Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:56:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008731.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_SRR6008731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008731.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:56:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,582,048
Mapped reads	1,276,408 / 80.68%
Unmapped reads	305,640 / 19.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,438 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	92,778 / 5.86%
Duplication rate	5.87%
Clipped reads	641,440 / 40.54%

2.2. ACGT Content

Number/percentage of A's	22,272,091 / 26.74%
Number/percentage of C's	15,248,796 / 18.31%
Number/percentage of T's	26,425,311 / 31.73%
Number/percentage of G's	19,276,266 / 23.14%
Number/percentage of N's	71,497 / 0.09%
GC Percentage	41.45%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.2826

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

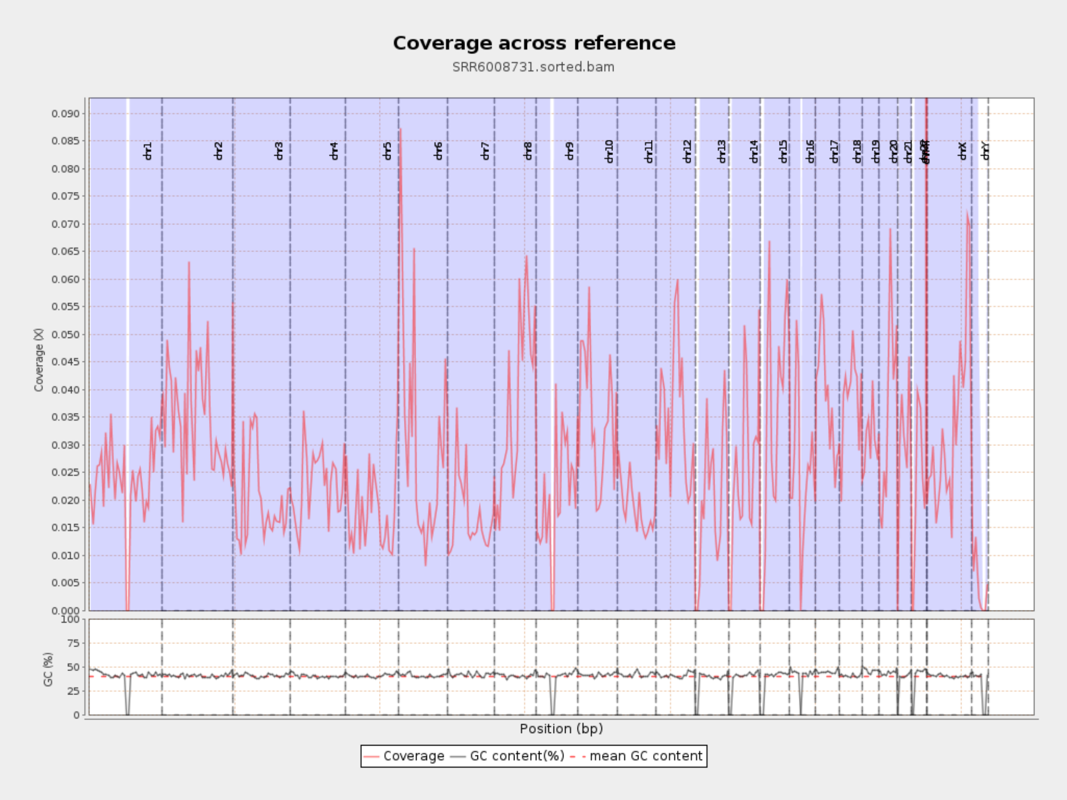
General error rate	0.91%
Mismatches	747,227
Insertions	6,986
Mapped reads with at least one insertion	0.54%
Deletions	24,244
Mapped reads with at least one deletion	1.88%
Homopolymer indels	47.65%

2.6. Chromosome stats

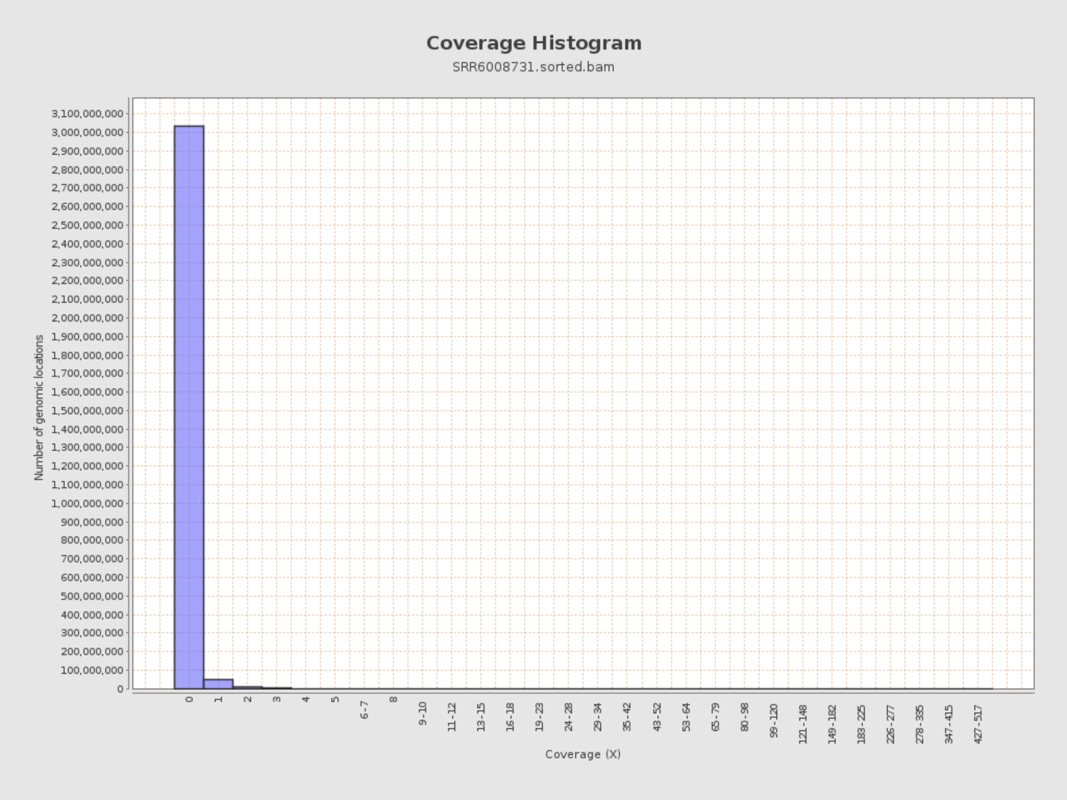
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5864194	0.0235	0.3449
chr2	243199373	8487153	0.0349	0.3784
chr3	198022430	4077223	0.0206	0.1781
chr4	191154276	4344565	0.0227	0.2015
chr5	180915260	3227913	0.0178	0.1687
chr6	171115067	5338697	0.0312	0.2527
chr7	159138663	2732938	0.0172	0.2477

chr8	146364022	5450880	0.0372	0.3757
chr9	141213431	2840984	0.0201	0.3048
chr10	135534747	4725796	0.0349	0.304
chr11	135006516	2527065	0.0187	0.2505
chr12	133851895	4632074	0.0346	0.2392
chr13	115169878	2369941	0.0206	0.1791
chr14	107349540	2567256	0.0239	0.2079
chr15	102531392	3521328	0.0343	0.2364
chr16	90354753	2312660	0.0256	0.2265
chr17	81195210	3132496	0.0386	0.3018
chr18	78077248	3005850	0.0385	0.6365
chr19	59128983	1836358	0.0311	0.2758
chr20	63025520	2285389	0.0363	0.2455
chr21	48129895	1452791	0.0302	0.2307
chr22	51304566	1090468	0.0213	0.1782
chrMT	16571	48520	2.928	3.1676
chrX	155270560	5186461	0.0334	0.2417
chrY	59373566	275535	0.0046	0.106

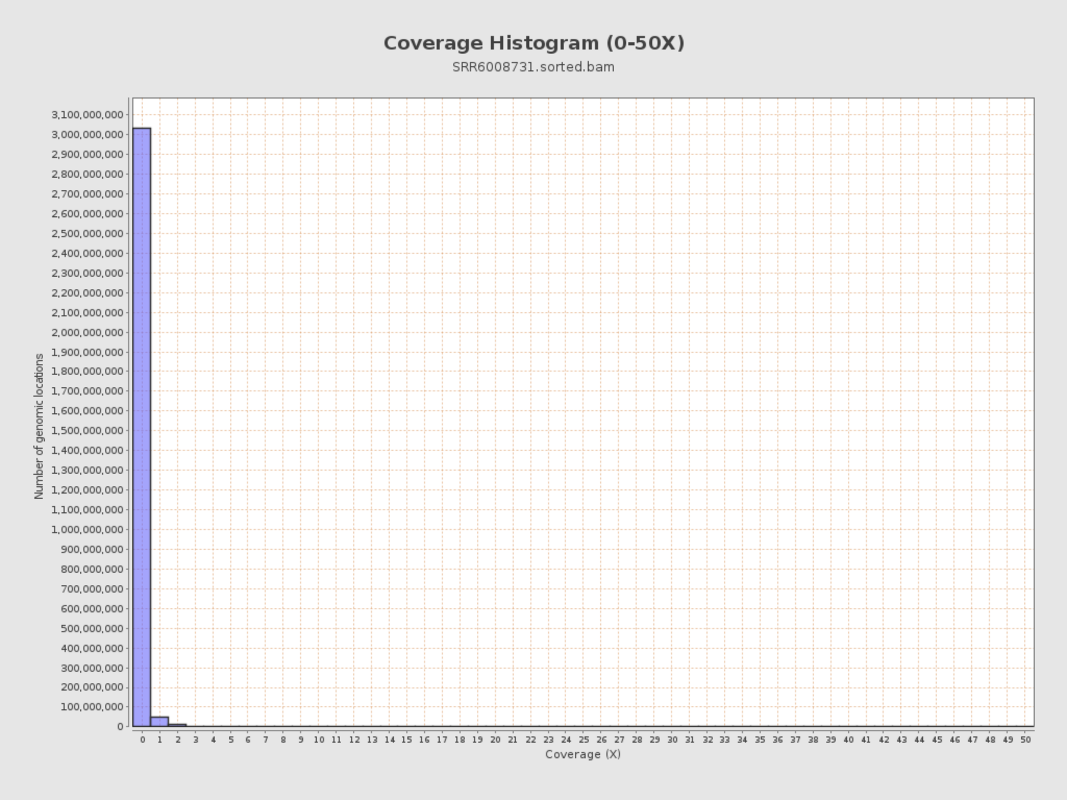
3. Results : Coverage across reference



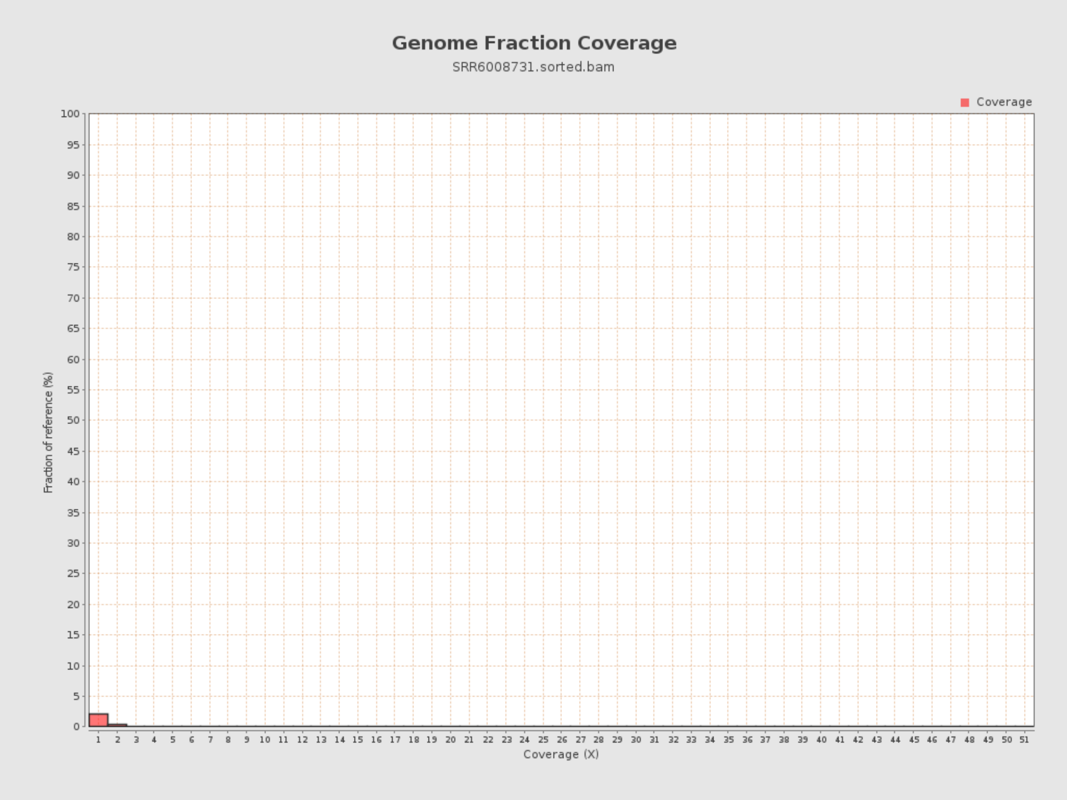
4. Results : Coverage Histogram



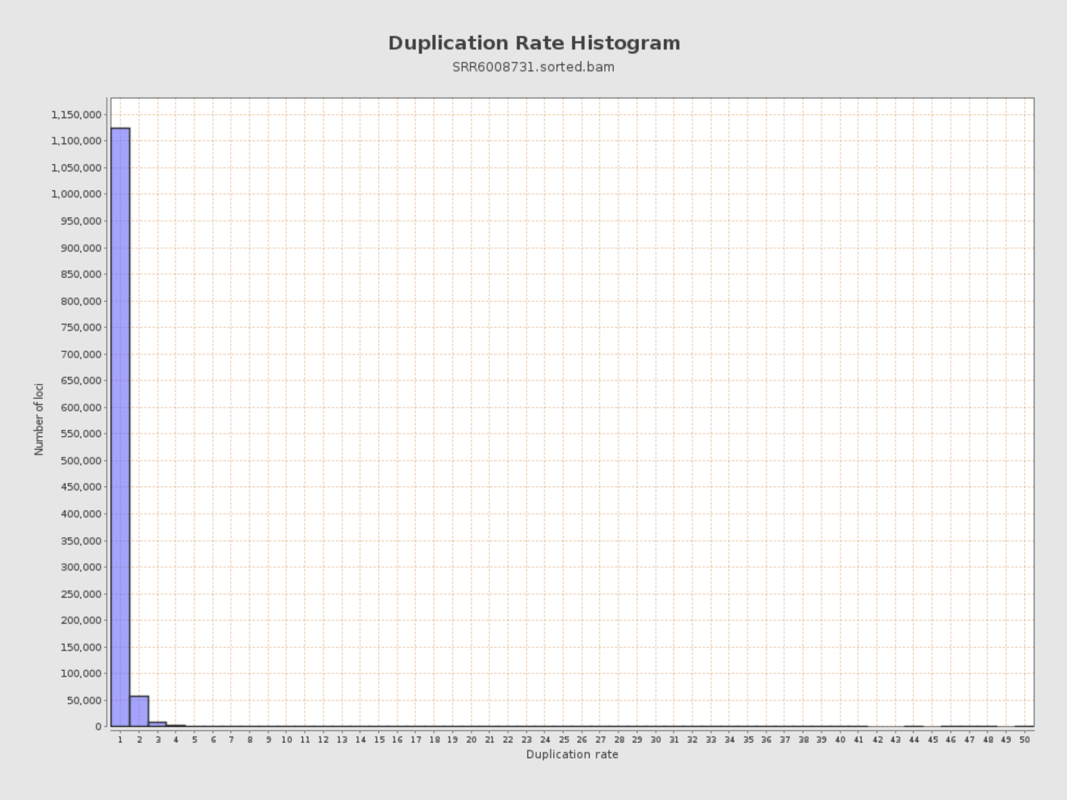
5. Results : Coverage Histogram (0-50X)



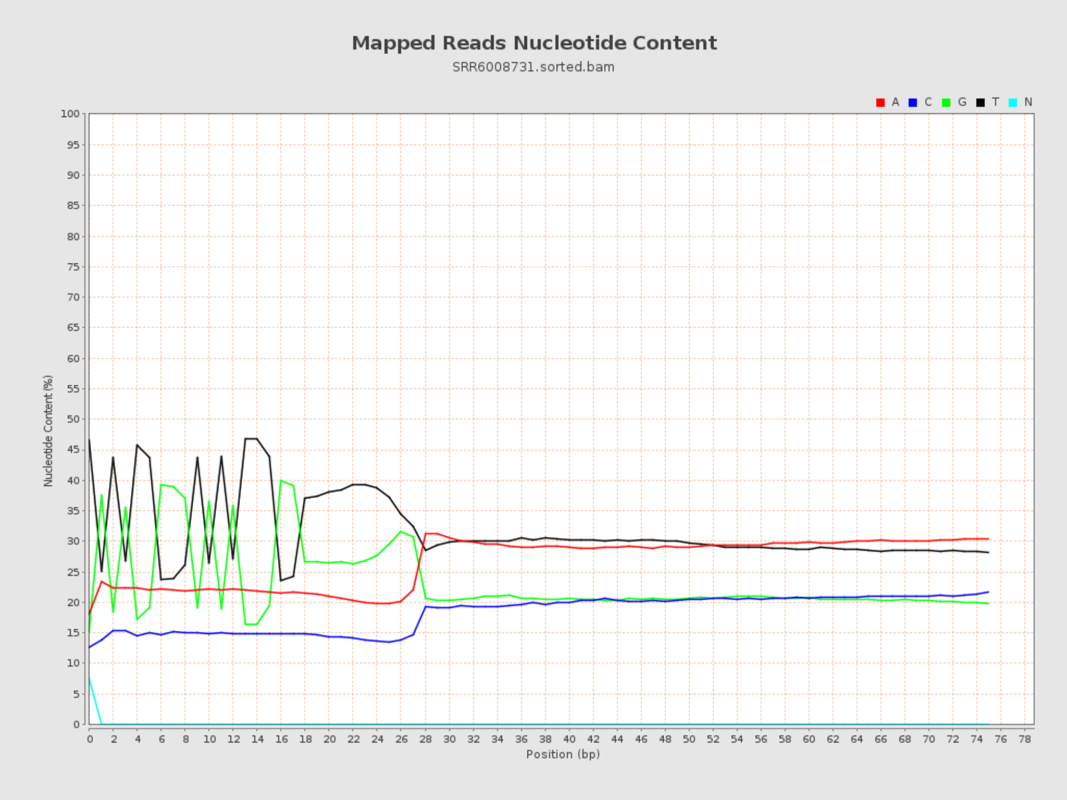
6. Results : Genome Fraction Coverage



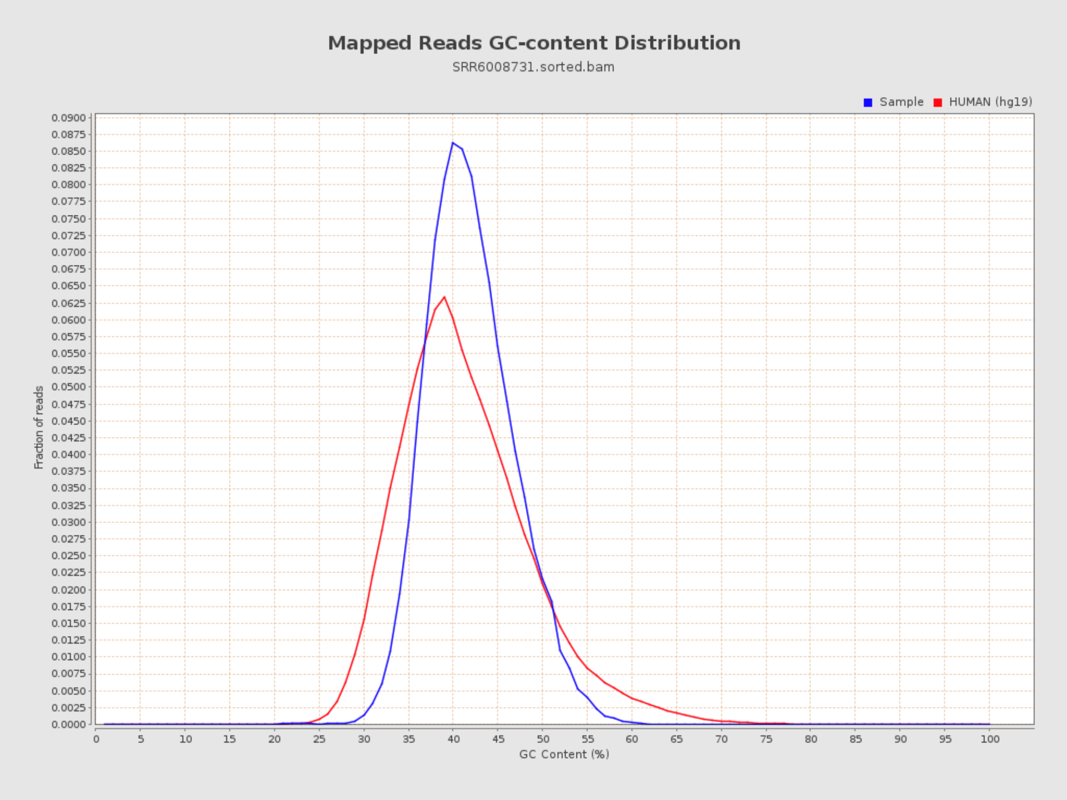
7. Results : Duplication Rate Histogram



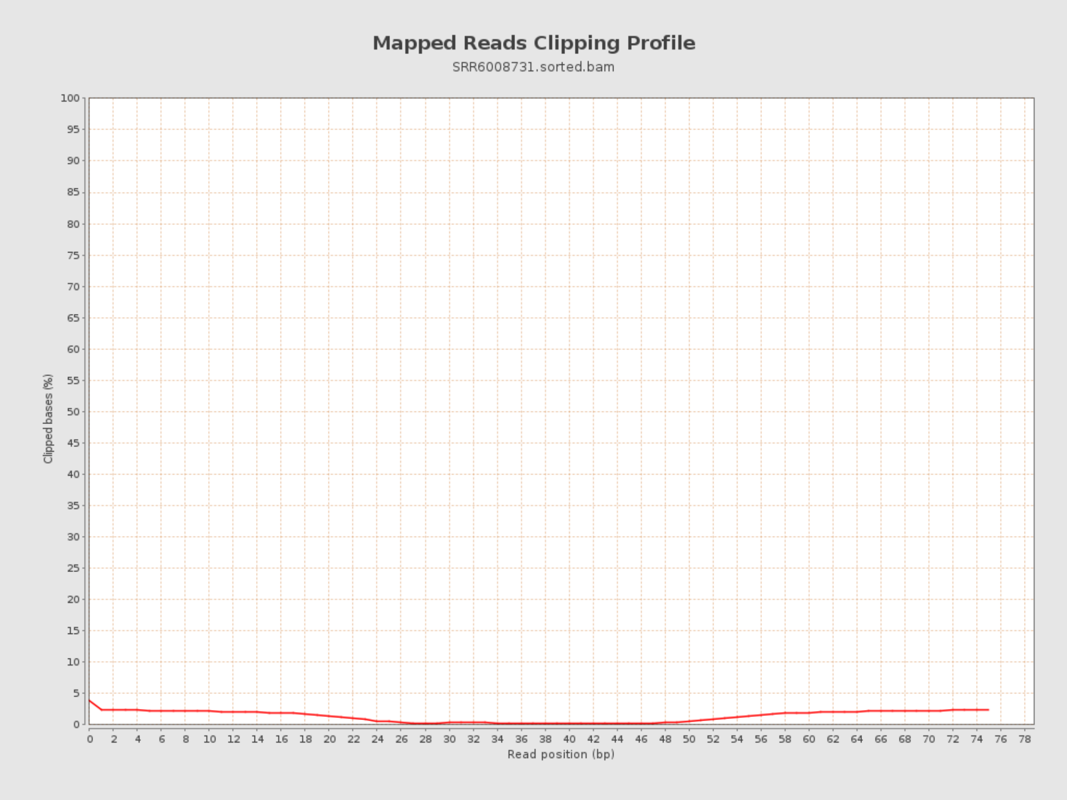
8. Results : Mapped Reads Nucleotide Content



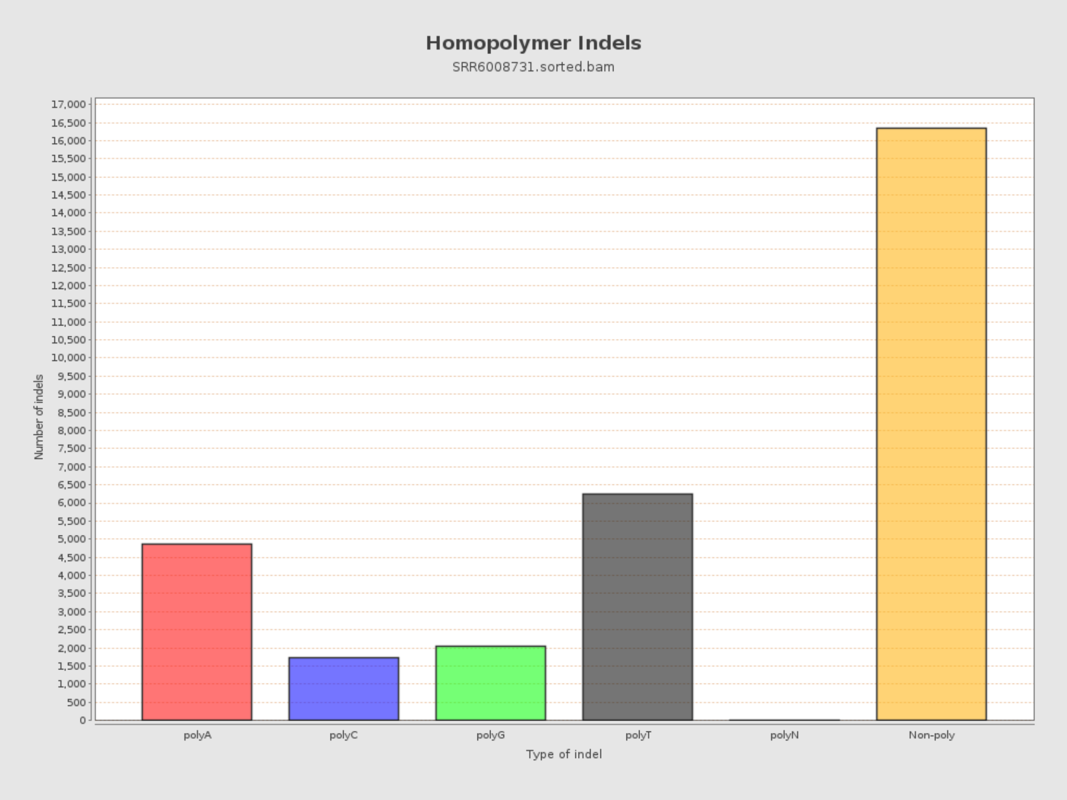
9. Results : Mapped Reads GC-content Distribution



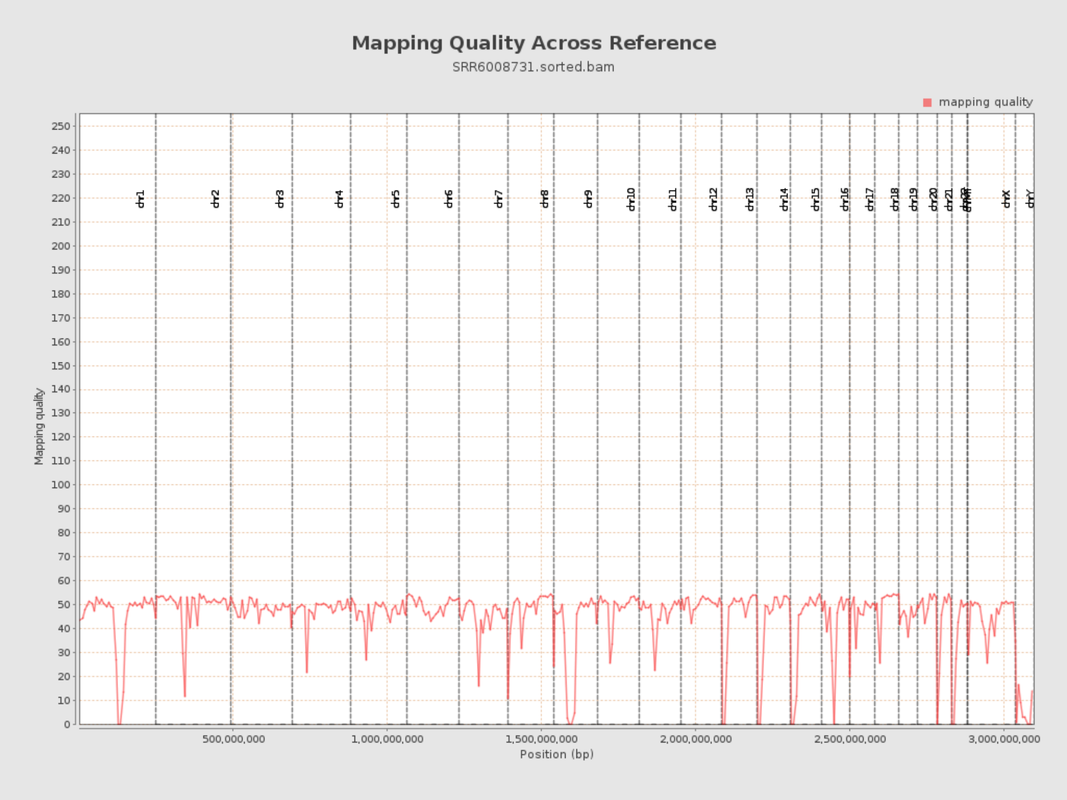
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram