Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:39:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068944.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_SRR6068944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:39:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,290,863
Mapped reads	761,550 / 59%
Unmapped reads	529,313 / 41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,427 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	59,178 / 4.58%
Duplication rate	6.54%
Clipped reads	423,391 / 32.8%

2.2. ACGT Content

Number/percentage of A's	12,973,852 / 26.72%
Number/percentage of C's	8,217,596 / 16.93%
Number/percentage of T's	16,335,182 / 33.65%
Number/percentage of G's	10,912,560 / 22.48%
Number/percentage of N's	108,088 / 0.22%
GC Percentage	39.41%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1901

2.4. Mapping Quality

Mean Mapping Quality	46.39

2.5. Mismatches and indels

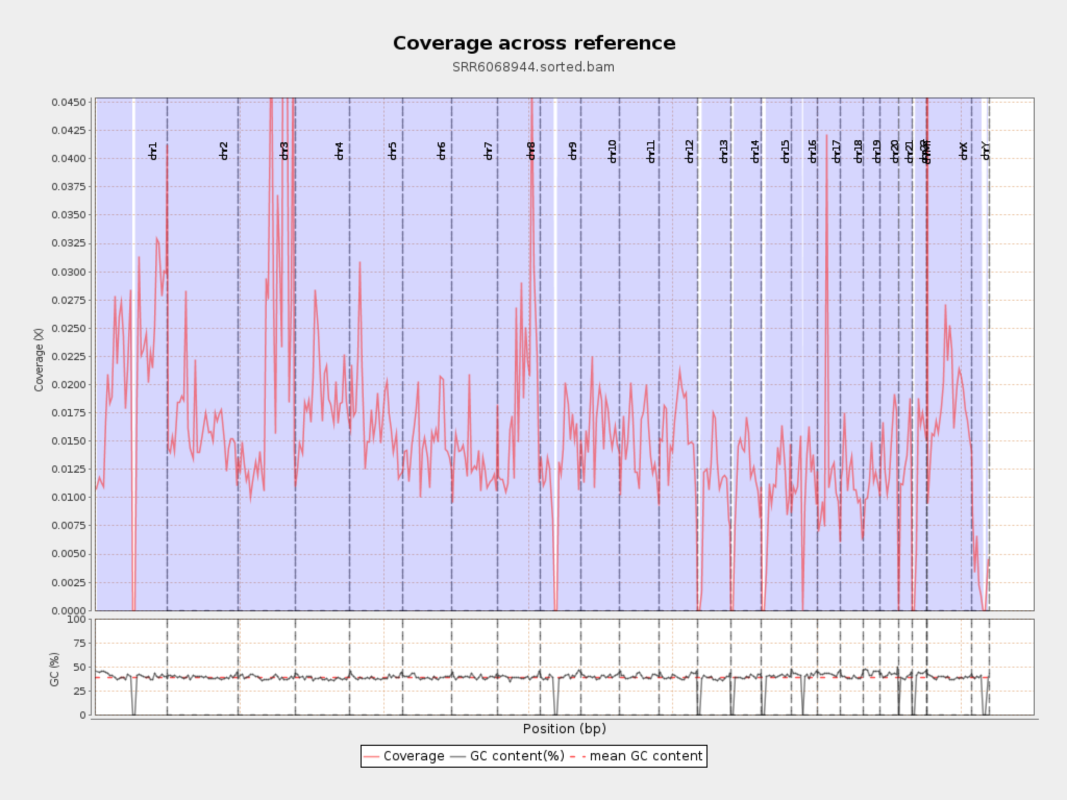
General error rate	1.13%
Mismatches	542,621
Insertions	4,190
Mapped reads with at least one insertion	0.55%
Deletions	16,639
Mapped reads with at least one deletion	2.16%
Homopolymer indels	48.88%

2.6. Chromosome stats

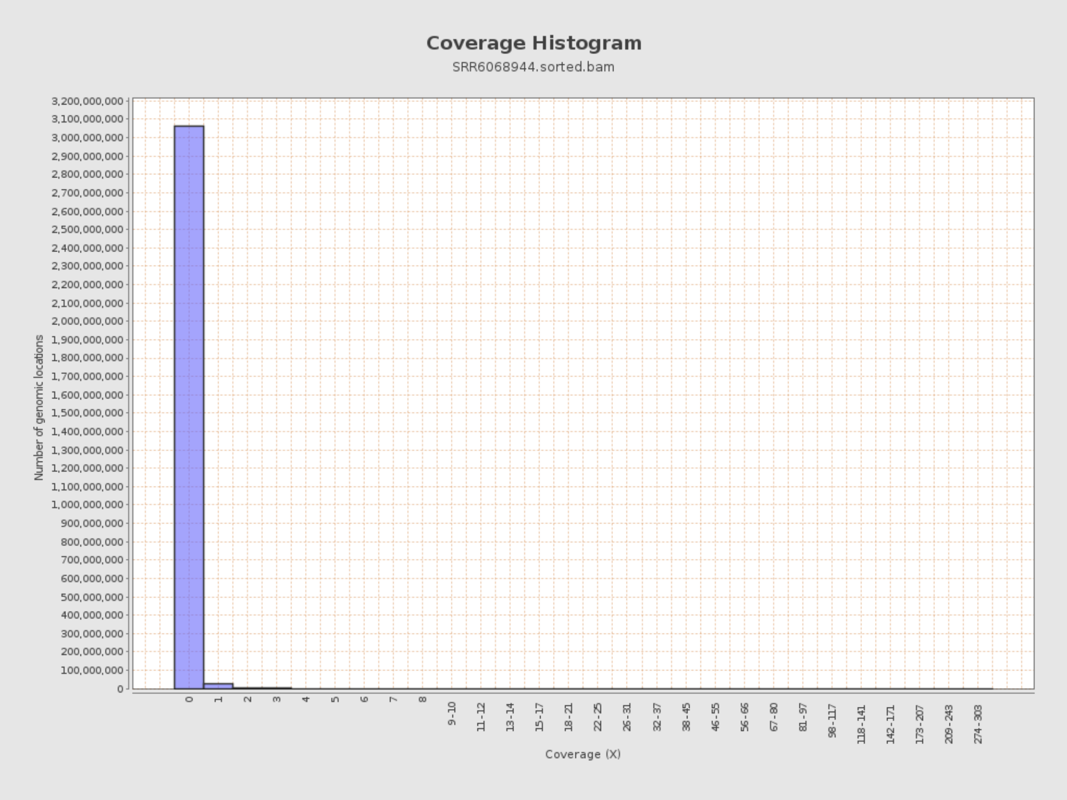
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5311587	0.0213	0.268
chr2	243199373	3951979	0.0162	0.1909
chr3	198022430	4842213	0.0245	0.212
chr4	191154276	3550974	0.0186	0.1863
chr5	180915260	3141448	0.0174	0.1784
chr6	171115067	2565931	0.015	0.1757
chr7	159138663	2072040	0.013	0.1885

chr8	146364022	2862441	0.0196	0.2592
chr9	141213431	1752519	0.0124	0.1651
chr10	135534747	2177236	0.0161	0.1843
chr11	135006516	1987819	0.0147	0.1713
chr12	133851895	2151818	0.0161	0.1716
chr13	115169878	1190729	0.0103	0.1362
chr14	107349540	1198947	0.0112	0.1425
chr15	102531392	979302	0.0096	0.1294
chr16	90354753	996835	0.011	0.1413
chr17	81195210	1034686	0.0127	0.1543
chr18	78077248	905199	0.0116	0.2401
chr19	59128983	663708	0.0112	0.1799
chr20	63025520	894320	0.0142	0.1627
chr21	48129895	586754	0.0122	0.1503
chr22	51304566	600187	0.0117	0.1433
chrMT	16571	97263	5.8695	4.2278
chrX	155270560	2873184	0.0185	0.1883
chrY	59373566	184153	0.0031	0.0699

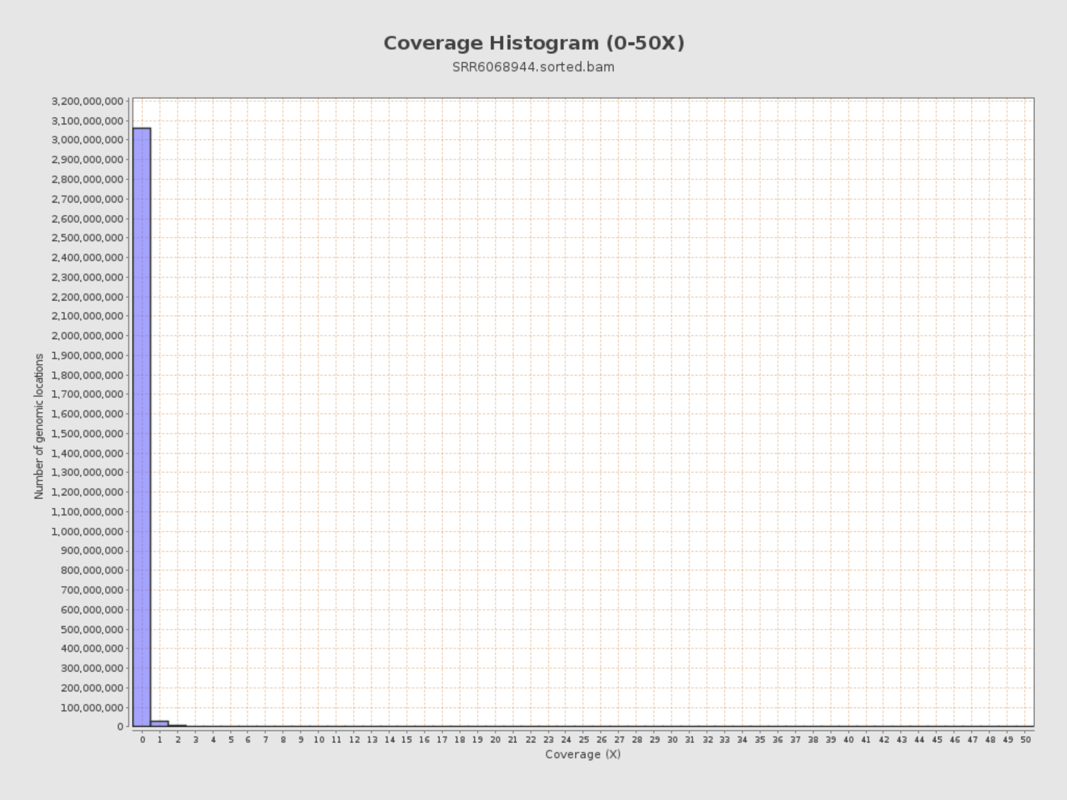
3. Results : Coverage across reference



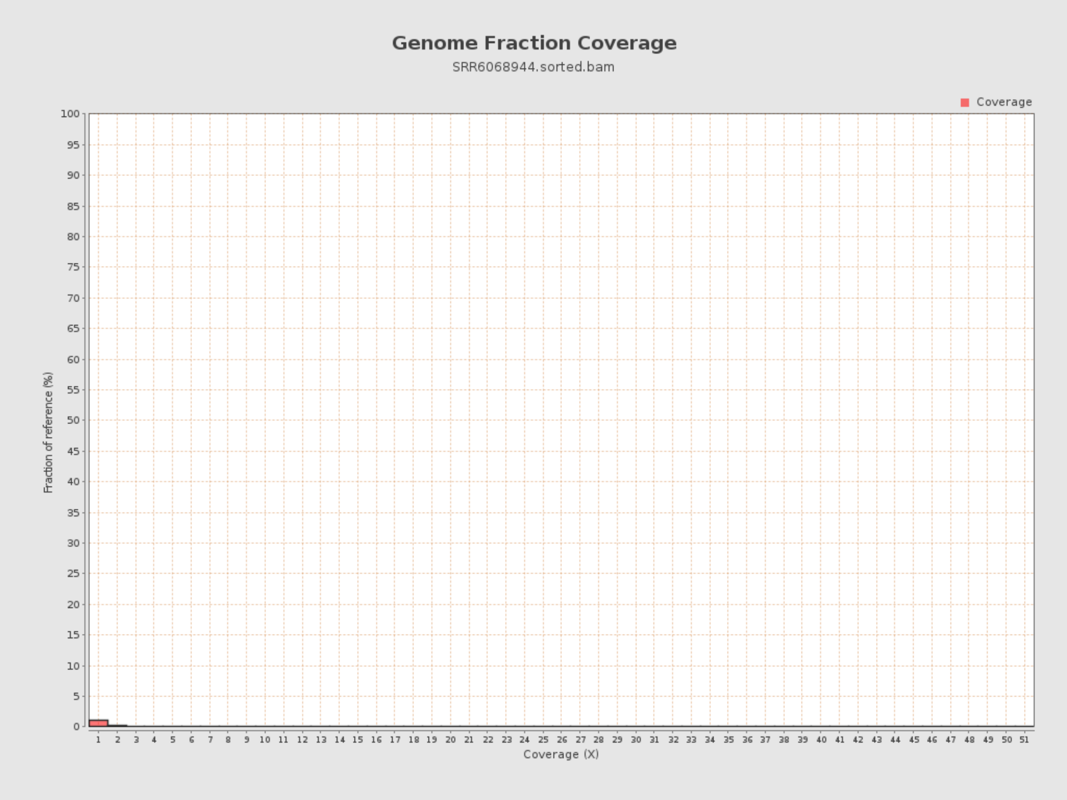
4. Results : Coverage Histogram



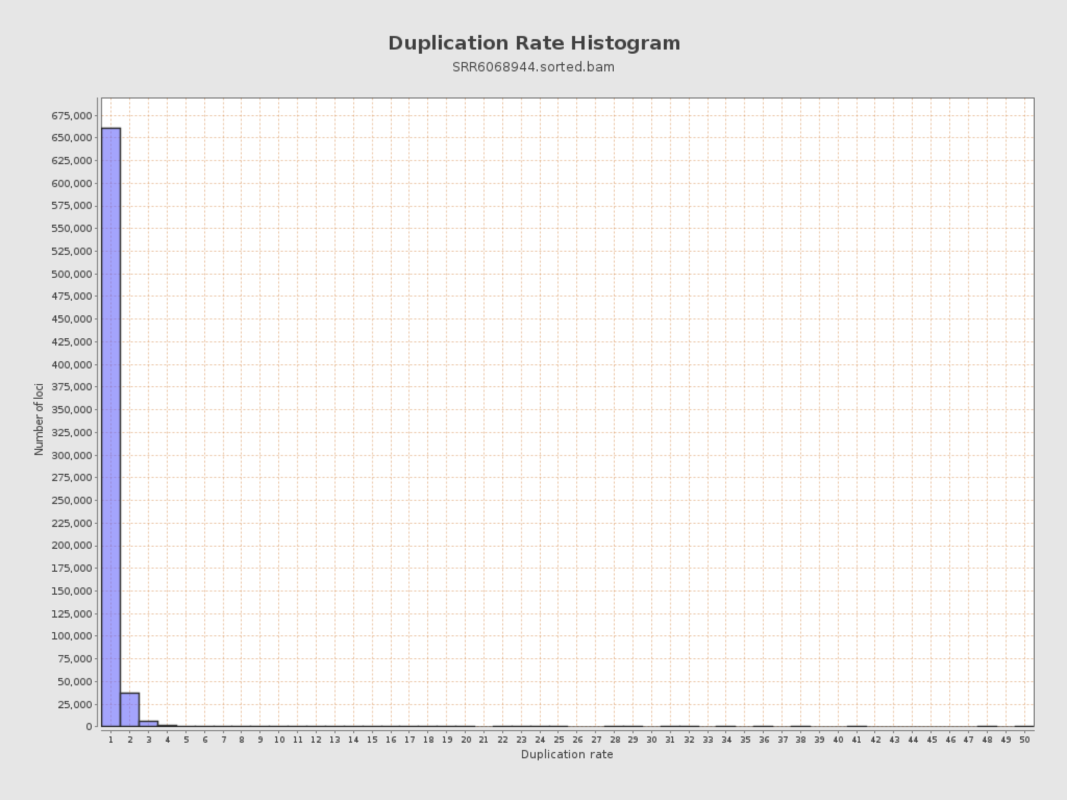
5. Results : Coverage Histogram (0-50X)



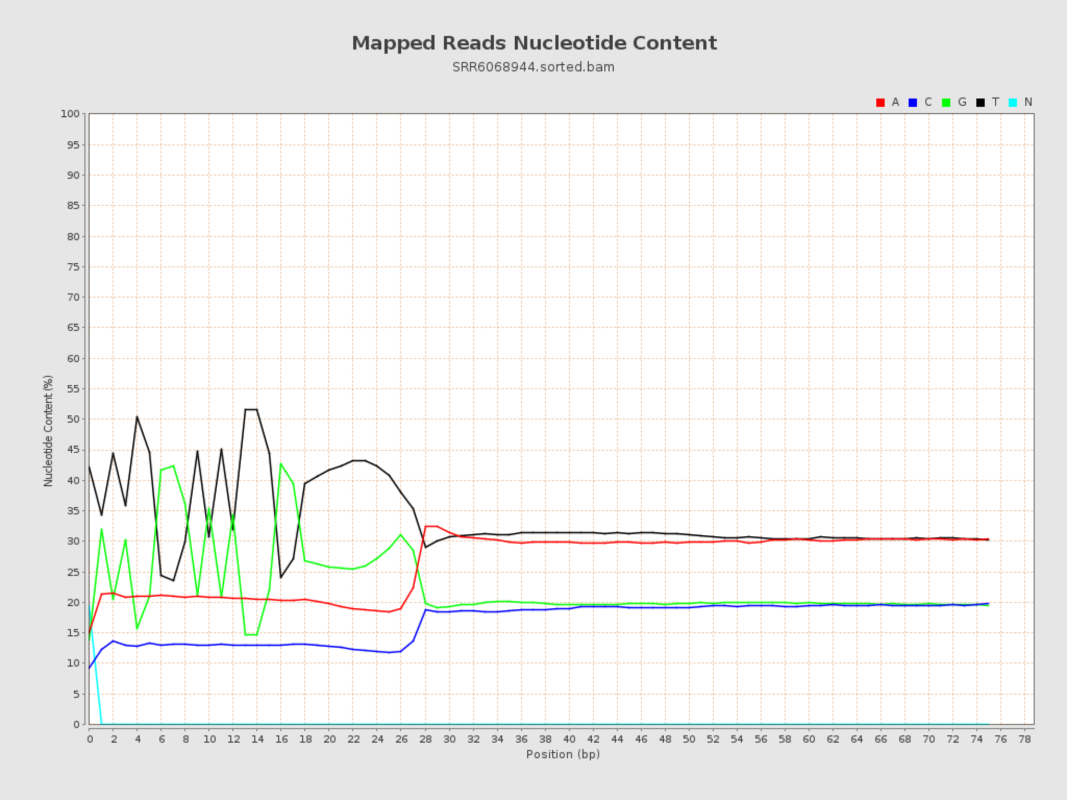
6. Results : Genome Fraction Coverage



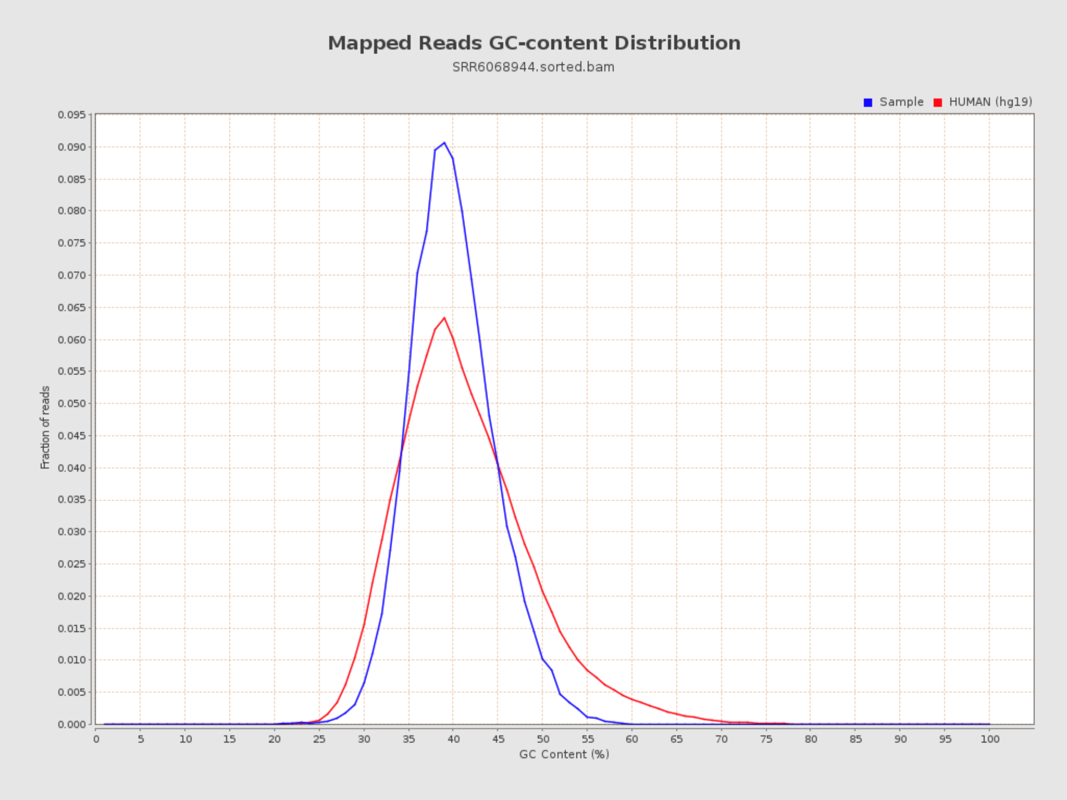
7. Results : Duplication Rate Histogram



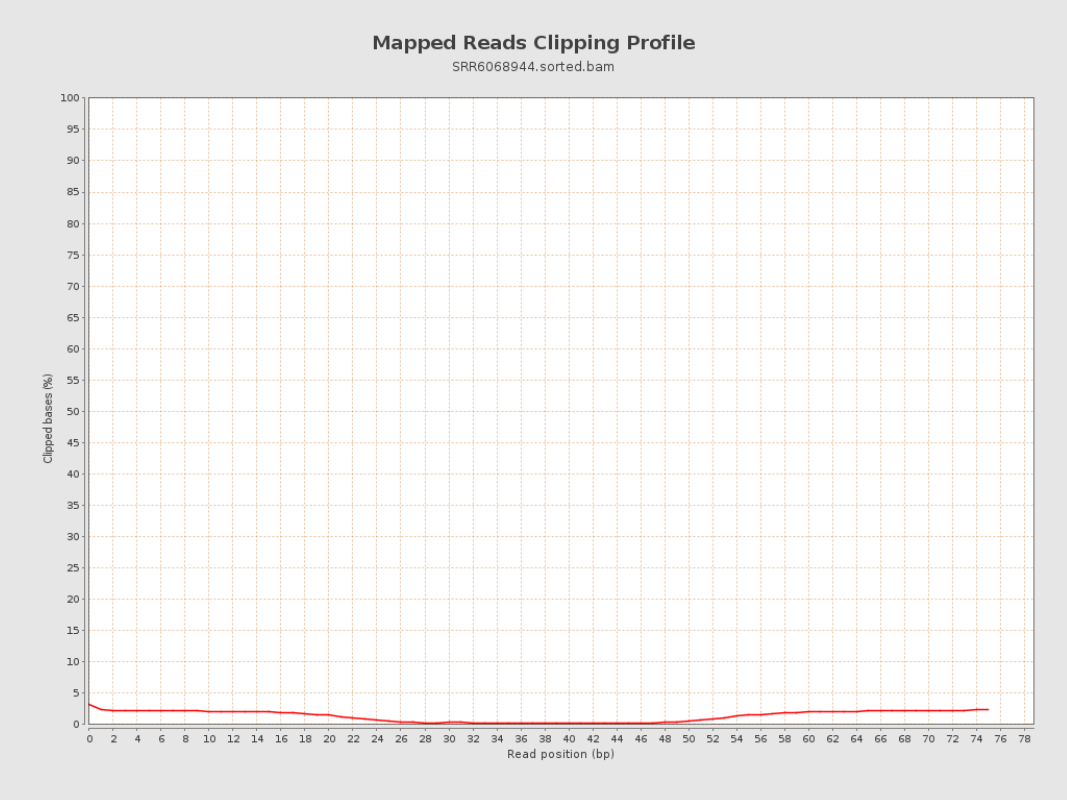
8. Results : Mapped Reads Nucleotide Content



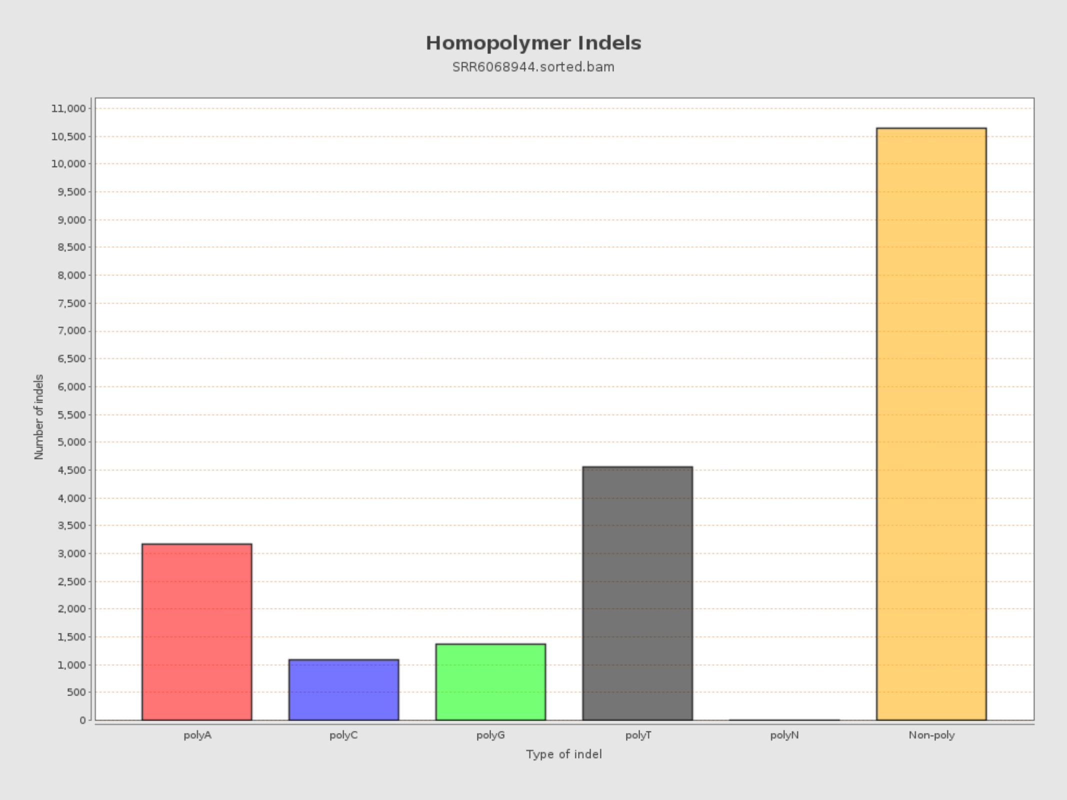
9. Results : Mapped Reads GC-content Distribution



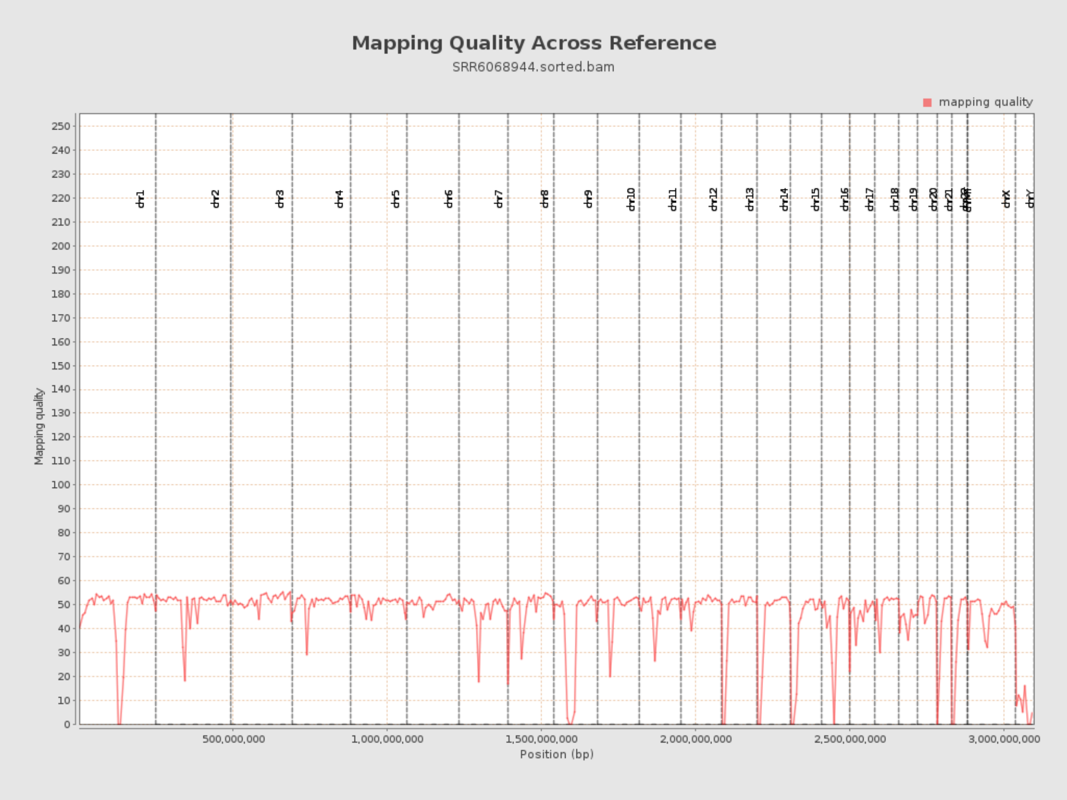
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram