Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:24:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085040.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_SRR3085040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:24:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,491,833
Mapped reads	3,171,148 / 90.82%
Unmapped reads	320,685 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,868 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	201,171 / 5.76%
Duplication rate	5.1%
Clipped reads	1,515,625 / 43.4%

2.2. ACGT Content

Number/percentage of A's	59,703,491 / 28.43%
Number/percentage of C's	39,778,054 / 18.94%
Number/percentage of T's	65,598,099 / 31.24%
Number/percentage of G's	44,879,748 / 21.37%
Number/percentage of N's	22,312 / 0.01%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0679

Standard Deviation	0.5092

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

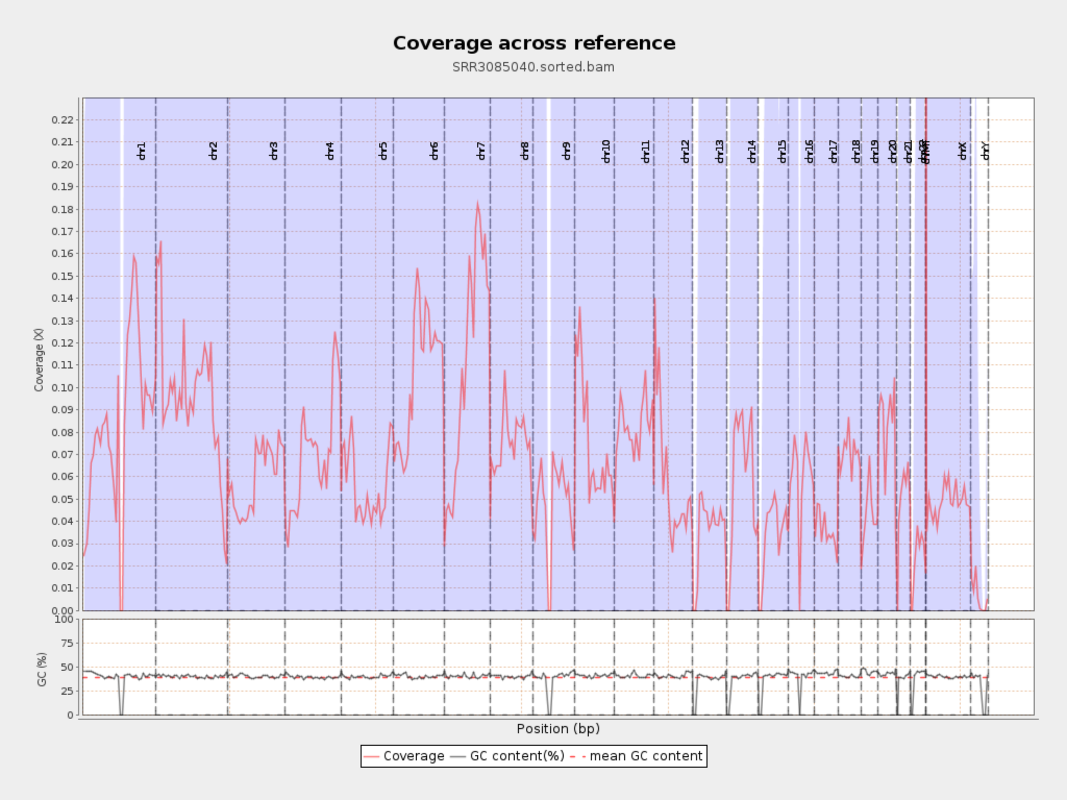
General error rate	0.86%
Mismatches	1,777,322
Insertions	14,426
Mapped reads with at least one insertion	0.45%
Deletions	38,859
Mapped reads with at least one deletion	1.21%
Homopolymer indels	46.27%

2.6. Chromosome stats

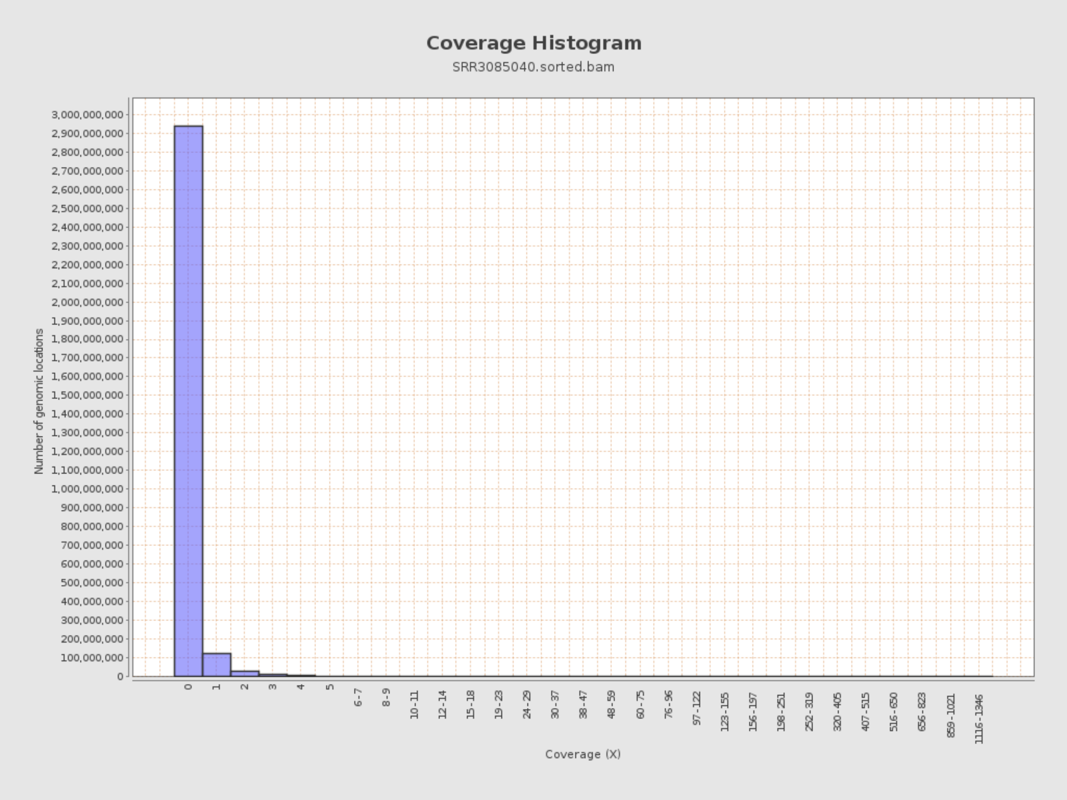
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20764388	0.0833	0.7583
chr2	243199373	23518033	0.0967	0.6227
chr3	198022430	11688956	0.059	0.3139
chr4	191154276	13428439	0.0702	0.3466
chr5	180915260	10237142	0.0566	0.3056
chr6	171115067	18175014	0.1062	0.5621
chr7	159138663	17783219	0.1117	0.6704

chr8	146364022	10996596	0.0751	0.8777
chr9	141213431	6768774	0.0479	0.4476
chr10	135534747	10326704	0.0762	0.5677
chr11	135006516	11165392	0.0827	0.5391
chr12	133851895	7882805	0.0589	0.3239
chr13	115169878	4144761	0.036	0.2398
chr14	107349540	6531212	0.0608	0.3357
chr15	102531392	3445158	0.0336	0.2436
chr16	90354753	5280795	0.0584	0.3281
chr17	81195210	2900338	0.0357	0.2935
chr18	78077248	5546568	0.071	0.803
chr19	59128983	2613908	0.0442	0.4901
chr20	63025520	5340233	0.0847	0.3796
chr21	48129895	2379249	0.0494	0.2959
chr22	51304566	1191591	0.0232	0.1898
chrMT	16571	7066	0.4264	0.8305
chrX	155270560	7550331	0.0486	0.341
chrY	59373566	381801	0.0064	0.123

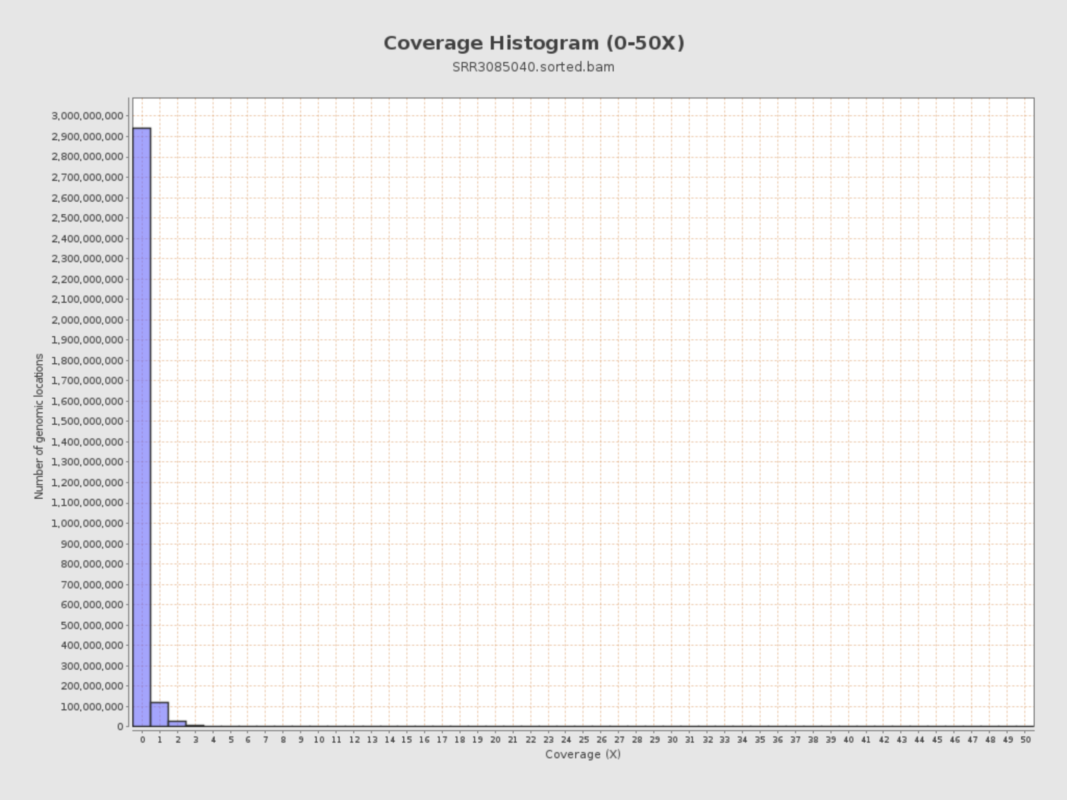
3. Results : Coverage across reference



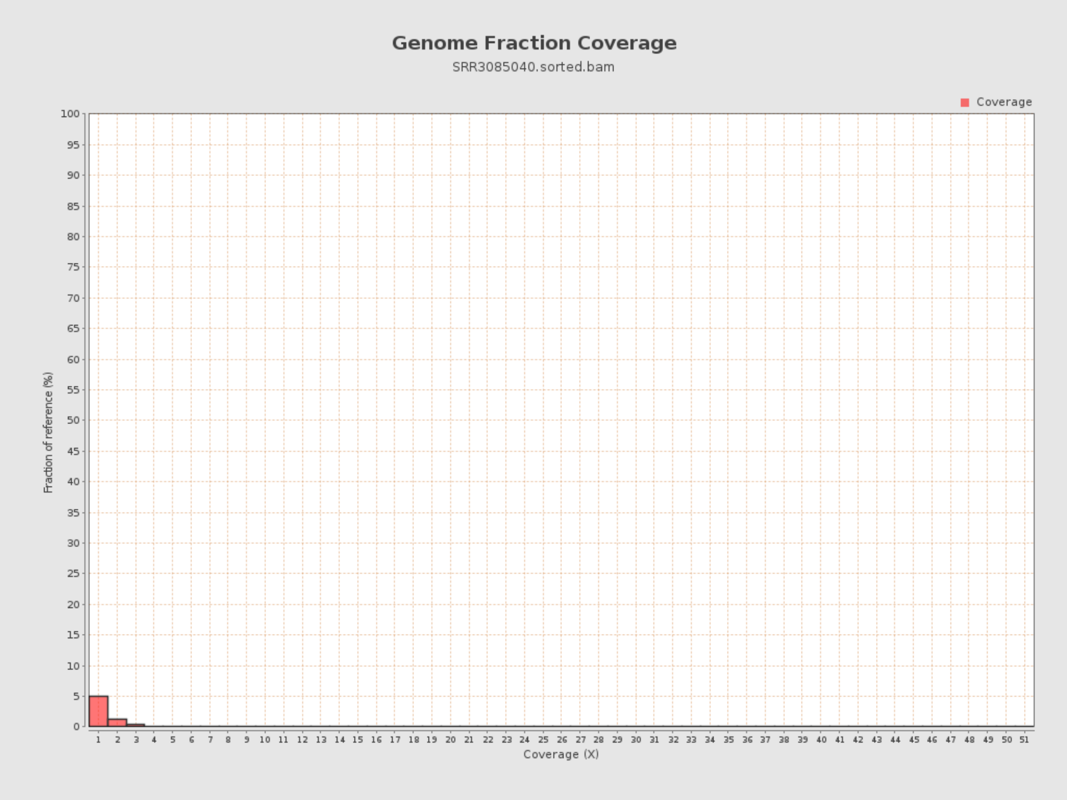
4. Results : Coverage Histogram



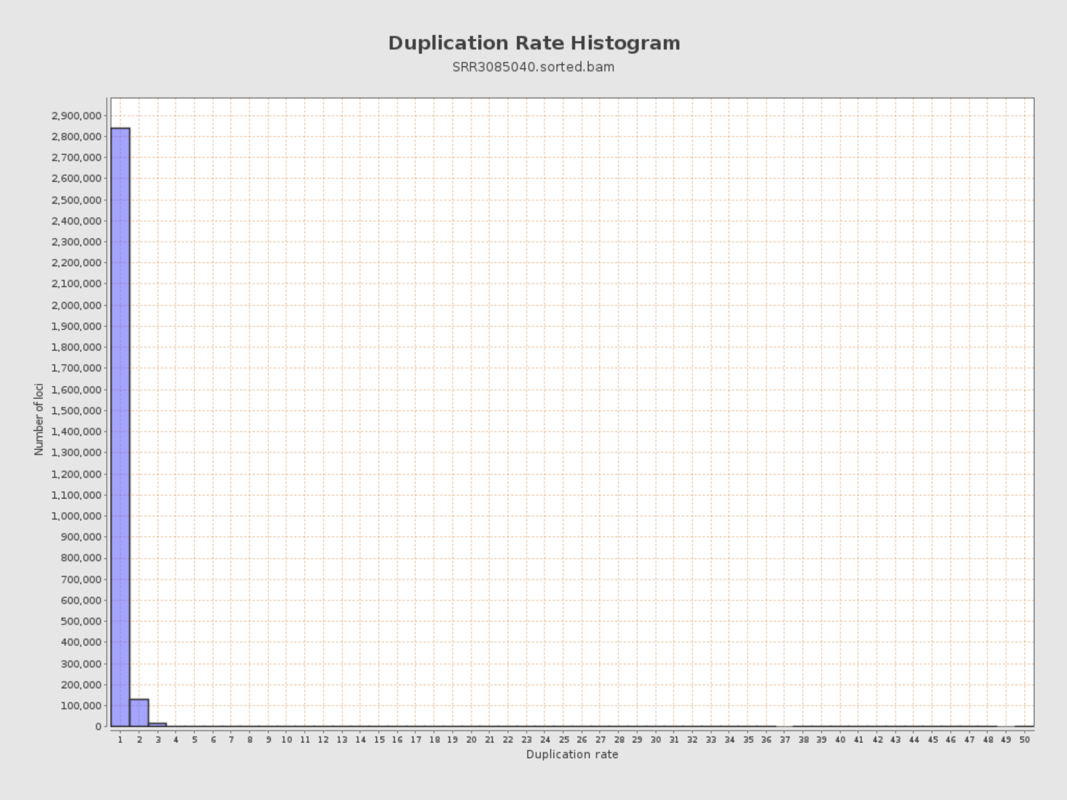
5. Results : Coverage Histogram (0-50X)



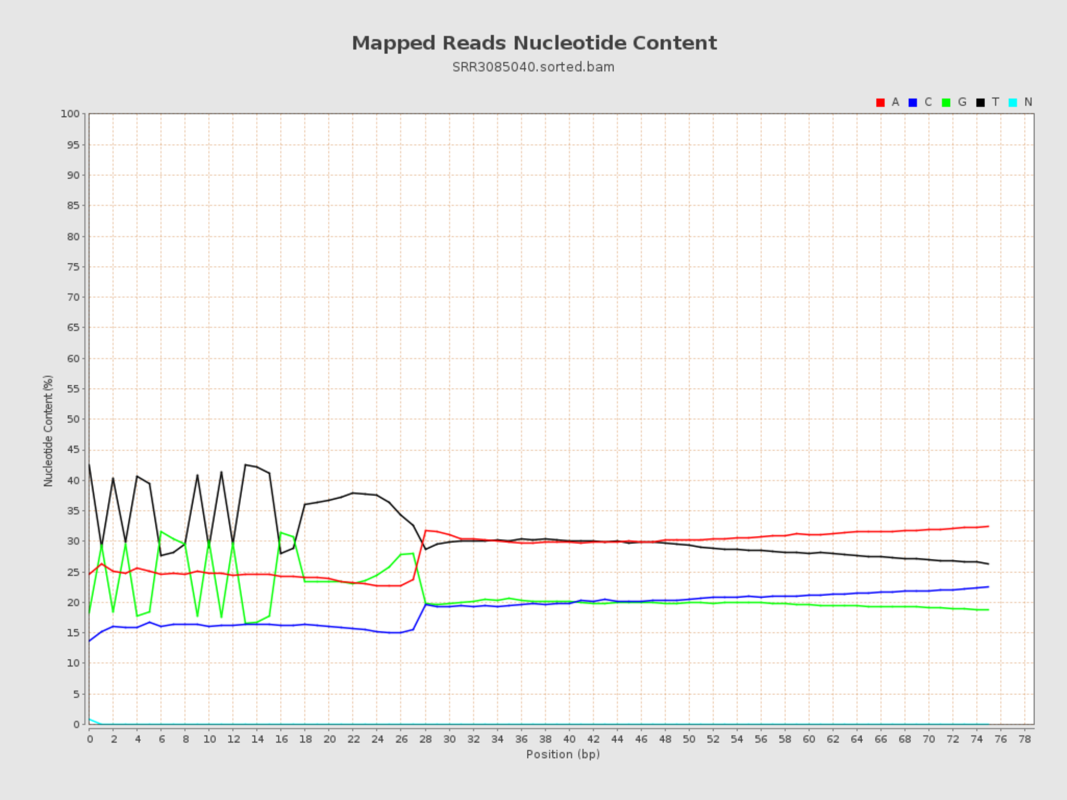
6. Results : Genome Fraction Coverage



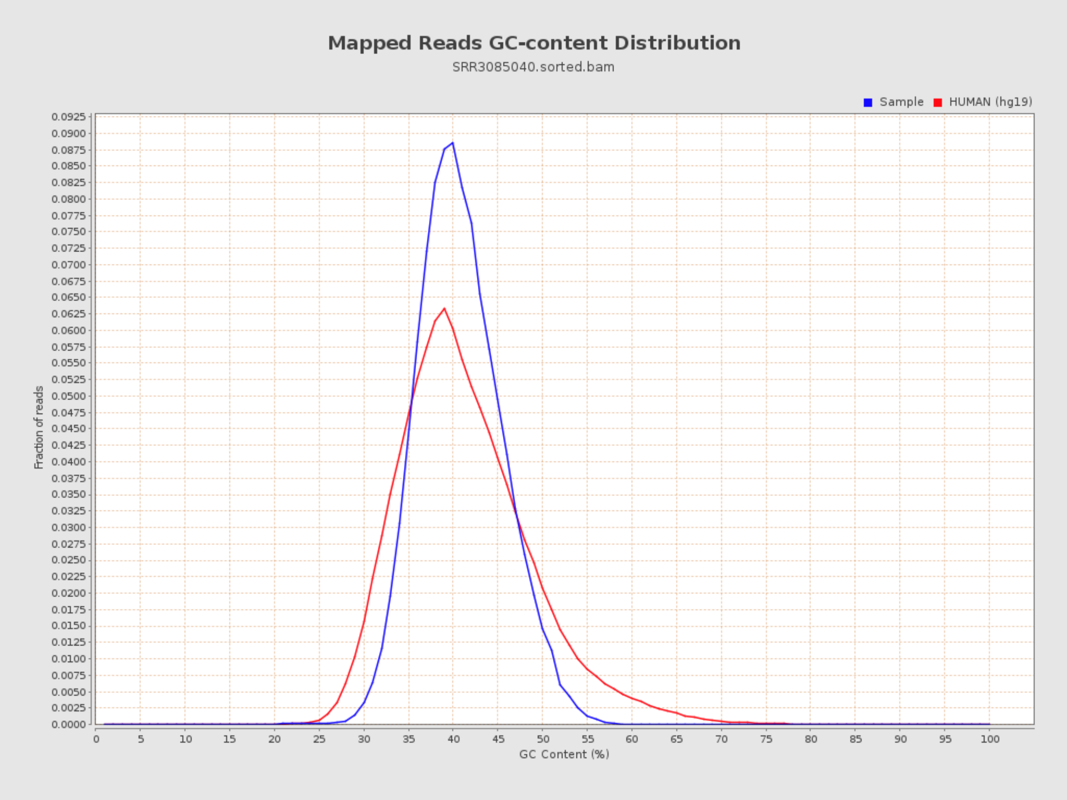
7. Results : Duplication Rate Histogram



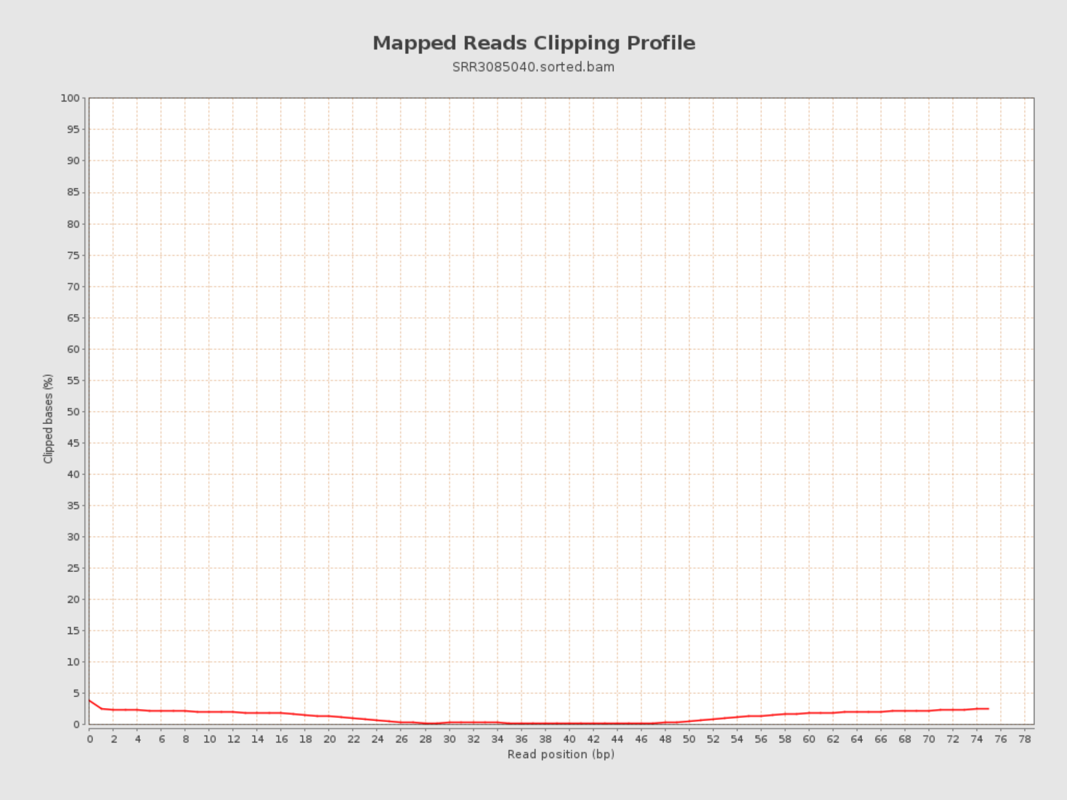
8. Results : Mapped Reads Nucleotide Content



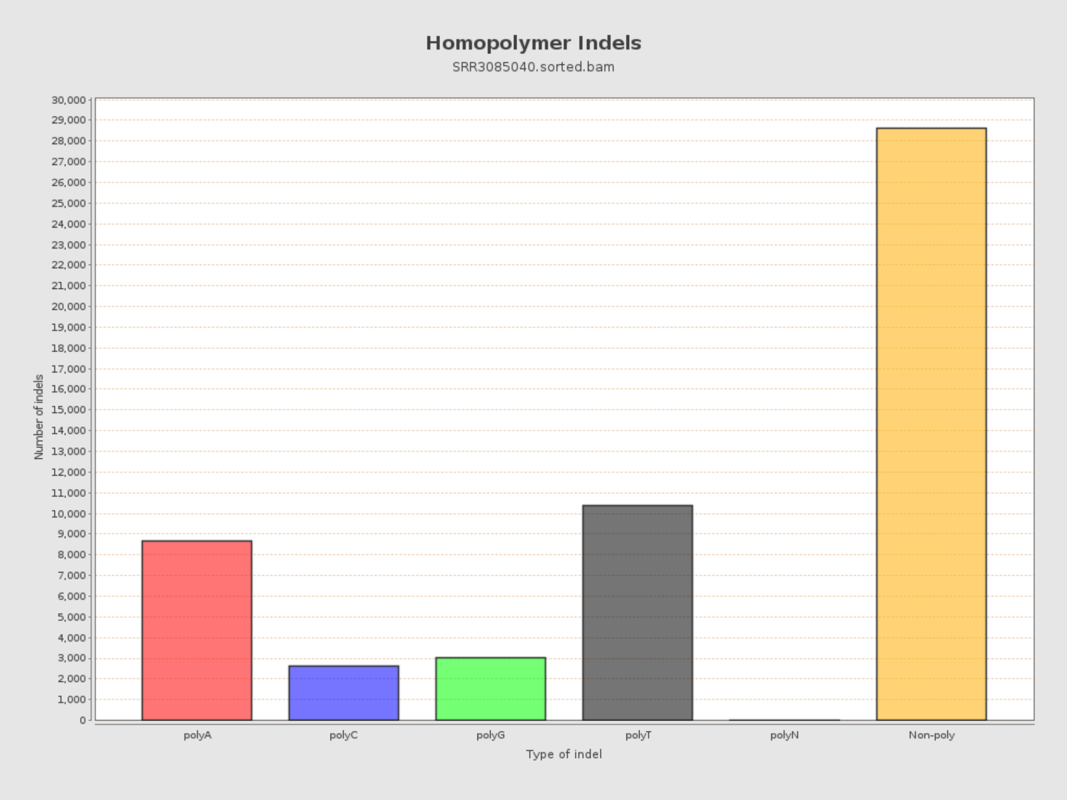
9. Results : Mapped Reads GC-content Distribution



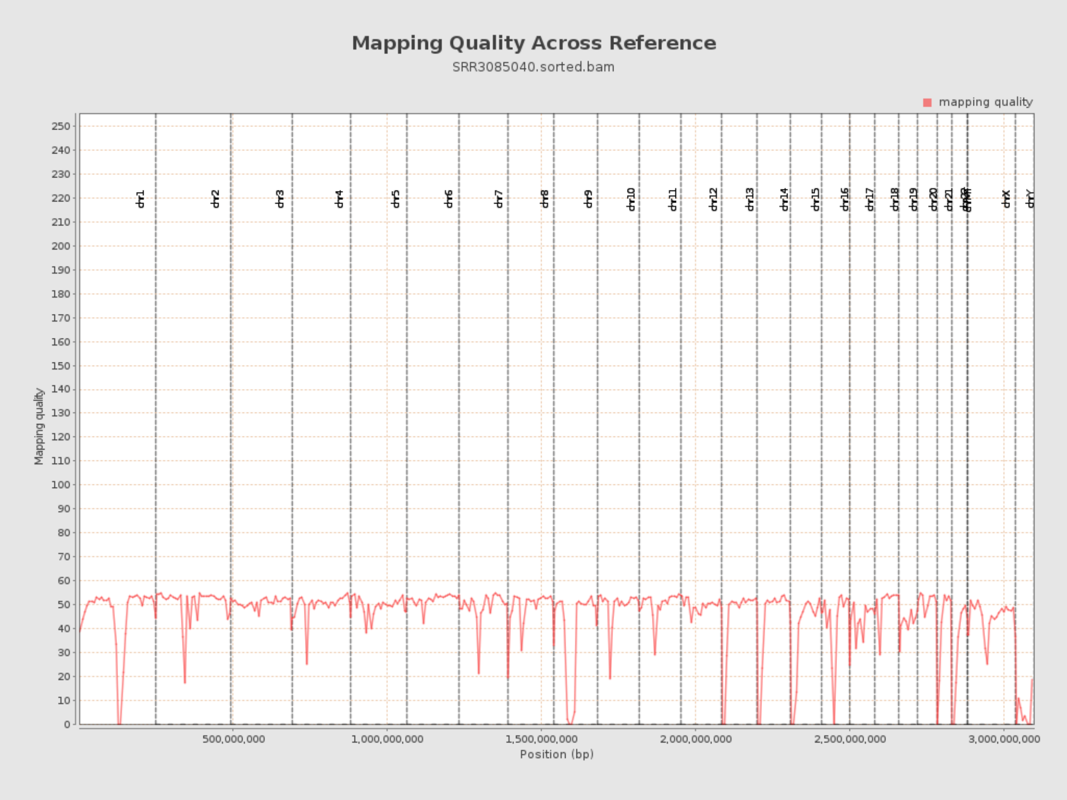
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram