Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:47:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008728.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_SRR6008728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008728.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:47:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,375,099
Mapped reads	2,068,811 / 87.1%
Unmapped reads	306,288 / 12.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,132 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	115,612 / 4.87%
Duplication rate	4.56%
Clipped reads	1,137,502 / 47.89%

2.2. ACGT Content

Number/percentage of A's	34,777,915 / 26.27%
Number/percentage of C's	24,322,867 / 18.37%
Number/percentage of T's	41,977,446 / 31.71%
Number/percentage of G's	31,219,776 / 23.58%
Number/percentage of N's	95,160 / 0.07%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.358

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

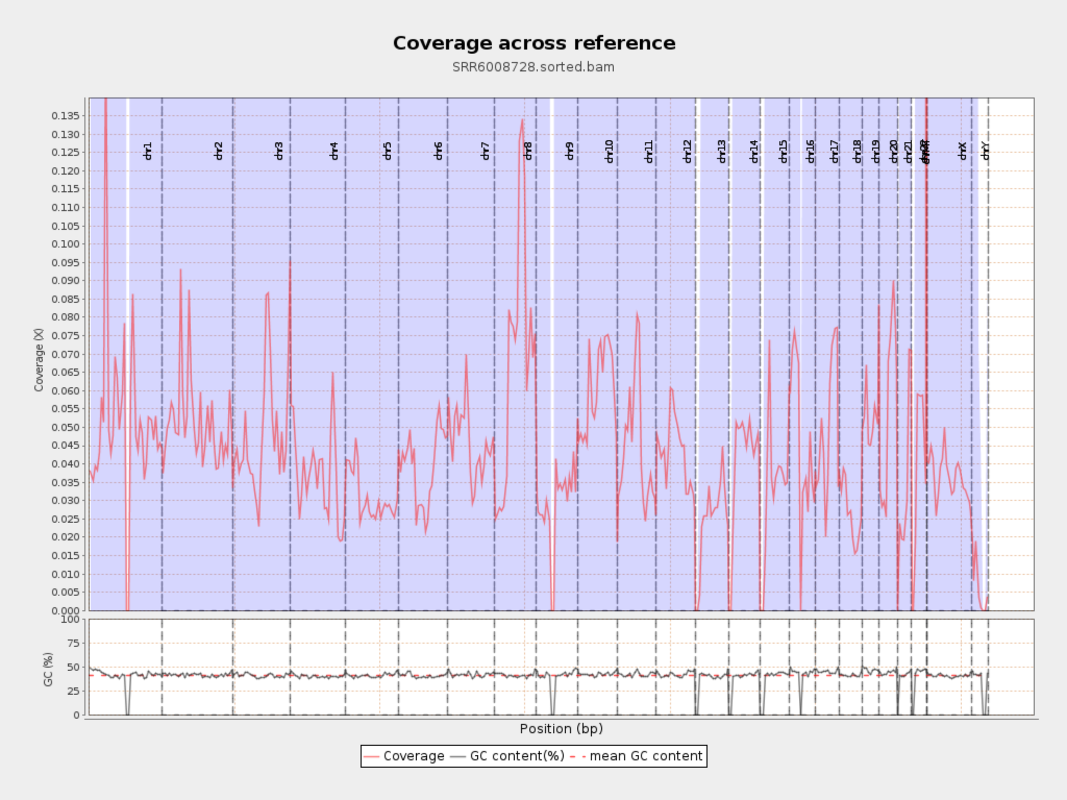
General error rate	0.91%
Mismatches	1,181,771
Insertions	10,071
Mapped reads with at least one insertion	0.48%
Deletions	52,874
Mapped reads with at least one deletion	2.52%
Homopolymer indels	44.15%

2.6. Chromosome stats

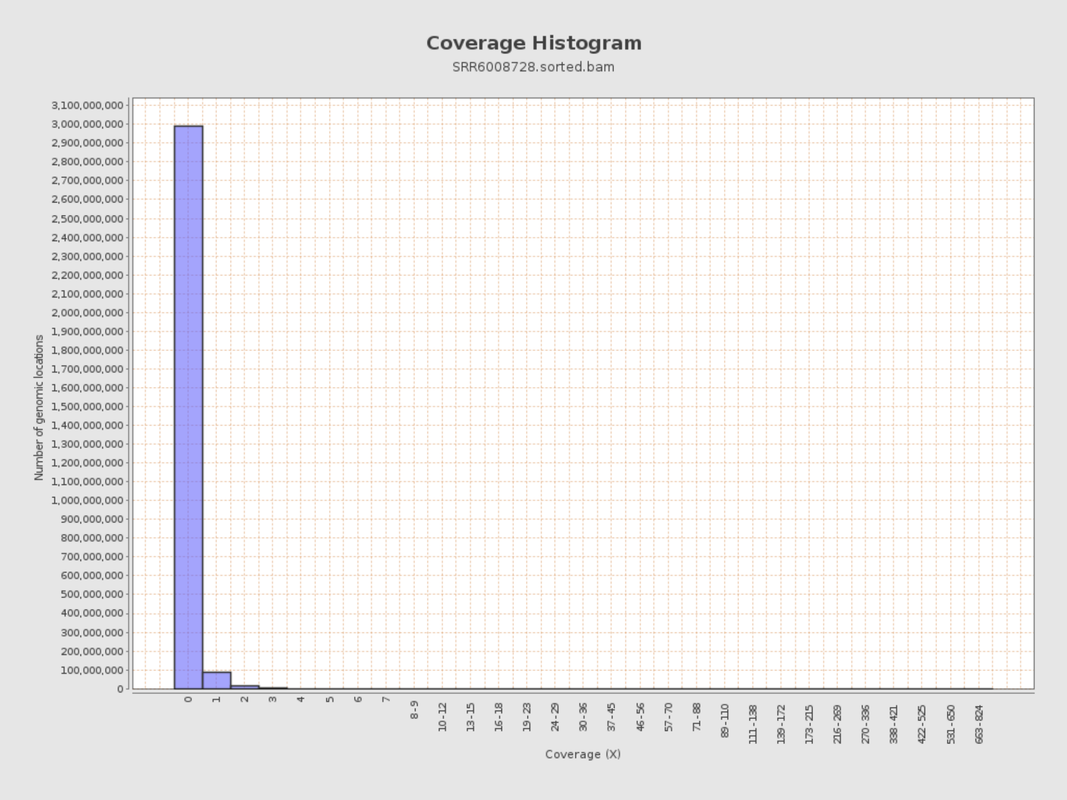
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12696490	0.0509	0.6489
chr2	243199373	12517399	0.0515	0.5059
chr3	198022430	9408424	0.0475	0.2596
chr4	191154276	6995783	0.0366	0.2389
chr5	180915260	5592697	0.0309	0.2087
chr6	171115067	6704453	0.0392	0.2667
chr7	159138663	7289118	0.0458	0.4157

chr8	146364022	10001464	0.0683	0.3962
chr9	141213431	4025006	0.0285	0.2766
chr10	135534747	8183954	0.0604	0.3665
chr11	135006516	6006452	0.0445	0.345
chr12	133851895	5848662	0.0437	0.2507
chr13	115169878	2844354	0.0247	0.186
chr14	107349540	4325966	0.0403	0.2445
chr15	102531392	3436161	0.0335	0.2211
chr16	90354753	4135519	0.0458	0.2896
chr17	81195210	4073906	0.0502	0.3097
chr18	78077248	2067107	0.0265	0.4548
chr19	59128983	3149422	0.0533	0.4296
chr20	63025520	3441430	0.0546	0.2844
chr21	48129895	1617219	0.0336	0.2289
chr22	51304566	1914020	0.0373	0.2264
chrMT	16571	121275	7.3185	5.4252
chrX	155270560	5717416	0.0368	0.2498
chrY	59373566	368287	0.0062	0.1708

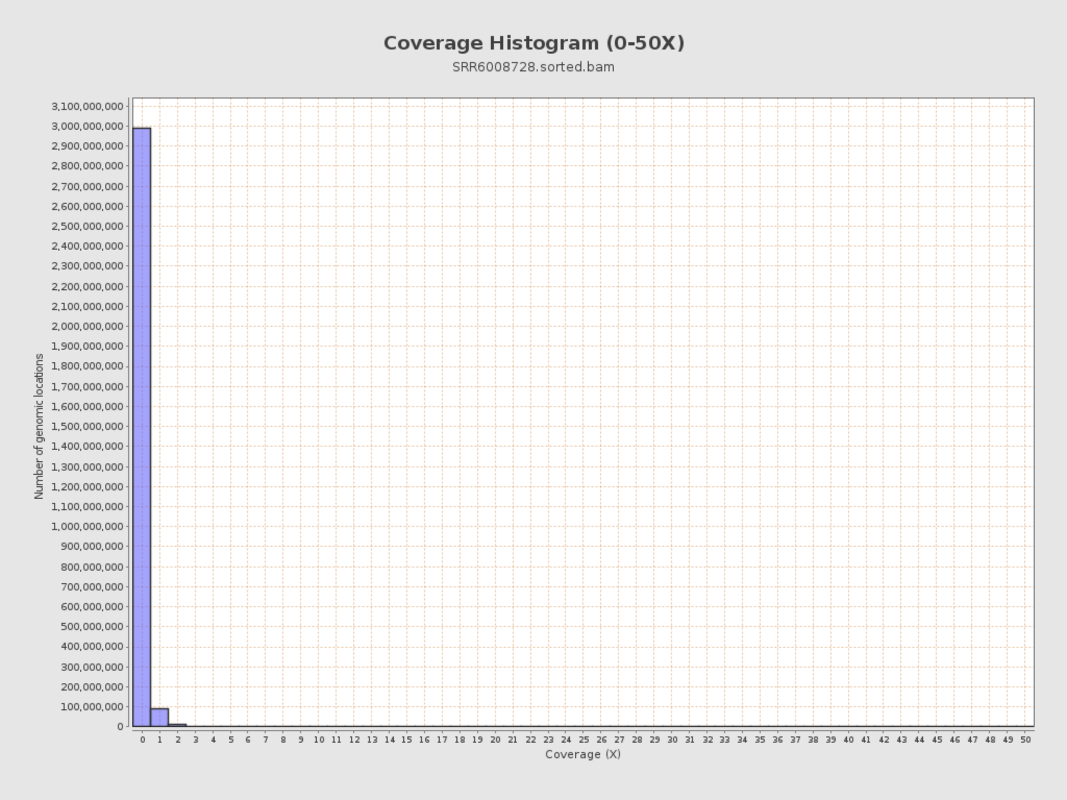
3. Results : Coverage across reference



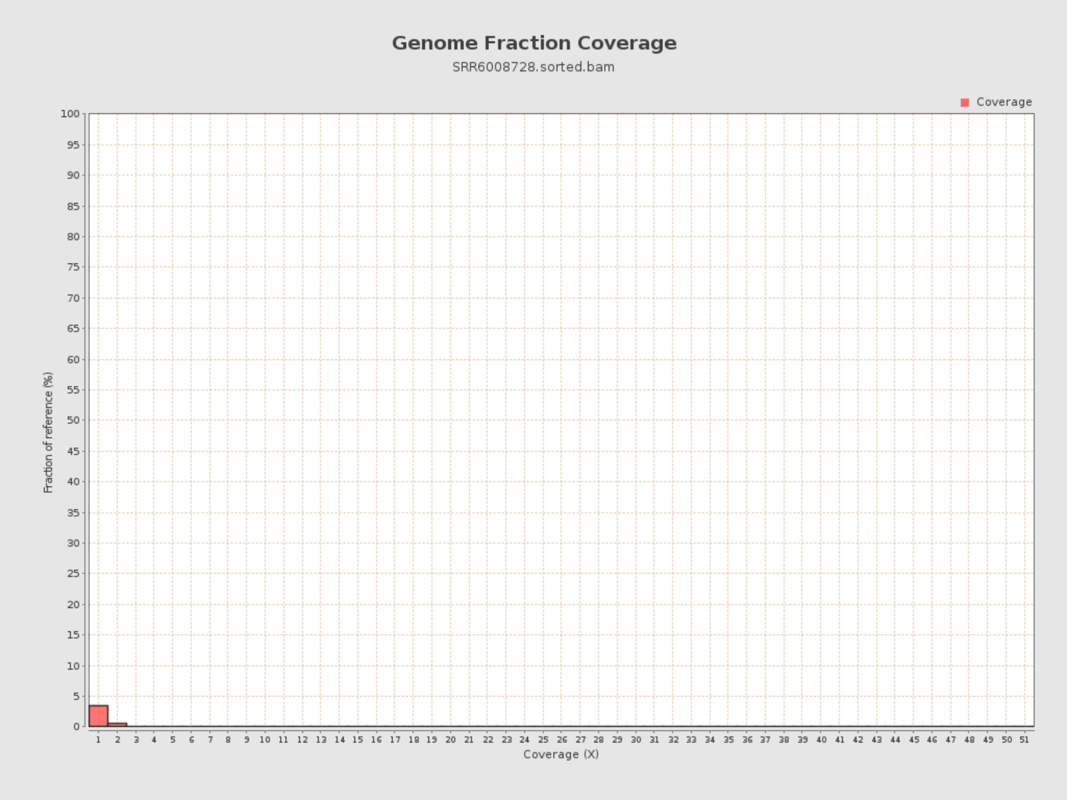
4. Results : Coverage Histogram



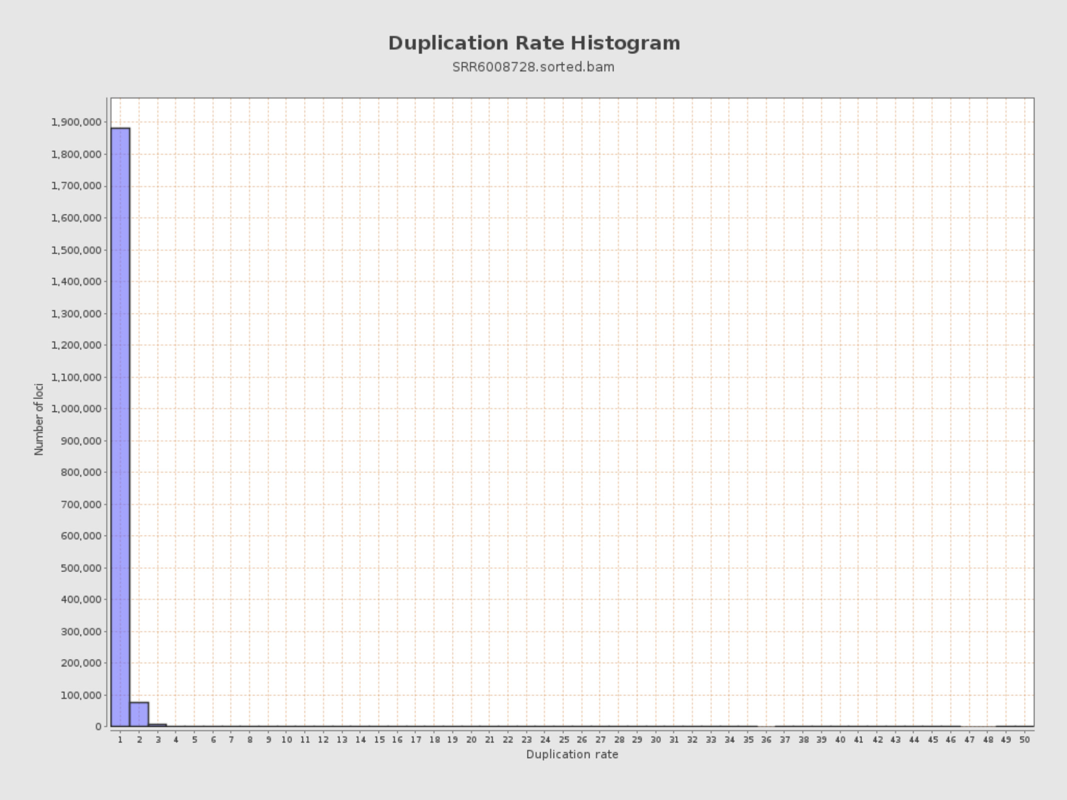
5. Results : Coverage Histogram (0-50X)



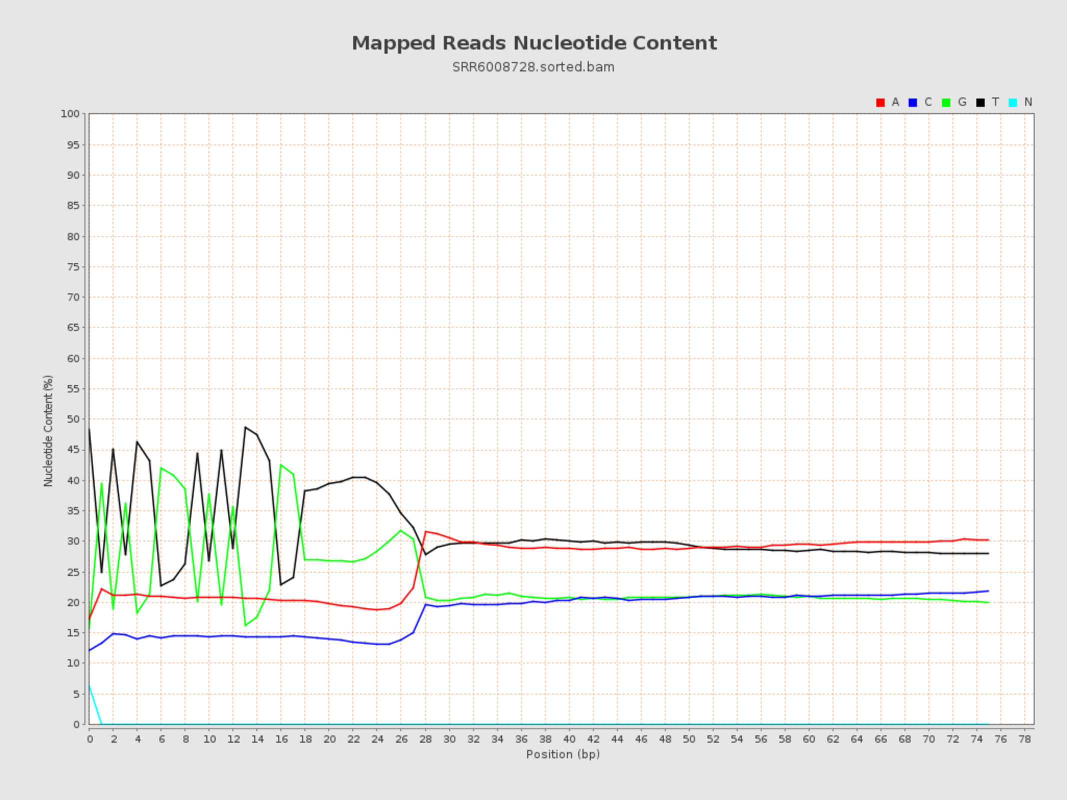
6. Results : Genome Fraction Coverage



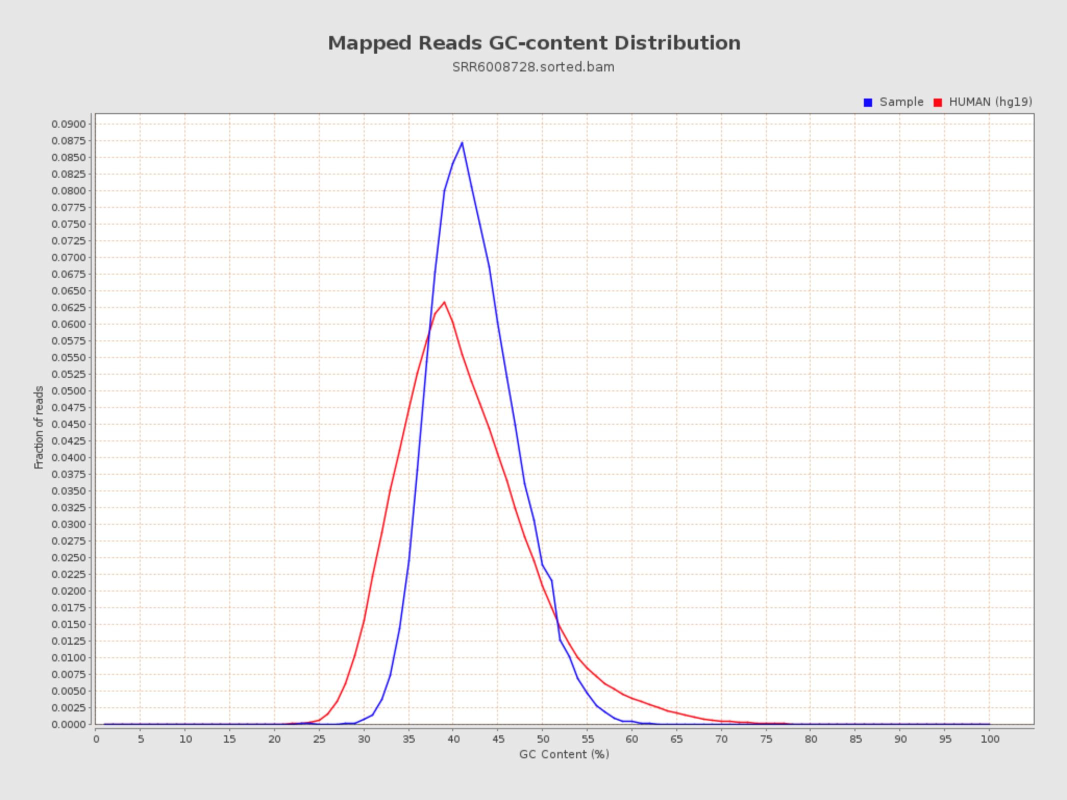
7. Results : Duplication Rate Histogram



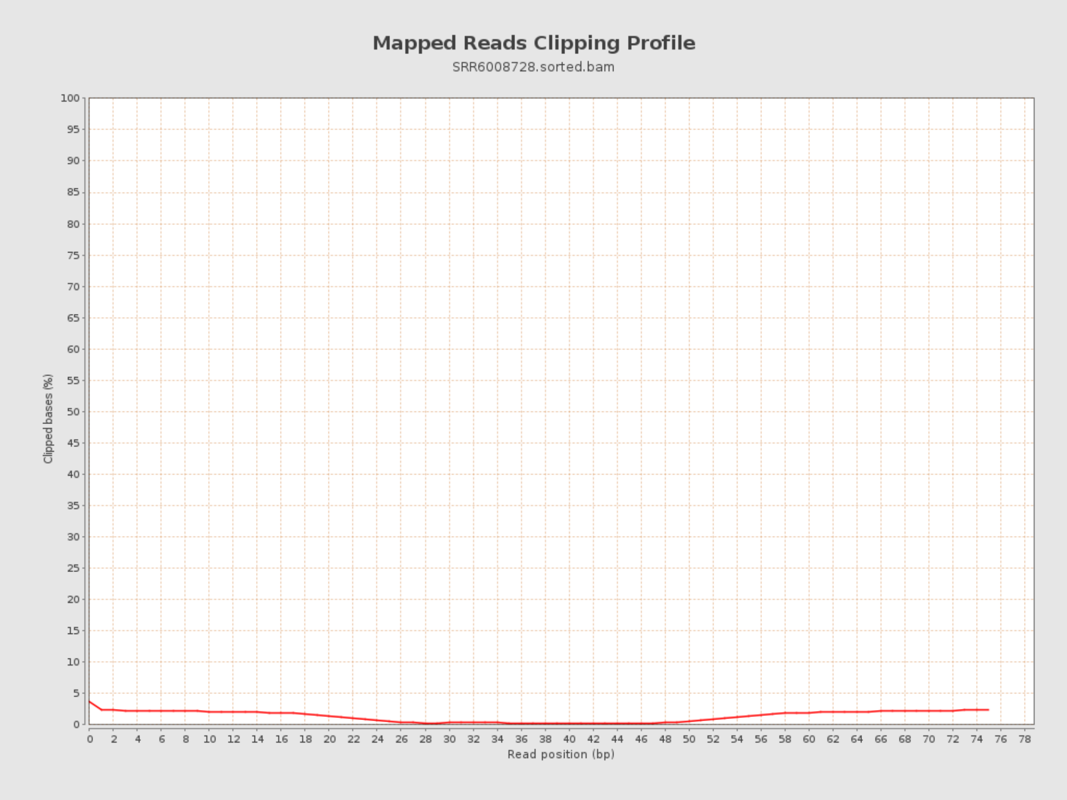
8. Results : Mapped Reads Nucleotide Content



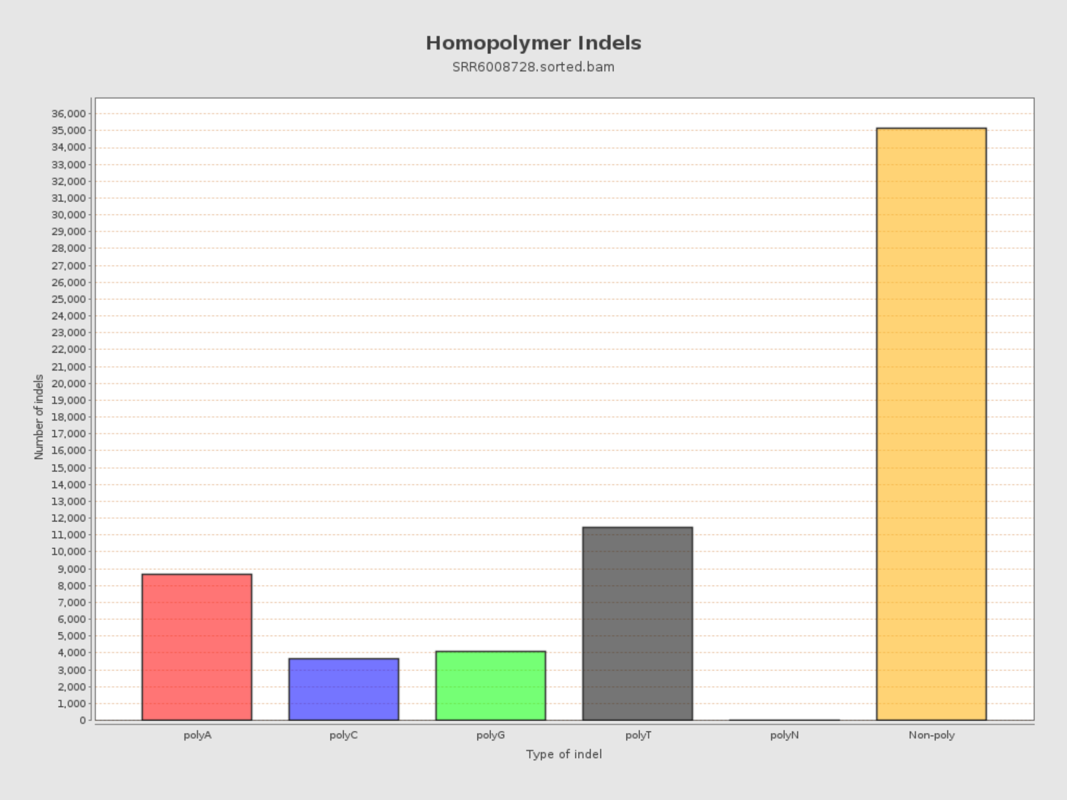
9. Results : Mapped Reads GC-content Distribution



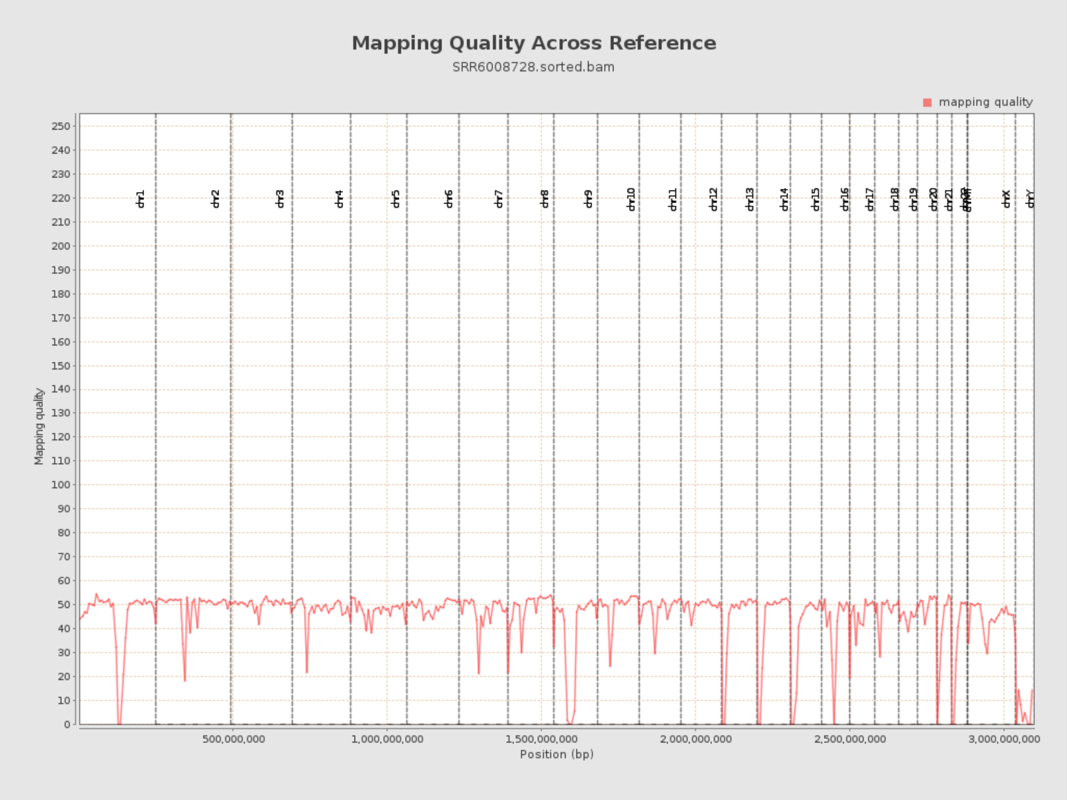
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram