Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:13:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008737.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_SRR6008737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008737.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:13:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,526,733
Mapped reads	1,103,422 / 72.27%
Unmapped reads	423,311 / 27.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,375 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	38,773 / 2.54%
Duplication rate	2.62%
Clipped reads	584,153 / 38.26%

2.2. ACGT Content

Number/percentage of A's	20,068,403 / 28.19%
Number/percentage of C's	12,119,774 / 17.02%
Number/percentage of T's	21,931,564 / 30.8%
Number/percentage of G's	17,075,852 / 23.98%
Number/percentage of N's	3,494 / 0%
GC Percentage	41.01%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2309

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

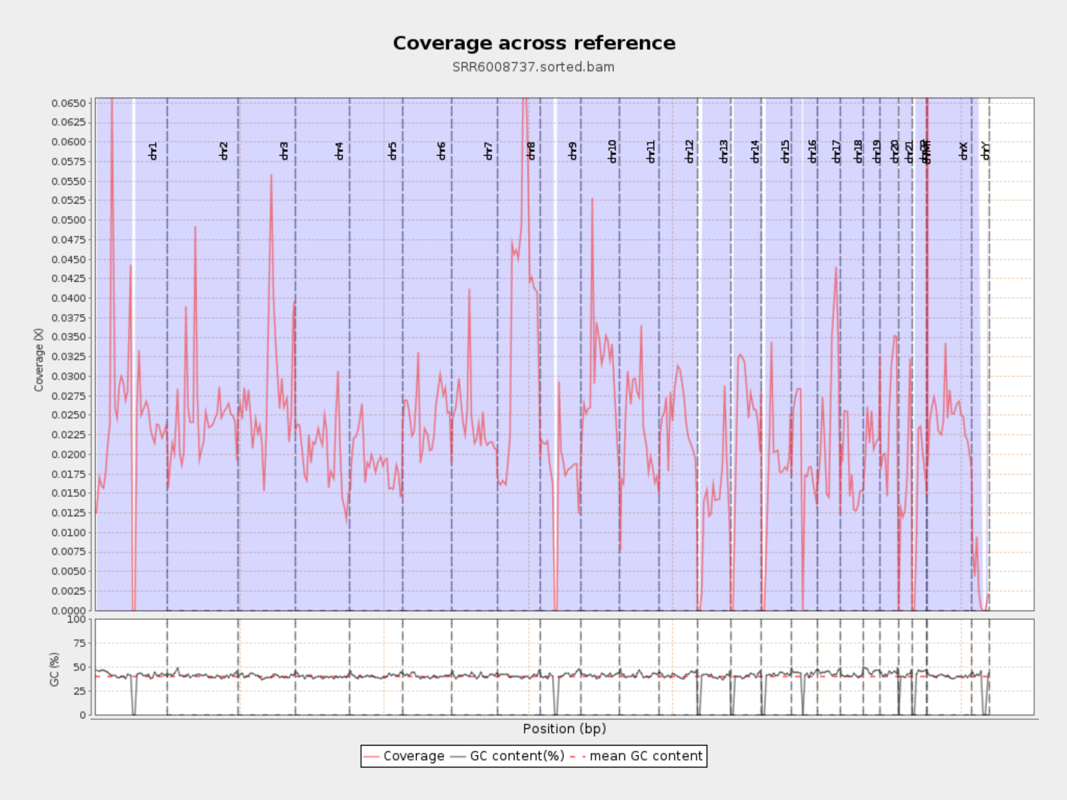
General error rate	0.96%
Mismatches	673,872
Insertions	5,869
Mapped reads with at least one insertion	0.53%
Deletions	27,023
Mapped reads with at least one deletion	2.42%
Homopolymer indels	47.25%

2.6. Chromosome stats

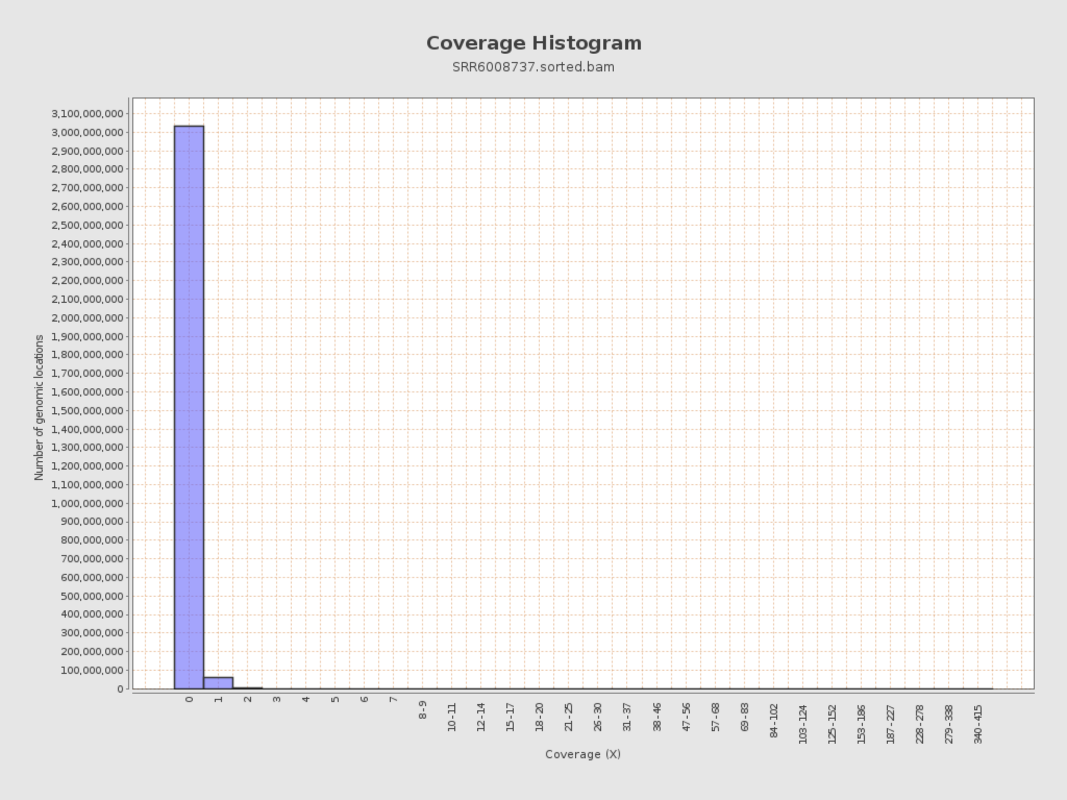
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6028161	0.0242	0.3724
chr2	243199373	6007991	0.0247	0.2936
chr3	198022430	5545559	0.028	0.1836
chr4	191154276	3855620	0.0202	0.1553
chr5	180915260	3462493	0.0191	0.1491
chr6	171115067	4260930	0.0249	0.1917
chr7	159138663	3882335	0.0244	0.3064

chr8	146364022	5666417	0.0387	0.2508
chr9	141213431	2456934	0.0174	0.2212
chr10	135534747	4145632	0.0306	0.2902
chr11	135006516	3128558	0.0232	0.2198
chr12	133851895	3318269	0.0248	0.1718
chr13	115169878	1530176	0.0133	0.1258
chr14	107349540	2508057	0.0234	0.171
chr15	102531392	1753696	0.0171	0.1419
chr16	90354753	1727773	0.0191	0.1622
chr17	81195210	2123463	0.0262	0.2009
chr18	78077248	1363405	0.0175	0.3351
chr19	59128983	1330385	0.0225	0.2585
chr20	63025520	1566843	0.0249	0.1715
chr21	48129895	778415	0.0162	0.1407
chr22	51304566	745231	0.0145	0.1282
chrMT	16571	14913	0.8999	1.1636
chrX	155270560	3854472	0.0248	0.1869
chrY	59373566	186696	0.0031	0.0792

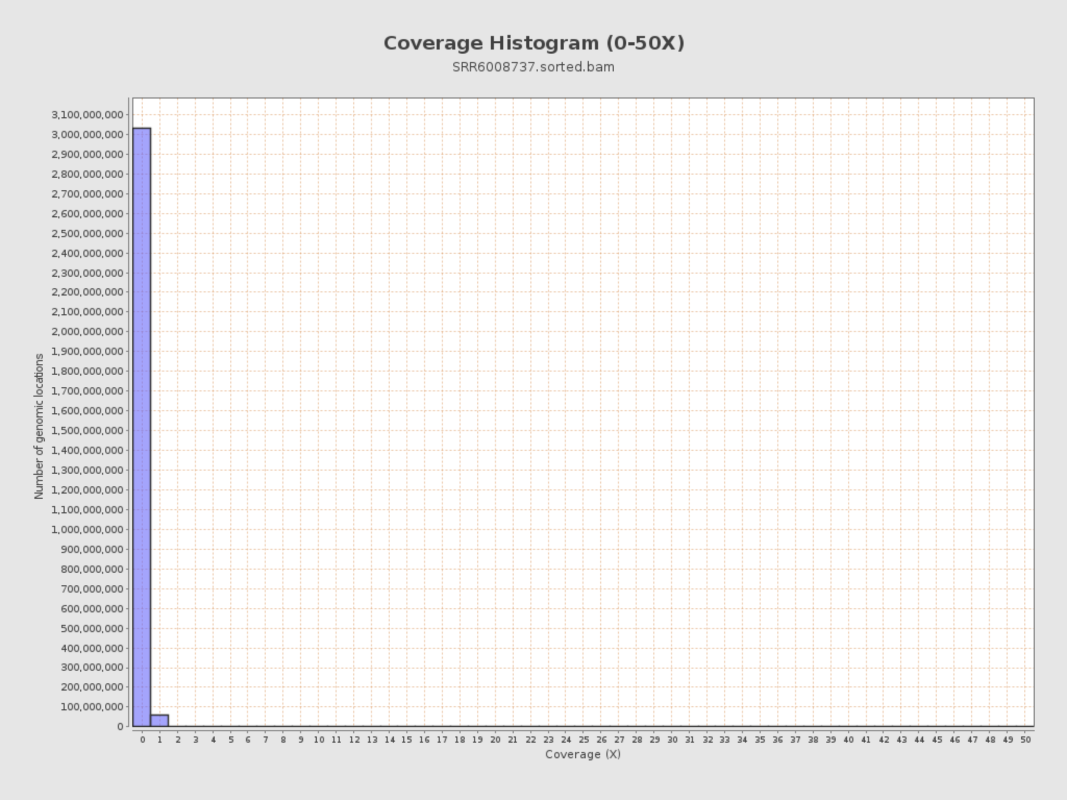
3. Results : Coverage across reference



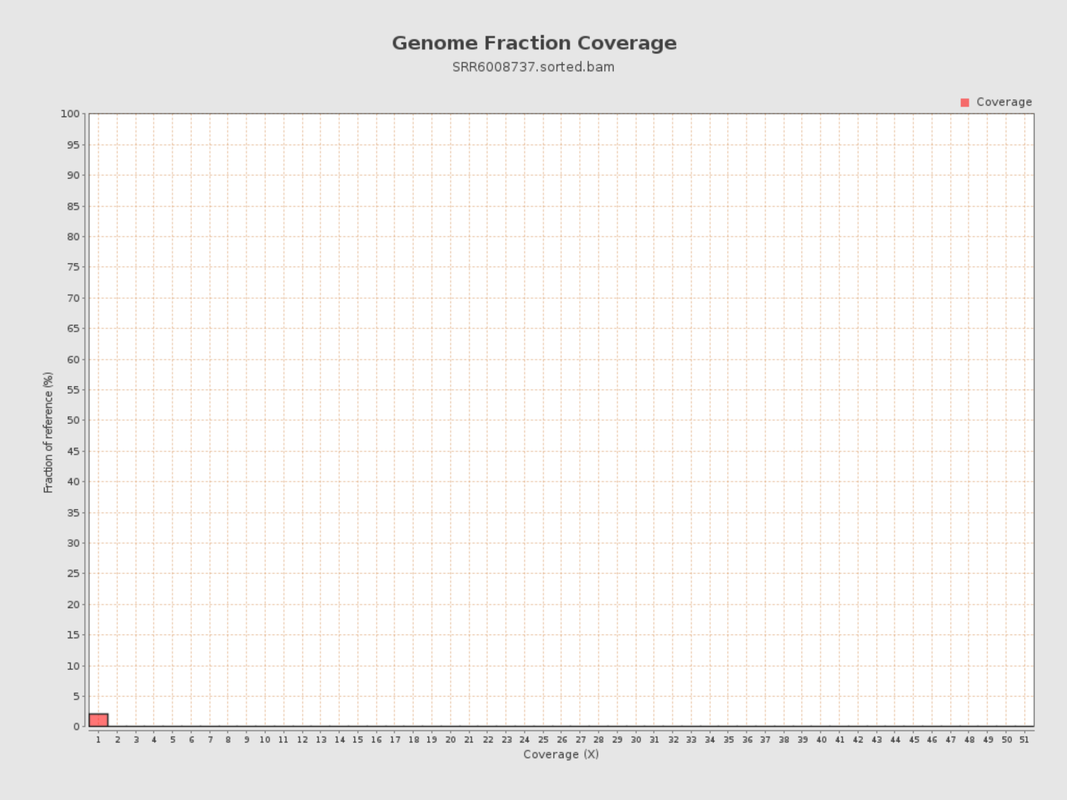
4. Results : Coverage Histogram



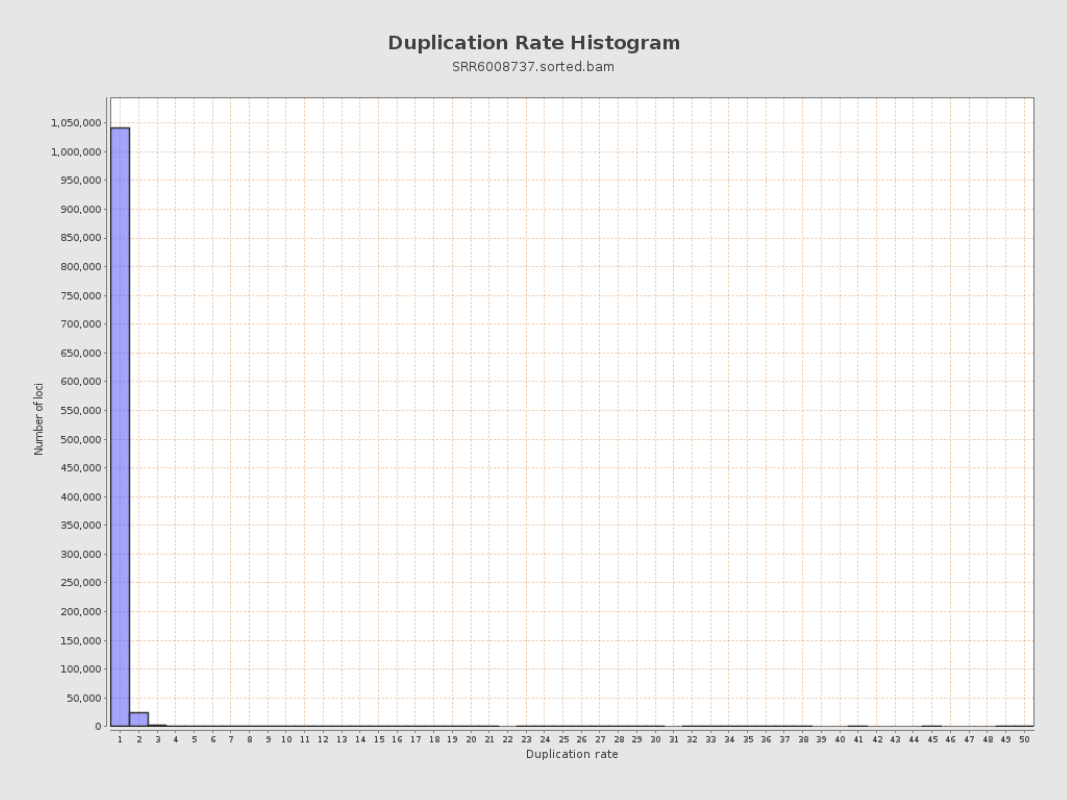
5. Results : Coverage Histogram (0-50X)



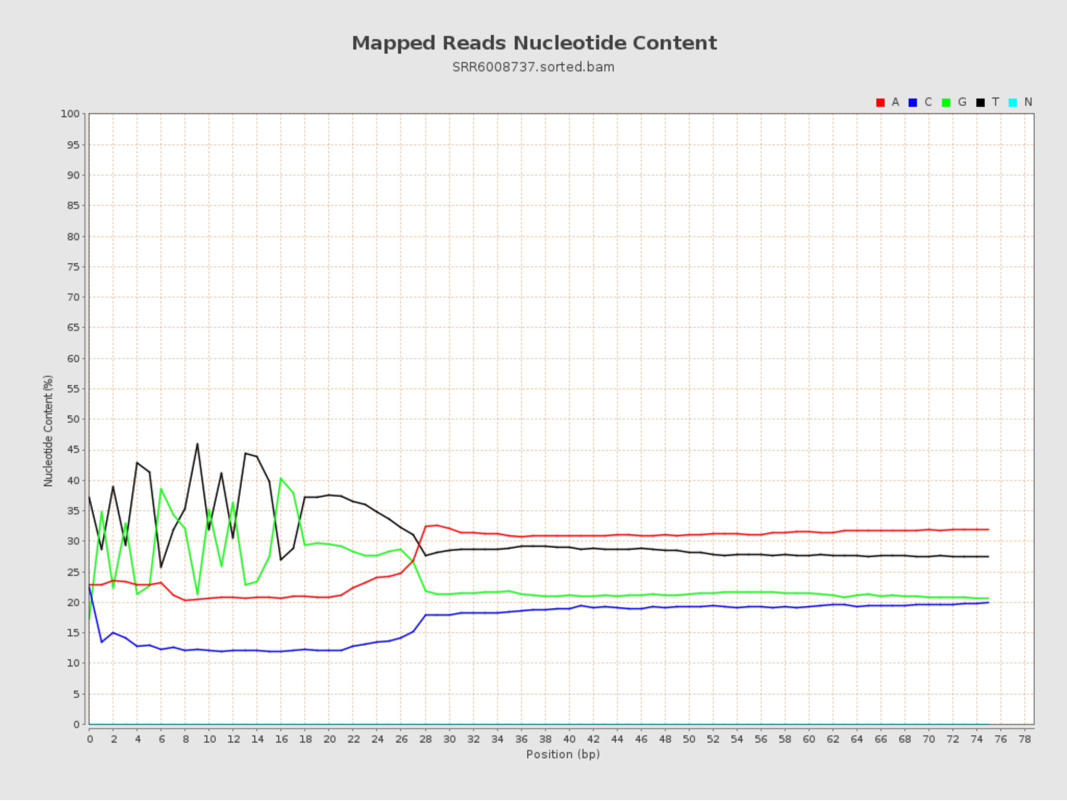
6. Results : Genome Fraction Coverage



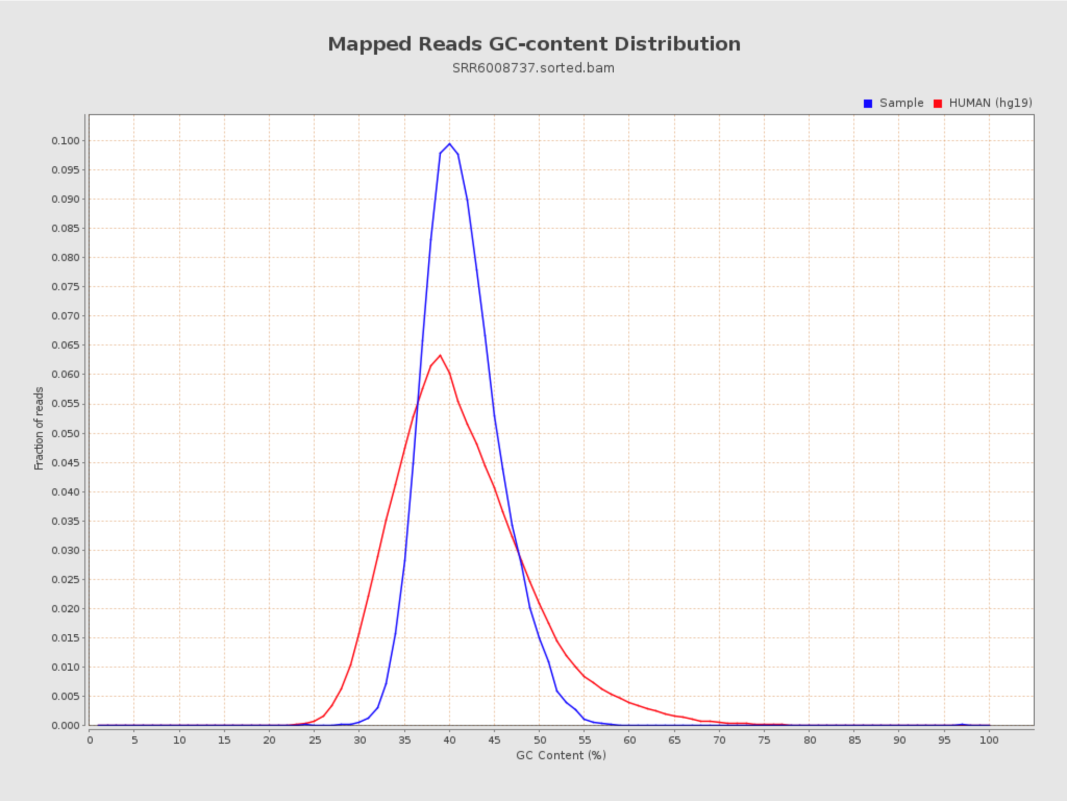
7. Results : Duplication Rate Histogram



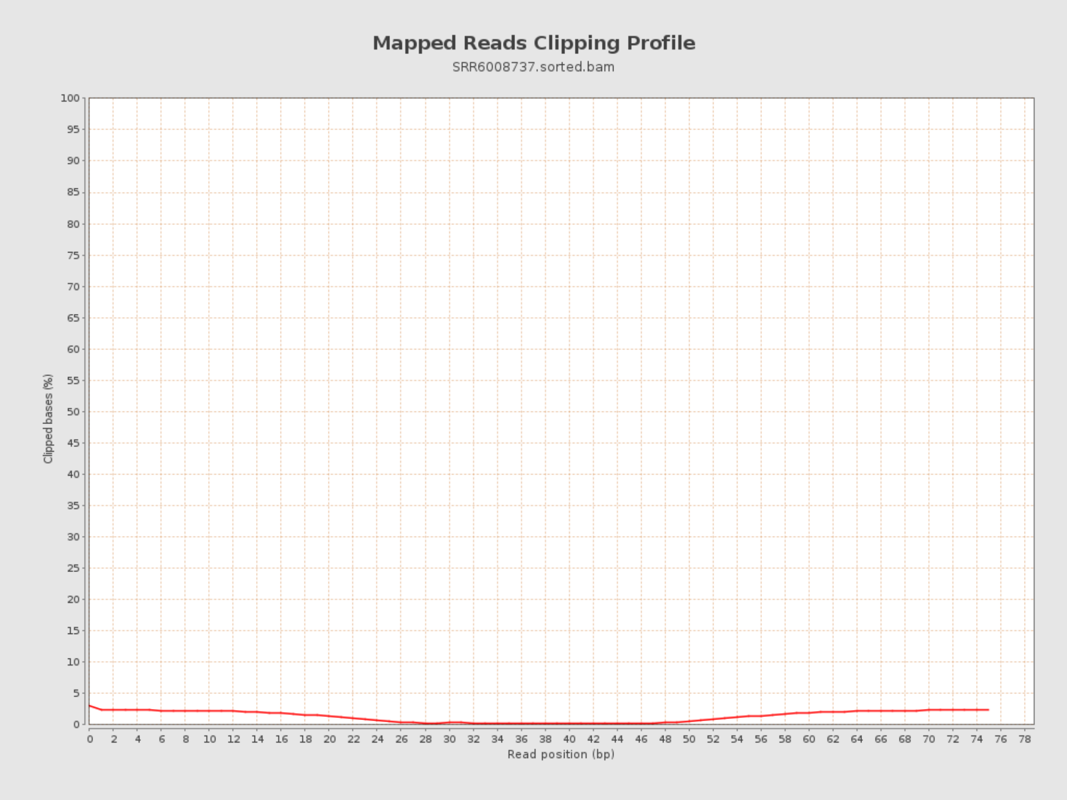
8. Results : Mapped Reads Nucleotide Content



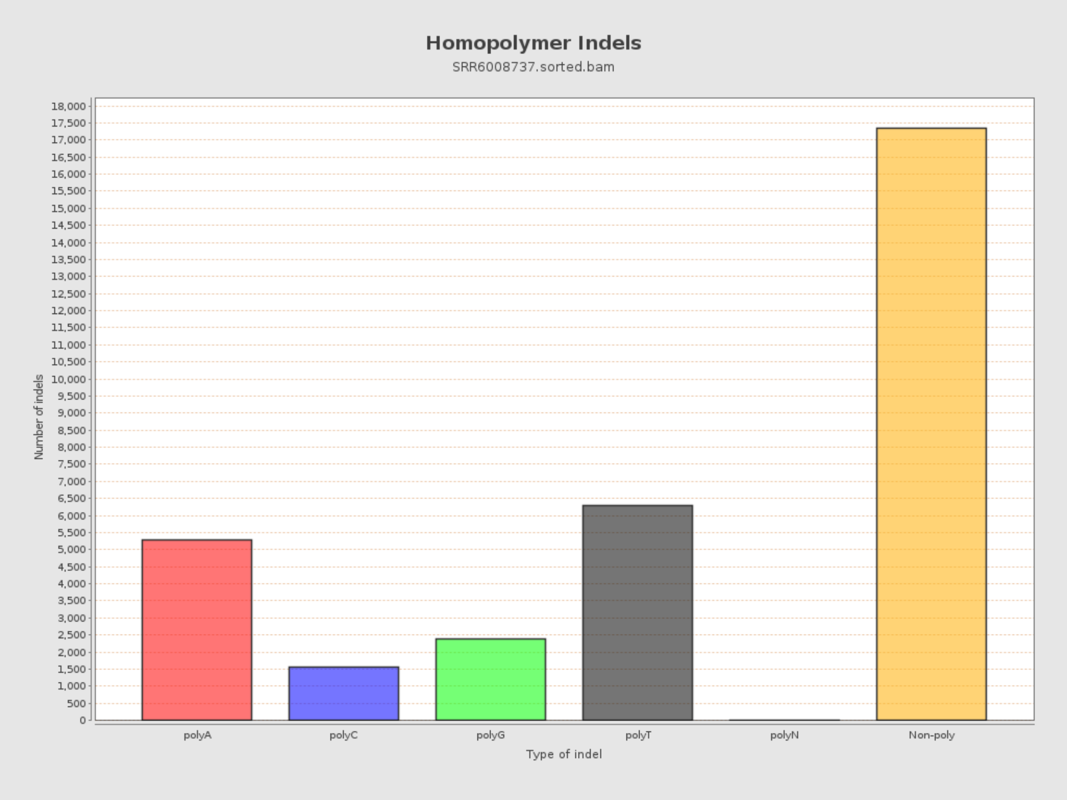
9. Results : Mapped Reads GC-content Distribution



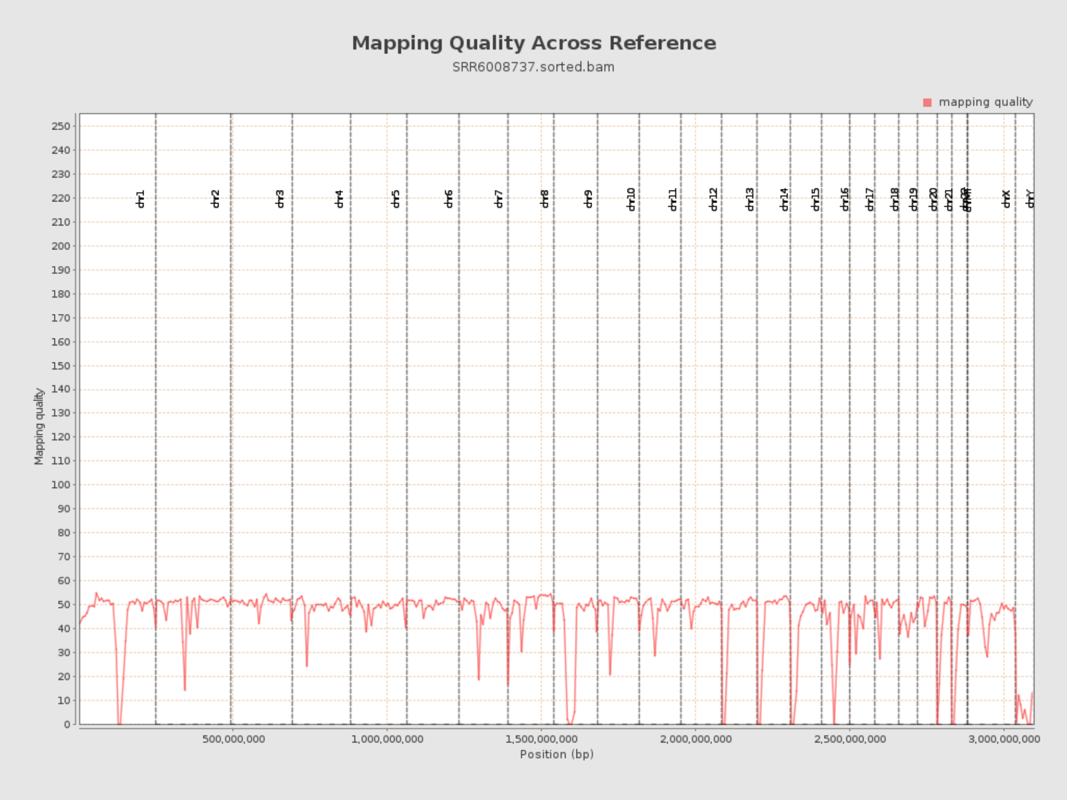
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram