Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:04:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008733.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_SRR6008733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008733.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:04:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,172,230
Mapped reads	1,824,981 / 84.01%
Unmapped reads	347,249 / 15.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,748 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	189,902 / 8.74%
Duplication rate	7.93%
Clipped reads	724,552 / 33.36%

2.2. ACGT Content

Number/percentage of A's	34,740,411 / 28.1%
Number/percentage of C's	23,210,631 / 18.78%
Number/percentage of T's	38,992,388 / 31.54%
Number/percentage of G's	26,604,638 / 21.52%
Number/percentage of N's	75,648 / 0.06%
GC Percentage	40.3%

2.3. Coverage

Mean	0.04

Standard Deviation	0.4451

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

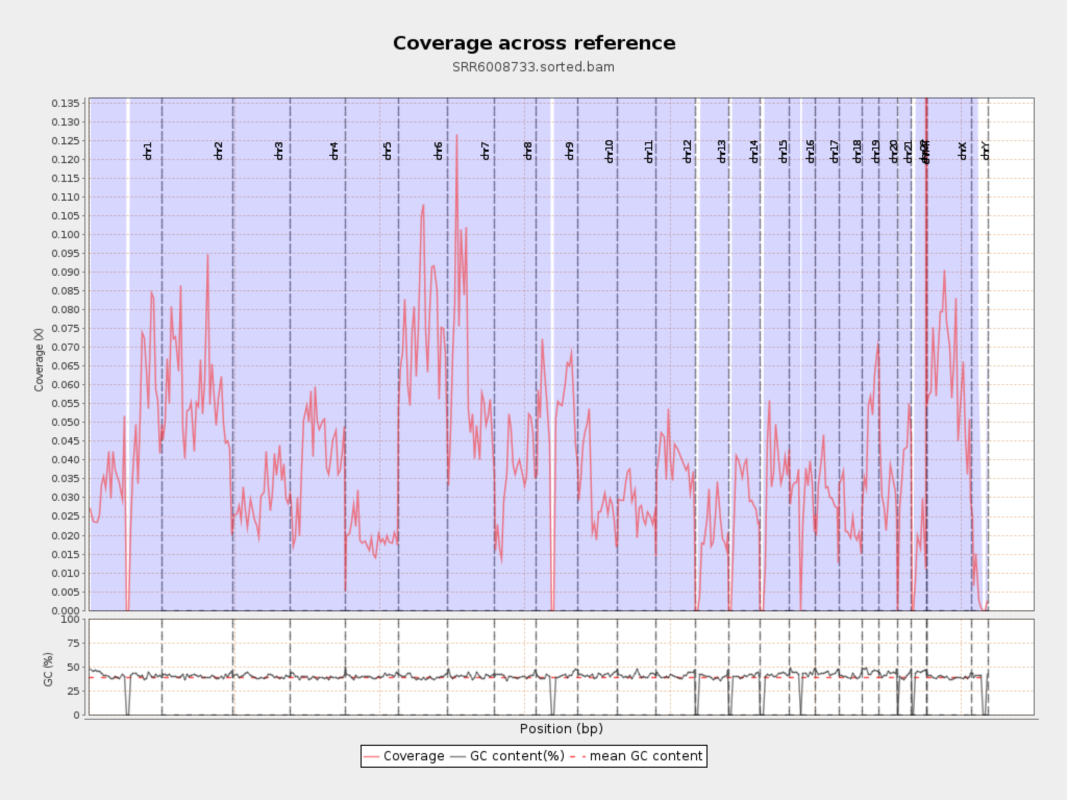
General error rate	0.83%
Mismatches	1,008,044
Insertions	9,753
Mapped reads with at least one insertion	0.53%
Deletions	36,748
Mapped reads with at least one deletion	1.99%
Homopolymer indels	49.11%

2.6. Chromosome stats

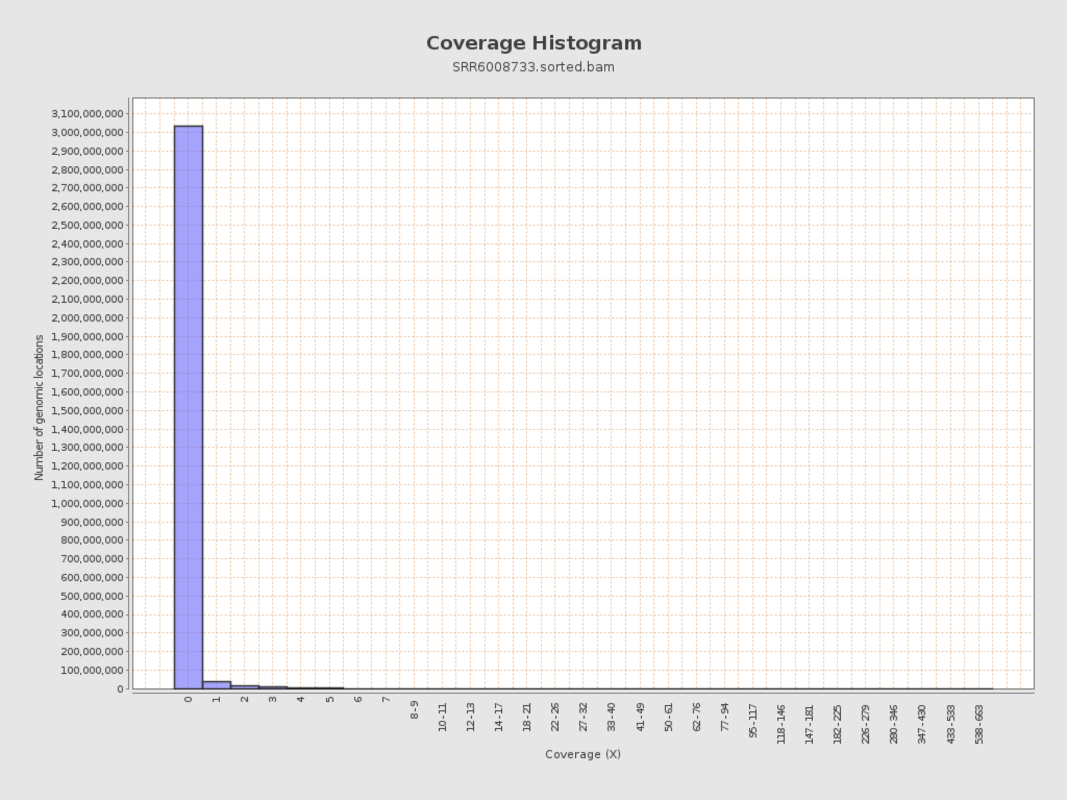
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10218272	0.041	0.649
chr2	243199373	13945535	0.0573	0.4718
chr3	198022430	5966537	0.0301	0.2882
chr4	191154276	7975955	0.0417	0.3612
chr5	180915260	3560617	0.0197	0.2299
chr6	171115067	12792161	0.0748	0.4982
chr7	159138663	10058255	0.0632	0.9285

chr8	146364022	5244308	0.0358	0.4597
chr9	141213431	7230098	0.0512	0.4235
chr10	135534747	4256665	0.0314	0.3772
chr11	135006516	3770293	0.0279	0.34
chr12	133851895	5361824	0.0401	0.3407
chr13	115169878	2115999	0.0184	0.2247
chr14	107349540	3003103	0.028	0.289
chr15	102531392	3363078	0.0328	0.3055
chr16	90354753	2677453	0.0296	0.2924
chr17	81195210	2532833	0.0312	0.3313
chr18	78077248	1872834	0.024	0.4764
chr19	59128983	3044629	0.0515	0.4514
chr20	63025520	1984789	0.0315	0.3017
chr21	48129895	1800730	0.0374	0.3358
chr22	51304566	727494	0.0142	0.1892
chrMT	16571	34429	2.0777	2.7537
chrX	155270560	9808179	0.0632	0.443
chrY	59373566	339908	0.0057	0.164

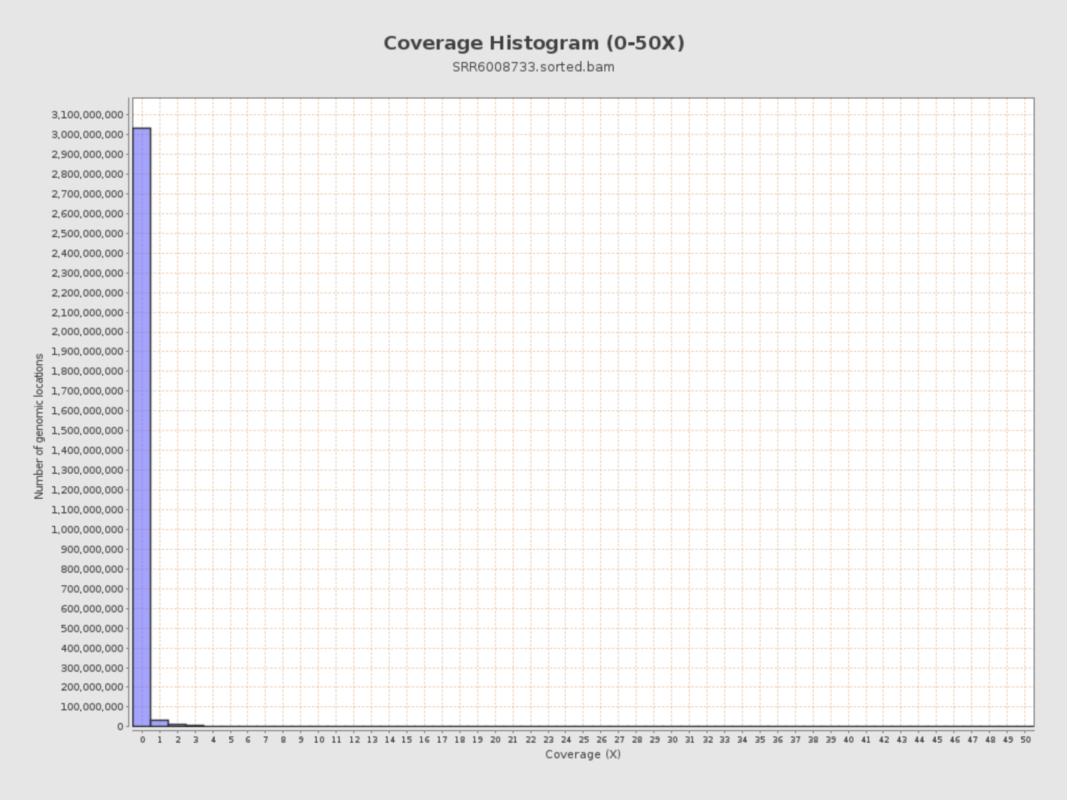
3. Results : Coverage across reference



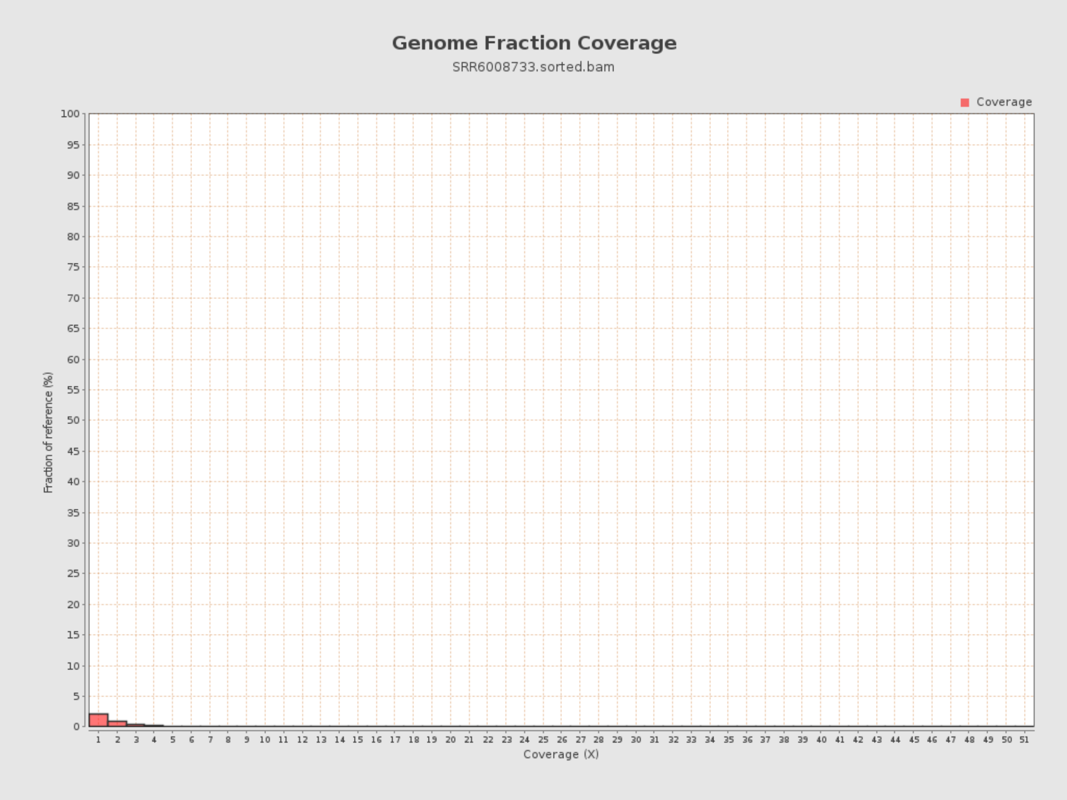
4. Results : Coverage Histogram



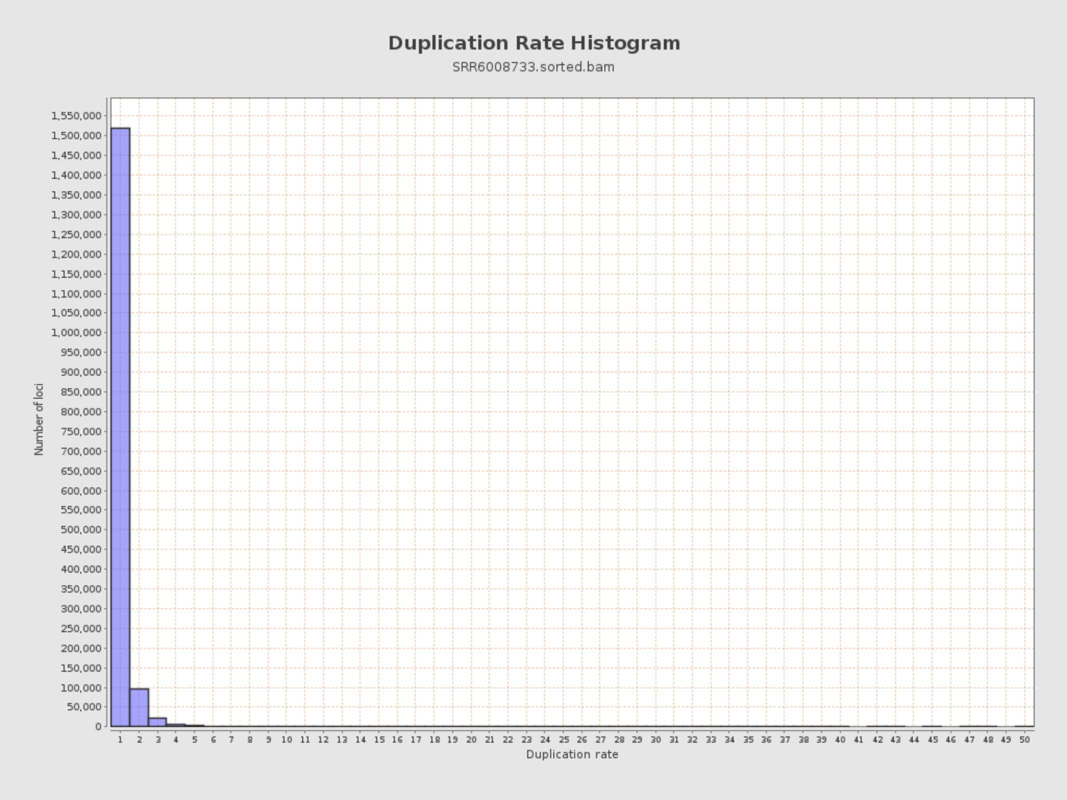
5. Results : Coverage Histogram (0-50X)



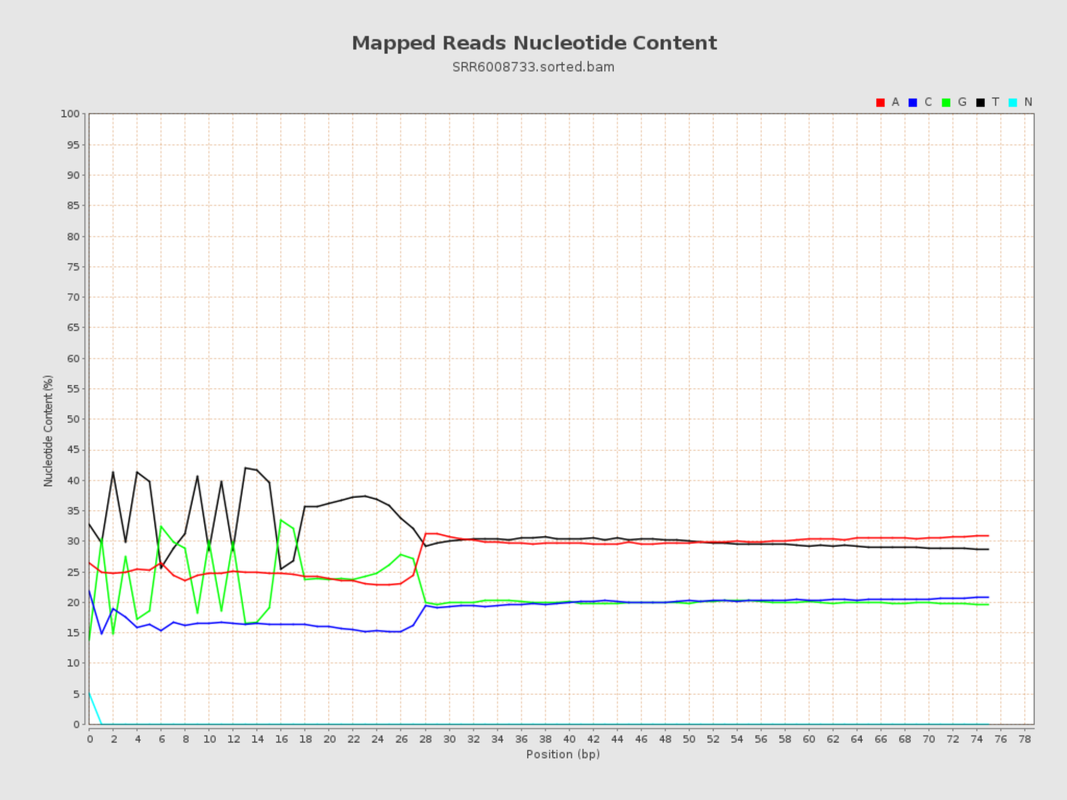
6. Results : Genome Fraction Coverage



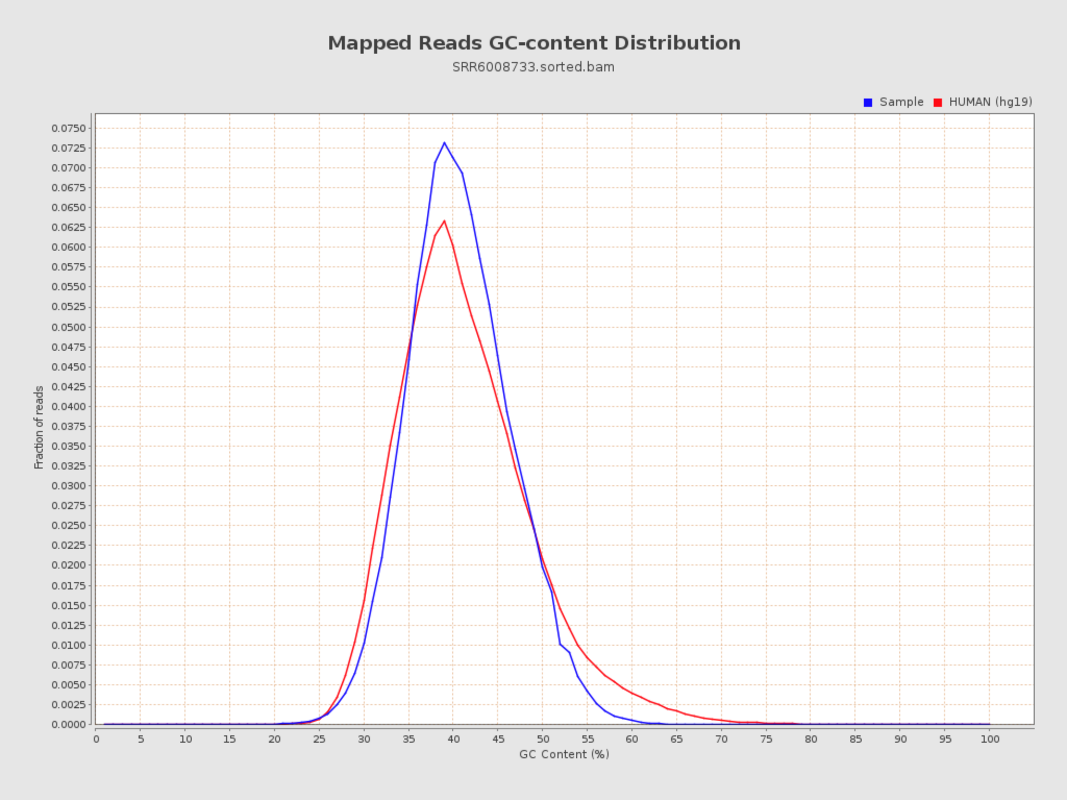
7. Results : Duplication Rate Histogram



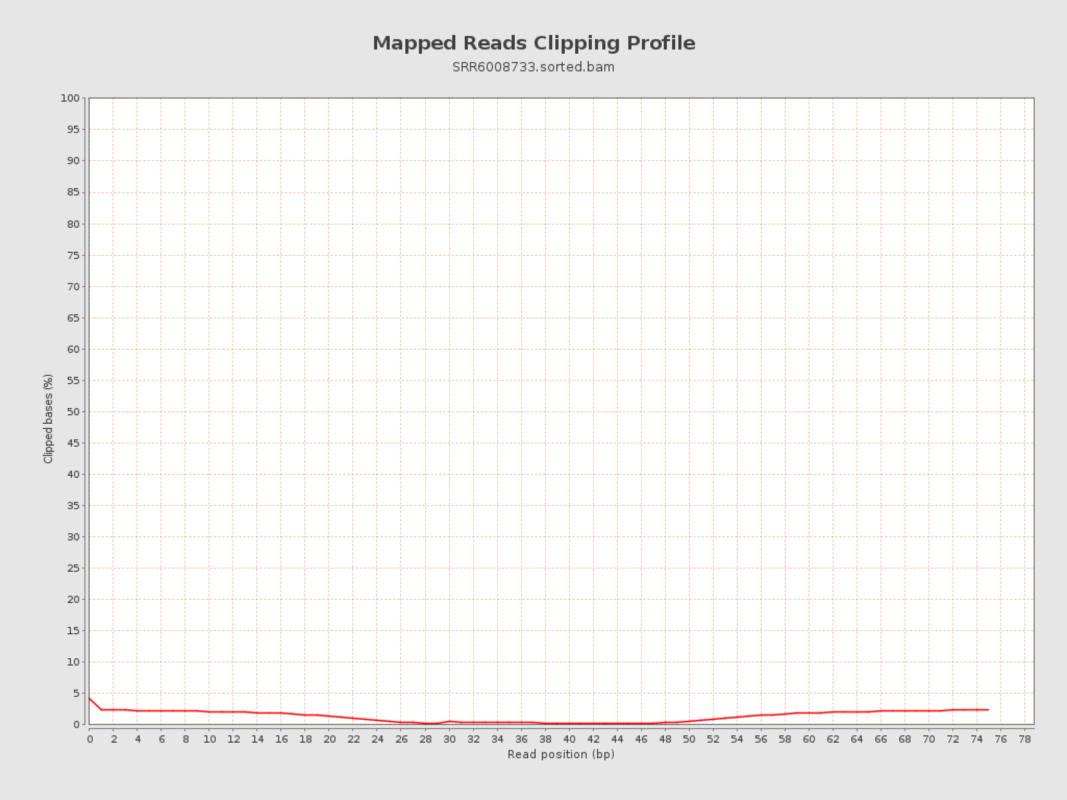
8. Results : Mapped Reads Nucleotide Content



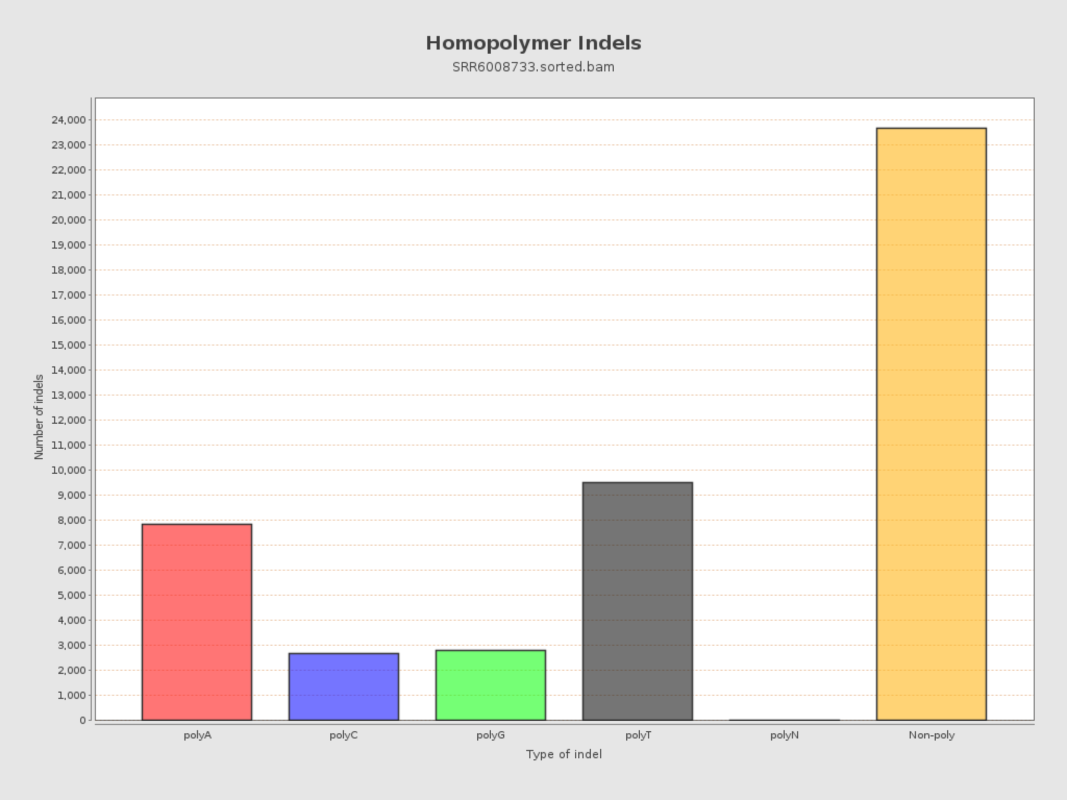
9. Results : Mapped Reads GC-content Distribution



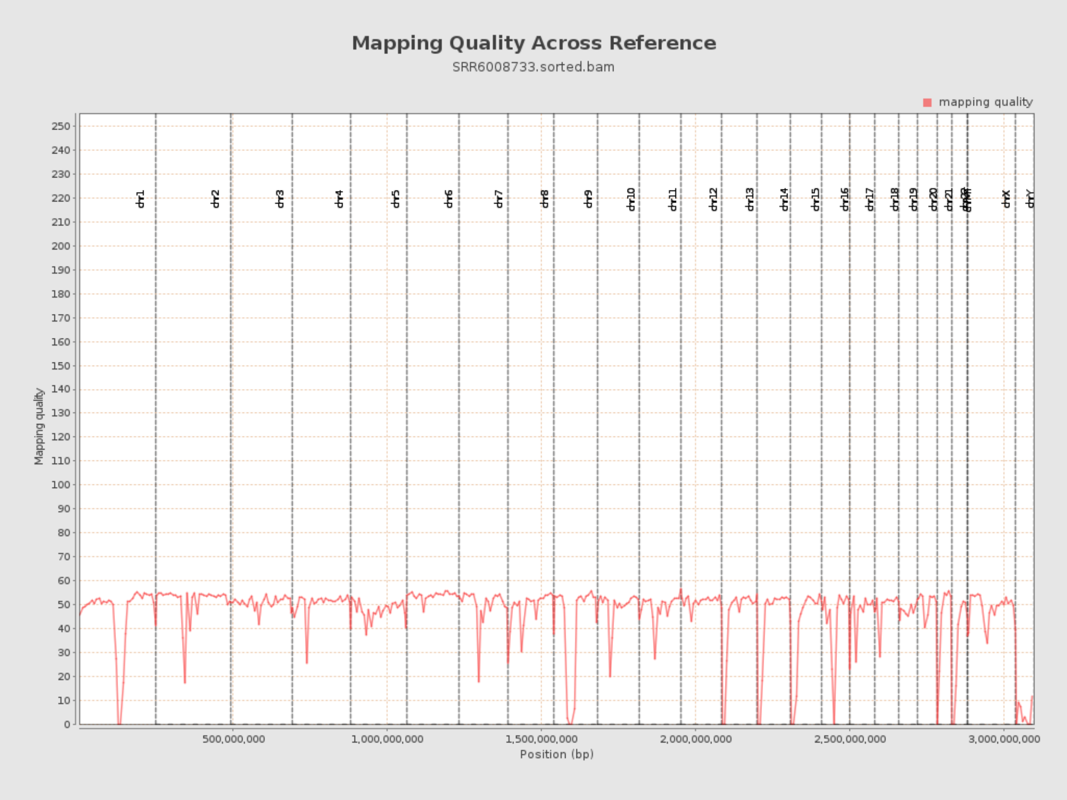
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram