Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:38:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085044.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_SRR3085044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:38:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,512,243
Mapped reads	2,319,399 / 92.32%
Unmapped reads	192,844 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,809 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	73,663 / 2.93%
Duplication rate	2.43%
Clipped reads	950,406 / 37.83%

2.2. ACGT Content

Number/percentage of A's	45,058,865 / 28.67%
Number/percentage of C's	29,549,234 / 18.8%
Number/percentage of T's	48,819,804 / 31.06%
Number/percentage of G's	33,733,656 / 21.46%
Number/percentage of N's	17,945 / 0.01%
GC Percentage	40.26%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.3991

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

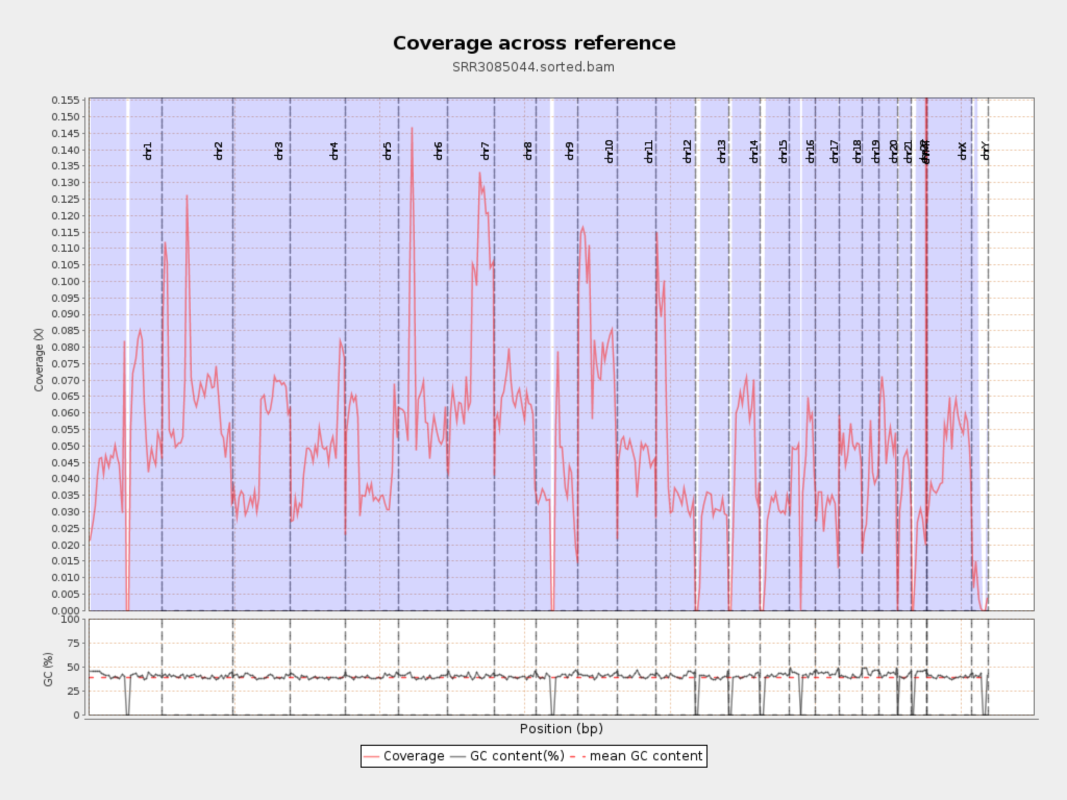
General error rate	0.89%
Mismatches	1,379,974
Insertions	11,382
Mapped reads with at least one insertion	0.49%
Deletions	33,543
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.21%

2.6. Chromosome stats

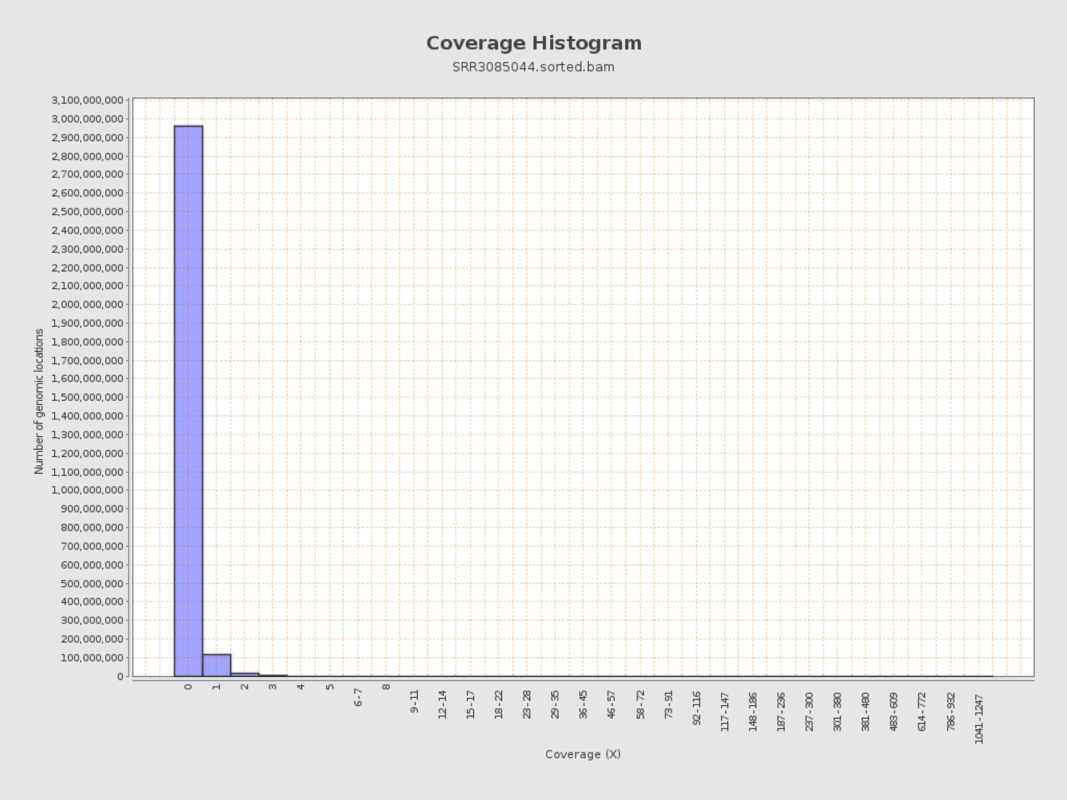
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12059275	0.0484	0.5911
chr2	243199373	16418426	0.0675	0.4708
chr3	198022430	9873239	0.0499	0.2577
chr4	191154276	9303119	0.0487	0.2559
chr5	180915260	7965720	0.044	0.2361
chr6	171115067	11234070	0.0657	0.3733
chr7	159138663	13893449	0.0873	0.4359

chr8	146364022	9199798	0.0629	0.791
chr9	141213431	5061804	0.0358	0.3351
chr10	135534747	11680066	0.0862	0.5162
chr11	135006516	6329356	0.0469	0.3764
chr12	133851895	6669104	0.0498	0.2592
chr13	115169878	3038135	0.0264	0.181
chr14	107349540	5218289	0.0486	0.2663
chr15	102531392	2616308	0.0255	0.1863
chr16	90354753	4065962	0.045	0.2575
chr17	81195210	2430104	0.0299	0.2289
chr18	78077248	3914595	0.0501	0.6454
chr19	59128983	2218974	0.0375	0.4294
chr20	63025520	3435013	0.0545	0.2653
chr21	48129895	1743477	0.0362	0.2284
chr22	51304566	965138	0.0188	0.1501
chrMT	16571	66125	3.9904	3.0517
chrX	155270560	7535860	0.0485	0.2755
chrY	59373566	301921	0.0051	0.1086

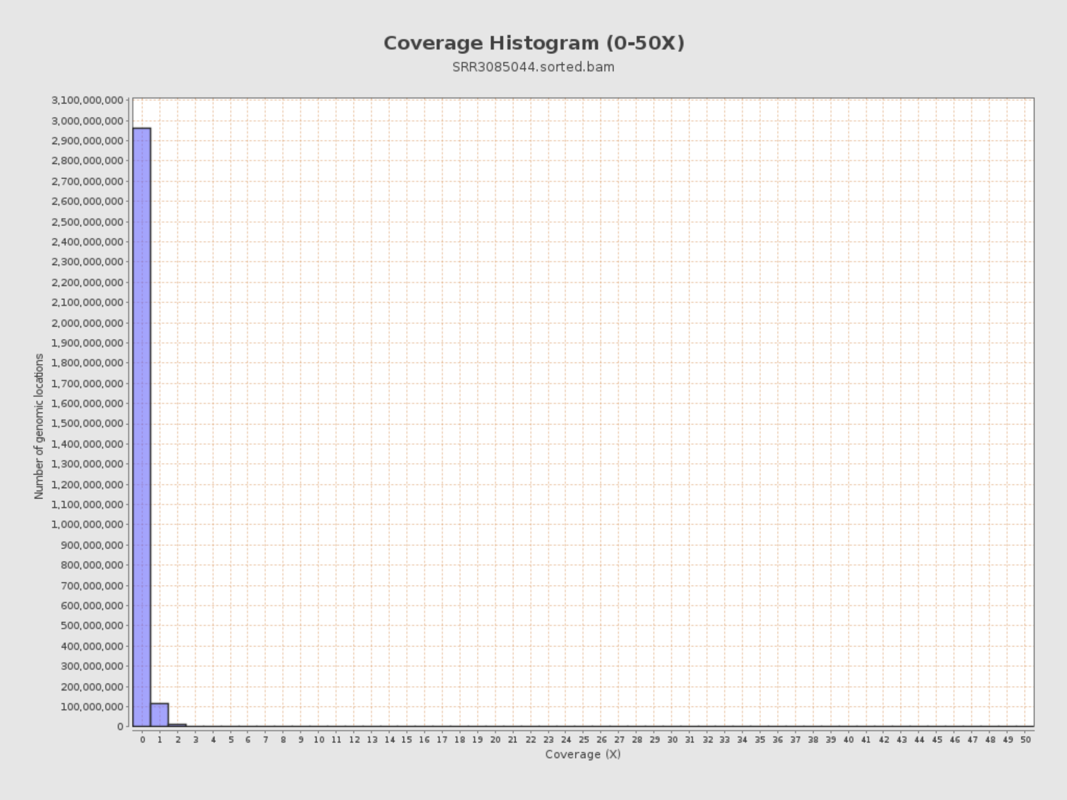
3. Results : Coverage across reference



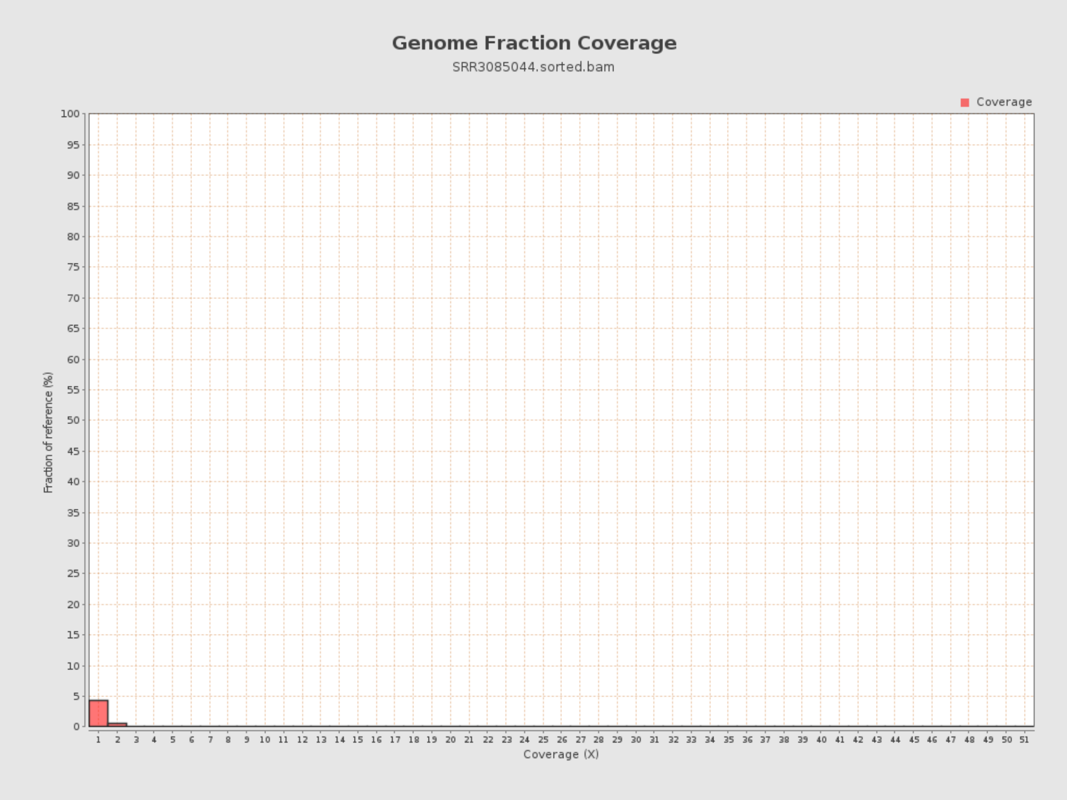
4. Results : Coverage Histogram



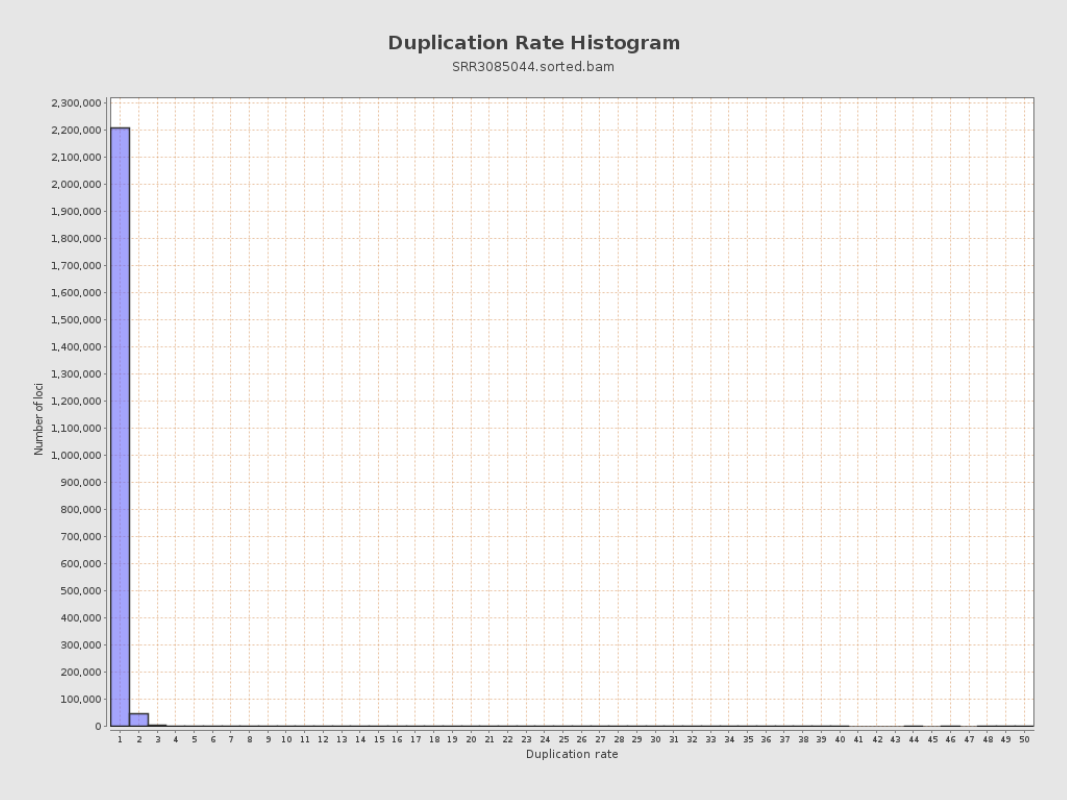
5. Results : Coverage Histogram (0-50X)



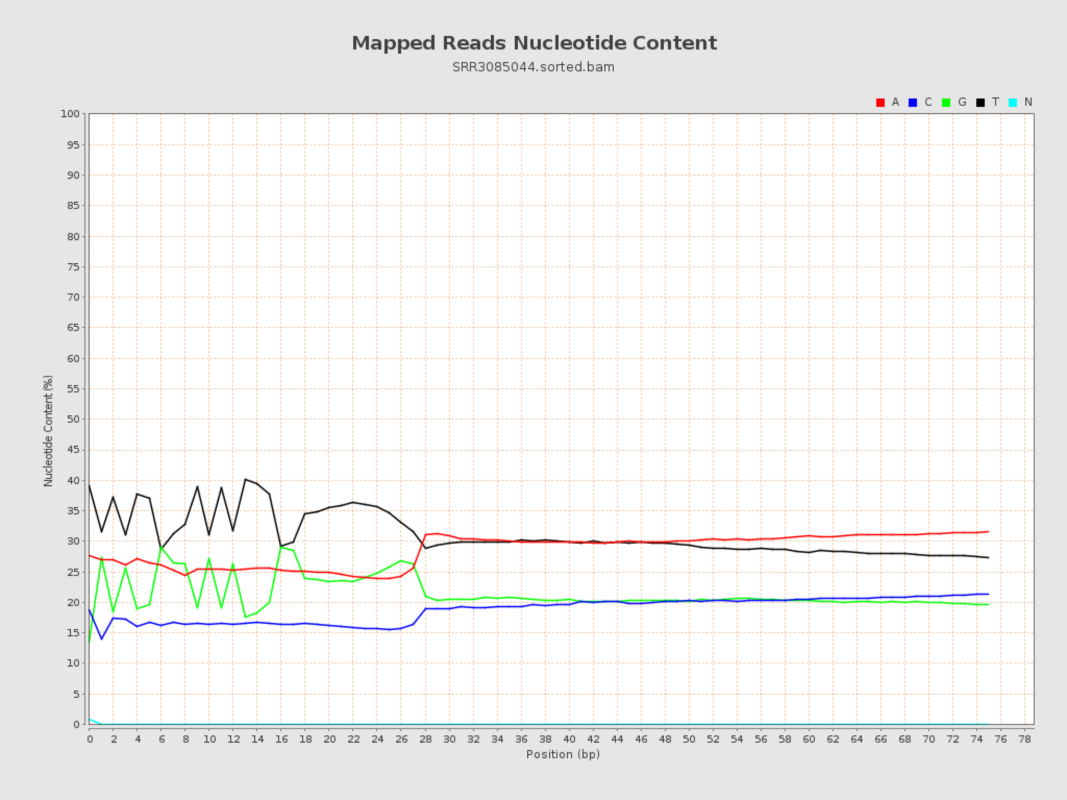
6. Results : Genome Fraction Coverage



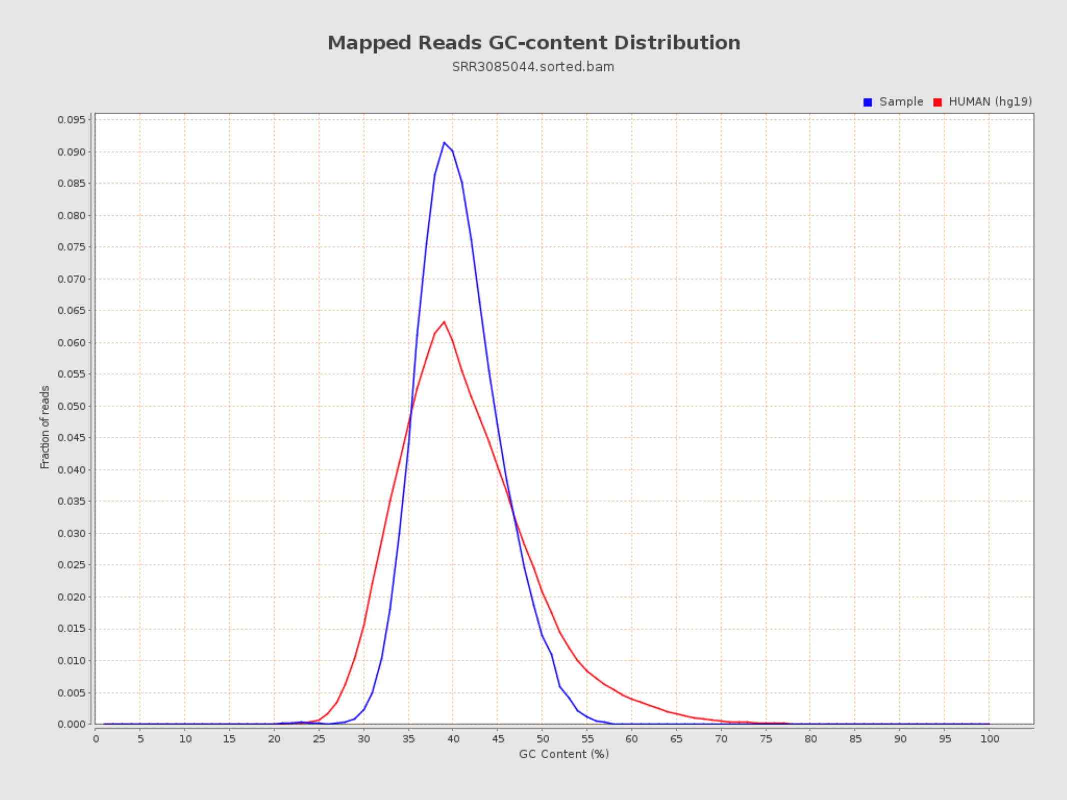
7. Results : Duplication Rate Histogram



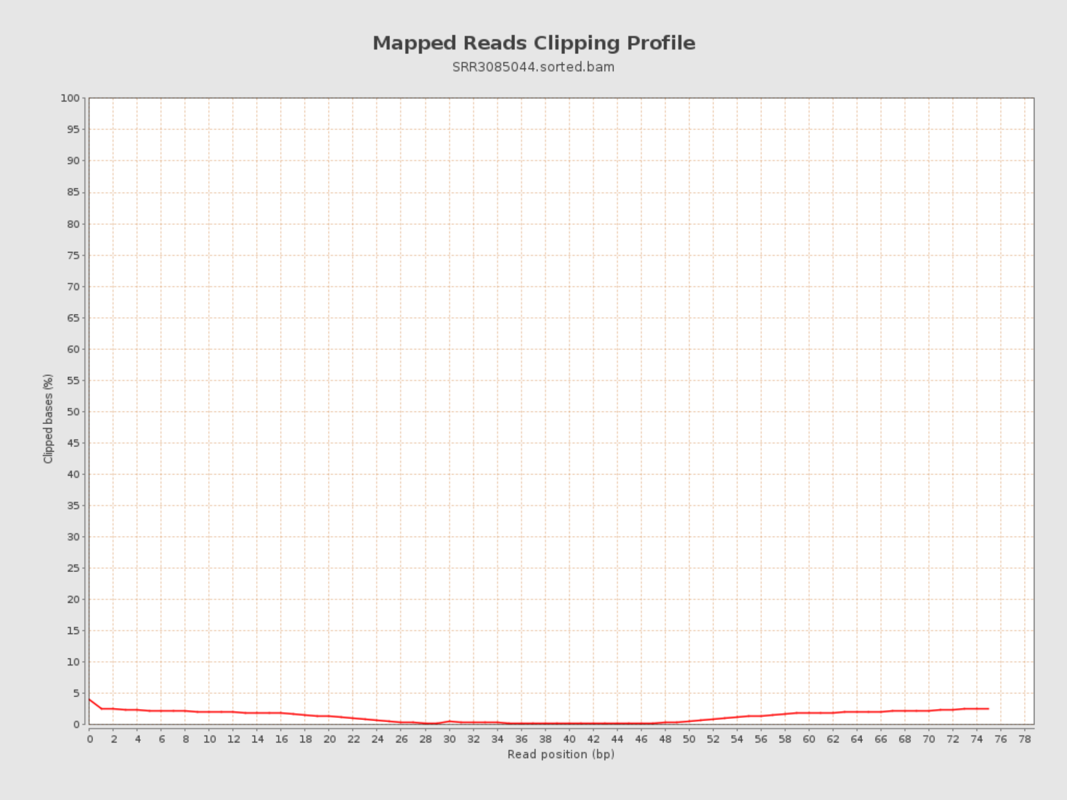
8. Results : Mapped Reads Nucleotide Content



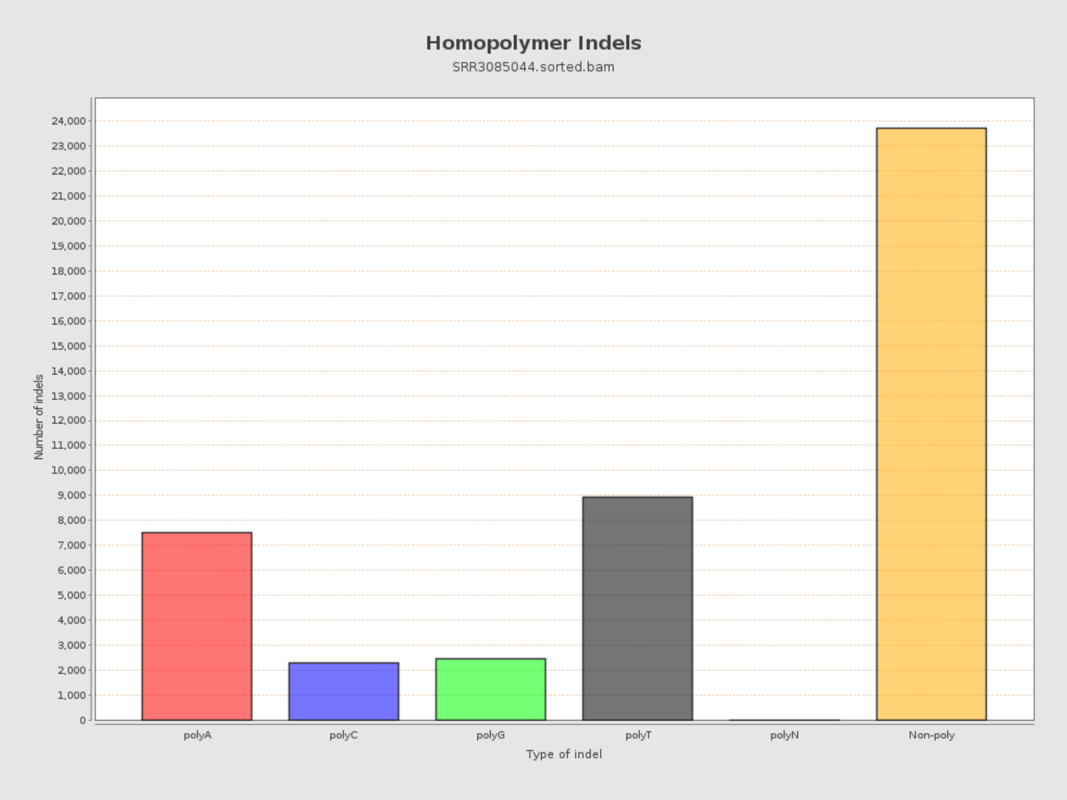
9. Results : Mapped Reads GC-content Distribution



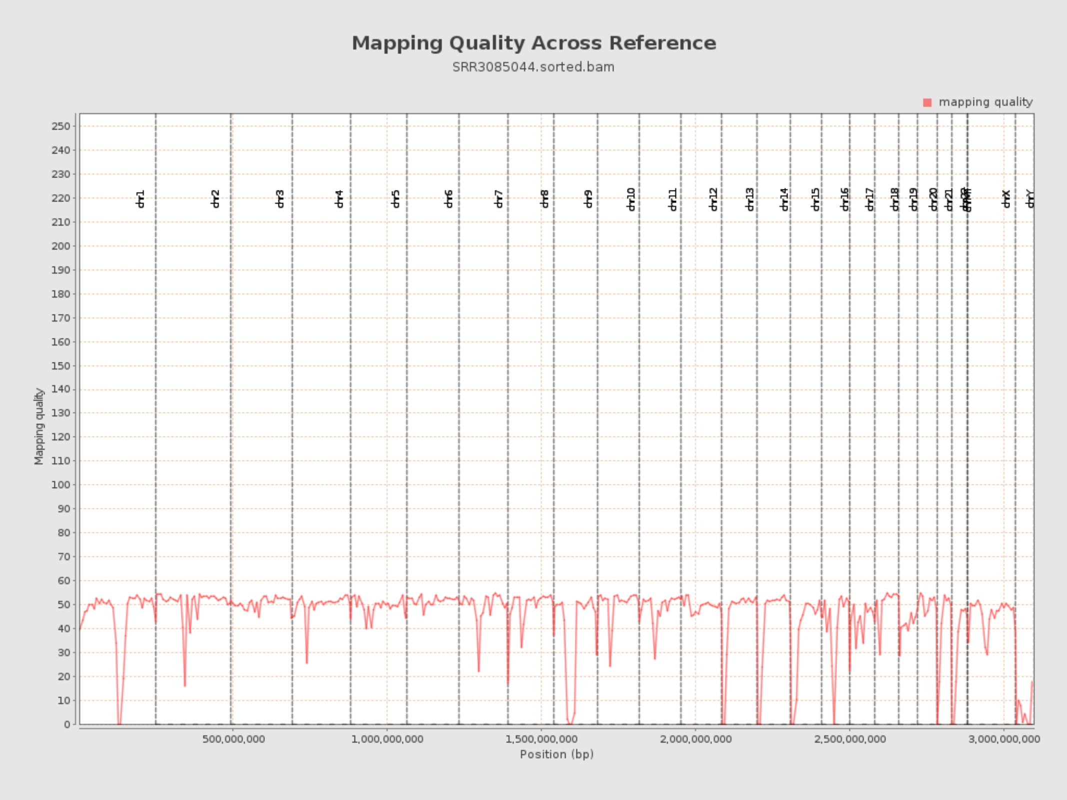
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram