Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:46:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084805.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_SRR3084805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:46:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,908,861
Mapped reads	1,753,032 / 91.84%
Unmapped reads	155,829 / 8.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,114 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	73,031 / 3.83%
Duplication rate	3.63%
Clipped reads	736,783 / 38.6%

2.2. ACGT Content

Number/percentage of A's	32,815,430 / 27.77%
Number/percentage of C's	21,951,570 / 18.58%
Number/percentage of T's	37,336,553 / 31.6%
Number/percentage of G's	26,044,248 / 22.04%
Number/percentage of N's	16,637 / 0.01%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.2644

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

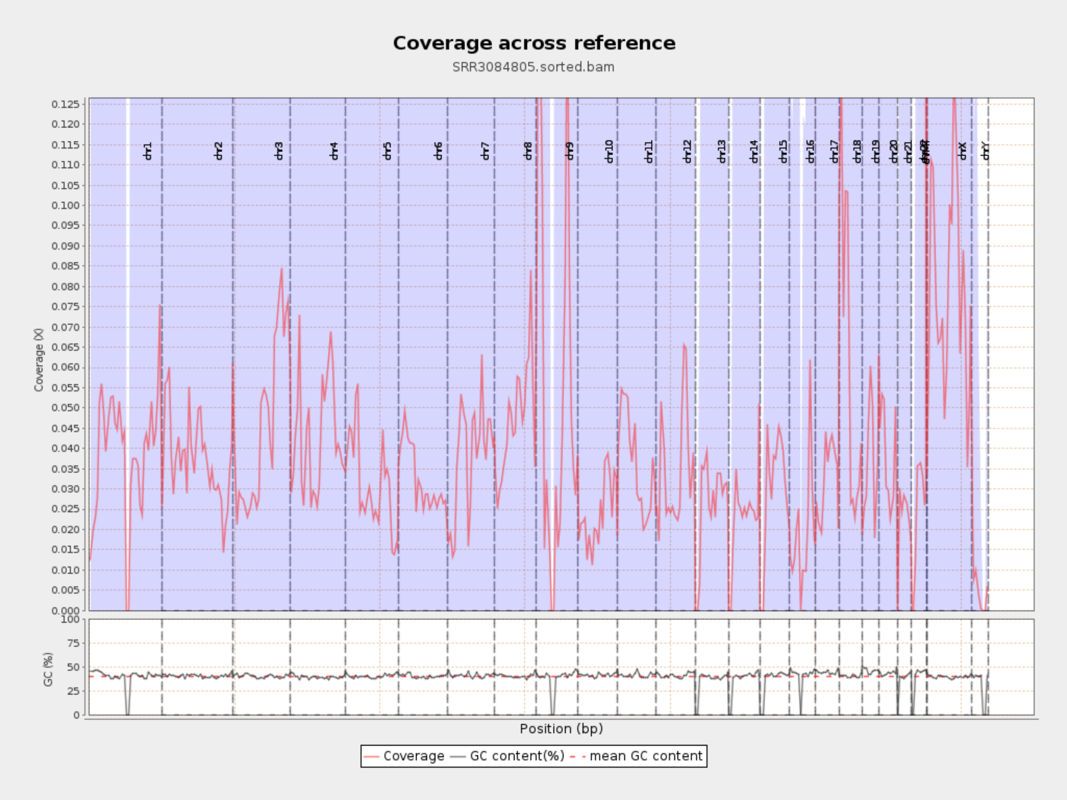
General error rate	0.75%
Mismatches	875,325
Insertions	9,103
Mapped reads with at least one insertion	0.51%
Deletions	27,321
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.16%

2.6. Chromosome stats

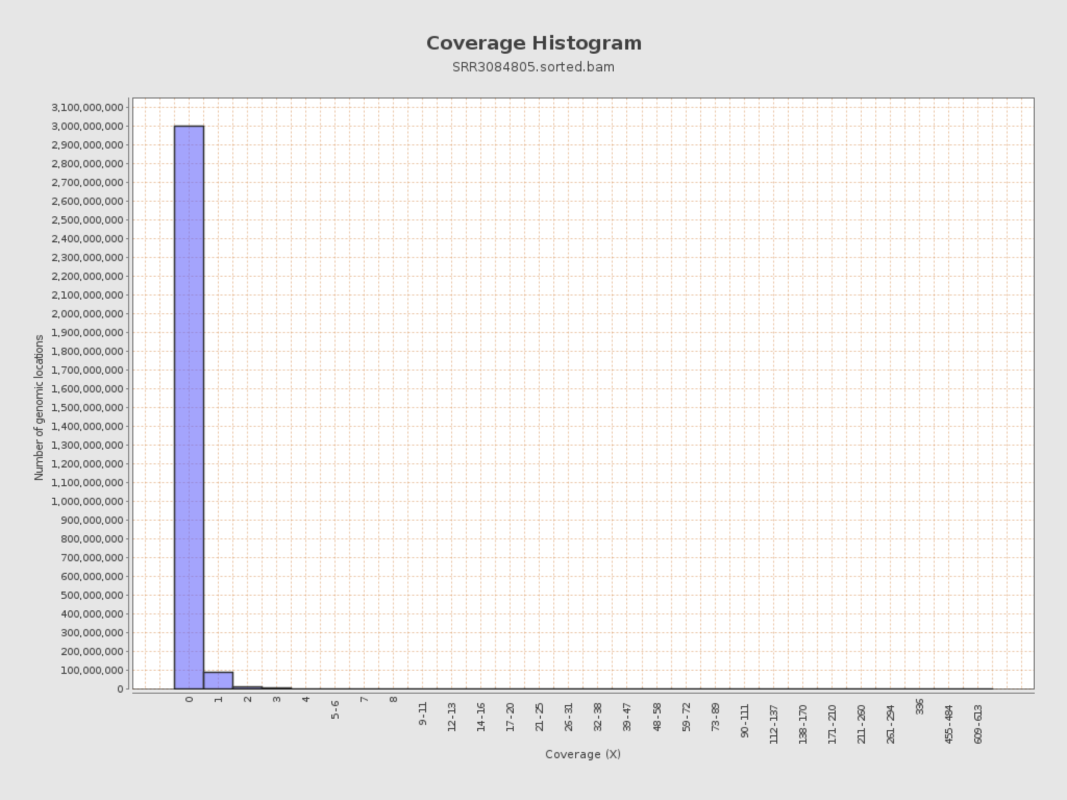
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9657284	0.0387	0.3079
chr2	243199373	9142323	0.0376	0.3762
chr3	198022430	9102395	0.046	0.2479
chr4	191154276	8215078	0.043	0.2436
chr5	180915260	5668360	0.0313	0.2065
chr6	171115067	5555812	0.0325	0.2195
chr7	159138663	6019662	0.0378	0.2552

chr8	146364022	6904585	0.0472	0.3068
chr9	141213431	8004657	0.0567	0.3285
chr10	135534747	3221917	0.0238	0.1845
chr11	135006516	4879715	0.0361	0.2422
chr12	133851895	4642155	0.0347	0.2165
chr13	115169878	2964918	0.0257	0.1863
chr14	107349540	2342830	0.0218	0.175
chr15	102531392	3066408	0.0299	0.2059
chr16	90354753	1778613	0.0197	0.1678
chr17	81195210	2688685	0.0331	0.2109
chr18	78077248	4824032	0.0618	0.4159
chr19	59128983	2246512	0.038	0.2652
chr20	63025520	2411890	0.0383	0.2271
chr21	48129895	1102808	0.0229	0.1795
chr22	51304566	1163530	0.0227	0.1714
chrMT	16571	30928	1.8664	1.6676
chrX	155270560	12249181	0.0789	0.338
chrY	59373566	325647	0.0055	0.0921

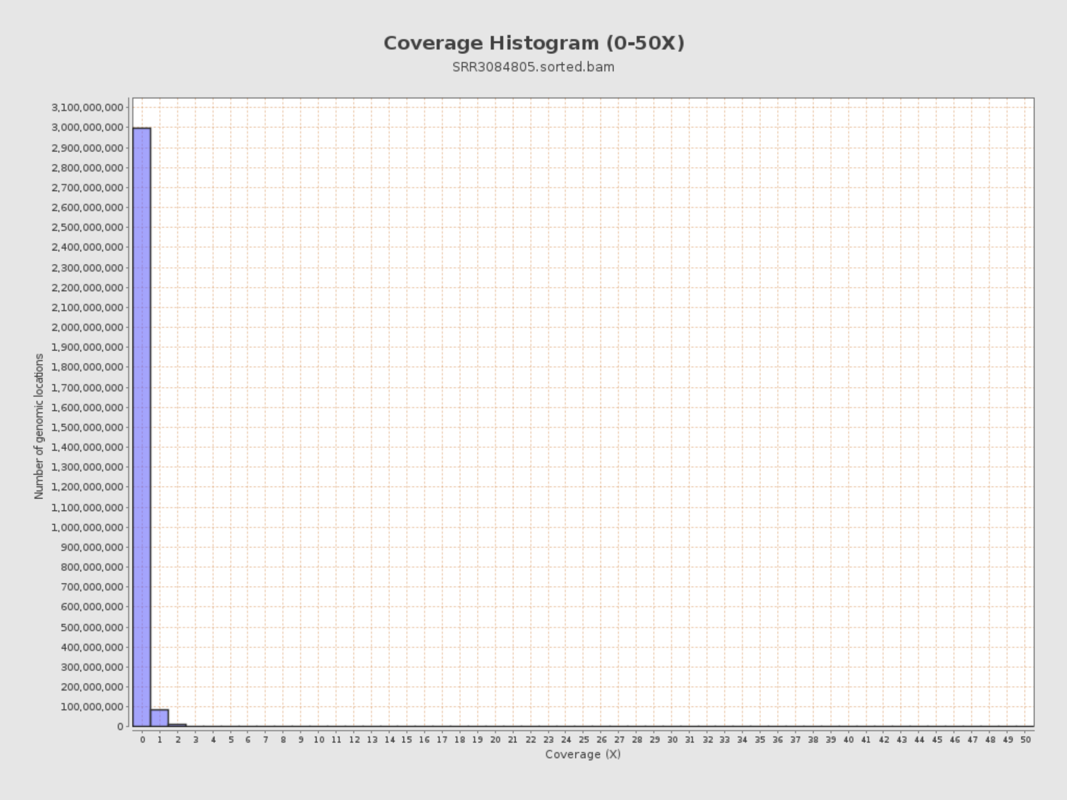
3. Results : Coverage across reference



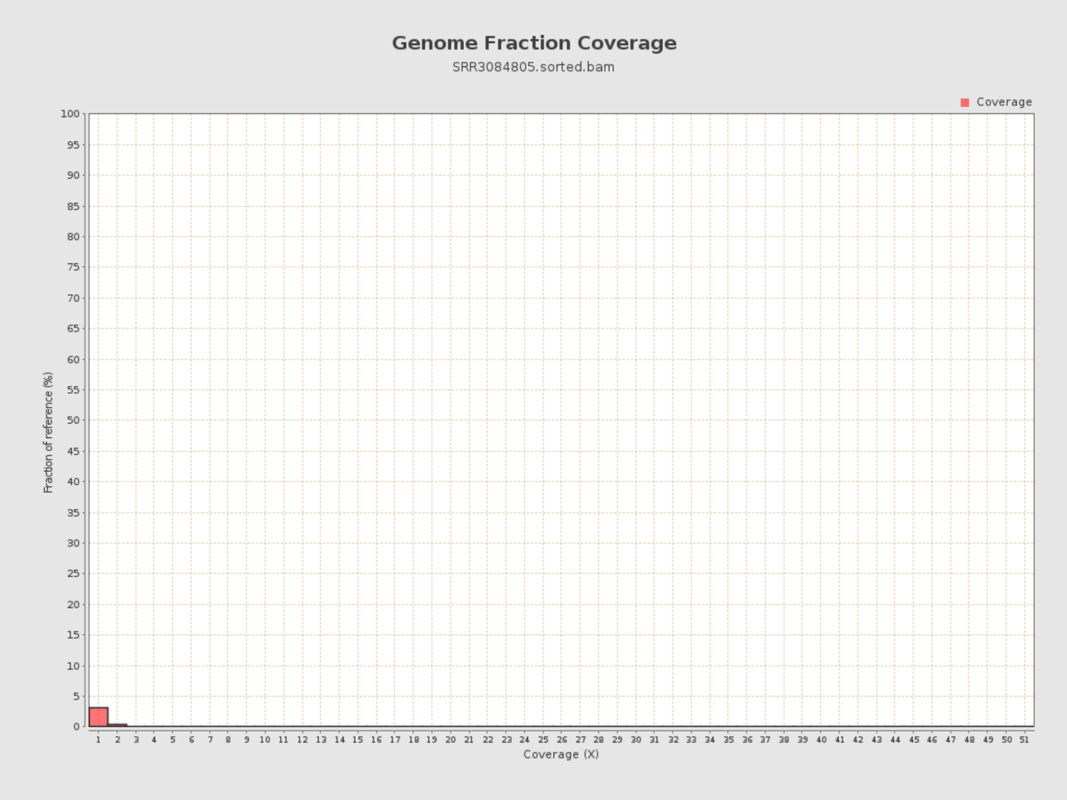
4. Results : Coverage Histogram



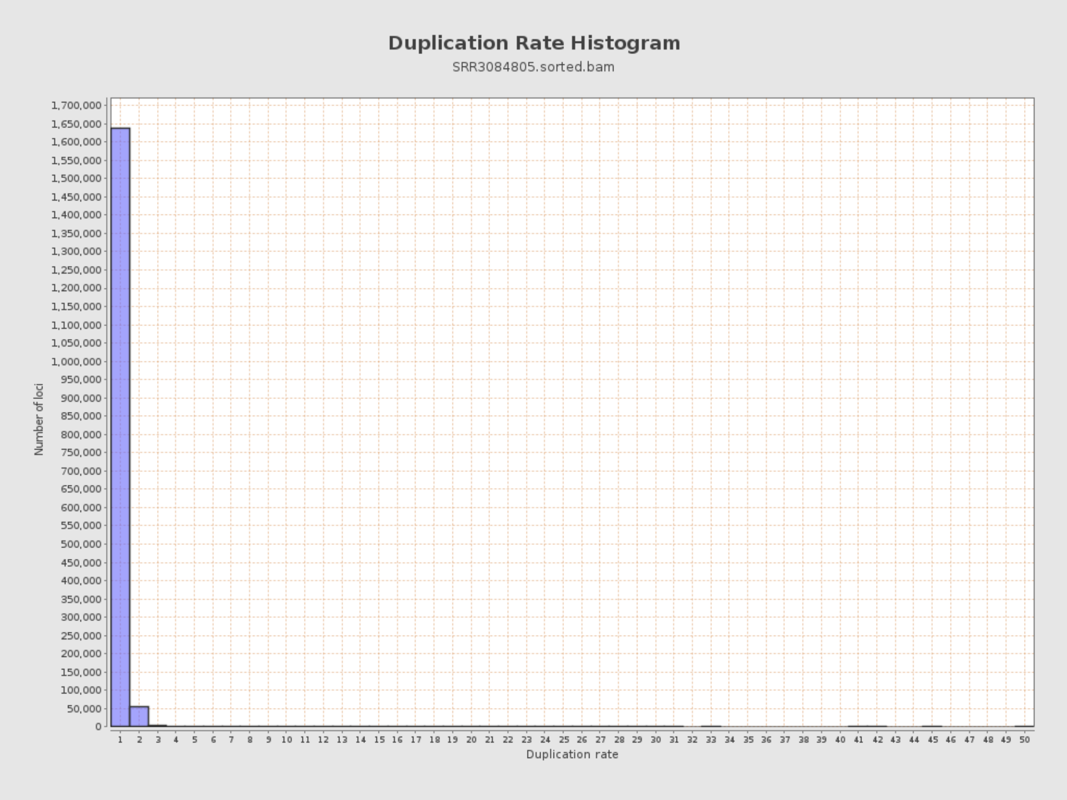
5. Results : Coverage Histogram (0-50X)



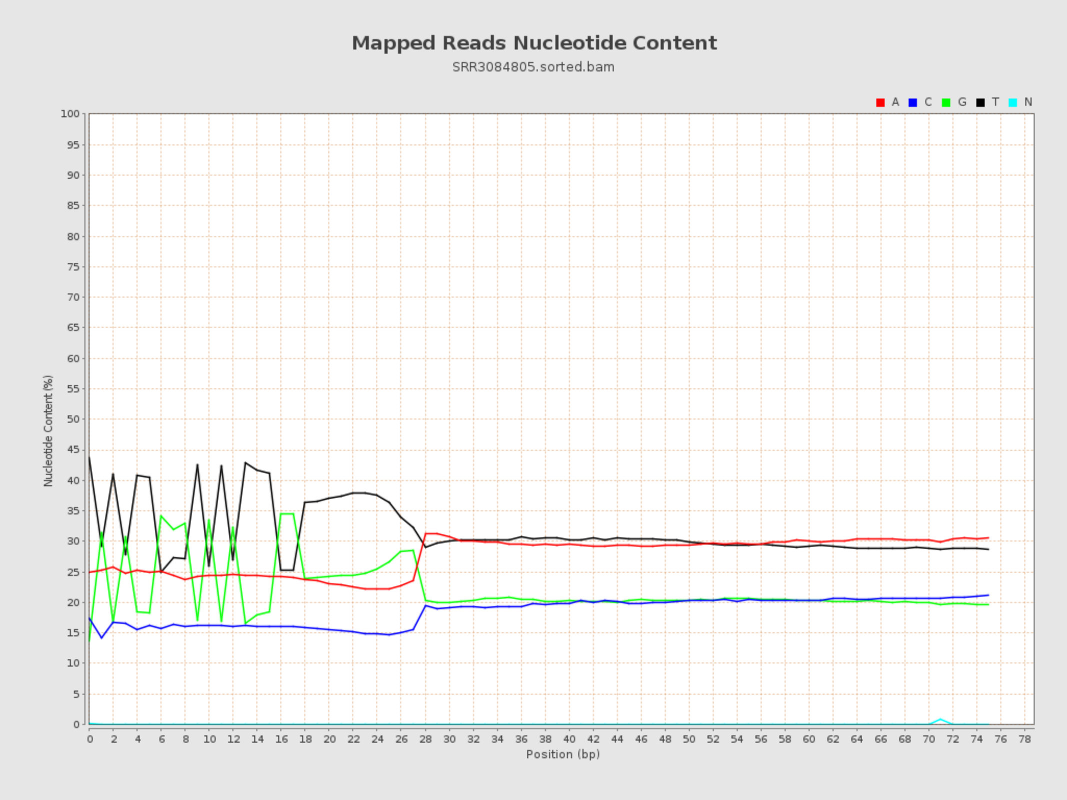
6. Results : Genome Fraction Coverage



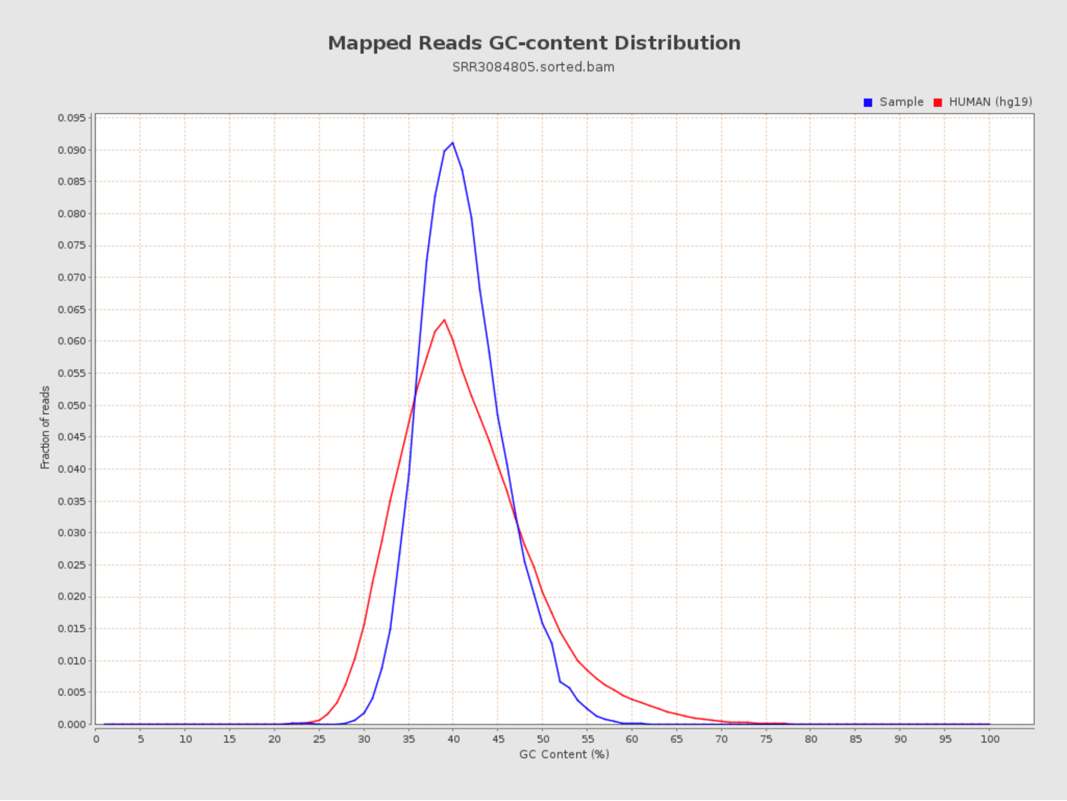
7. Results : Duplication Rate Histogram



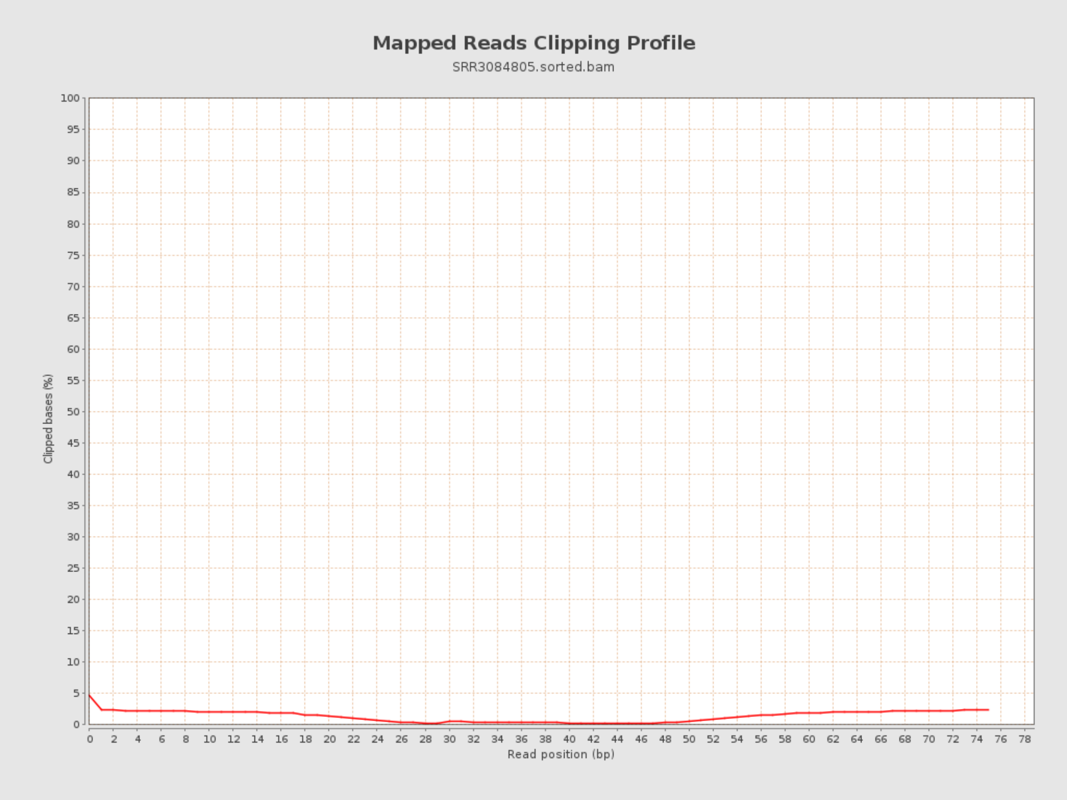
8. Results : Mapped Reads Nucleotide Content



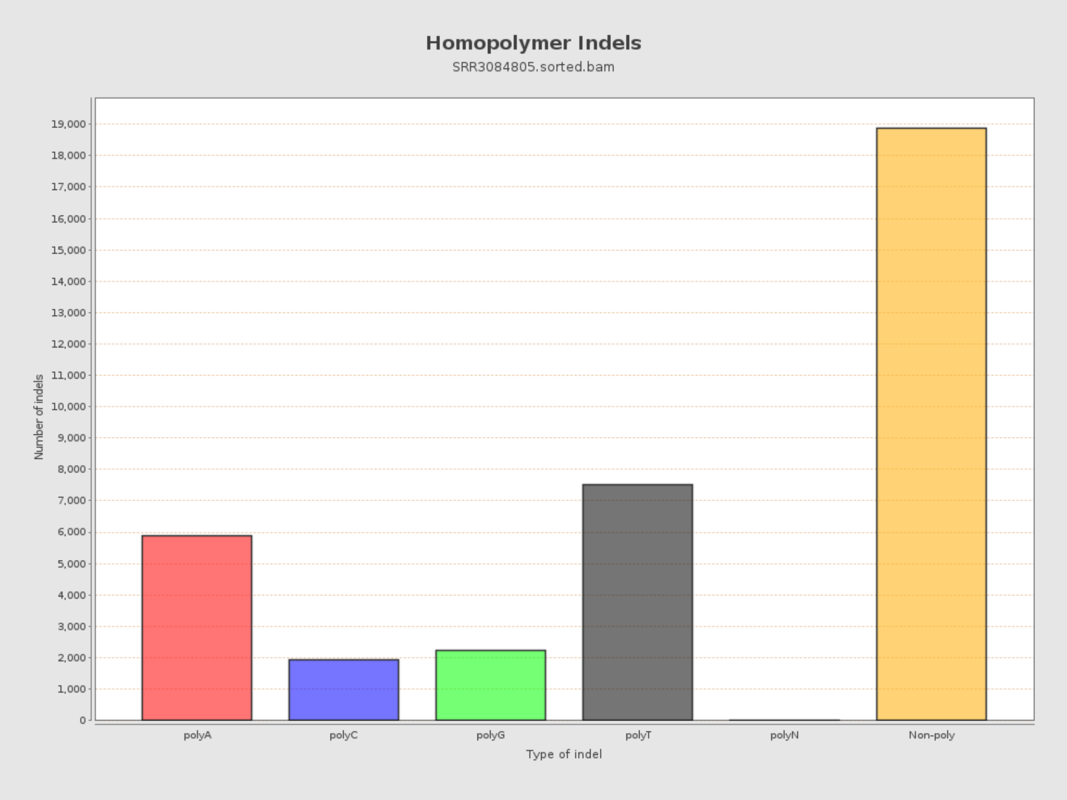
9. Results : Mapped Reads GC-content Distribution



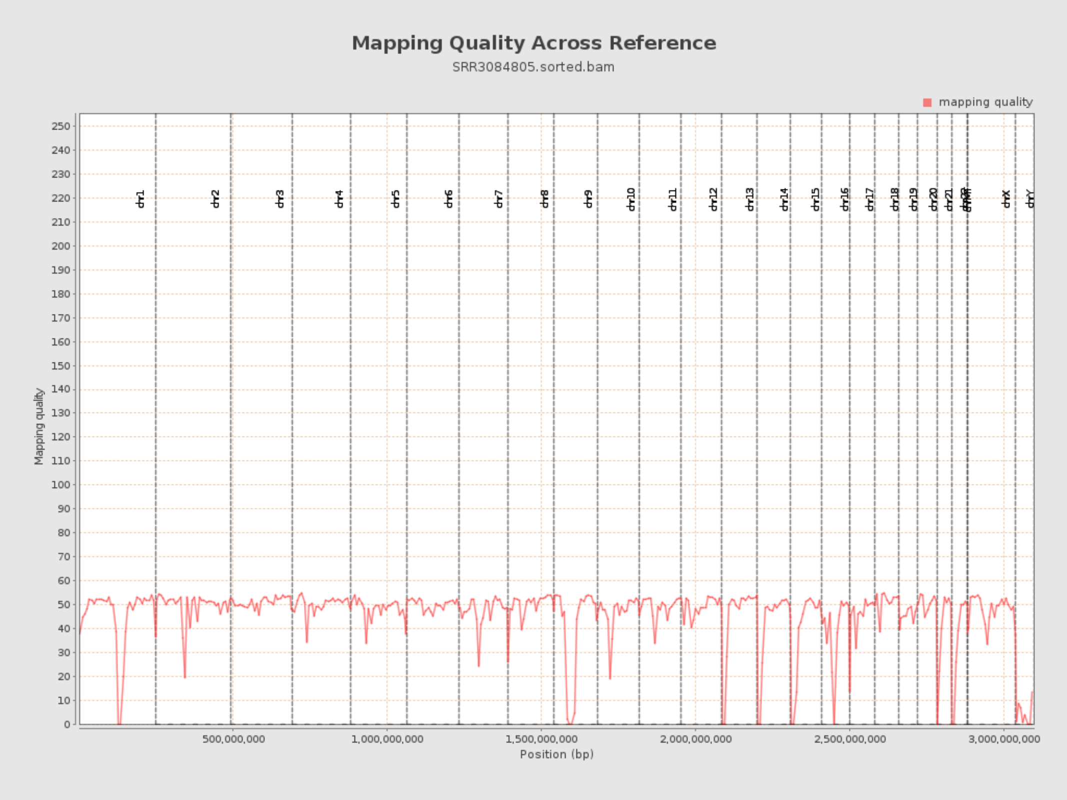
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram