Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:24:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008765.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_SRR6008765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008765.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:24:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008765.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,759,872
Mapped reads	2,346,496 / 85.02%
Unmapped reads	413,376 / 14.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,396 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	242,570 / 8.79%
Duplication rate	8.82%
Clipped reads	1,330,707 / 48.22%

2.2. ACGT Content

Number/percentage of A's	38,973,007 / 26.31%
Number/percentage of C's	25,542,944 / 17.24%
Number/percentage of T's	48,928,792 / 33.03%
Number/percentage of G's	34,647,262 / 23.39%
Number/percentage of N's	54,299 / 0.04%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.3757

2.4. Mapping Quality

Mean Mapping Quality	37.37

2.5. Mismatches and indels

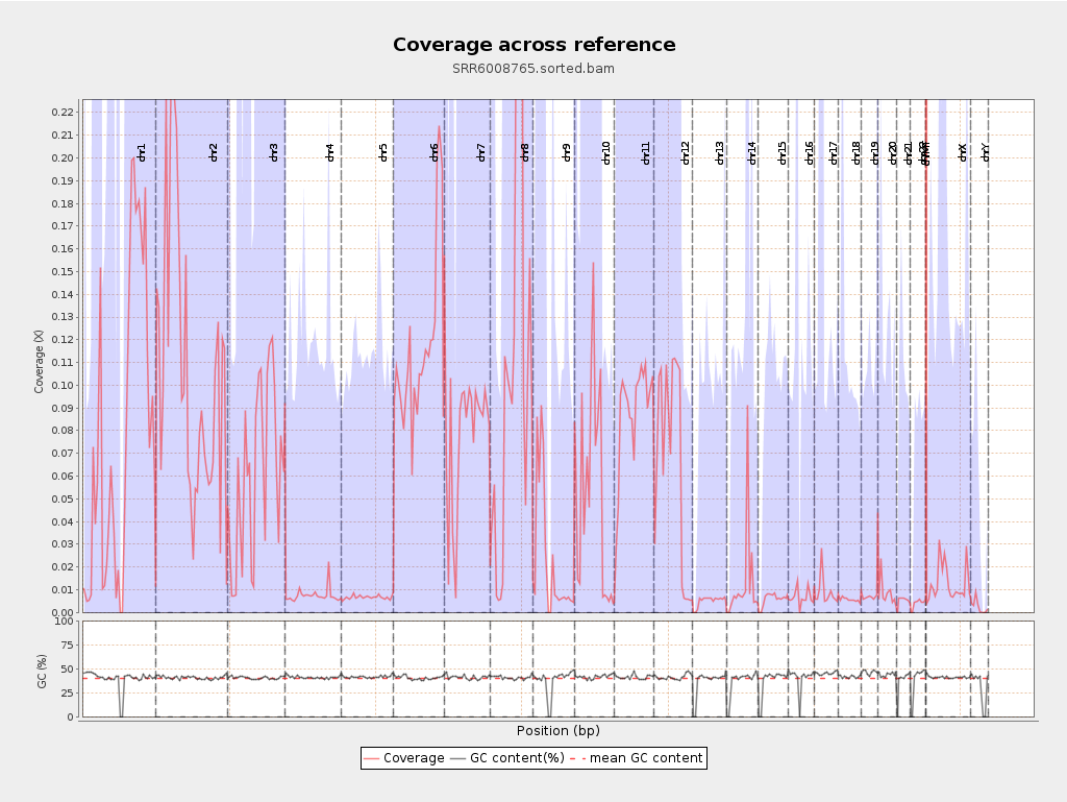
General error rate	0.83%
Mismatches	1,212,792
Insertions	9,214
Mapped reads with at least one insertion	0.39%
Deletions	36,703
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.42%

2.6. Chromosome stats

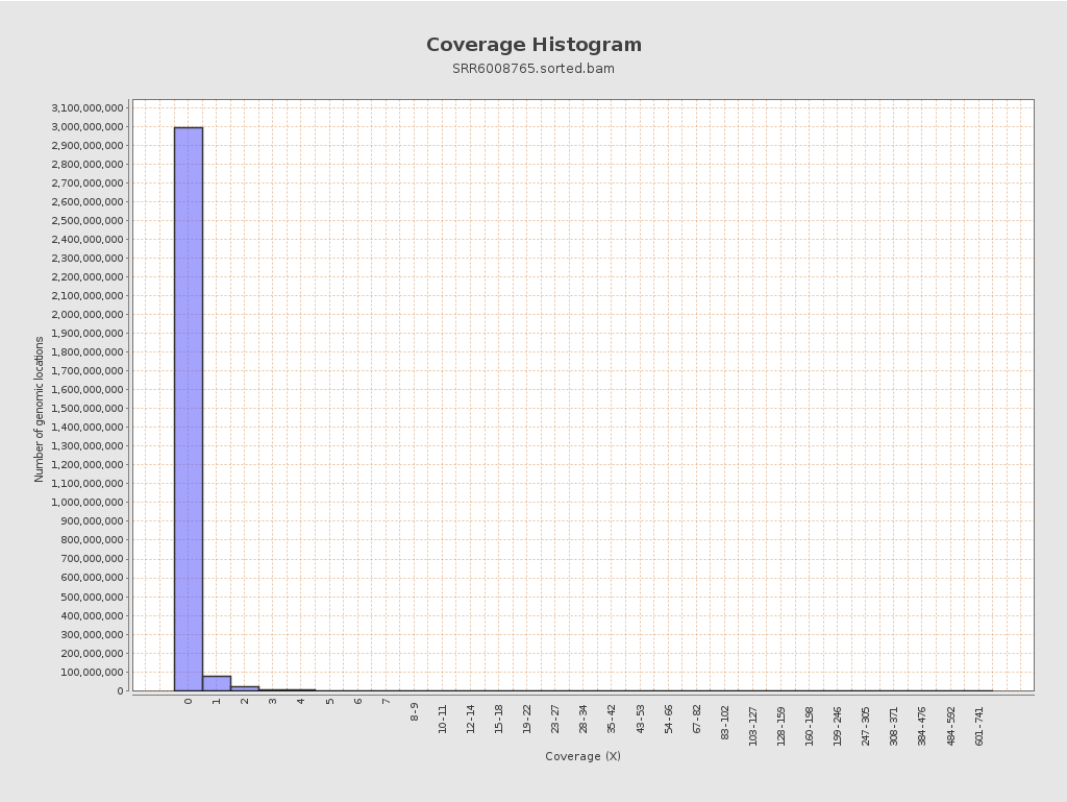
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19096142	0.0766	0.3948
chr2	243199373	26342735	0.1083	0.5033
chr3	198022430	11917822	0.0602	0.3414
chr4	191154276	1451703	0.0076	0.1152
chr5	180915260	1201298	0.0066	0.108
chr6	171115067	19991577	0.1168	0.5704
chr7	159138663	12683477	0.0797	0.5175

chr8	146364022	16414120	0.1121	0.4777
chr9	141213431	3398373	0.0241	0.2084
chr10	135534747	6946592	0.0513	0.6353
chr11	135006516	11802259	0.0874	0.6619
chr12	133851895	8602464	0.0643	0.3382
chr13	115169878	581431	0.005	0.1067
chr14	107349540	1432877	0.0133	0.1529
chr15	102531392	589344	0.0057	0.0976
chr16	90354753	589308	0.0065	0.1404
chr17	81195210	716746	0.0088	0.2512
chr18	78077248	450884	0.0058	0.127
chr19	59128983	478664	0.0081	0.1158
chr20	63025520	547694	0.0087	0.1242
chr21	48129895	251516	0.0052	0.1039
chr22	51304566	201706	0.0039	0.0766
chrMT	16571	408573	24.6559	16.7346
chrX	155270560	1952919	0.0126	0.1972
chrY	59373566	154433	0.0026	0.0652

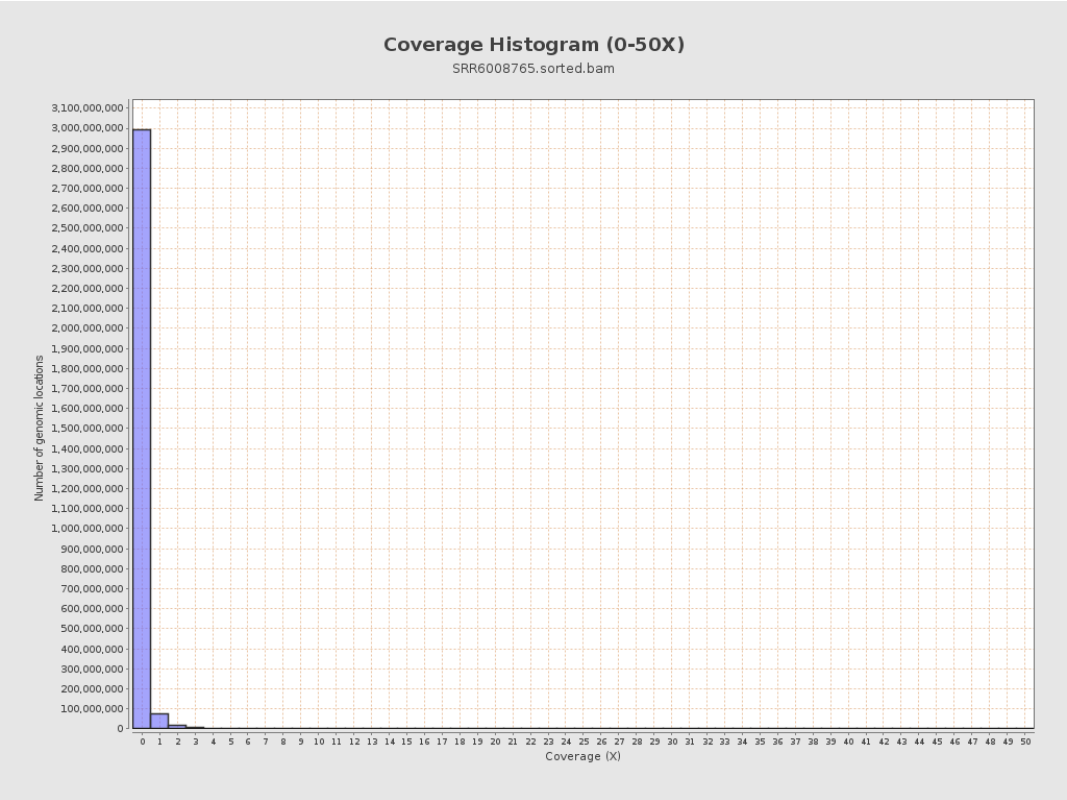
3. Results : Coverage across reference



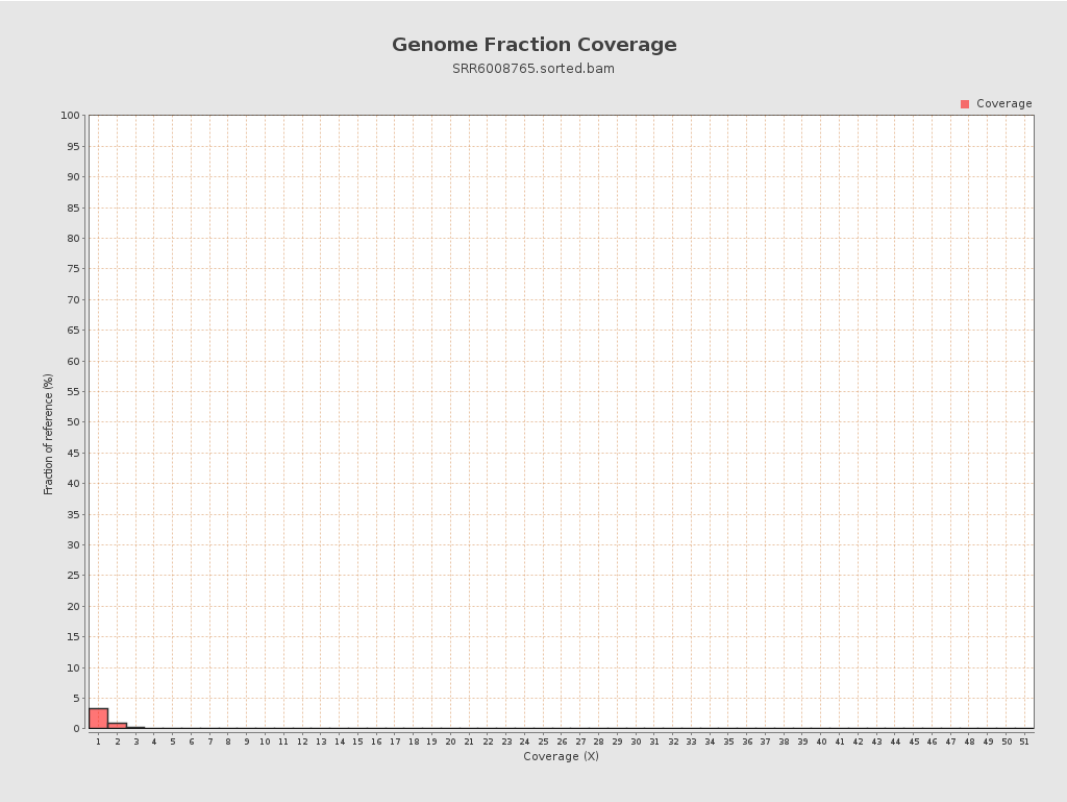
4. Results : Coverage Histogram



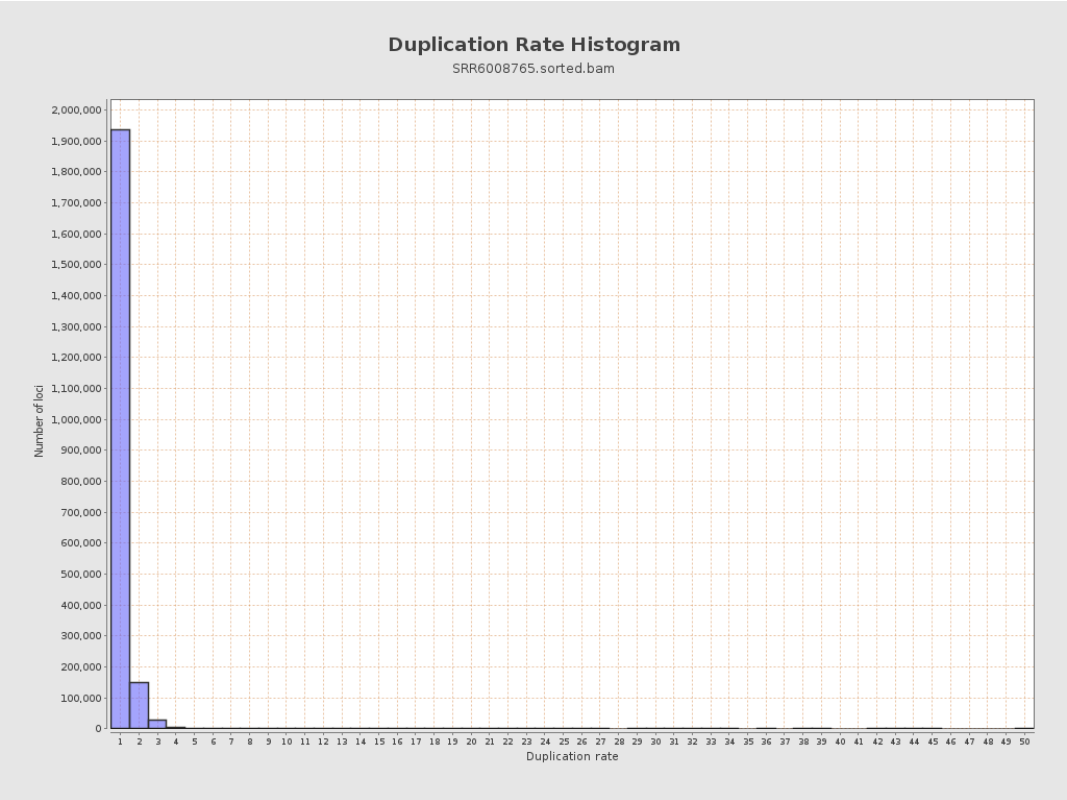
5. Results : Coverage Histogram (0-50X)



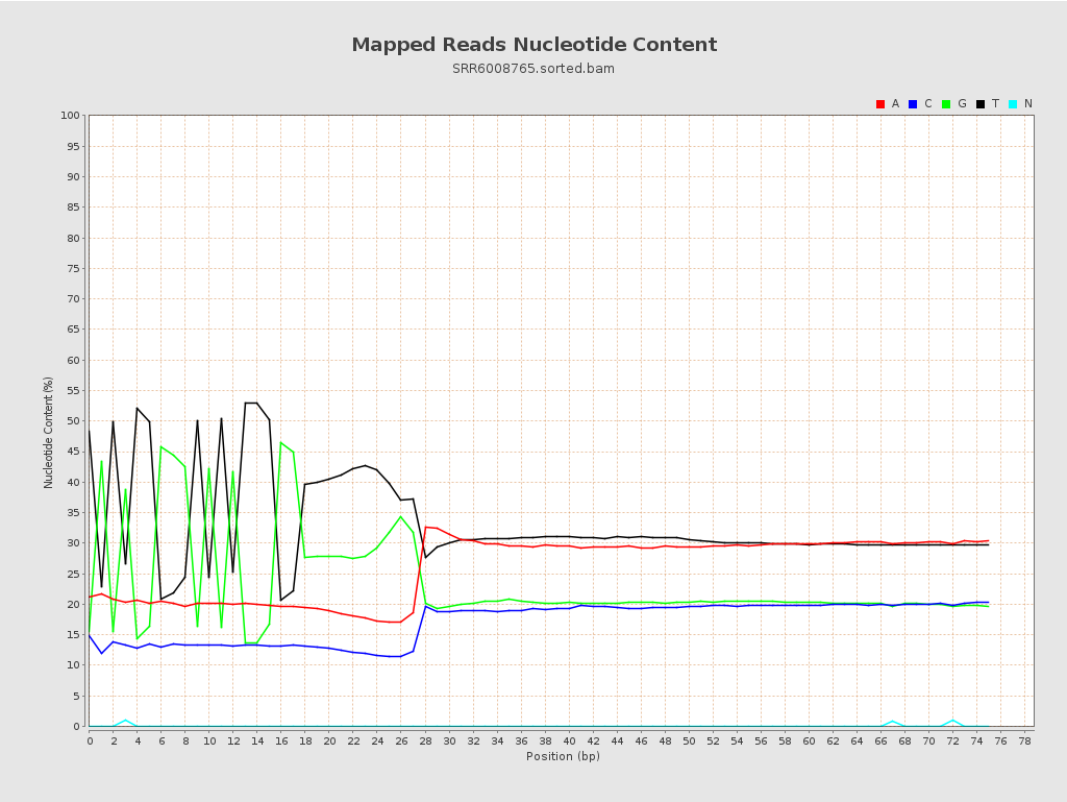
6. Results : Genome Fraction Coverage



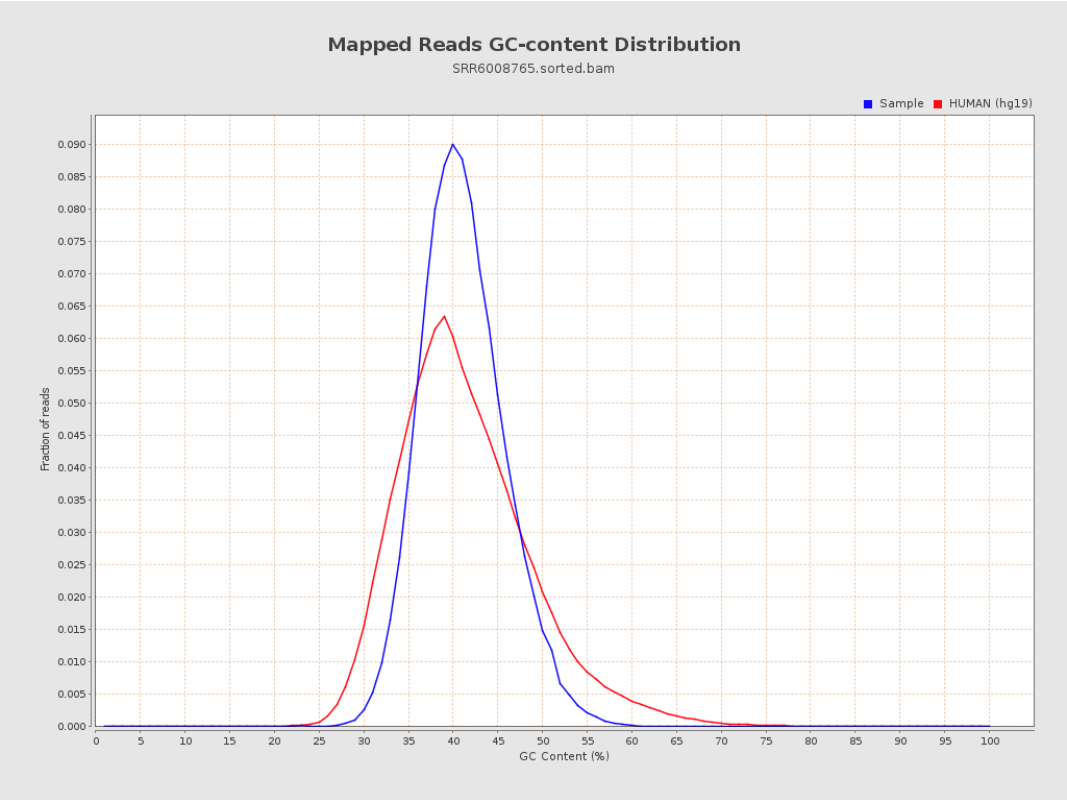
7. Results : Duplication Rate Histogram



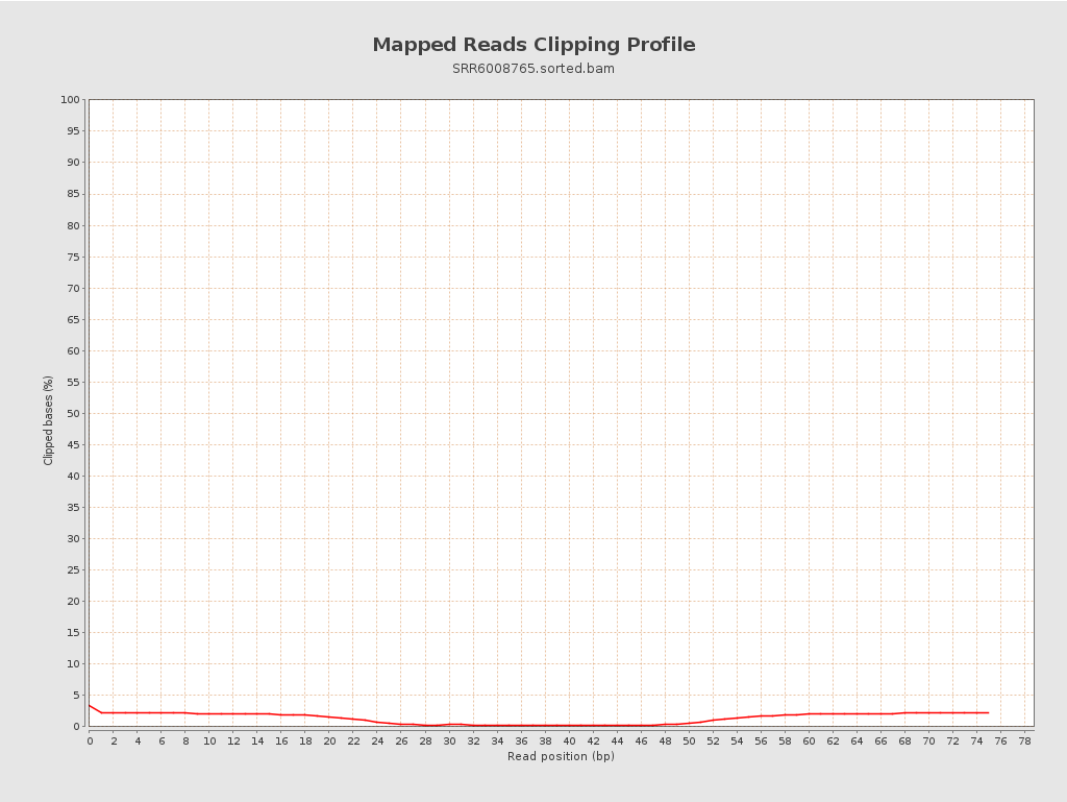
8. Results : Mapped Reads Nucleotide Content



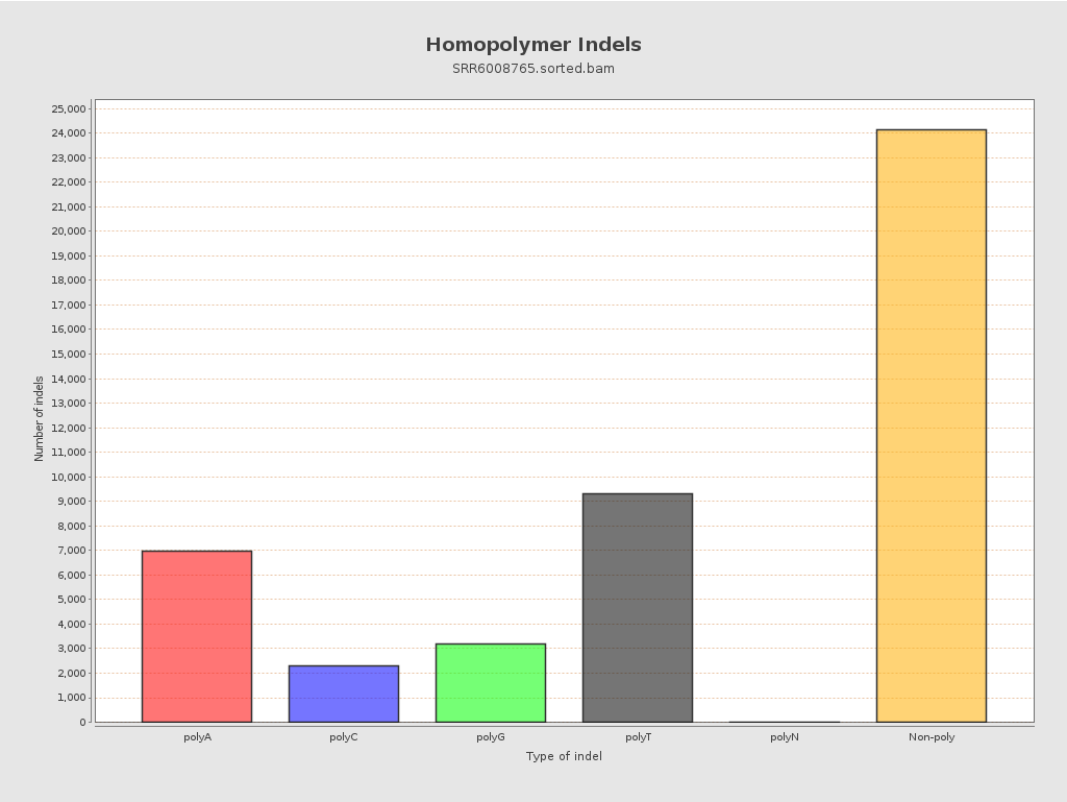
9. Results : Mapped Reads GC-content Distribution



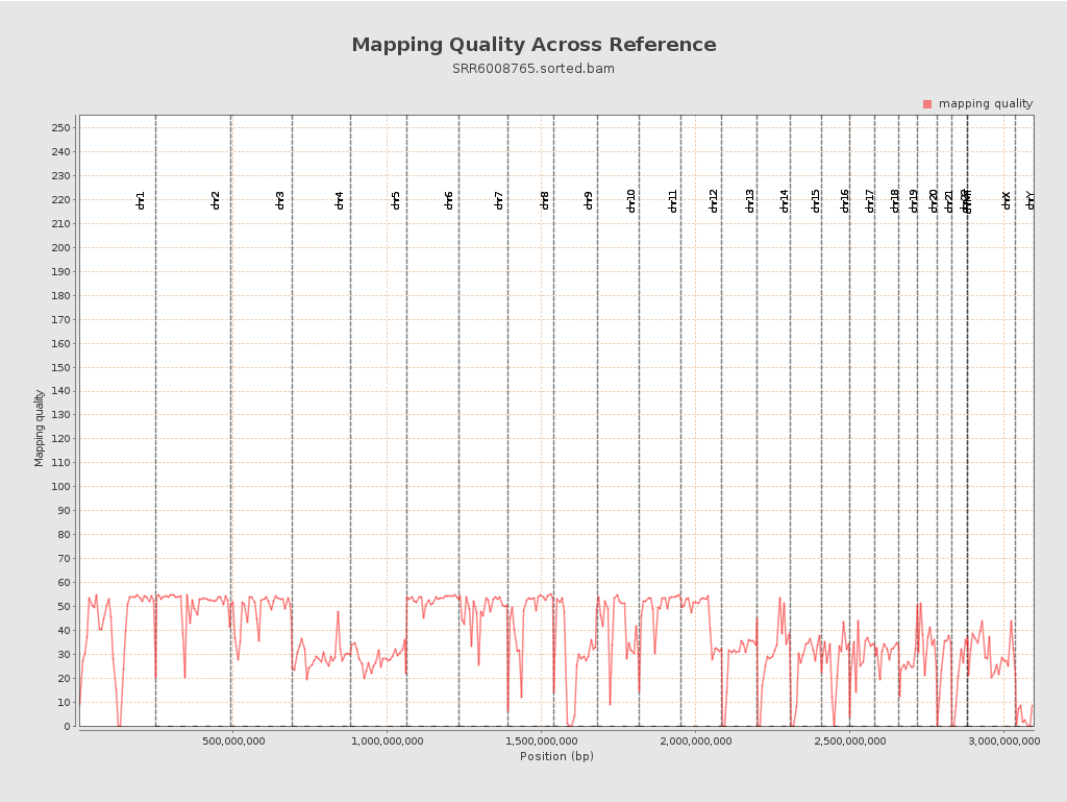
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram