Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:33:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082485.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_SRR3082485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082485.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:33:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,544,581
Mapped reads	1,405,794 / 91.01%
Unmapped reads	138,787 / 8.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,527 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	40,820 / 2.64%
Duplication rate	2.09%
Clipped reads	490,536 / 31.76%

2.2. ACGT Content

Number/percentage of A's	29,029,580 / 29.66%
Number/percentage of C's	18,433,008 / 18.83%
Number/percentage of T's	29,935,177 / 30.58%
Number/percentage of G's	20,484,365 / 20.93%
Number/percentage of N's	2,103 / 0%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3187

2.4. Mapping Quality

Mean Mapping Quality	47.53

2.5. Mismatches and indels

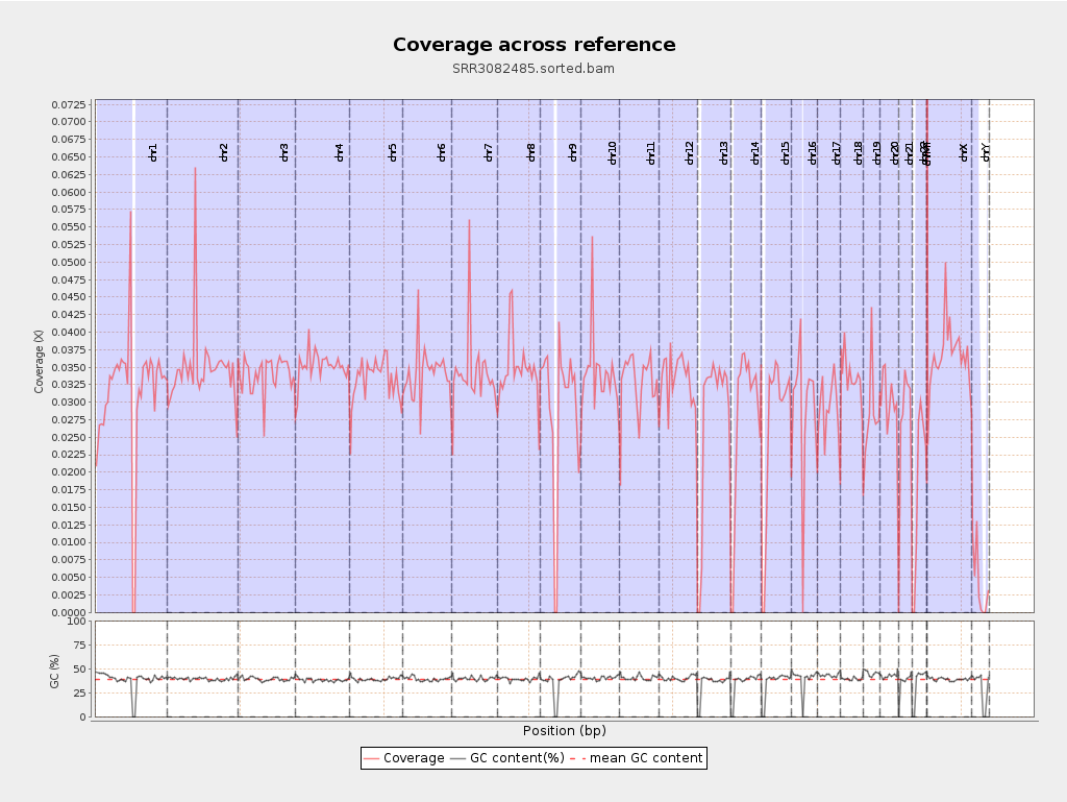
General error rate	0.88%
Mismatches	847,075
Insertions	8,283
Mapped reads with at least one insertion	0.58%
Deletions	22,826
Mapped reads with at least one deletion	1.61%
Homopolymer indels	46.35%

2.6. Chromosome stats

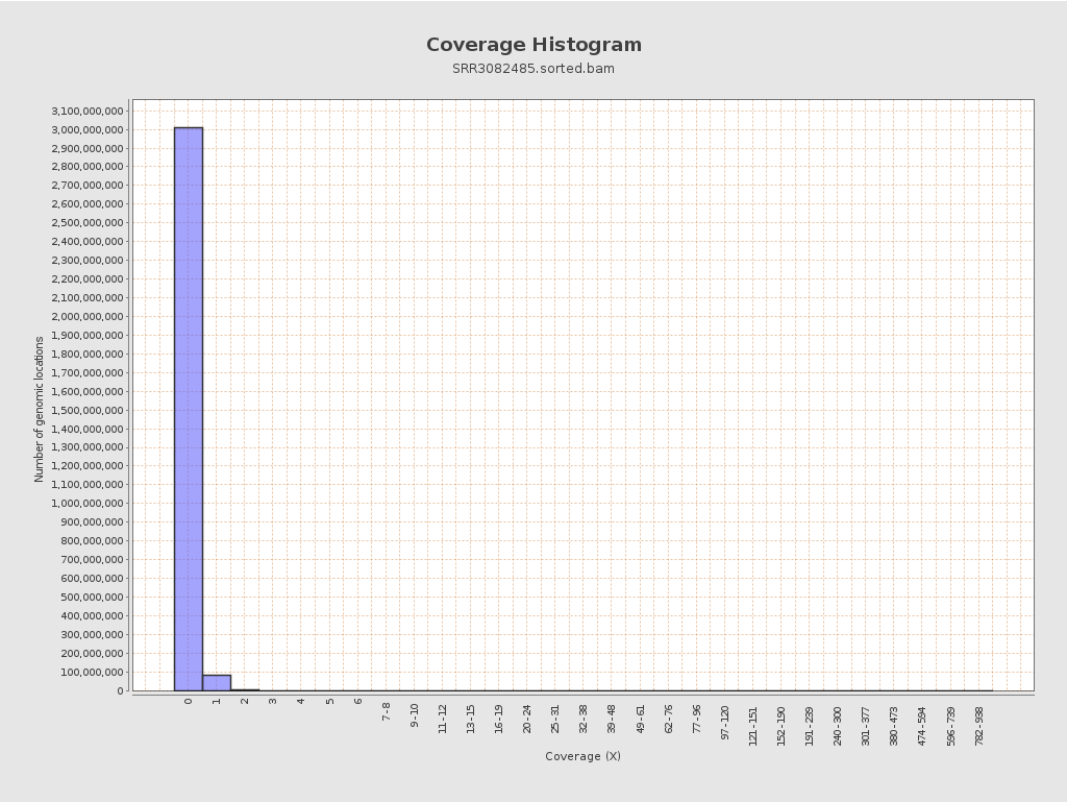
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7766398	0.0312	0.5665
chr2	243199373	8462632	0.0348	0.3296
chr3	198022430	6734553	0.034	0.1972
chr4	191154276	6702643	0.0351	0.2069
chr5	180915260	6065868	0.0335	0.1968
chr6	171115067	5828049	0.0341	0.2353
chr7	159138663	5436467	0.0342	0.3998

chr8	146364022	5079024	0.0347	0.5982
chr9	141213431	4099133	0.029	0.2768
chr10	135534747	4604462	0.034	0.2866
chr11	135006516	4469929	0.0331	0.2677
chr12	133851895	4448165	0.0332	0.1976
chr13	115169878	3183582	0.0276	0.1768
chr14	107349540	2975311	0.0277	0.1872
chr15	102531392	2720065	0.0265	0.1737
chr16	90354753	2577634	0.0285	0.2039
chr17	81195210	2361351	0.0291	0.2069
chr18	78077248	2635276	0.0338	0.4885
chr19	59128983	1681715	0.0284	0.4283
chr20	63025520	1887514	0.0299	0.1886
chr21	48129895	1297865	0.027	0.1859
chr22	51304566	953609	0.0186	0.1441
chrMT	16571	2872	0.1733	0.4401
chrX	155270560	5704685	0.0367	0.2267
chrY	59373566	243179	0.0041	0.1072

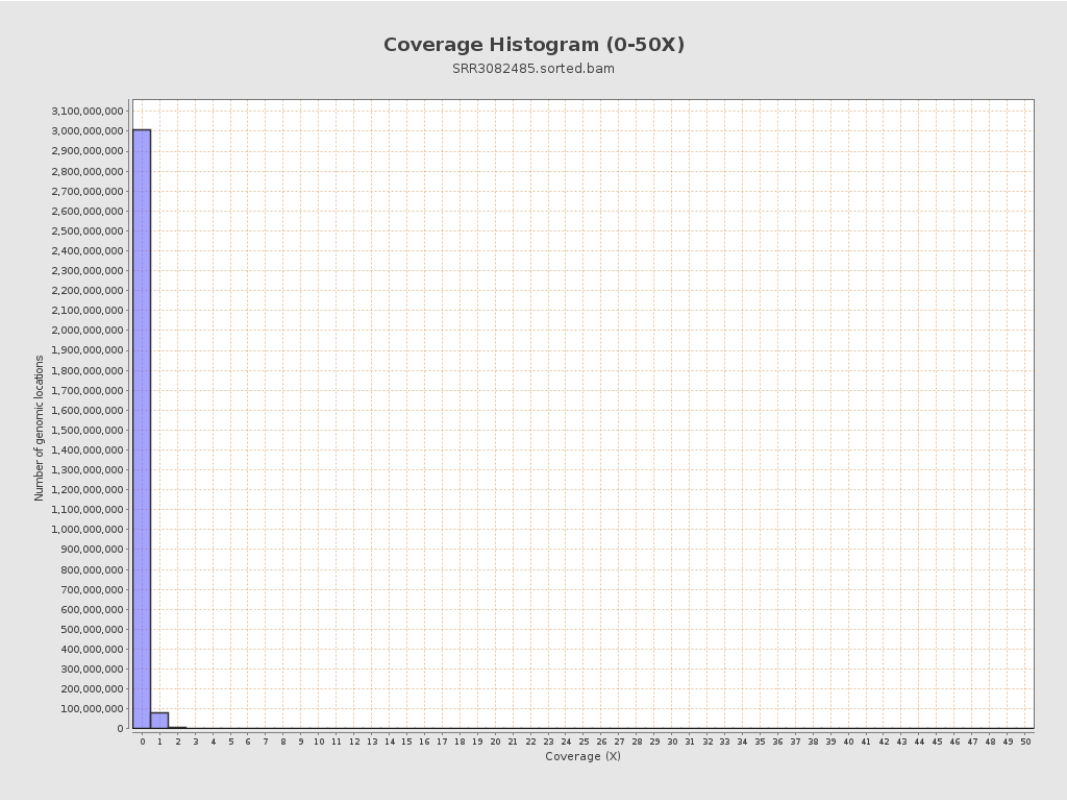
3. Results : Coverage across reference



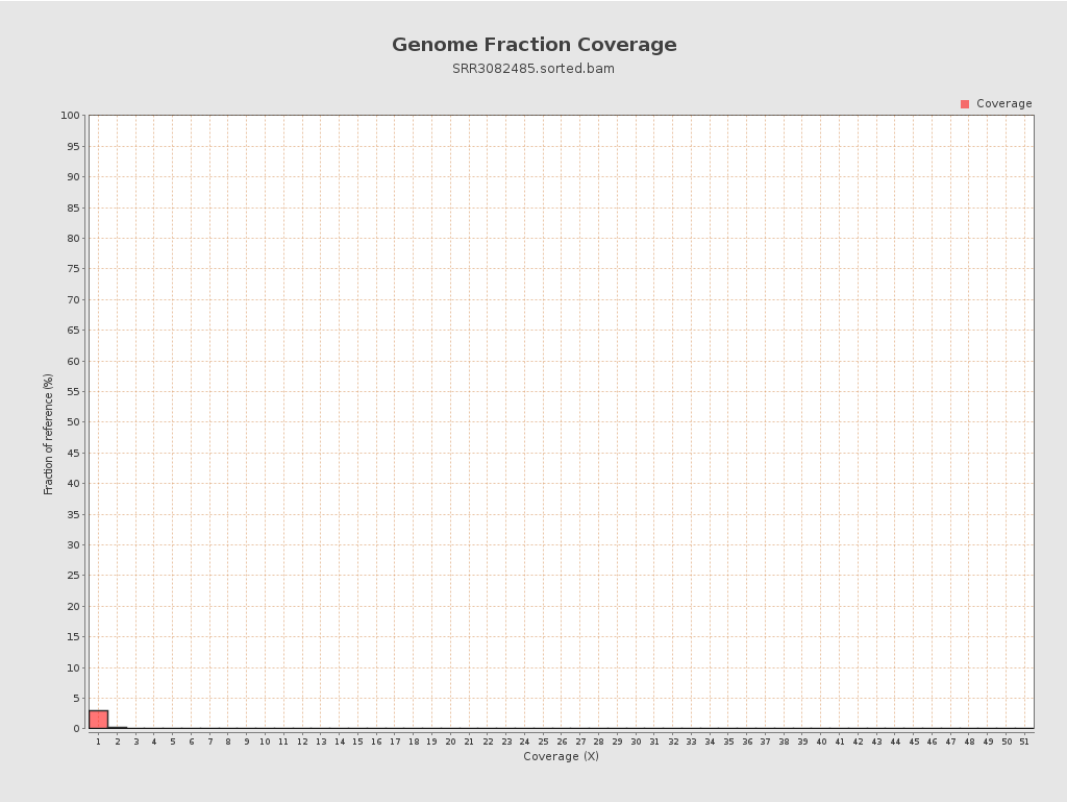
4. Results : Coverage Histogram



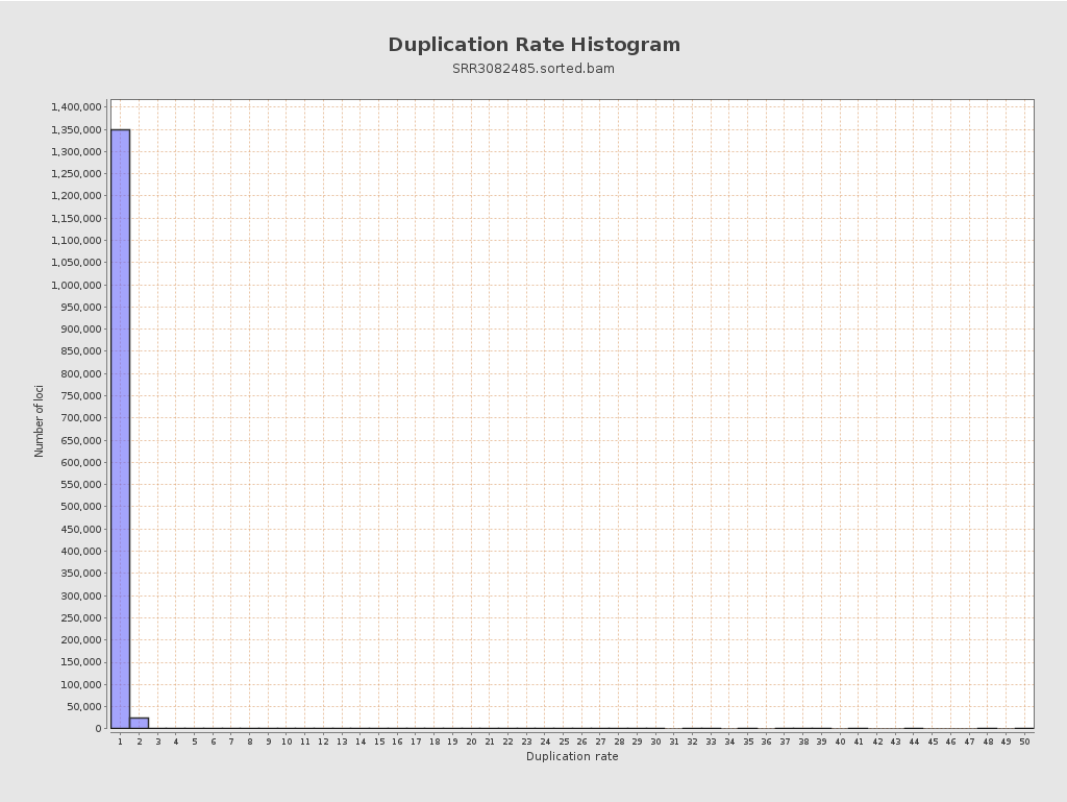
5. Results : Coverage Histogram (0-50X)



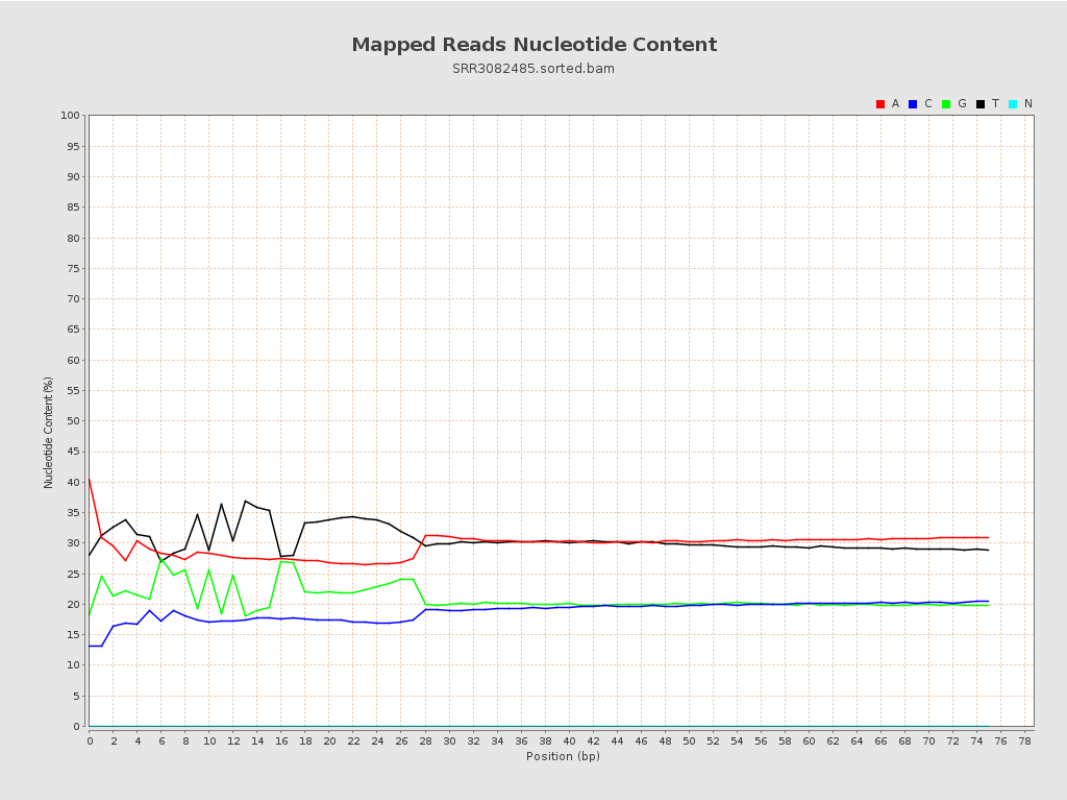
6. Results : Genome Fraction Coverage



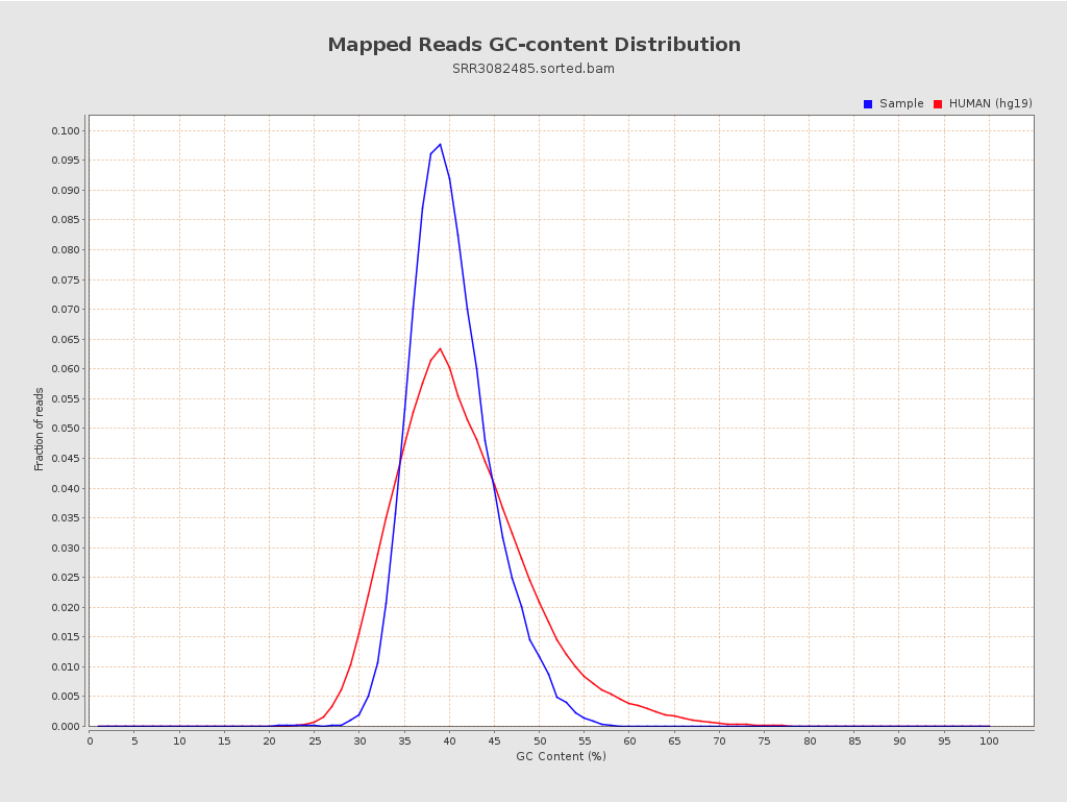
7. Results : Duplication Rate Histogram



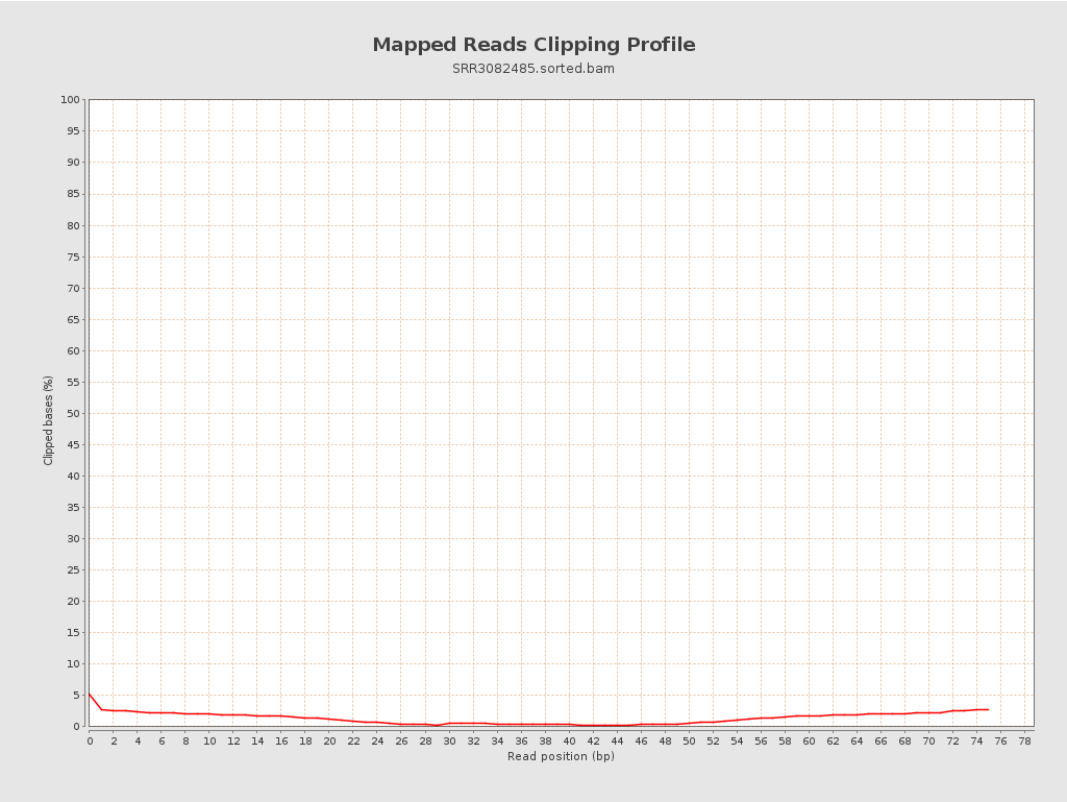
8. Results : Mapped Reads Nucleotide Content



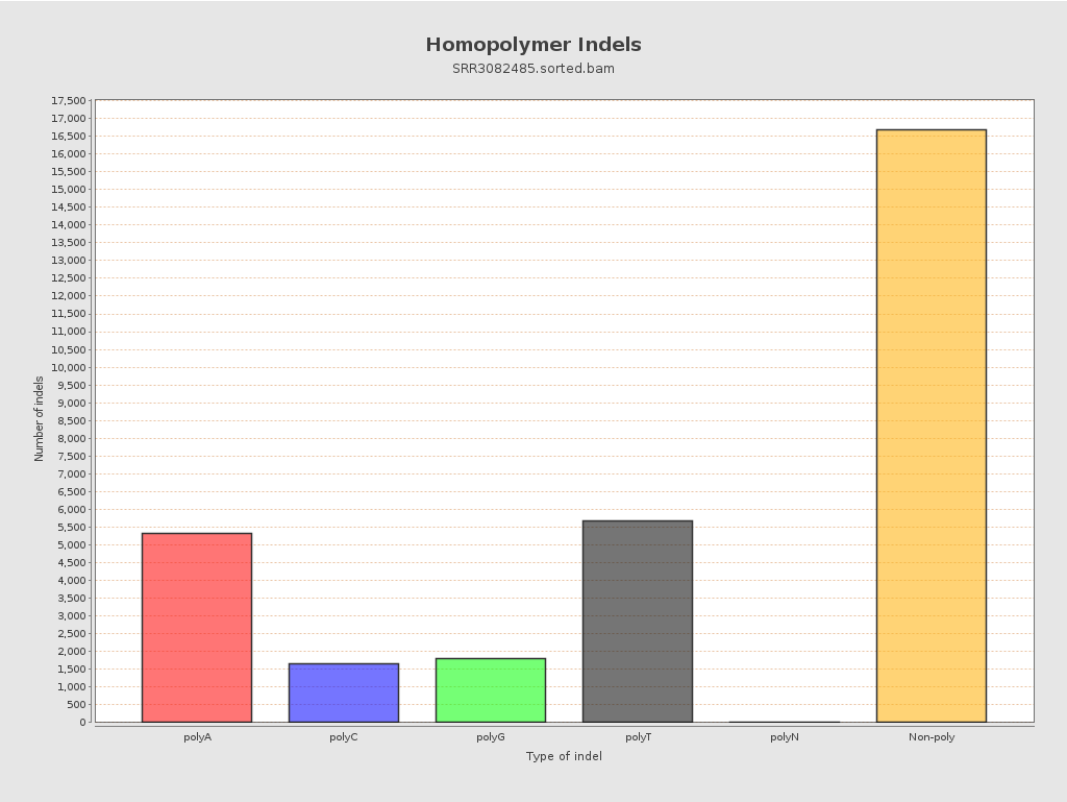
9. Results : Mapped Reads GC-content Distribution



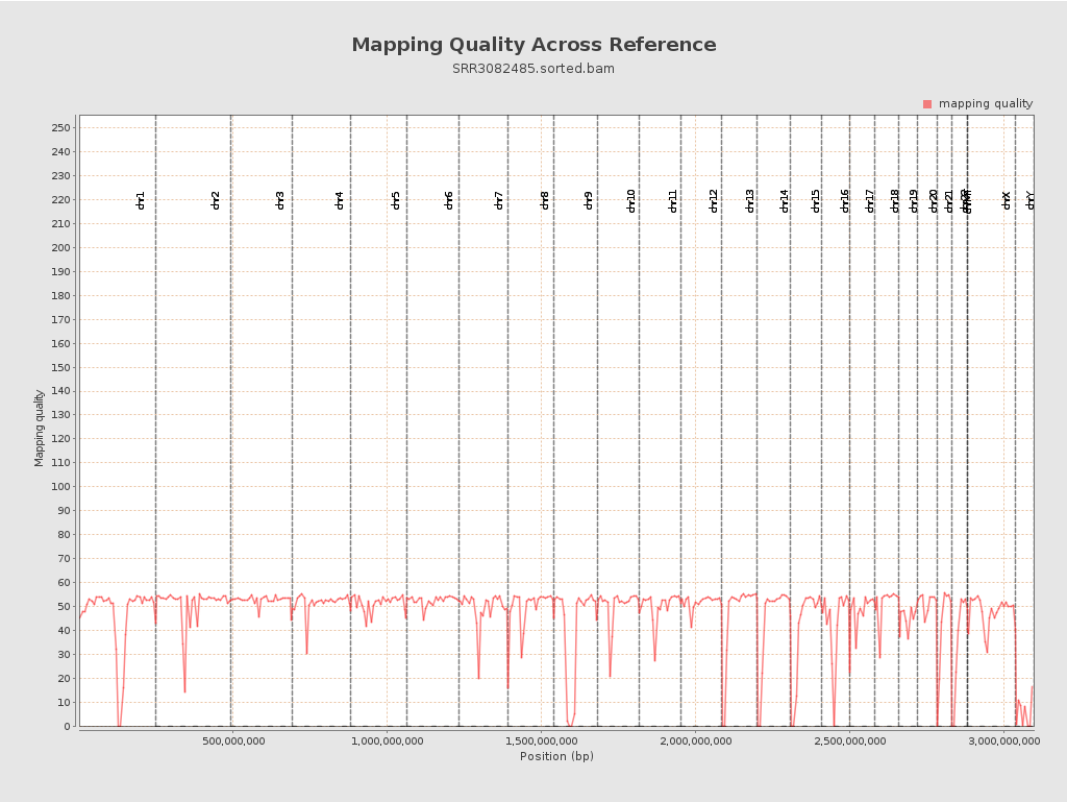
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram