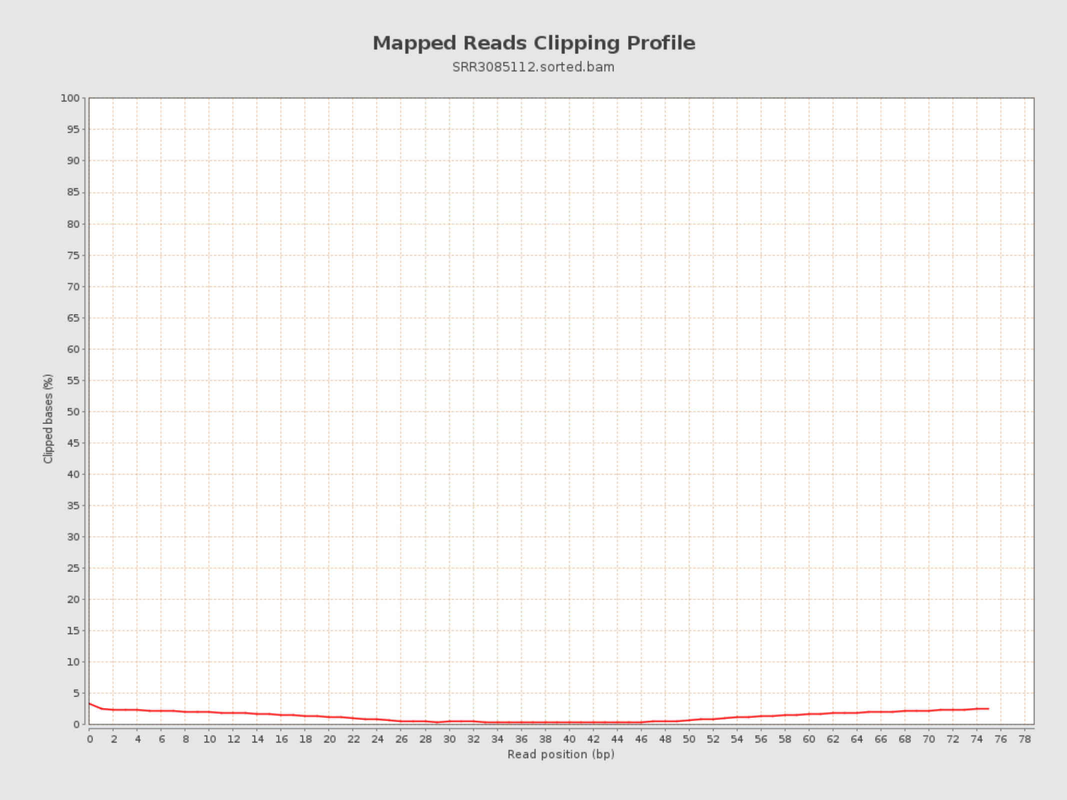
8. Results : Mapped Reads Nucleotide Content



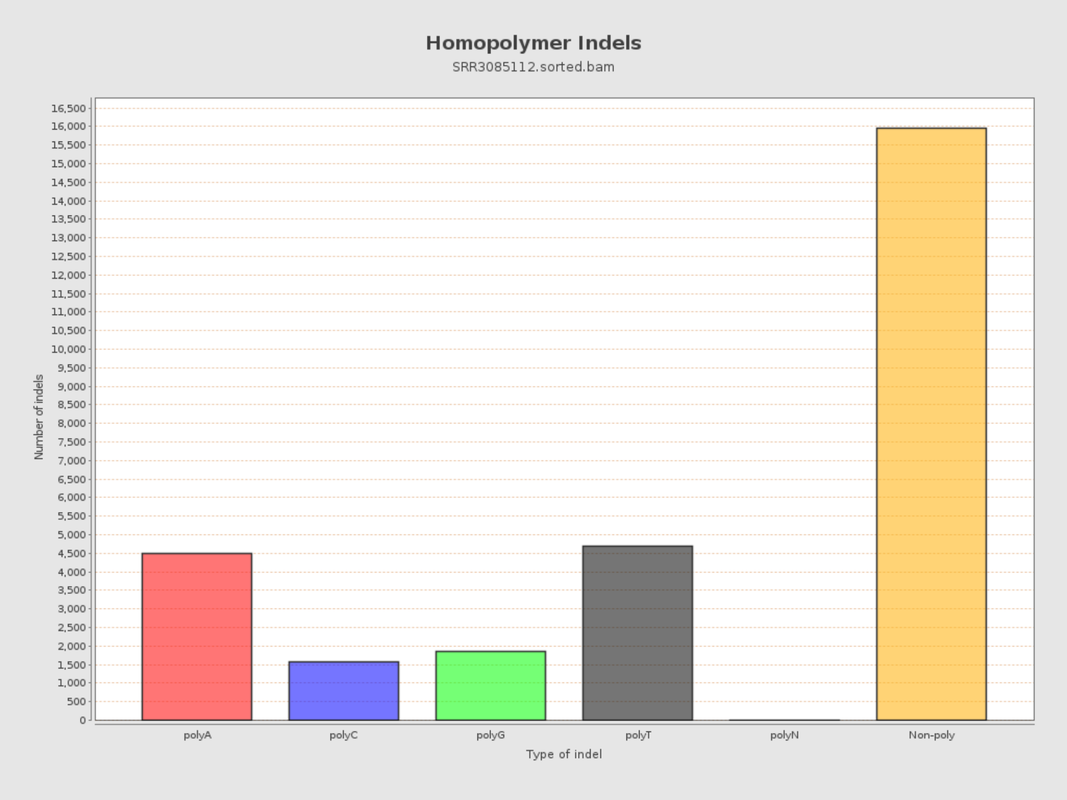
9. Results : Mapped Reads GC-content Distribution



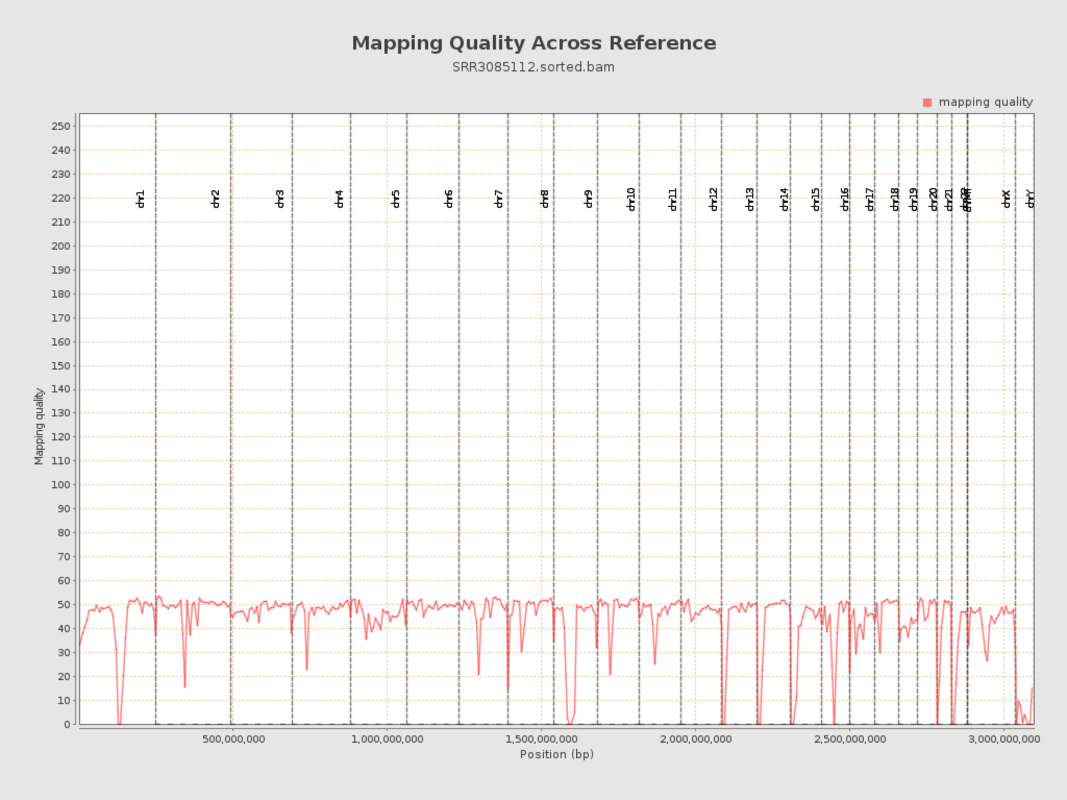
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram