Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:45:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004086.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_SRR6004086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:45:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,936,269
Mapped reads	2,618,147 / 89.17%
Unmapped reads	318,122 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,977 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	164,263 / 5.59%
Duplication rate	4.81%
Clipped reads	1,289,231 / 43.91%

2.2. ACGT Content

Number/percentage of A's	48,597,368 / 28.3%
Number/percentage of C's	30,414,368 / 17.71%
Number/percentage of T's	55,538,110 / 32.35%
Number/percentage of G's	37,074,670 / 21.59%
Number/percentage of N's	76,036 / 0.04%
GC Percentage	39.31%

2.3. Coverage

Mean	0.0555

Standard Deviation	0.5474

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

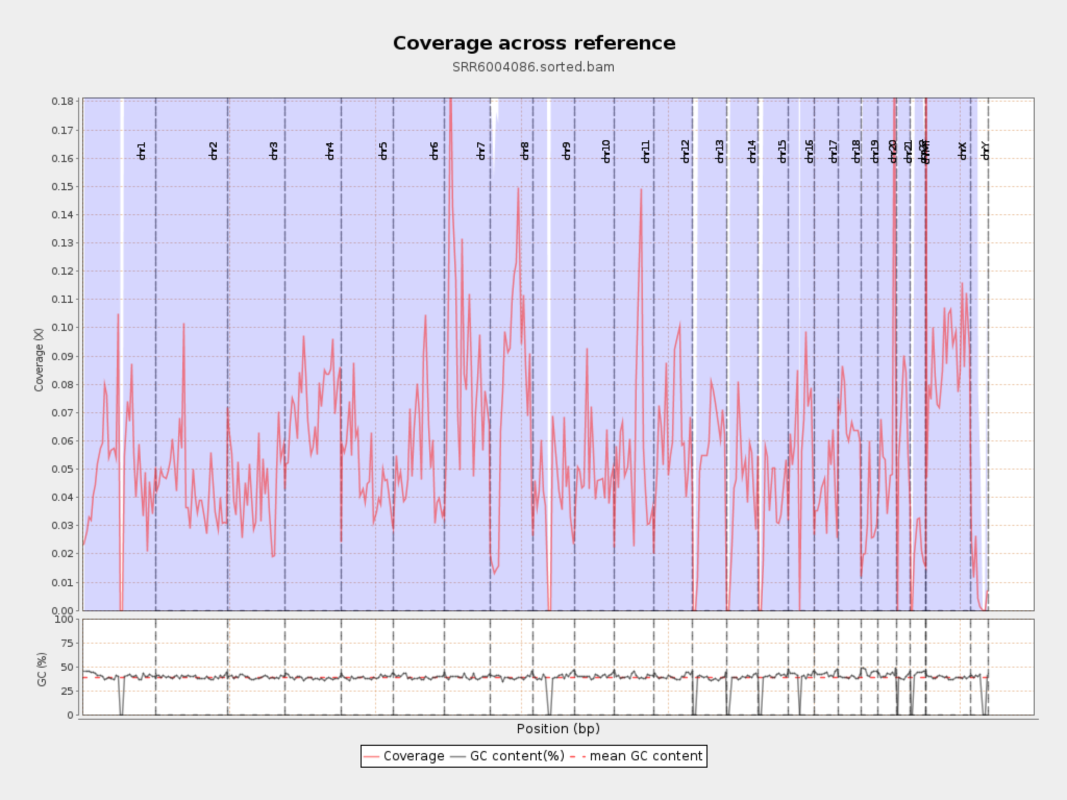
General error rate	0.91%
Mismatches	1,545,185
Insertions	13,465
Mapped reads with at least one insertion	0.51%
Deletions	68,634
Mapped reads with at least one deletion	2.58%
Homopolymer indels	43.76%

2.6. Chromosome stats

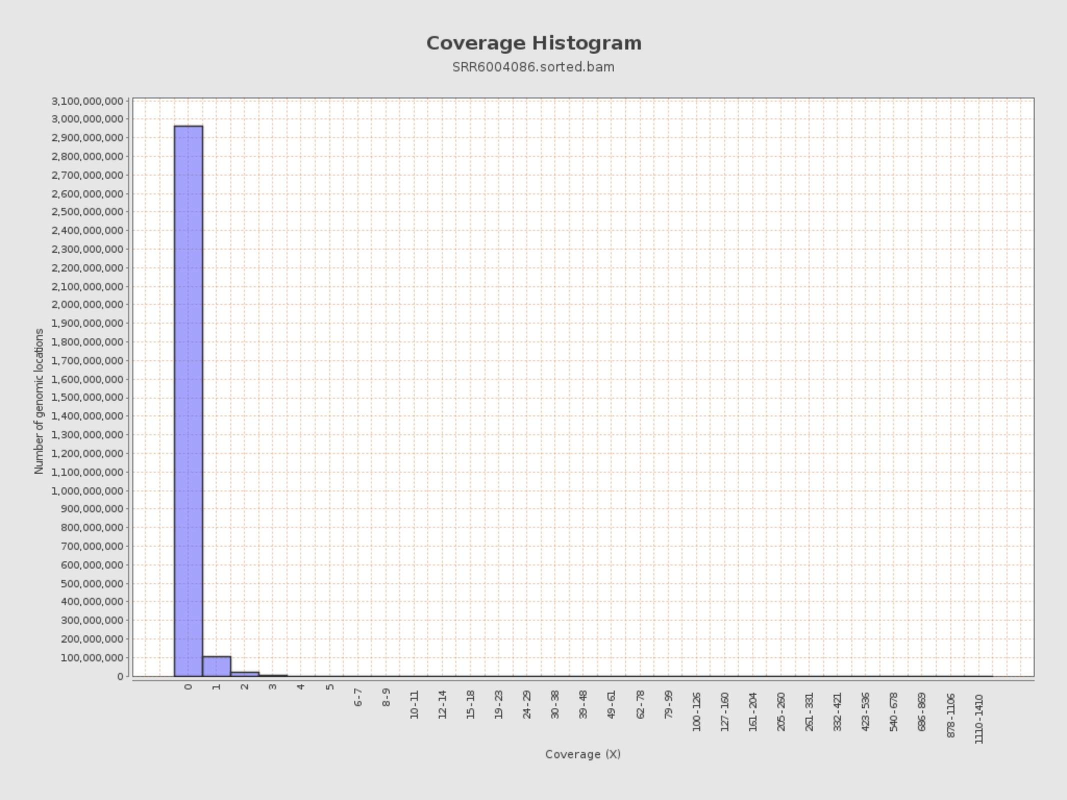
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12190888	0.0489	1.0319
chr2	243199373	10813088	0.0445	0.5465
chr3	198022430	8700234	0.0439	0.259
chr4	191154276	14139938	0.074	0.3498
chr5	180915260	8943588	0.0494	0.2793
chr6	171115067	9350096	0.0546	0.3637
chr7	159138663	14083737	0.0885	0.8601

chr8	146364022	11390528	0.0778	0.9072
chr9	141213431	5796865	0.0411	0.4635
chr10	135534747	6847617	0.0505	0.448
chr11	135006516	7882979	0.0584	0.4295
chr12	133851895	8504941	0.0635	0.3222
chr13	115169878	6068229	0.0527	0.2816
chr14	107349540	4558056	0.0425	0.2792
chr15	102531392	3695476	0.036	0.2364
chr16	90354753	5384101	0.0596	0.3604
chr17	81195210	3531454	0.0435	0.3054
chr18	78077248	5340174	0.0684	0.8874
chr19	59128983	1761434	0.0298	0.7292
chr20	63025520	4608429	0.0731	0.3638
chr21	48129895	2893415	0.0601	0.3259
chr22	51304566	984068	0.0192	0.1657
chrMT	16571	7599	0.4586	0.7824
chrX	155270560	13823272	0.089	0.4263
chrY	59373566	515863	0.0087	0.1816

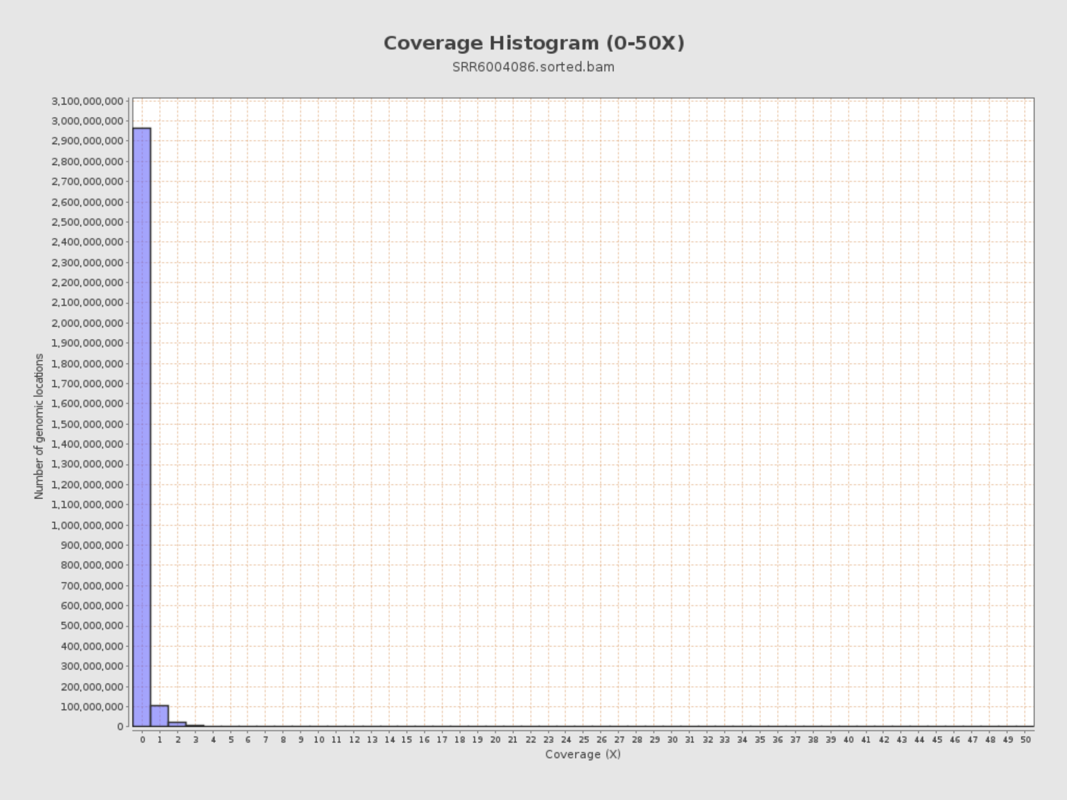
3. Results : Coverage across reference



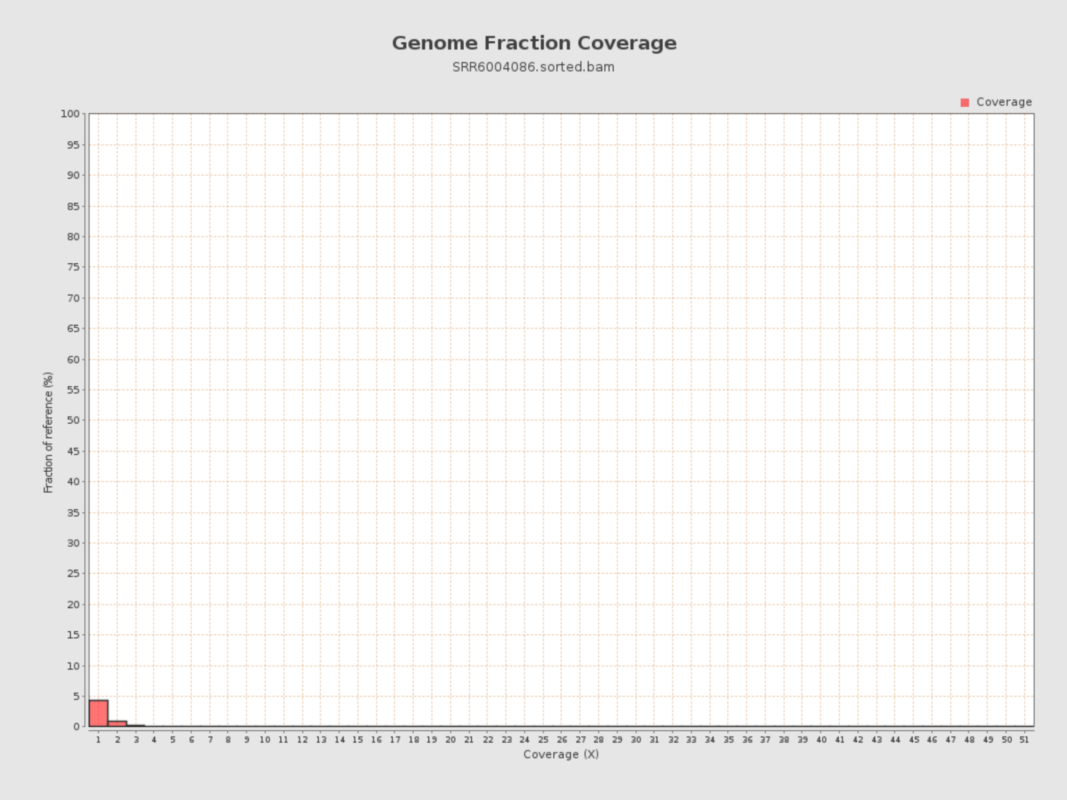
4. Results : Coverage Histogram



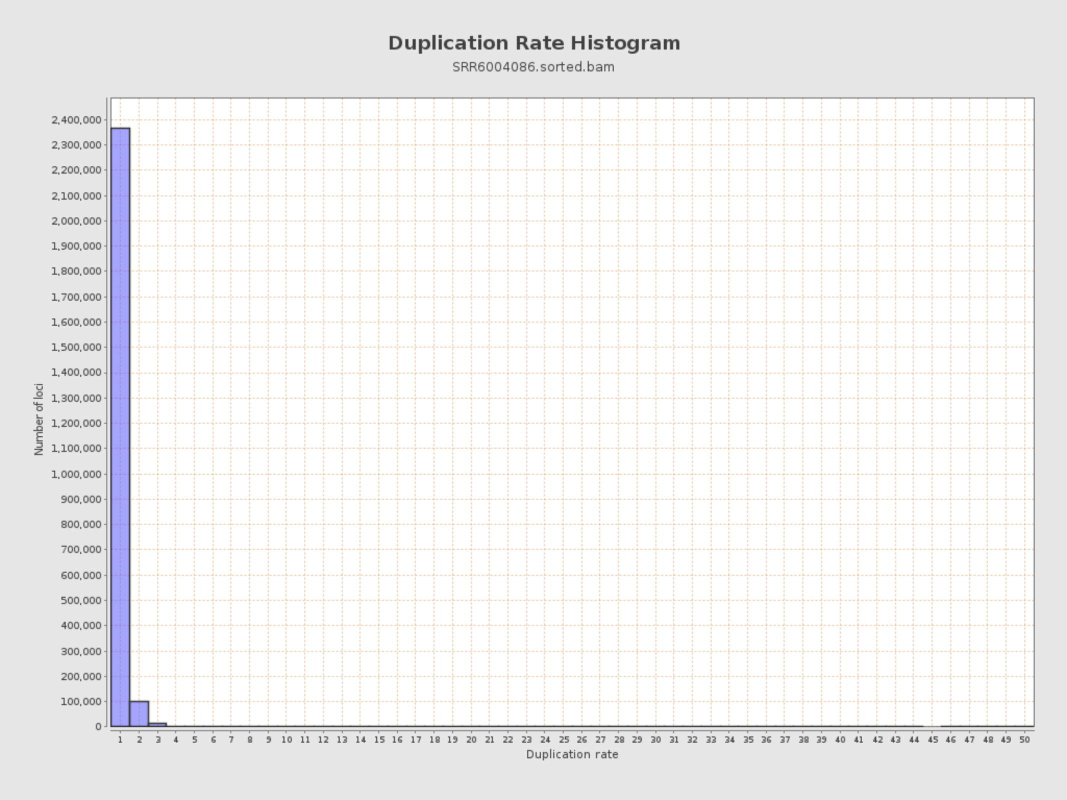
5. Results : Coverage Histogram (0-50X)



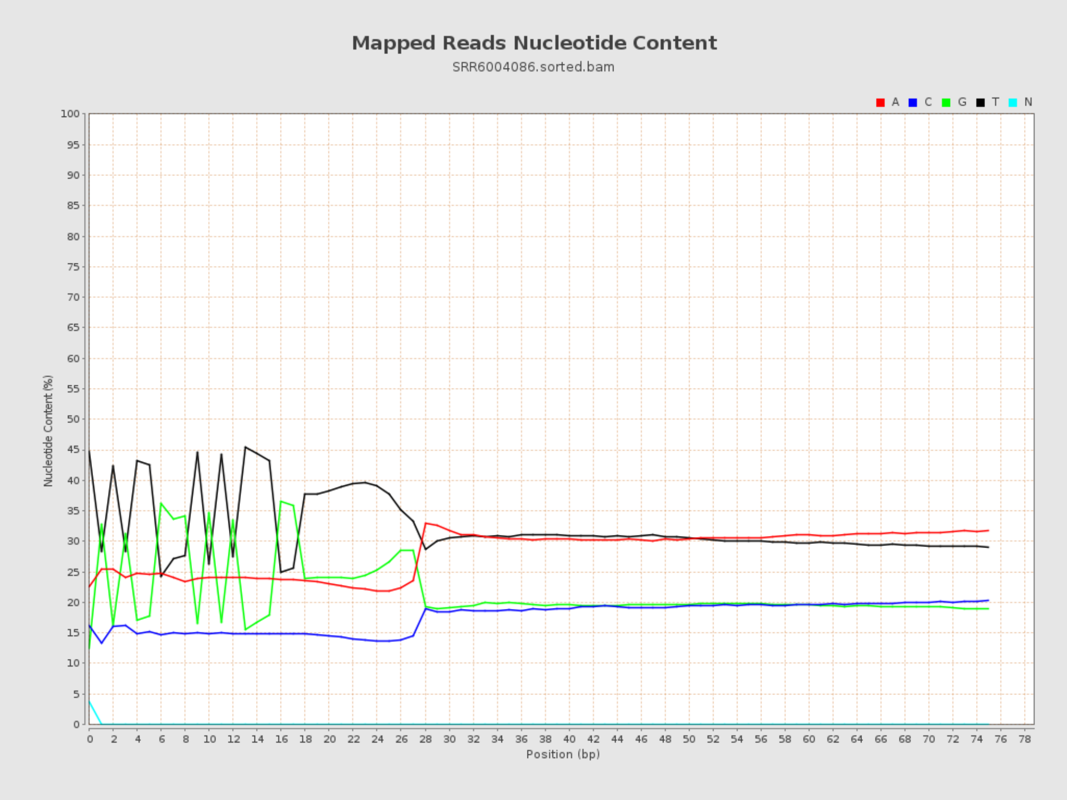
6. Results : Genome Fraction Coverage



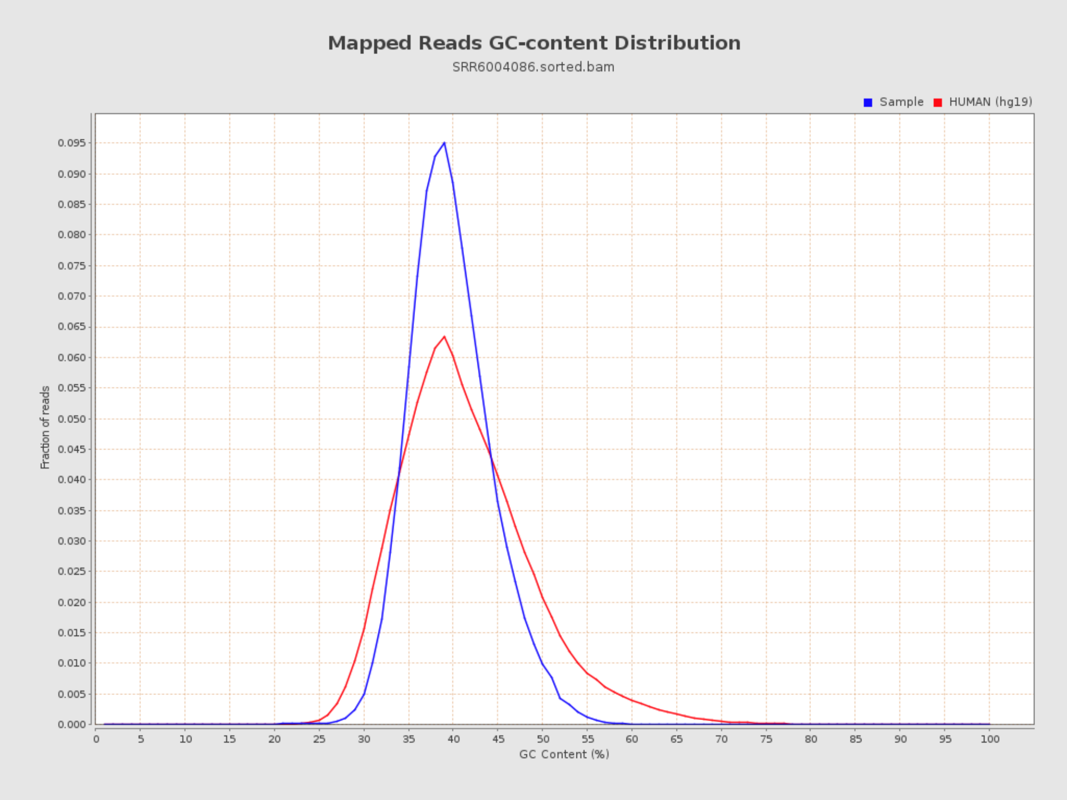
7. Results : Duplication Rate Histogram



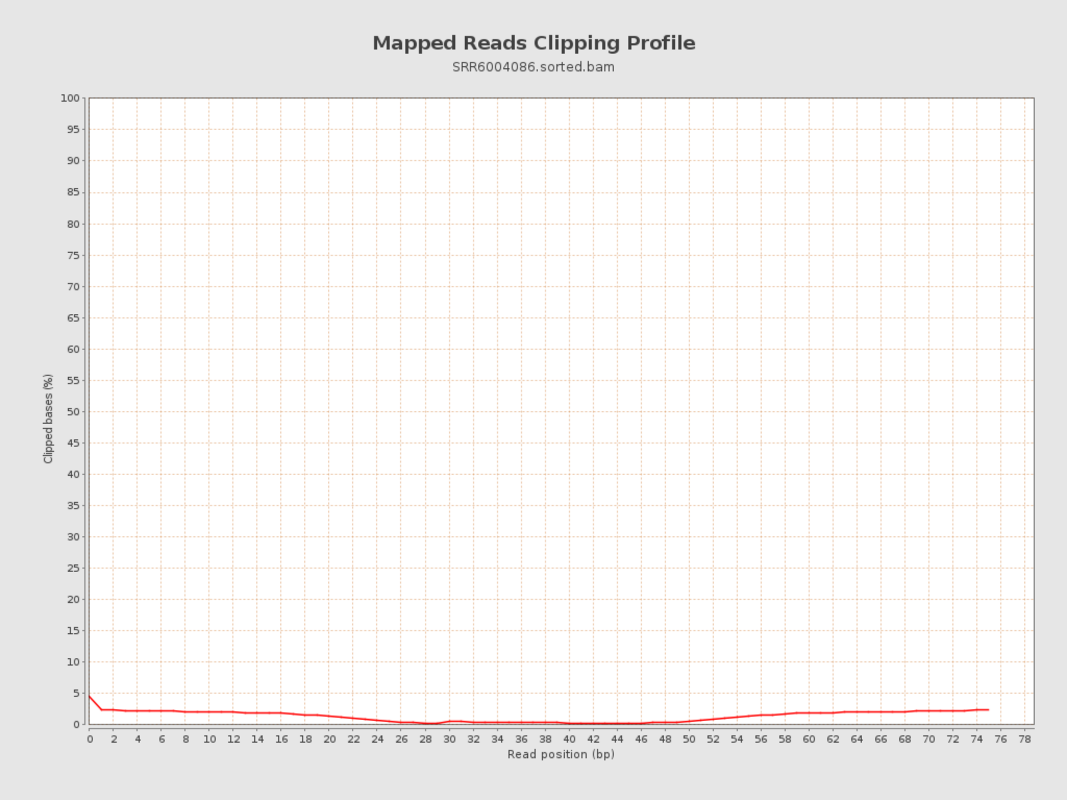
8. Results : Mapped Reads Nucleotide Content



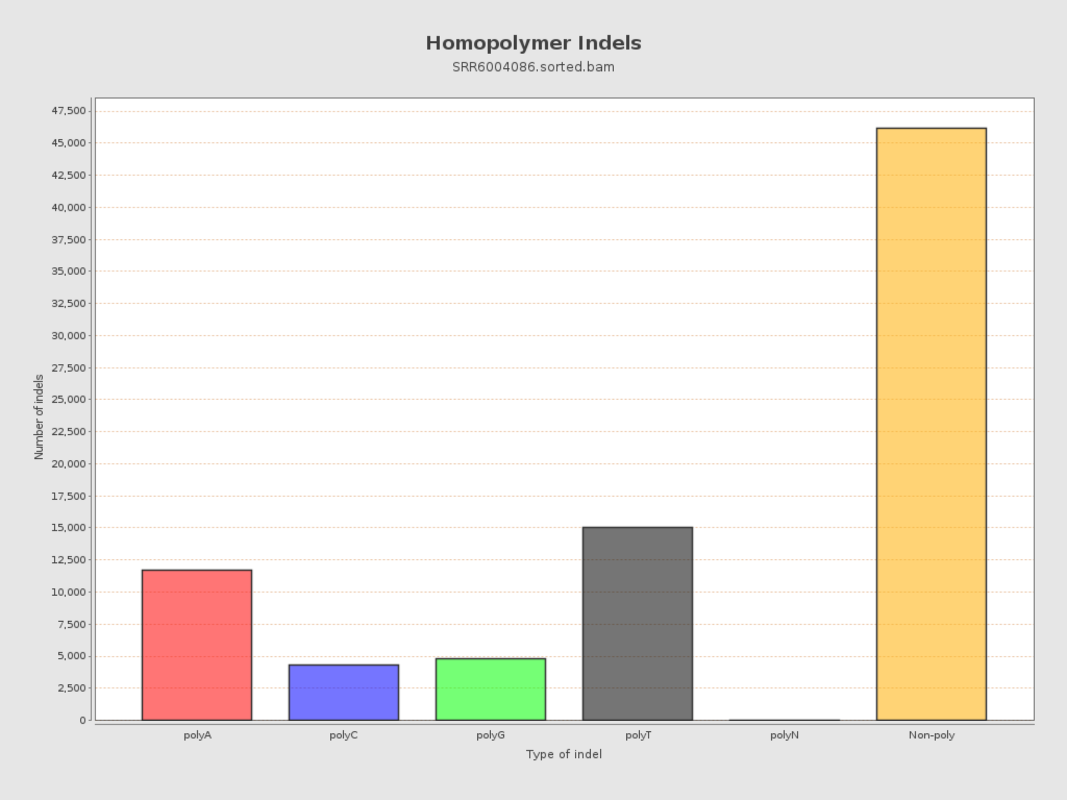
9. Results : Mapped Reads GC-content Distribution



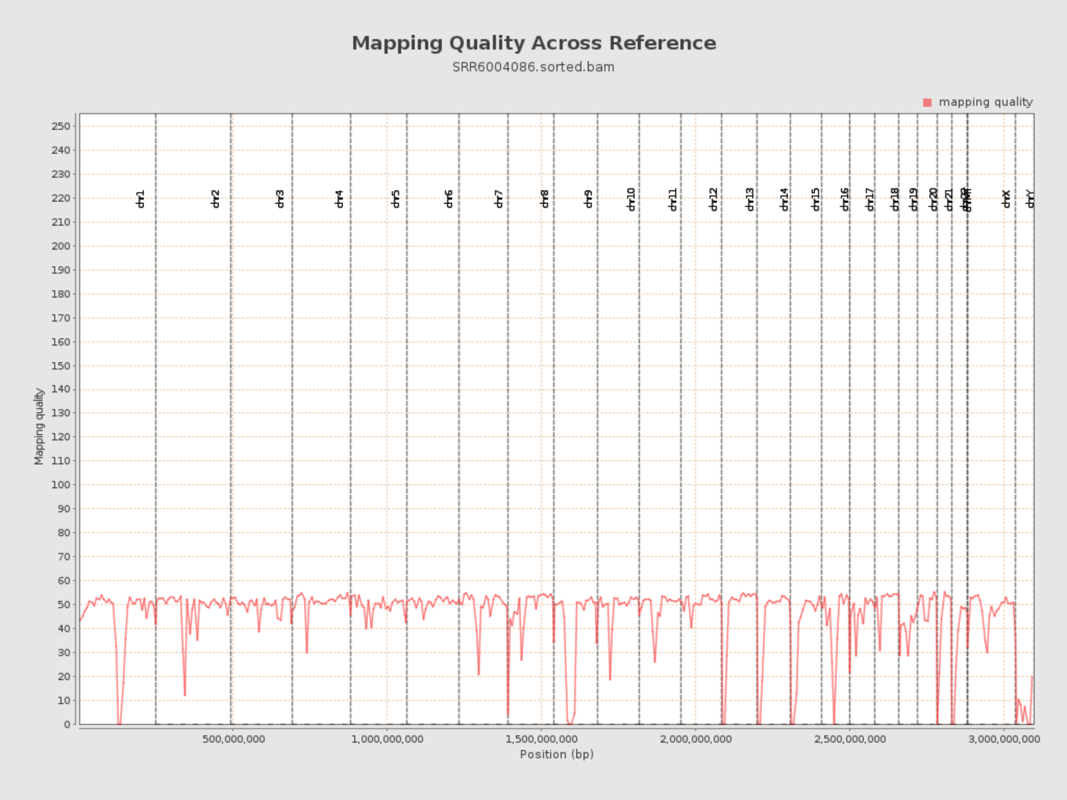
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram