Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:42:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008680.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_SRR6008680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008680.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:42:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,606,339
Mapped reads	1,461,955 / 91.01%
Unmapped reads	144,384 / 8.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,448 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	51,980 / 3.24%
Duplication rate	2.67%
Clipped reads	683,829 / 42.57%

2.2. ACGT Content

Number/percentage of A's	27,107,910 / 28.19%
Number/percentage of C's	17,430,277 / 18.12%
Number/percentage of T's	30,357,895 / 31.56%
Number/percentage of G's	21,263,112 / 22.11%
Number/percentage of N's	16,958 / 0.02%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.2963

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

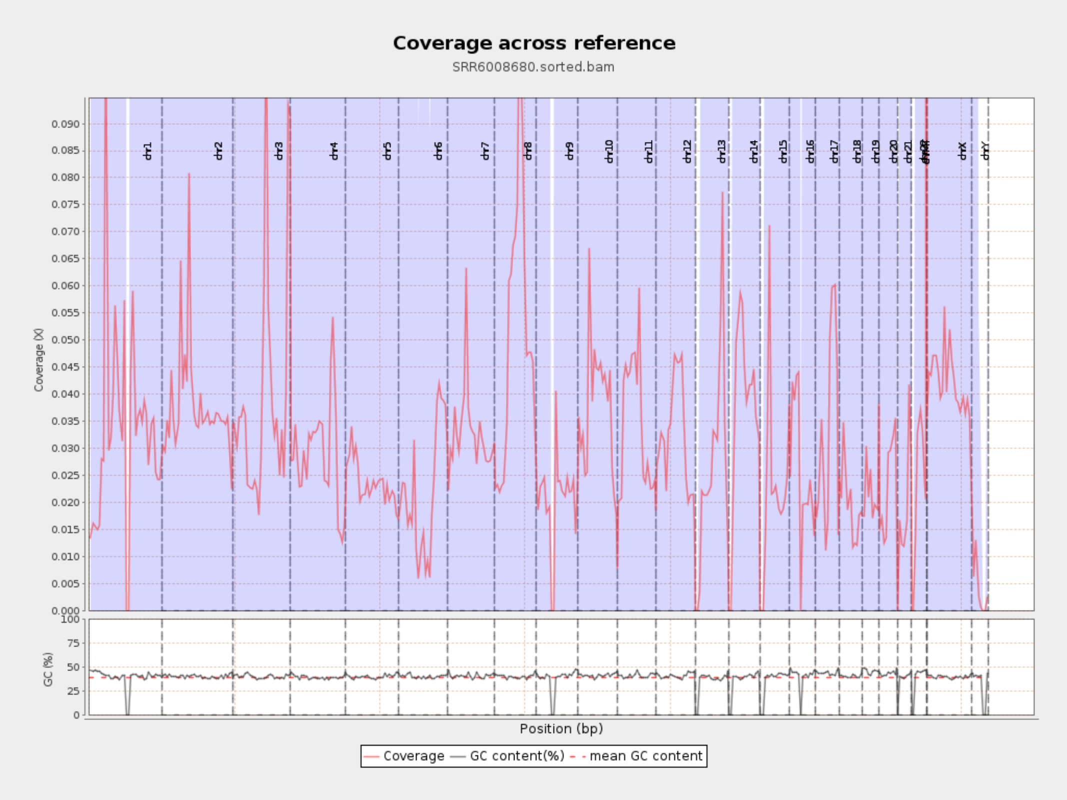
General error rate	0.71%
Mismatches	672,172
Insertions	8,197
Mapped reads with at least one insertion	0.56%
Deletions	25,657
Mapped reads with at least one deletion	1.74%
Homopolymer indels	48.52%

2.6. Chromosome stats

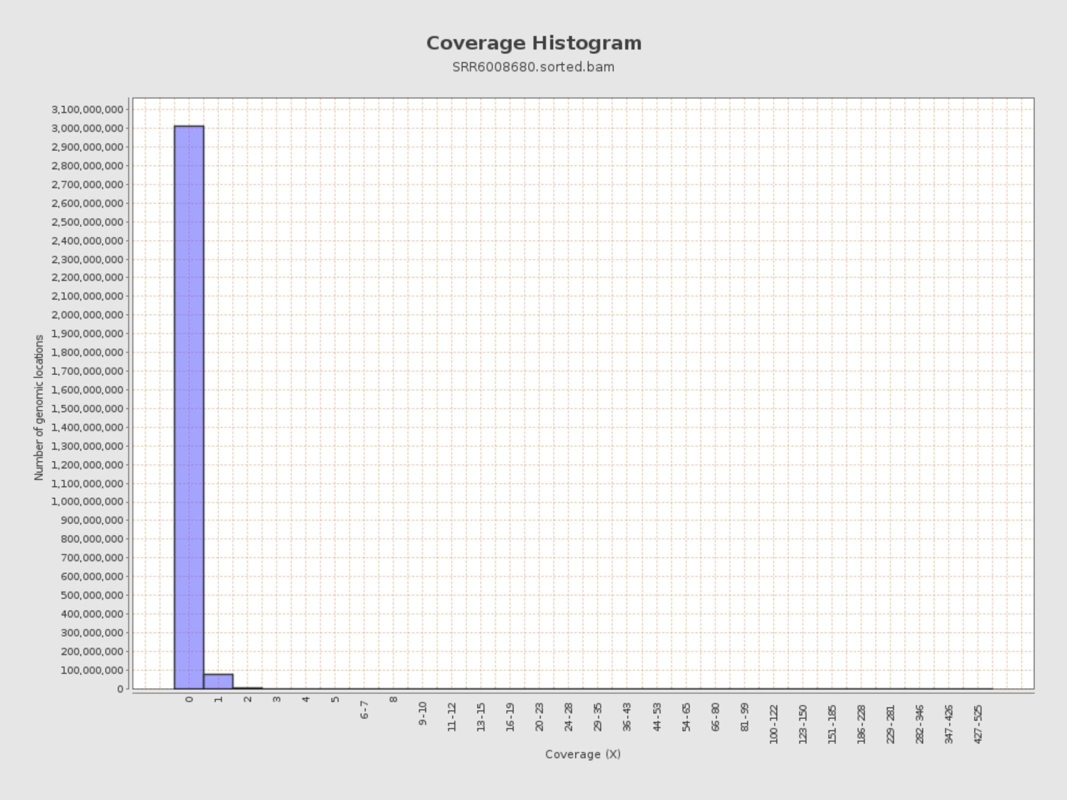
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8279487	0.0332	0.4565
chr2	243199373	9269732	0.0381	0.3511
chr3	198022430	7768124	0.0392	0.2178
chr4	191154276	5481899	0.0287	0.1902
chr5	180915260	4304397	0.0238	0.1672
chr6	171115067	3689052	0.0216	0.1802
chr7	159138663	5268906	0.0331	0.4302

chr8	146364022	7486997	0.0512	0.4098
chr9	141213431	2876056	0.0204	0.2777
chr10	135534747	5117717	0.0378	0.336
chr11	135006516	4623624	0.0342	0.315
chr12	133851895	4365413	0.0326	0.198
chr13	115169878	3097062	0.0269	0.1768
chr14	107349540	4056033	0.0378	0.216
chr15	102531392	2309087	0.0225	0.1629
chr16	90354753	2338912	0.0259	0.2121
chr17	81195210	2685140	0.0331	0.2499
chr18	78077248	1545674	0.0198	0.5333
chr19	59128983	1294014	0.0219	0.3045
chr20	63025520	1455592	0.0231	0.1684
chr21	48129895	906588	0.0188	0.1601
chr22	51304566	1115074	0.0217	0.158
chrMT	16571	86033	5.1918	3.7268
chrX	155270560	6529527	0.0421	0.251
chrY	59373566	268383	0.0045	0.1225

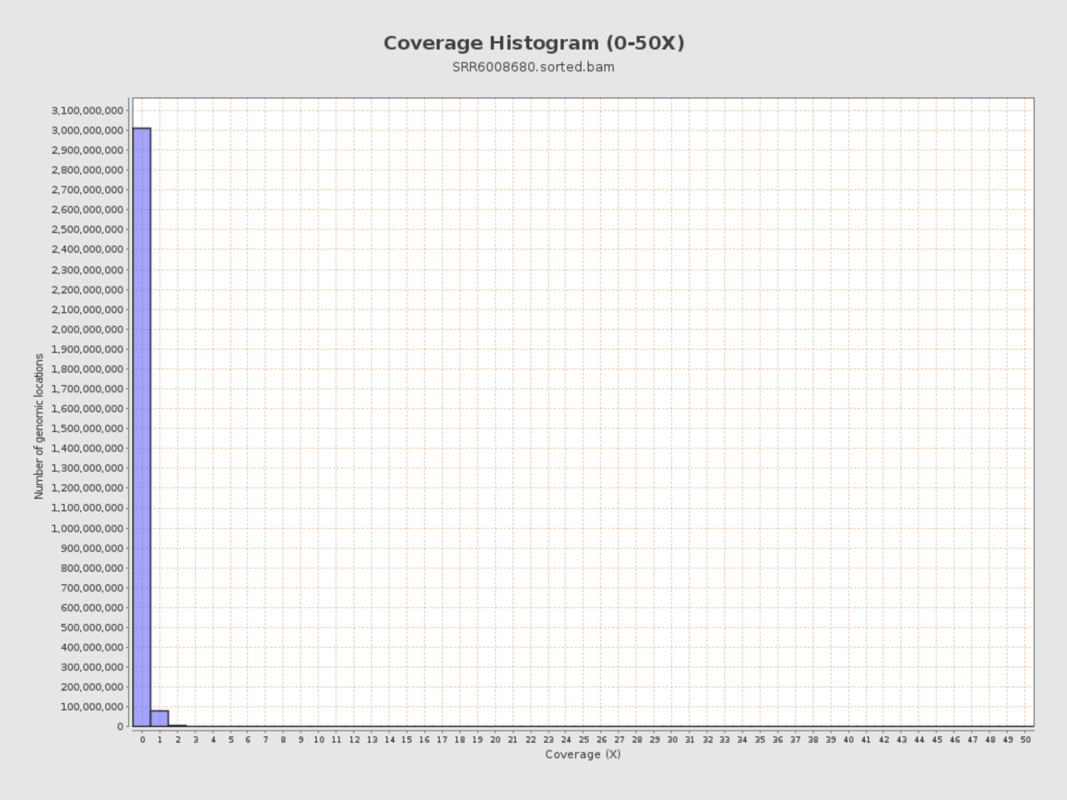
3. Results : Coverage across reference



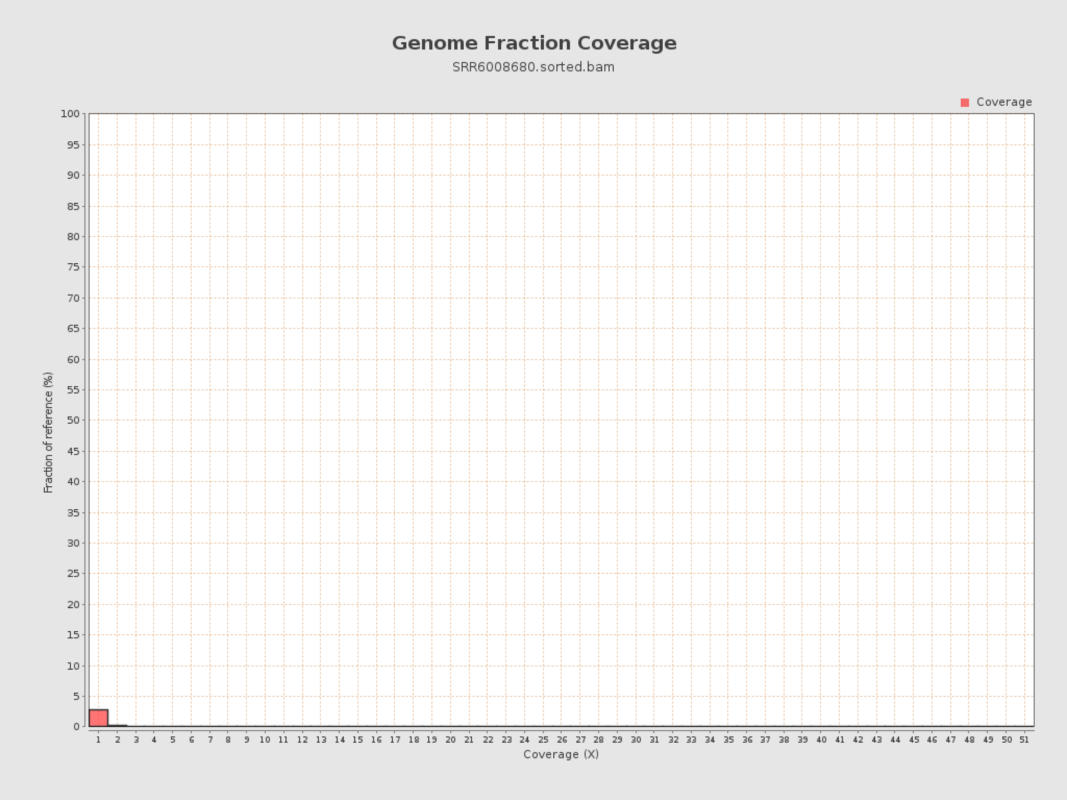
4. Results : Coverage Histogram



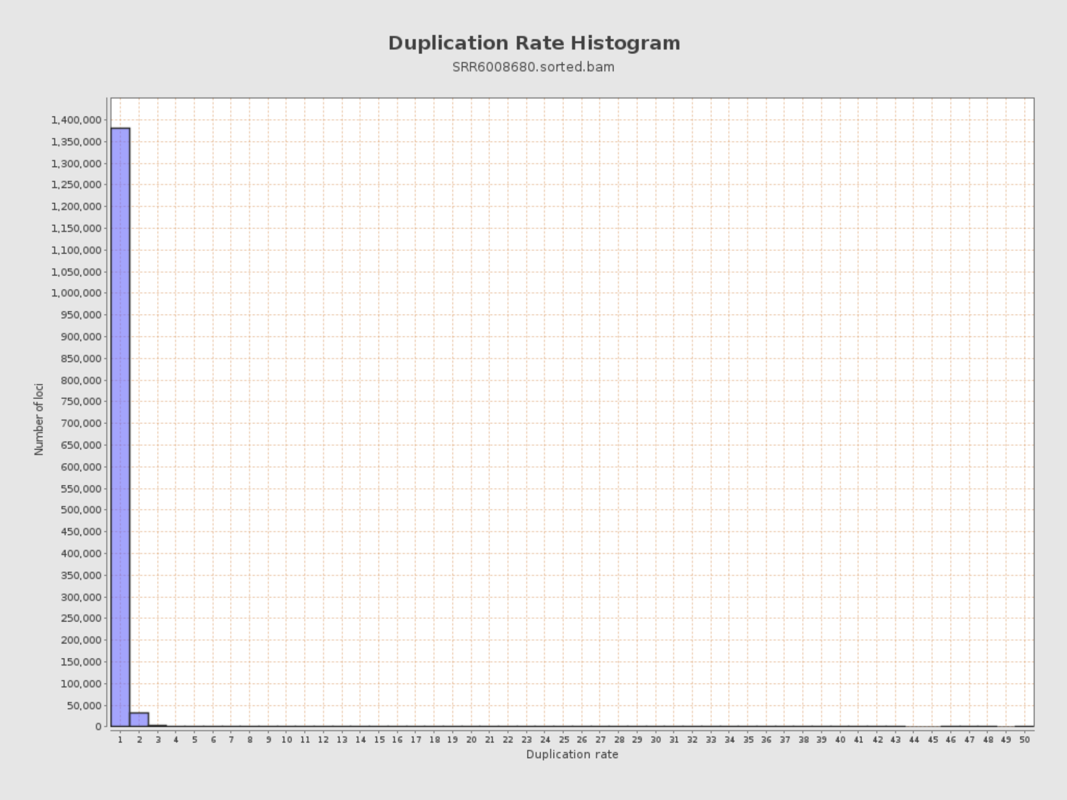
5. Results : Coverage Histogram (0-50X)



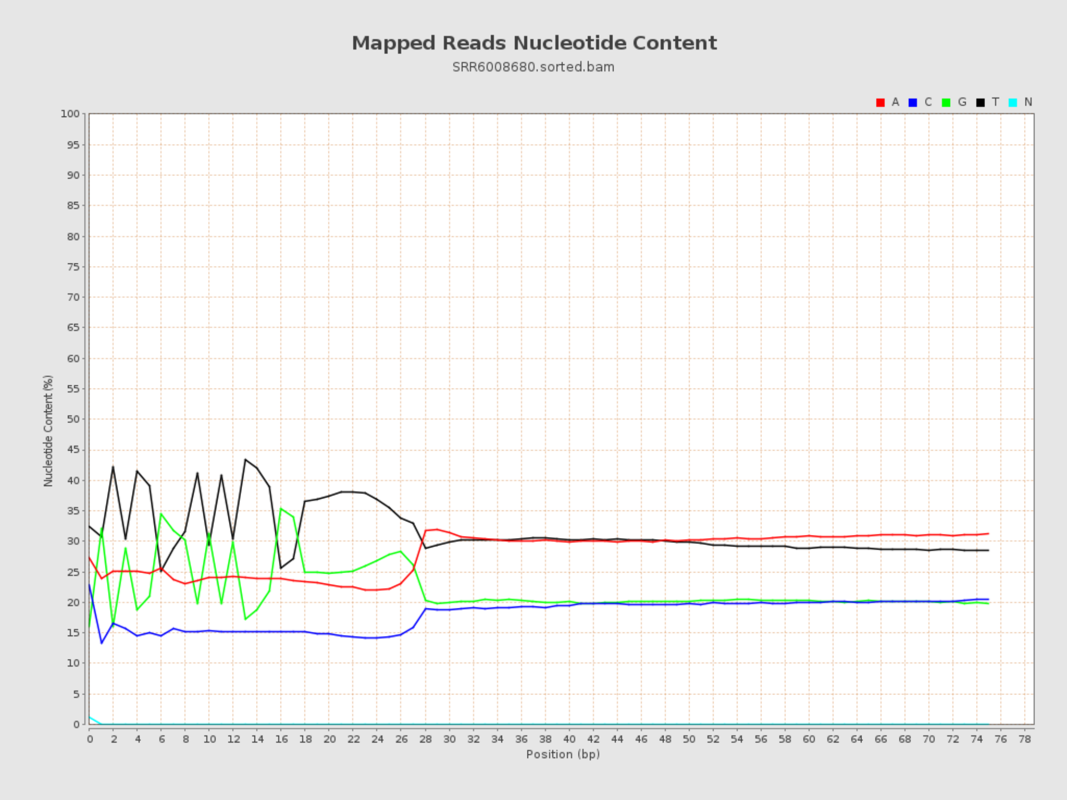
6. Results : Genome Fraction Coverage



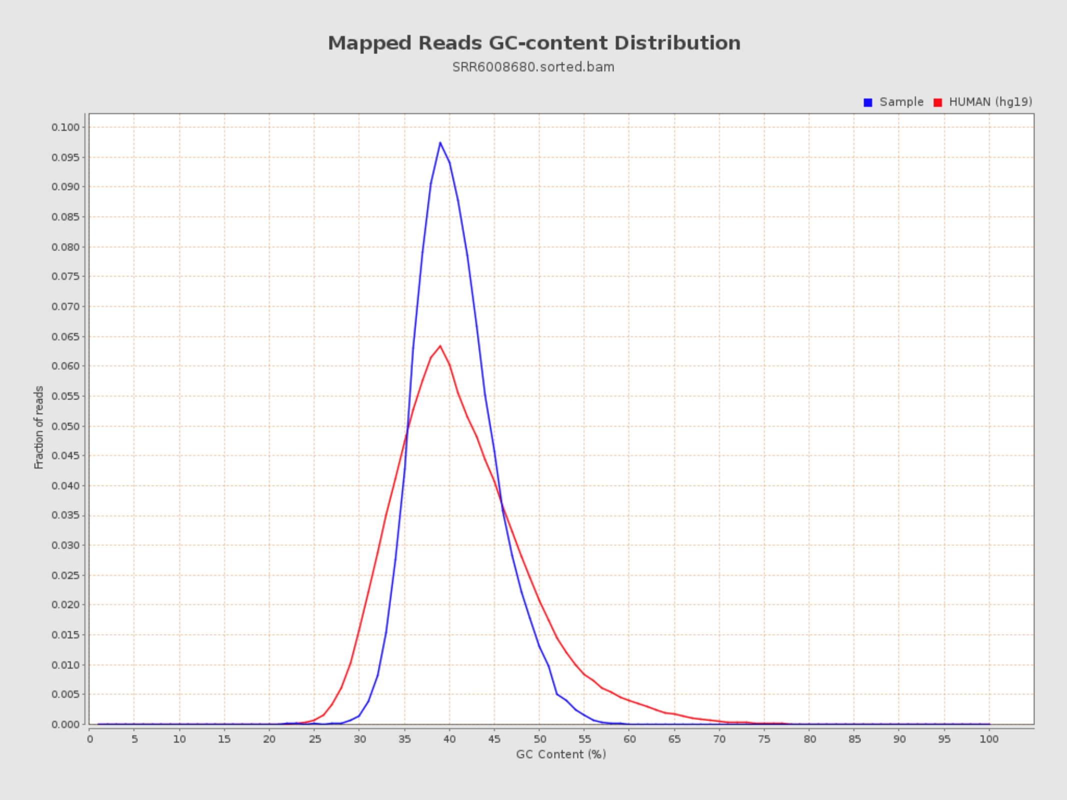
7. Results : Duplication Rate Histogram



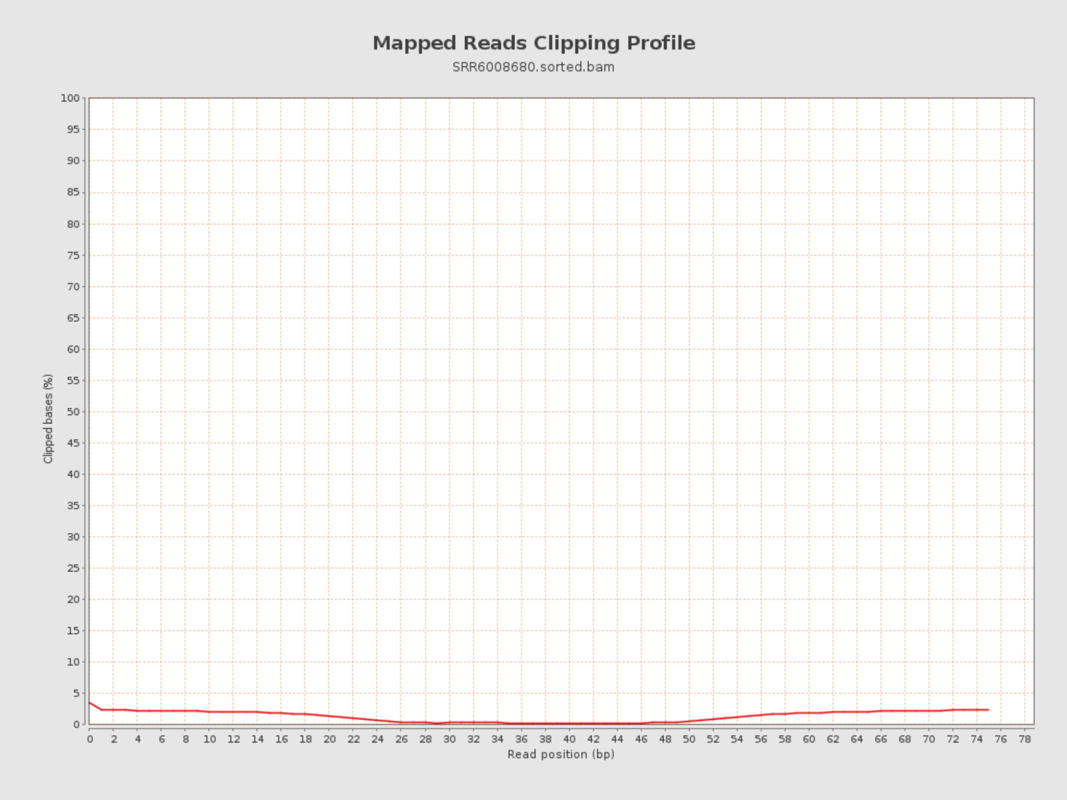
8. Results : Mapped Reads Nucleotide Content



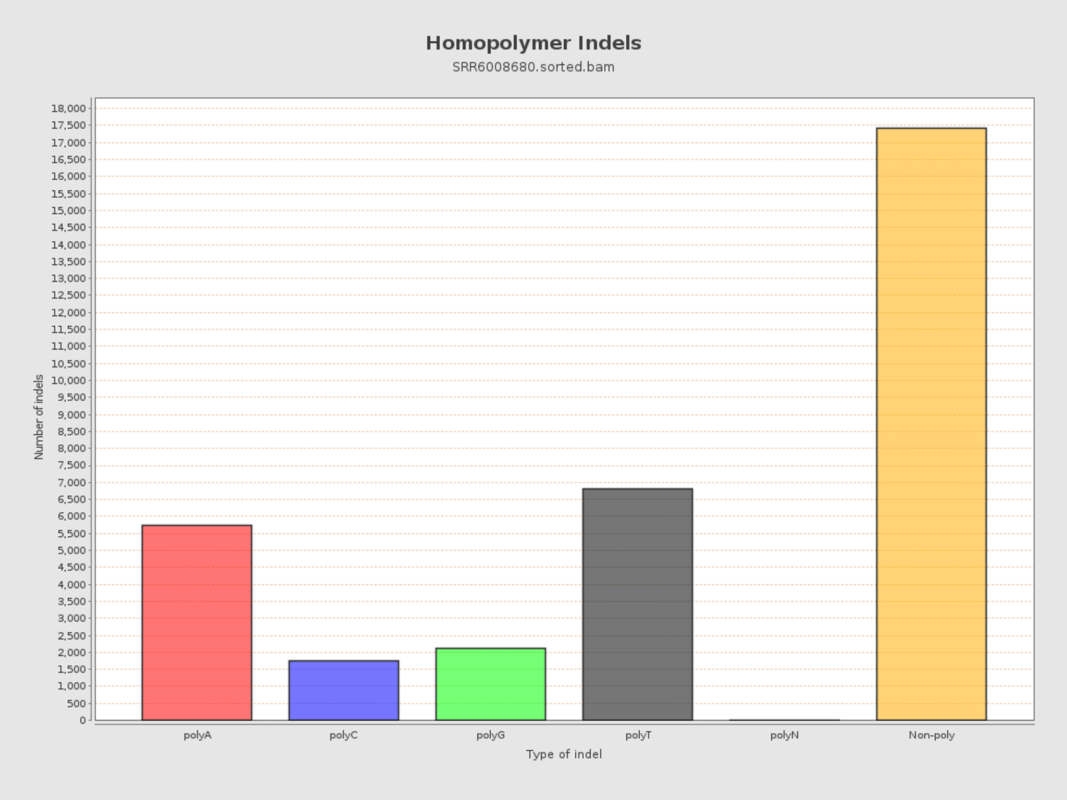
9. Results : Mapped Reads GC-content Distribution



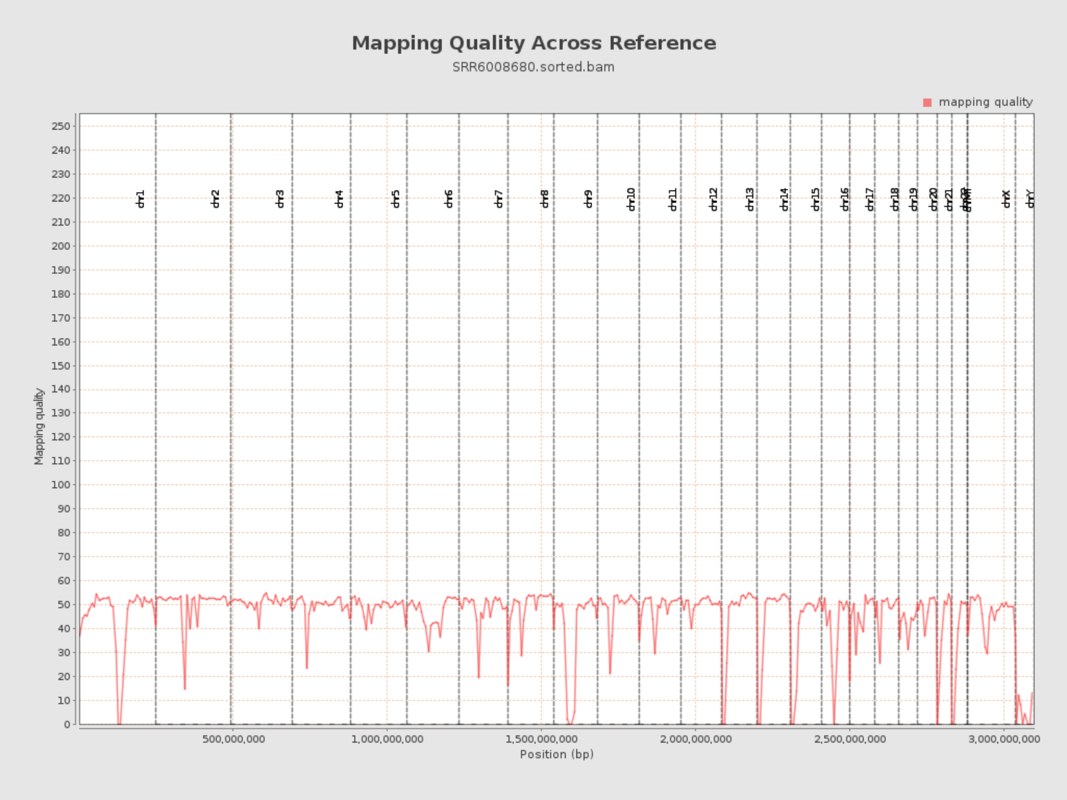
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram