Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:19:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008763.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_SRR6008763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:19:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,447,857
Mapped reads	1,294,529 / 89.41%
Unmapped reads	153,328 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,059 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	53,126 / 3.67%
Duplication rate	3.25%
Clipped reads	577,539 / 39.89%

2.2. ACGT Content

Number/percentage of A's	22,898,923 / 26.69%
Number/percentage of C's	16,507,968 / 19.24%
Number/percentage of T's	26,579,430 / 30.98%
Number/percentage of G's	19,698,760 / 22.96%
Number/percentage of N's	110,429 / 0.13%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2767

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

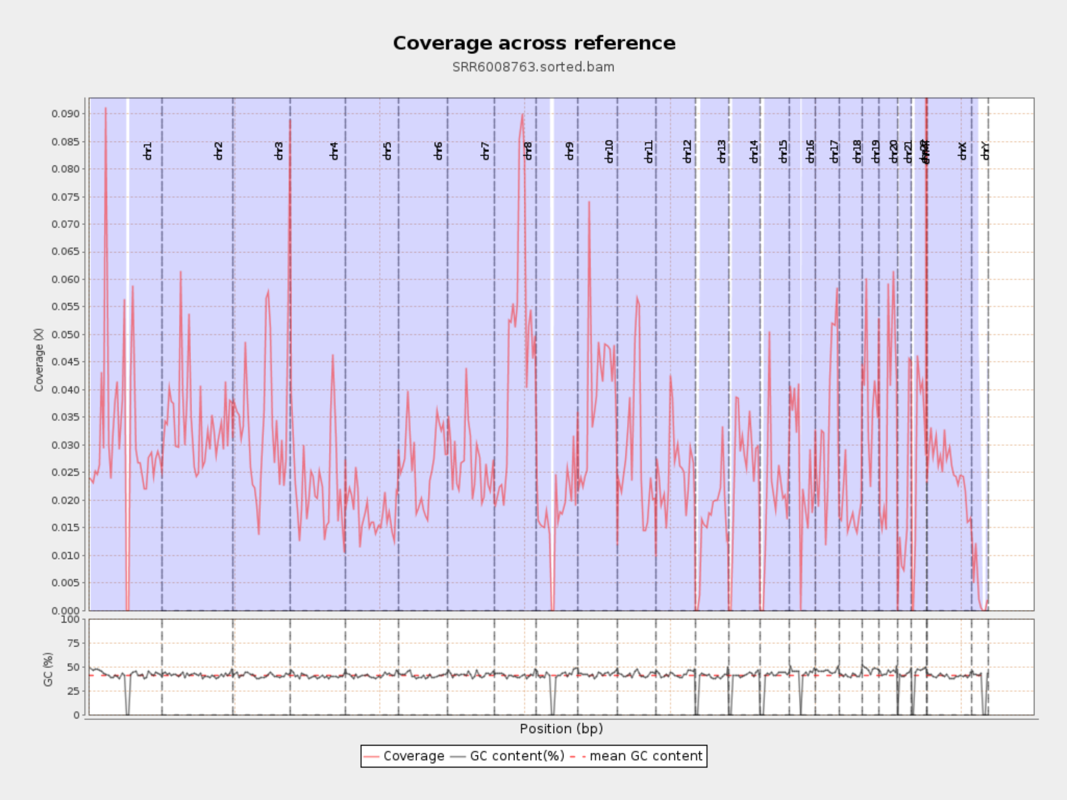
General error rate	0.85%
Mismatches	713,053
Insertions	6,196
Mapped reads with at least one insertion	0.47%
Deletions	24,760
Mapped reads with at least one deletion	1.89%
Homopolymer indels	44.99%

2.6. Chromosome stats

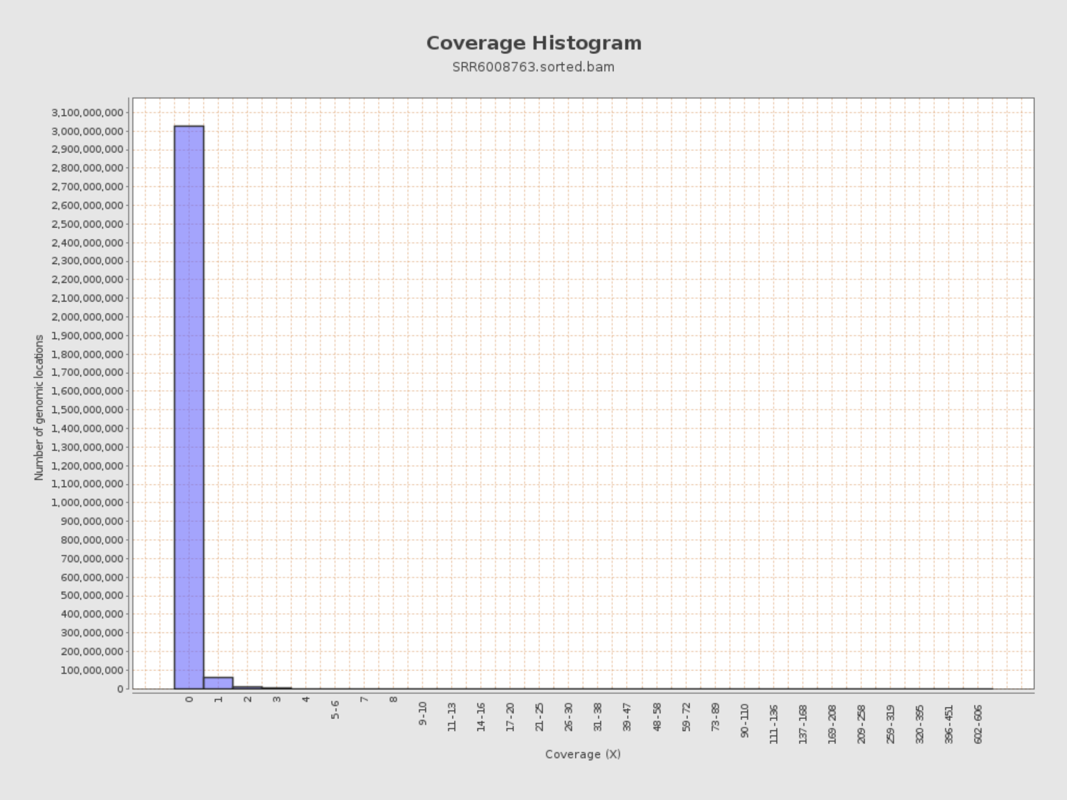
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7733731	0.031	0.4267
chr2	243199373	8347280	0.0343	0.3593
chr3	198022430	6765316	0.0342	0.2311
chr4	191154276	4344471	0.0227	0.1825
chr5	180915260	3207245	0.0177	0.154
chr6	171115067	4548233	0.0266	0.2044
chr7	159138663	4264582	0.0268	0.2805

chr8	146364022	6898758	0.0471	0.3536
chr9	141213431	2451145	0.0174	0.1915
chr10	135534747	5316011	0.0392	0.4181
chr11	135006516	3801112	0.0282	0.2265
chr12	133851895	3439106	0.0257	0.1843
chr13	115169878	1841803	0.016	0.1477
chr14	107349540	2763491	0.0257	0.1882
chr15	102531392	2082986	0.0203	0.1633
chr16	90354753	2322870	0.0257	0.2369
chr17	81195210	2801189	0.0345	0.2402
chr18	78077248	1415409	0.0181	0.2821
chr19	59128983	2306260	0.039	0.3191
chr20	63025520	2223954	0.0353	0.219
chr21	48129895	909359	0.0189	0.1648
chr22	51304566	1397538	0.0272	0.1918
chrMT	16571	457081	27.5832	15.2779
chrX	155270560	3974264	0.0256	0.1945
chrY	59373566	226172	0.0038	0.1268

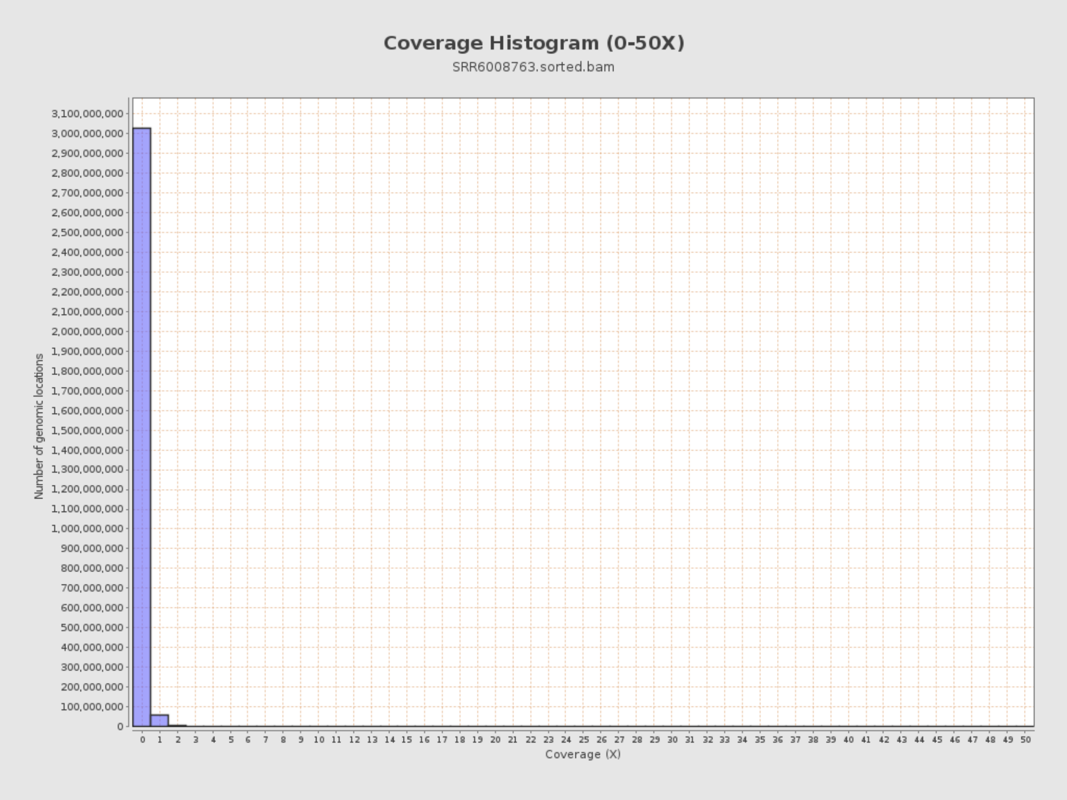
3. Results : Coverage across reference



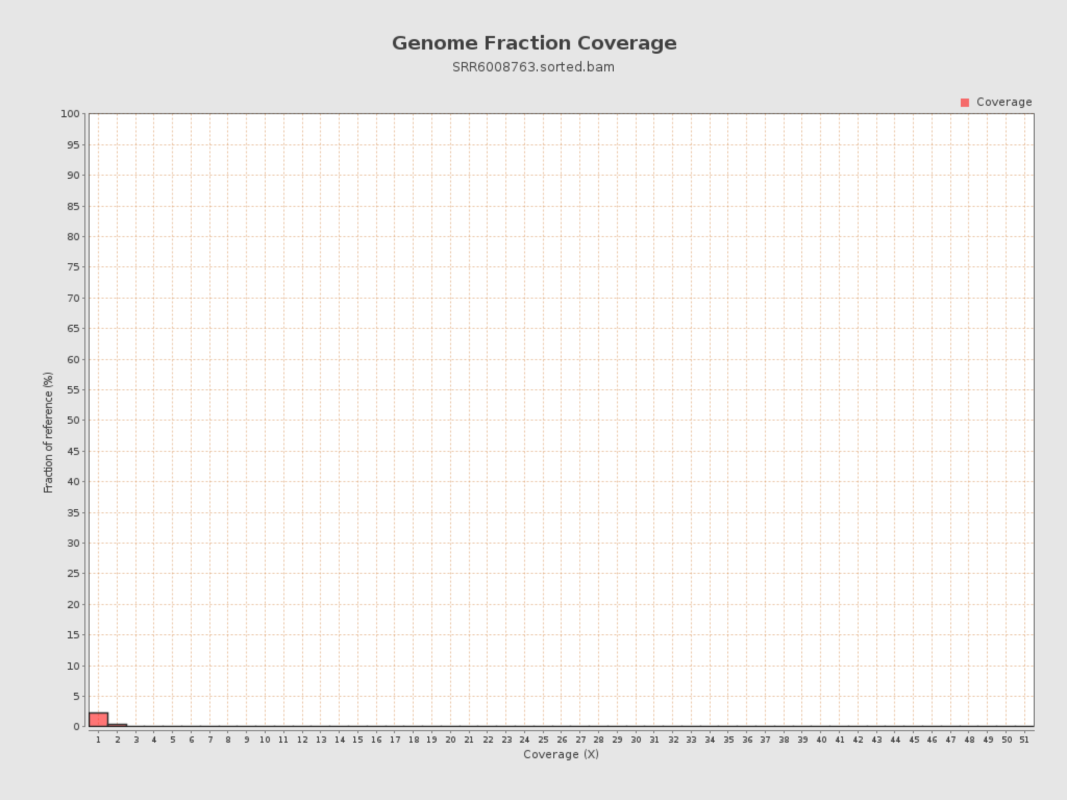
4. Results : Coverage Histogram



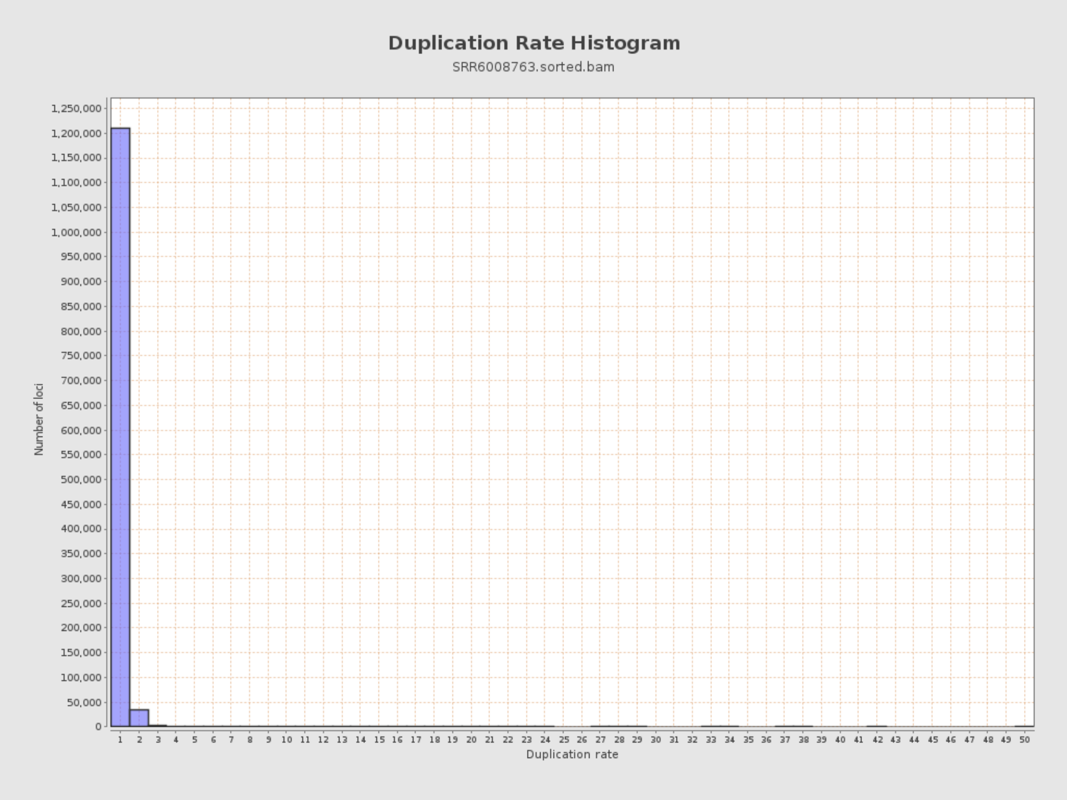
5. Results : Coverage Histogram (0-50X)



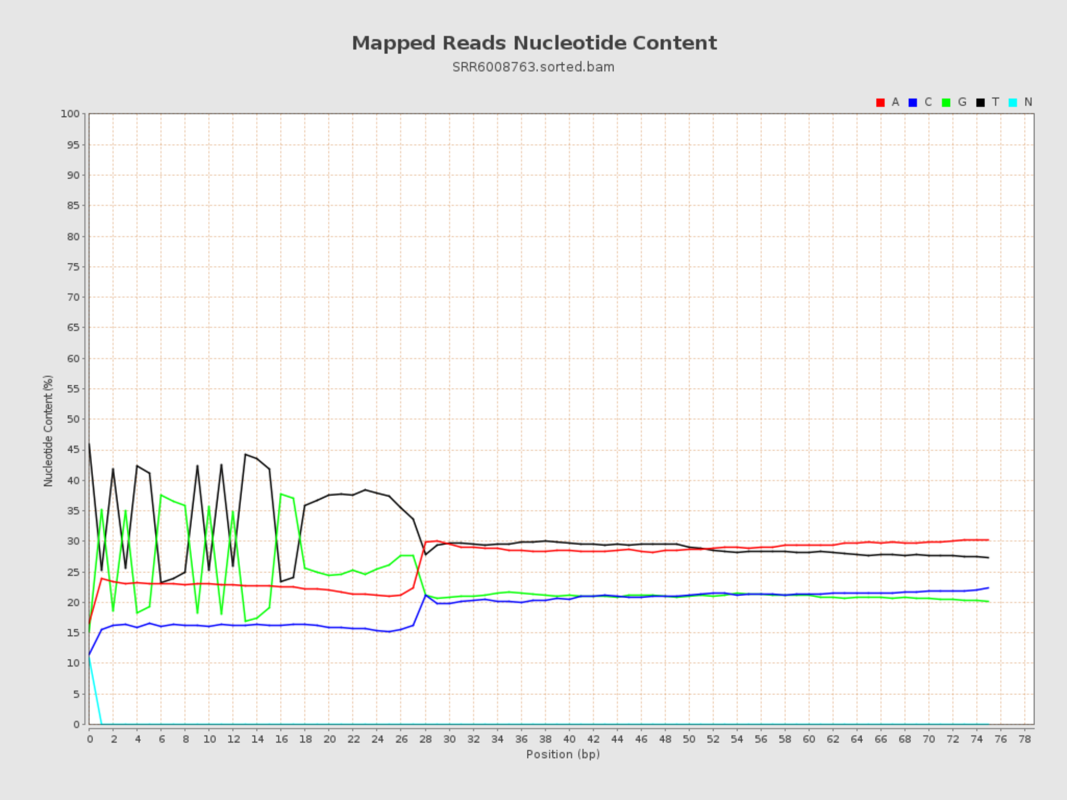
6. Results : Genome Fraction Coverage



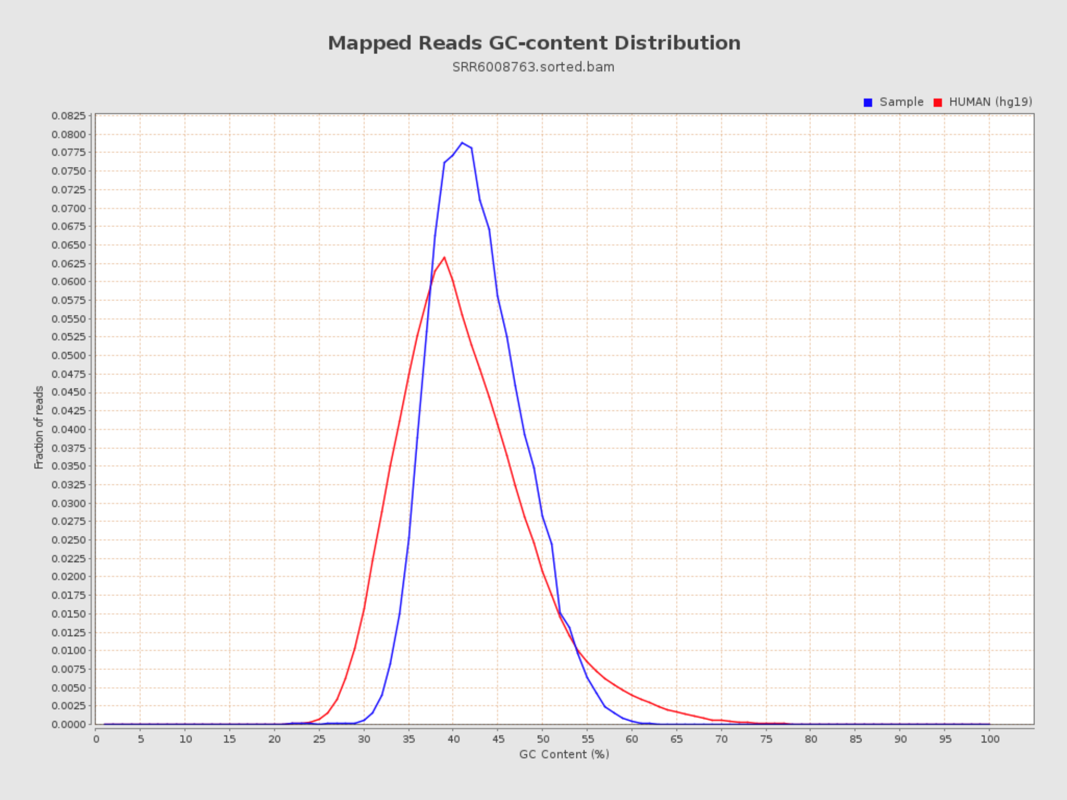
7. Results : Duplication Rate Histogram



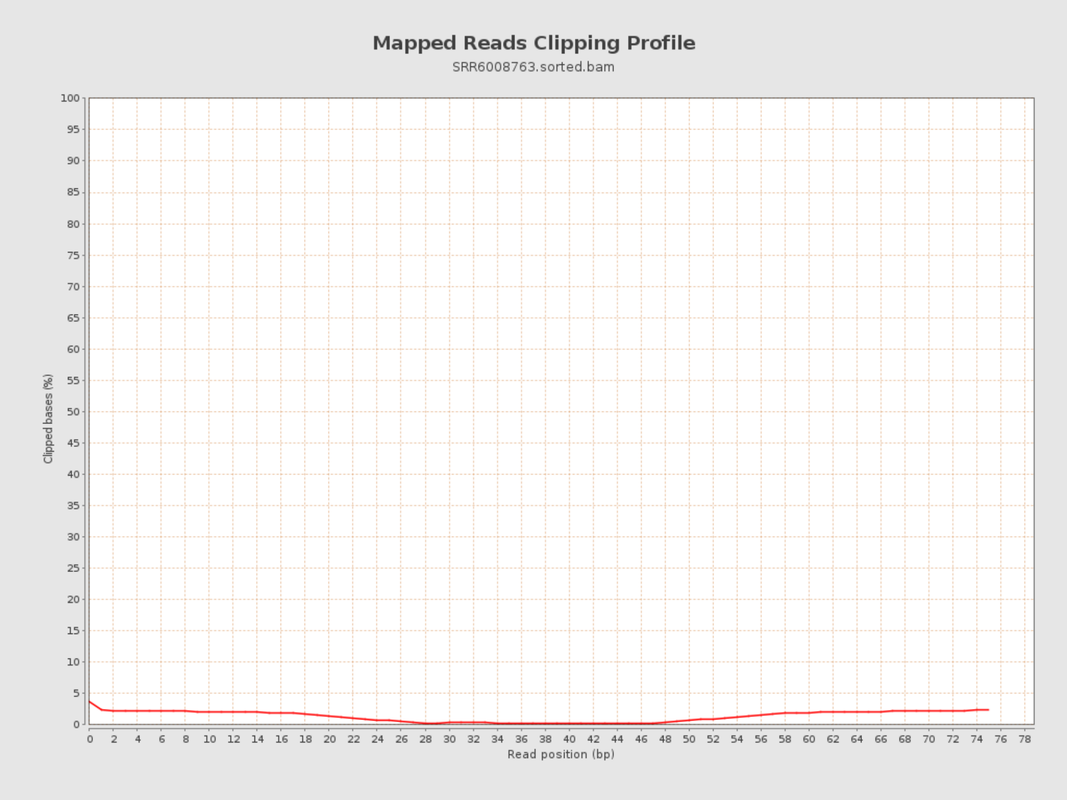
8. Results : Mapped Reads Nucleotide Content



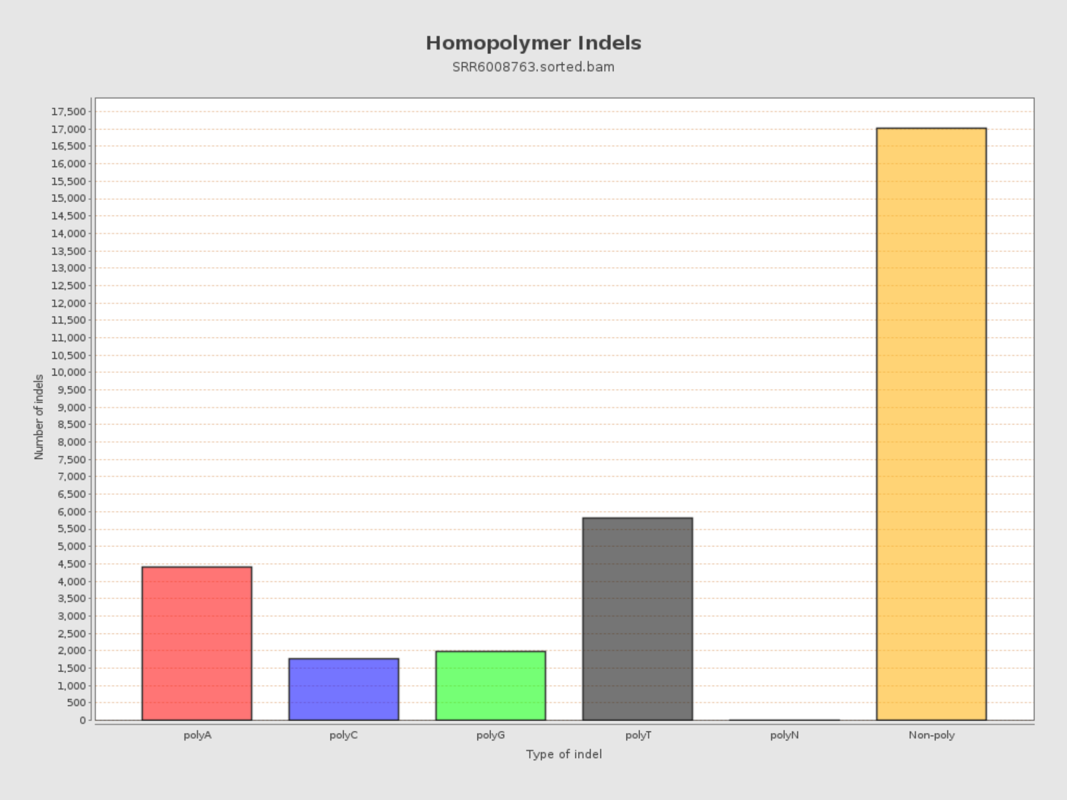
9. Results : Mapped Reads GC-content Distribution



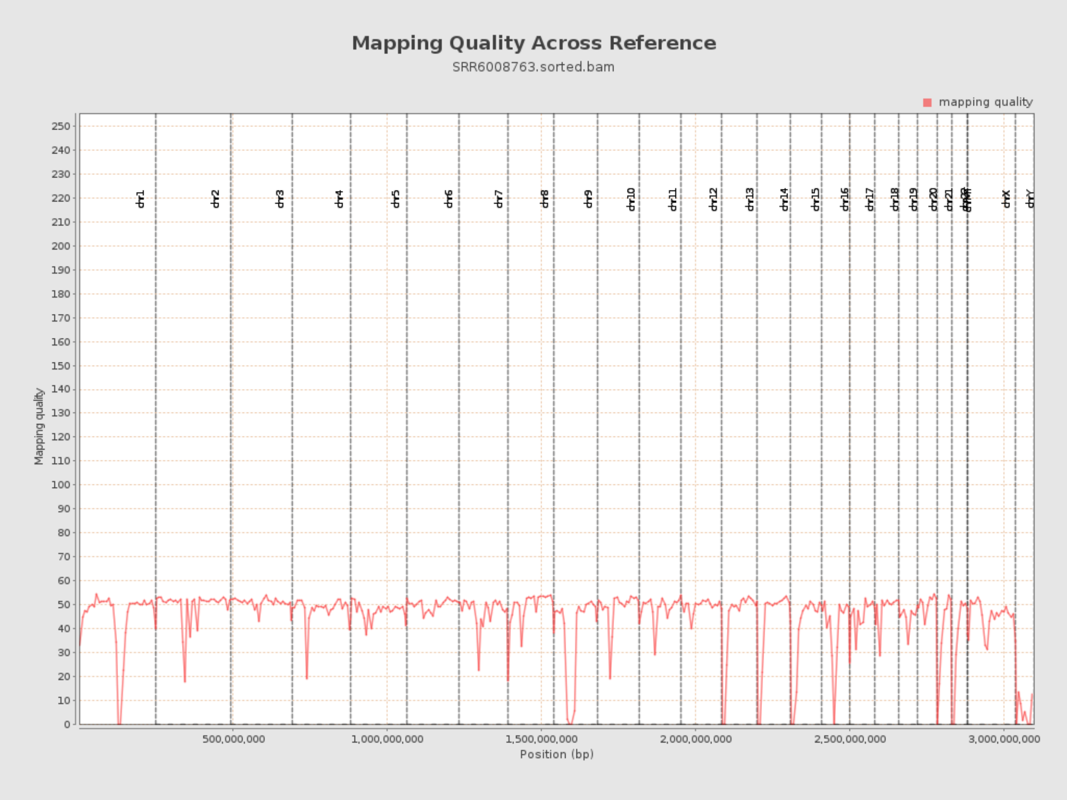
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram