Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:22:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008695.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_SRR6008695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008695.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:22:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	761,741
Mapped reads	647,156 / 84.96%
Unmapped reads	114,585 / 15.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,051 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	17,135 / 2.25%
Duplication rate	1.89%
Clipped reads	374,358 / 49.15%

2.2. ACGT Content

Number/percentage of A's	11,123,765 / 27.17%
Number/percentage of C's	7,368,565 / 18%
Number/percentage of T's	12,653,929 / 30.91%
Number/percentage of G's	9,789,763 / 23.91%
Number/percentage of N's	4,435 / 0.01%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0132

Standard Deviation	0.1676

2.4. Mapping Quality

Mean Mapping Quality	42.86

2.5. Mismatches and indels

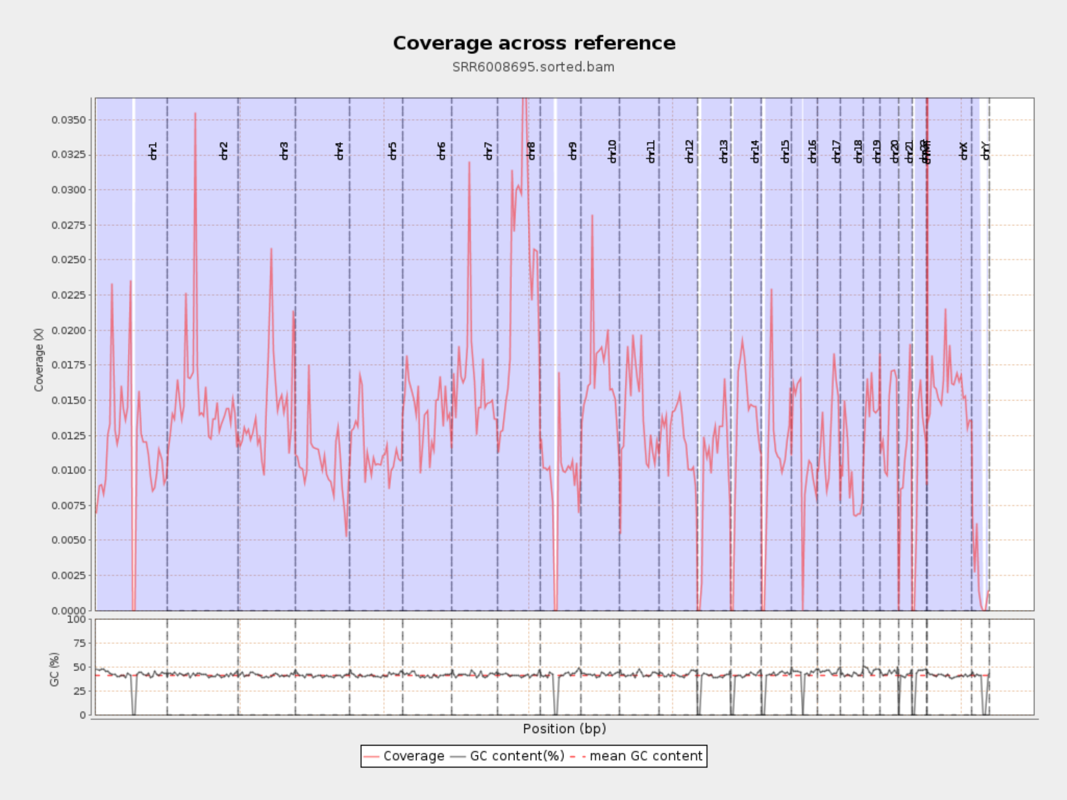
General error rate	1.01%
Mismatches	405,768
Insertions	3,947
Mapped reads with at least one insertion	0.6%
Deletions	17,384
Mapped reads with at least one deletion	2.65%
Homopolymer indels	48.81%

2.6. Chromosome stats

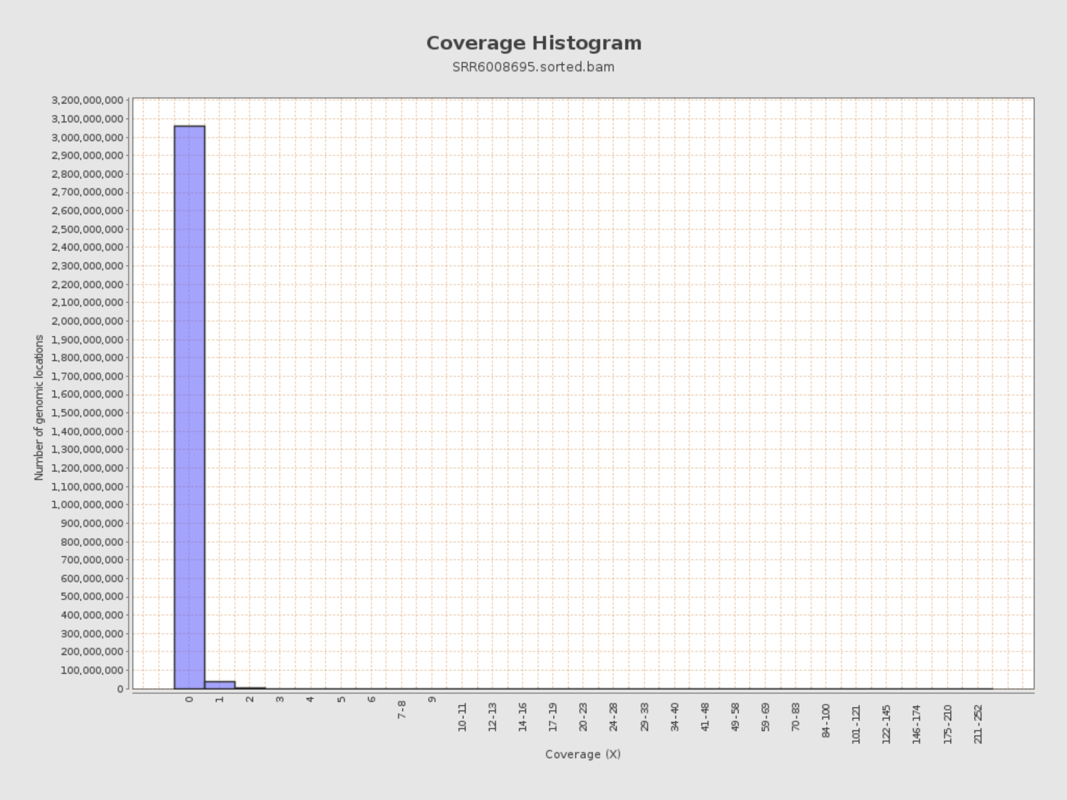
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2839430	0.0114	0.2287
chr2	243199373	3700045	0.0152	0.2142
chr3	198022430	2838690	0.0143	0.1292
chr4	191154276	1991672	0.0104	0.1136
chr5	180915260	2075691	0.0115	0.1143
chr6	171115067	2416271	0.0141	0.1379
chr7	159138663	2626189	0.0165	0.27

chr8	146364022	3552375	0.0243	0.1936
chr9	141213431	1301422	0.0092	0.1558
chr10	135534747	2292441	0.0169	0.1684
chr11	135006516	1904510	0.0141	0.215
chr12	133851895	1651310	0.0123	0.1203
chr13	115169878	1167818	0.0101	0.1082
chr14	107349540	1394352	0.013	0.1281
chr15	102531392	1097370	0.0107	0.1122
chr16	90354753	992926	0.011	0.1181
chr17	81195210	1029899	0.0127	0.1398
chr18	78077248	709225	0.0091	0.2275
chr19	59128983	871409	0.0147	0.1697
chr20	63025520	850626	0.0135	0.1295
chr21	48129895	528139	0.011	0.1163
chr22	51304566	503639	0.0098	0.1053
chrMT	16571	30713	1.8534	1.8454
chrX	155270560	2475762	0.0159	0.1423
chrY	59373566	127092	0.0021	0.0611

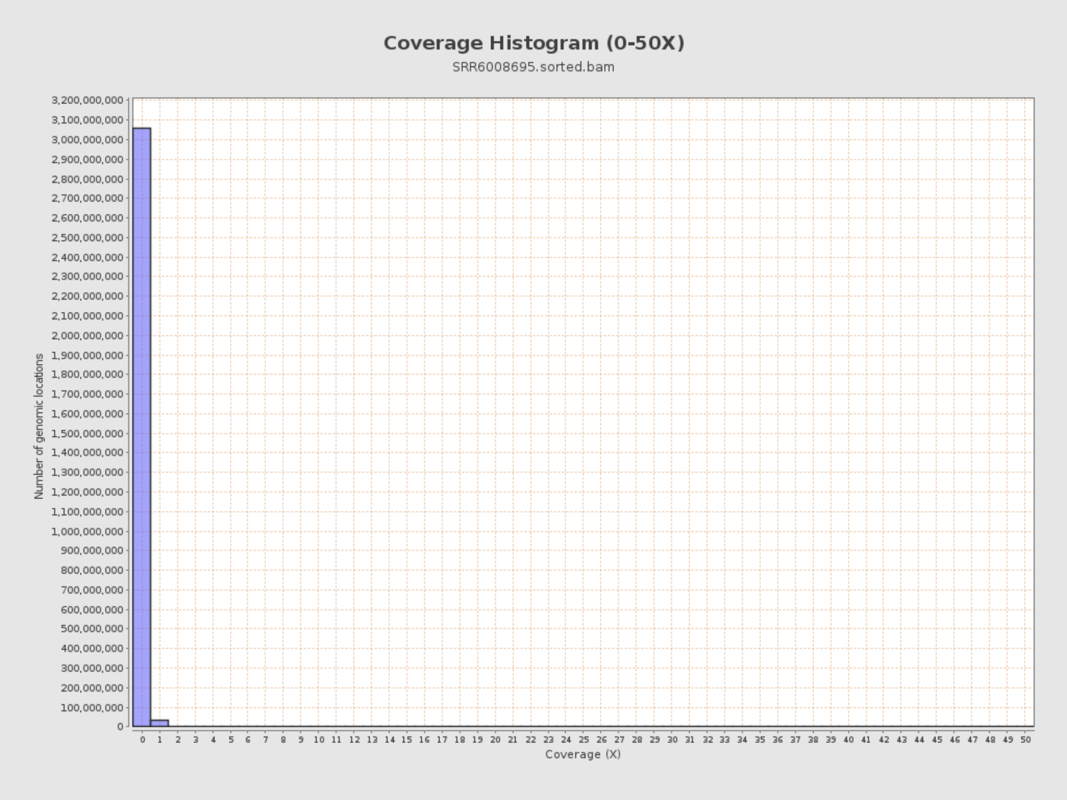
3. Results : Coverage across reference



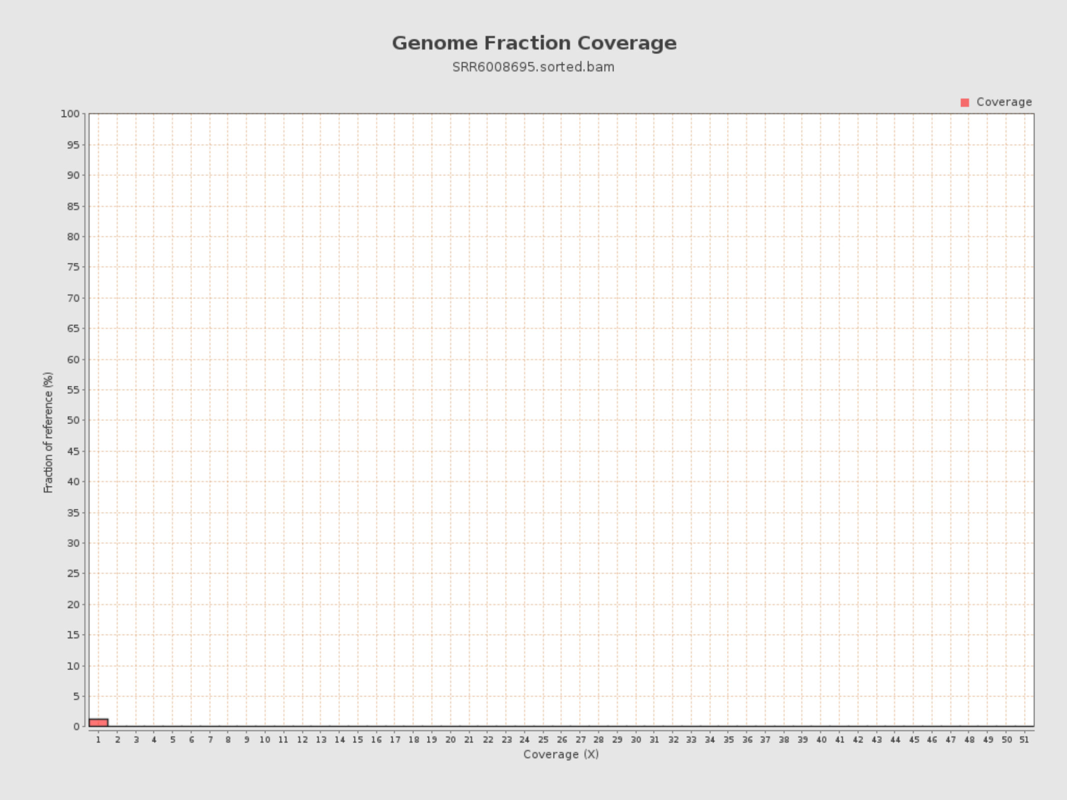
4. Results : Coverage Histogram



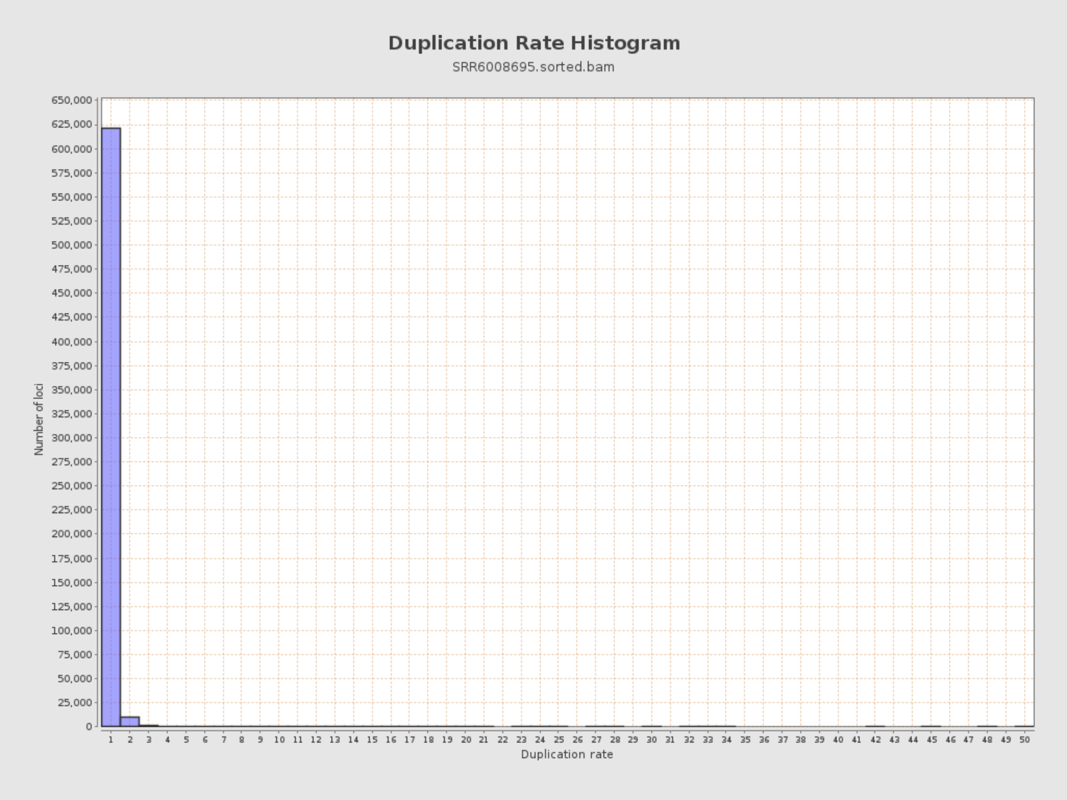
5. Results : Coverage Histogram (0-50X)



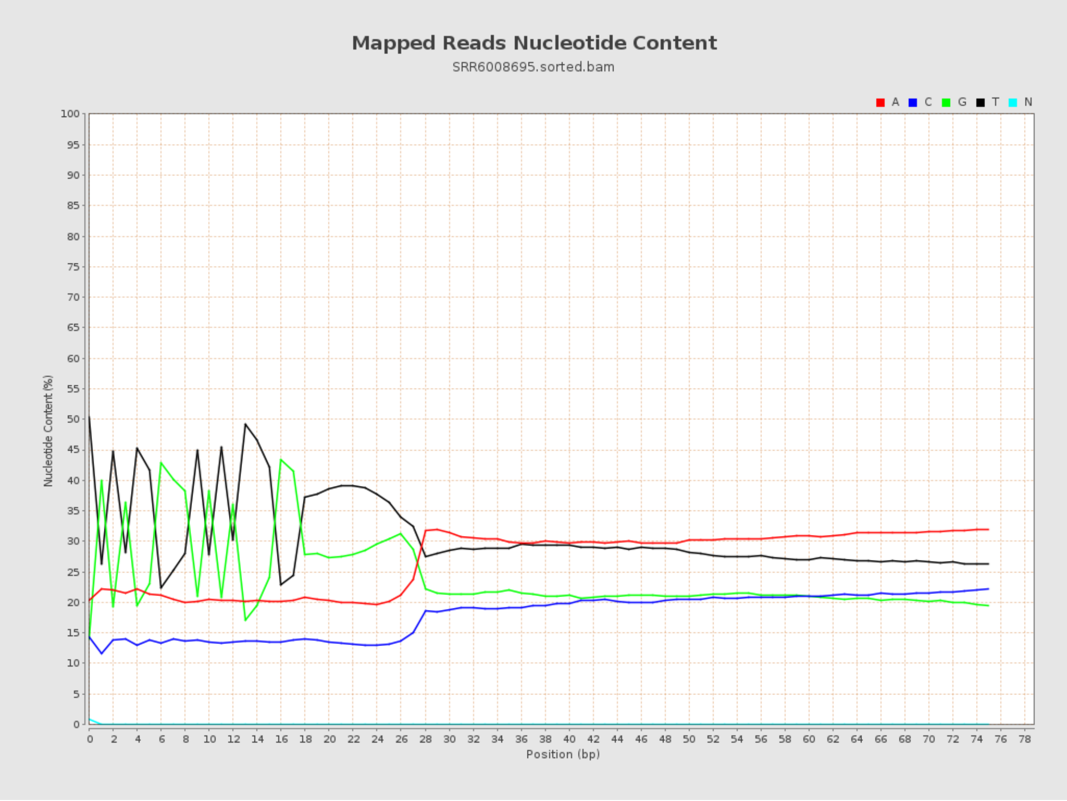
6. Results : Genome Fraction Coverage



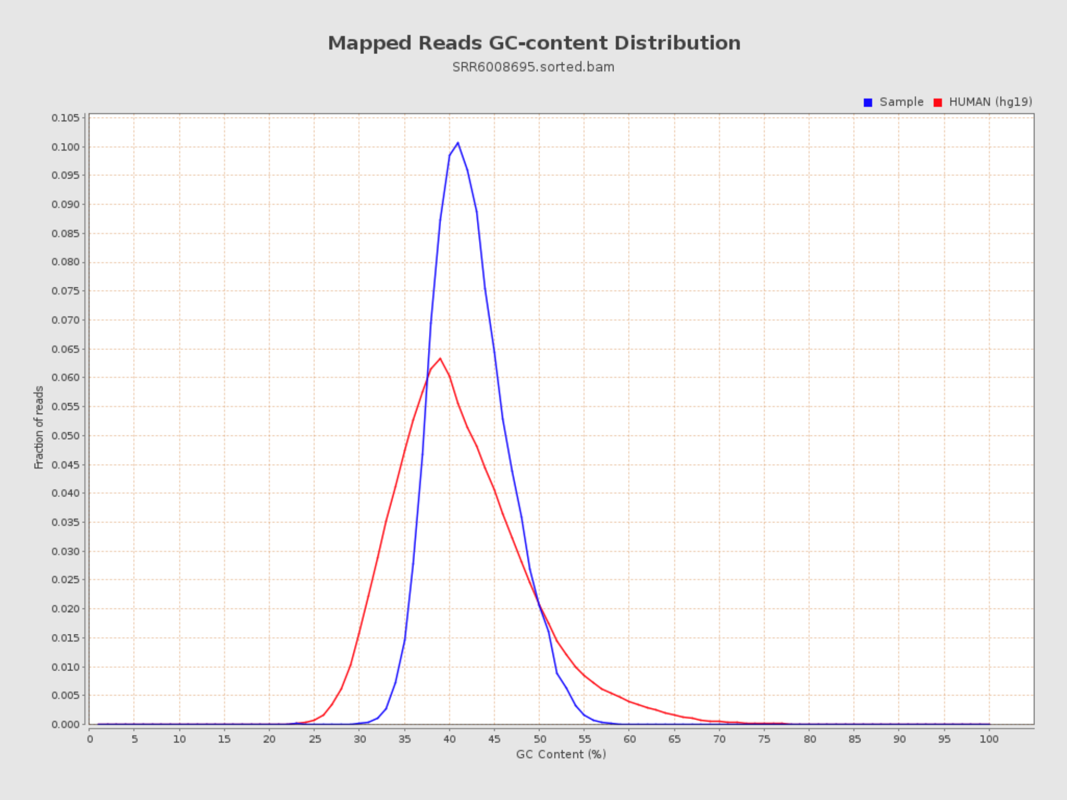
7. Results : Duplication Rate Histogram



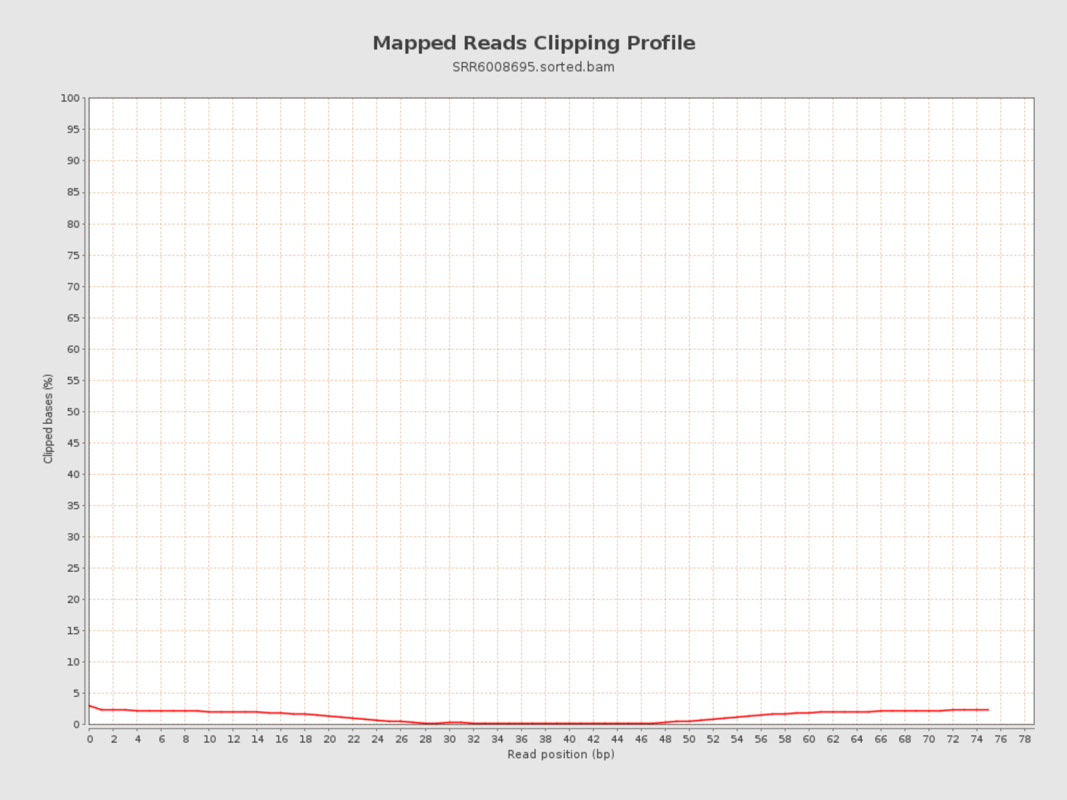
8. Results : Mapped Reads Nucleotide Content



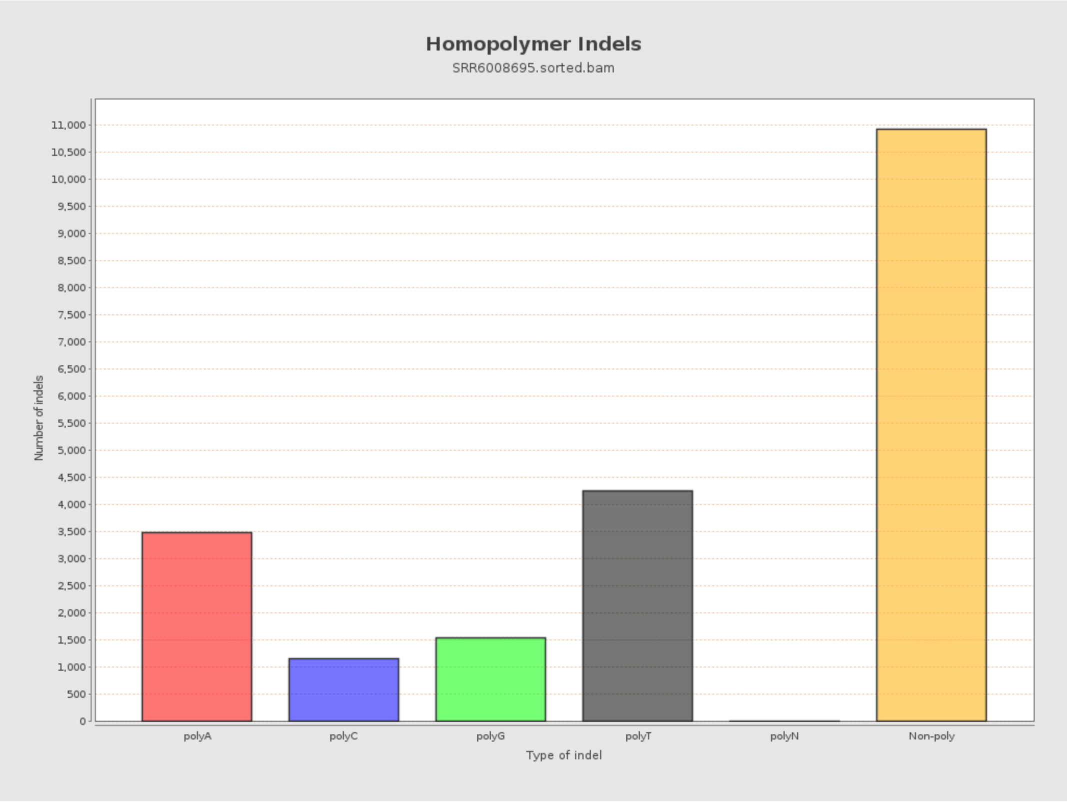
9. Results : Mapped Reads GC-content Distribution



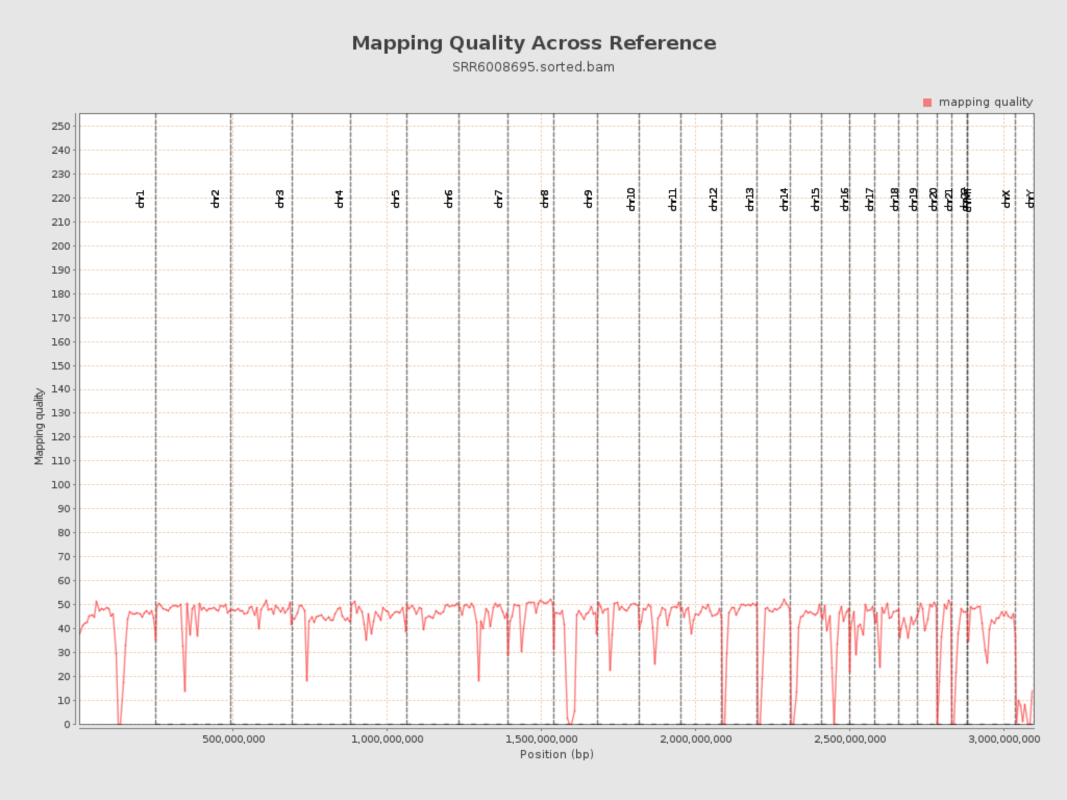
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram