Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:11:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004094.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_SRR6004094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004094.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:11:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,529,195
Mapped reads	2,768,266 / 78.44%
Unmapped reads	760,929 / 21.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,789 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	199,232 / 5.65%
Duplication rate	5.85%
Clipped reads	1,333,738 / 37.79%

2.2. ACGT Content

Number/percentage of A's	51,203,441 / 27.95%
Number/percentage of C's	32,981,454 / 18.01%
Number/percentage of T's	59,506,546 / 32.49%
Number/percentage of G's	39,458,883 / 21.54%
Number/percentage of N's	24,235 / 0.01%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.4939

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

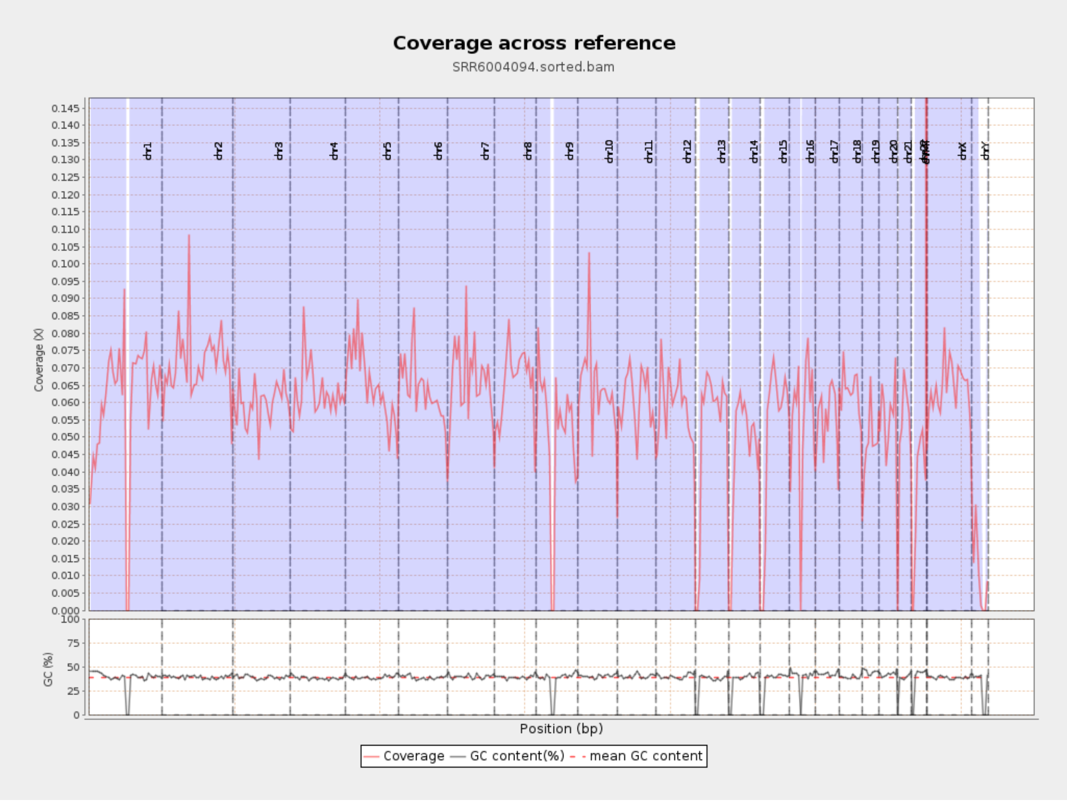
General error rate	0.98%
Mismatches	1,765,148
Insertions	15,979
Mapped reads with at least one insertion	0.57%
Deletions	52,368
Mapped reads with at least one deletion	1.87%
Homopolymer indels	47.67%

2.6. Chromosome stats

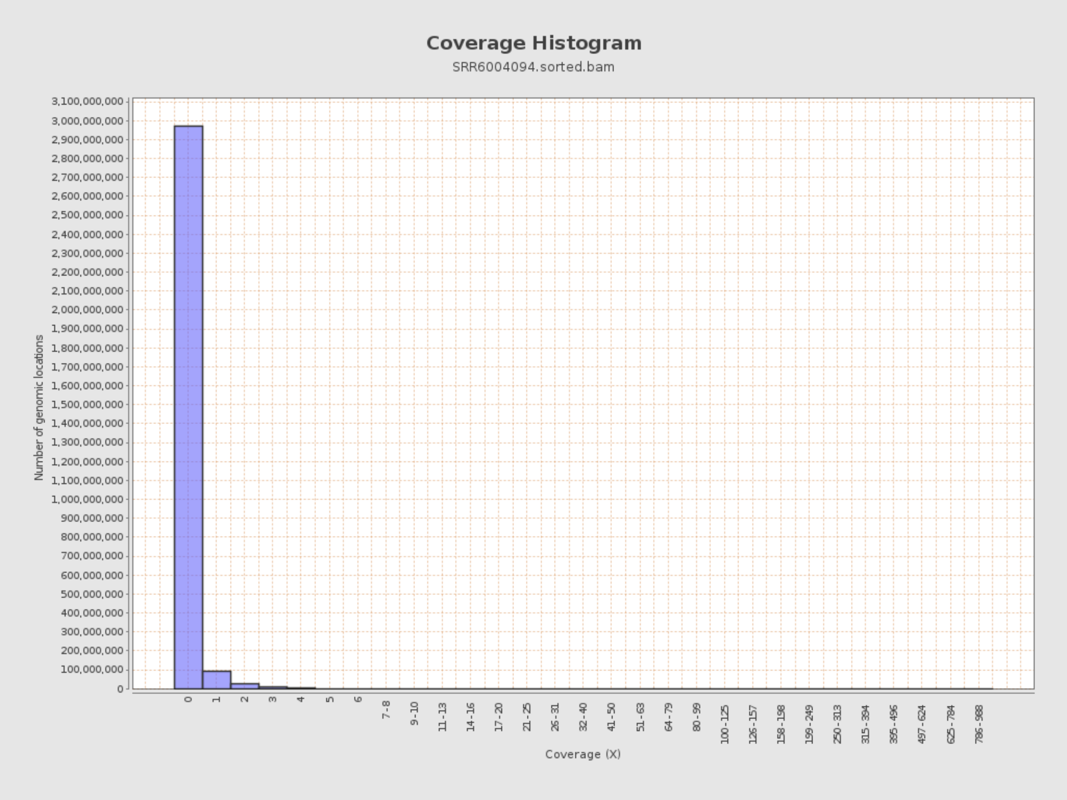
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15047118	0.0604	0.7754
chr2	243199373	17428073	0.0717	0.6328
chr3	198022430	11882021	0.06	0.3351
chr4	191154276	12004886	0.0628	0.3581
chr5	180915260	11820442	0.0653	0.3489
chr6	171115067	10889266	0.0636	0.4308
chr7	159138663	10744954	0.0675	0.6381

chr8	146364022	9610112	0.0657	0.6962
chr9	141213431	7270015	0.0515	0.4478
chr10	135534747	8830878	0.0652	0.5016
chr11	135006516	8137616	0.0603	0.4499
chr12	133851895	7929300	0.0592	0.3391
chr13	115169878	5946957	0.0516	0.3112
chr14	107349540	4874524	0.0454	0.3118
chr15	102531392	5236903	0.0511	0.3124
chr16	90354753	4997927	0.0553	0.3412
chr17	81195210	4461160	0.0549	0.3654
chr18	78077248	4958825	0.0635	0.8356
chr19	59128983	2869905	0.0485	0.57
chr20	63025520	3527199	0.056	0.3312
chr21	48129895	2452573	0.051	0.3316
chr22	51304566	1676014	0.0327	0.2388
chrMT	16571	78822	4.7566	4.1453
chrX	155270560	9978894	0.0643	0.3748
chrY	59373566	606531	0.0102	0.1774

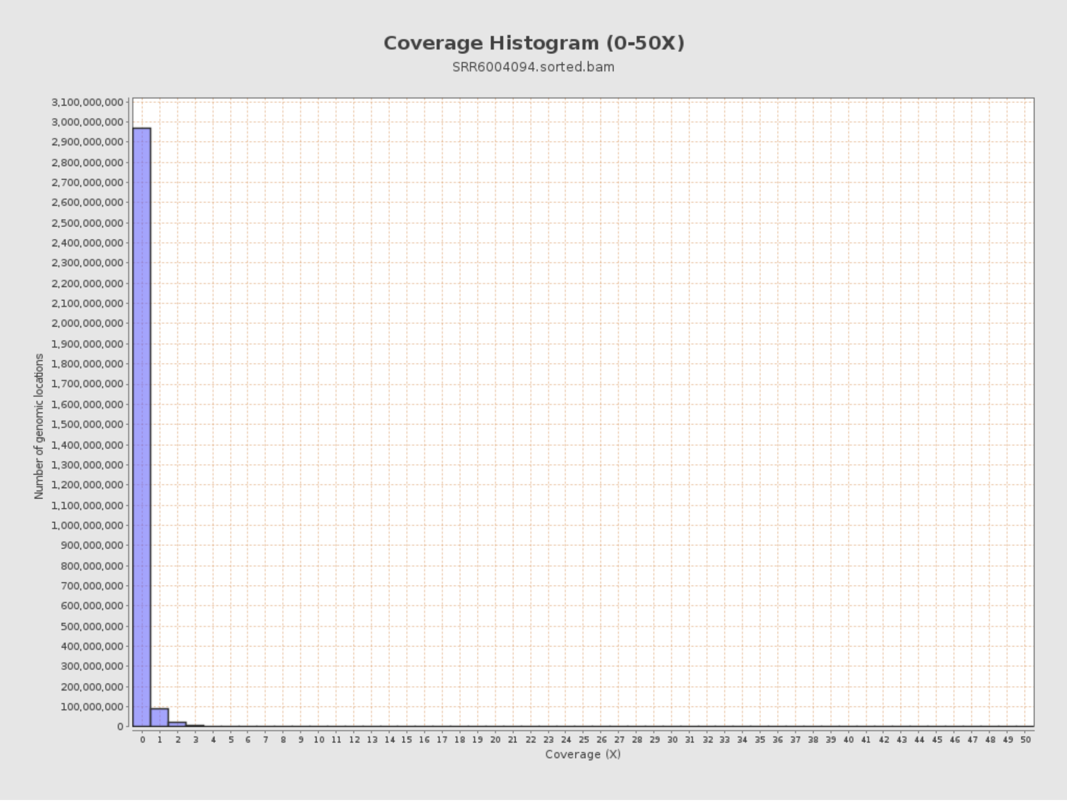
3. Results : Coverage across reference



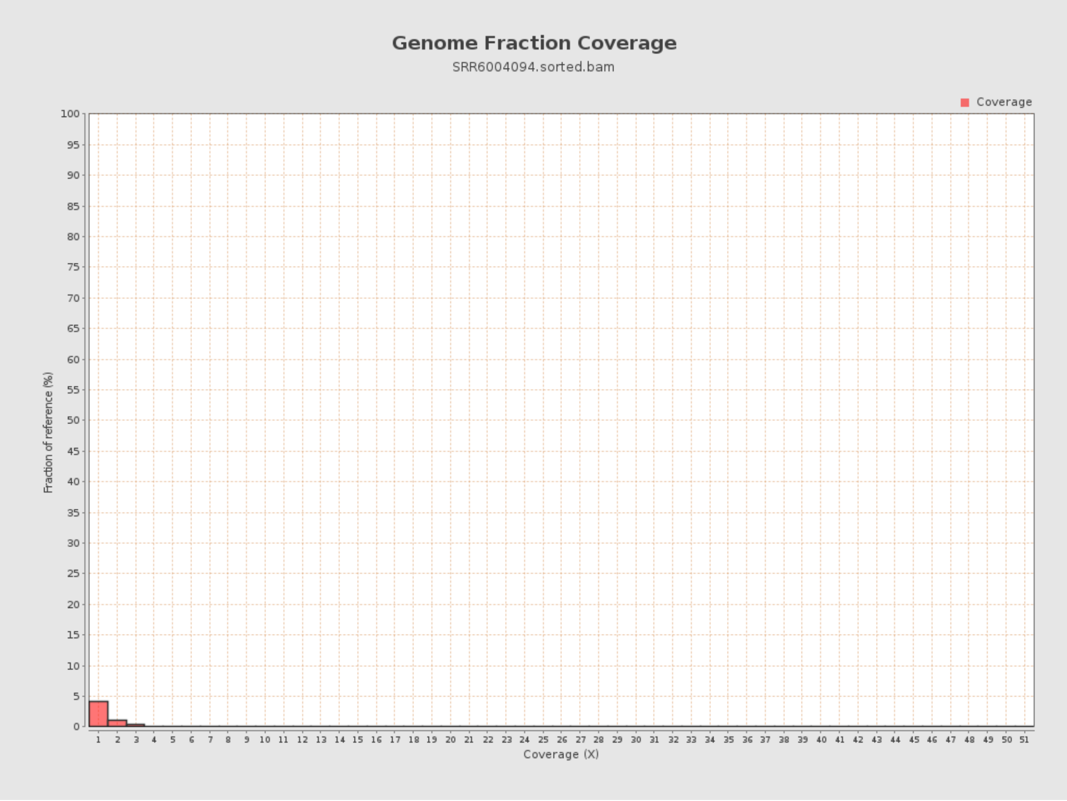
4. Results : Coverage Histogram



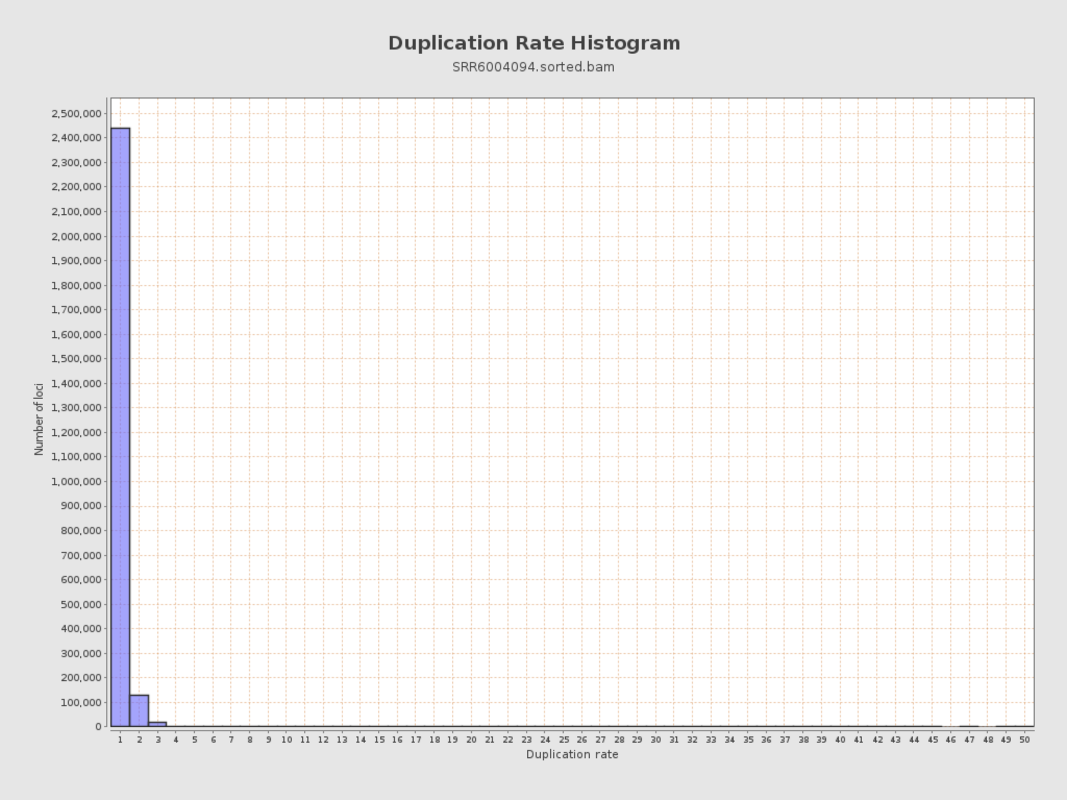
5. Results : Coverage Histogram (0-50X)



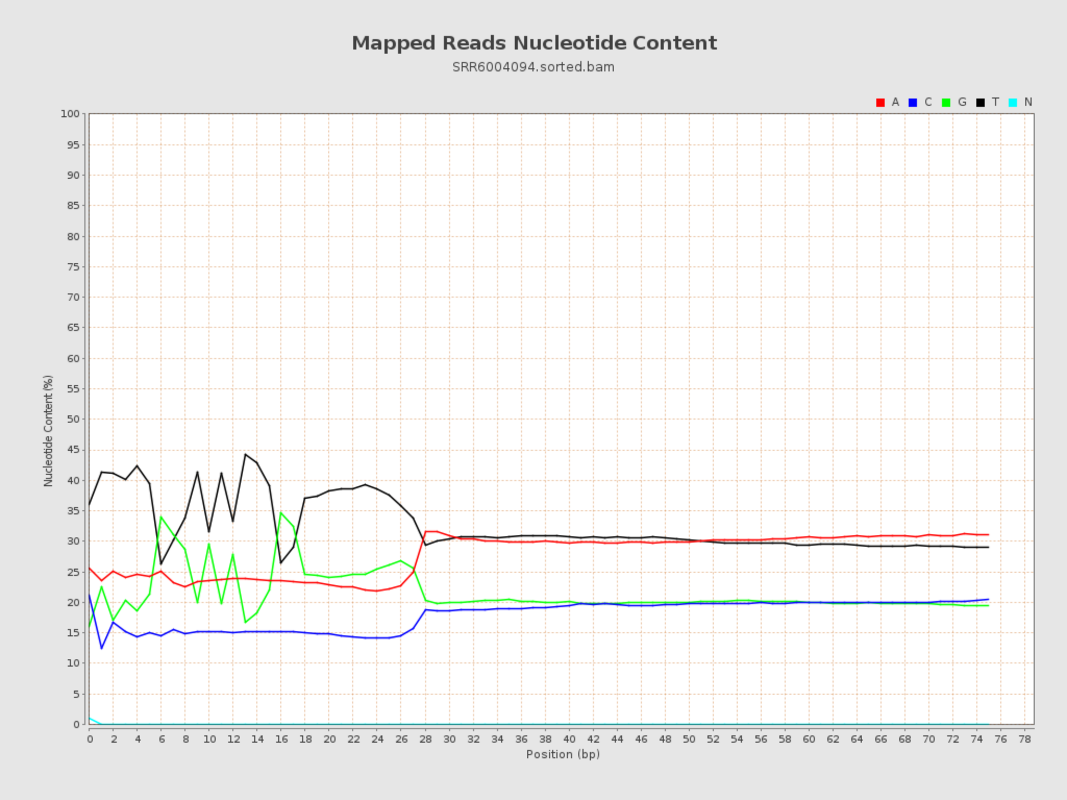
6. Results : Genome Fraction Coverage



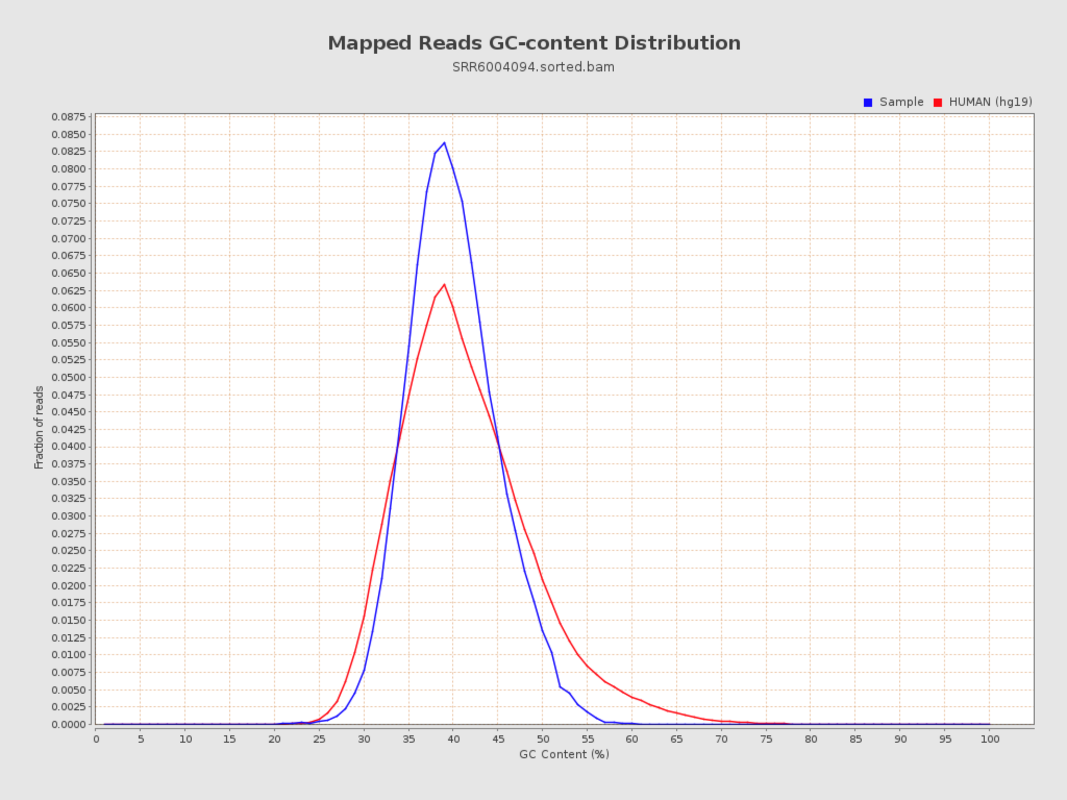
7. Results : Duplication Rate Histogram



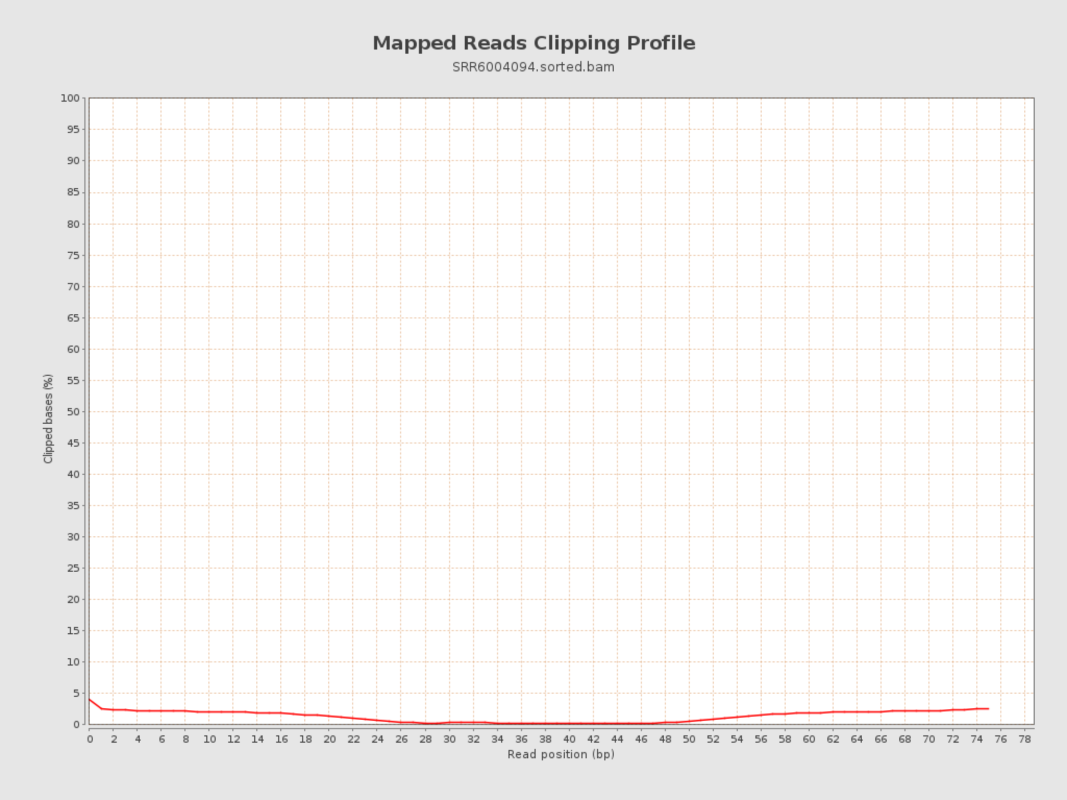
8. Results : Mapped Reads Nucleotide Content



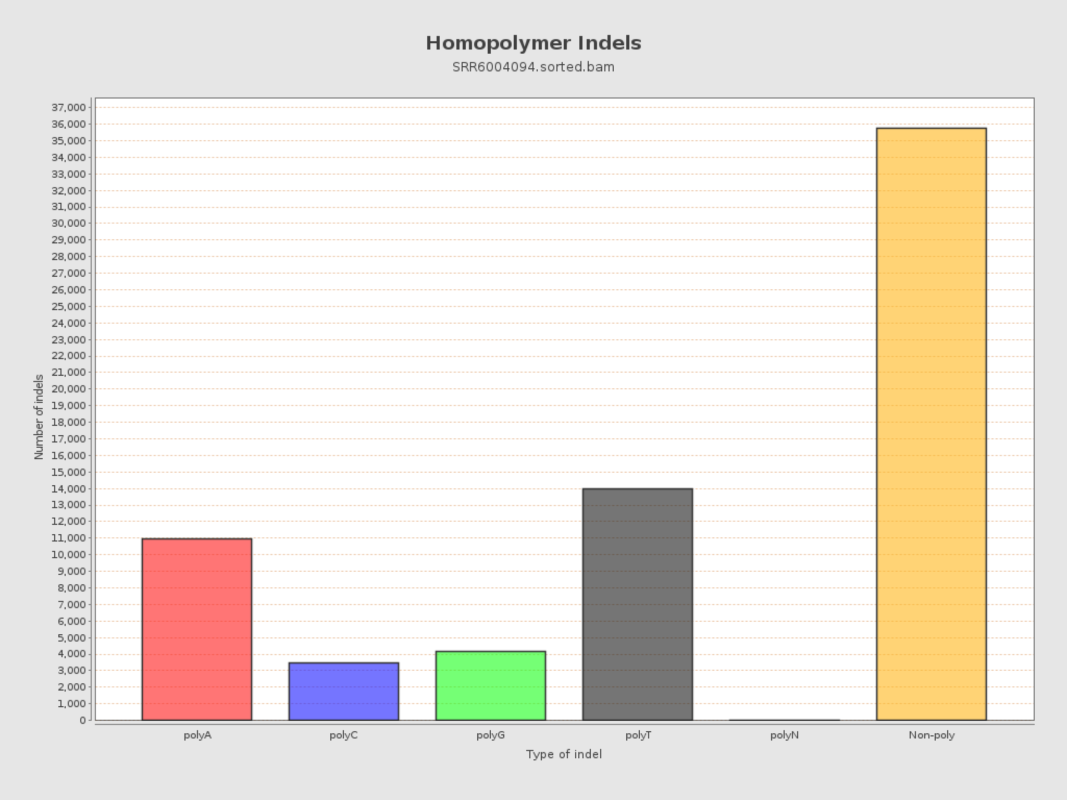
9. Results : Mapped Reads GC-content Distribution



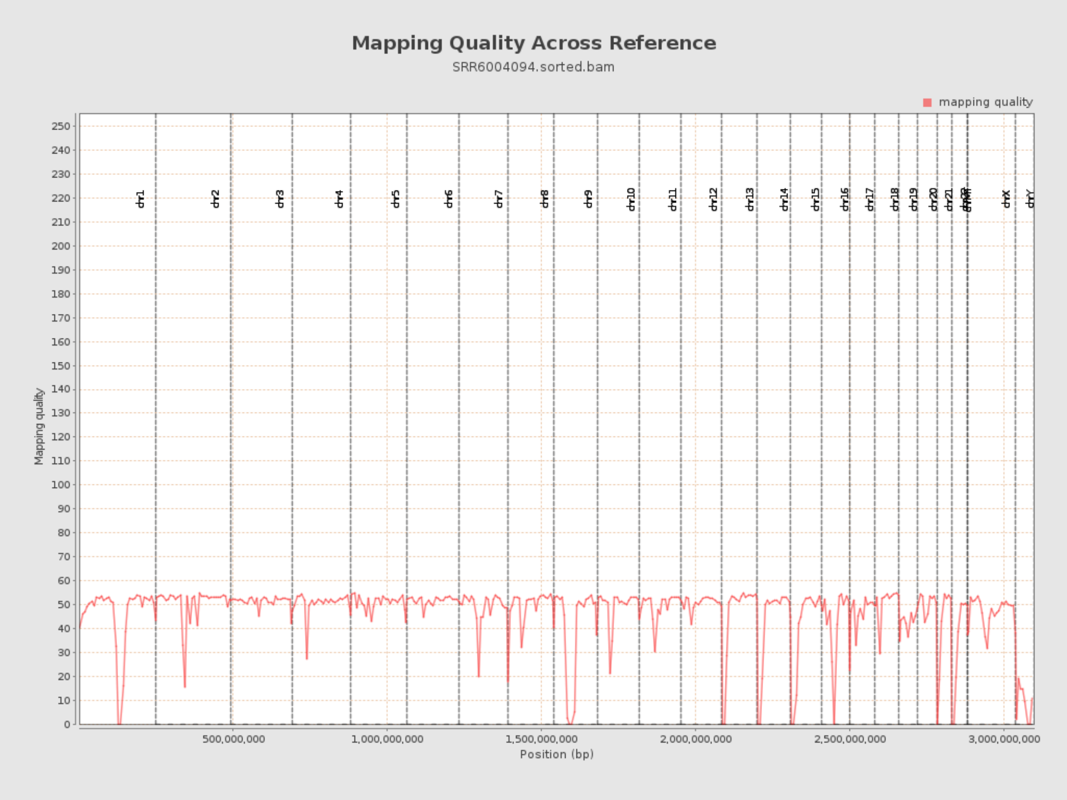
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram