Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:02:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085034.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_SRR3085034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:02:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,687,753
Mapped reads	2,442,114 / 90.86%
Unmapped reads	245,639 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,288 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	88,177 / 3.28%
Duplication rate	2.84%
Clipped reads	1,111,750 / 41.36%

2.2. ACGT Content

Number/percentage of A's	45,838,505 / 28.09%
Number/percentage of C's	31,730,472 / 19.44%
Number/percentage of T's	49,688,829 / 30.44%
Number/percentage of G's	35,934,030 / 22.02%
Number/percentage of N's	17,922 / 0.01%
GC Percentage	41.46%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.3943

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

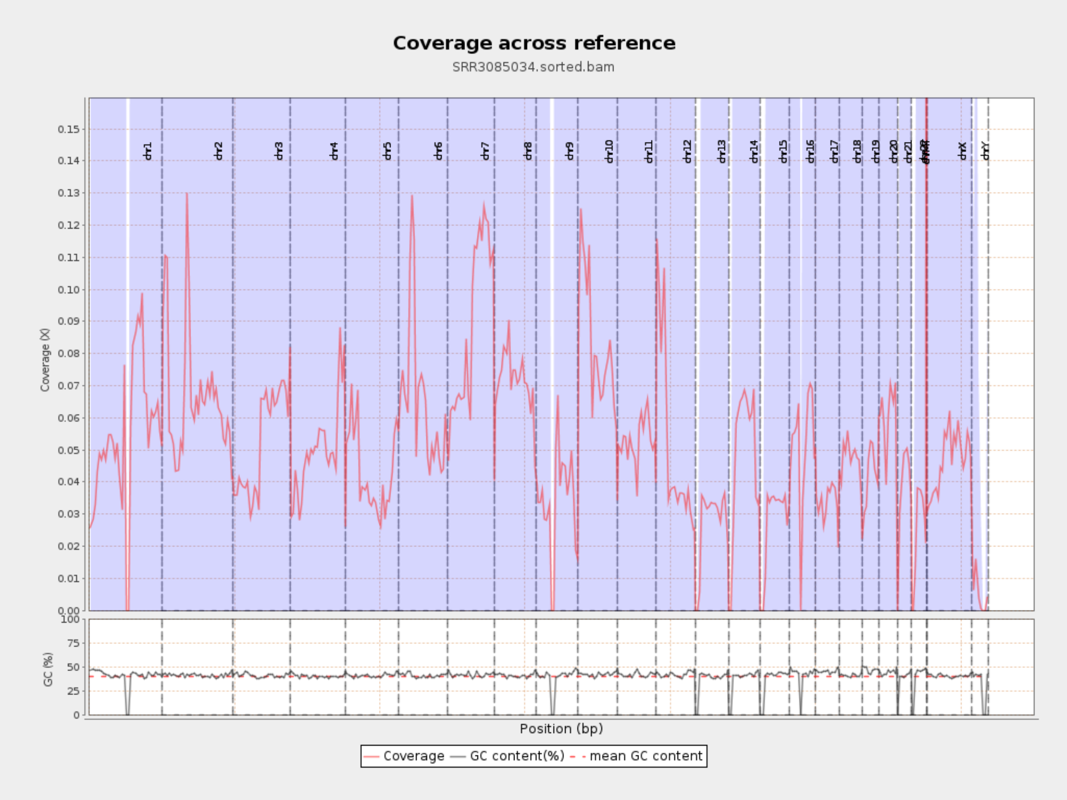
General error rate	0.88%
Mismatches	1,423,410
Insertions	11,452
Mapped reads with at least one insertion	0.46%
Deletions	34,633
Mapped reads with at least one deletion	1.4%
Homopolymer indels	46.23%

2.6. Chromosome stats

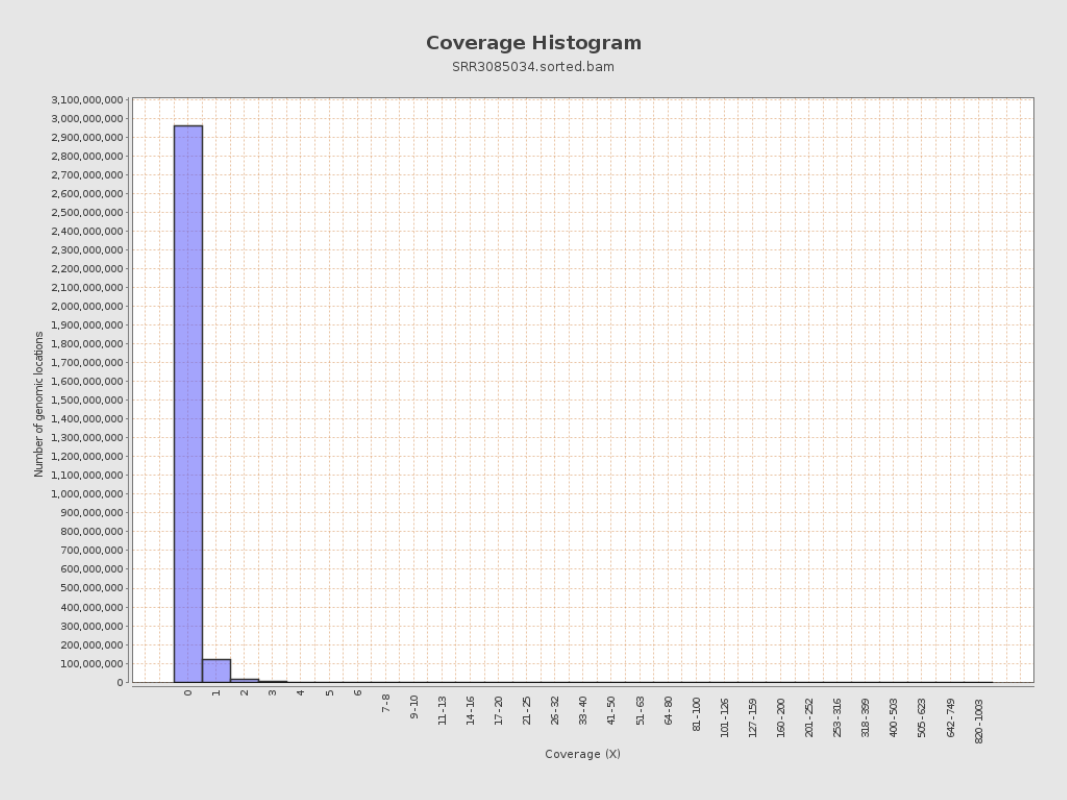
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13503828	0.0542	0.578
chr2	243199373	16453556	0.0677	0.5167
chr3	198022430	10338991	0.0522	0.2681
chr4	191154276	9633509	0.0504	0.2646
chr5	180915260	7827886	0.0433	0.238
chr6	171115067	11245594	0.0657	0.3895
chr7	159138663	14259966	0.0896	0.4688

chr8	146364022	10472187	0.0715	0.6745
chr9	141213431	4893326	0.0347	0.3246
chr10	135534747	11449463	0.0845	0.5506
chr11	135006516	7125659	0.0528	0.3853
chr12	133851895	6887553	0.0515	0.2676
chr13	115169878	3118728	0.0271	0.1869
chr14	107349540	5210854	0.0485	0.2656
chr15	102531392	2802083	0.0273	0.1985
chr16	90354753	4668537	0.0517	0.277
chr17	81195210	2727138	0.0336	0.2437
chr18	78077248	3711668	0.0475	0.5223
chr19	59128983	2503520	0.0423	0.4231
chr20	63025520	3779506	0.06	0.2844
chr21	48129895	1838085	0.0382	0.2343
chr22	51304566	1225937	0.0239	0.1758
chrMT	16571	11808	0.7126	0.9738
chrX	155270560	7261209	0.0468	0.2752
chrY	59373566	318629	0.0054	0.1099

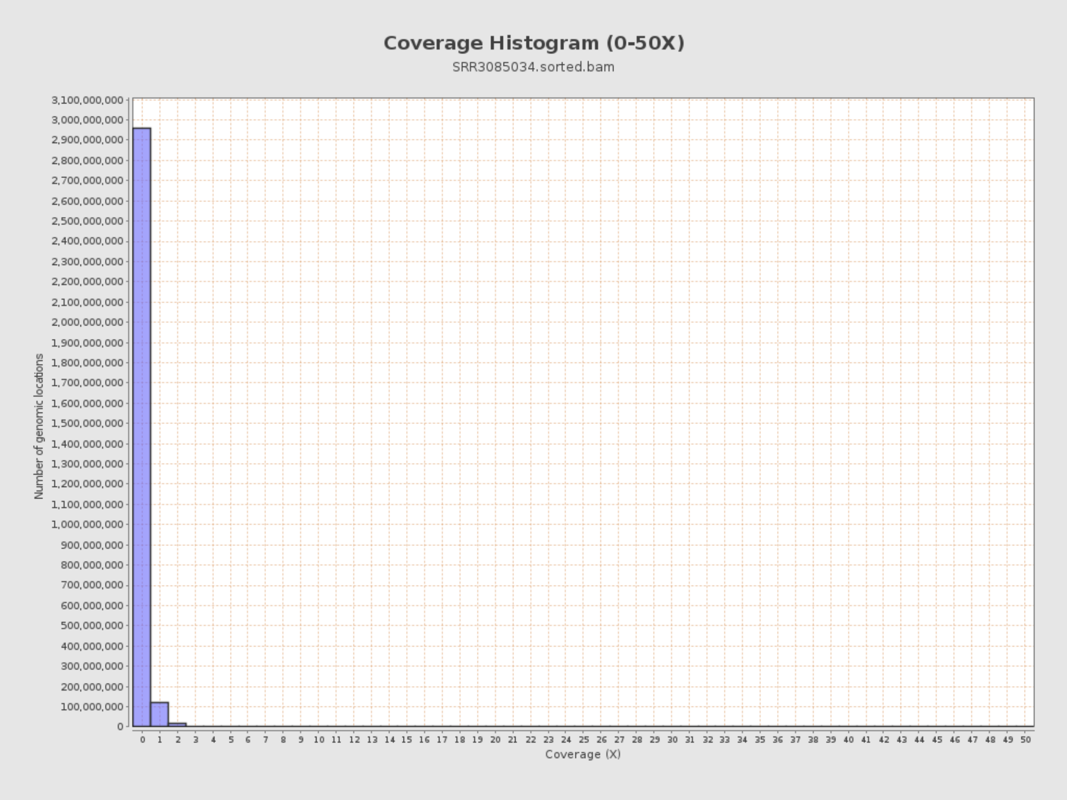
3. Results : Coverage across reference



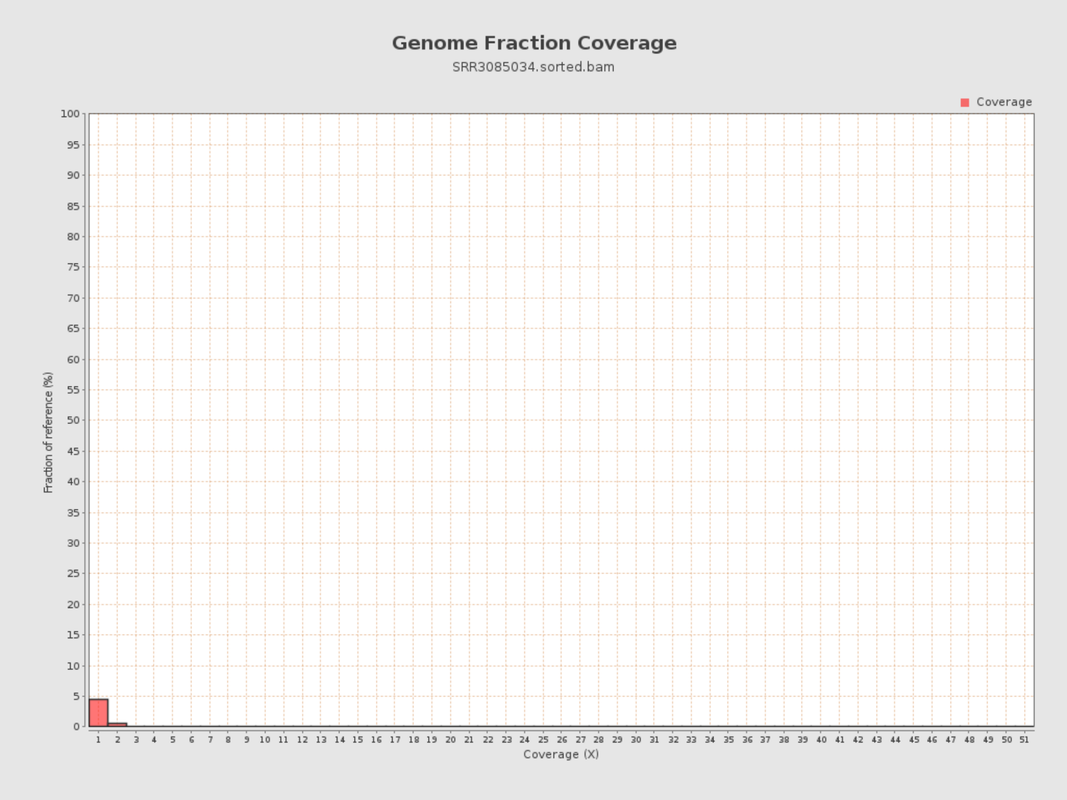
4. Results : Coverage Histogram



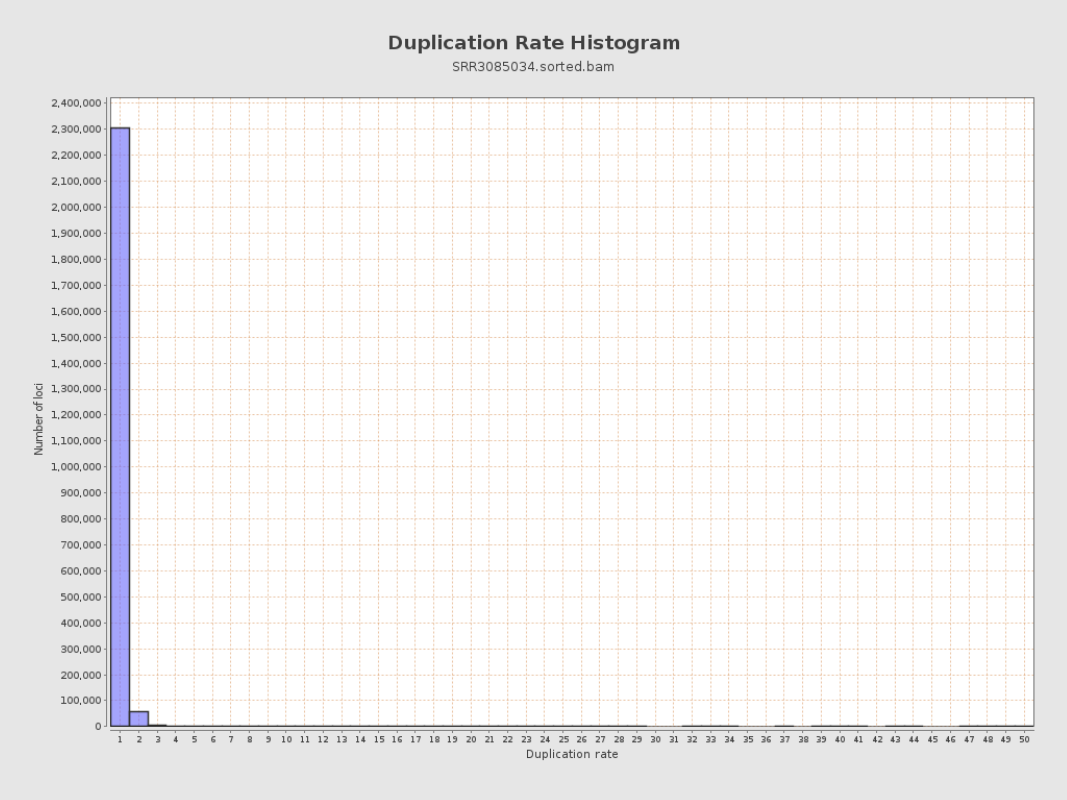
5. Results : Coverage Histogram (0-50X)



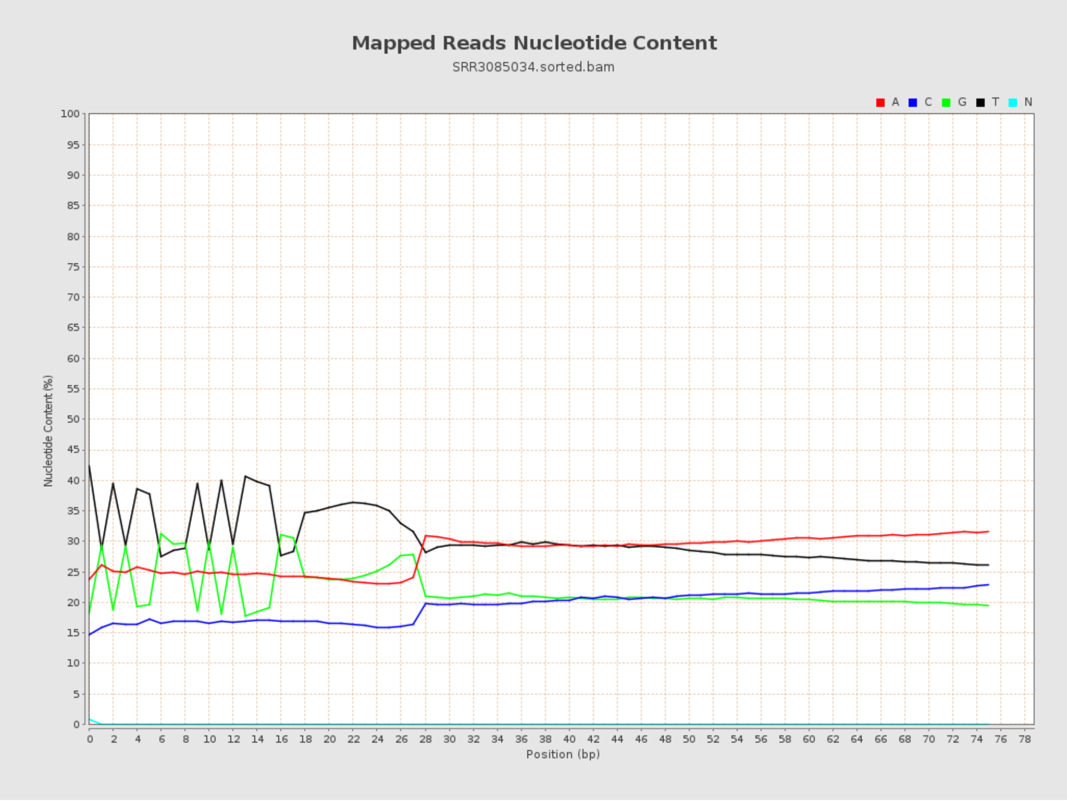
6. Results : Genome Fraction Coverage



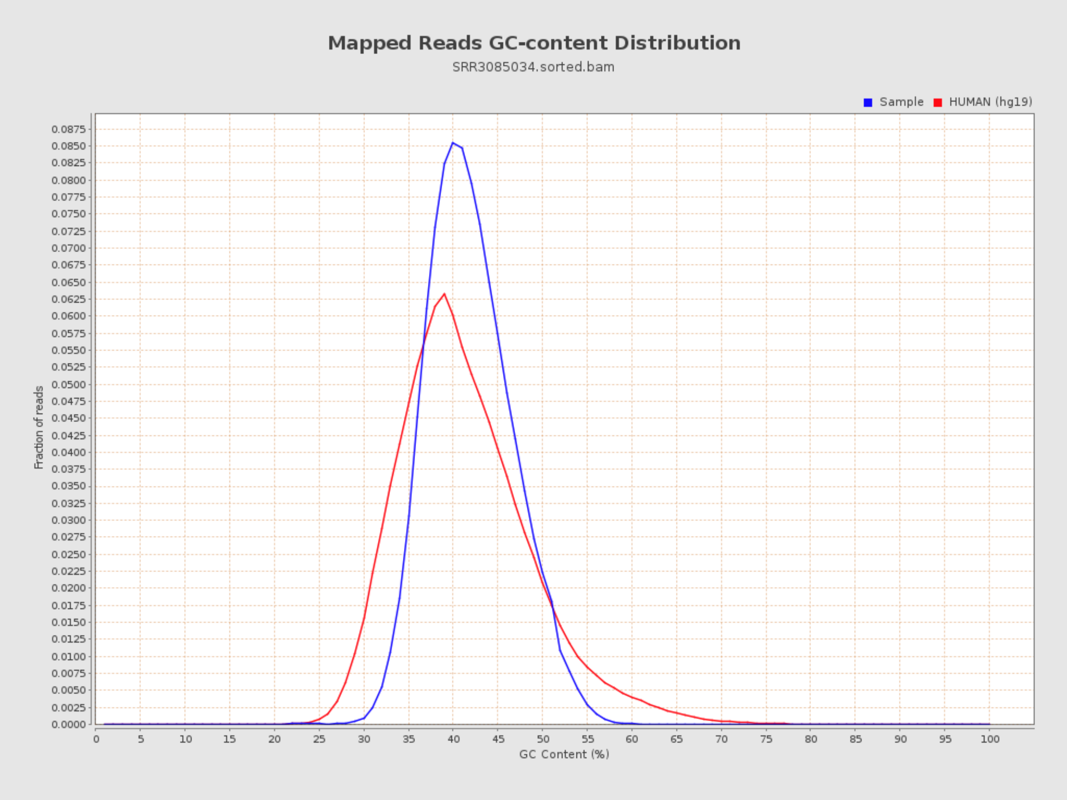
7. Results : Duplication Rate Histogram



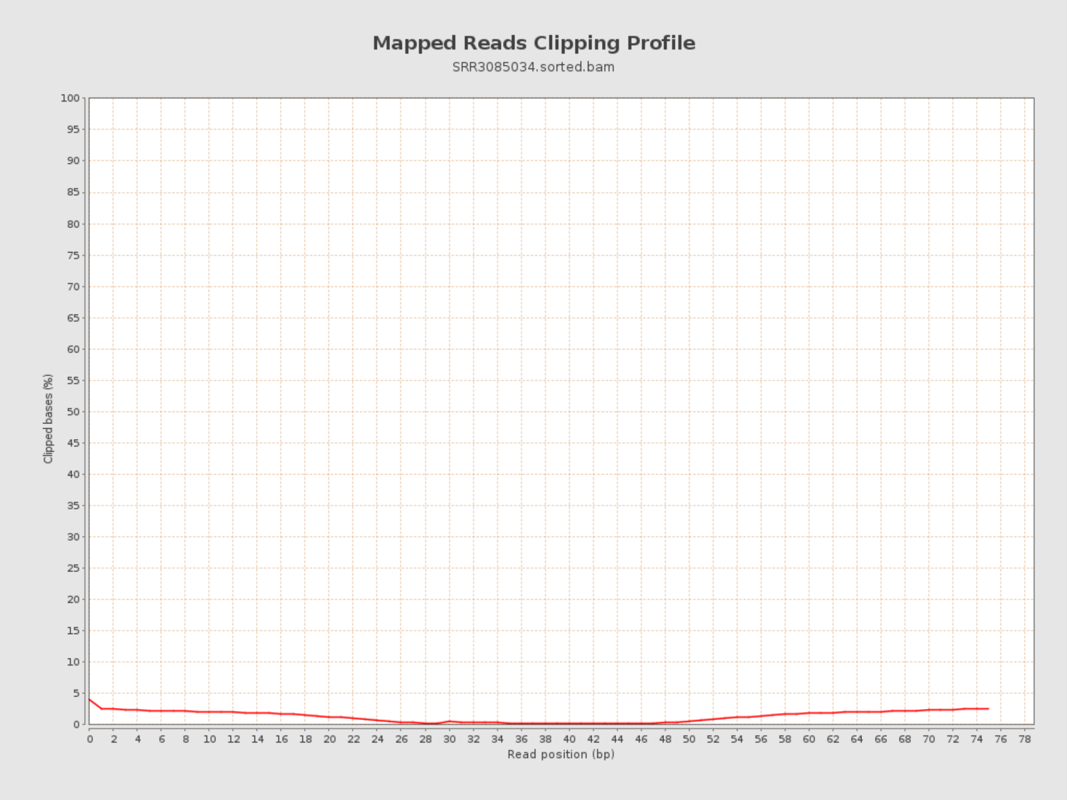
8. Results : Mapped Reads Nucleotide Content



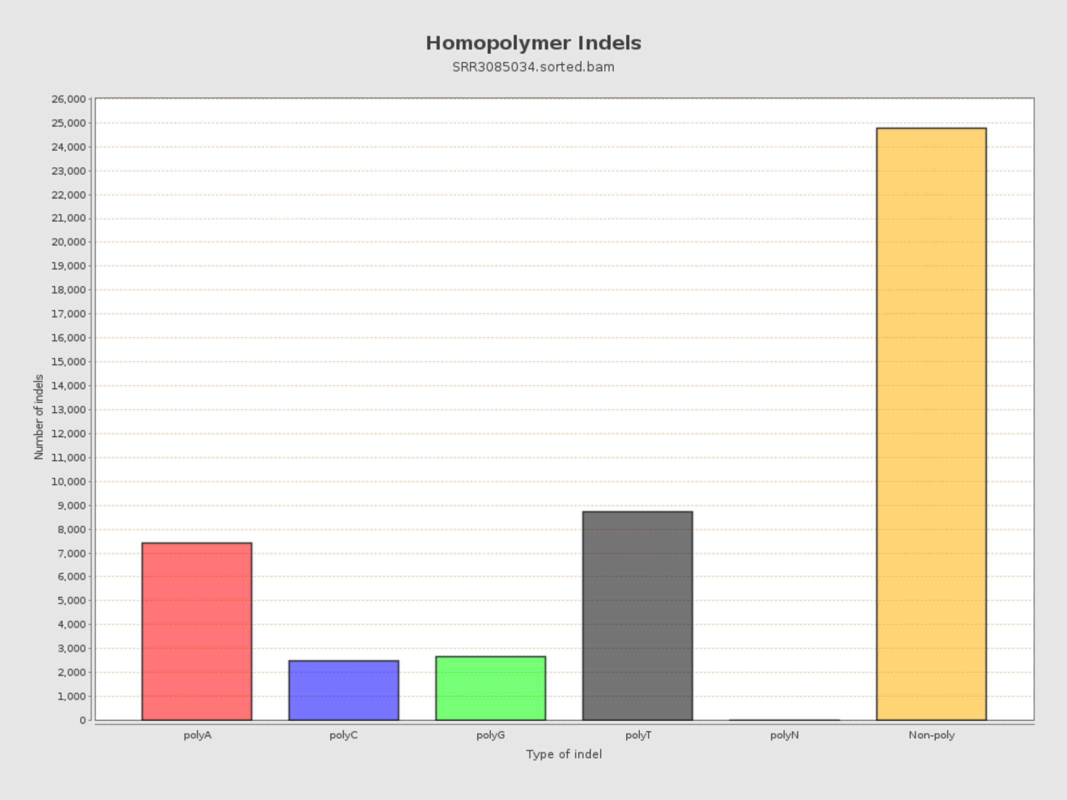
9. Results : Mapped Reads GC-content Distribution



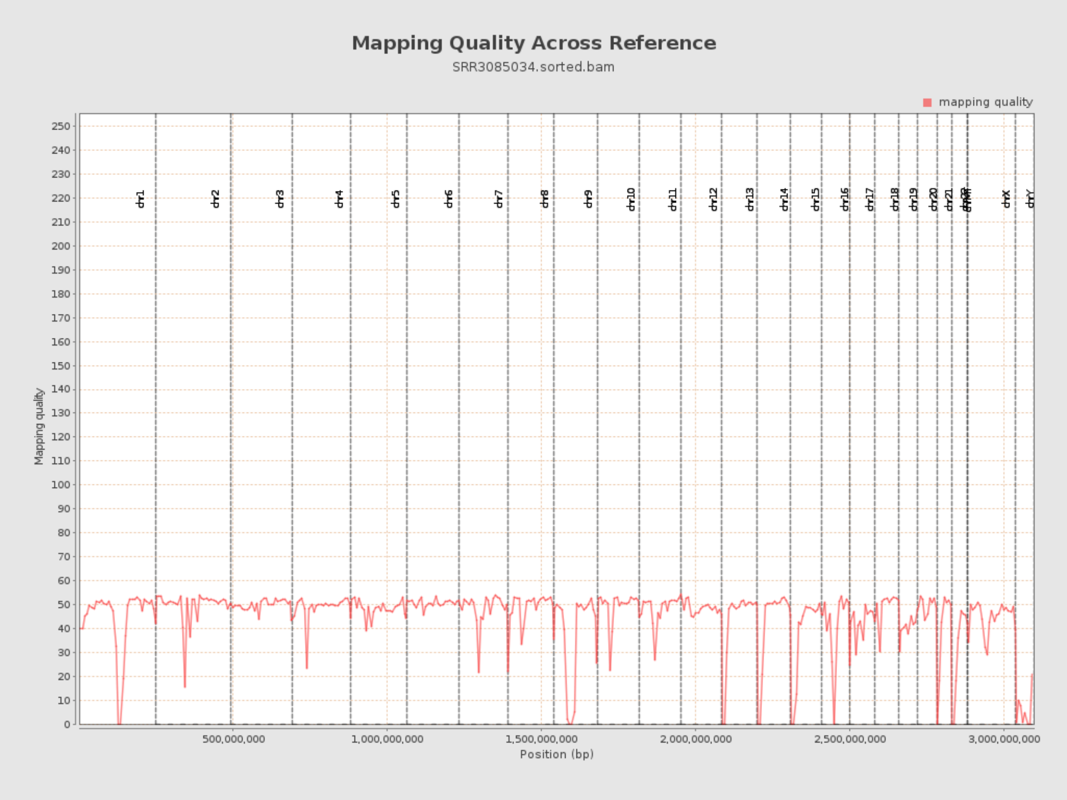
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram