Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:06:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084407.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_SRR3084407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084407.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:06:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,469,330
Mapped reads	1,382,518 / 55.99%
Unmapped reads	1,086,812 / 44.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,809 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	39,213 / 1.59%
Duplication rate	2.36%
Clipped reads	722,110 / 29.24%

2.2. ACGT Content

Number/percentage of A's	25,436,715 / 28.67%
Number/percentage of C's	16,499,980 / 18.6%
Number/percentage of T's	26,835,980 / 30.25%
Number/percentage of G's	19,953,788 / 22.49%
Number/percentage of N's	998 / 0%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2241

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

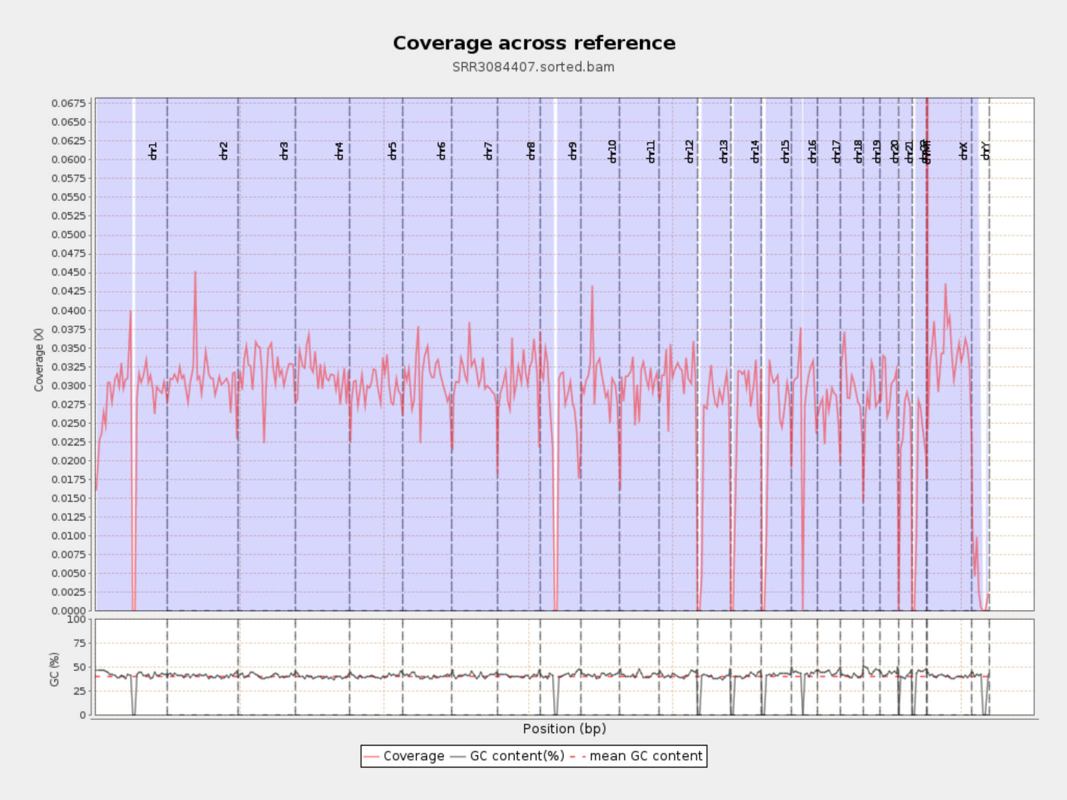
General error rate	0.86%
Mismatches	755,626
Insertions	6,455
Mapped reads with at least one insertion	0.46%
Deletions	18,229
Mapped reads with at least one deletion	1.31%
Homopolymer indels	46.48%

2.6. Chromosome stats

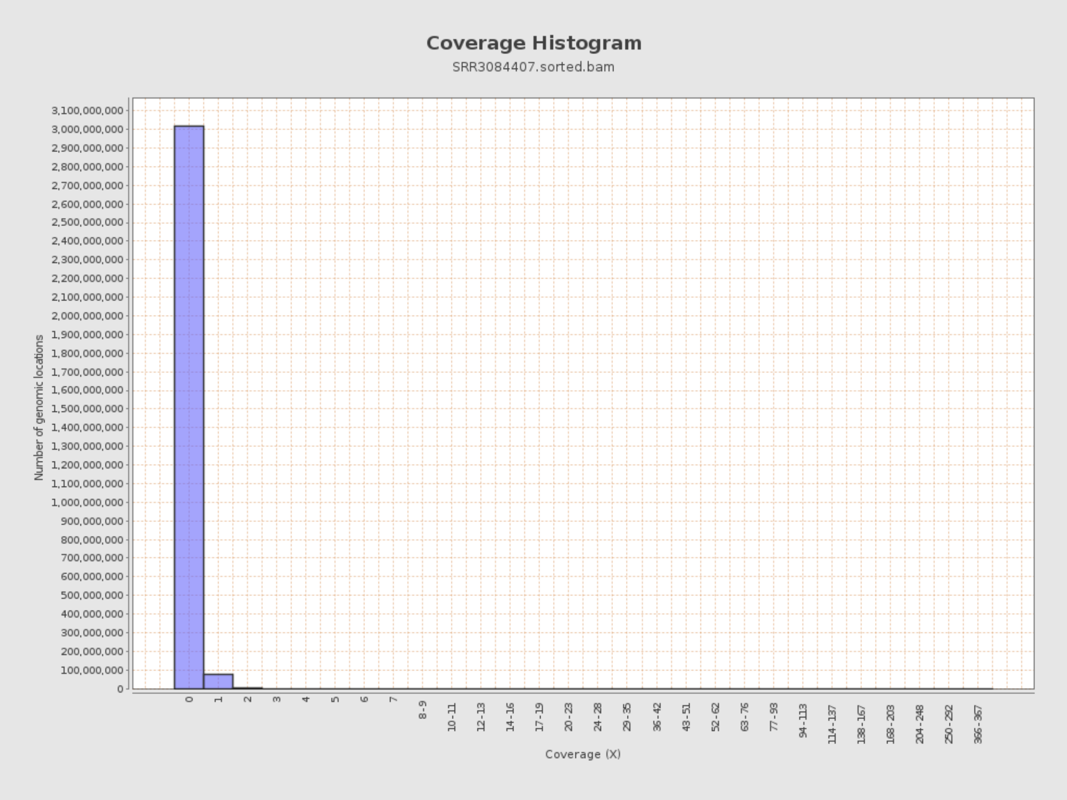
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6841726	0.0274	0.296
chr2	243199373	7519299	0.0309	0.2785
chr3	198022430	6363998	0.0321	0.1937
chr4	191154276	6006299	0.0314	0.1948
chr5	180915260	5412060	0.0299	0.1864
chr6	171115067	5258552	0.0307	0.2109
chr7	159138663	4912681	0.0309	0.2466

chr8	146364022	4489654	0.0307	0.2332
chr9	141213431	3596609	0.0255	0.2112
chr10	135534747	4116271	0.0304	0.2338
chr11	135006516	4061016	0.0301	0.211
chr12	133851895	4186997	0.0313	0.1914
chr13	115169878	2763977	0.024	0.1684
chr14	107349540	2683770	0.025	0.1762
chr15	102531392	2420283	0.0236	0.1691
chr16	90354753	2489663	0.0276	0.193
chr17	81195210	2184698	0.0269	0.1878
chr18	78077248	2346855	0.0301	0.3868
chr19	59128983	1661699	0.0281	0.264
chr20	63025520	1868402	0.0296	0.1904
chr21	48129895	1101422	0.0229	0.1693
chr22	51304566	885445	0.0173	0.1411
chrMT	16571	43851	2.6462	2.1513
chrX	155270560	5336779	0.0344	0.2142
chrY	59373566	203871	0.0034	0.0762

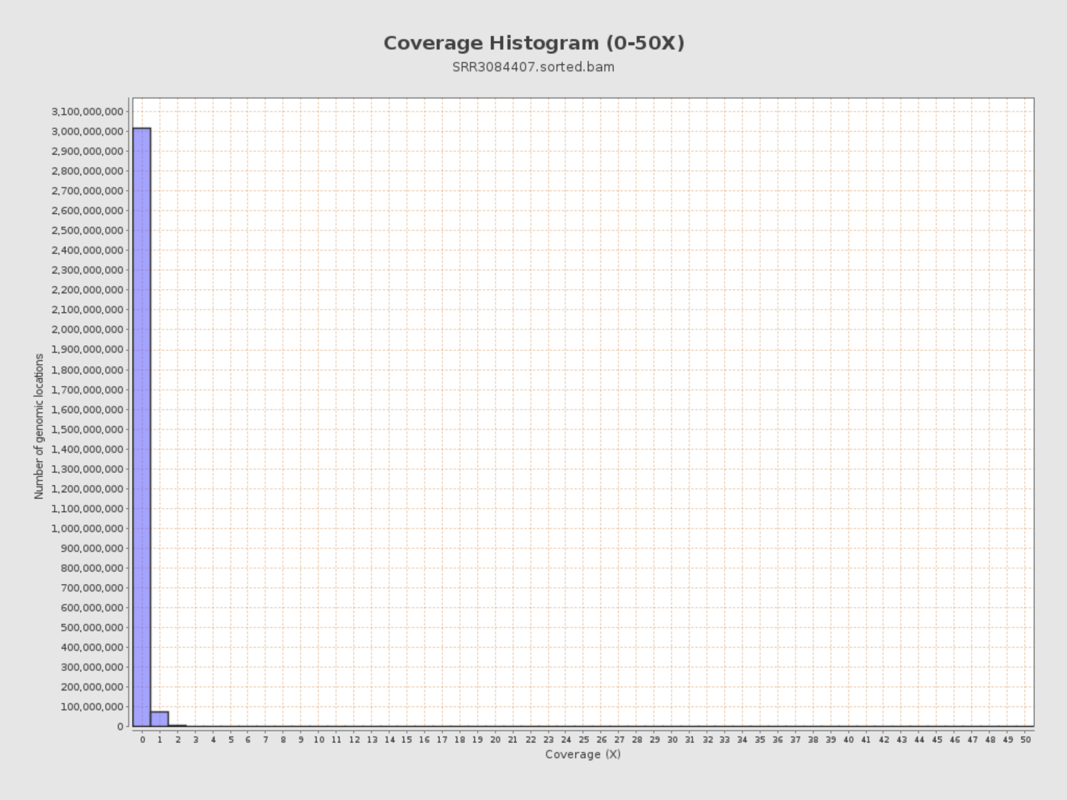
3. Results : Coverage across reference



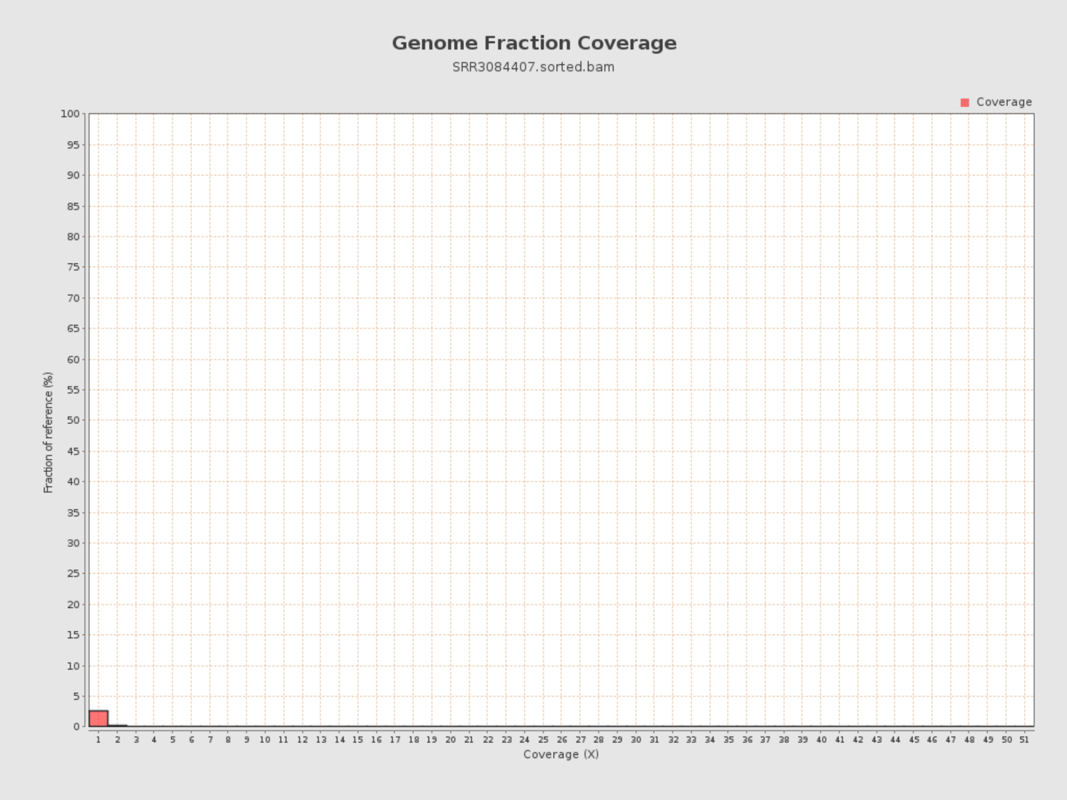
4. Results : Coverage Histogram



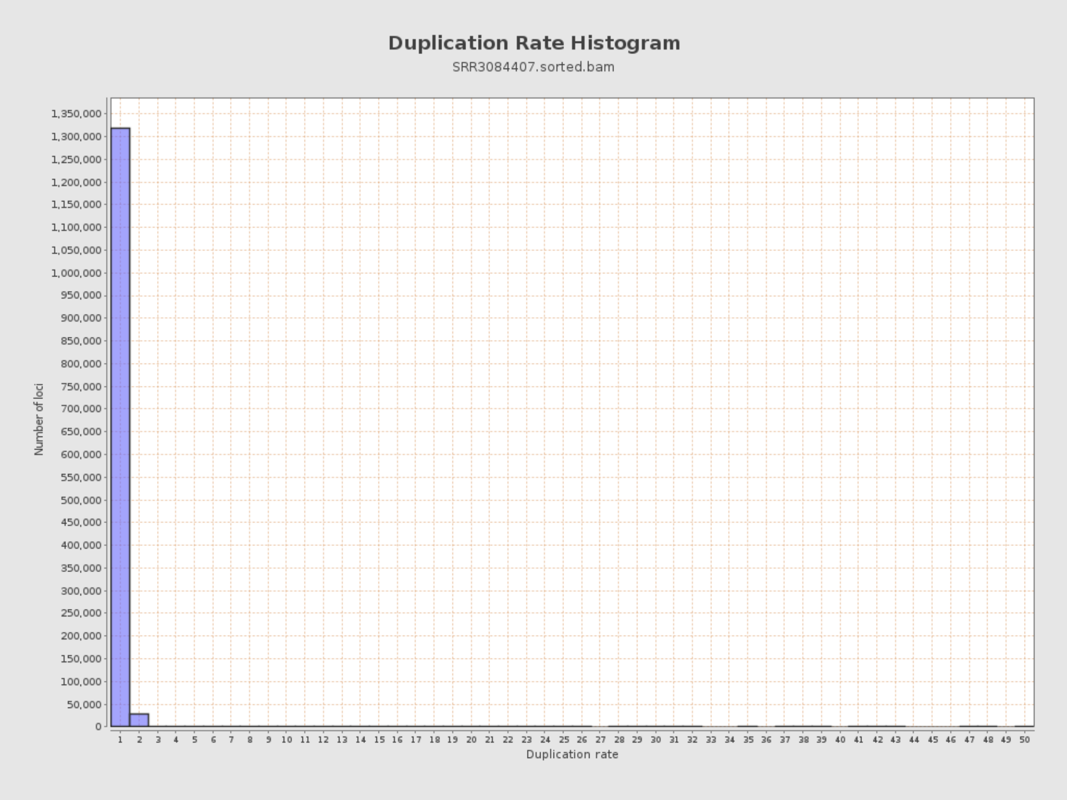
5. Results : Coverage Histogram (0-50X)



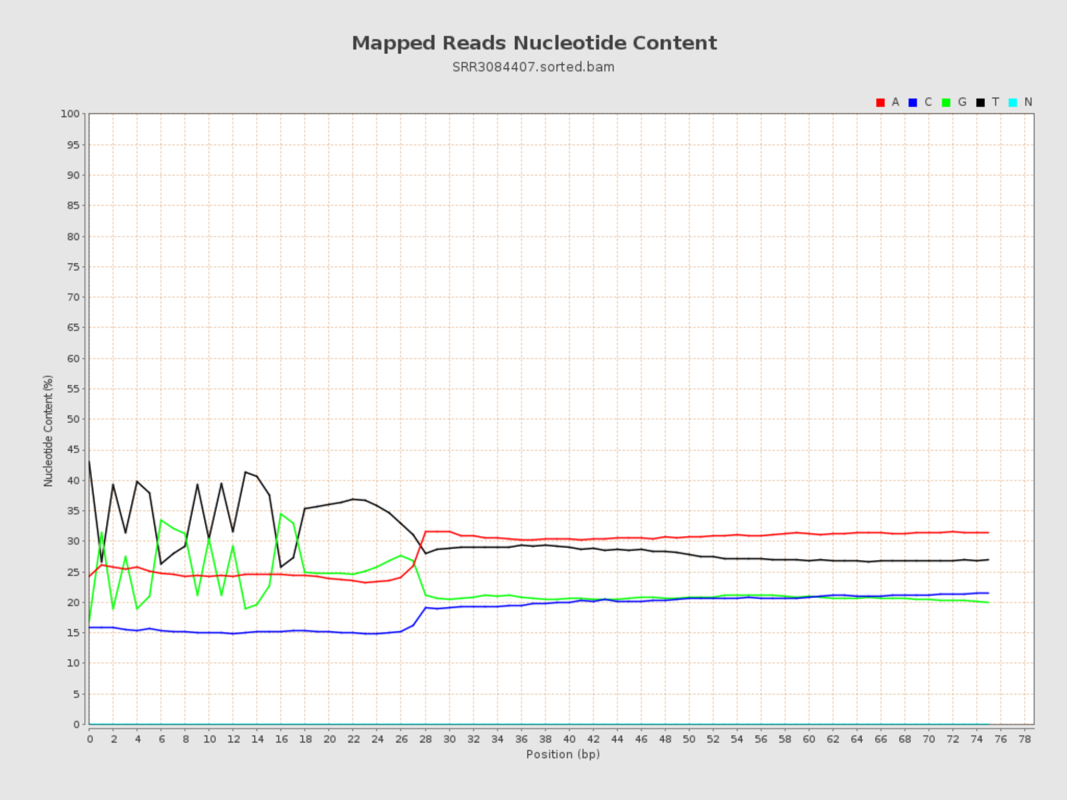
6. Results : Genome Fraction Coverage



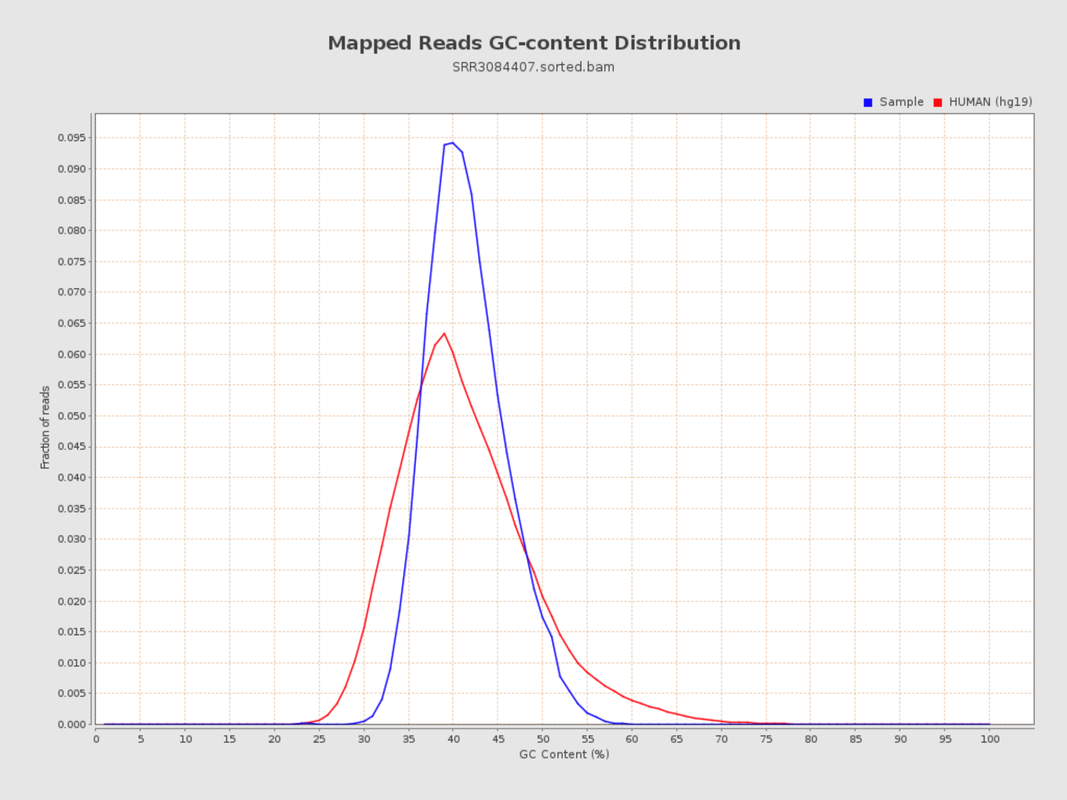
7. Results : Duplication Rate Histogram



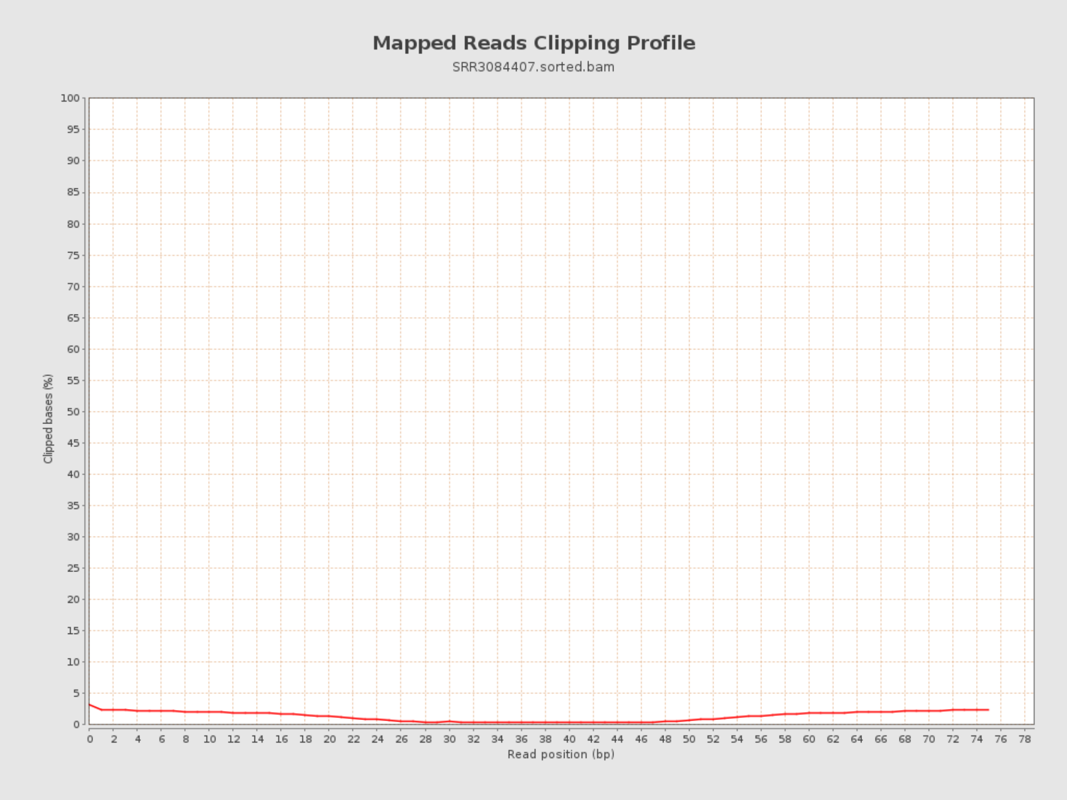
8. Results : Mapped Reads Nucleotide Content



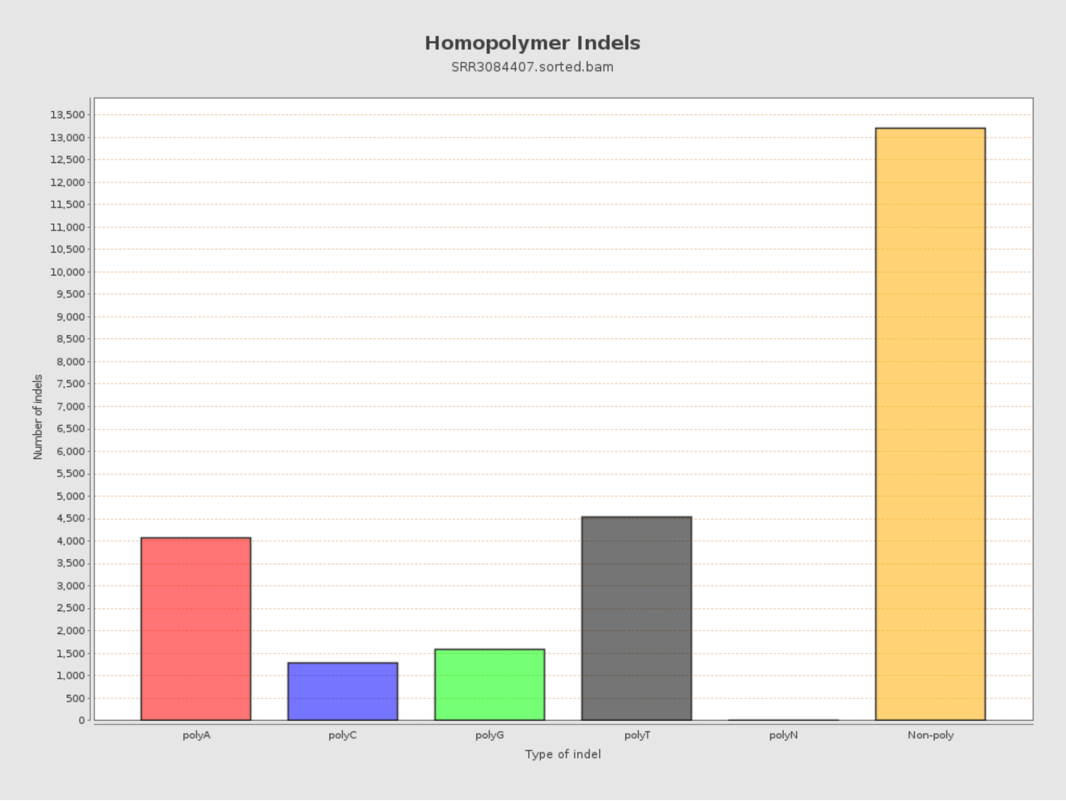
9. Results : Mapped Reads GC-content Distribution



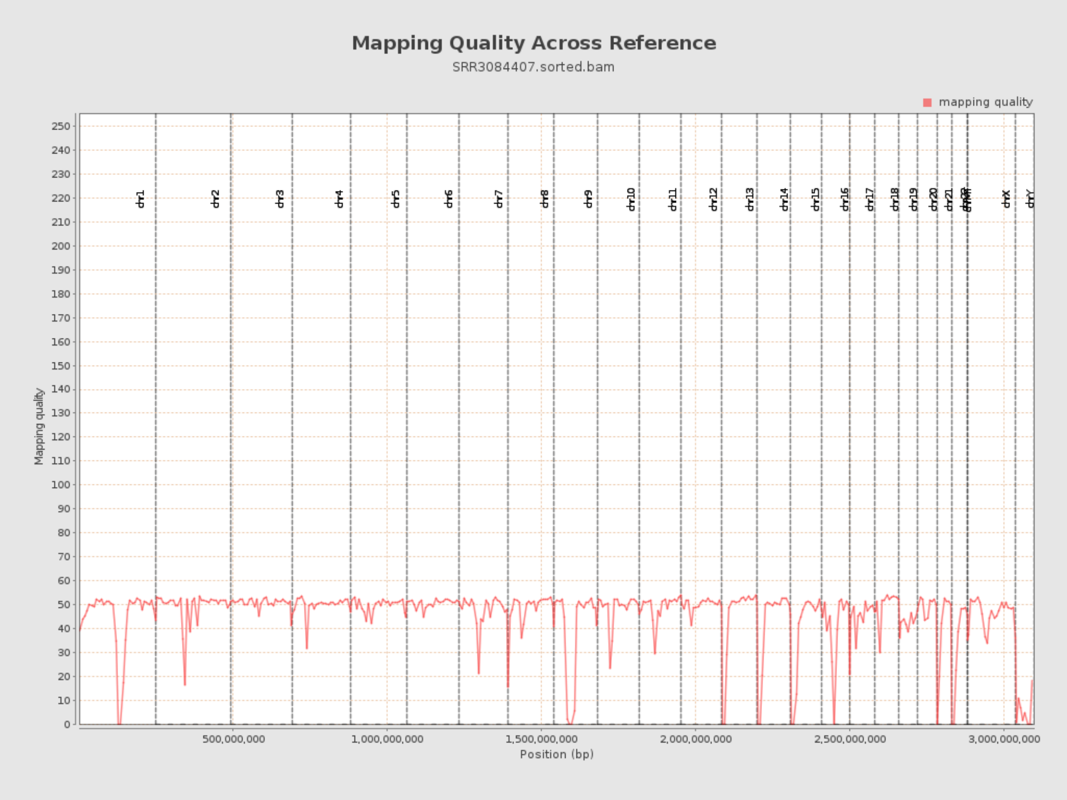
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram