Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:13:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085056.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_SRR3085056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:13:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,659,055
Mapped reads	2,216,645 / 83.36%
Unmapped reads	442,410 / 16.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,463 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	79,352 / 2.98%
Duplication rate	2.85%
Clipped reads	1,608,168 / 60.48%

2.2. ACGT Content

Number/percentage of A's	39,886,161 / 30.11%
Number/percentage of C's	26,335,746 / 19.88%
Number/percentage of T's	38,348,808 / 28.95%
Number/percentage of G's	27,875,006 / 21.05%
Number/percentage of N's	2,940 / 0%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.3288

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

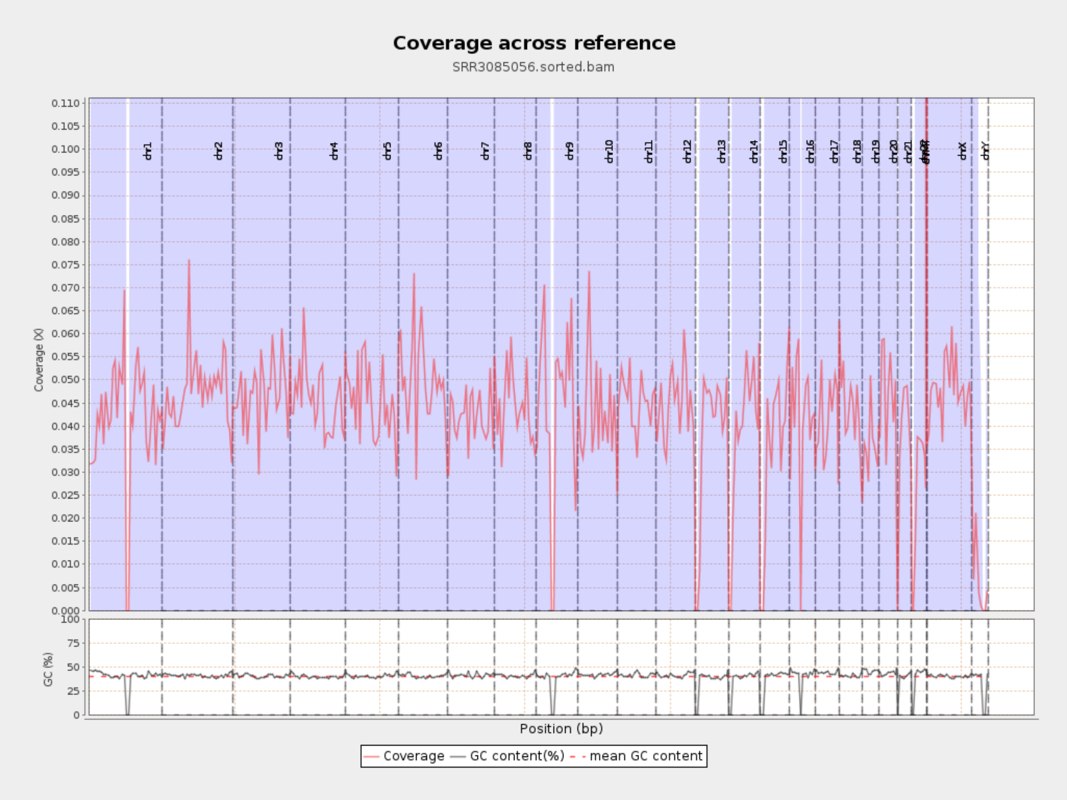
General error rate	0.85%
Mismatches	1,108,508
Insertions	10,404
Mapped reads with at least one insertion	0.47%
Deletions	26,442
Mapped reads with at least one deletion	1.18%
Homopolymer indels	45.63%

2.6. Chromosome stats

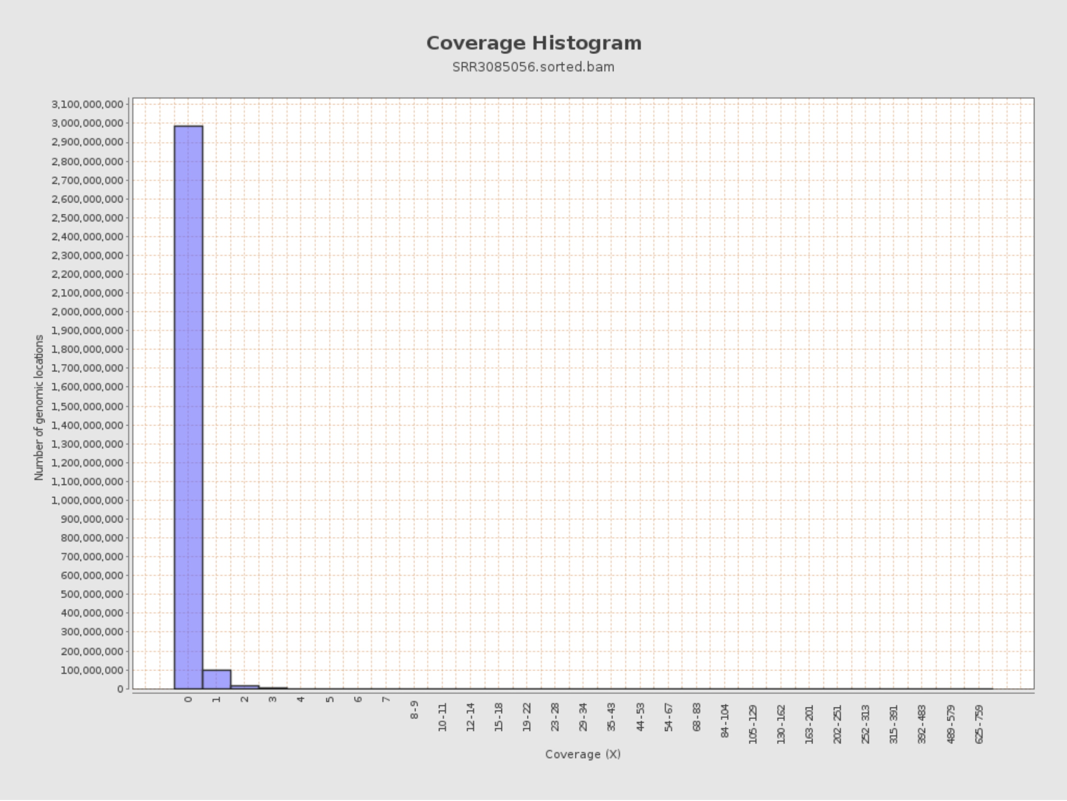
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10356851	0.0416	0.4715
chr2	243199373	11583774	0.0476	0.4014
chr3	198022430	9356980	0.0473	0.2494
chr4	191154276	8660773	0.0453	0.2735
chr5	180915260	8138746	0.045	0.2448
chr6	171115067	8565901	0.0501	0.2873
chr7	159138663	6633678	0.0417	0.2651

chr8	146364022	6472099	0.0442	0.5219
chr9	141213431	6294544	0.0446	0.345
chr10	135534747	5889635	0.0435	0.3504
chr11	135006516	6098457	0.0452	0.29
chr12	133851895	5978152	0.0447	0.2491
chr13	115169878	4295100	0.0373	0.2202
chr14	107349540	4046702	0.0377	0.2436
chr15	102531392	3539254	0.0345	0.2125
chr16	90354753	3765277	0.0417	0.2561
chr17	81195210	3363651	0.0414	0.2912
chr18	78077248	3469897	0.0444	0.559
chr19	59128983	2117267	0.0358	0.3687
chr20	63025520	2931002	0.0465	0.2558
chr21	48129895	1803358	0.0375	0.2558
chr22	51304566	1289830	0.0251	0.18
chrMT	16571	28149	1.6987	1.5957
chrX	155270560	7428333	0.0478	0.2771
chrY	59373566	383712	0.0065	0.1545

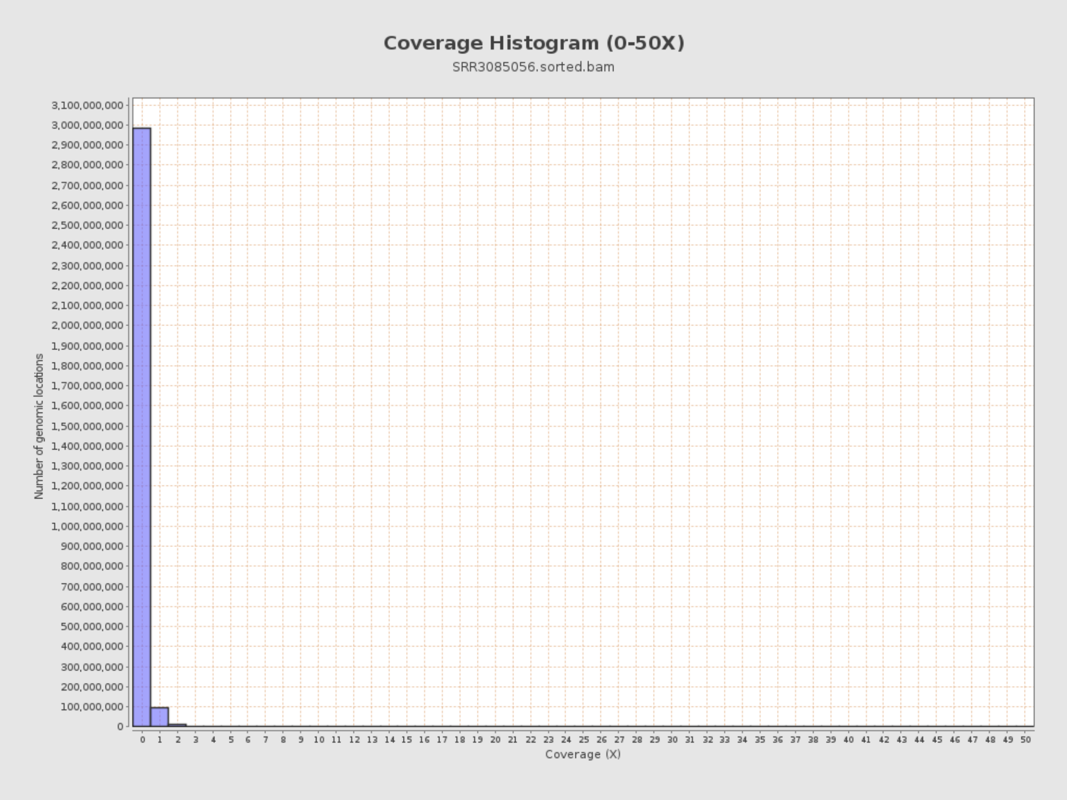
3. Results : Coverage across reference



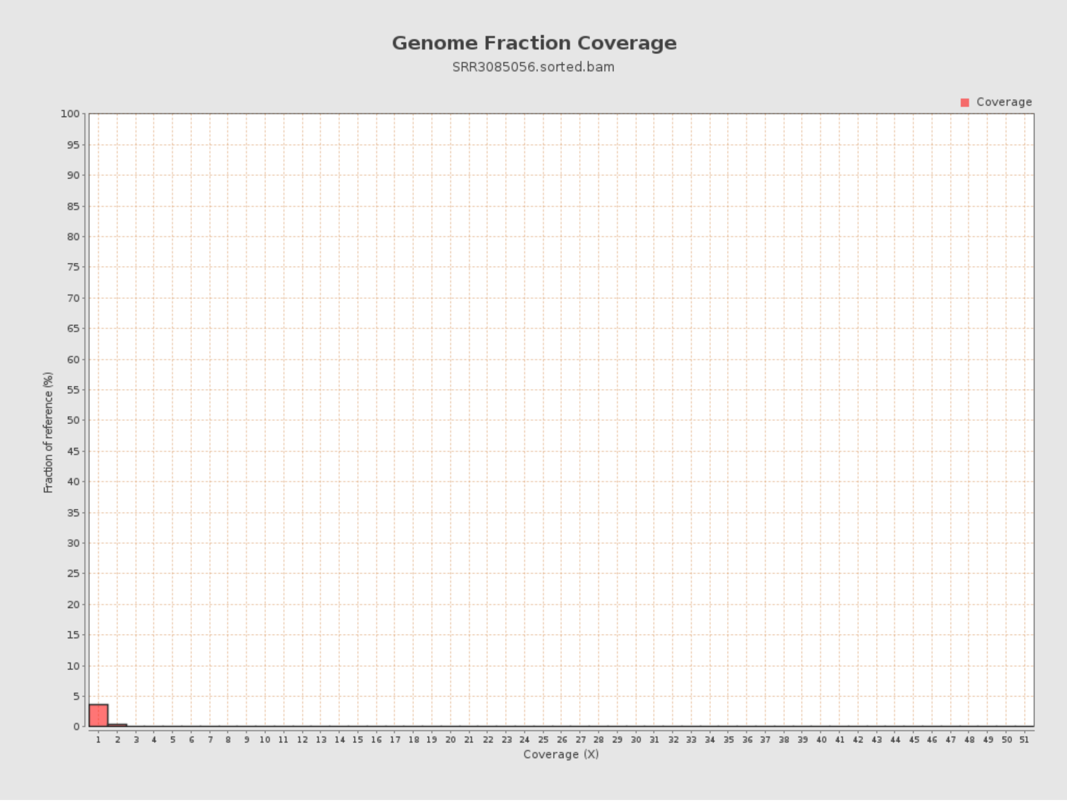
4. Results : Coverage Histogram



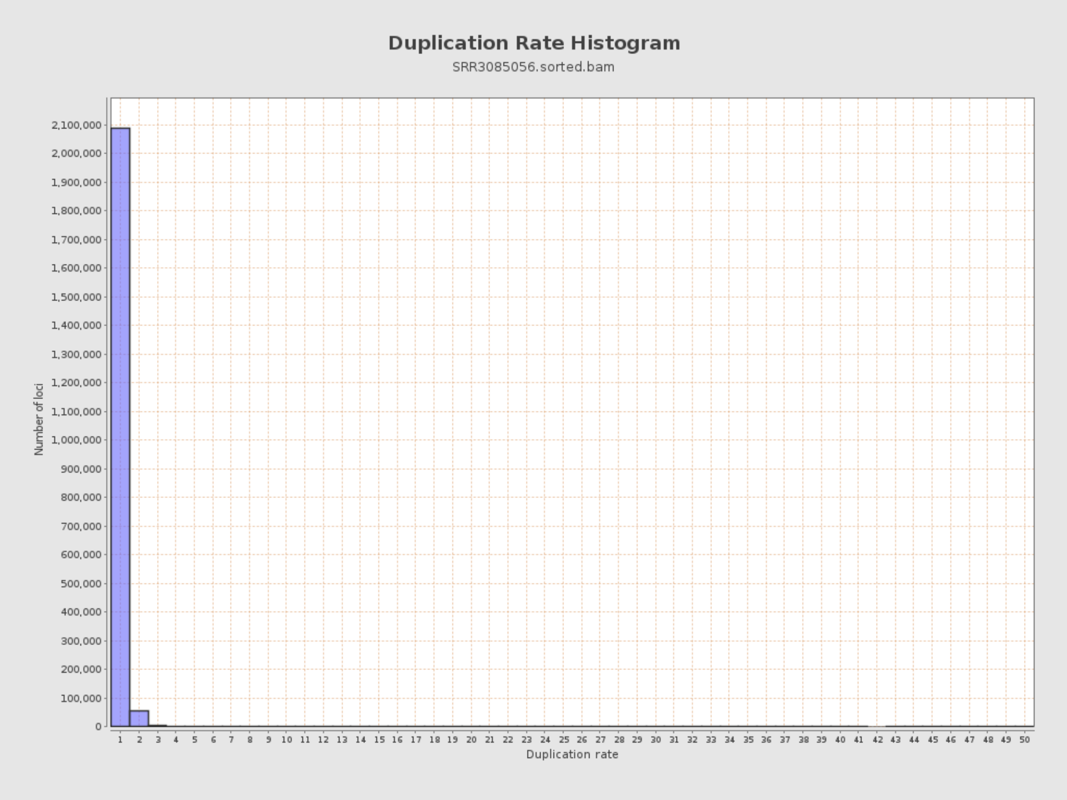
5. Results : Coverage Histogram (0-50X)



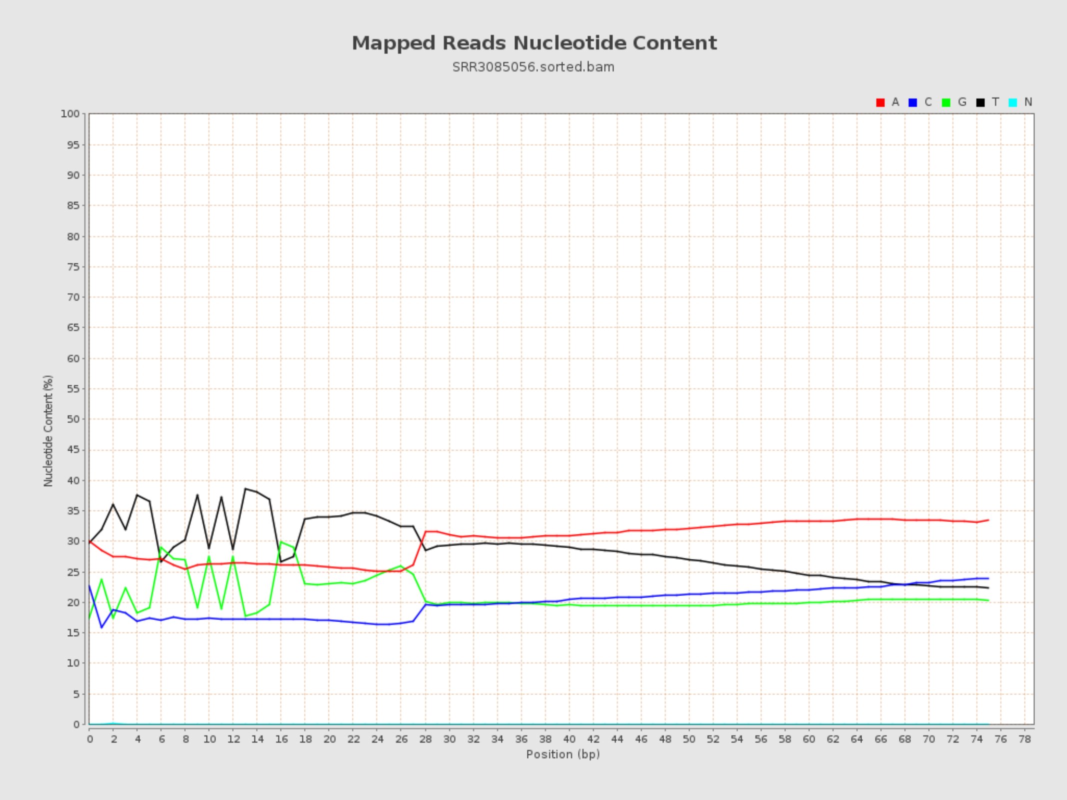
6. Results : Genome Fraction Coverage



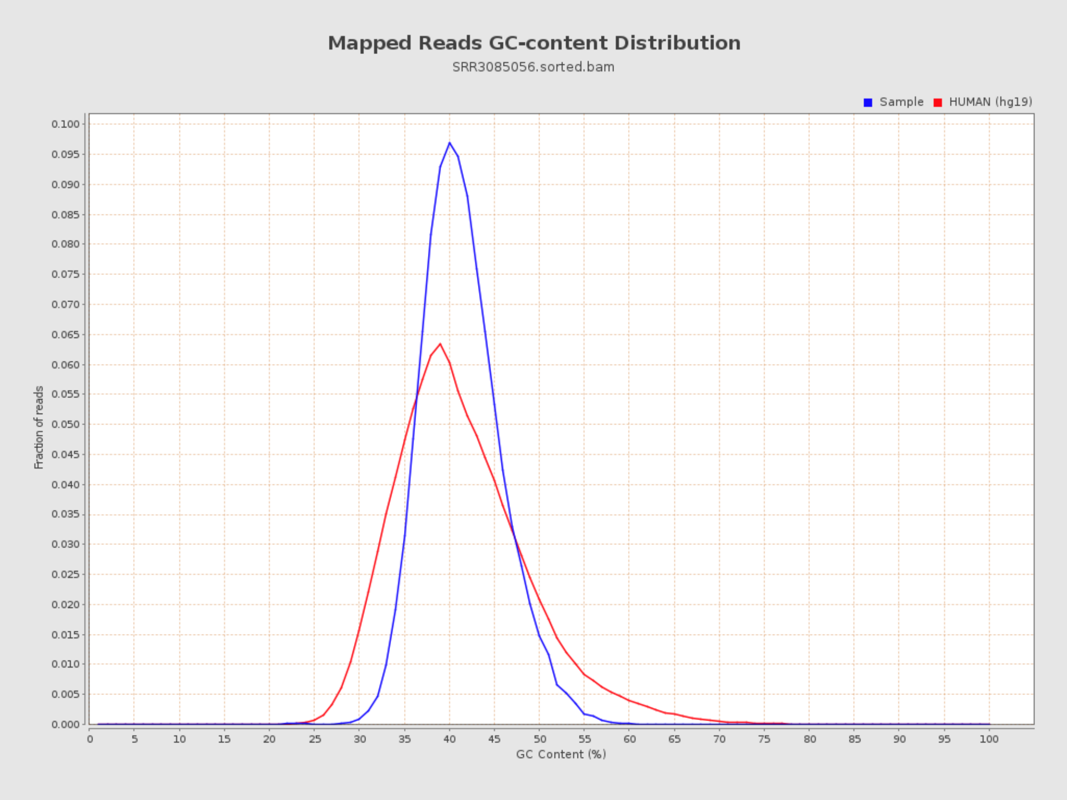
7. Results : Duplication Rate Histogram



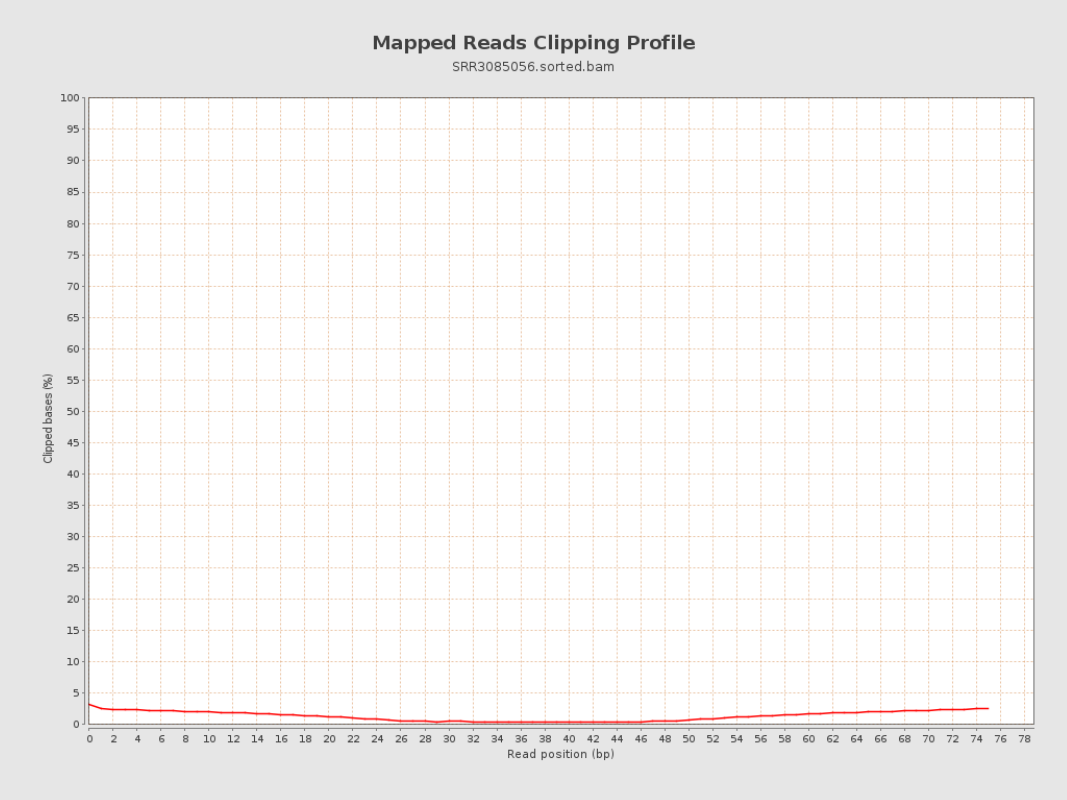
8. Results : Mapped Reads Nucleotide Content



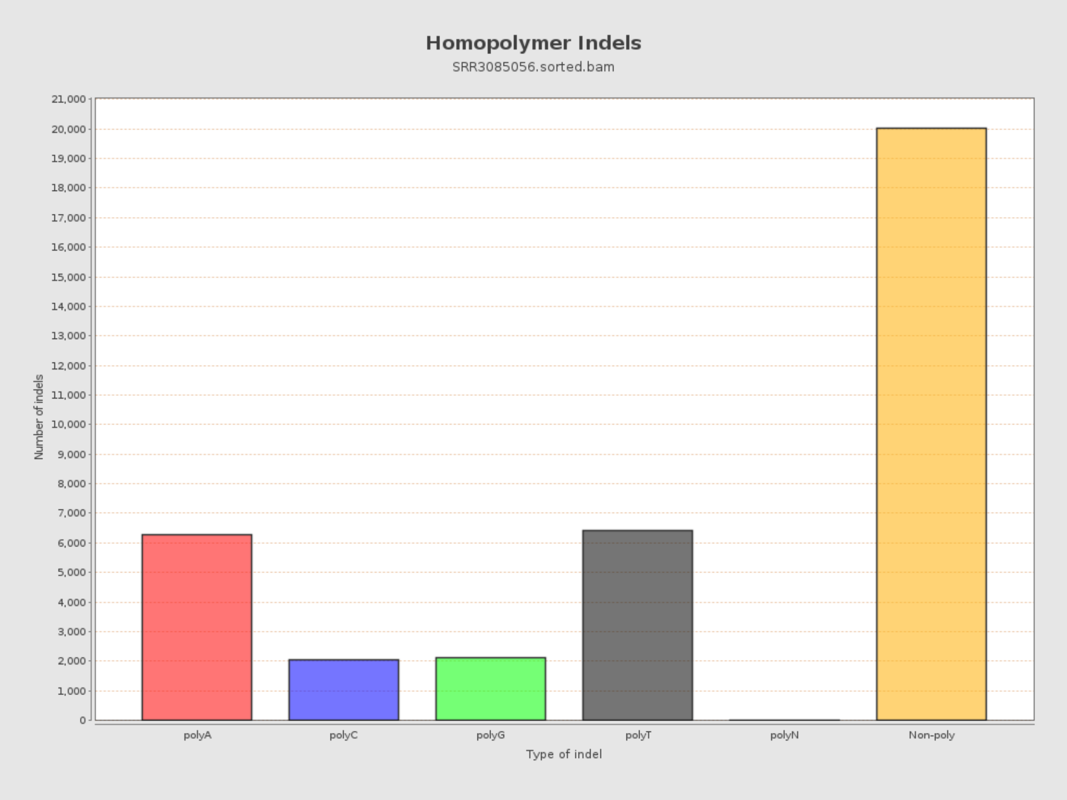
9. Results : Mapped Reads GC-content Distribution



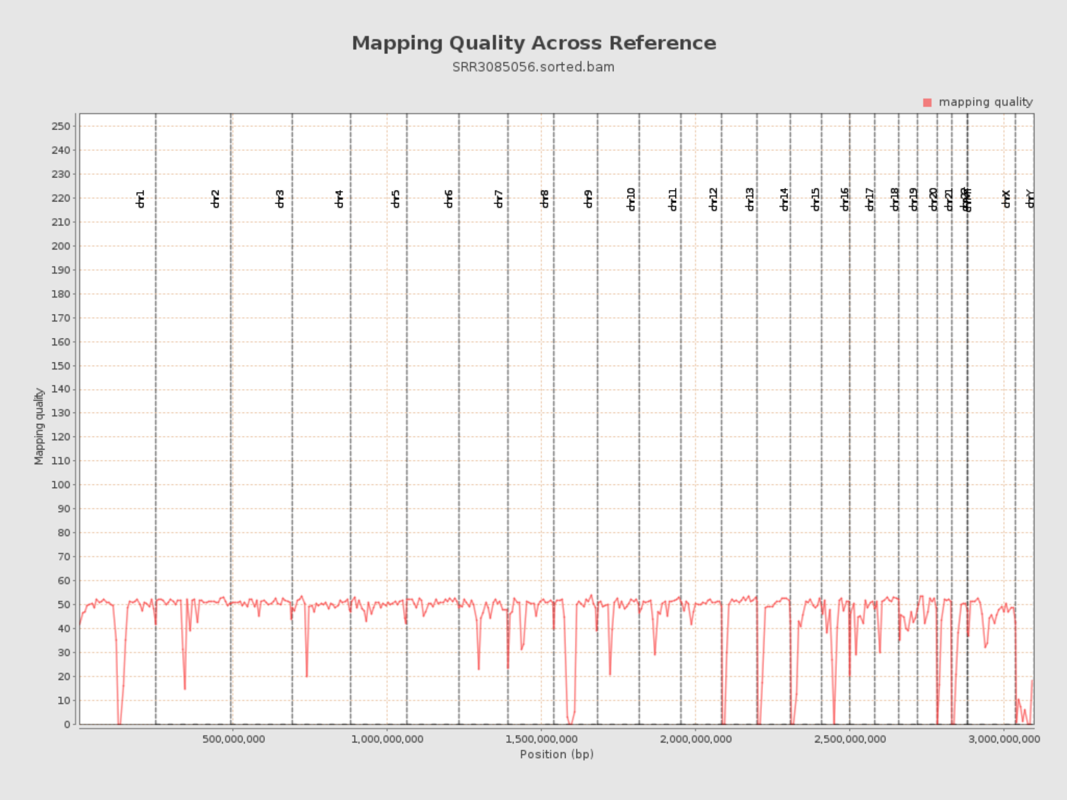
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram