Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:53:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085049.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_SRR3085049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,142,090
Mapped reads	2,841,307 / 90.43%
Unmapped reads	300,783 / 9.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,521 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	122,584 / 3.9%
Duplication rate	3.24%
Clipped reads	1,365,639 / 43.46%

2.2. ACGT Content

Number/percentage of A's	53,530,720 / 28.44%
Number/percentage of C's	35,471,431 / 18.85%
Number/percentage of T's	57,822,358 / 30.72%
Number/percentage of G's	41,358,293 / 21.97%
Number/percentage of N's	25,872 / 0.01%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0608

Standard Deviation	0.5044

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

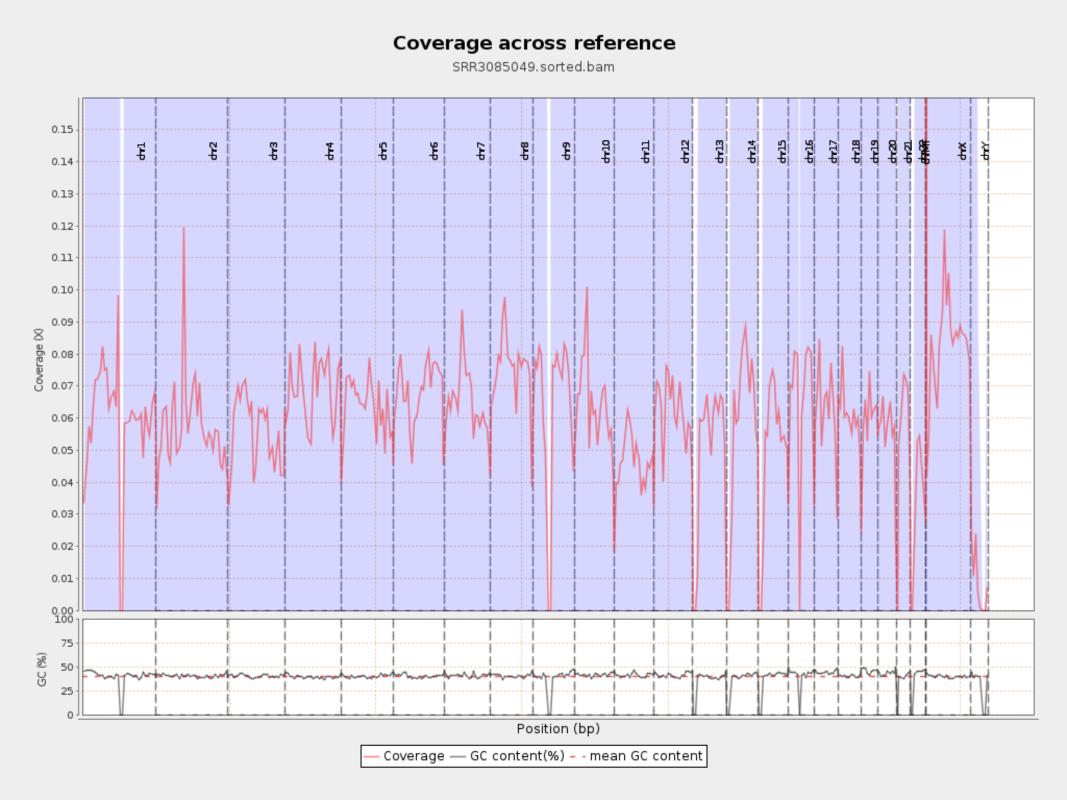
General error rate	0.85%
Mismatches	1,574,397
Insertions	15,246
Mapped reads with at least one insertion	0.53%
Deletions	42,384
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.64%

2.6. Chromosome stats

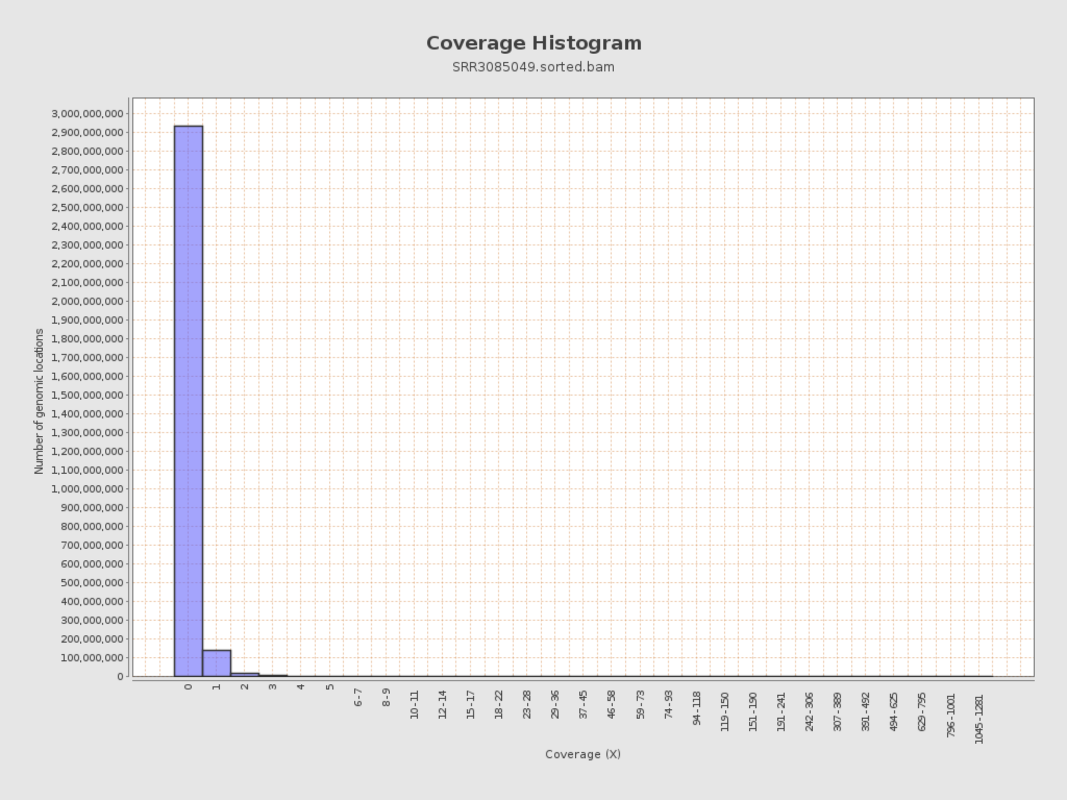
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14829012	0.0595	0.9014
chr2	243199373	14068772	0.0578	0.6136
chr3	198022430	11077149	0.0559	0.2702
chr4	191154276	13321767	0.0697	0.3136
chr5	180915260	11547233	0.0638	0.2899
chr6	171115067	11731326	0.0686	0.3291
chr7	159138663	10374065	0.0652	0.4734

chr8	146364022	11023447	0.0753	0.8441
chr9	141213431	9008742	0.0638	0.494
chr10	135534747	8806699	0.065	0.4462
chr11	135006516	6266528	0.0464	0.4421
chr12	133851895	8373597	0.0626	0.293
chr13	115169878	5760479	0.05	0.2521
chr14	107349540	6347115	0.0591	0.3149
chr15	102531392	5000692	0.0488	0.2572
chr16	90354753	5778613	0.064	0.3499
chr17	81195210	5185430	0.0639	0.3612
chr18	78077248	4839515	0.062	0.9887
chr19	59128983	3570612	0.0604	0.6593
chr20	63025520	3588466	0.0569	0.2938
chr21	48129895	2714560	0.0564	0.2911
chr22	51304566	1682111	0.0328	0.2046
chrMT	16571	25073	1.5131	1.5285
chrX	155270560	12869322	0.0829	0.4034
chrY	59373566	486437	0.0082	0.156

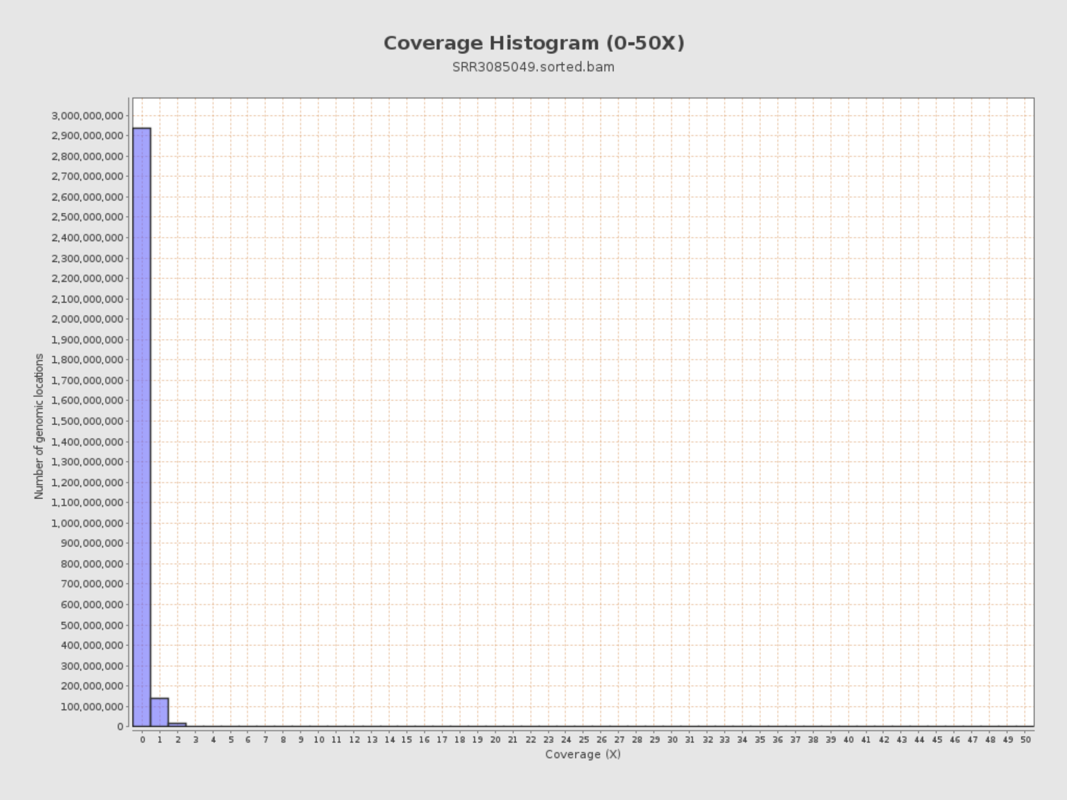
3. Results : Coverage across reference



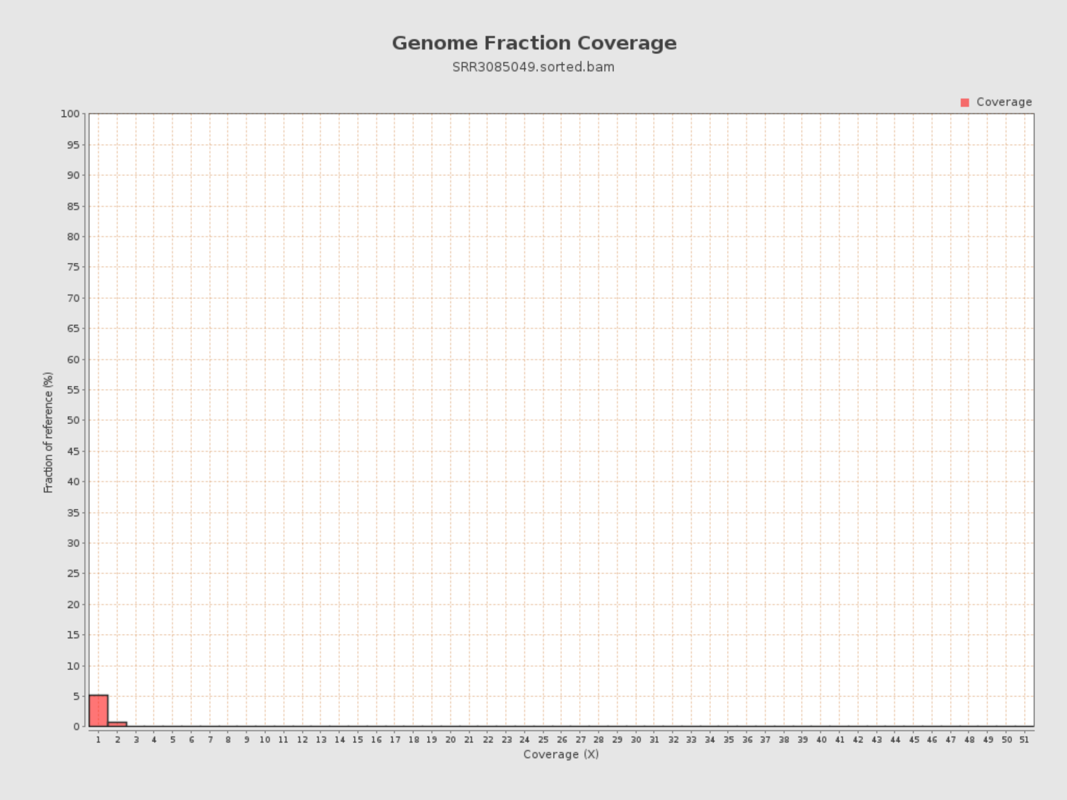
4. Results : Coverage Histogram



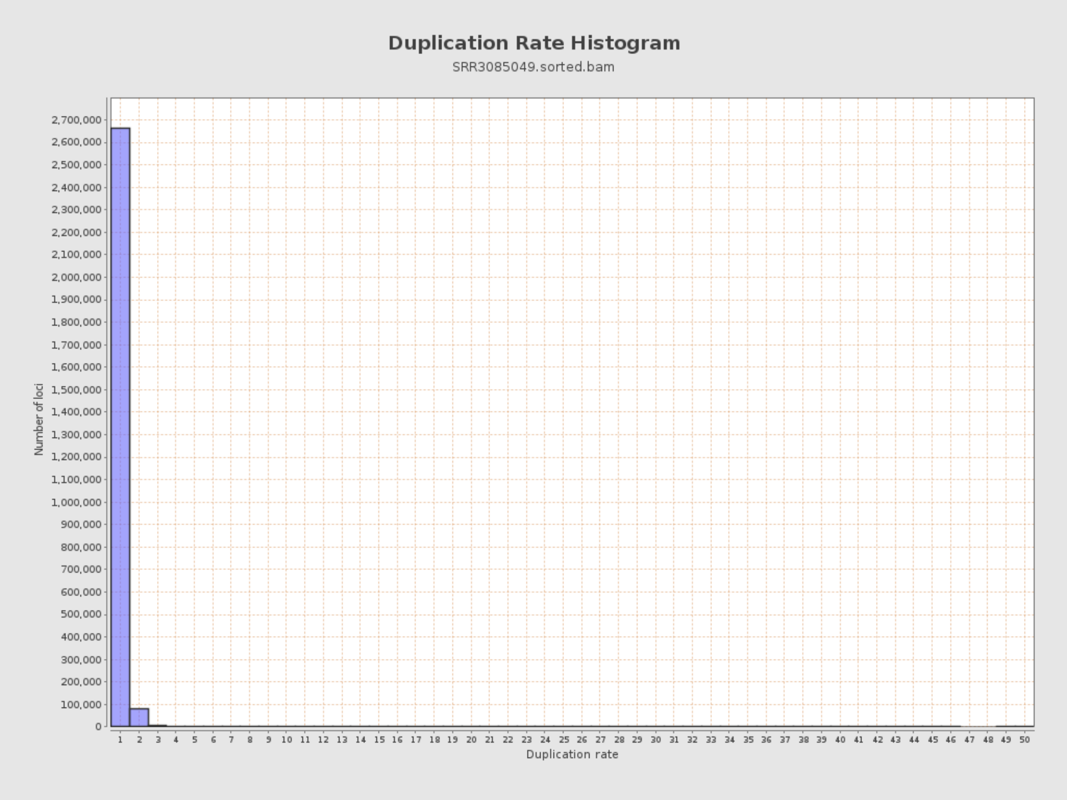
5. Results : Coverage Histogram (0-50X)



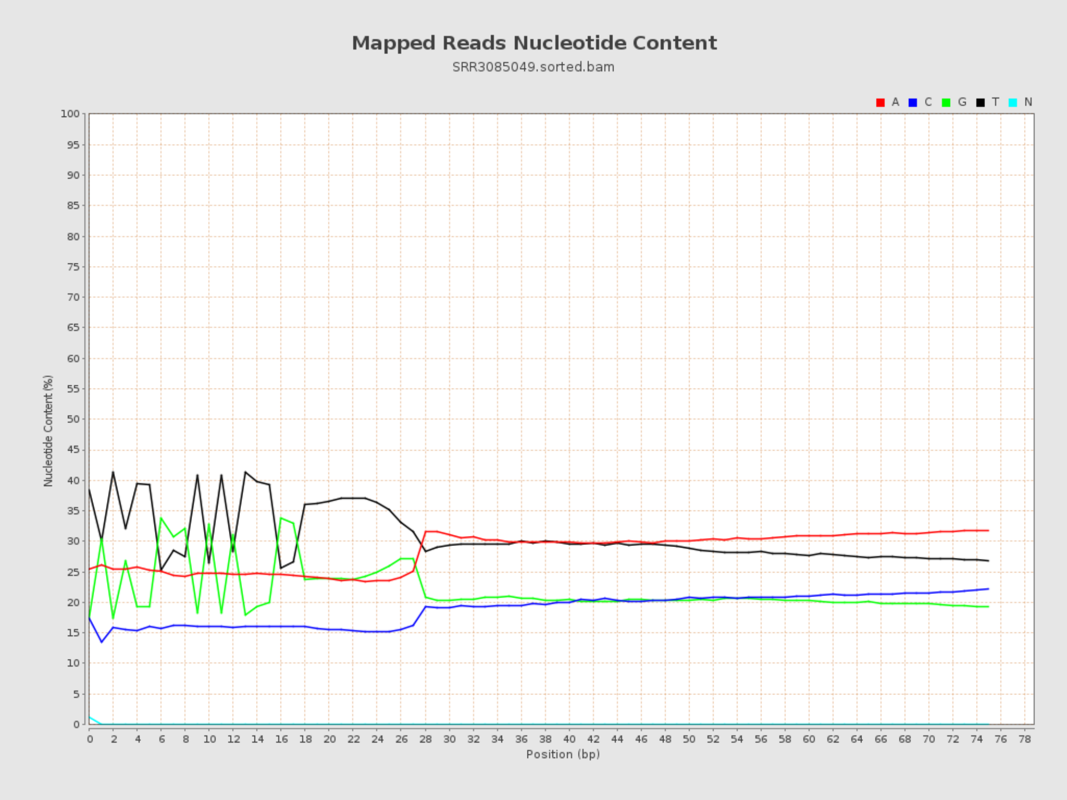
6. Results : Genome Fraction Coverage



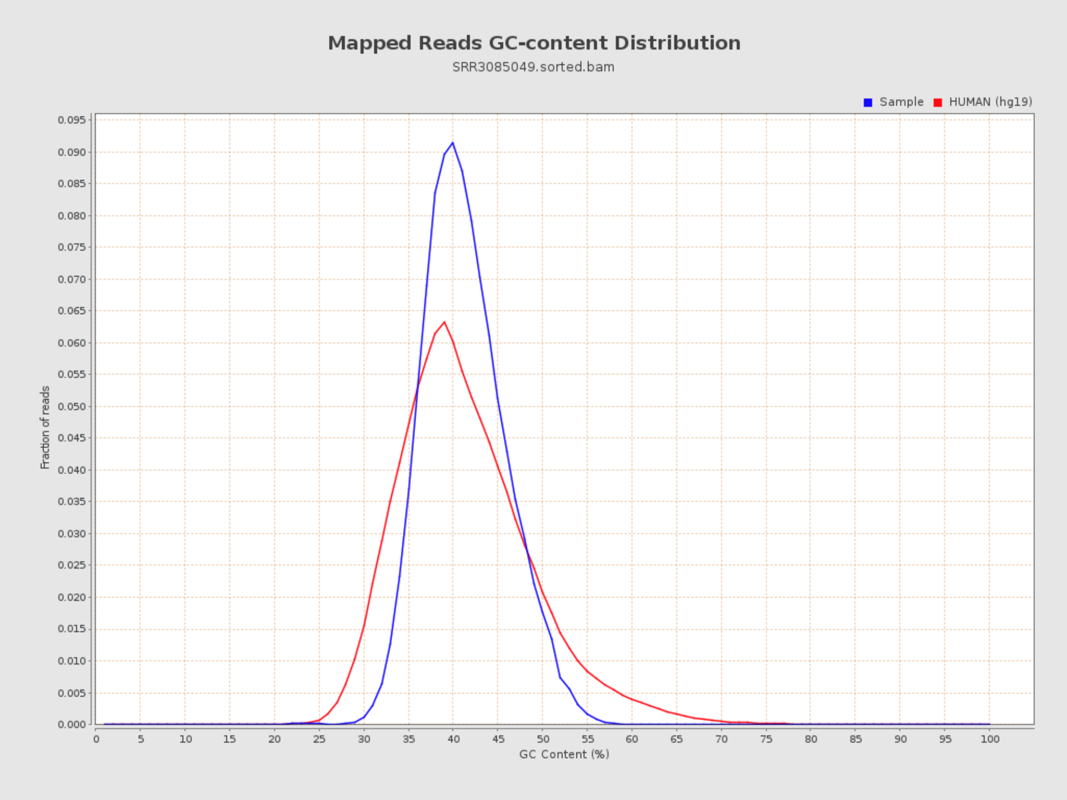
7. Results : Duplication Rate Histogram



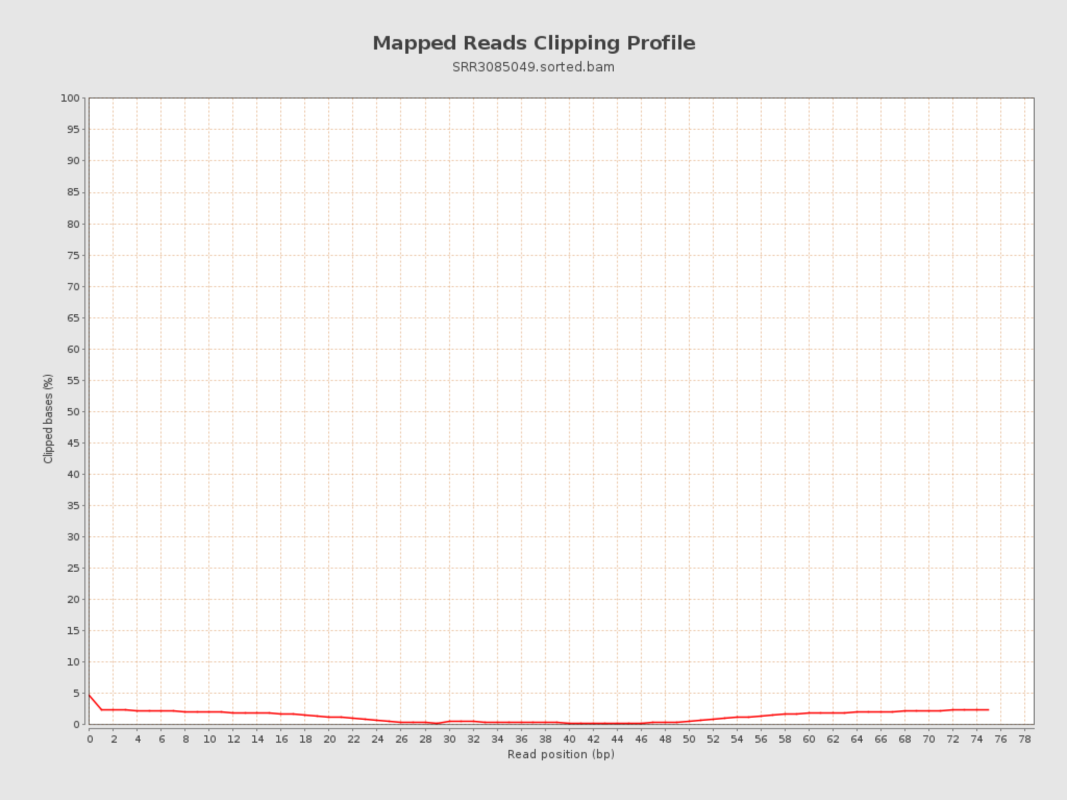
8. Results : Mapped Reads Nucleotide Content



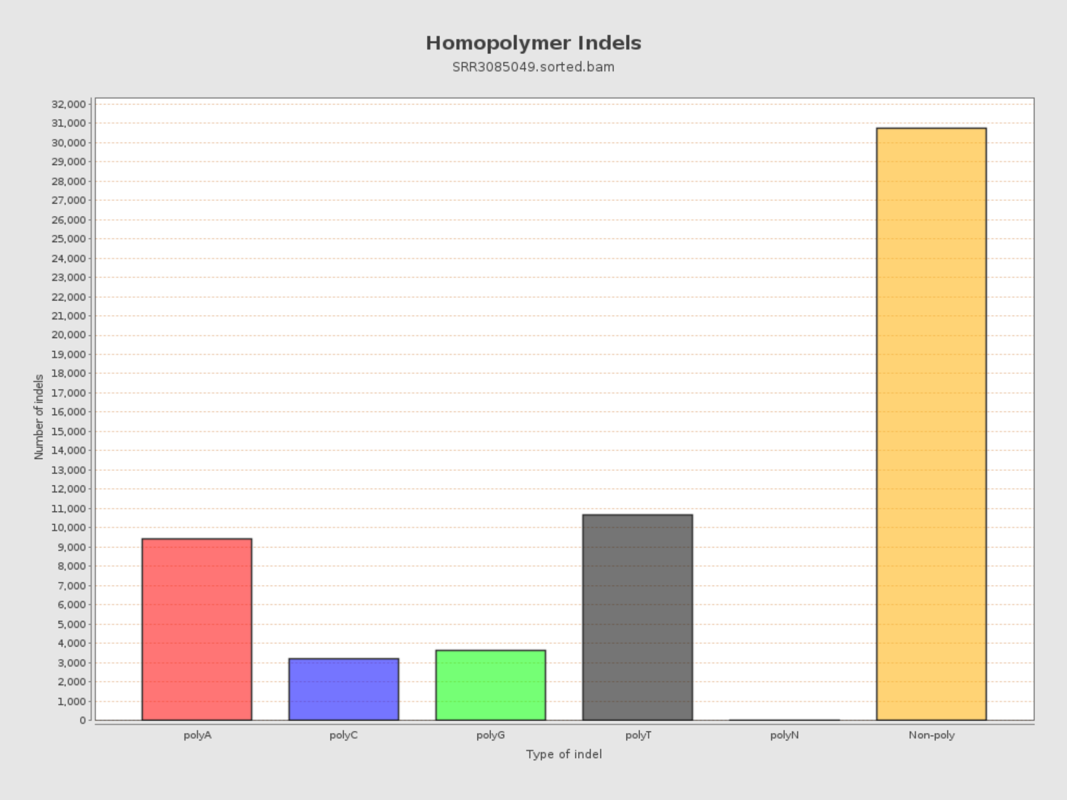
9. Results : Mapped Reads GC-content Distribution



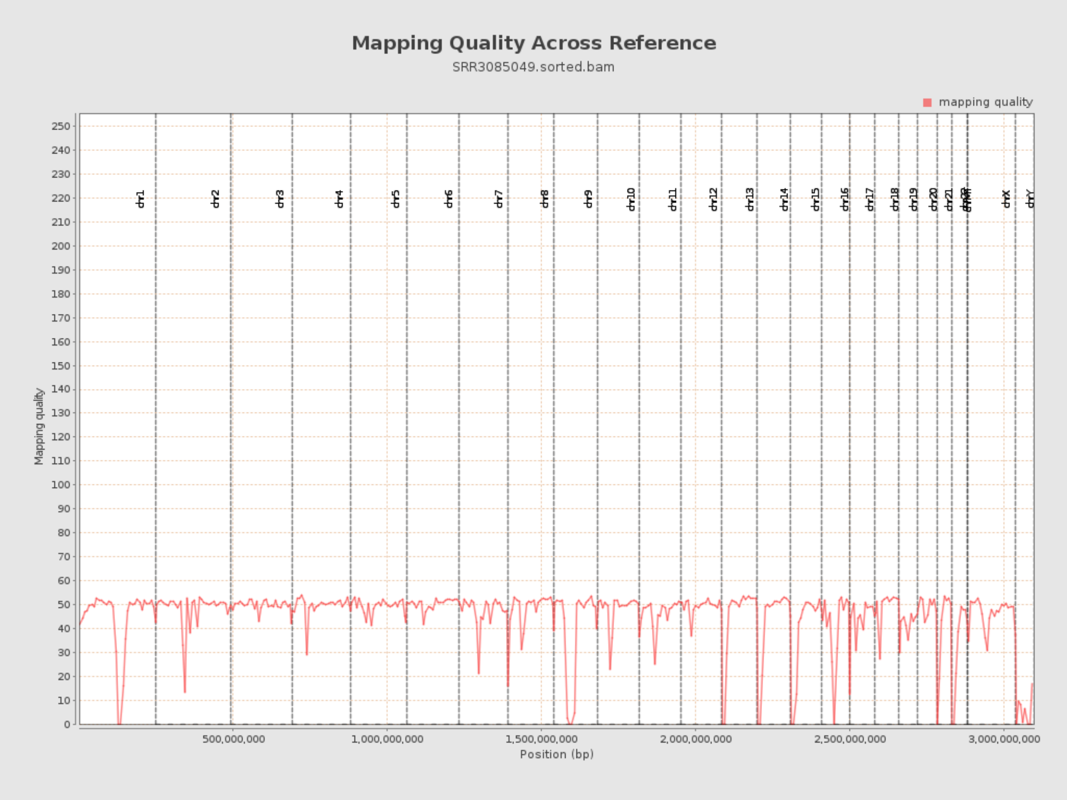
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram