Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:22:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085124.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_SRR3085124 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085124.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:22:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085124.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,114,984
Mapped reads	1,890,603 / 89.39%
Unmapped reads	224,381 / 10.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,604 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	70,988 / 3.36%
Duplication rate	2.84%
Clipped reads	849,440 / 40.16%

2.2. ACGT Content

Number/percentage of A's	35,197,684 / 27.9%
Number/percentage of C's	23,224,573 / 18.41%
Number/percentage of T's	39,864,085 / 31.6%
Number/percentage of G's	27,863,745 / 22.08%
Number/percentage of N's	19,701 / 0.02%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.3671

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

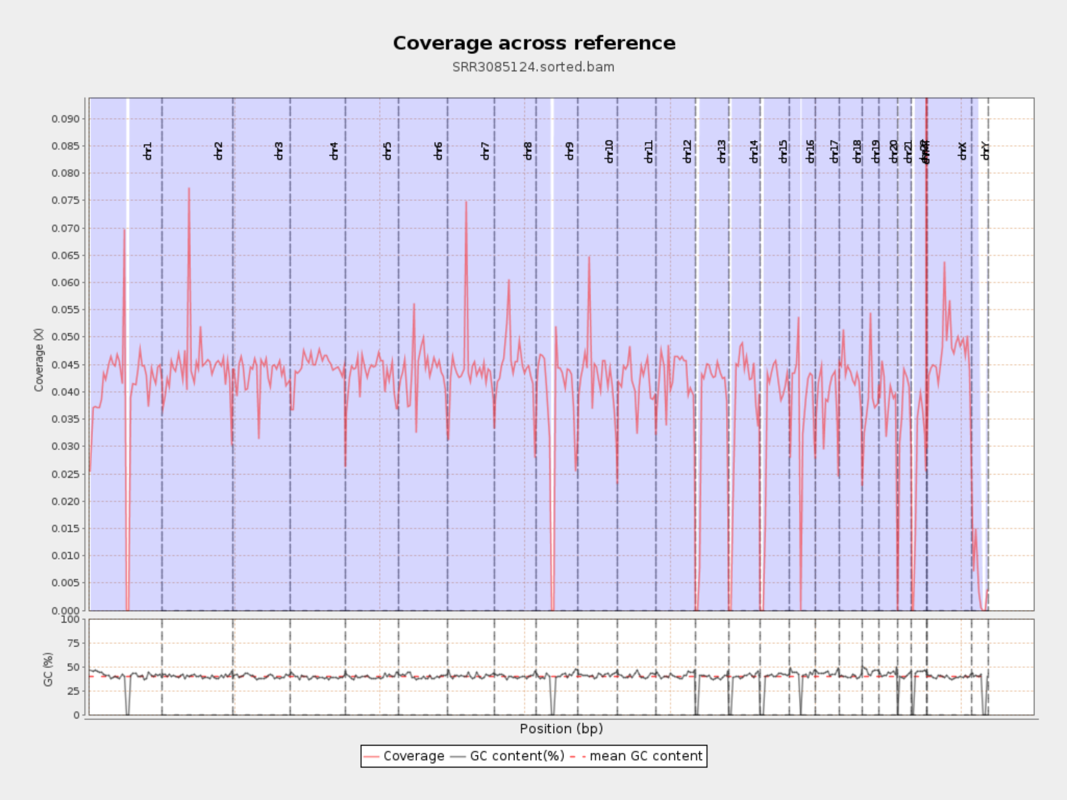
General error rate	0.91%
Mismatches	1,124,447
Insertions	9,943
Mapped reads with at least one insertion	0.52%
Deletions	27,777
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.5%

2.6. Chromosome stats

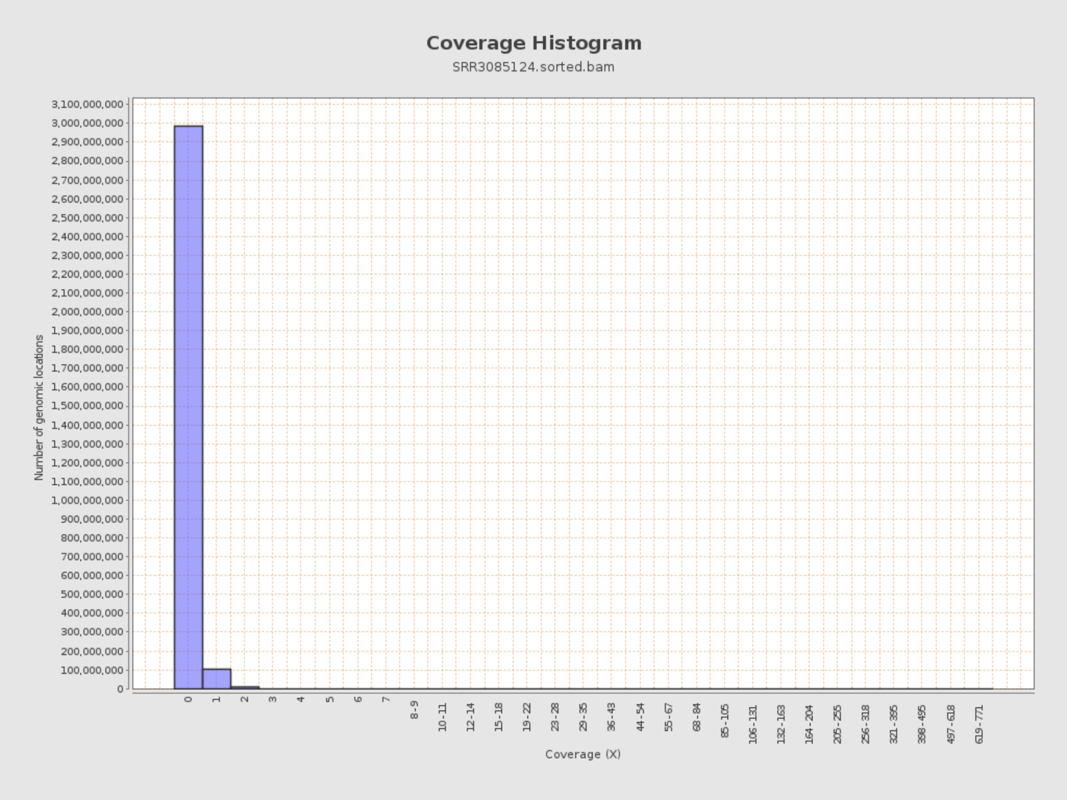
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10015496	0.0402	0.6643
chr2	243199373	10933013	0.045	0.4392
chr3	198022430	8564812	0.0433	0.2264
chr4	191154276	8526201	0.0446	0.2361
chr5	180915260	7817074	0.0432	0.2282
chr6	171115067	7476751	0.0437	0.2749
chr7	159138663	7106171	0.0447	0.5

chr8	146364022	6530983	0.0446	0.5277
chr9	141213431	5304137	0.0376	0.3406
chr10	135534747	5895378	0.0435	0.3378
chr11	135006516	5631442	0.0417	0.294
chr12	133851895	5727001	0.0428	0.2298
chr13	115169878	4109926	0.0357	0.2087
chr14	107349540	3900037	0.0363	0.225
chr15	102531392	3508244	0.0342	0.2068
chr16	90354753	3371506	0.0373	0.2329
chr17	81195210	3112474	0.0383	0.2363
chr18	78077248	3405813	0.0436	0.5981
chr19	59128983	2281559	0.0386	0.5061
chr20	63025520	2428965	0.0385	0.219
chr21	48129895	1647453	0.0342	0.2122
chr22	51304566	1272496	0.0248	0.1694
chrMT	16571	4821	0.2909	0.5786
chrX	155270560	7333780	0.0472	0.2666
chrY	59373566	308865	0.0052	0.1134

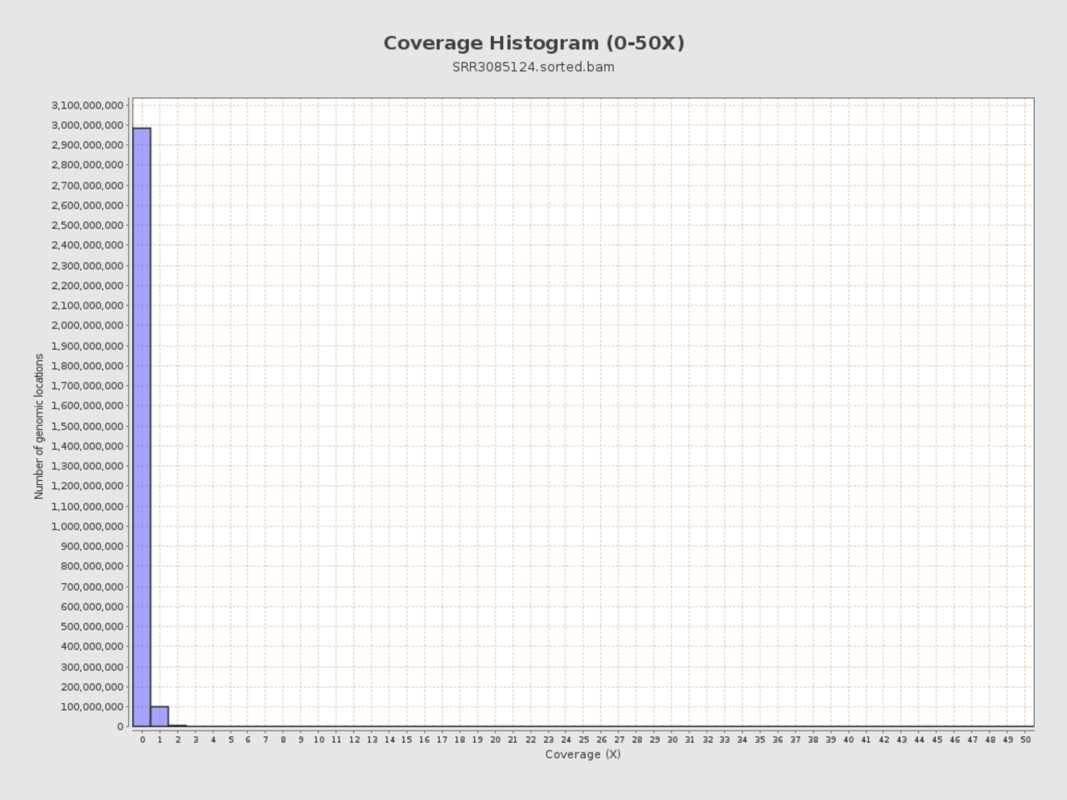
3. Results : Coverage across reference



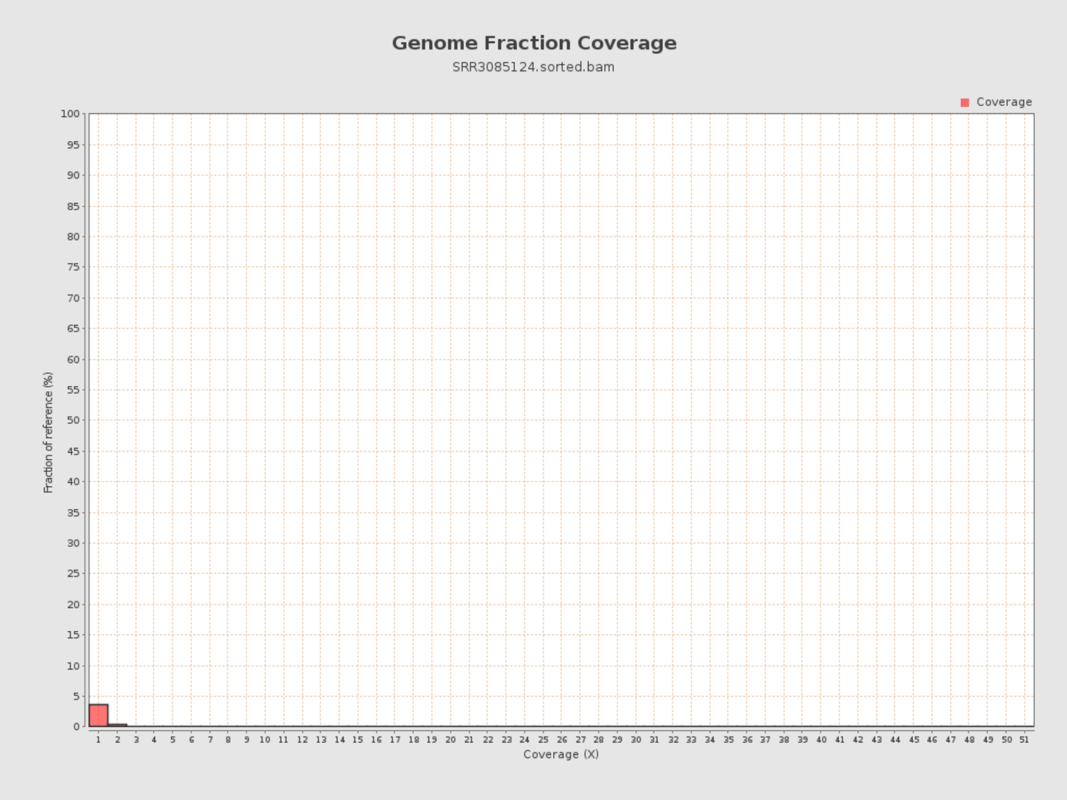
4. Results : Coverage Histogram



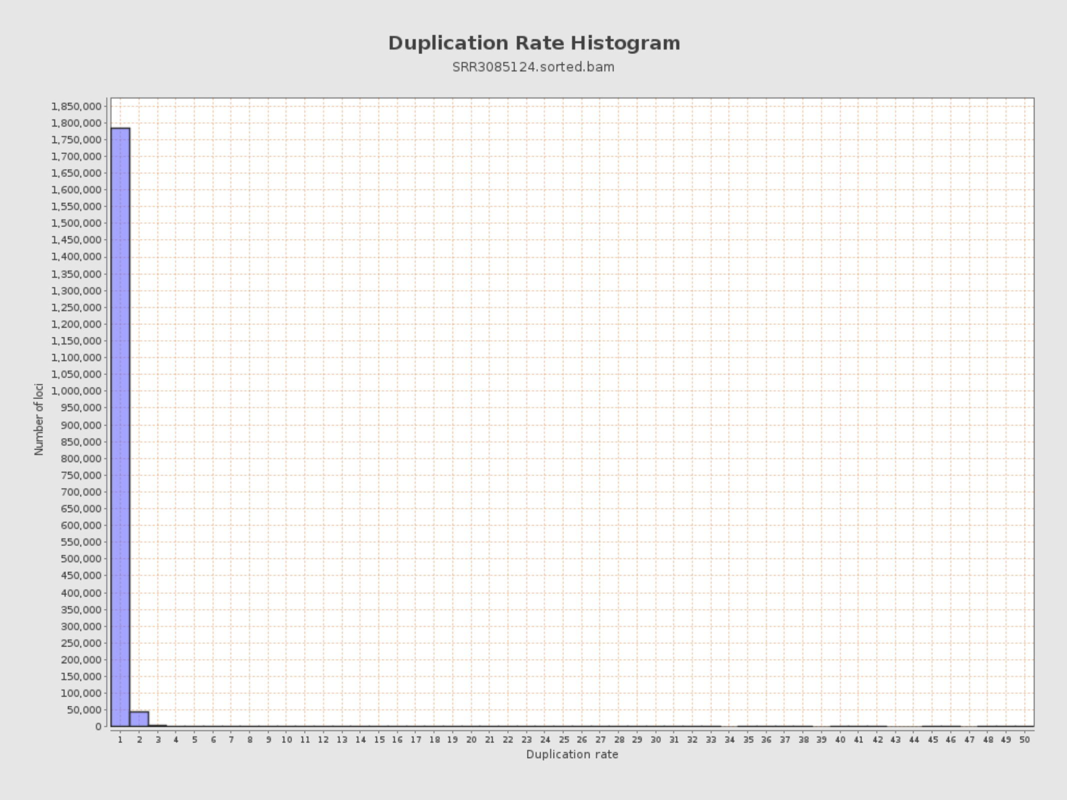
5. Results : Coverage Histogram (0-50X)



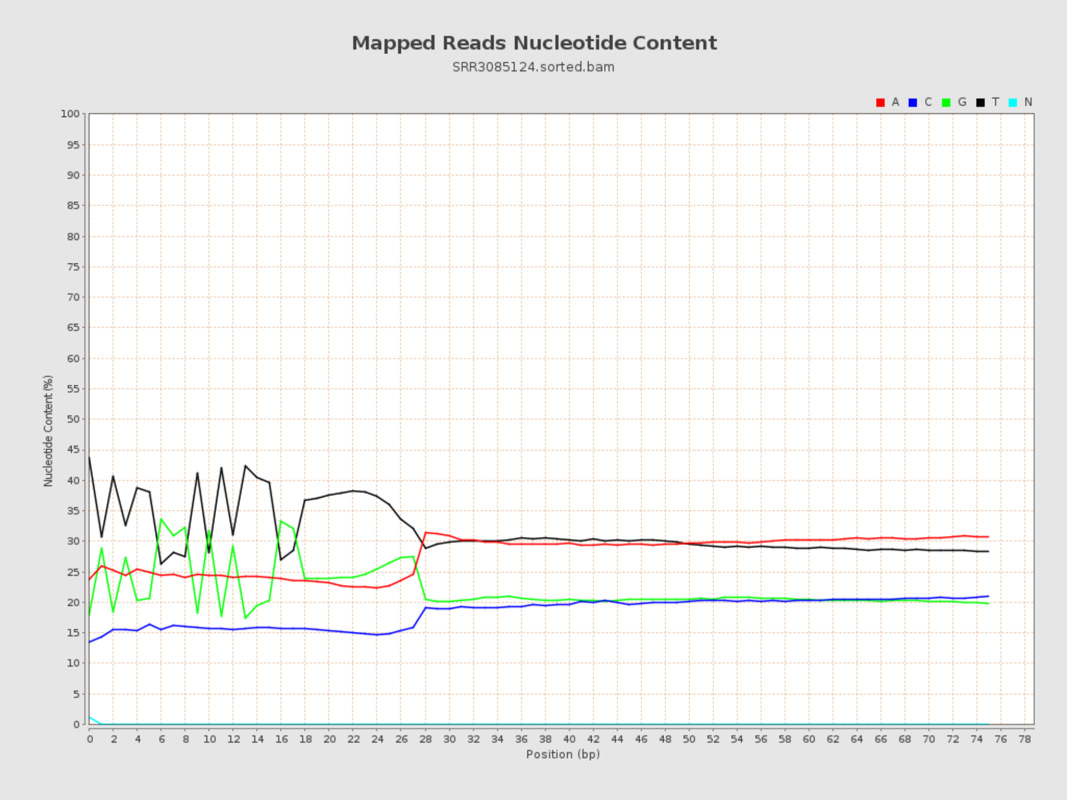
6. Results : Genome Fraction Coverage



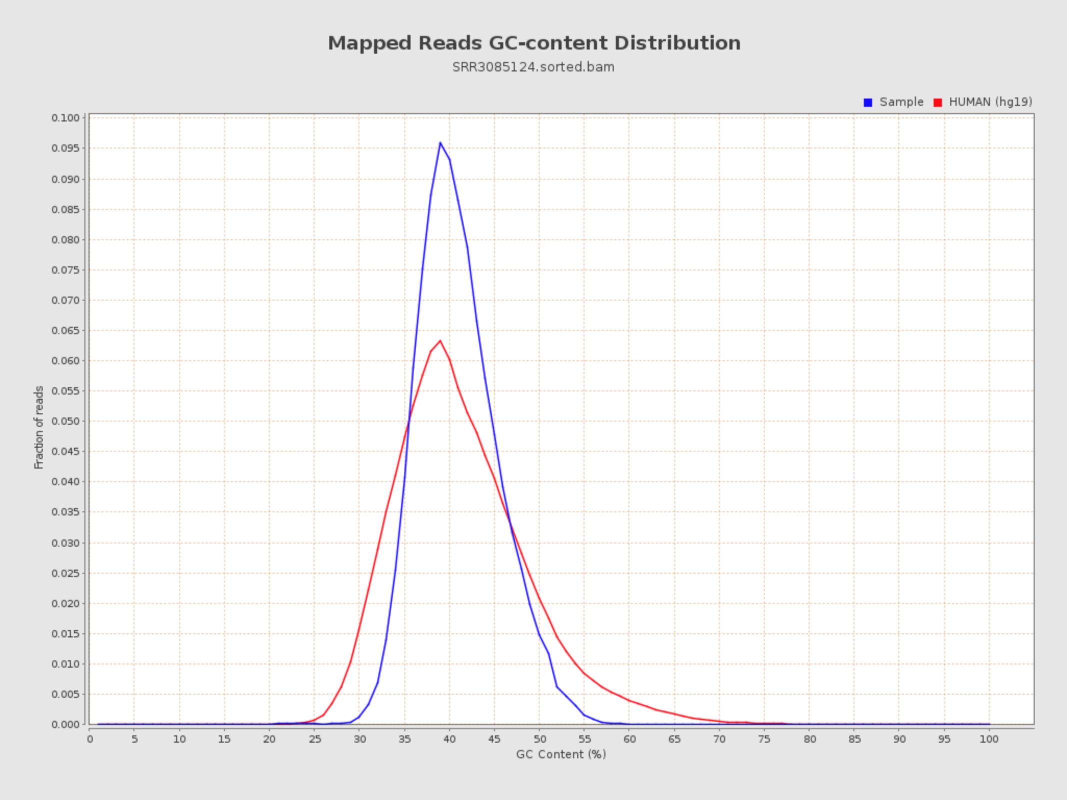
7. Results : Duplication Rate Histogram



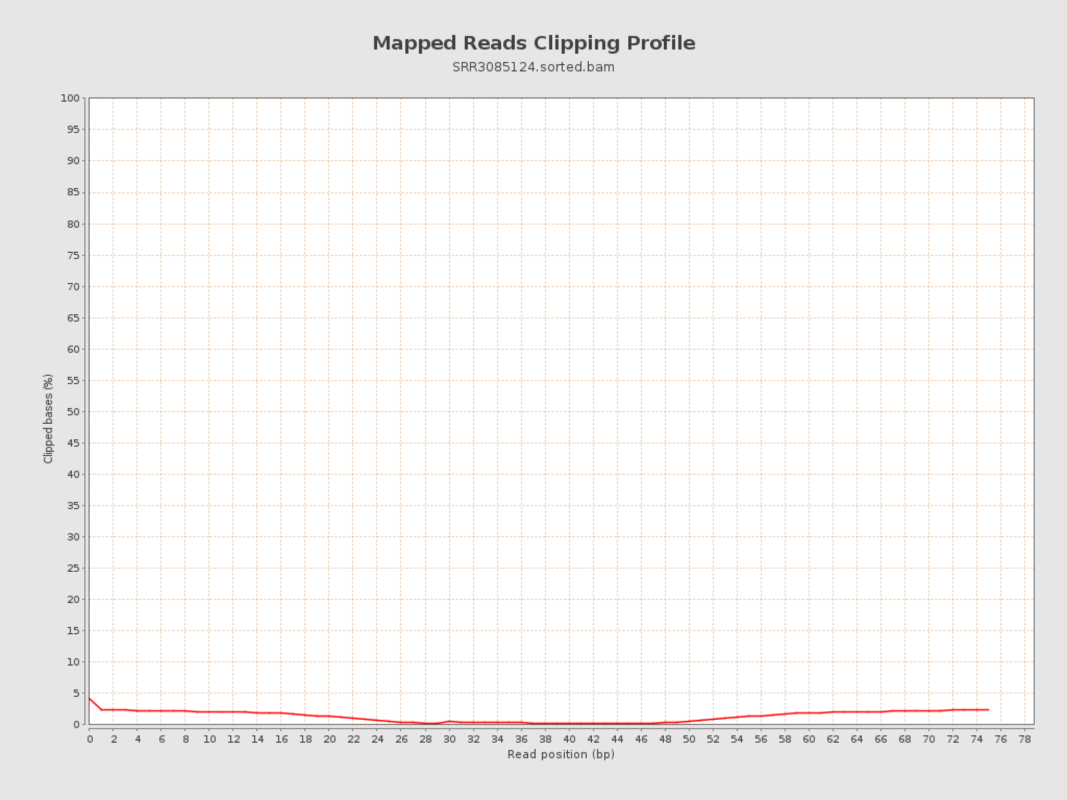
8. Results : Mapped Reads Nucleotide Content



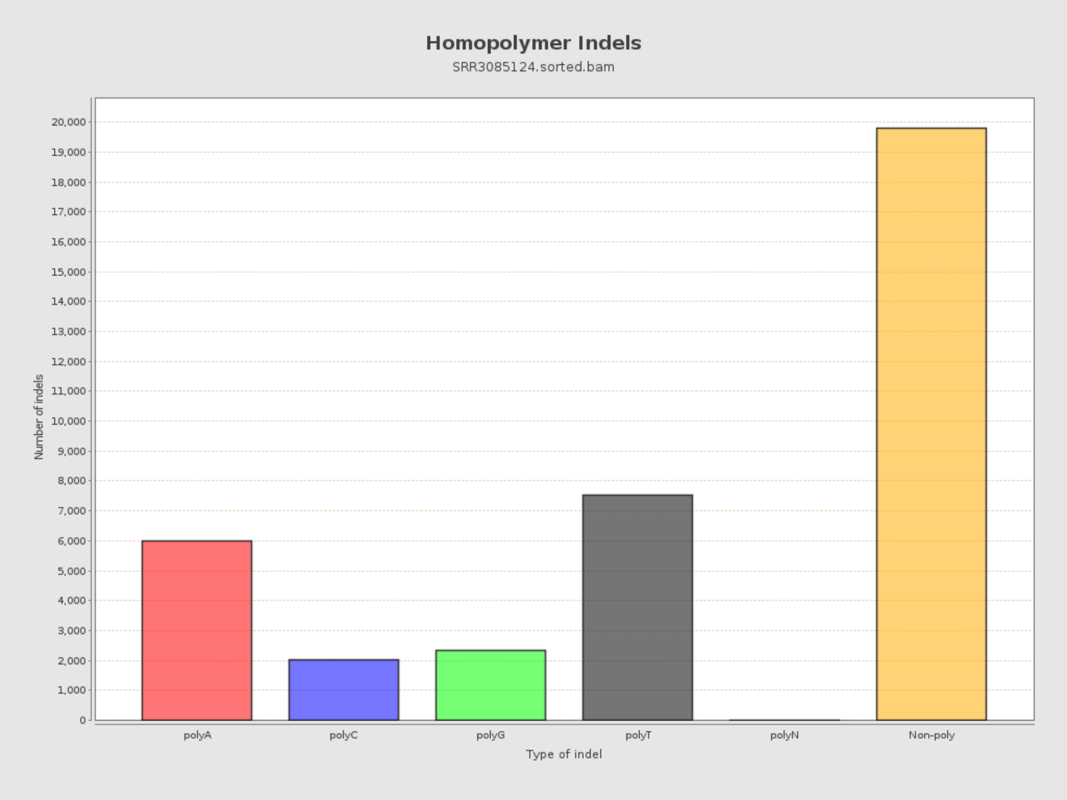
9. Results : Mapped Reads GC-content Distribution



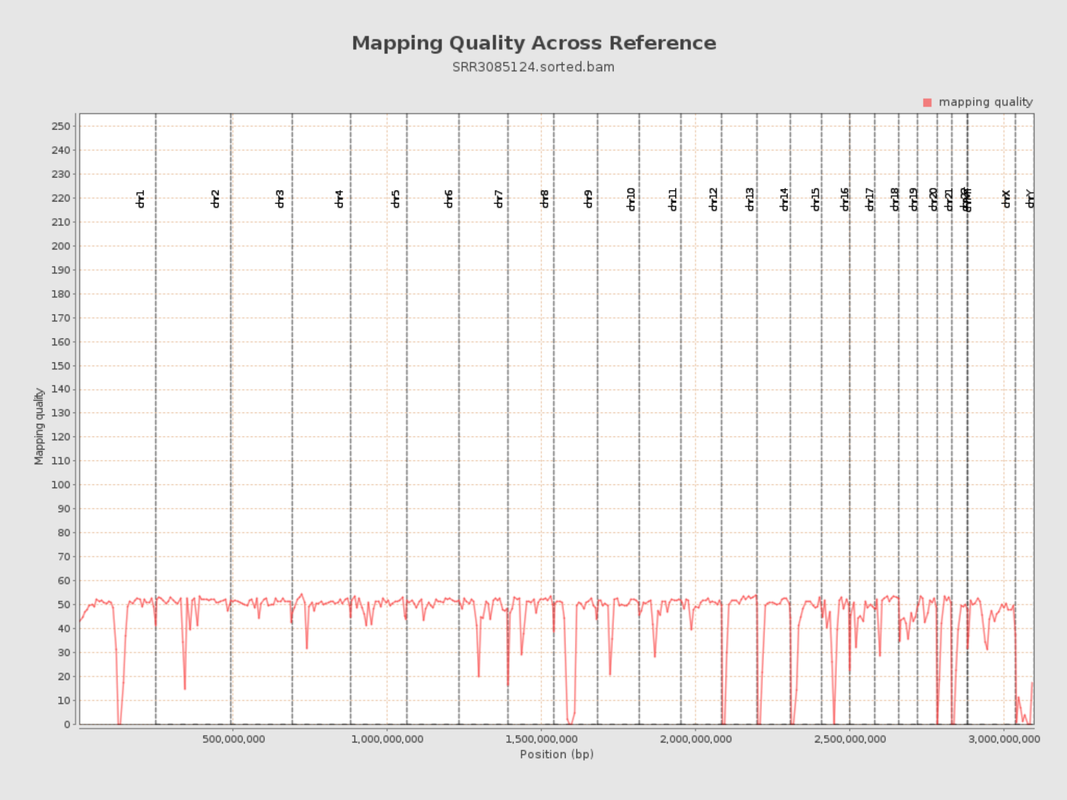
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram