Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:53:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084807.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_SRR3084807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084807.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:53:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,791,230
Mapped reads	1,635,151 / 91.29%
Unmapped reads	156,079 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,299 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	67,922 / 3.79%
Duplication rate	3.66%
Clipped reads	683,578 / 38.16%

2.2. ACGT Content

Number/percentage of A's	30,581,434 / 27.78%
Number/percentage of C's	20,383,360 / 18.51%
Number/percentage of T's	34,937,325 / 31.73%
Number/percentage of G's	24,177,123 / 21.96%
Number/percentage of N's	15,869 / 0.01%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.2502

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

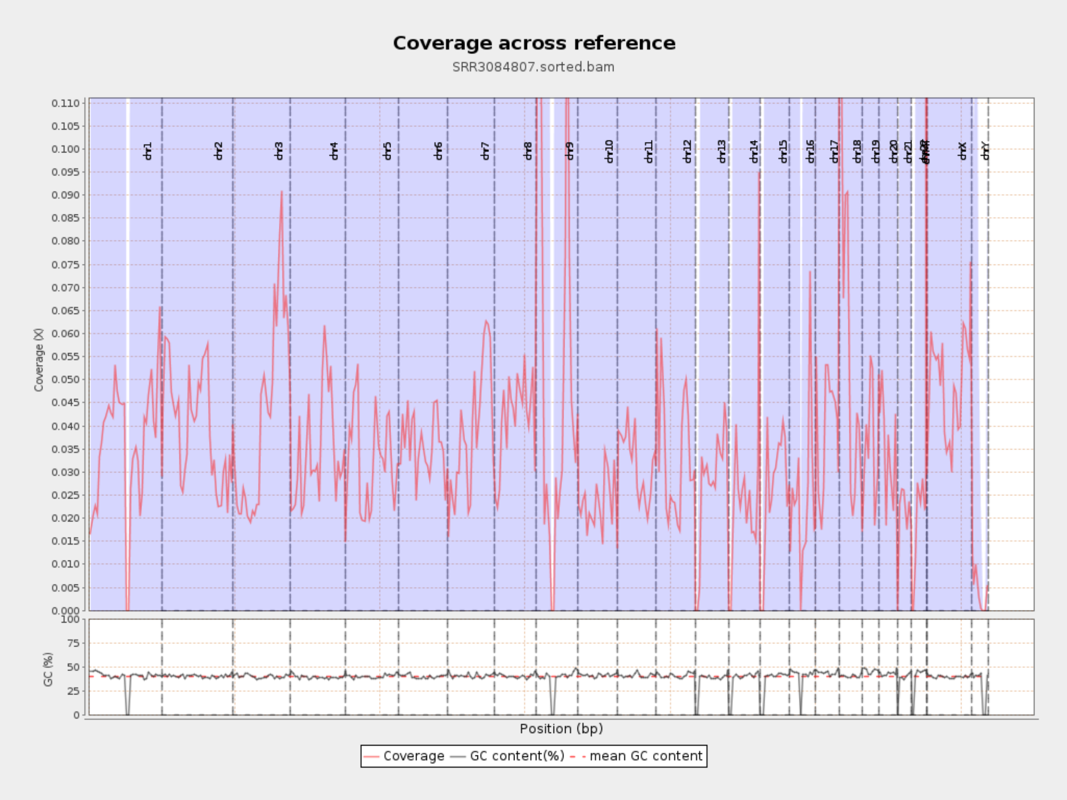
General error rate	0.76%
Mismatches	816,219
Insertions	8,841
Mapped reads with at least one insertion	0.54%
Deletions	25,505
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.69%

2.6. Chromosome stats

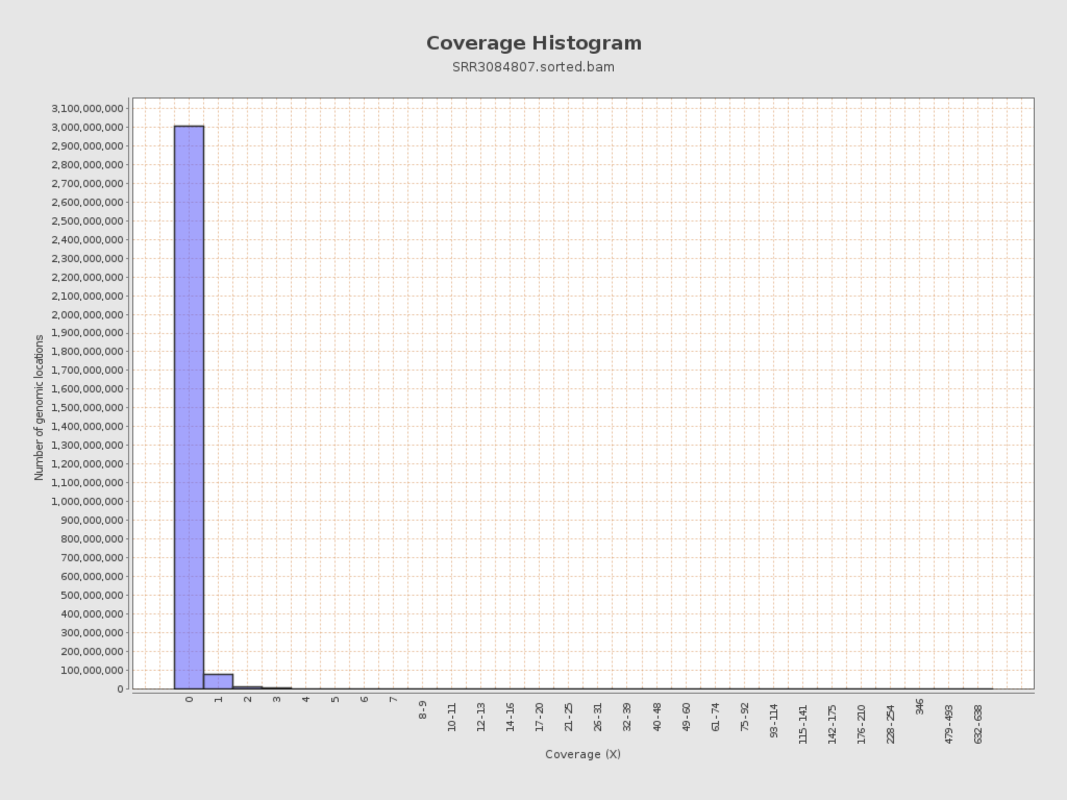
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8958508	0.0359	0.2644
chr2	243199373	9748457	0.0401	0.3715
chr3	198022430	8348911	0.0422	0.2401
chr4	191154276	6677607	0.0349	0.2188
chr5	180915260	5916181	0.0327	0.2103
chr6	171115067	6079696	0.0355	0.2311
chr7	159138663	6215109	0.0391	0.2466

chr8	146364022	6091313	0.0416	0.2931
chr9	141213431	7658723	0.0542	0.3043
chr10	135534747	3165373	0.0234	0.1864
chr11	135006516	4252766	0.0315	0.228
chr12	133851895	4537003	0.0339	0.2155
chr13	115169878	3117746	0.0271	0.1923
chr14	107349540	2319626	0.0216	0.1757
chr15	102531392	2700836	0.0263	0.1918
chr16	90354753	2294470	0.0254	0.1907
chr17	81195210	3296663	0.0406	0.2355
chr18	78077248	4681812	0.06	0.3898
chr19	59128983	2167524	0.0367	0.2461
chr20	63025520	2206388	0.035	0.2199
chr21	48129895	996238	0.0207	0.1703
chr22	51304566	914588	0.0178	0.1535
chrMT	16571	25031	1.5105	1.5916
chrX	155270560	7519085	0.0484	0.2629
chrY	59373566	248266	0.0042	0.092

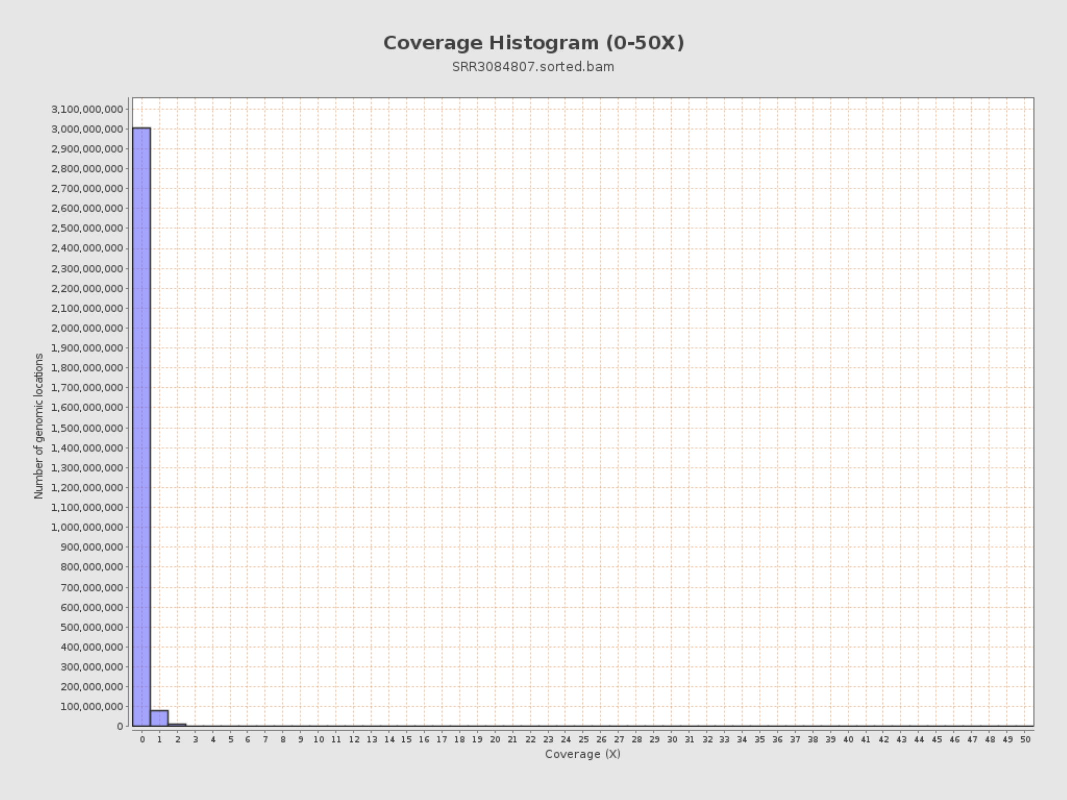
3. Results : Coverage across reference



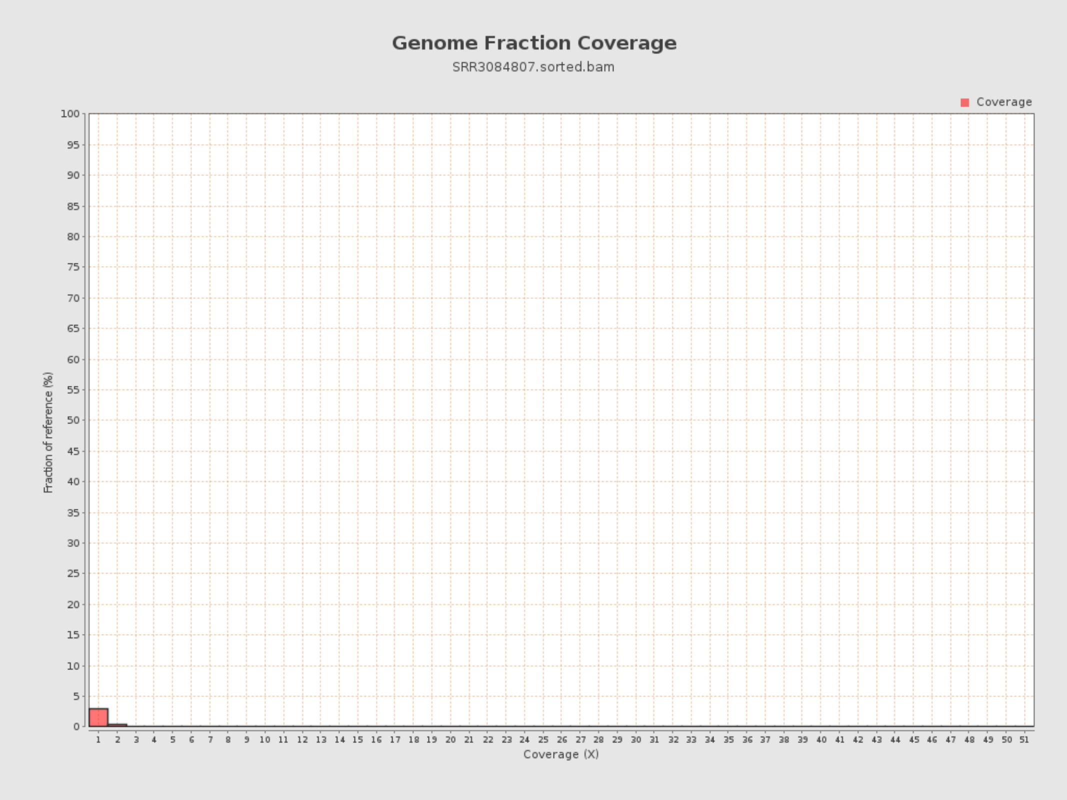
4. Results : Coverage Histogram



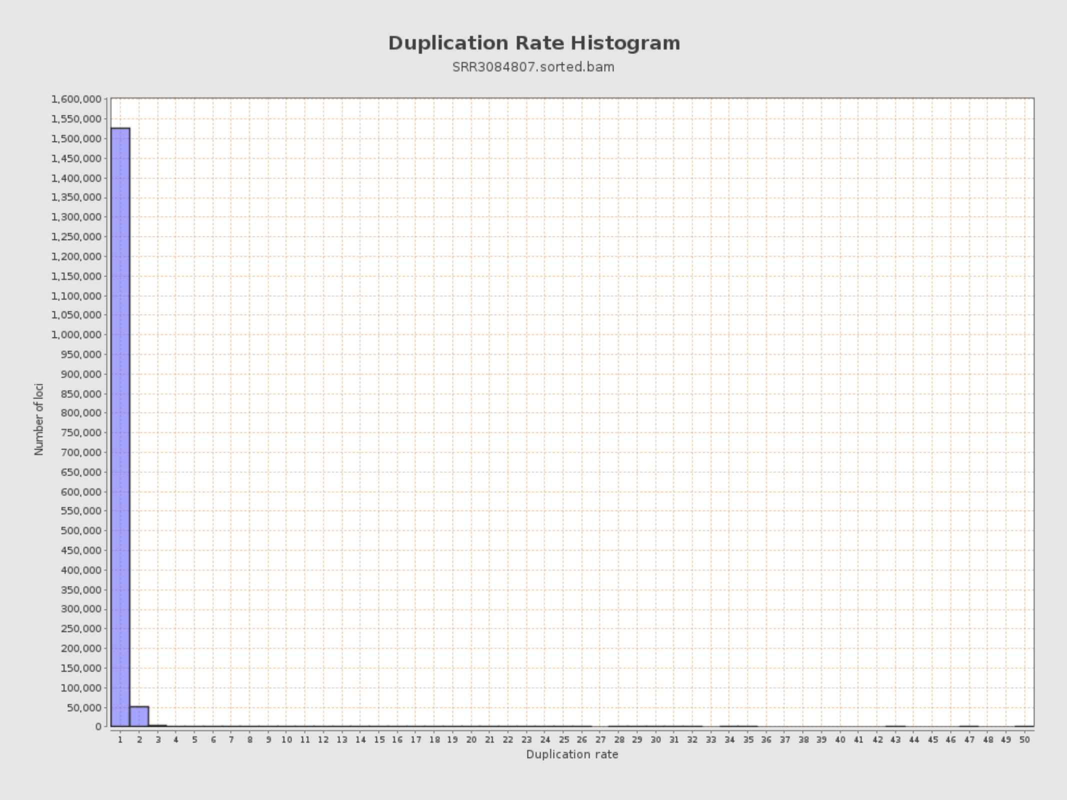
5. Results : Coverage Histogram (0-50X)



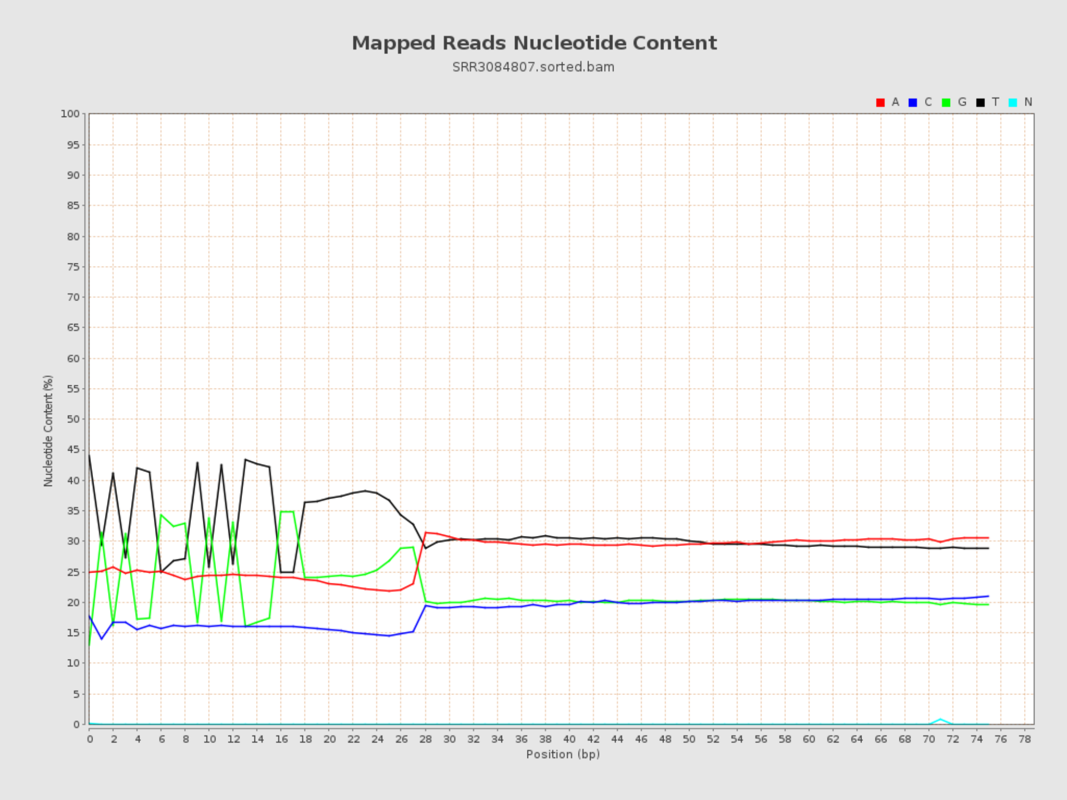
6. Results : Genome Fraction Coverage



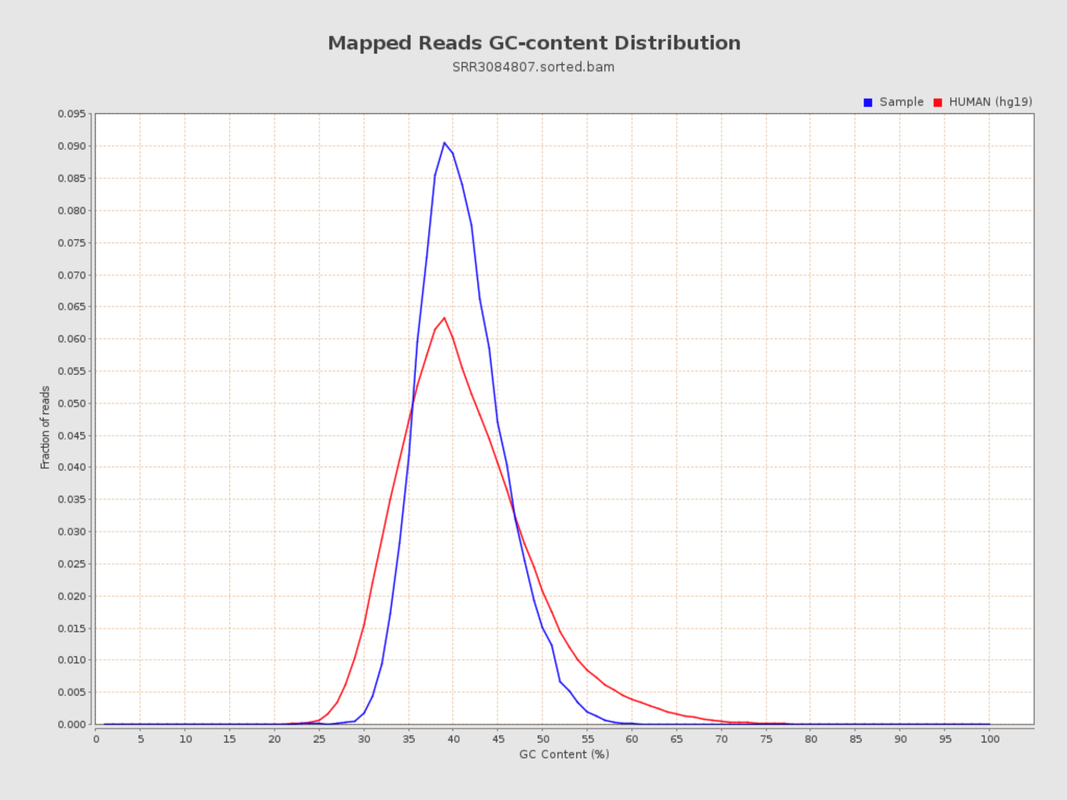
7. Results : Duplication Rate Histogram



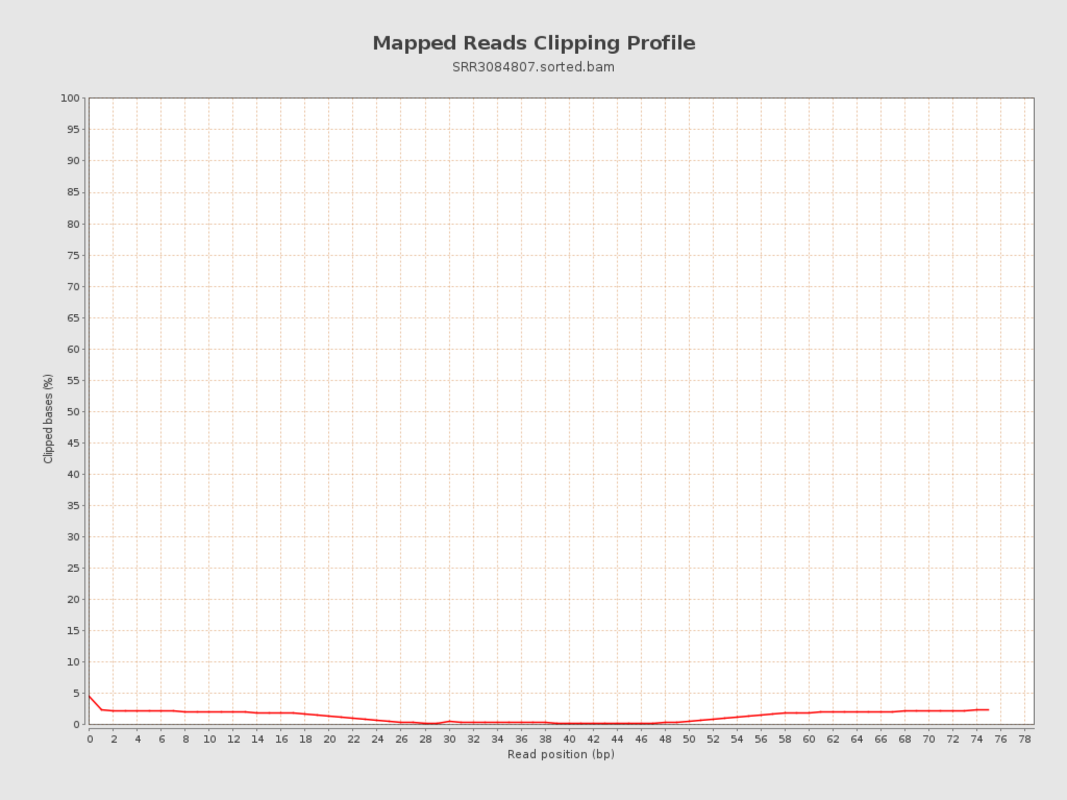
8. Results : Mapped Reads Nucleotide Content



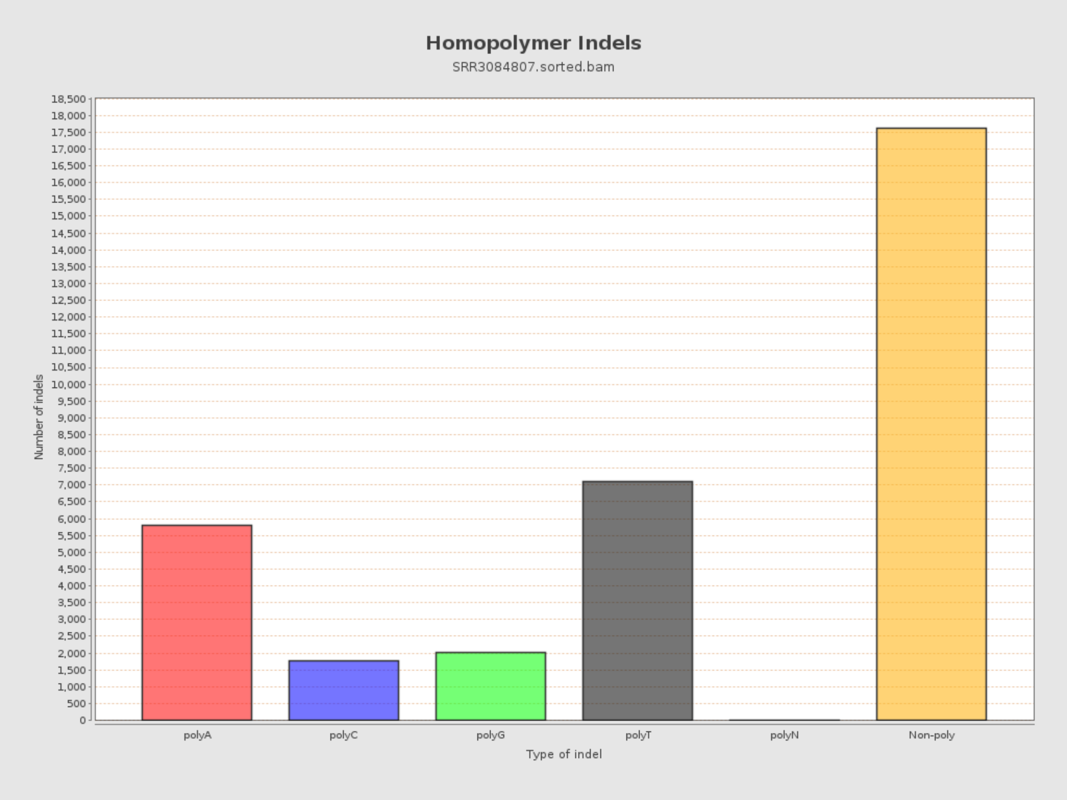
9. Results : Mapped Reads GC-content Distribution



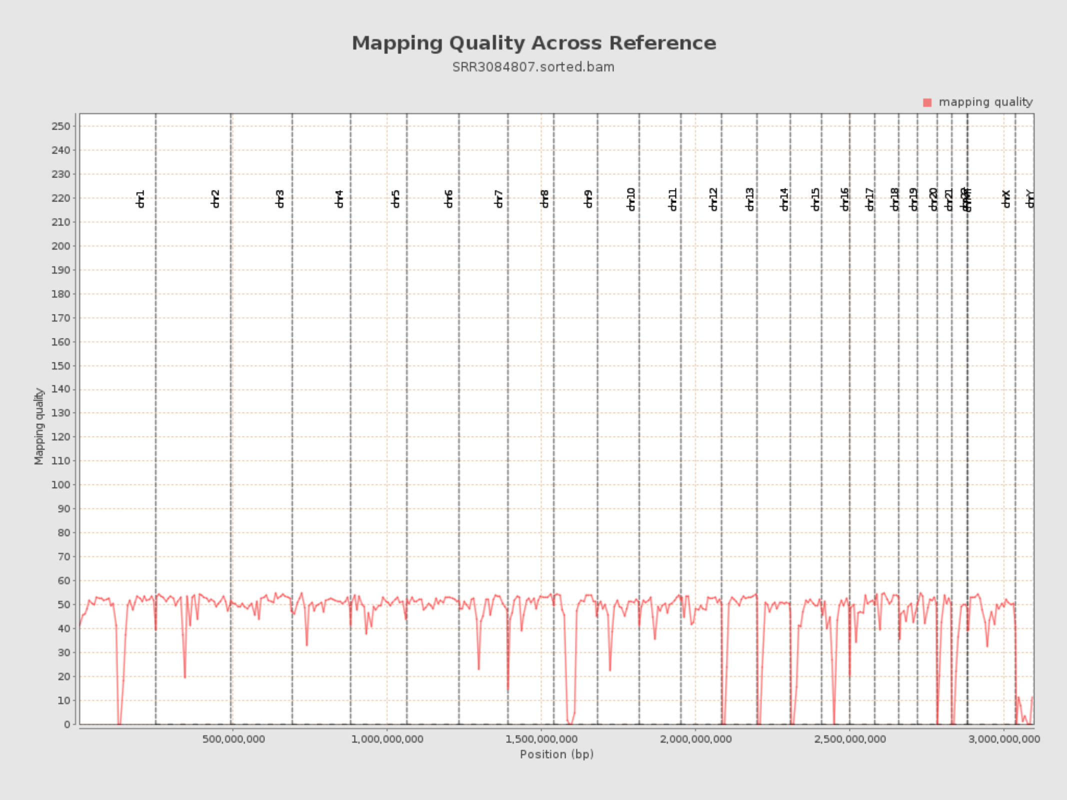
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram