Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:59:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084340.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_SRR3084340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:59:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,330,484
Mapped reads	2,101,541 / 90.18%
Unmapped reads	228,943 / 9.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,464 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	65,430 / 2.81%
Duplication rate	2.57%
Clipped reads	1,086,724 / 46.63%

2.2. ACGT Content

Number/percentage of A's	37,915,132 / 27.51%
Number/percentage of C's	26,524,623 / 19.25%
Number/percentage of T's	41,871,890 / 30.39%
Number/percentage of G's	31,325,848 / 22.73%
Number/percentage of N's	165,993 / 0.12%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.3145

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

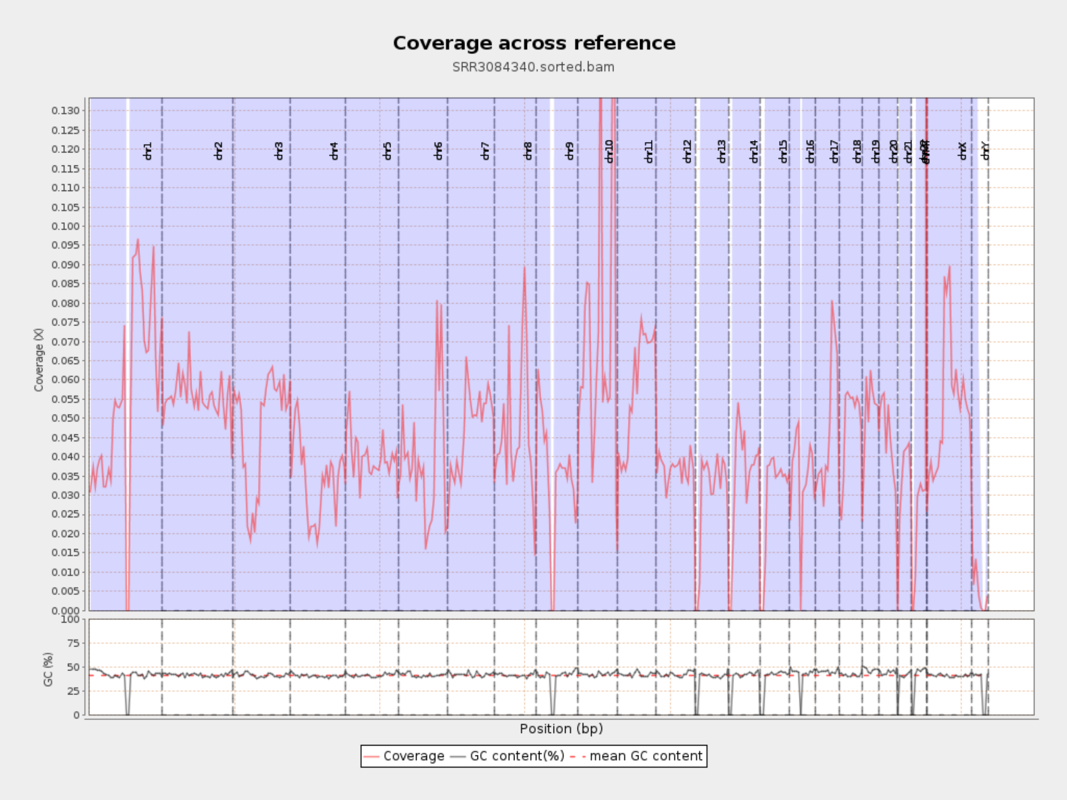
General error rate	1%
Mismatches	1,359,576
Insertions	10,477
Mapped reads with at least one insertion	0.49%
Deletions	29,235
Mapped reads with at least one deletion	1.38%
Homopolymer indels	45.62%

2.6. Chromosome stats

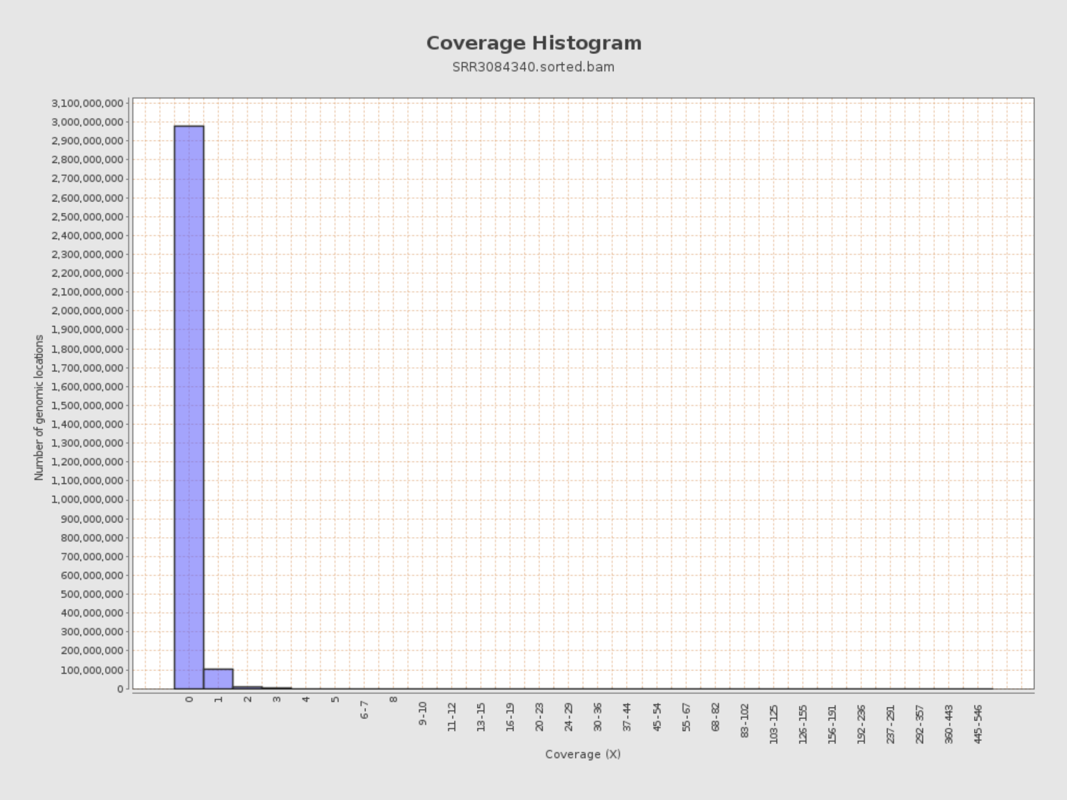
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13792915	0.0553	0.5351
chr2	243199373	13563846	0.0558	0.3748
chr3	198022430	9427275	0.0476	0.2482
chr4	191154276	6535096	0.0342	0.2161
chr5	180915260	7245033	0.04	0.2241
chr6	171115067	6675981	0.039	0.2428
chr7	159138663	7641305	0.048	0.3785

chr8	146364022	6834077	0.0467	0.2917
chr9	141213431	4999126	0.0354	0.2478
chr10	135534747	10348128	0.0764	0.4862
chr11	135006516	7772815	0.0576	0.3089
chr12	133851895	4903368	0.0366	0.2159
chr13	115169878	3434036	0.0298	0.1937
chr14	107349540	3719935	0.0347	0.2159
chr15	102531392	3031234	0.0296	0.2011
chr16	90354753	3152517	0.0349	0.2273
chr17	81195210	3866006	0.0476	0.254
chr18	78077248	3766581	0.0482	0.3913
chr19	59128983	3085729	0.0522	0.4008
chr20	63025520	2816722	0.0447	0.2393
chr21	48129895	1581628	0.0329	0.2098
chr22	51304566	1100571	0.0215	0.1645
chrMT	16571	12584	0.7594	1.228
chrX	155270560	8250893	0.0531	0.2787
chrY	59373566	293367	0.0049	0.1075

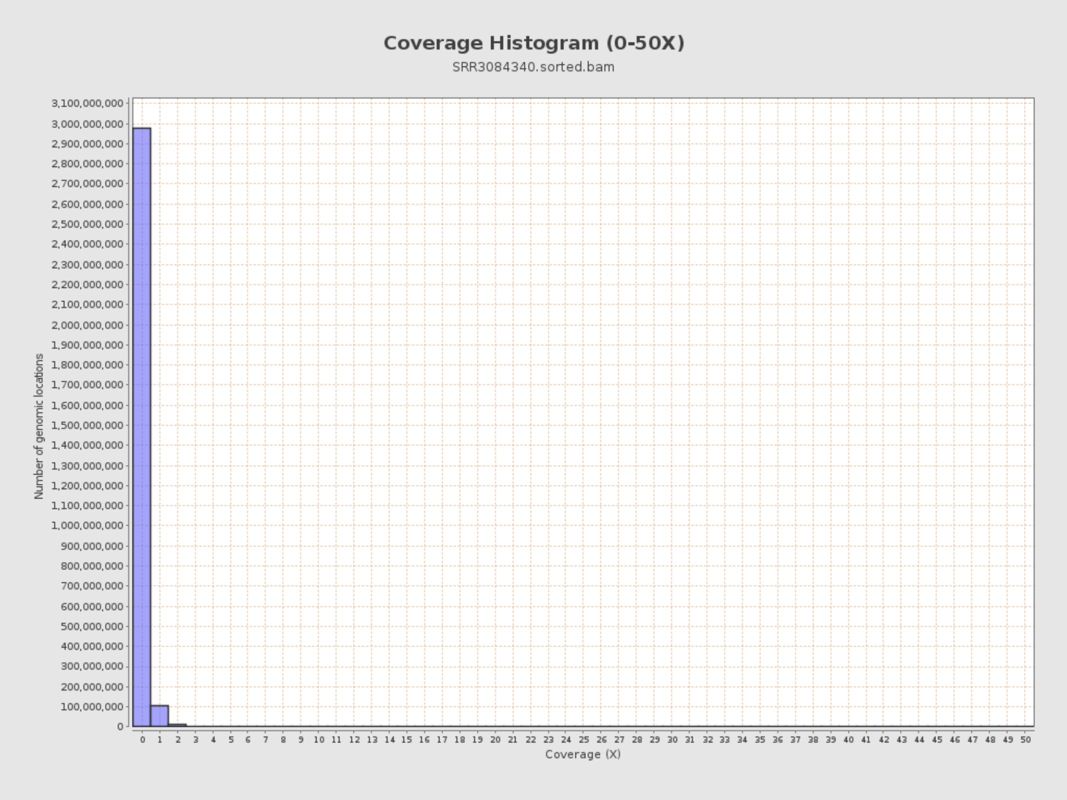
3. Results : Coverage across reference



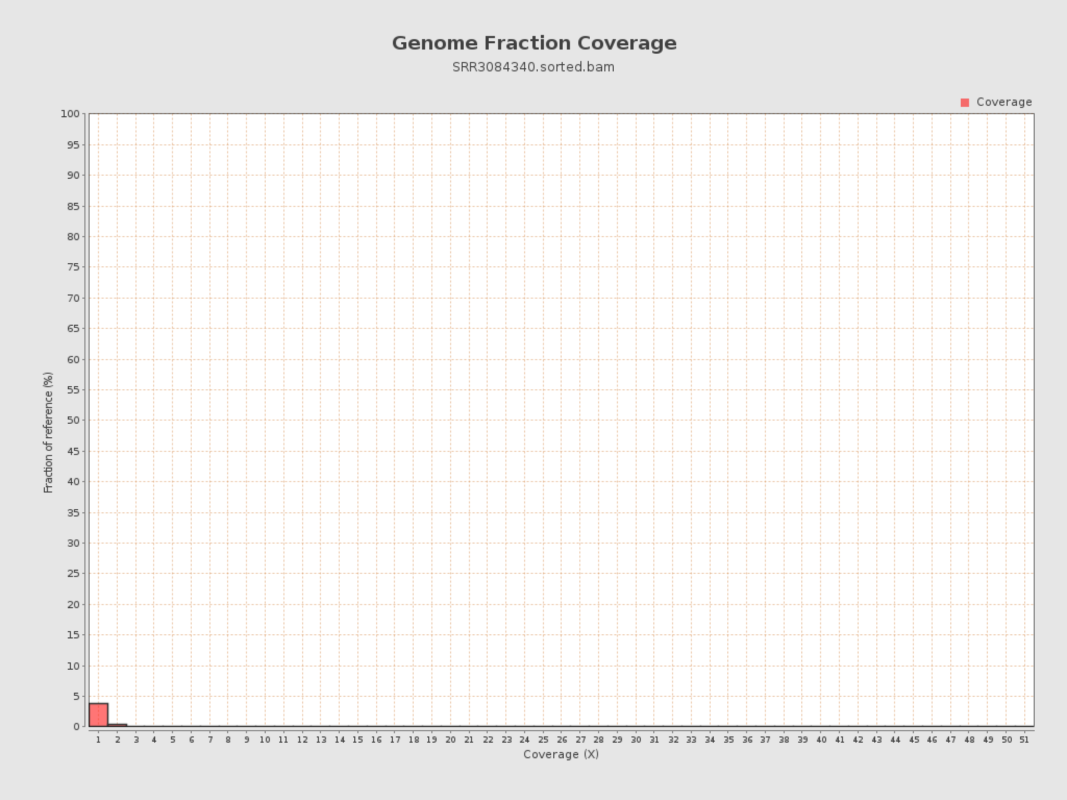
4. Results : Coverage Histogram



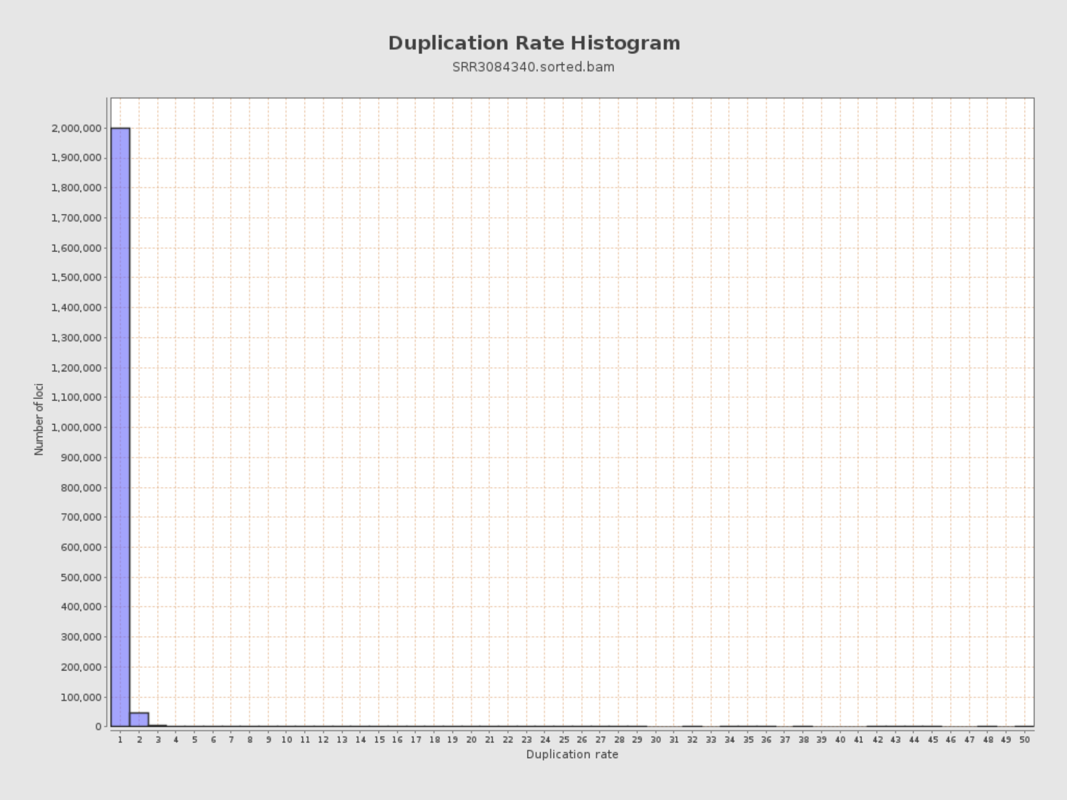
5. Results : Coverage Histogram (0-50X)



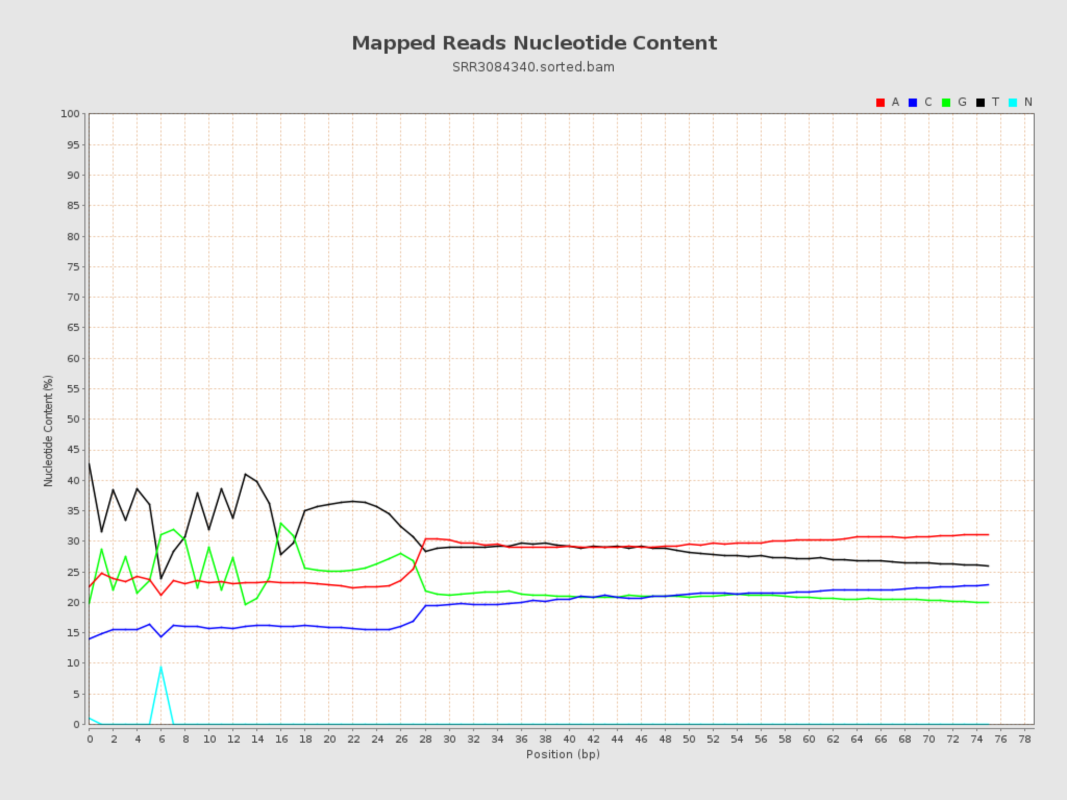
6. Results : Genome Fraction Coverage



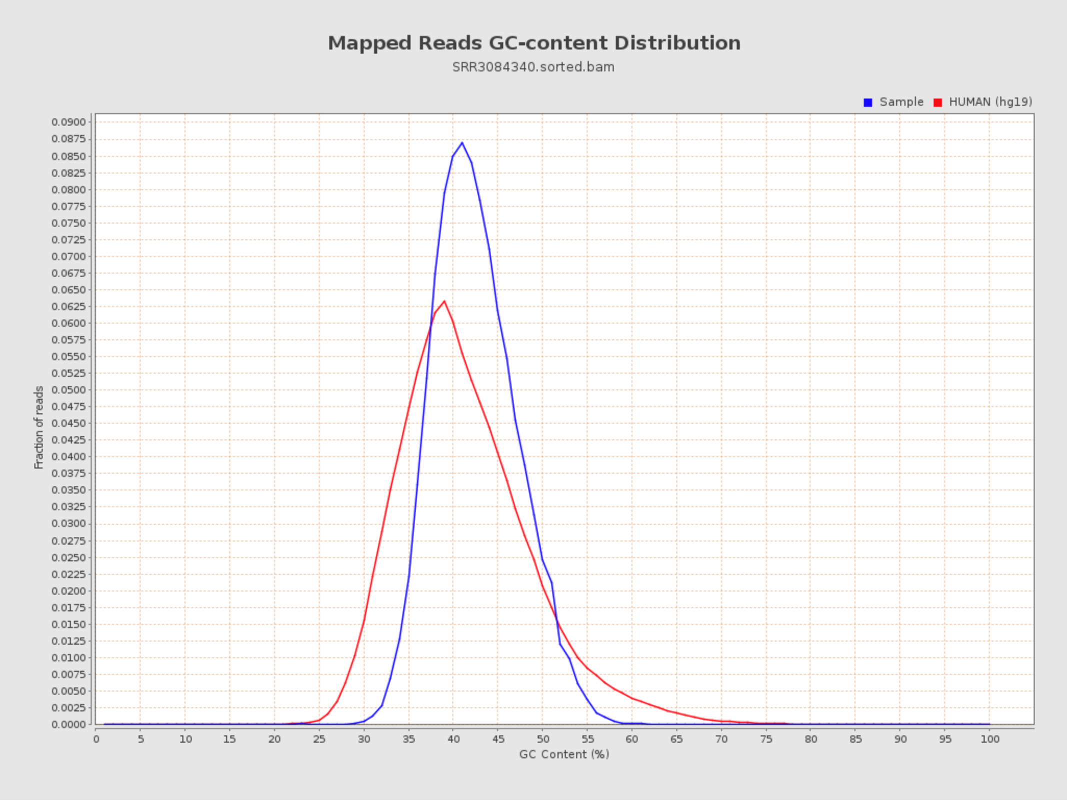
7. Results : Duplication Rate Histogram



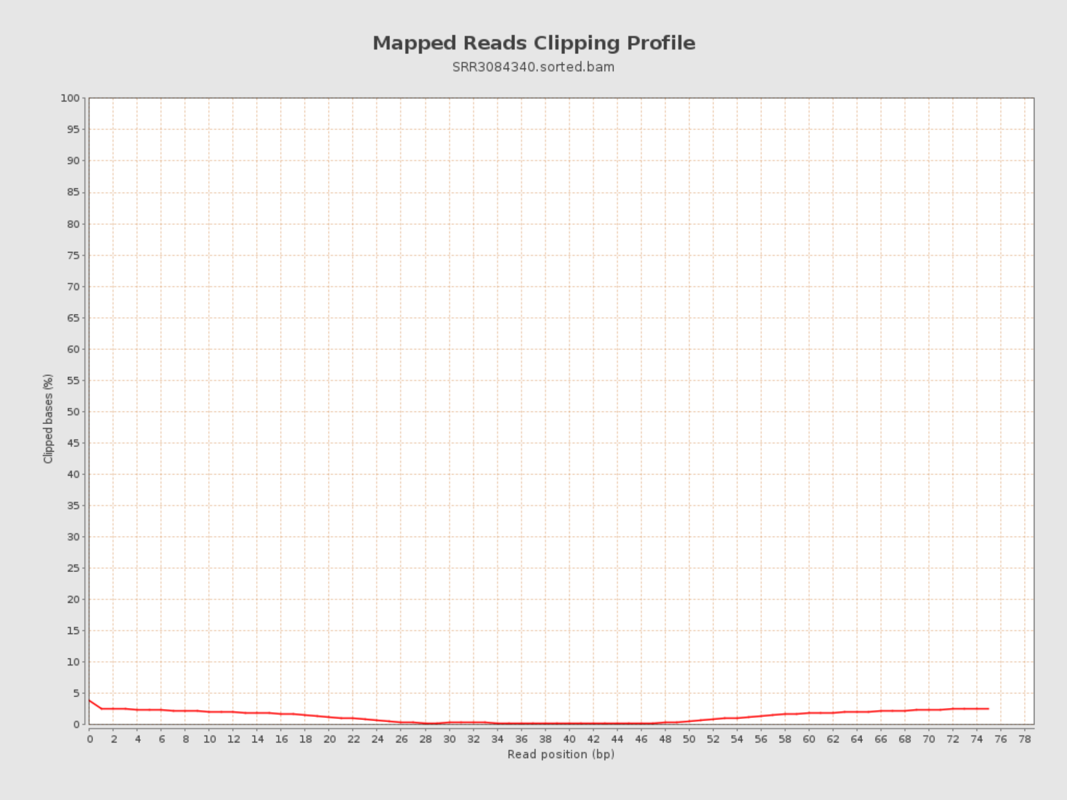
8. Results : Mapped Reads Nucleotide Content



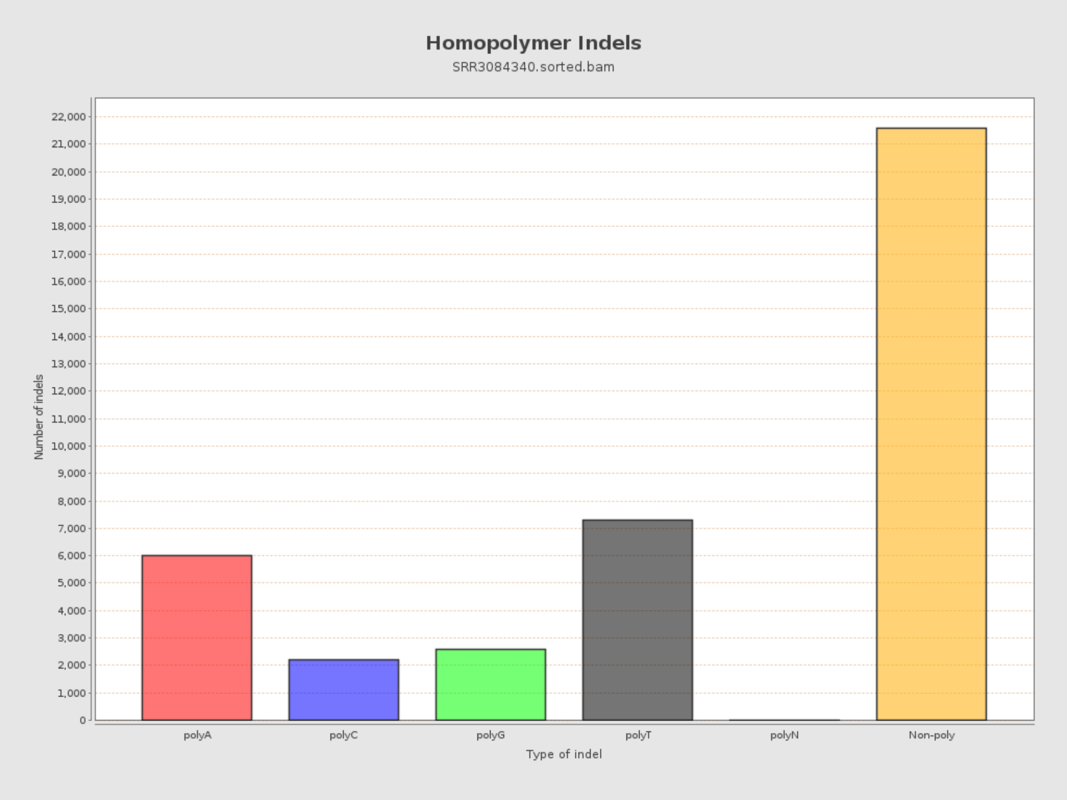
9. Results : Mapped Reads GC-content Distribution



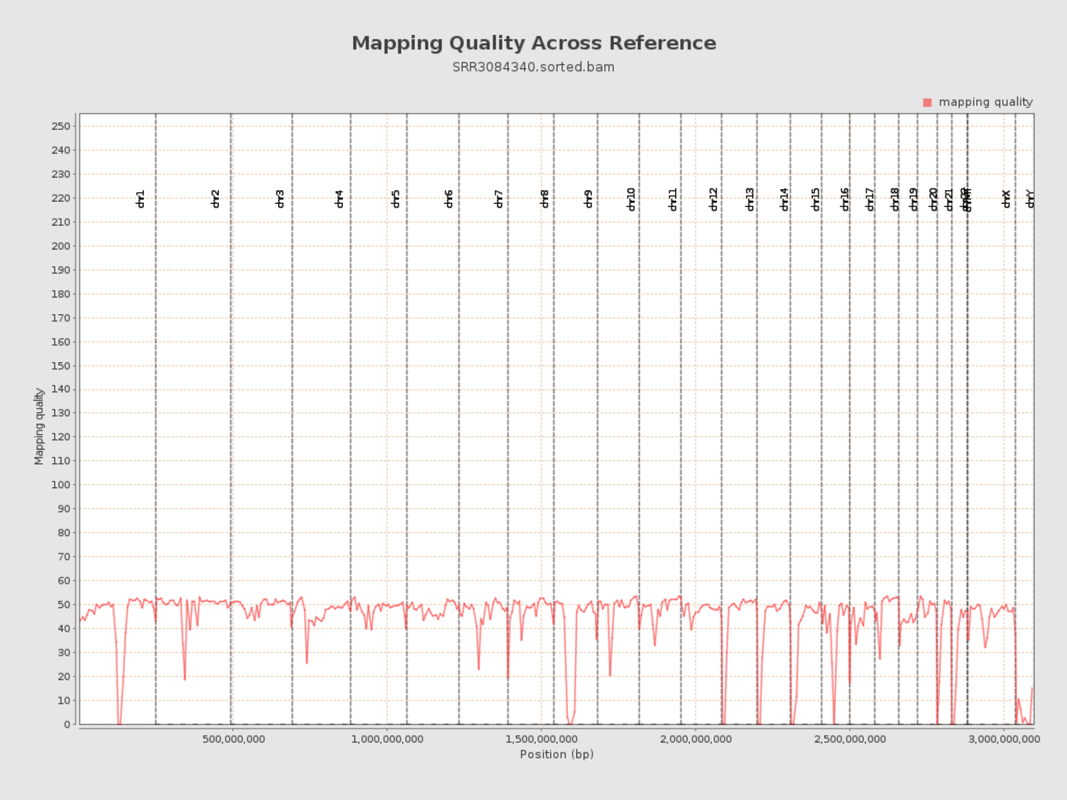
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram