Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:57:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083645.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_SRR3083645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083645.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:57:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083645.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,948,823
Mapped reads	1,609,150 / 82.57%
Unmapped reads	339,673 / 17.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,423 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	49,461 / 2.54%
Duplication rate	2.7%
Clipped reads	1,140,240 / 58.51%

2.2. ACGT Content

Number/percentage of A's	28,402,839 / 29.62%
Number/percentage of C's	18,477,133 / 19.27%
Number/percentage of T's	28,431,588 / 29.65%
Number/percentage of G's	20,557,857 / 21.44%
Number/percentage of N's	12,147 / 0.01%
GC Percentage	40.71%

2.3. Coverage

Mean	0.031

Standard Deviation	0.2303

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

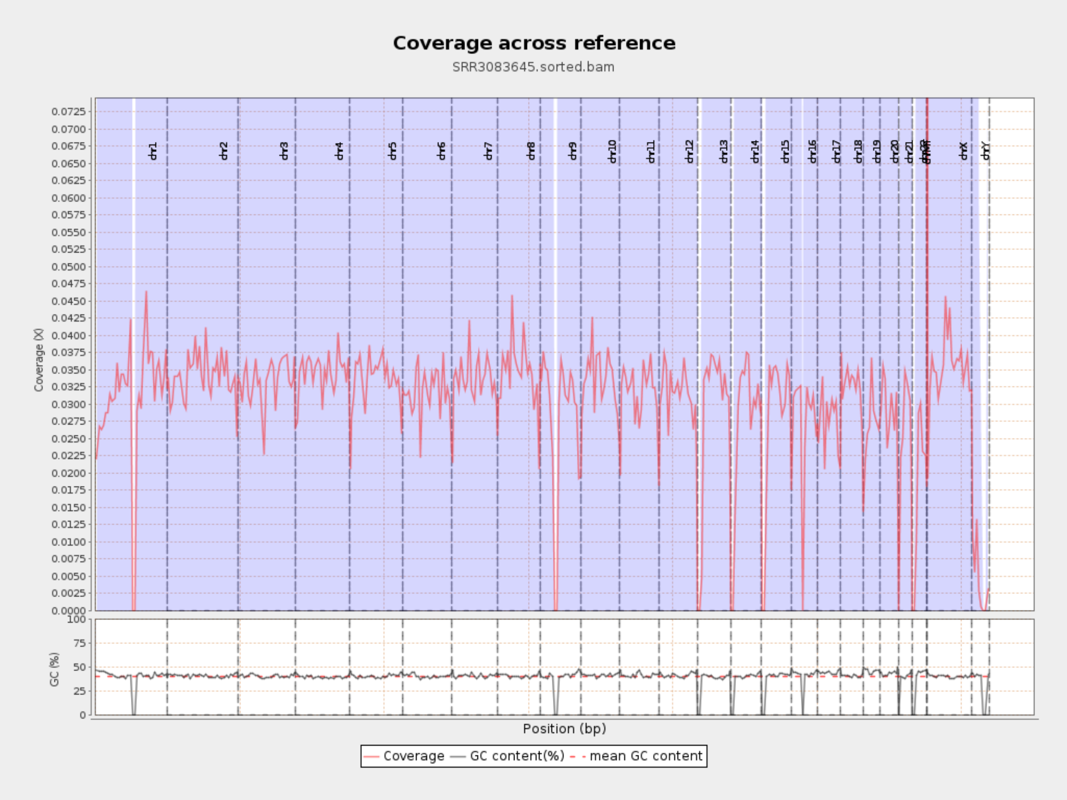
General error rate	0.84%
Mismatches	791,364
Insertions	6,542
Mapped reads with at least one insertion	0.4%
Deletions	19,006
Mapped reads with at least one deletion	1.17%
Homopolymer indels	46.3%

2.6. Chromosome stats

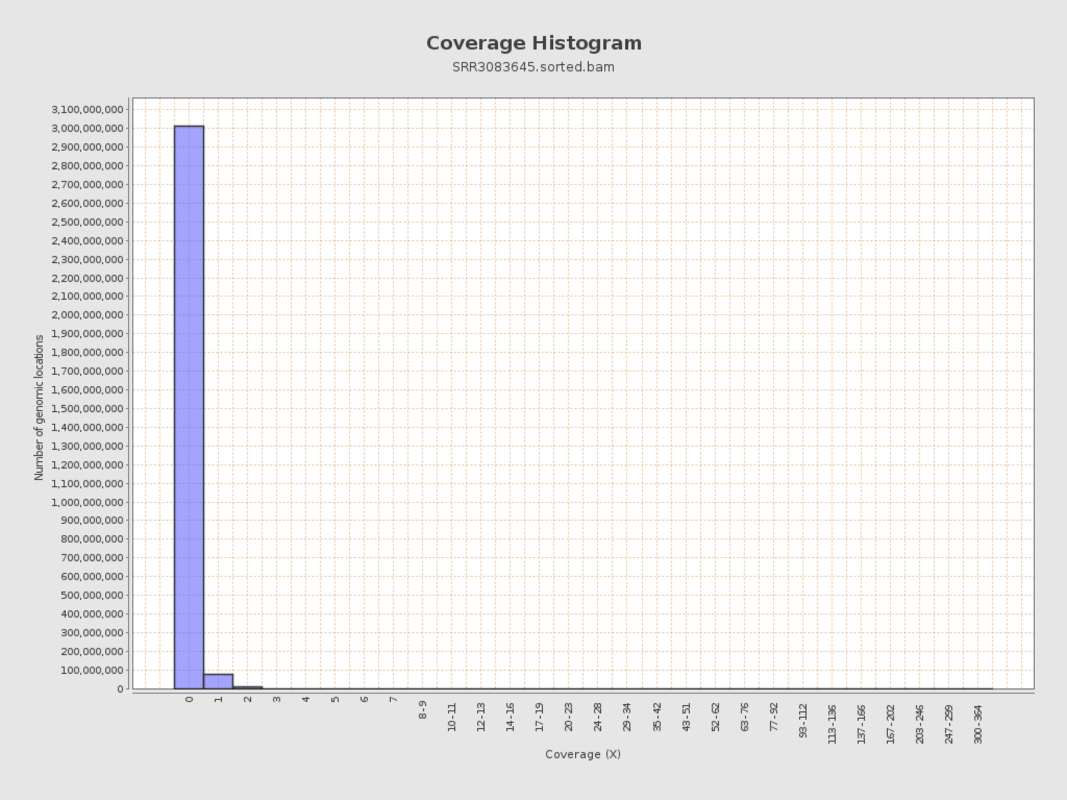
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7690301	0.0309	0.3331
chr2	243199373	8291324	0.0341	0.2304
chr3	198022430	6583501	0.0332	0.2002
chr4	191154276	6603064	0.0345	0.2067
chr5	180915260	6135756	0.0339	0.2024
chr6	171115067	5445091	0.0318	0.2064
chr7	159138663	5360401	0.0337	0.2884

chr8	146364022	5086029	0.0347	0.3055
chr9	141213431	3963864	0.0281	0.2036
chr10	135534747	4569923	0.0337	0.2337
chr11	135006516	4338418	0.0321	0.208
chr12	133851895	4261426	0.0318	0.1969
chr13	115169878	3262377	0.0283	0.1848
chr14	107349540	2900666	0.027	0.1857
chr15	102531392	2797586	0.0273	0.1821
chr16	90354753	2420746	0.0268	0.1865
chr17	81195210	2230575	0.0275	0.1906
chr18	78077248	2573063	0.033	0.3004
chr19	59128983	1602627	0.0271	0.2798
chr20	63025520	1845329	0.0293	0.192
chr21	48129895	1236940	0.0257	0.1808
chr22	51304566	923340	0.018	0.1472
chrMT	16571	22163	1.3375	1.3073
chrX	155270560	5514306	0.0355	0.2139
chrY	59373566	252752	0.0043	0.0974

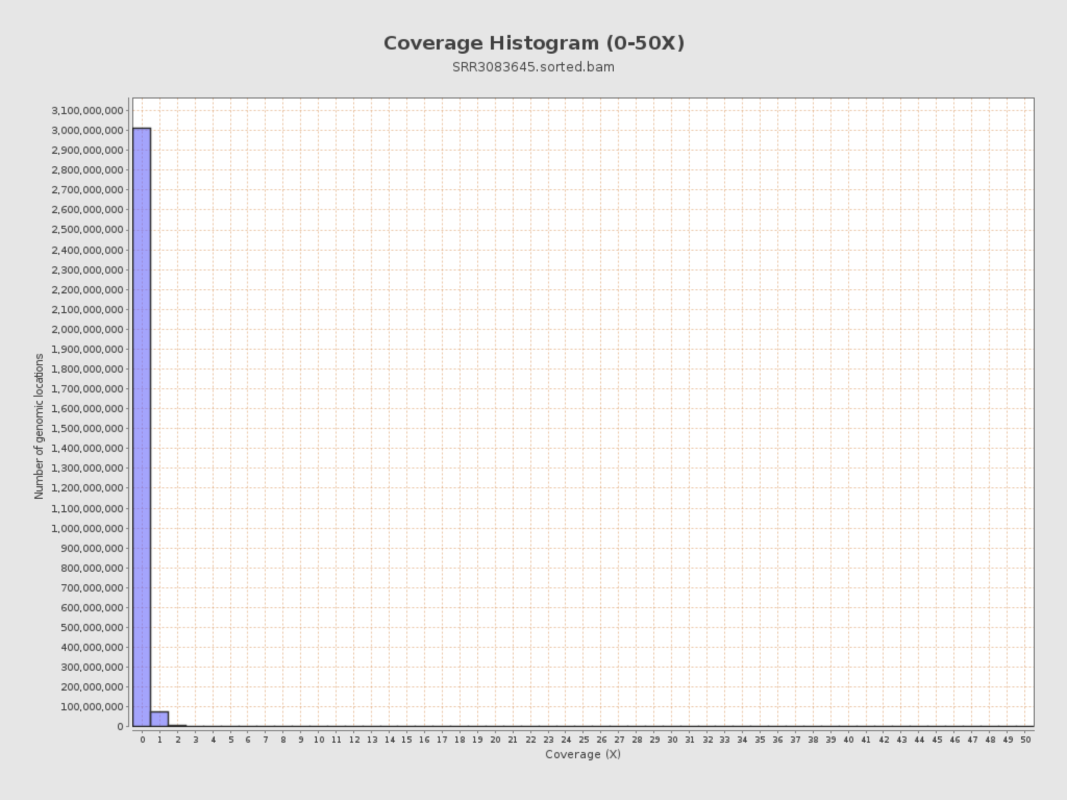
3. Results : Coverage across reference



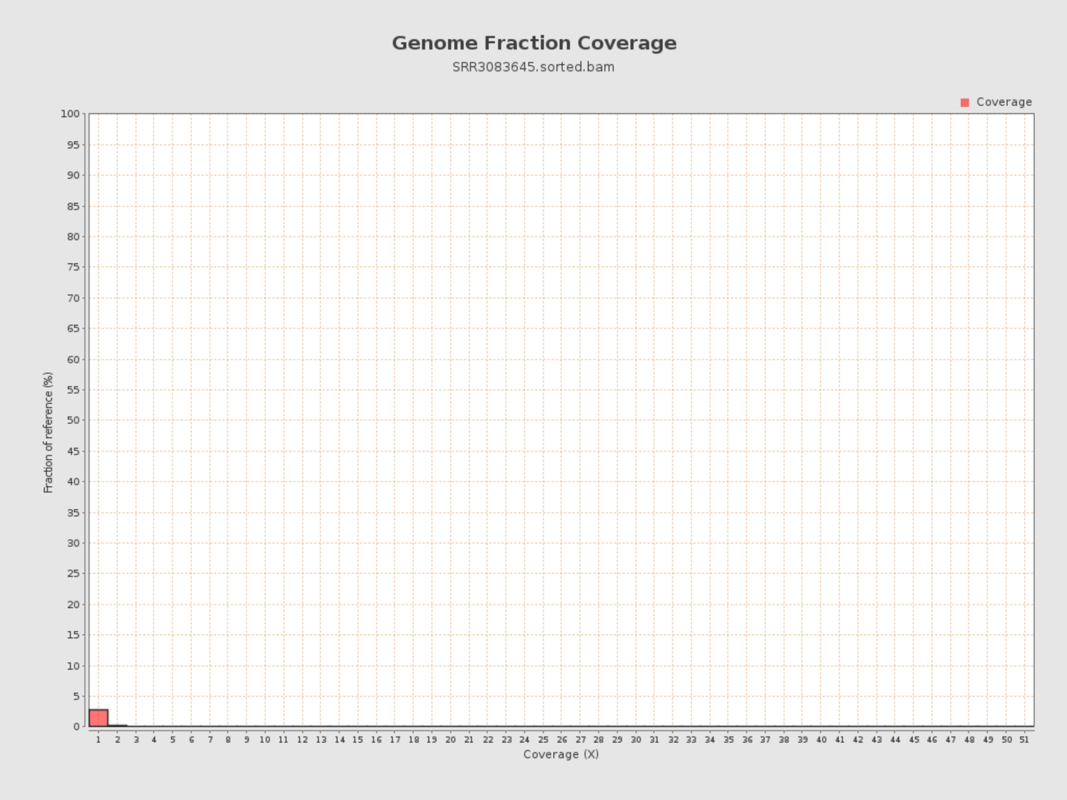
4. Results : Coverage Histogram



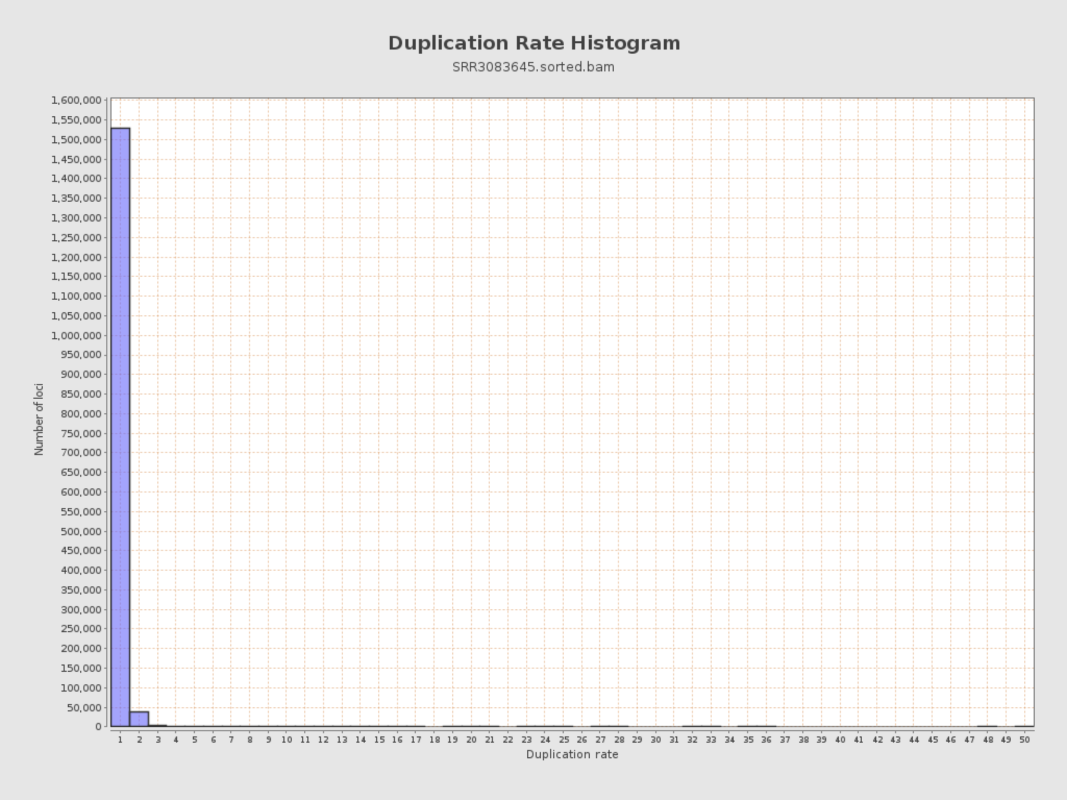
5. Results : Coverage Histogram (0-50X)



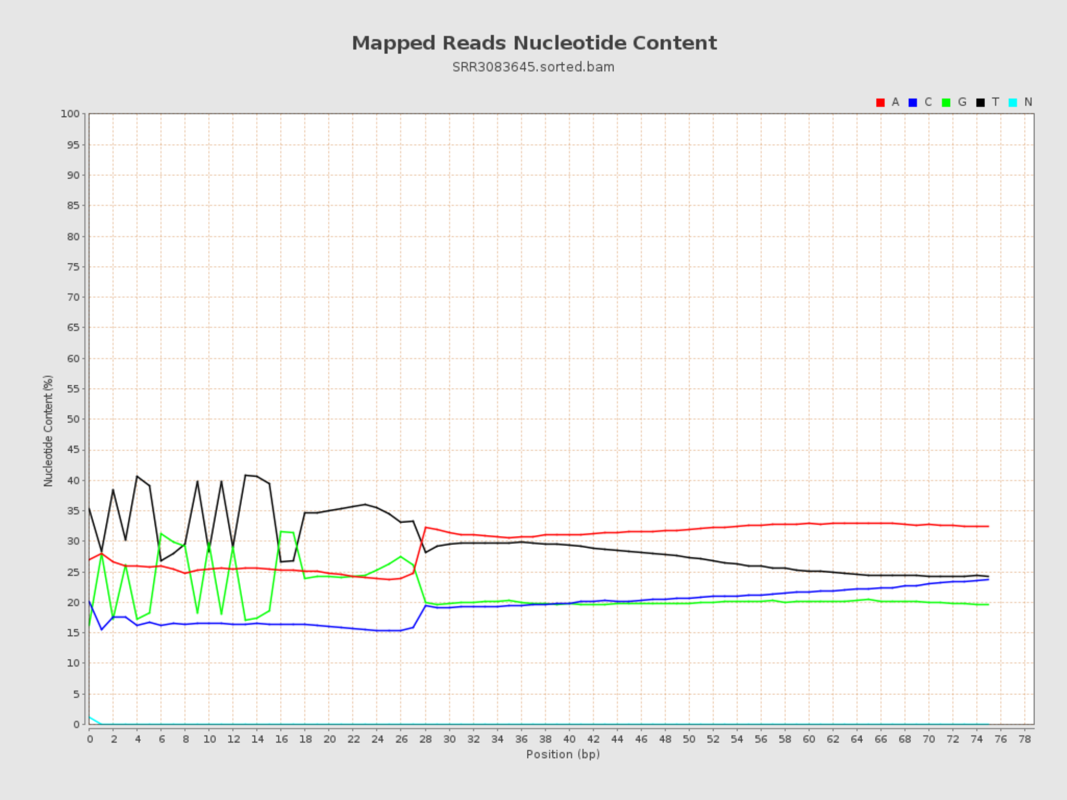
6. Results : Genome Fraction Coverage



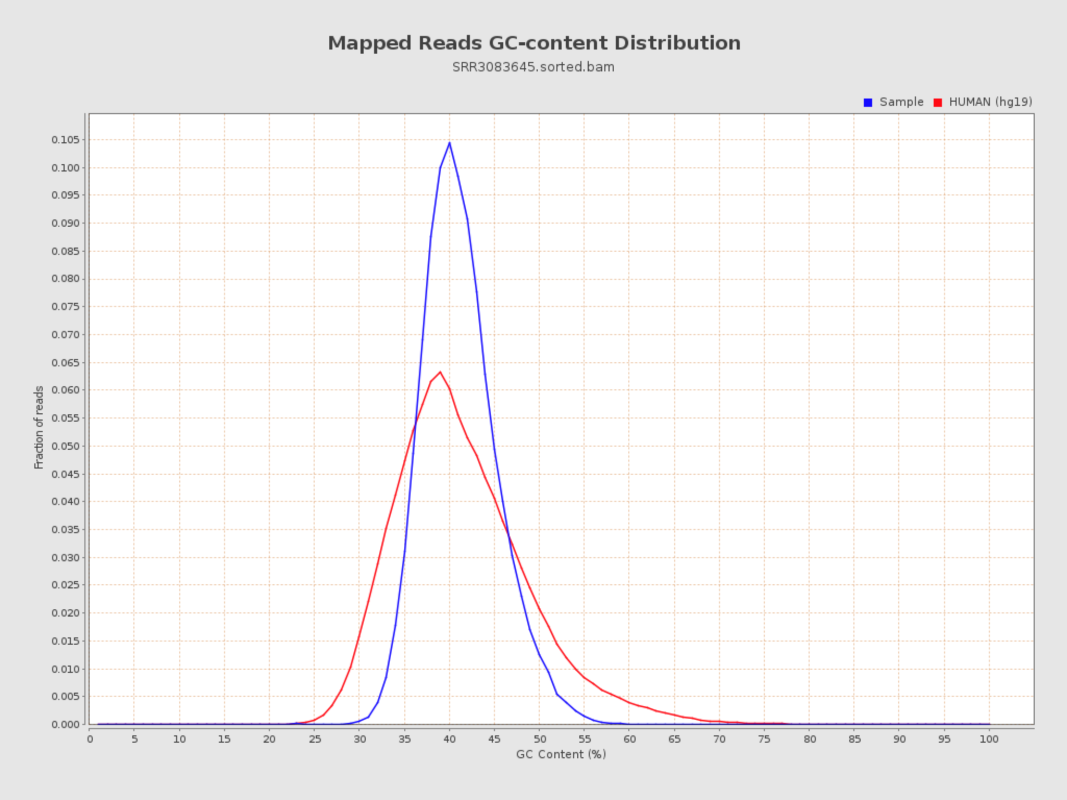
7. Results : Duplication Rate Histogram



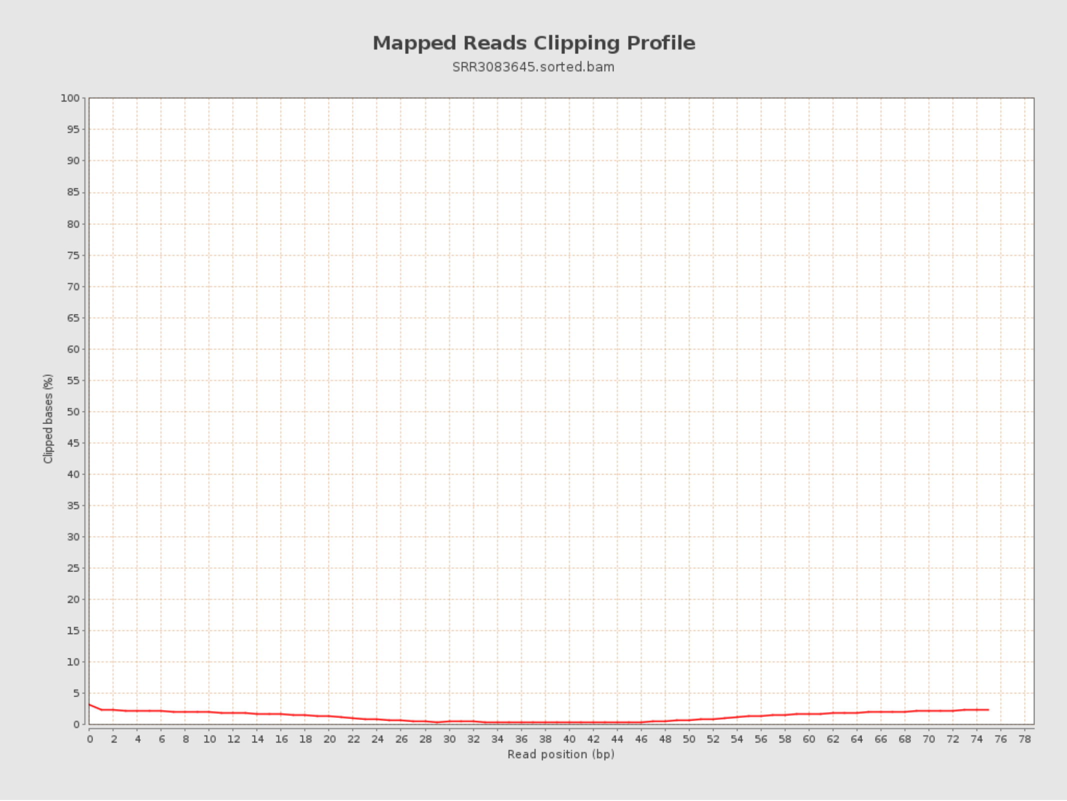
8. Results : Mapped Reads Nucleotide Content



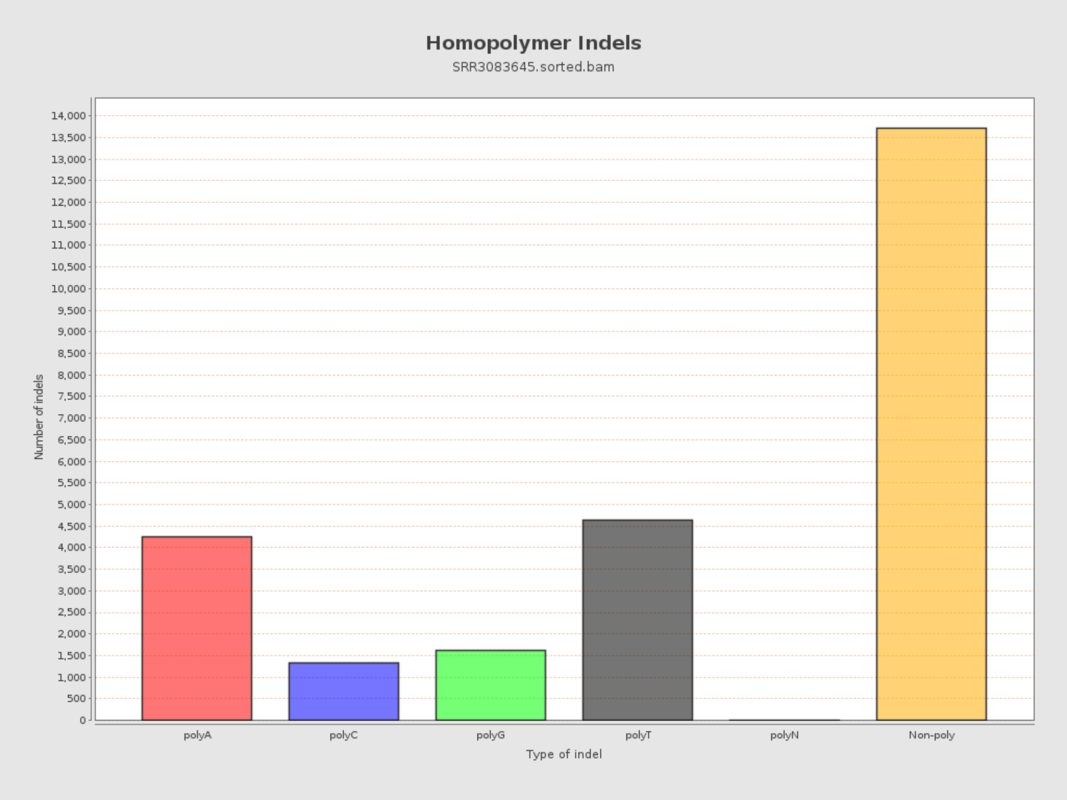
9. Results : Mapped Reads GC-content Distribution



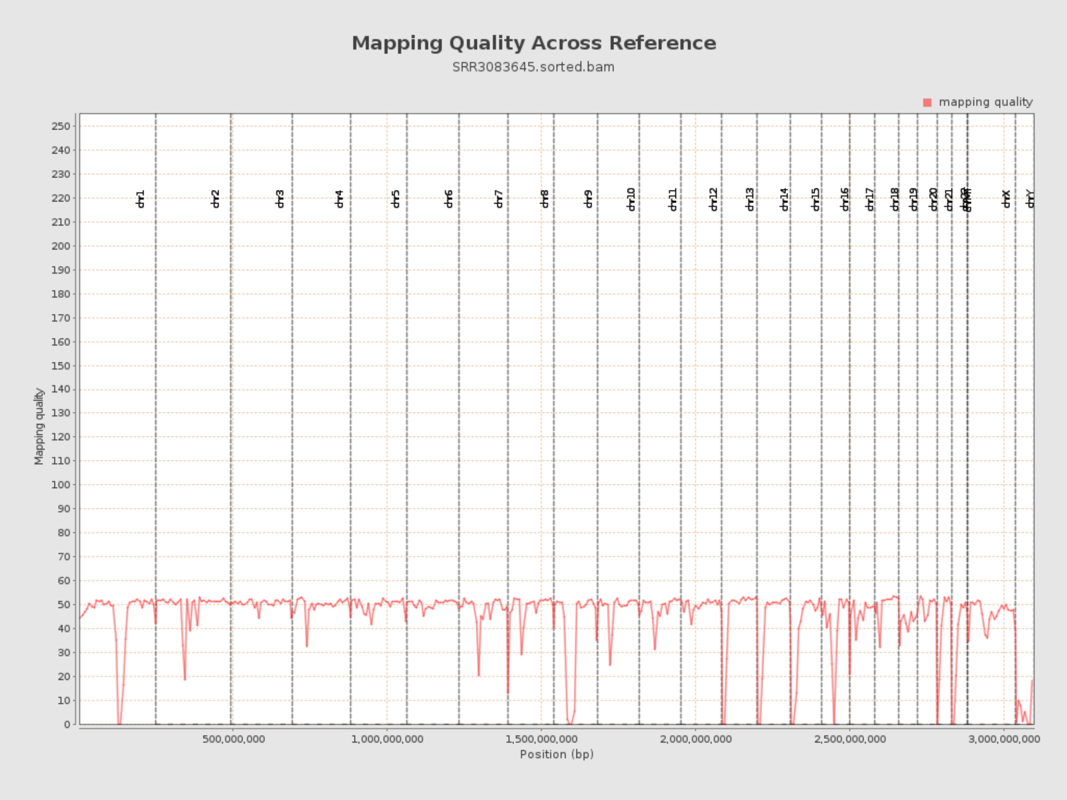
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram