Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:53:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085102.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_SRR3085102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:53:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,859,036
Mapped reads	2,624,789 / 91.81%
Unmapped reads	234,247 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,650 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	115,419 / 4.04%
Duplication rate	3.41%
Clipped reads	1,156,863 / 40.46%

2.2. ACGT Content

Number/percentage of A's	49,329,729 / 28.05%
Number/percentage of C's	33,085,809 / 18.81%
Number/percentage of T's	54,666,631 / 31.08%
Number/percentage of G's	38,778,368 / 22.05%
Number/percentage of N's	24,545 / 0.01%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0568

Standard Deviation	0.4558

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

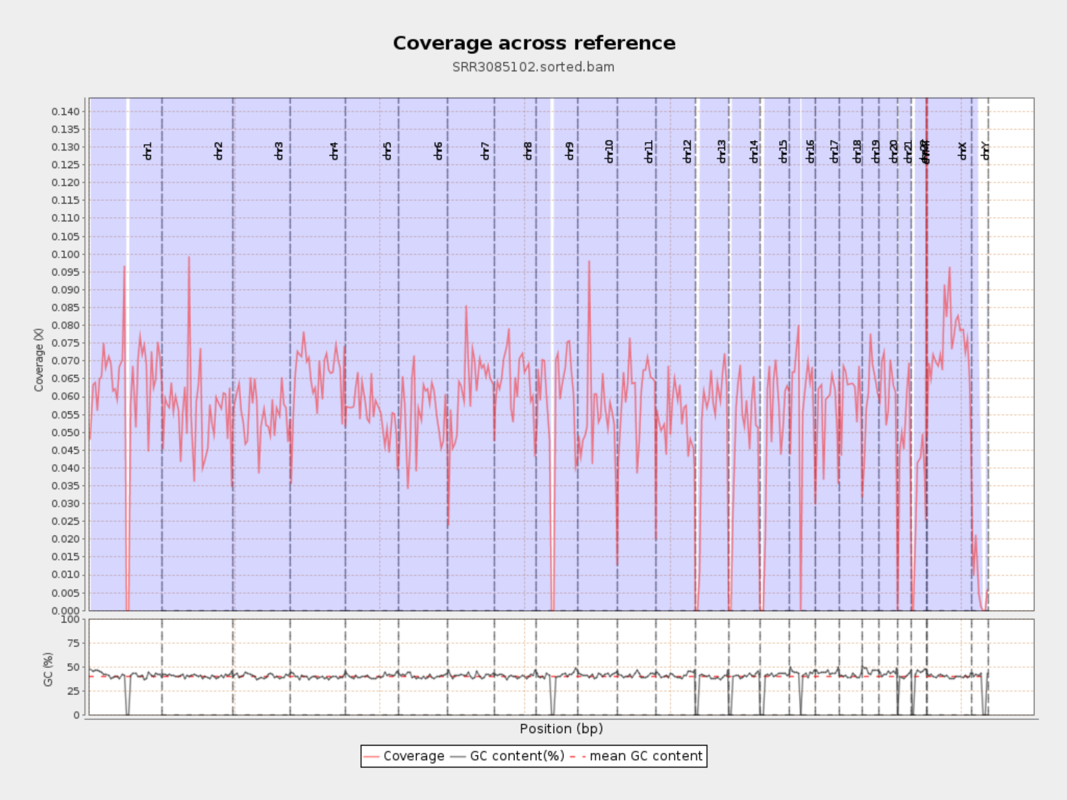
General error rate	0.82%
Mismatches	1,419,433
Insertions	13,911
Mapped reads with at least one insertion	0.53%
Deletions	39,924
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.74%

2.6. Chromosome stats

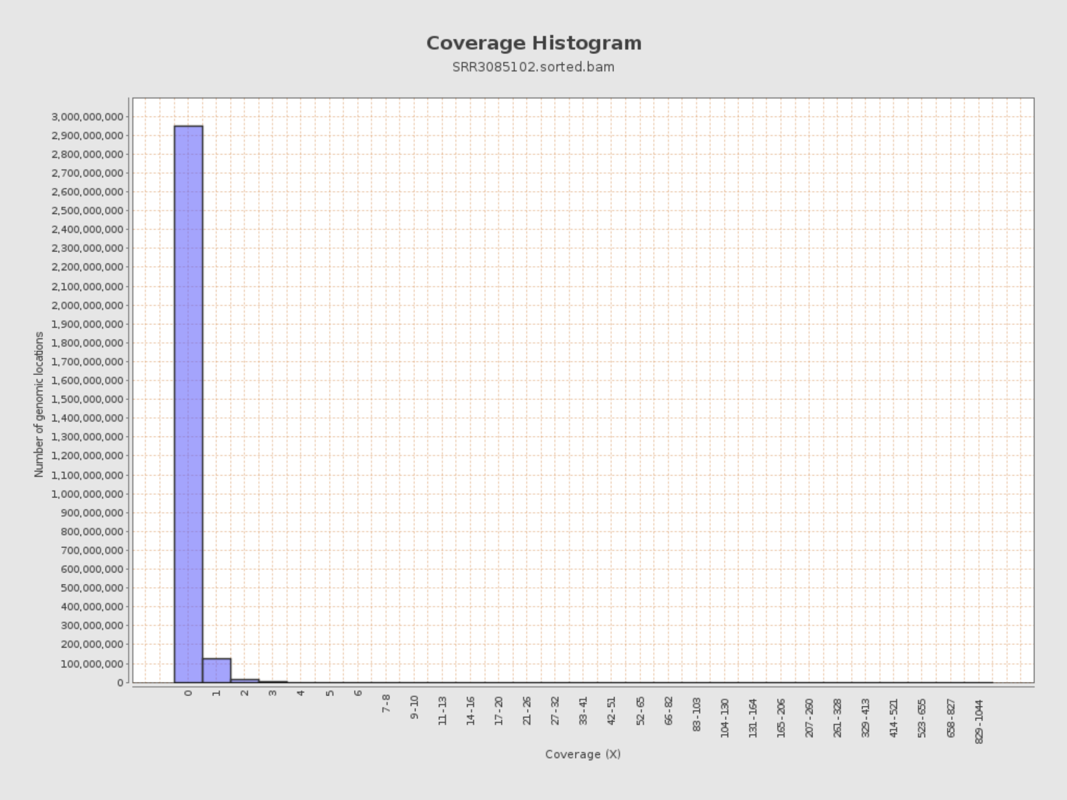
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15547248	0.0624	0.823
chr2	243199373	13607287	0.056	0.5475
chr3	198022430	10916138	0.0551	0.277
chr4	191154276	12633910	0.0661	0.3056
chr5	180915260	10076403	0.0557	0.272
chr6	171115067	9432997	0.0551	0.3429
chr7	159138663	9937726	0.0624	0.4282

chr8	146364022	9386370	0.0641	0.7097
chr9	141213431	8045106	0.057	0.4231
chr10	135534747	7459820	0.055	0.5119
chr11	135006516	8097552	0.06	0.398
chr12	133851895	7232634	0.054	0.2719
chr13	115169878	5844939	0.0508	0.2582
chr14	107349540	5103470	0.0475	0.2723
chr15	102531392	4906389	0.0479	0.2534
chr16	90354753	5298788	0.0586	0.3186
chr17	81195210	4469419	0.055	0.3093
chr18	78077248	4790136	0.0614	0.7776
chr19	59128983	3564063	0.0603	0.6074
chr20	63025520	3892289	0.0618	0.2922
chr21	48129895	2191817	0.0455	0.2646
chr22	51304566	1533534	0.0299	0.1966
chrMT	16571	4237	0.2557	0.5243
chrX	155270560	11554768	0.0744	0.3539
chrY	59373566	422632	0.0071	0.1399

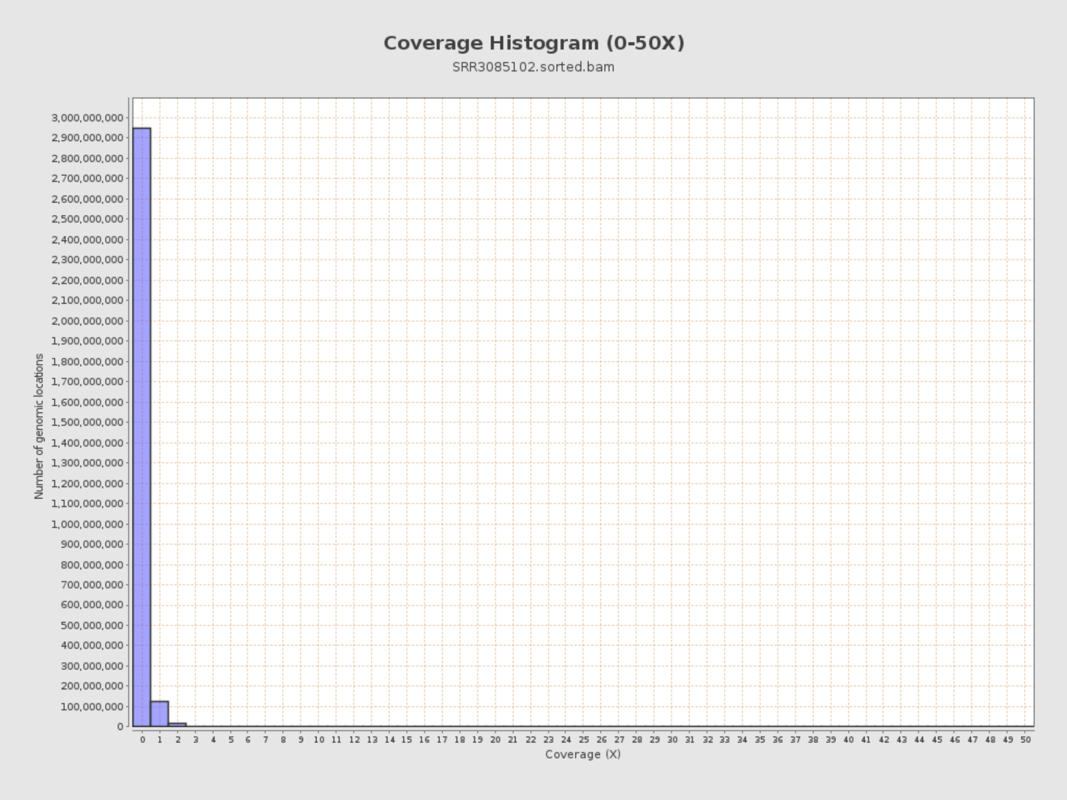
3. Results : Coverage across reference



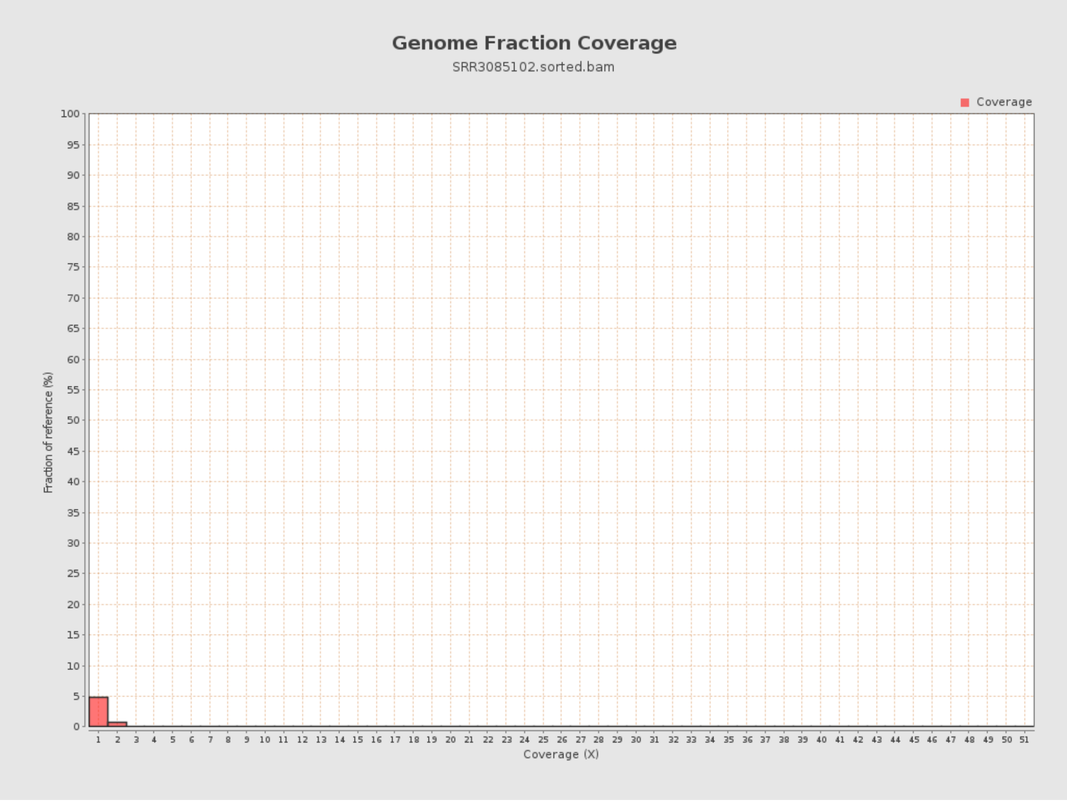
4. Results : Coverage Histogram



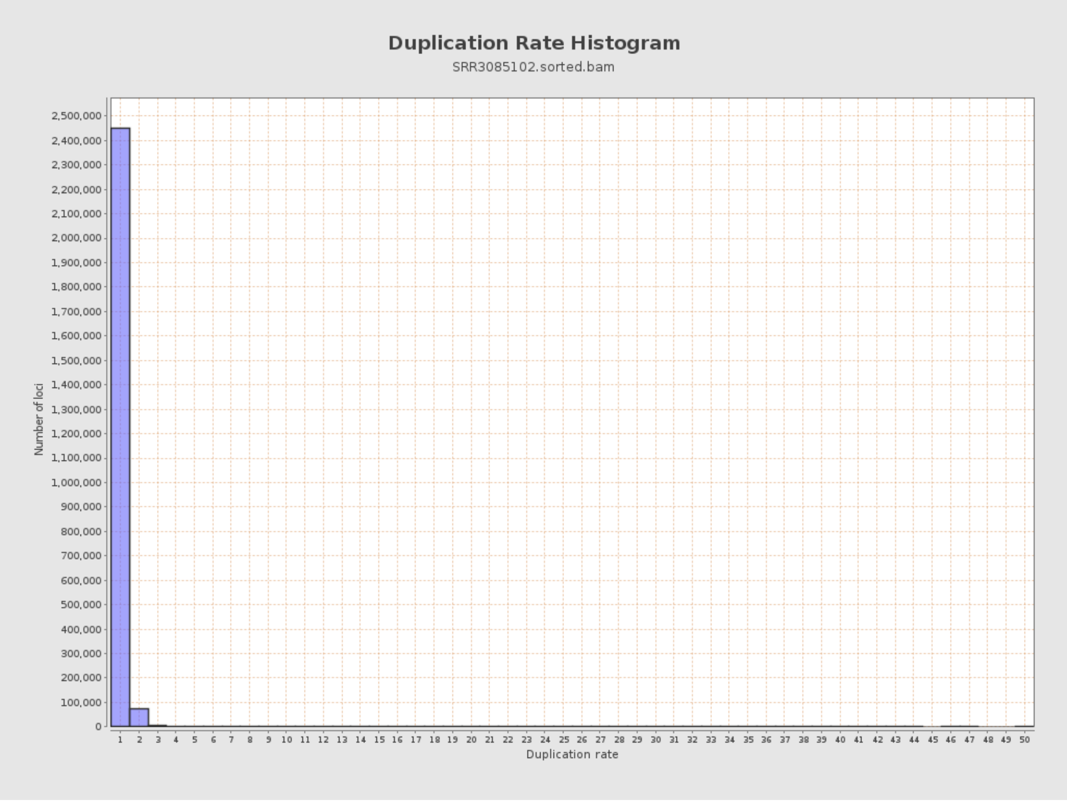
5. Results : Coverage Histogram (0-50X)



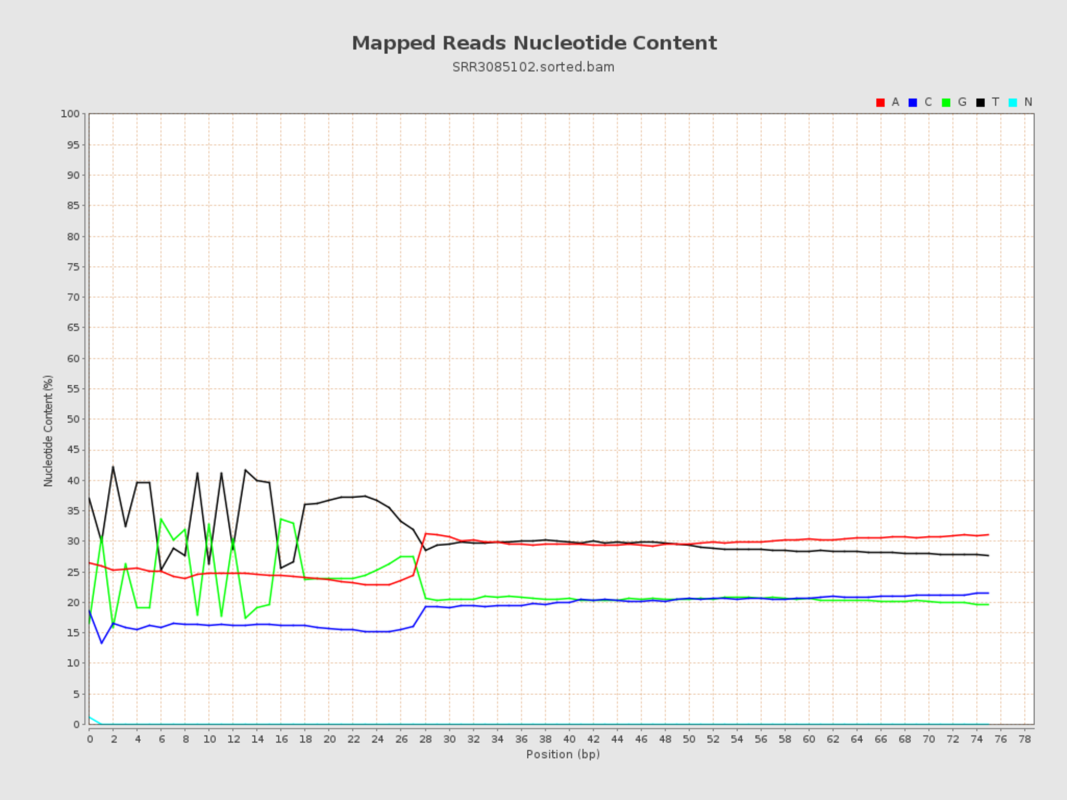
6. Results : Genome Fraction Coverage



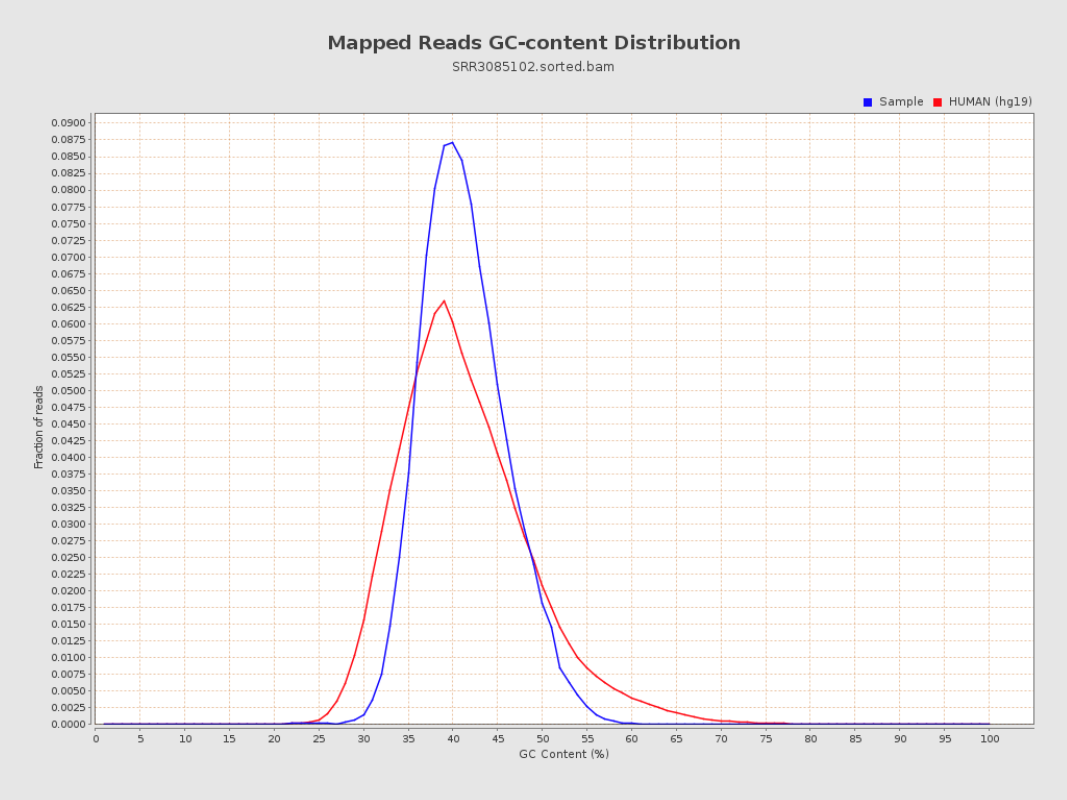
7. Results : Duplication Rate Histogram



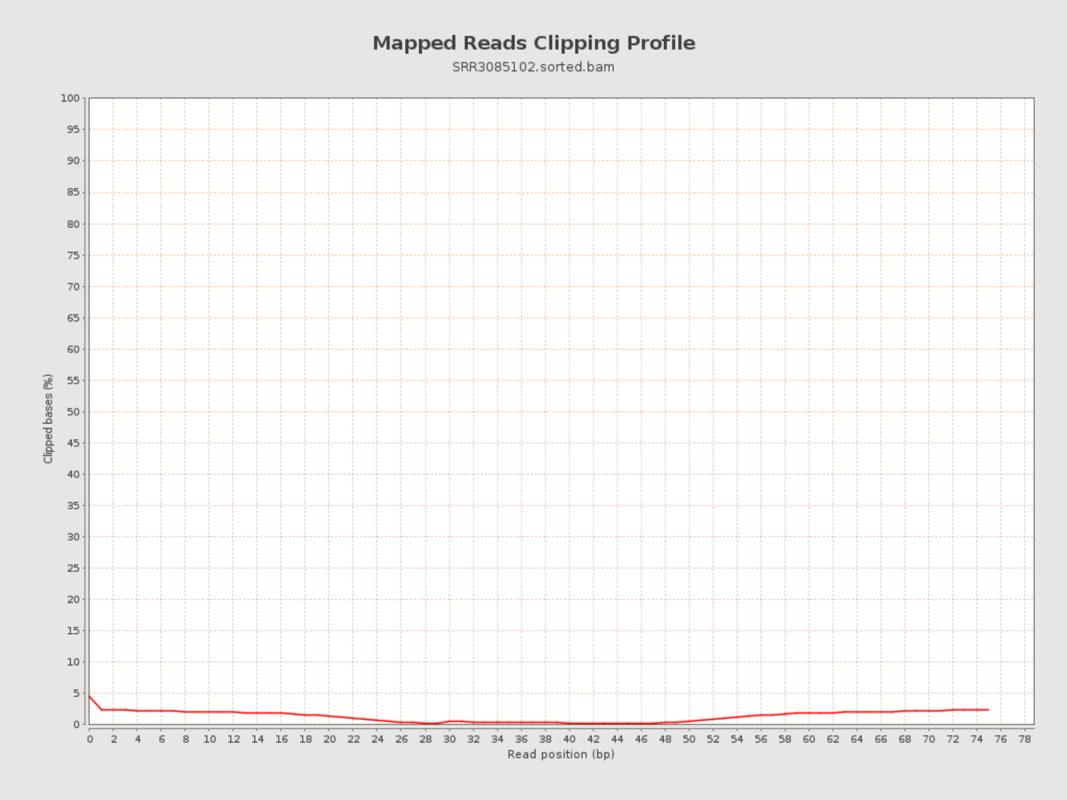
8. Results : Mapped Reads Nucleotide Content



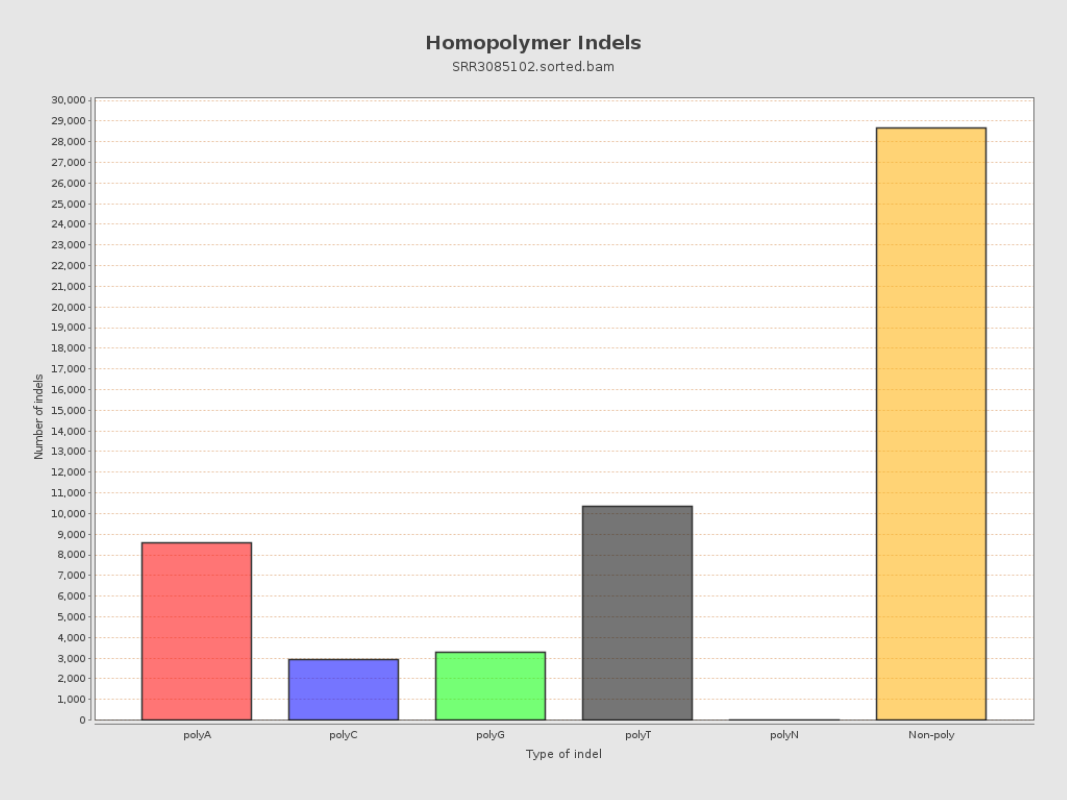
9. Results : Mapped Reads GC-content Distribution



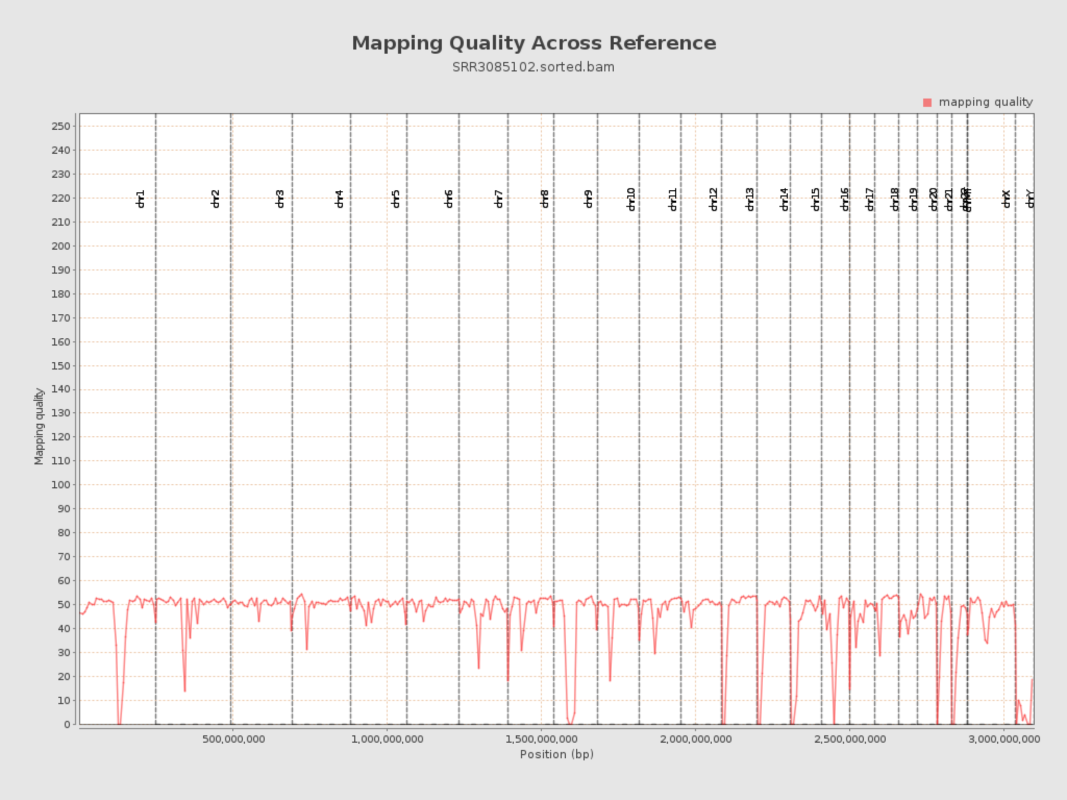
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram