Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:50:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085101.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_SRR3085101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:50:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,566,160
Mapped reads	1,228,199 / 78.42%
Unmapped reads	337,961 / 21.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,852 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	24,238 / 1.55%
Duplication rate	1.6%
Clipped reads	714,343 / 45.61%

2.2. ACGT Content

Number/percentage of A's	23,289,022 / 30.03%
Number/percentage of C's	14,598,733 / 18.83%
Number/percentage of T's	22,458,447 / 28.96%
Number/percentage of G's	17,196,781 / 22.18%
Number/percentage of N's	1,613 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2109

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

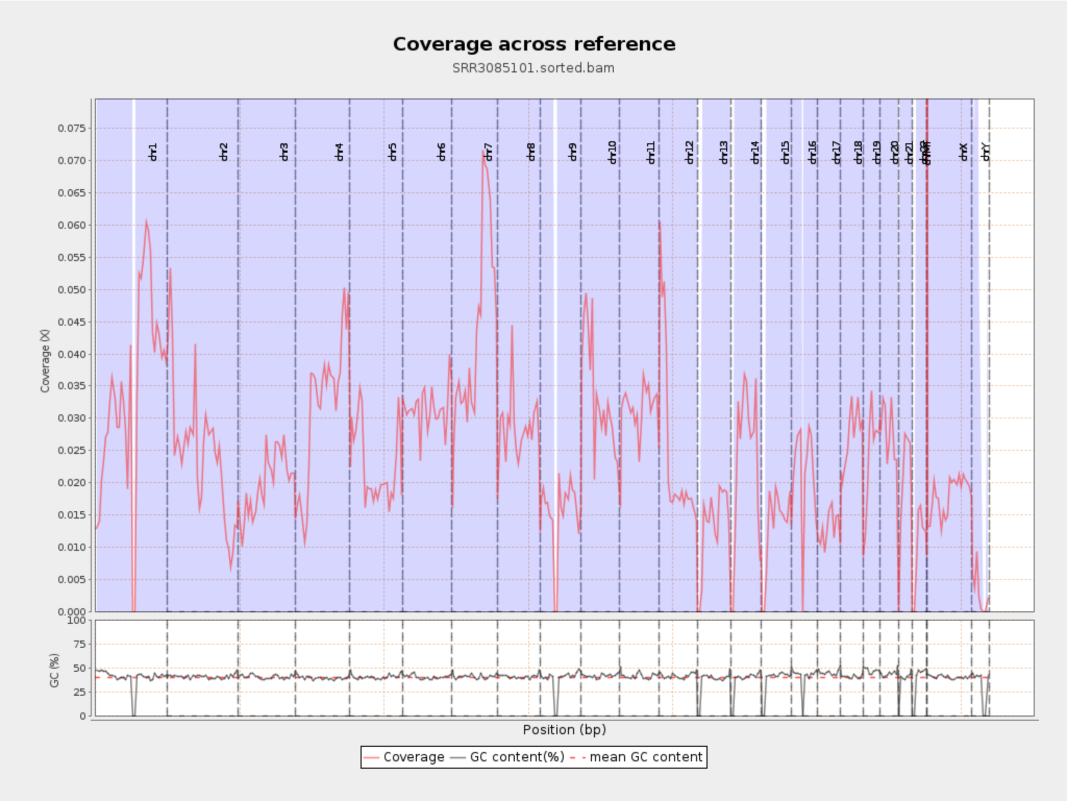
General error rate	0.91%
Mismatches	694,104
Insertions	5,776
Mapped reads with at least one insertion	0.47%
Deletions	15,654
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.42%

2.6. Chromosome stats

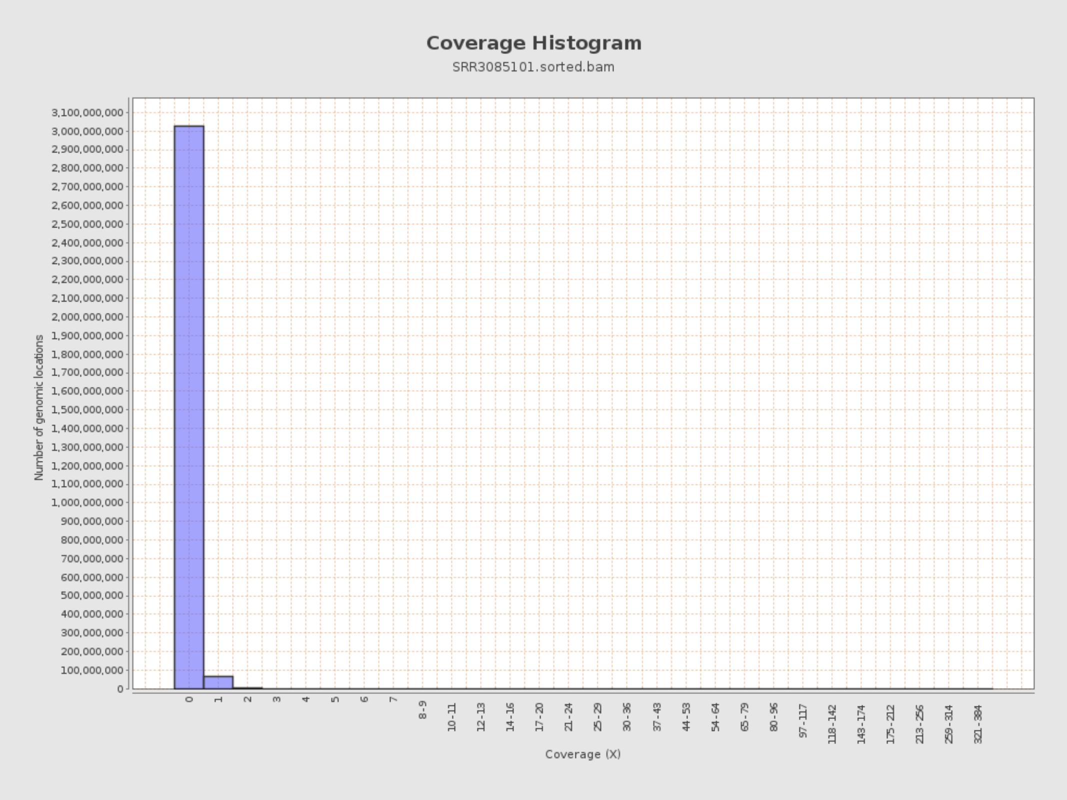
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8579698	0.0344	0.3354
chr2	243199373	5963540	0.0245	0.2128
chr3	198022430	3944103	0.0199	0.152
chr4	191154276	6115269	0.032	0.1922
chr5	180915260	4128850	0.0228	0.1601
chr6	171115067	5390949	0.0315	0.2049
chr7	159138663	6932998	0.0436	0.2512

chr8	146364022	4174909	0.0285	0.2835
chr9	141213431	2149490	0.0152	0.1678
chr10	135534747	4526137	0.0334	0.2853
chr11	135006516	4262669	0.0316	0.2377
chr12	133851895	3326729	0.0249	0.168
chr13	115169878	1505195	0.0131	0.1194
chr14	107349540	2483982	0.0231	0.163
chr15	102531392	1350468	0.0132	0.1218
chr16	90354753	1916055	0.0212	0.1631
chr17	81195210	1046846	0.0129	0.1312
chr18	78077248	2151175	0.0276	0.2923
chr19	59128983	1445444	0.0244	0.2175
chr20	63025520	1705961	0.0271	0.1762
chr21	48129895	984827	0.0205	0.1581
chr22	51304566	516190	0.0101	0.1046
chrMT	16571	5535	0.334	0.5841
chrX	155270560	2792744	0.018	0.1495
chrY	59373566	169724	0.0029	0.07

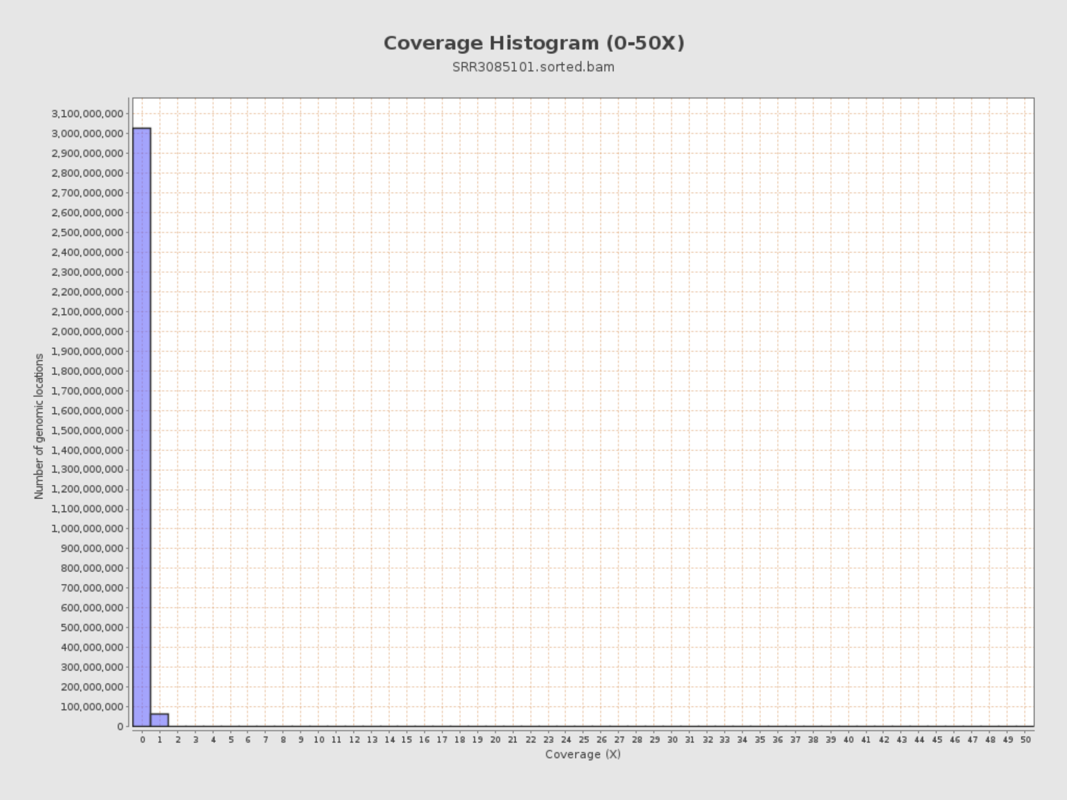
3. Results : Coverage across reference



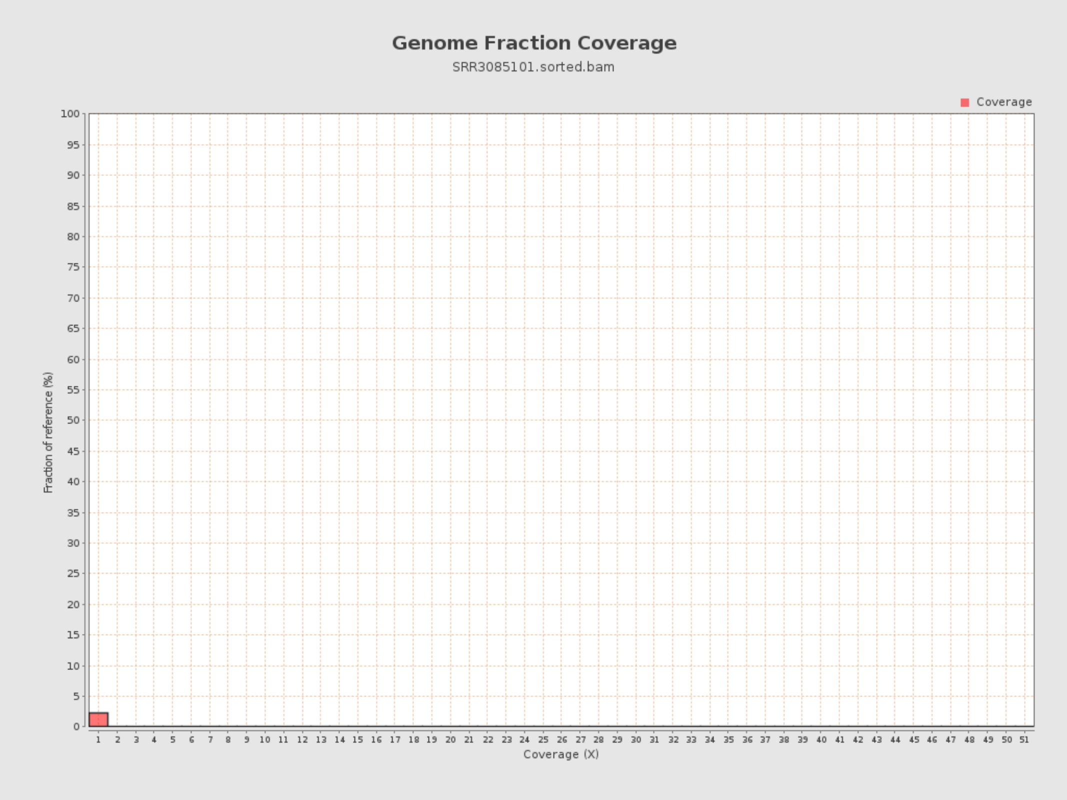
4. Results : Coverage Histogram



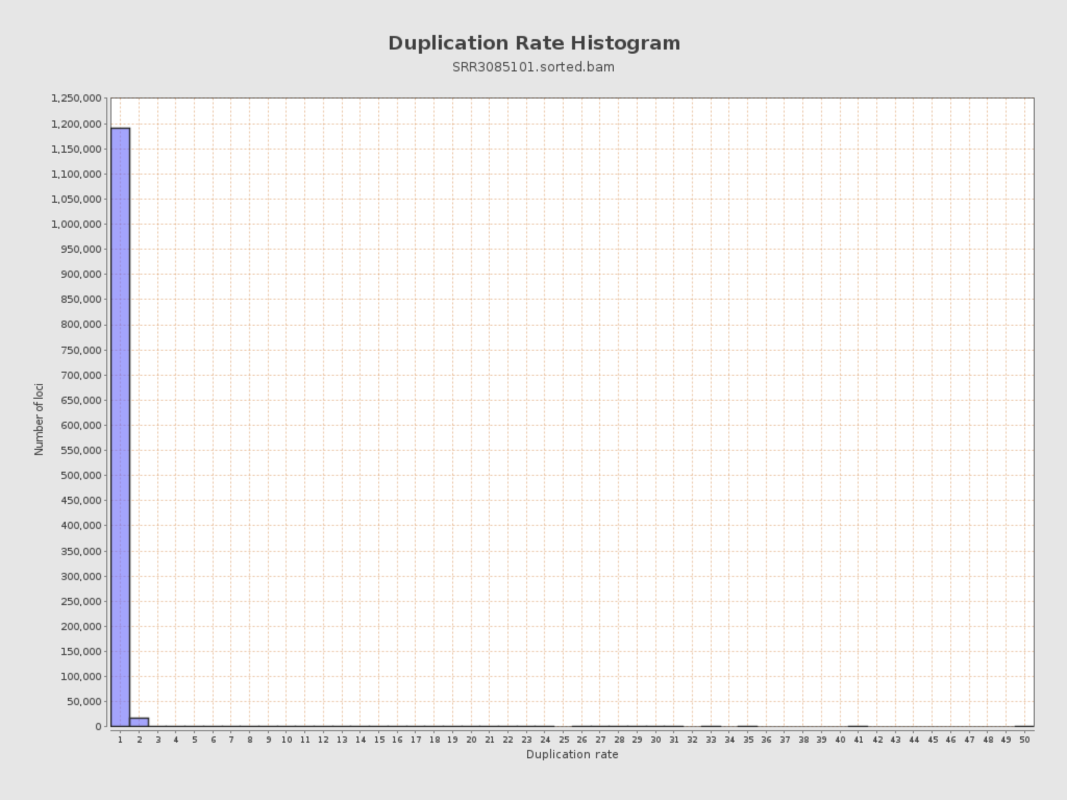
5. Results : Coverage Histogram (0-50X)



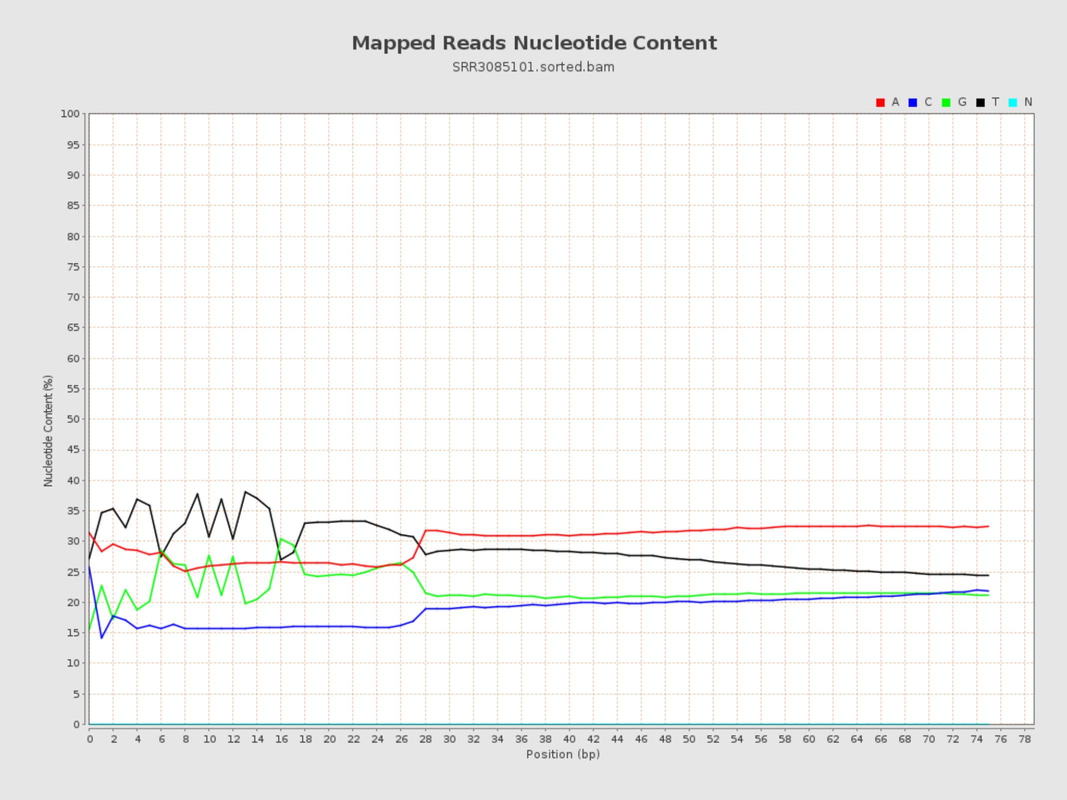
6. Results : Genome Fraction Coverage



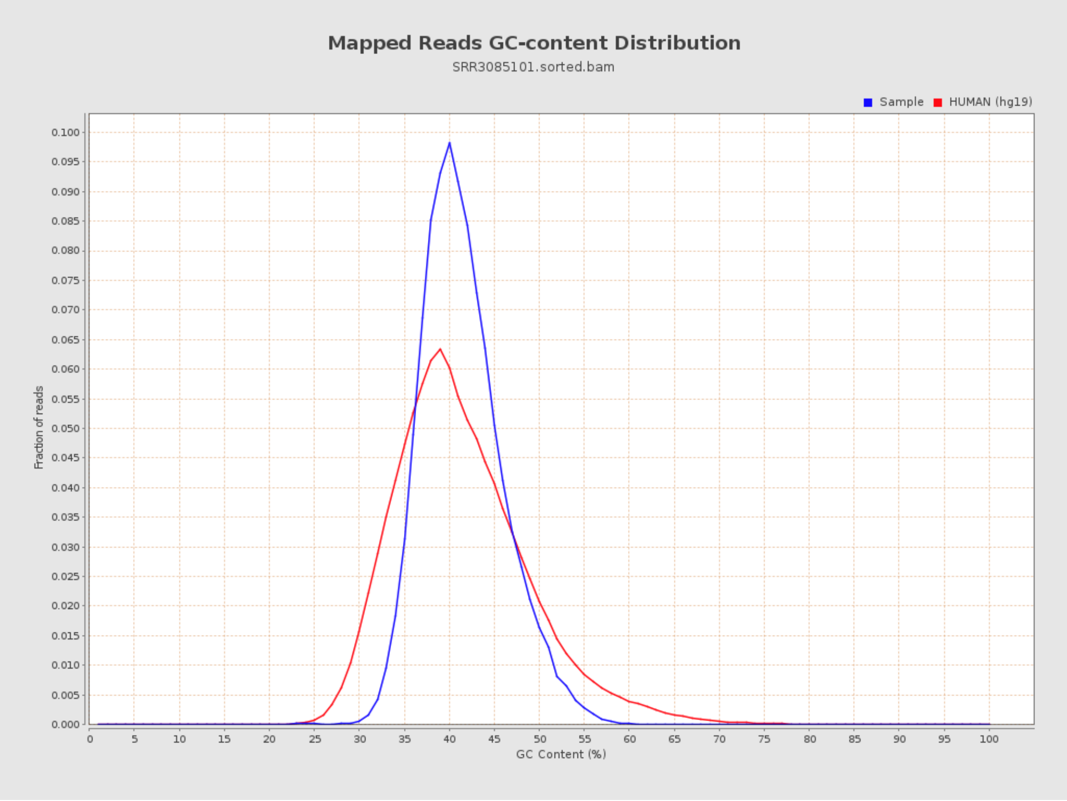
7. Results : Duplication Rate Histogram



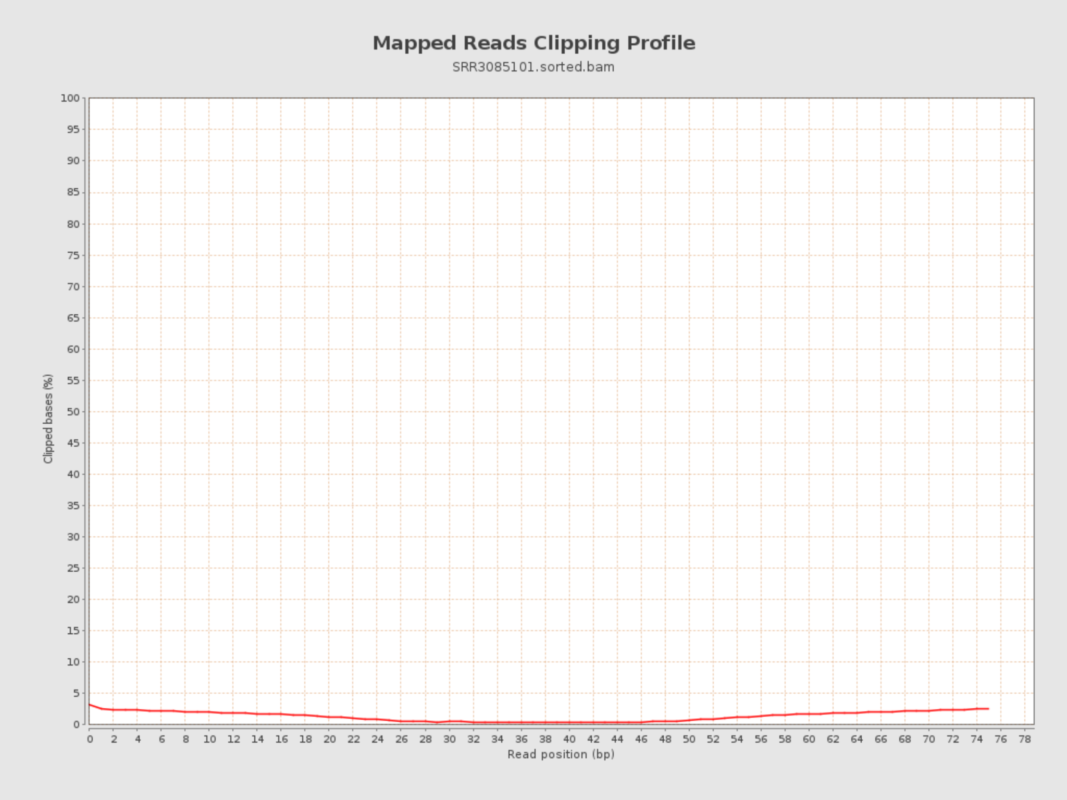
8. Results : Mapped Reads Nucleotide Content



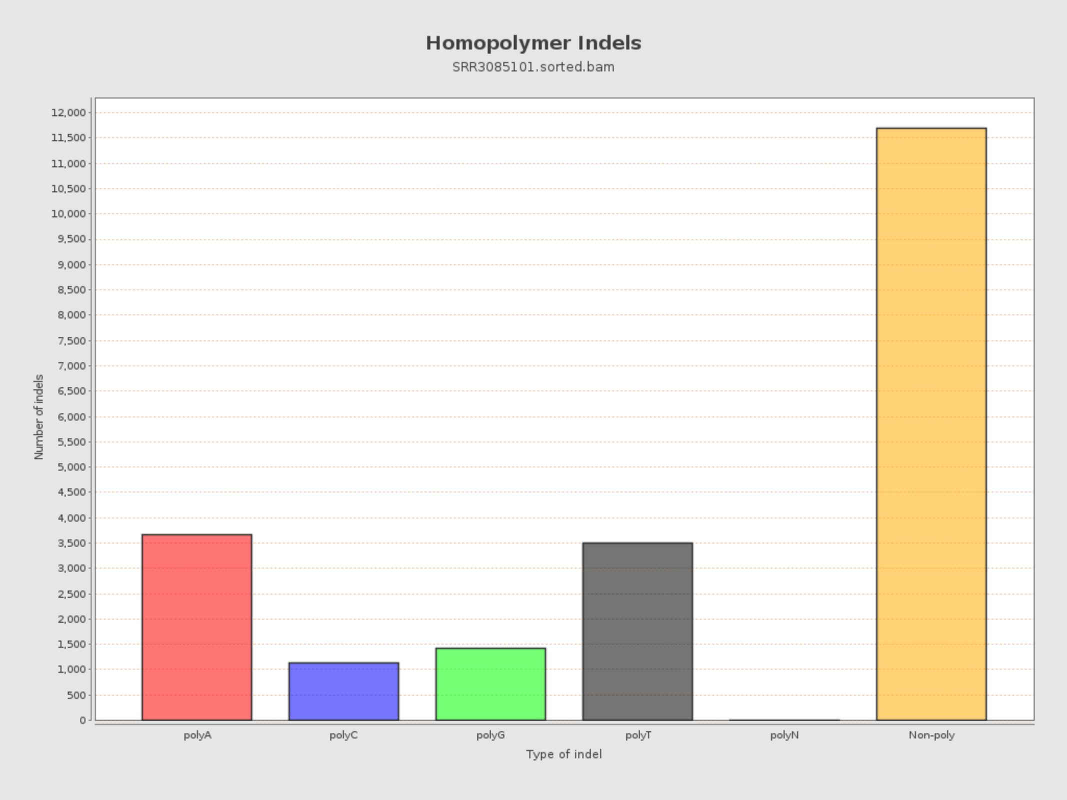
9. Results : Mapped Reads GC-content Distribution



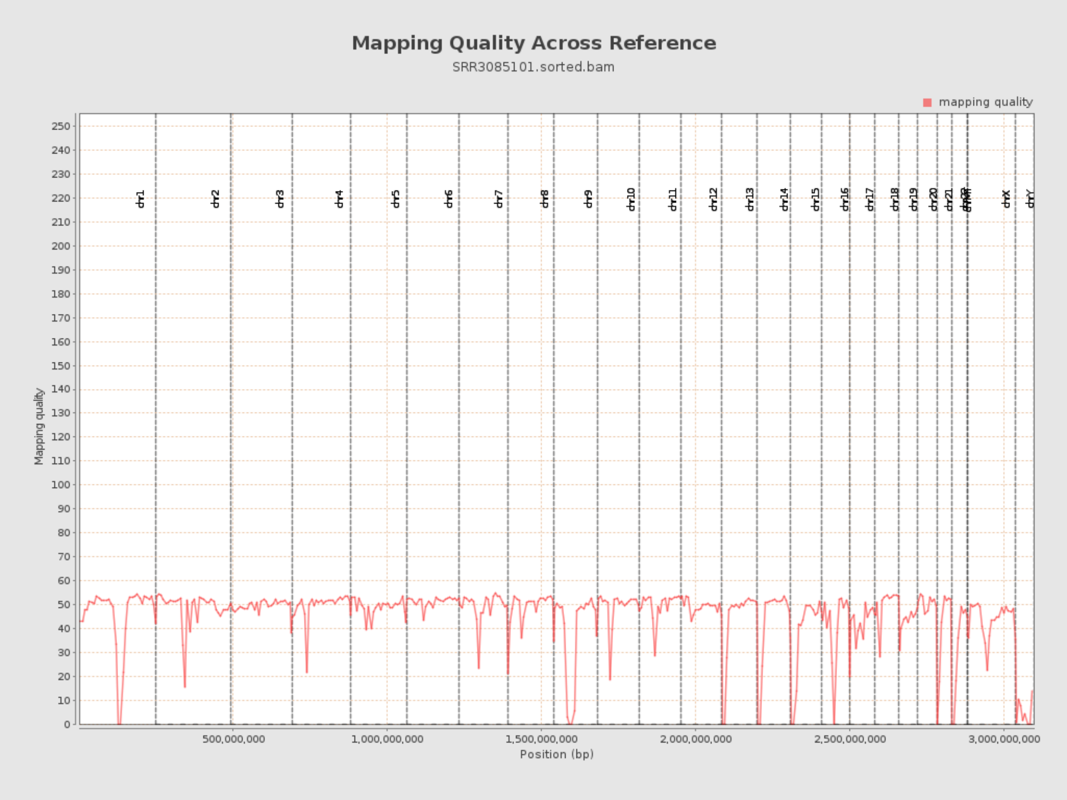
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram