Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:34:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084813.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_SRR3084813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:34:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,525,174
Mapped reads	2,276,514 / 90.15%
Unmapped reads	248,660 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,831 / 1.18%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	122,816 / 4.86%
Duplication rate	4.53%
Clipped reads	1,018,365 / 40.33%

2.2. ACGT Content

Number/percentage of A's	41,384,962 / 27.2%
Number/percentage of C's	28,721,429 / 18.88%
Number/percentage of T's	47,559,093 / 31.26%
Number/percentage of G's	34,448,617 / 22.64%
Number/percentage of N's	21,791 / 0.01%
GC Percentage	41.52%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.358

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

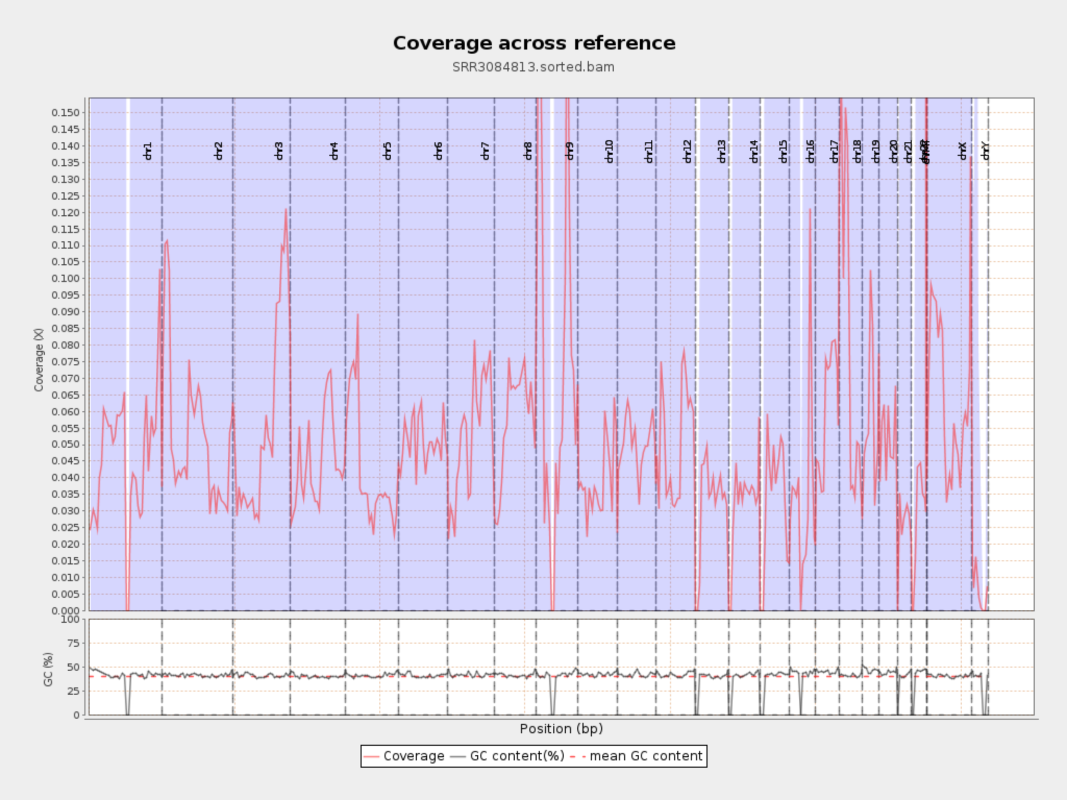
General error rate	0.8%
Mismatches	1,200,880
Insertions	12,124
Mapped reads with at least one insertion	0.53%
Deletions	34,860
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.54%

2.6. Chromosome stats

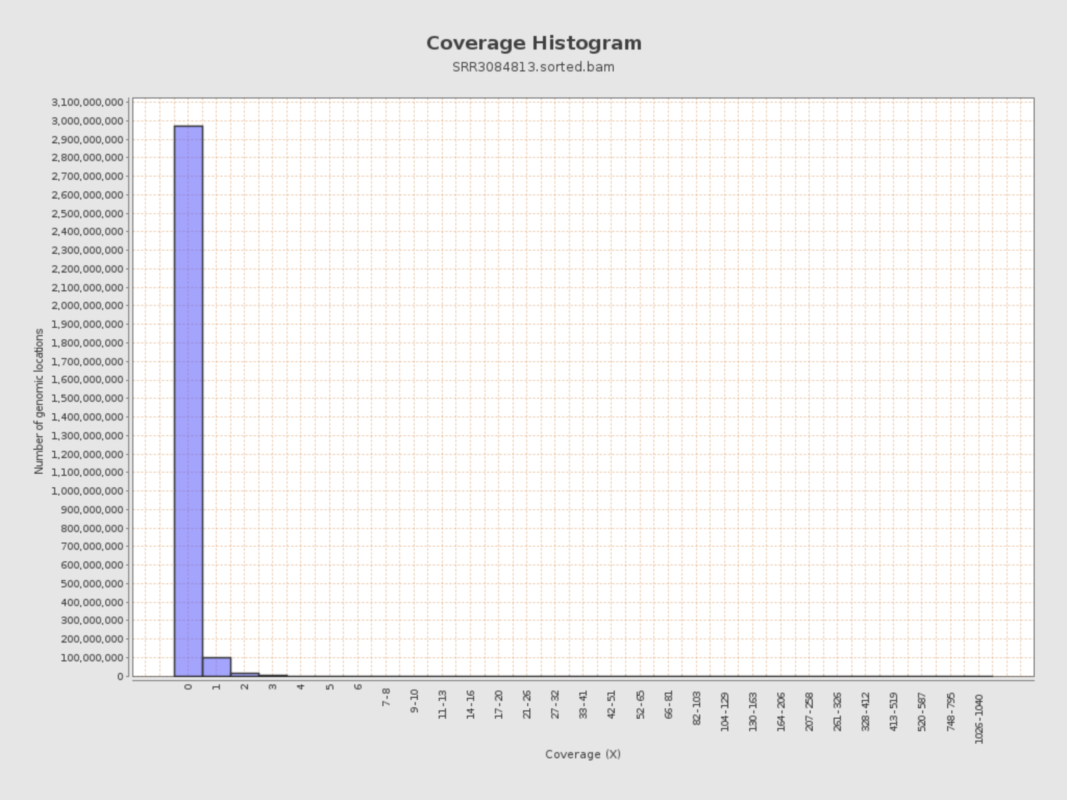
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11514264	0.0462	0.5366
chr2	243199373	12900884	0.053	0.5894
chr3	198022430	11265333	0.0569	0.2847
chr4	191154276	8622829	0.0451	0.2558
chr5	180915260	7663755	0.0424	0.2506
chr6	171115067	8661983	0.0506	0.2915
chr7	159138663	8407439	0.0528	0.3294

chr8	146364022	8423961	0.0576	0.379
chr9	141213431	10931555	0.0774	0.4201
chr10	135534747	5270177	0.0389	0.2649
chr11	135006516	6752610	0.05	0.3102
chr12	133851895	6764812	0.0505	0.2701
chr13	115169878	3632347	0.0315	0.2113
chr14	107349540	3337481	0.0311	0.2156
chr15	102531392	3502948	0.0342	0.2311
chr16	90354753	3227096	0.0357	0.239
chr17	81195210	5010863	0.0617	0.3011
chr18	78077248	6536290	0.0837	0.5784
chr19	59128983	3504432	0.0593	0.4156
chr20	63025520	3294554	0.0523	0.2764
chr21	48129895	1246759	0.0259	0.1985
chr22	51304566	1392058	0.0271	0.1929
chrMT	16571	35996	2.1722	1.8488
chrX	155270560	9951751	0.0641	0.3197
chrY	59373566	341434	0.0058	0.1291

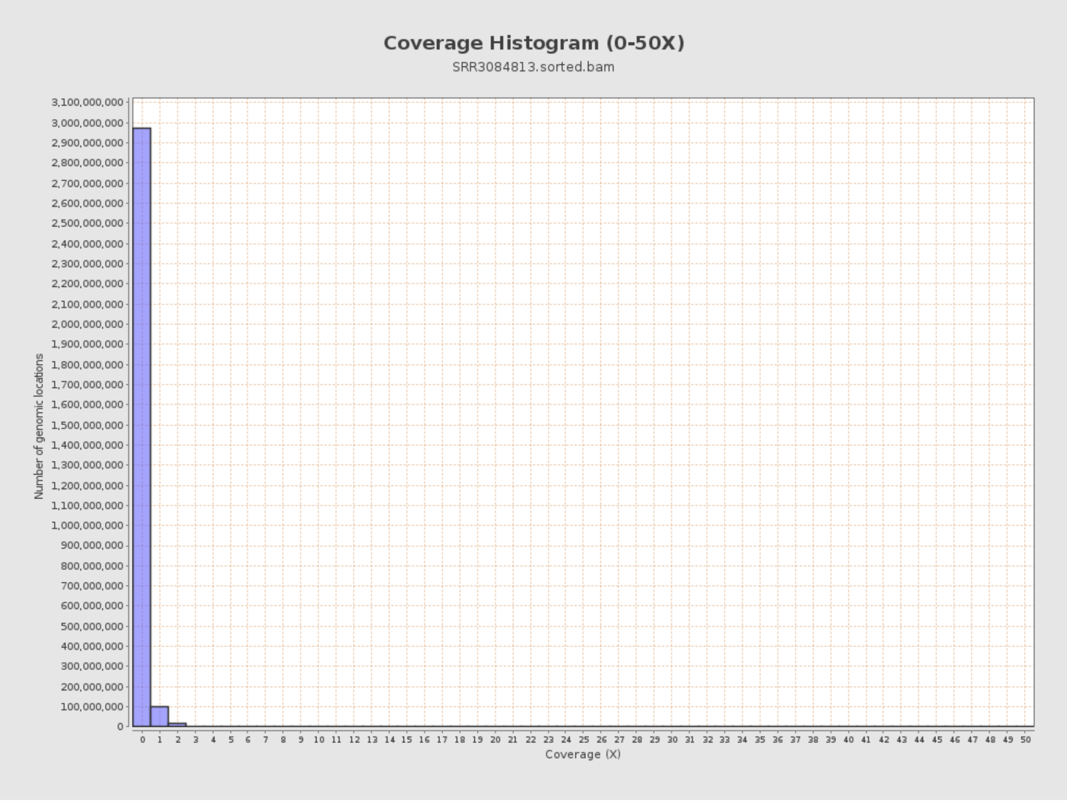
3. Results : Coverage across reference



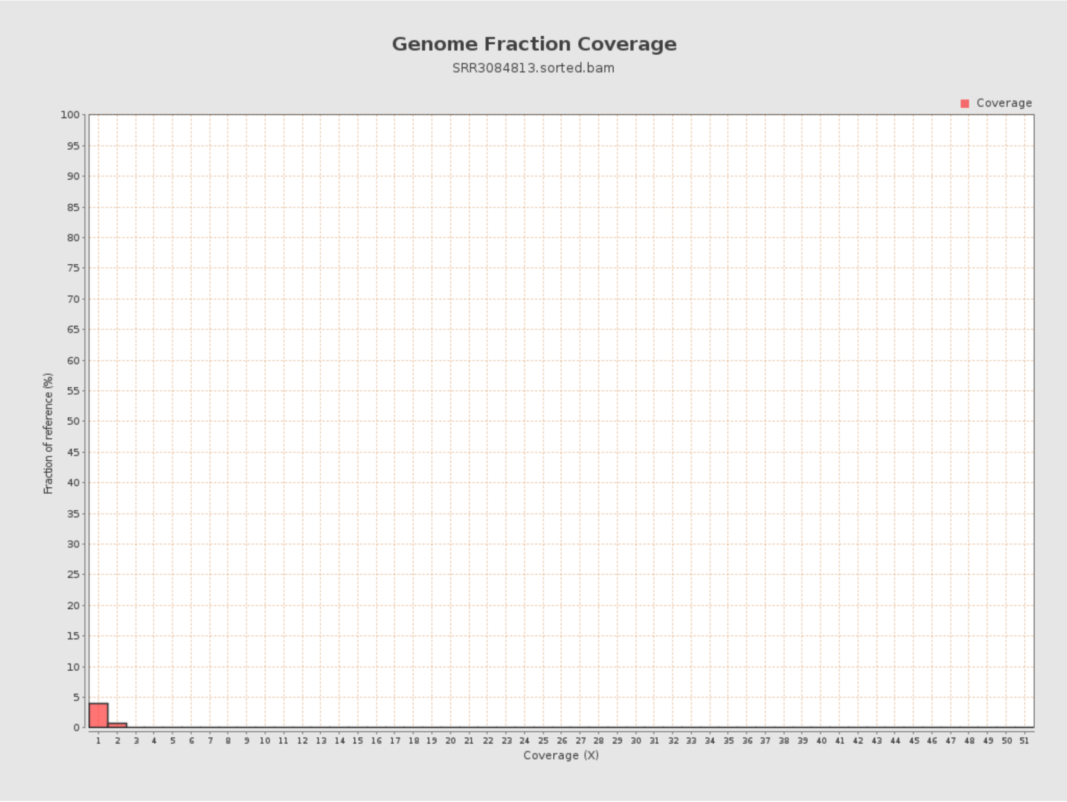
4. Results : Coverage Histogram



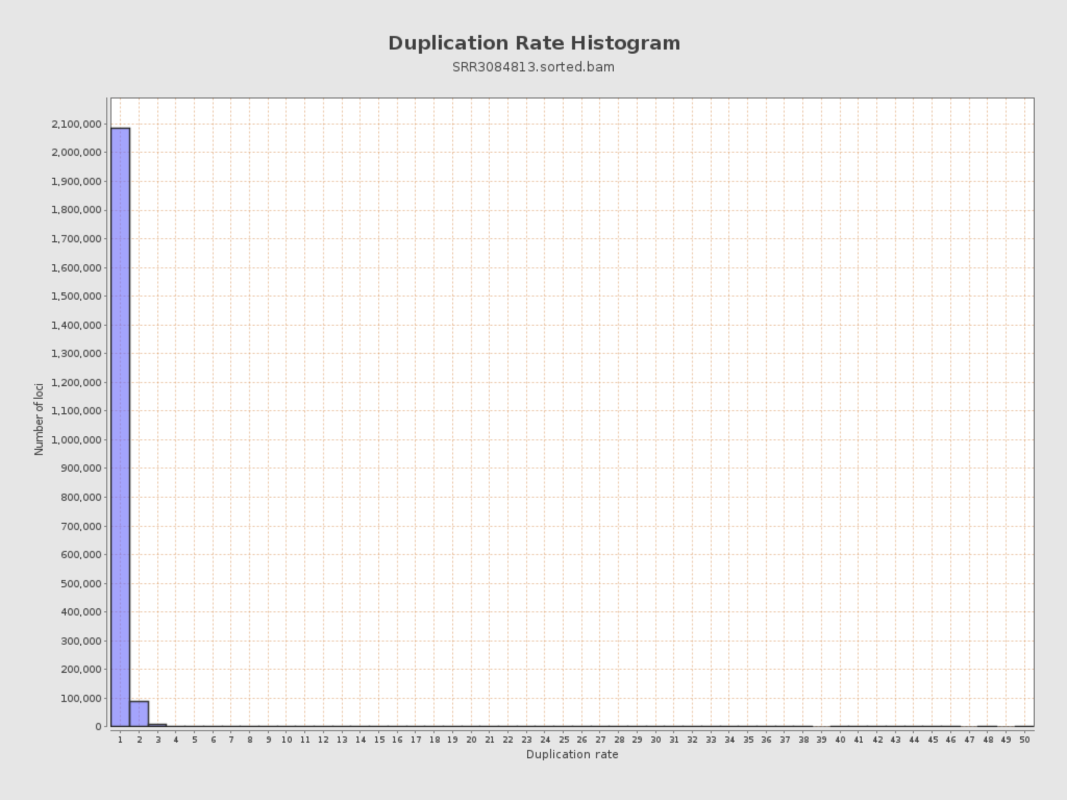
5. Results : Coverage Histogram (0-50X)



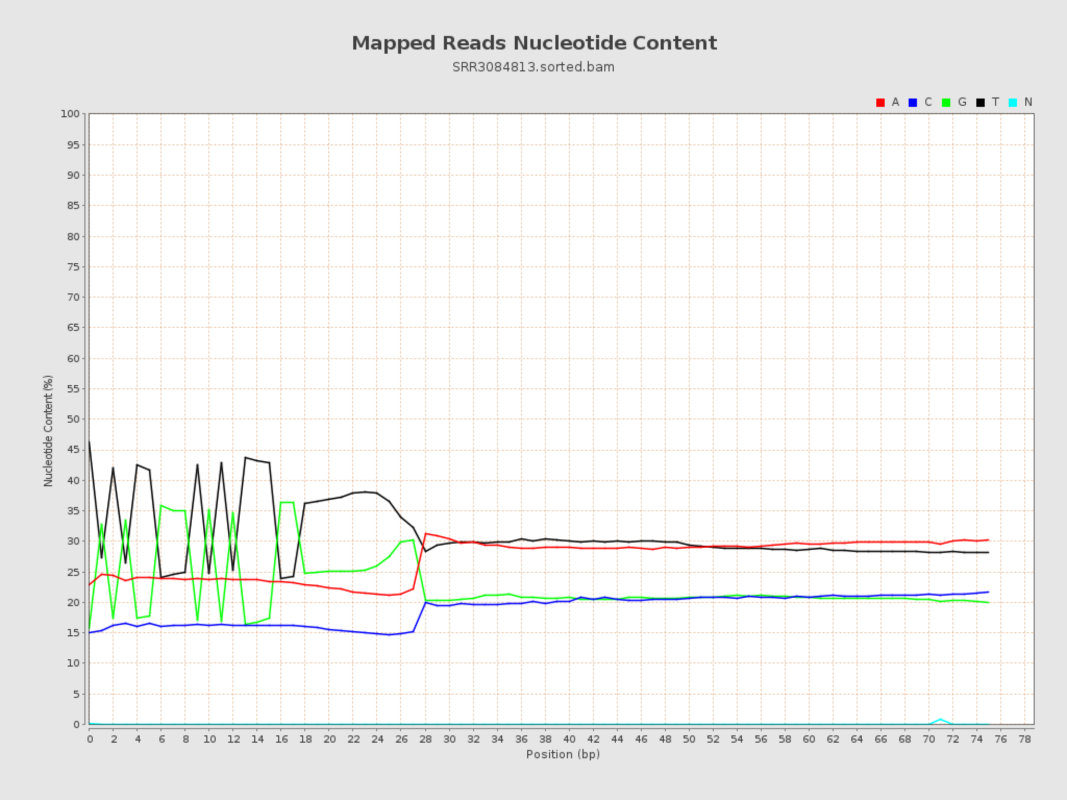
6. Results : Genome Fraction Coverage



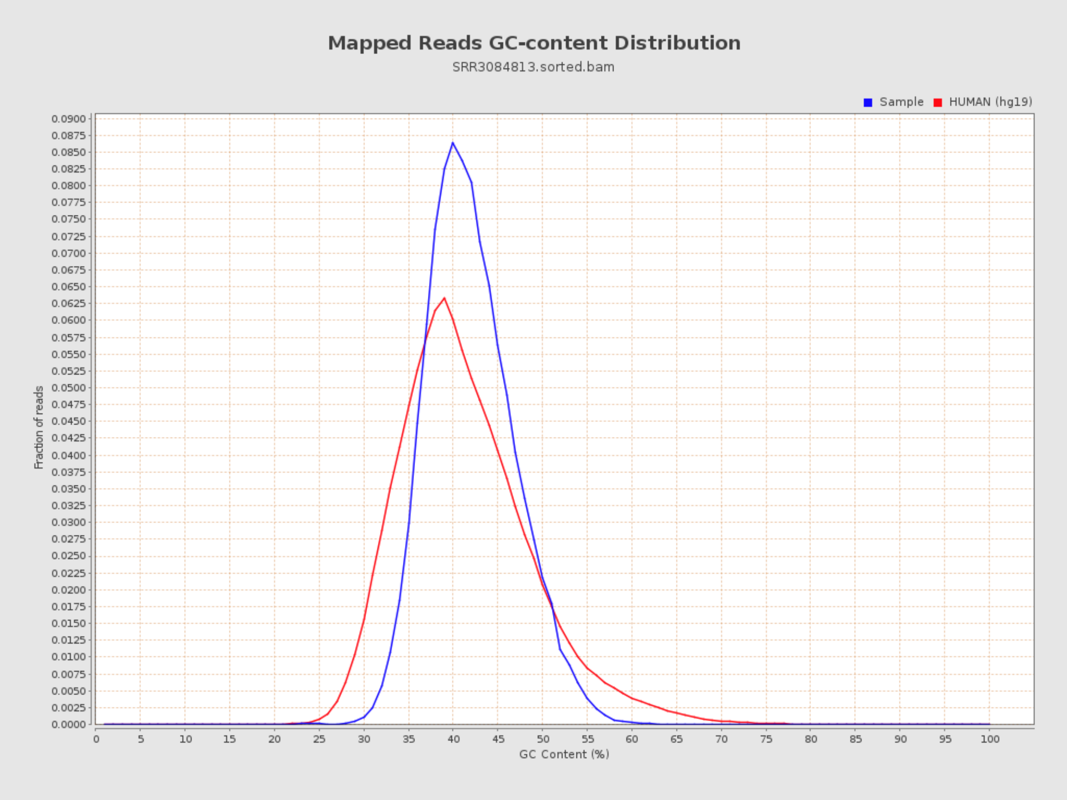
7. Results : Duplication Rate Histogram



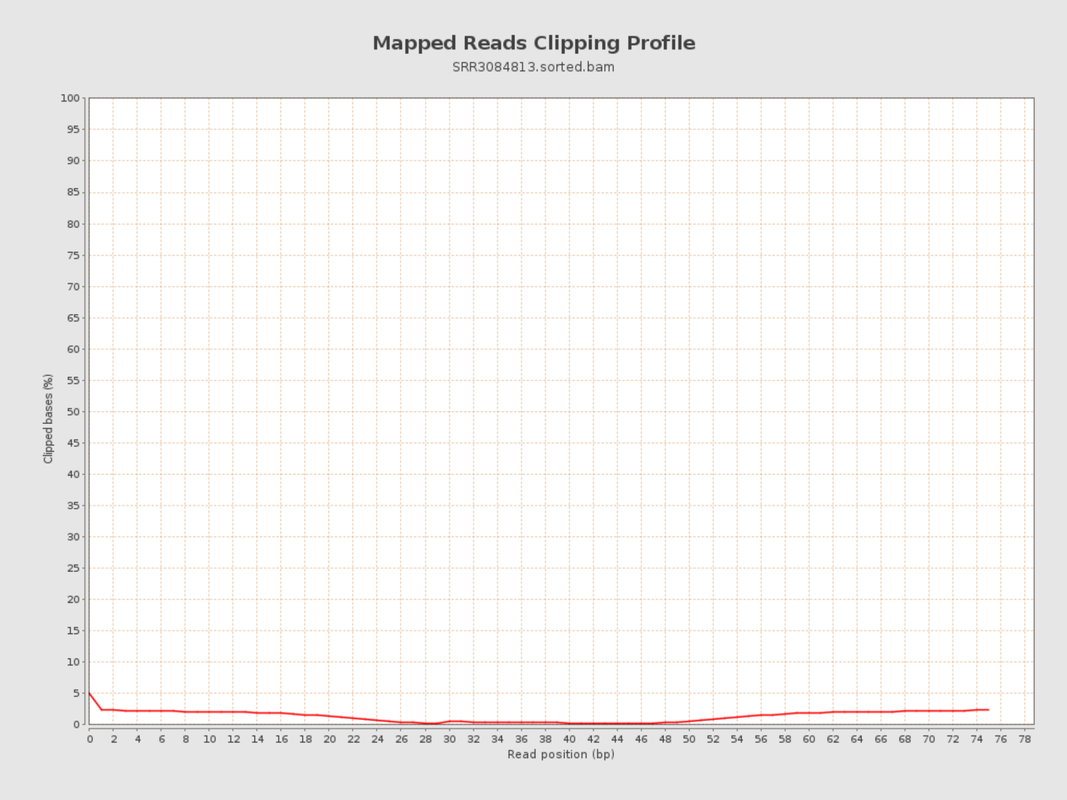
8. Results : Mapped Reads Nucleotide Content



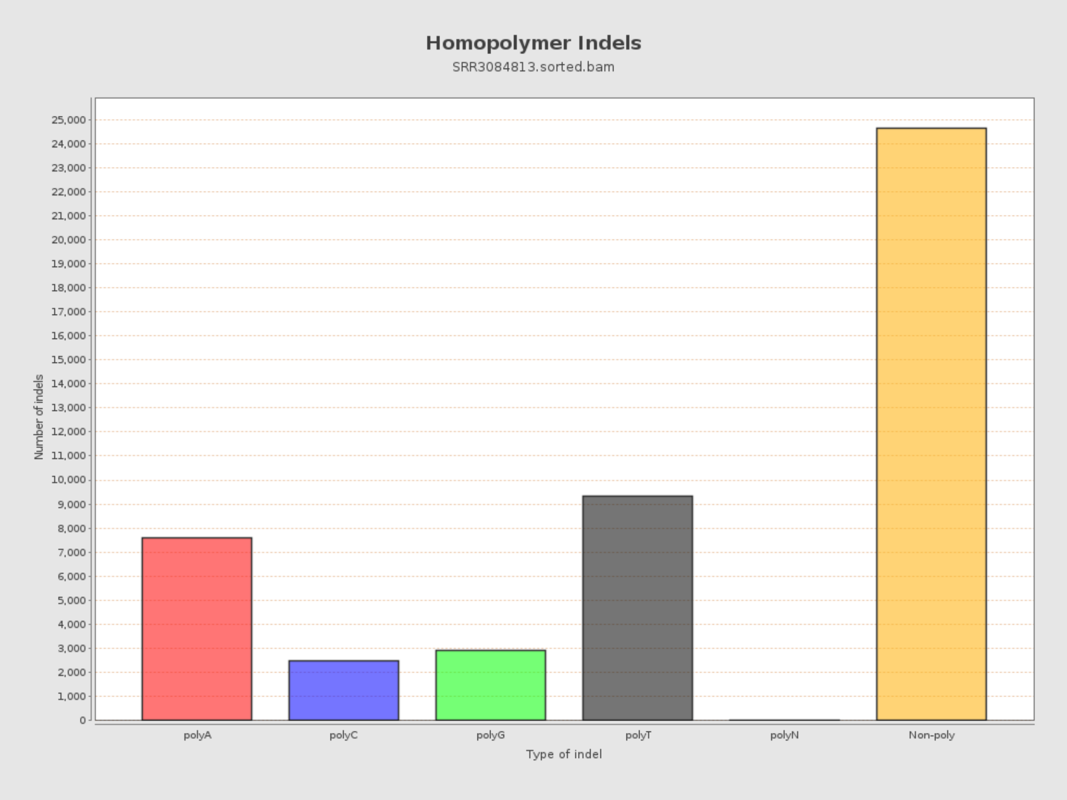
9. Results : Mapped Reads GC-content Distribution



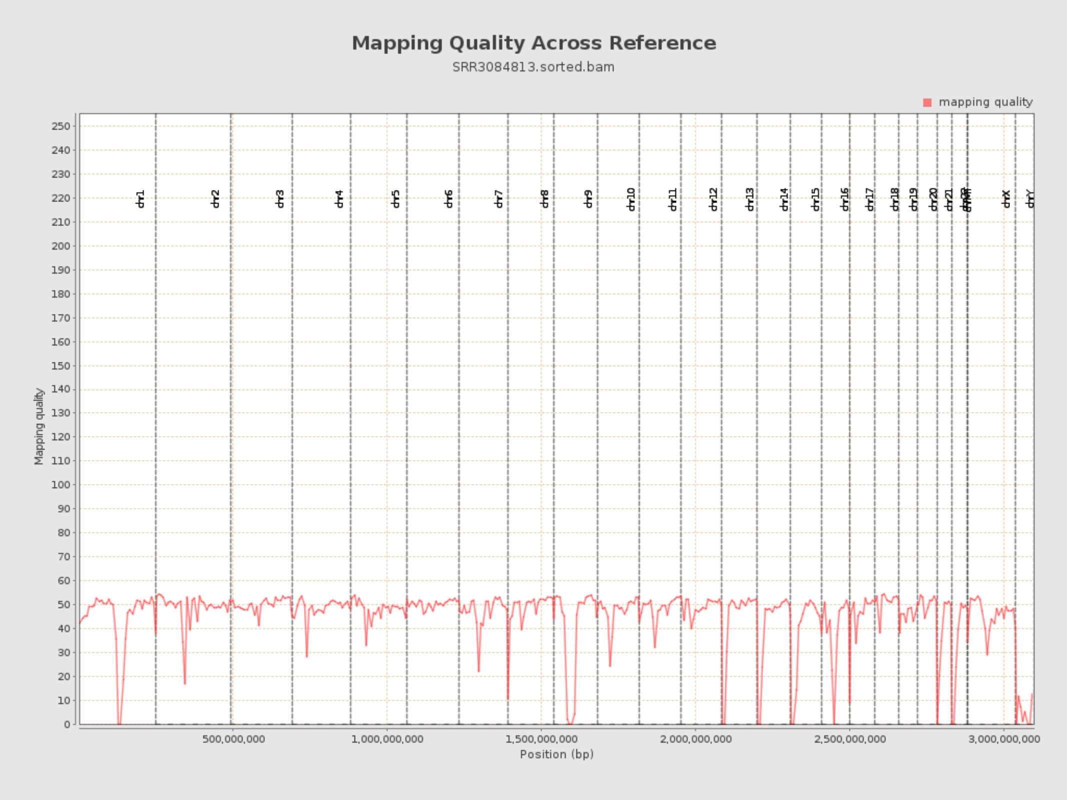
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram