Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:59:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083616.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_SRR3083616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:59:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,886,633
Mapped reads	1,668,544 / 88.44%
Unmapped reads	218,089 / 11.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,085 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	102,873 / 5.45%
Duplication rate	5.34%
Clipped reads	798,174 / 42.31%

2.2. ACGT Content

Number/percentage of A's	29,528,976 / 26.85%
Number/percentage of C's	20,470,094 / 18.61%
Number/percentage of T's	34,715,101 / 31.56%
Number/percentage of G's	25,268,647 / 22.97%
Number/percentage of N's	5,669 / 0.01%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.2857

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

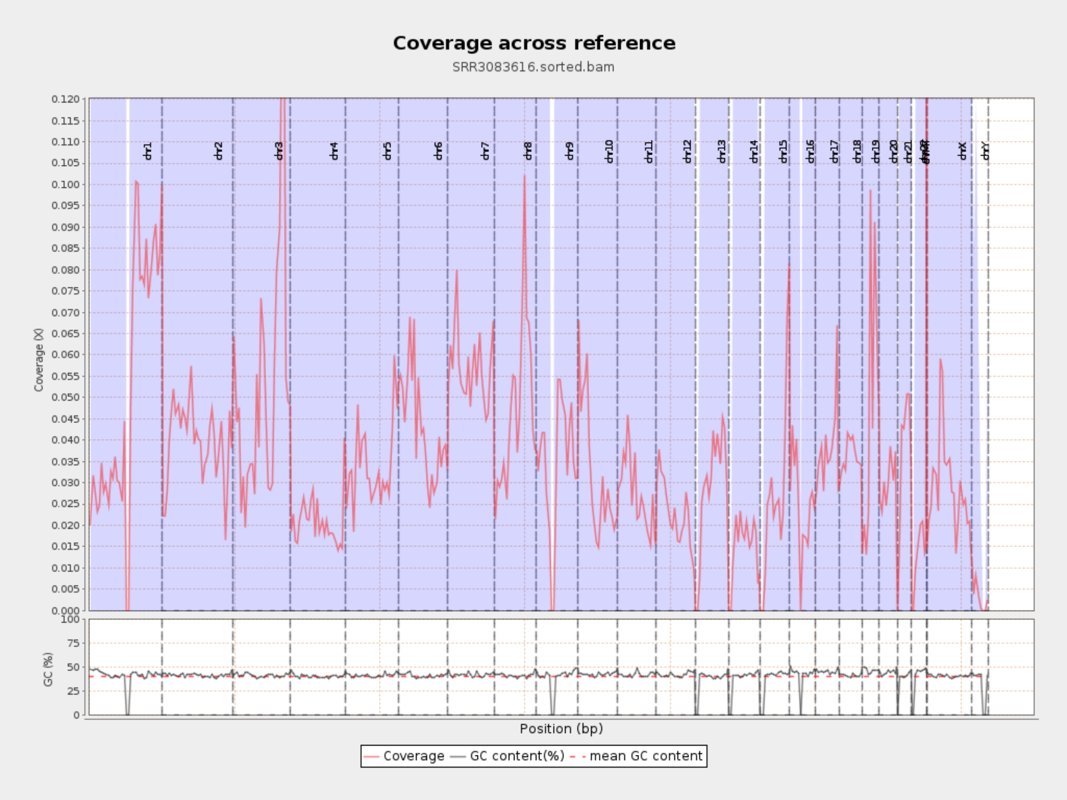
General error rate	0.71%
Mismatches	771,638
Insertions	8,025
Mapped reads with at least one insertion	0.48%
Deletions	24,758
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.13%

2.6. Chromosome stats

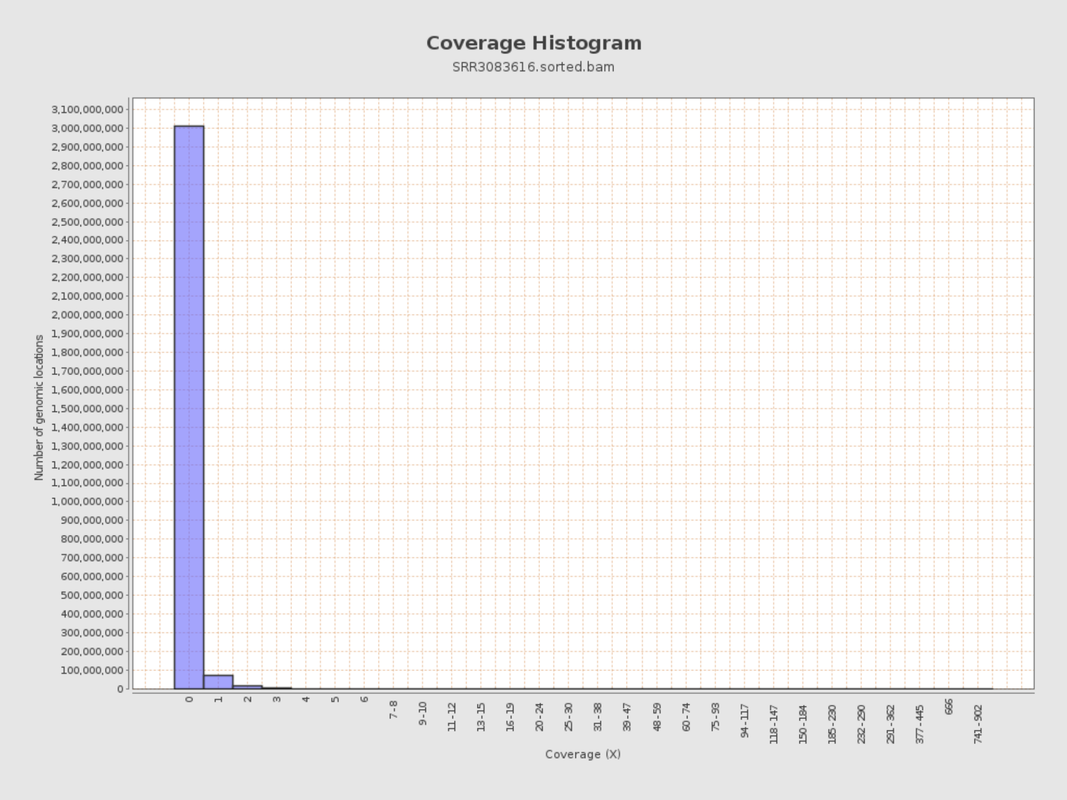
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12652318	0.0508	0.4397
chr2	243199373	9624480	0.0396	0.4507
chr3	198022430	10634690	0.0537	0.2907
chr4	191154276	3964864	0.0207	0.1811
chr5	180915260	6134820	0.0339	0.2258
chr6	171115067	7393154	0.0432	0.29
chr7	159138663	9096652	0.0572	0.3597

chr8	146364022	6978474	0.0477	0.3127
chr9	141213431	4860352	0.0344	0.2401
chr10	135534747	4407663	0.0325	0.2381
chr11	135006516	3722563	0.0276	0.2115
chr12	133851895	3060798	0.0229	0.1849
chr13	115169878	3312896	0.0288	0.2083
chr14	107349540	1613816	0.015	0.15
chr15	102531392	2664521	0.026	0.2065
chr16	90354753	2230221	0.0247	0.195
chr17	81195210	3120954	0.0384	0.2458
chr18	78077248	2821933	0.0361	0.2743
chr19	59128983	2801829	0.0474	0.3438
chr20	63025520	1849896	0.0294	0.2104
chr21	48129895	1757193	0.0365	0.2363
chr22	51304566	630793	0.0123	0.1332
chrMT	16571	3898	0.2352	0.5632
chrX	155270560	4502979	0.029	0.2132
chrY	59373566	186736	0.0031	0.0675

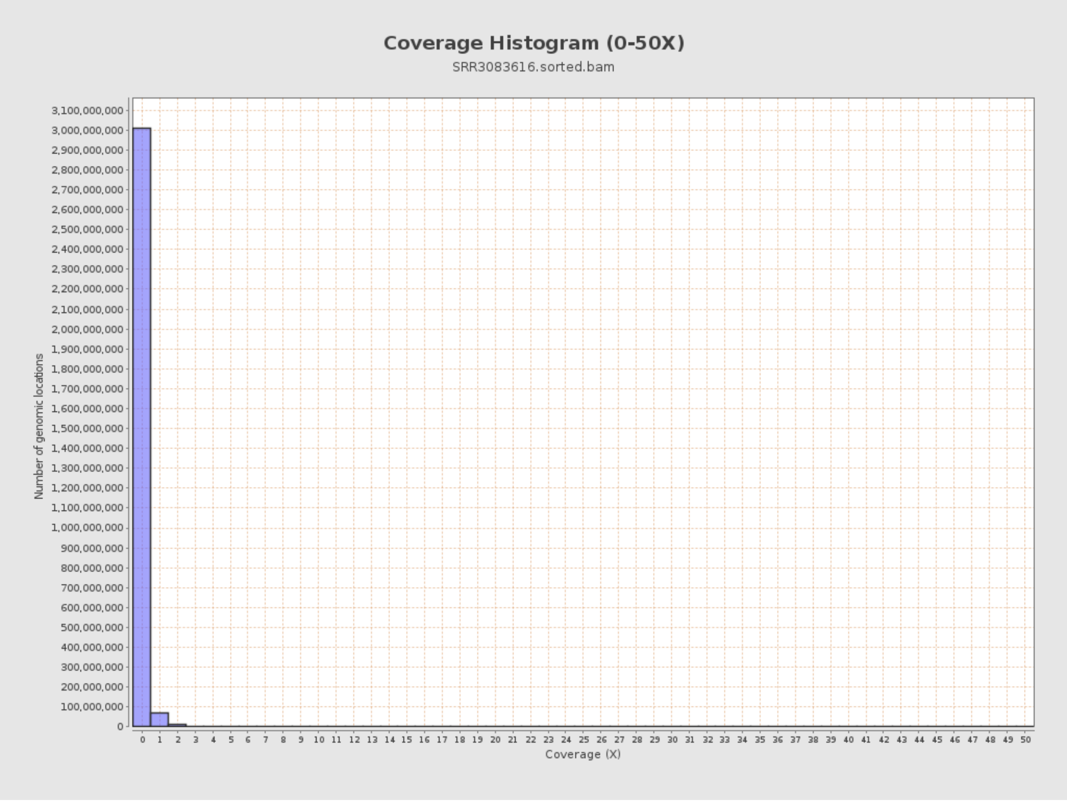
3. Results : Coverage across reference



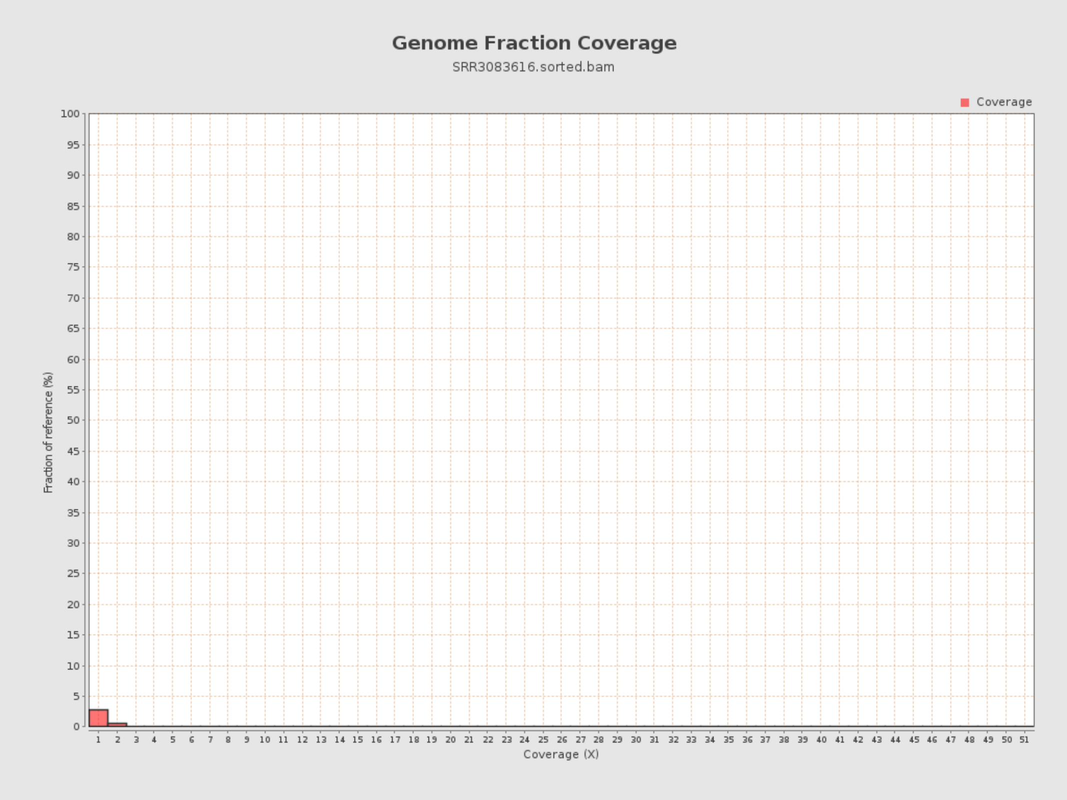
4. Results : Coverage Histogram



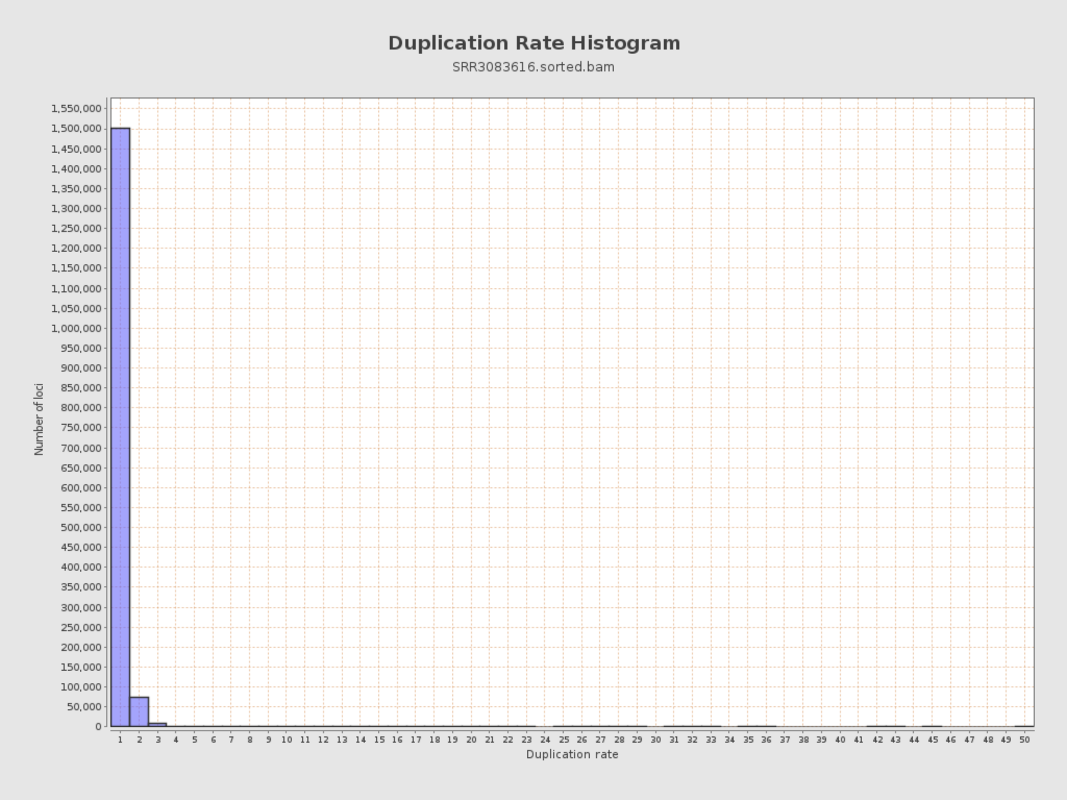
5. Results : Coverage Histogram (0-50X)



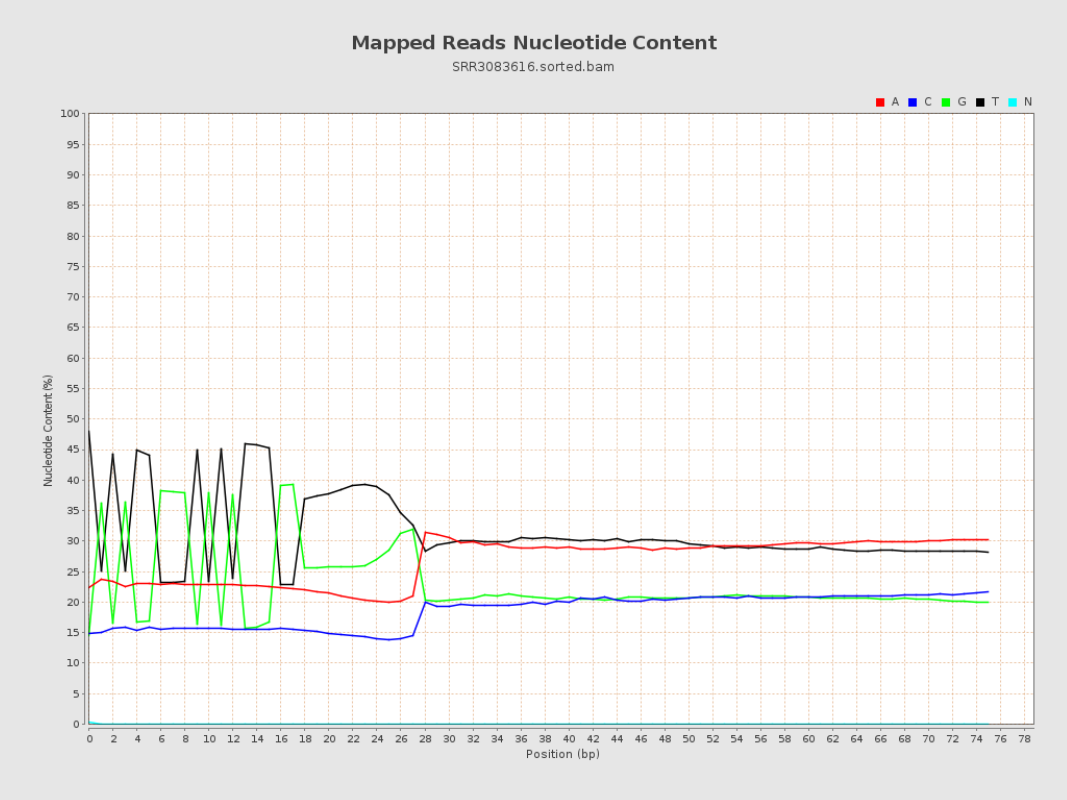
6. Results : Genome Fraction Coverage



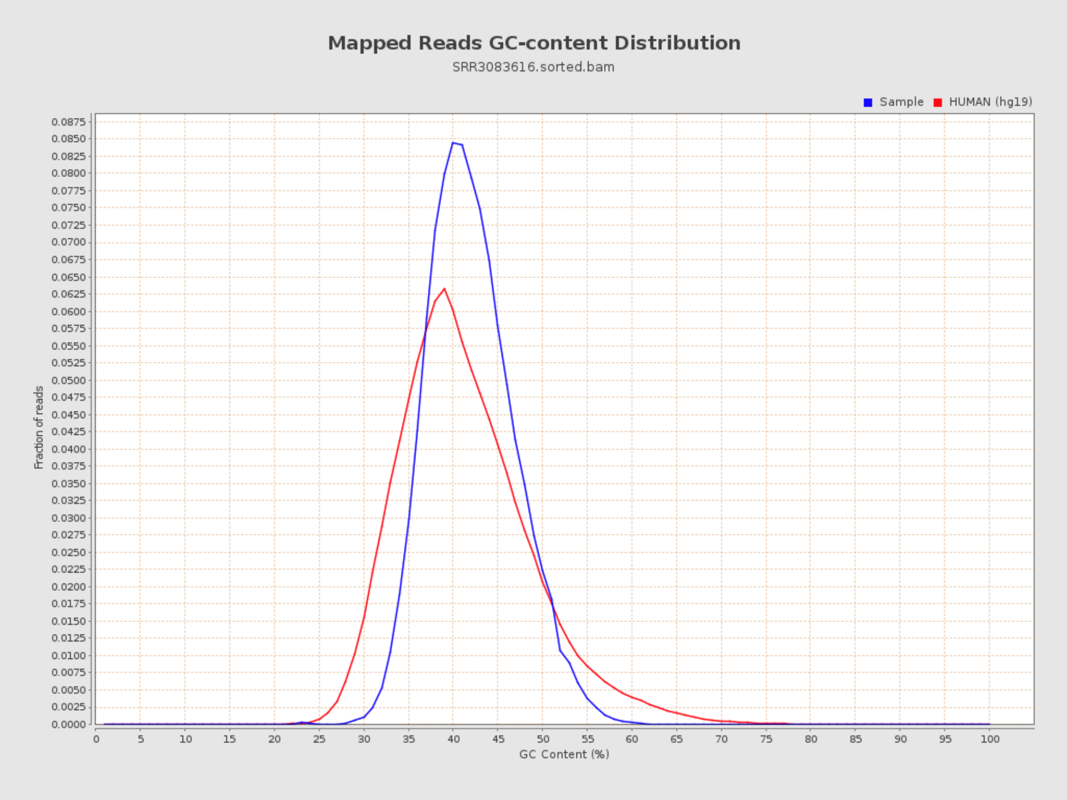
7. Results : Duplication Rate Histogram



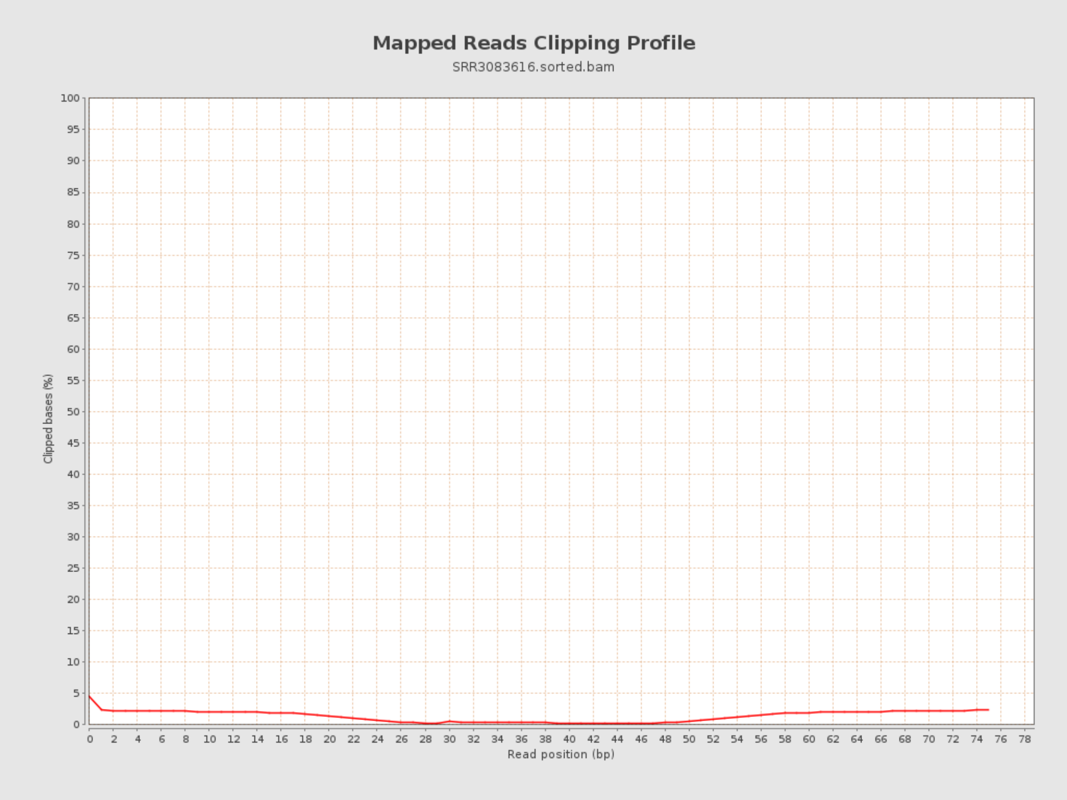
8. Results : Mapped Reads Nucleotide Content



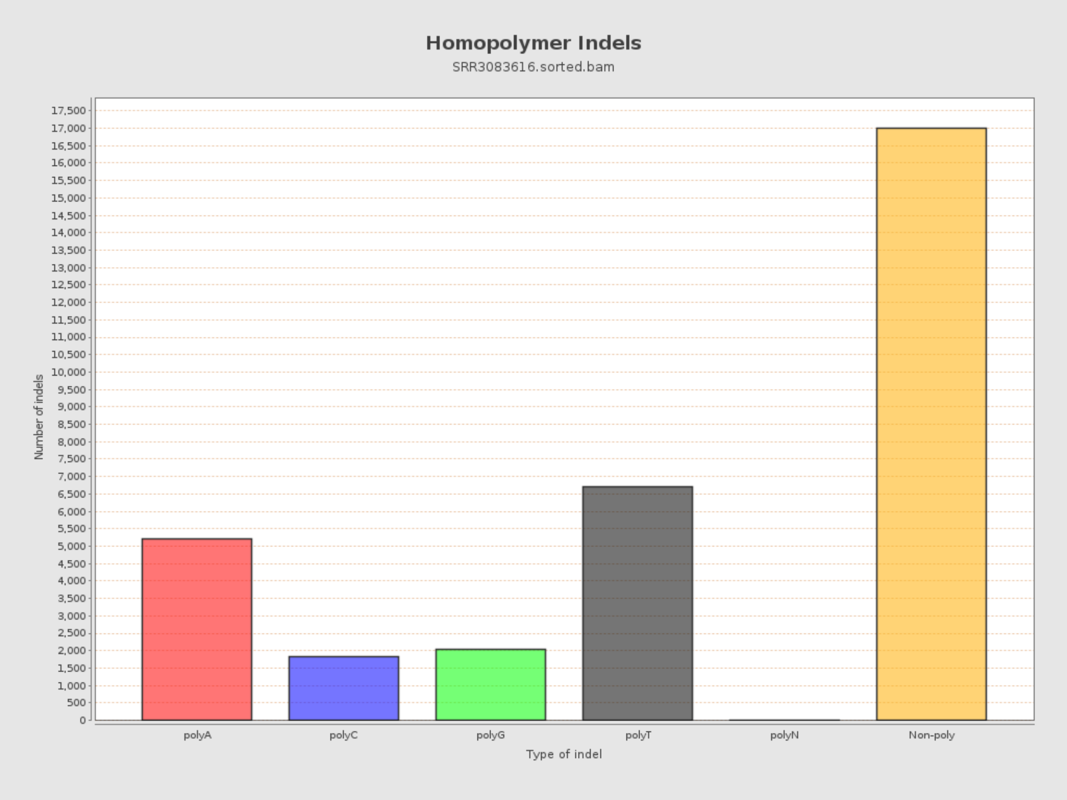
9. Results : Mapped Reads GC-content Distribution



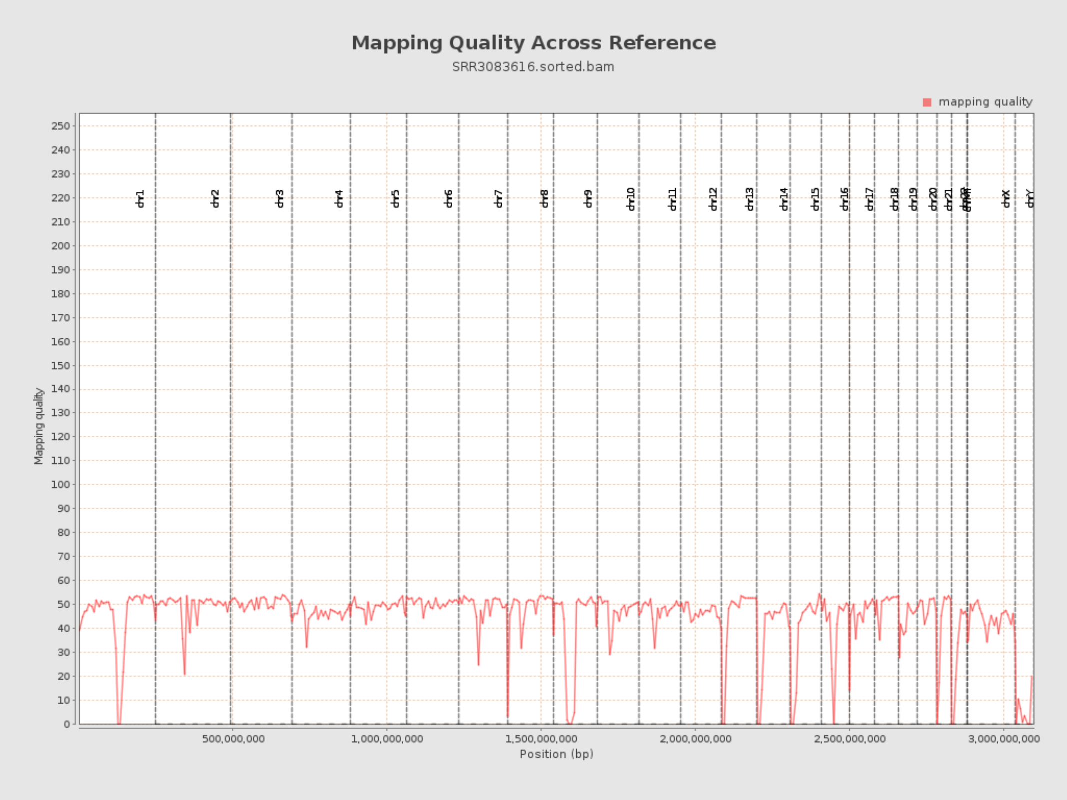
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram