Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:07:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085142.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_SRR3085142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:07:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,348,751
Mapped reads	2,111,417 / 89.9%
Unmapped reads	237,334 / 10.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,364 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	76,538 / 3.26%
Duplication rate	2.81%
Clipped reads	942,510 / 40.13%

2.2. ACGT Content

Number/percentage of A's	39,363,229 / 27.84%
Number/percentage of C's	26,417,535 / 18.68%
Number/percentage of T's	44,042,460 / 31.15%
Number/percentage of G's	31,548,643 / 22.31%
Number/percentage of N's	30,008 / 0.02%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.3722

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

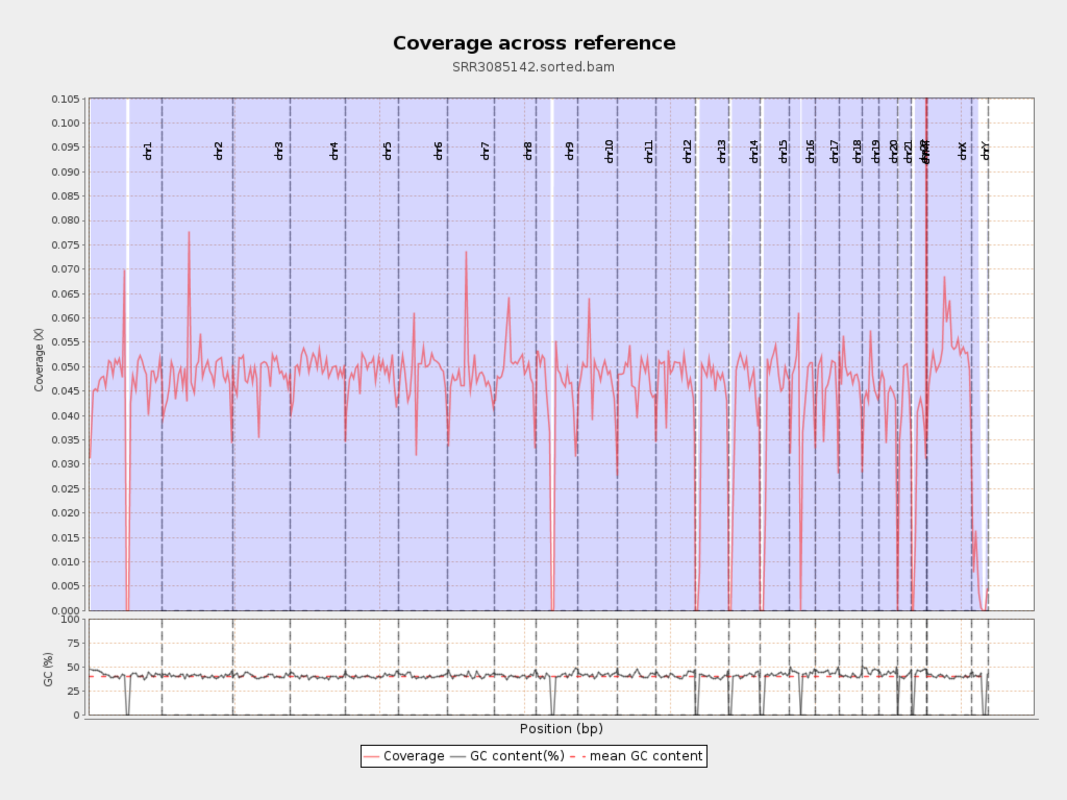
General error rate	0.89%
Mismatches	1,242,877
Insertions	11,144
Mapped reads with at least one insertion	0.52%
Deletions	31,900
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.05%

2.6. Chromosome stats

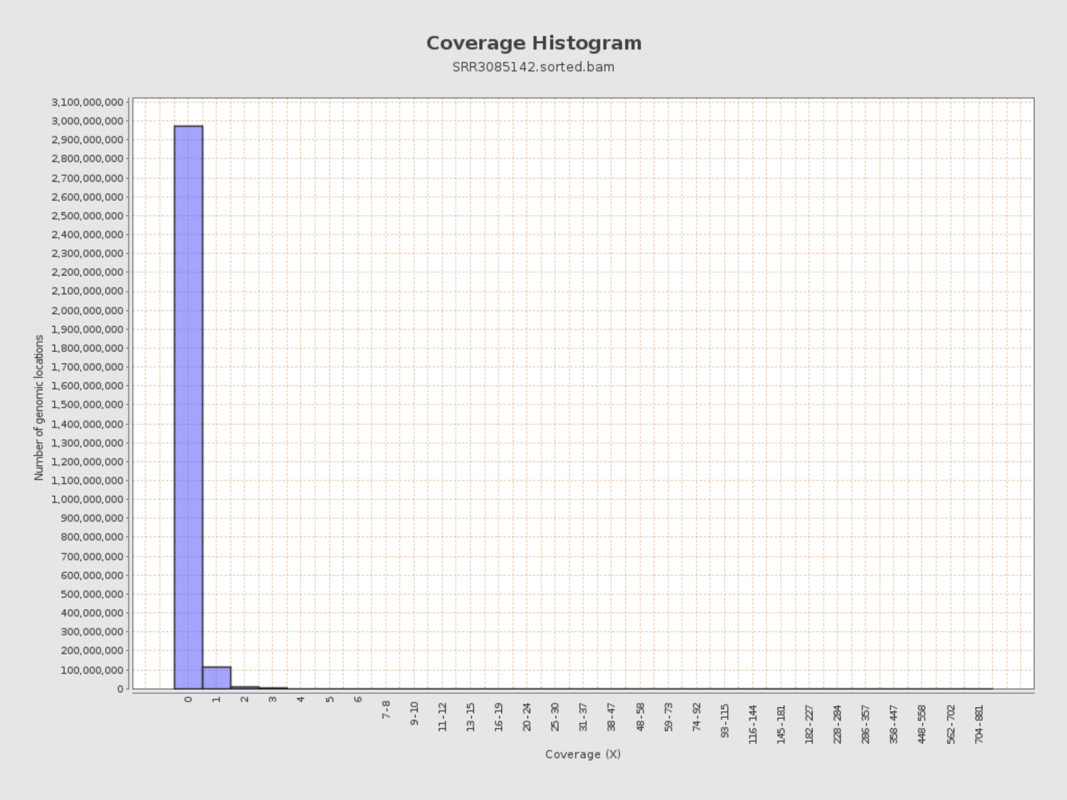
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11314396	0.0454	0.6266
chr2	243199373	11833343	0.0487	0.4563
chr3	198022430	9619737	0.0486	0.2427
chr4	191154276	9506451	0.0497	0.2541
chr5	180915260	8805472	0.0487	0.2446
chr6	171115067	8381880	0.049	0.2898
chr7	159138663	7681753	0.0483	0.4775

chr8	146364022	7276401	0.0497	0.5866
chr9	141213431	5898645	0.0418	0.3438
chr10	135534747	6573886	0.0485	0.3285
chr11	135006516	6405693	0.0474	0.3124
chr12	133851895	6448600	0.0482	0.2447
chr13	115169878	4594103	0.0399	0.2235
chr14	107349540	4303544	0.0401	0.2325
chr15	102531392	4121988	0.0402	0.2275
chr16	90354753	3903927	0.0432	0.2543
chr17	81195210	3687325	0.0454	0.2547
chr18	78077248	3794564	0.0486	0.6094
chr19	59128983	2692843	0.0455	0.4857
chr20	63025520	2728424	0.0433	0.2353
chr21	48129895	1883319	0.0391	0.2301
chr22	51304566	1427707	0.0278	0.1827
chrMT	16571	5943	0.3586	0.6771
chrX	155270560	8219420	0.0529	0.2807
chrY	59373566	344248	0.0058	0.1194

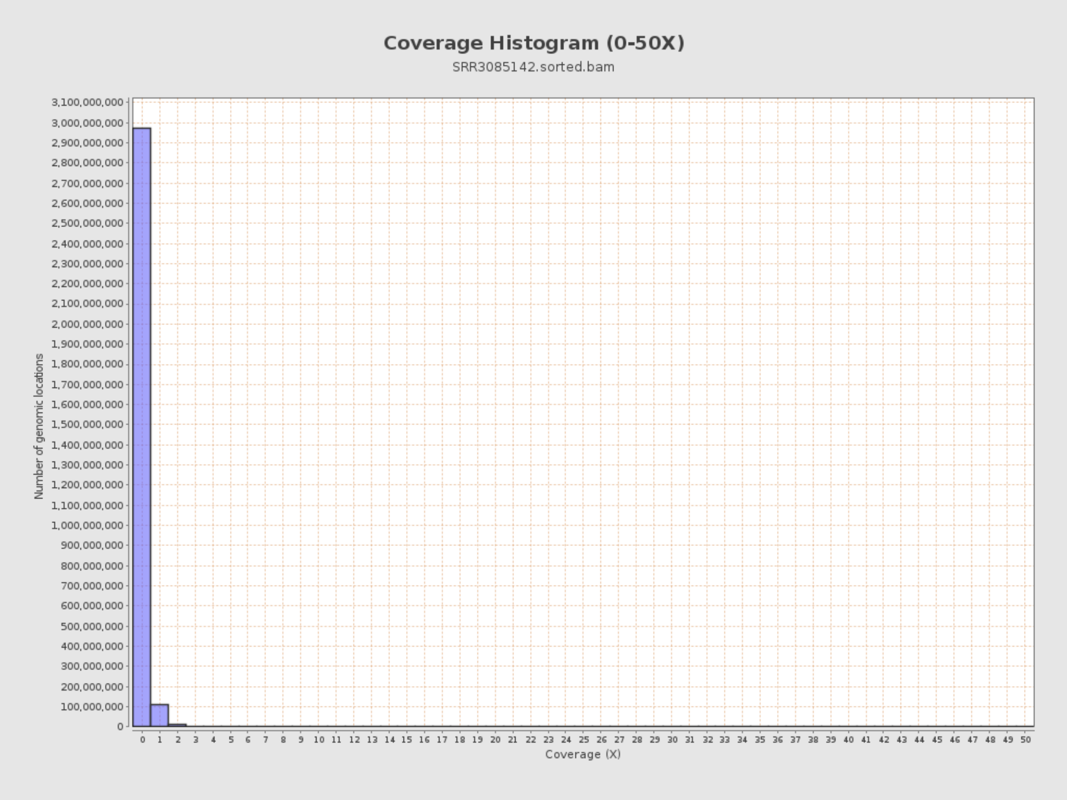
3. Results : Coverage across reference



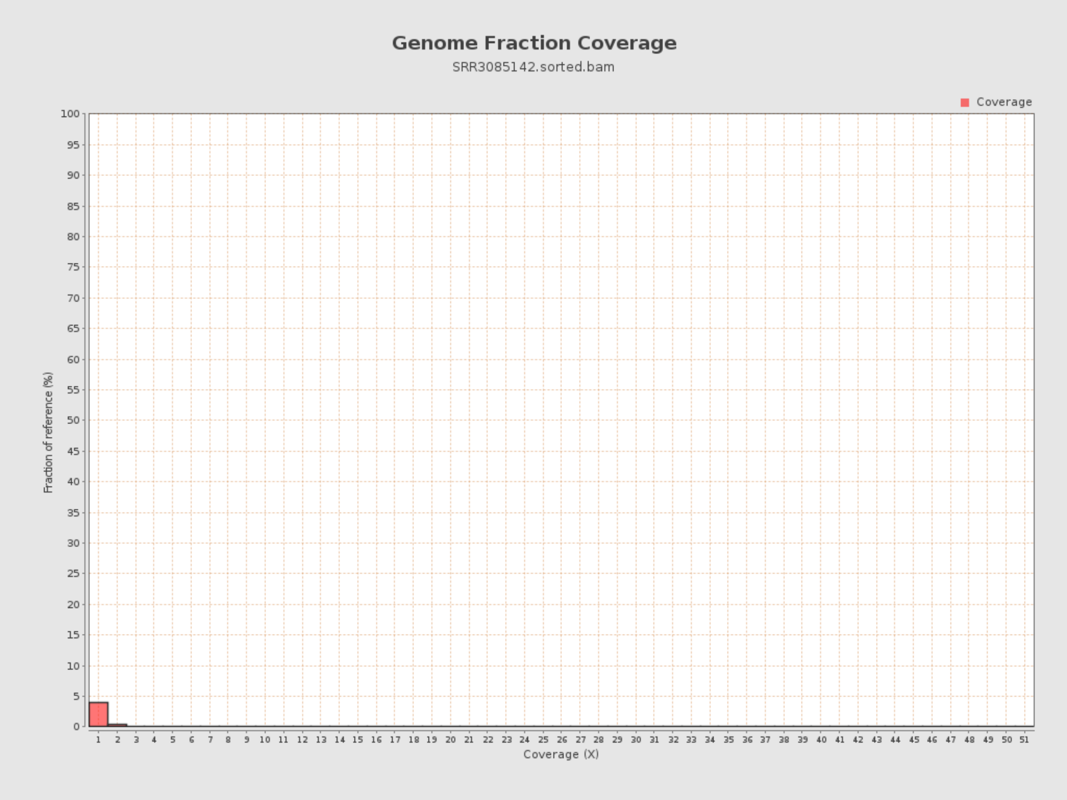
4. Results : Coverage Histogram



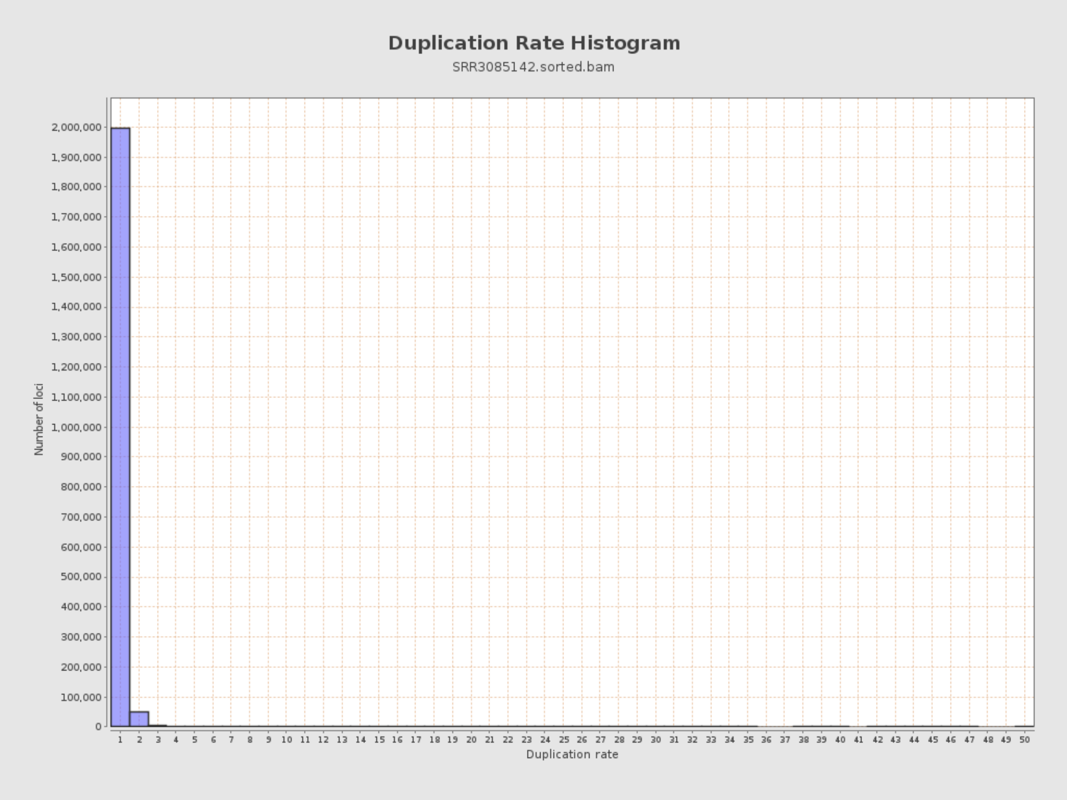
5. Results : Coverage Histogram (0-50X)



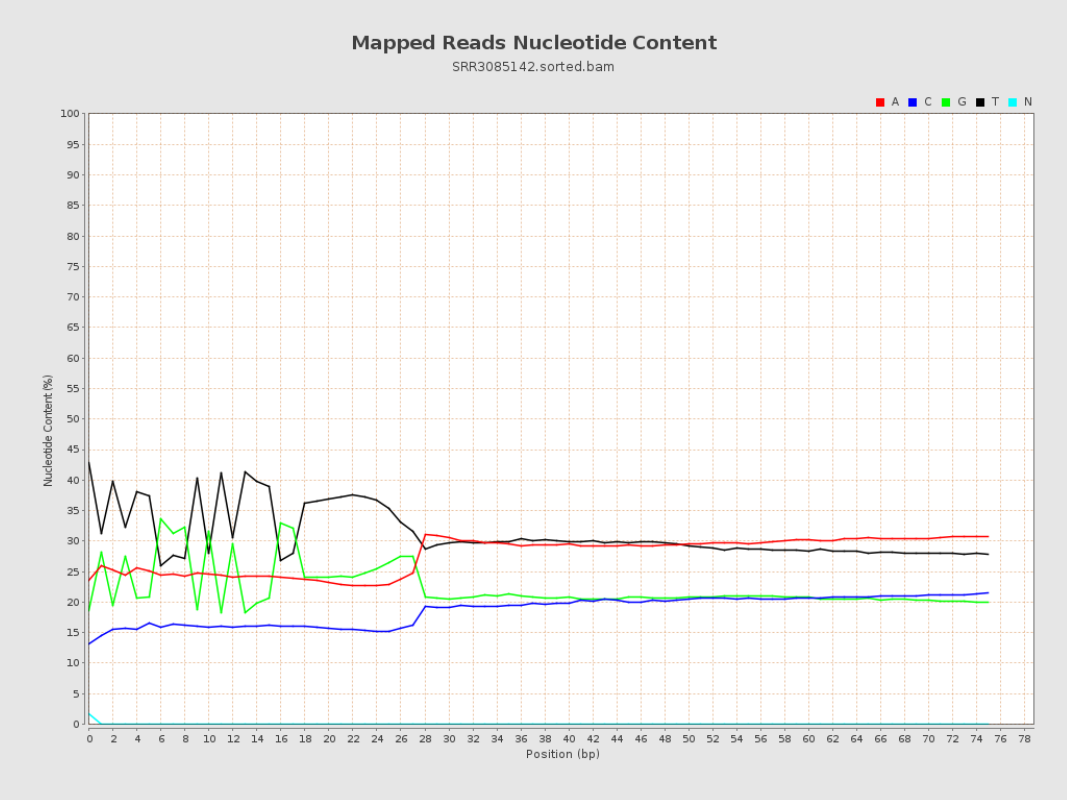
6. Results : Genome Fraction Coverage



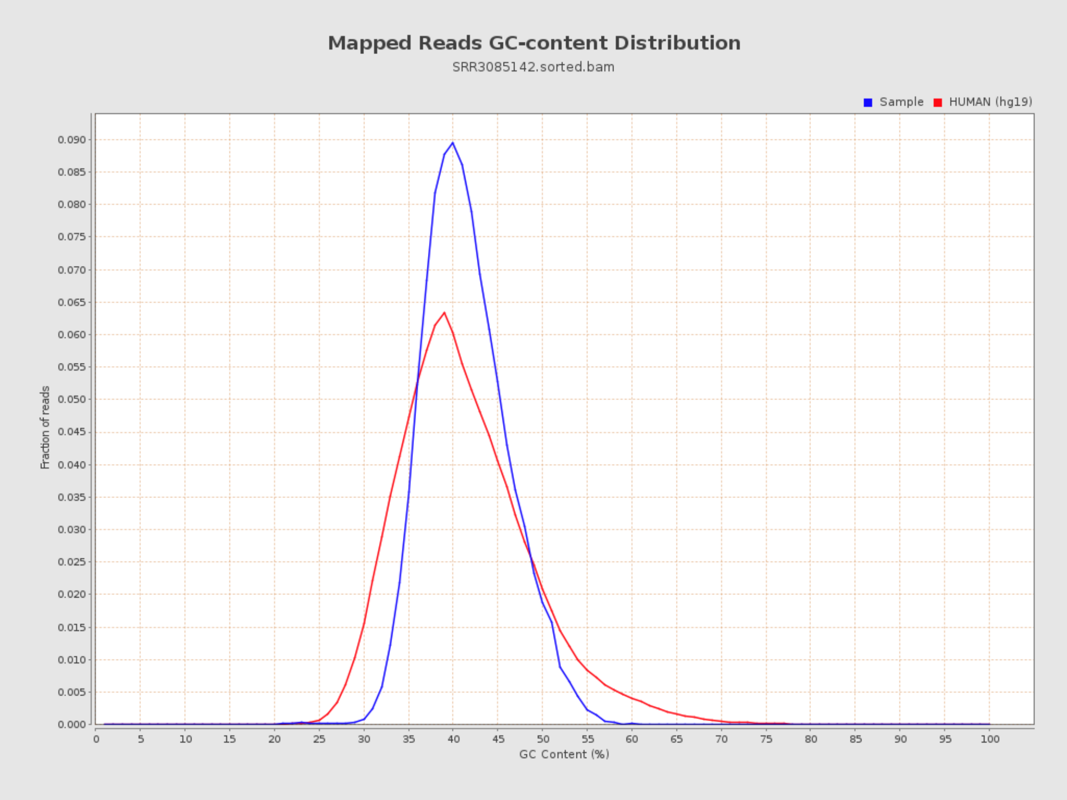
7. Results : Duplication Rate Histogram



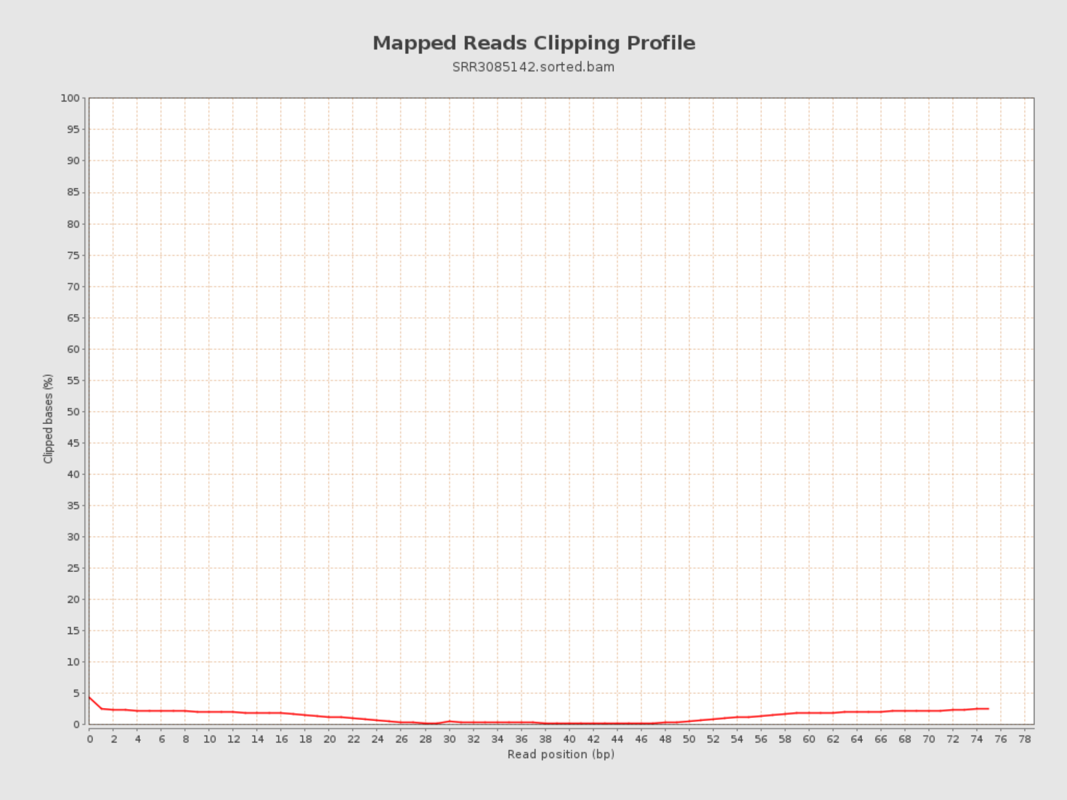
8. Results : Mapped Reads Nucleotide Content



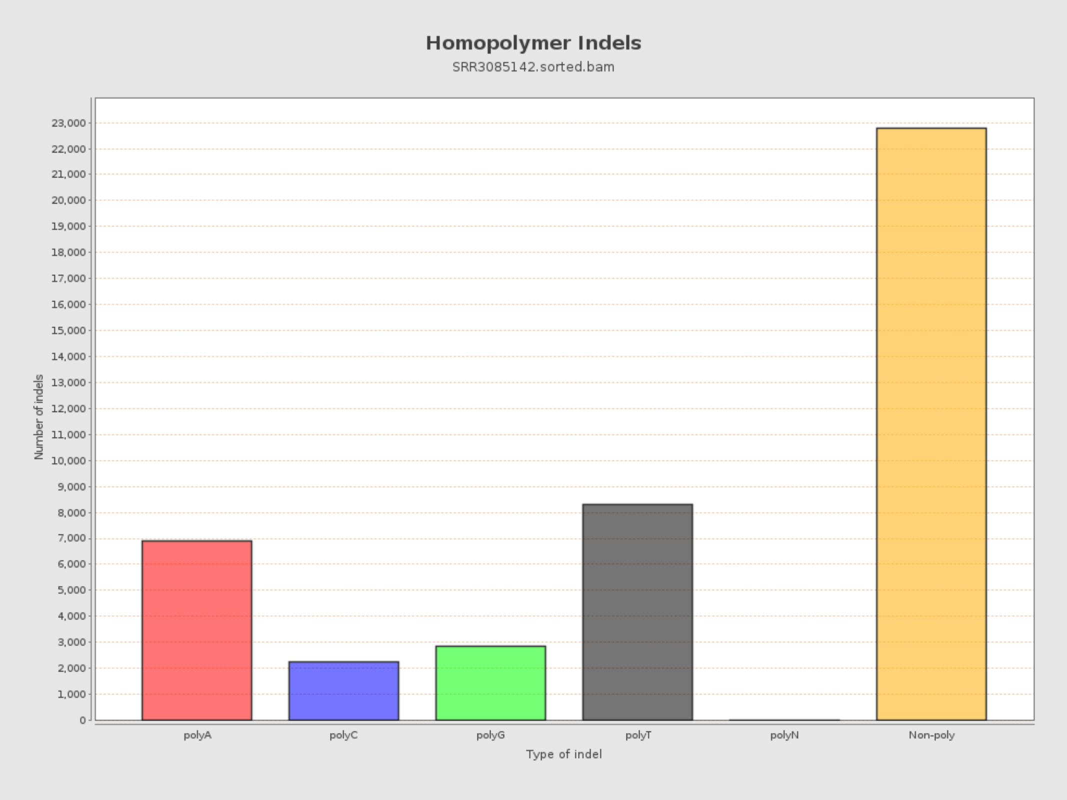
9. Results : Mapped Reads GC-content Distribution



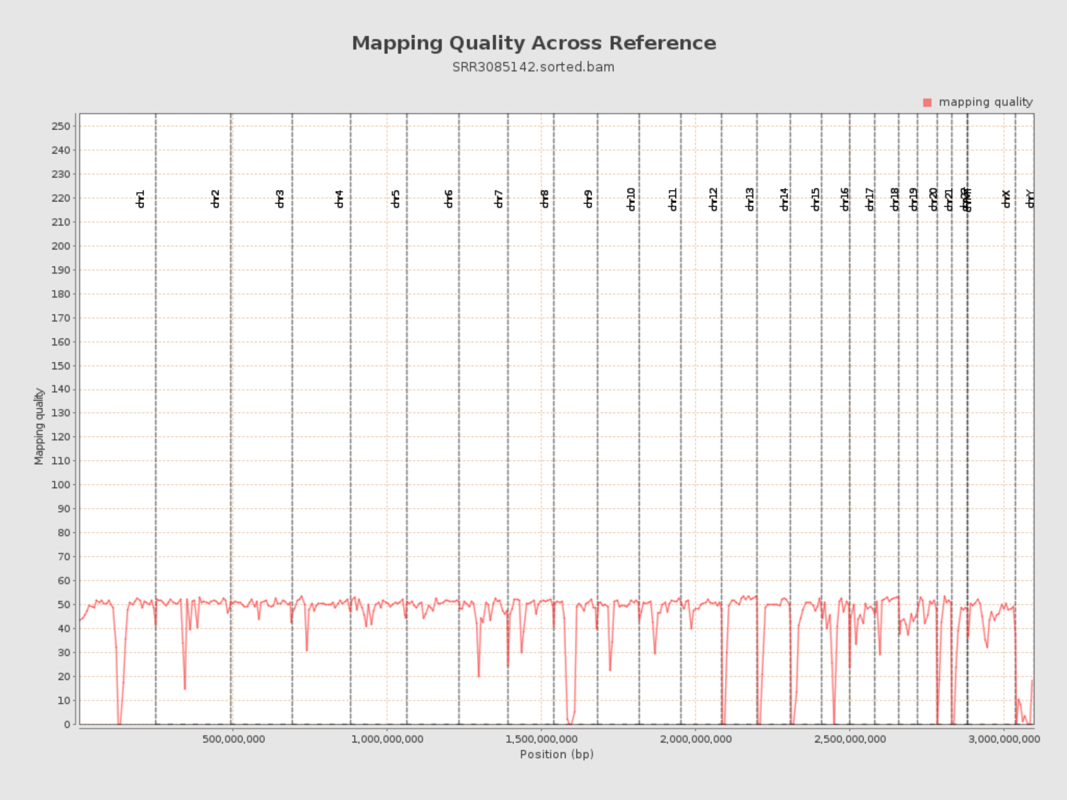
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram