Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:31:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008767.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_SRR6008767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:30:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,822,612
Mapped reads	1,618,269 / 88.79%
Unmapped reads	204,343 / 11.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,866 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	96,940 / 5.32%
Duplication rate	4.94%
Clipped reads	917,453 / 50.34%

2.2. ACGT Content

Number/percentage of A's	26,642,324 / 26.06%
Number/percentage of C's	17,931,722 / 17.54%
Number/percentage of T's	33,132,564 / 32.4%
Number/percentage of G's	24,520,953 / 23.98%
Number/percentage of N's	18,161 / 0.02%
GC Percentage	41.52%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3391

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

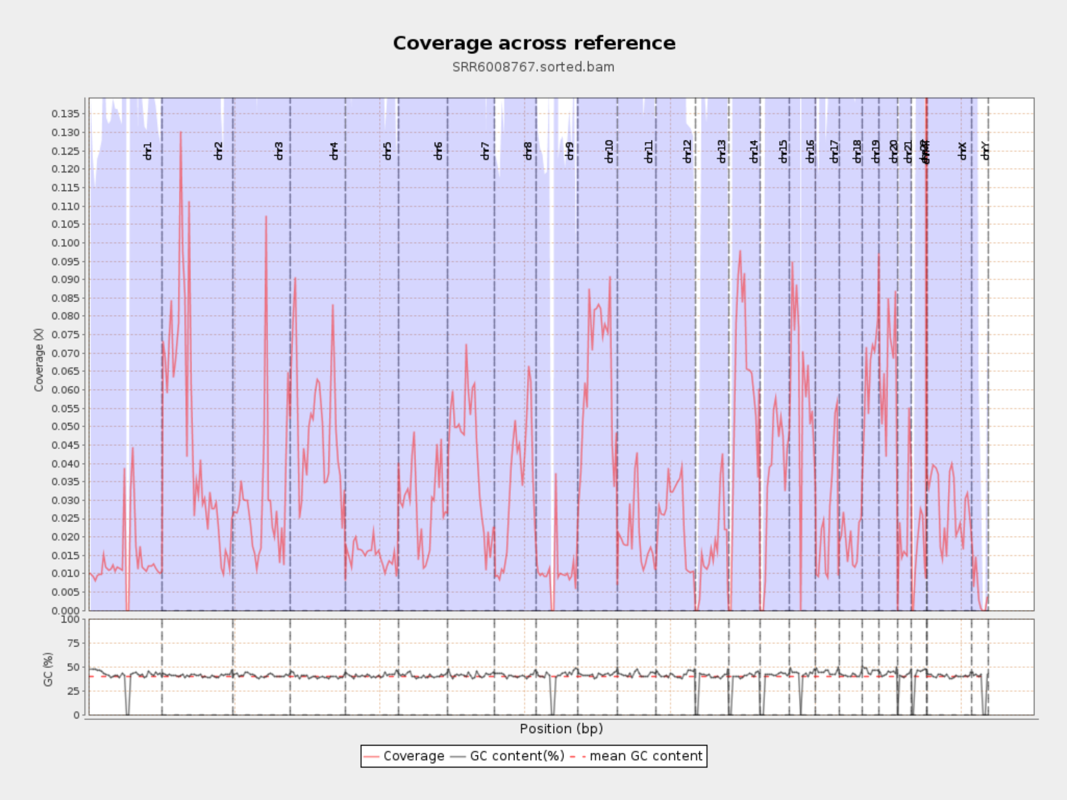
General error rate	0.75%
Mismatches	756,299
Insertions	7,746
Mapped reads with at least one insertion	0.48%
Deletions	31,280
Mapped reads with at least one deletion	1.91%
Homopolymer indels	45.82%

2.6. Chromosome stats

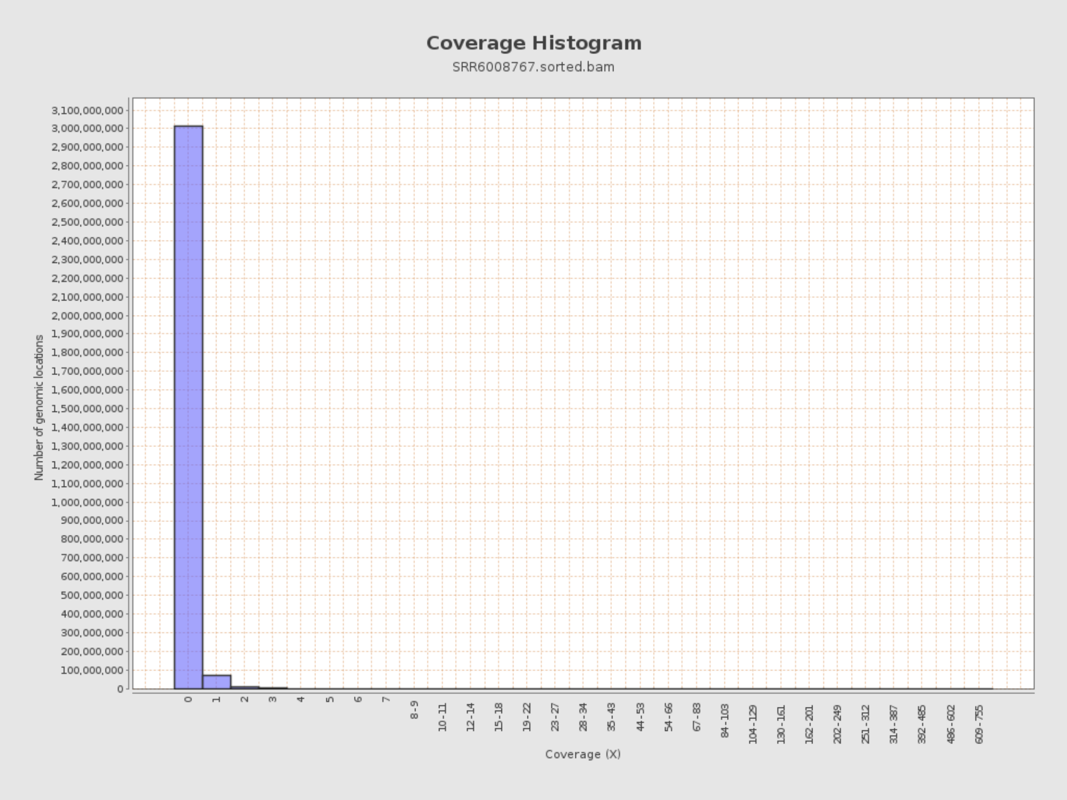
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3341911	0.0134	0.6065
chr2	243199373	11739571	0.0483	0.5082
chr3	198022430	5936649	0.03	0.2036
chr4	191154276	9577875	0.0501	0.2668
chr5	180915260	2724094	0.0151	0.1495
chr6	171115067	4959816	0.029	0.2493
chr7	159138663	6864300	0.0431	0.5154

chr8	146364022	4888707	0.0334	0.2907
chr9	141213431	1454716	0.0103	0.2649
chr10	135534747	8900713	0.0657	0.3564
chr11	135006516	2647142	0.0196	0.2011
chr12	133851895	3391551	0.0253	0.1961
chr13	115169878	1900385	0.0165	0.1506
chr14	107349540	6387857	0.0595	0.2877
chr15	102531392	3671756	0.0358	0.2198
chr16	90354753	5547367	0.0614	0.3546
chr17	81195210	2052923	0.0253	0.1893
chr18	78077248	1457210	0.0187	0.3545
chr19	59128983	3909678	0.0661	0.4862
chr20	63025520	4166072	0.0661	0.3058
chr21	48129895	1159529	0.0241	0.1882
chr22	51304566	756392	0.0147	0.1394
chrMT	16571	111931	6.7546	4.3455
chrX	155270560	4447741	0.0286	0.2085
chrY	59373566	301216	0.0051	0.1149

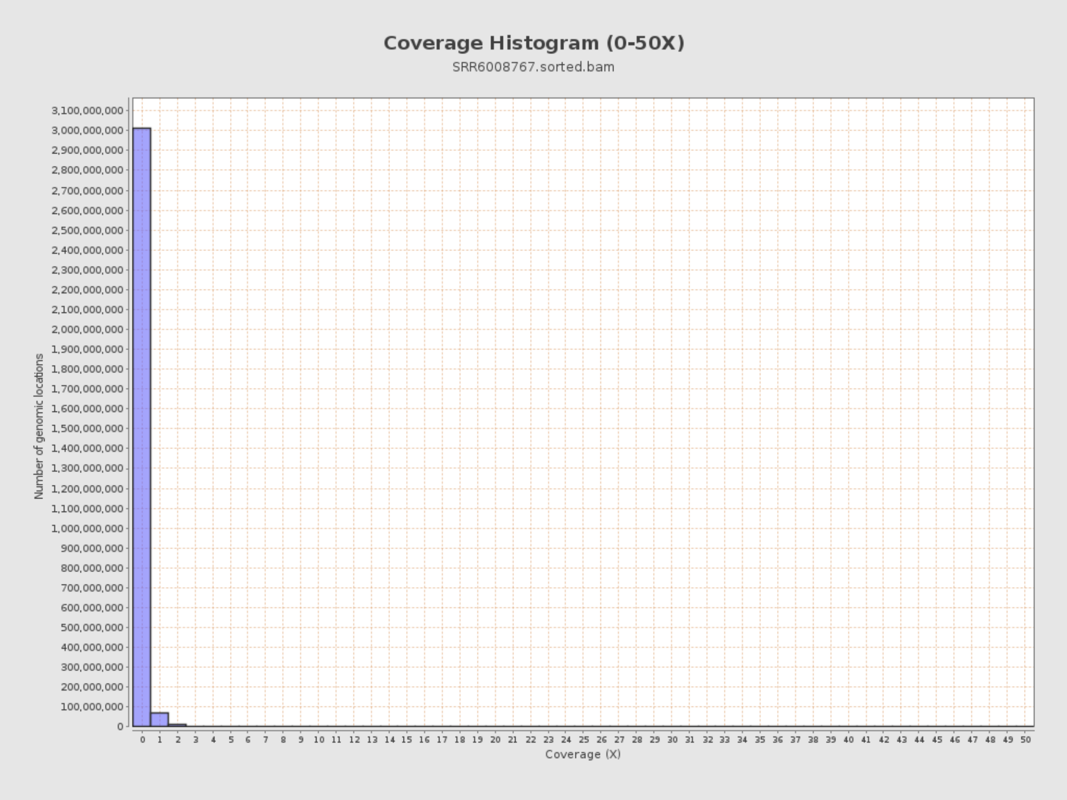
3. Results : Coverage across reference



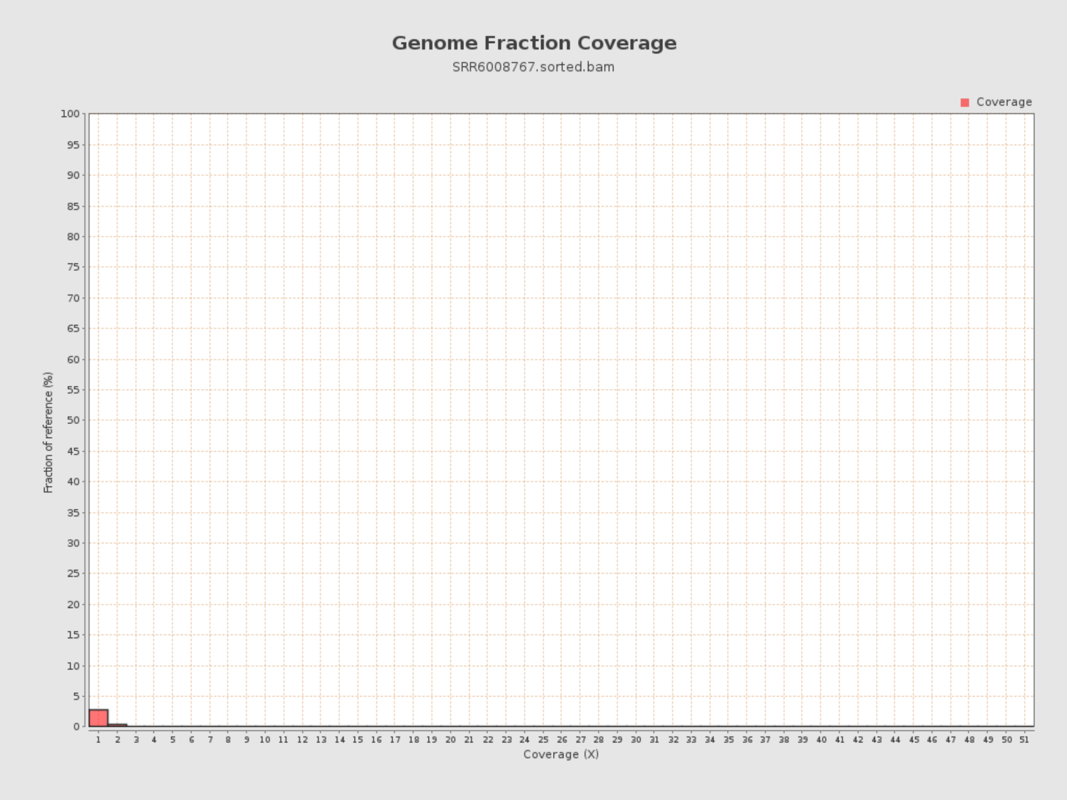
4. Results : Coverage Histogram



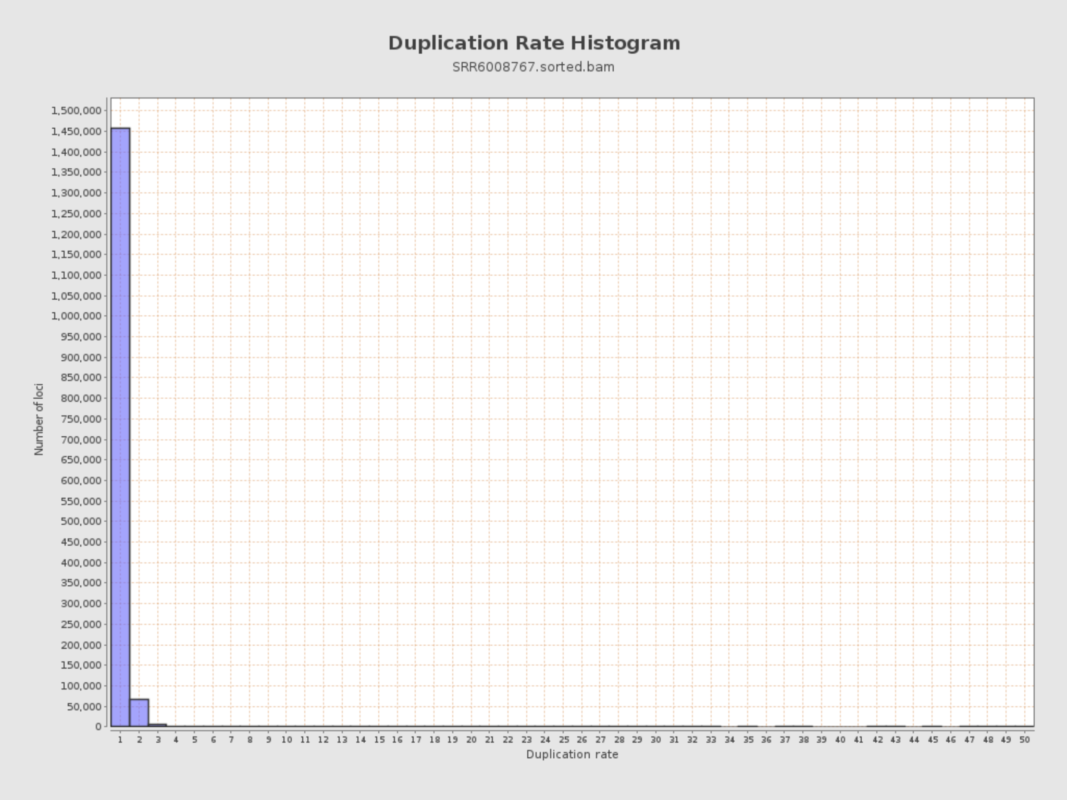
5. Results : Coverage Histogram (0-50X)



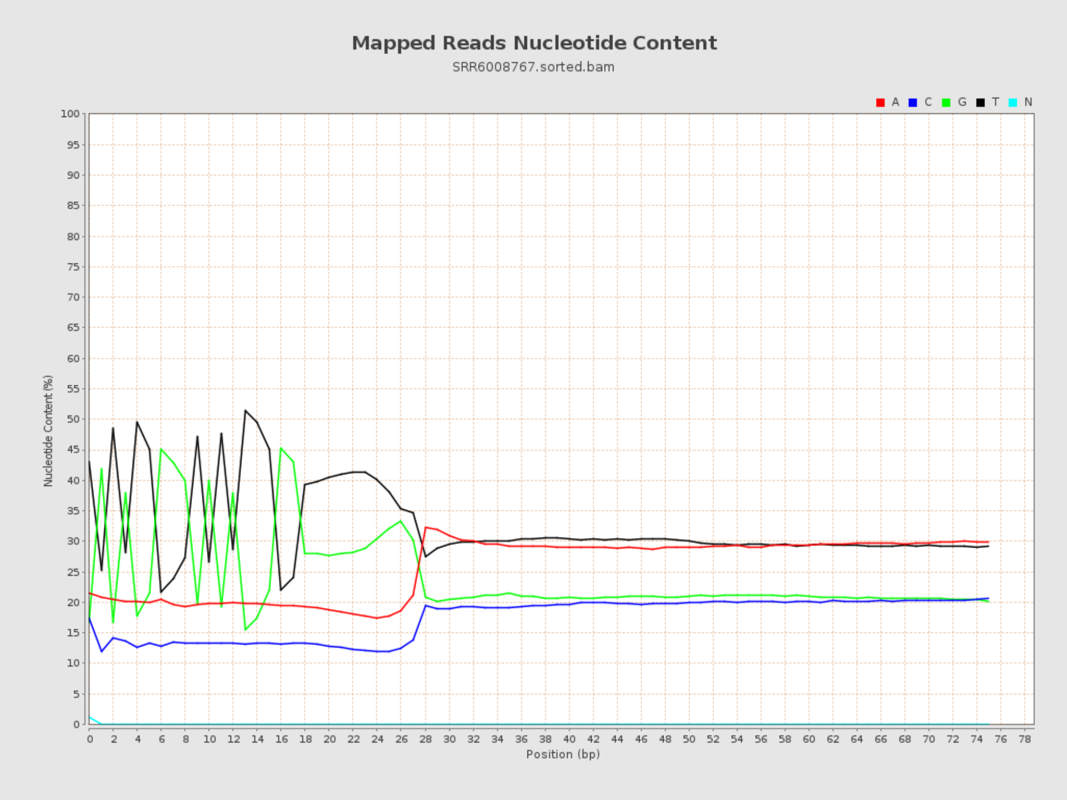
6. Results : Genome Fraction Coverage



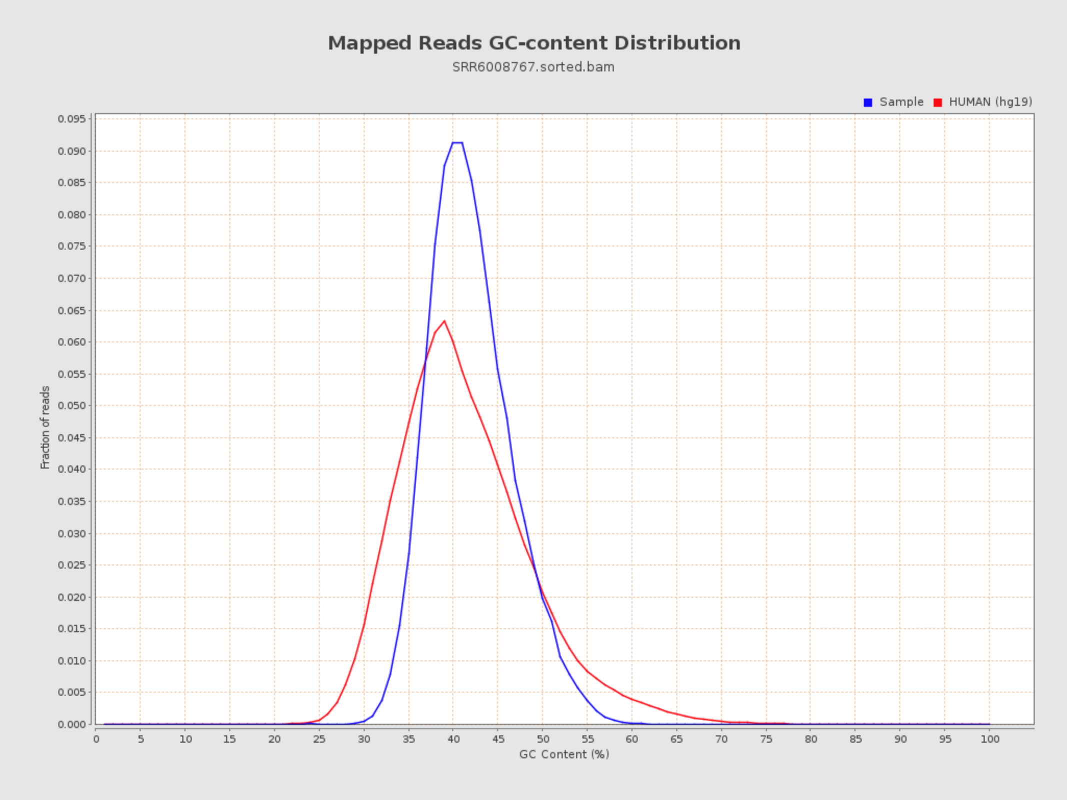
7. Results : Duplication Rate Histogram



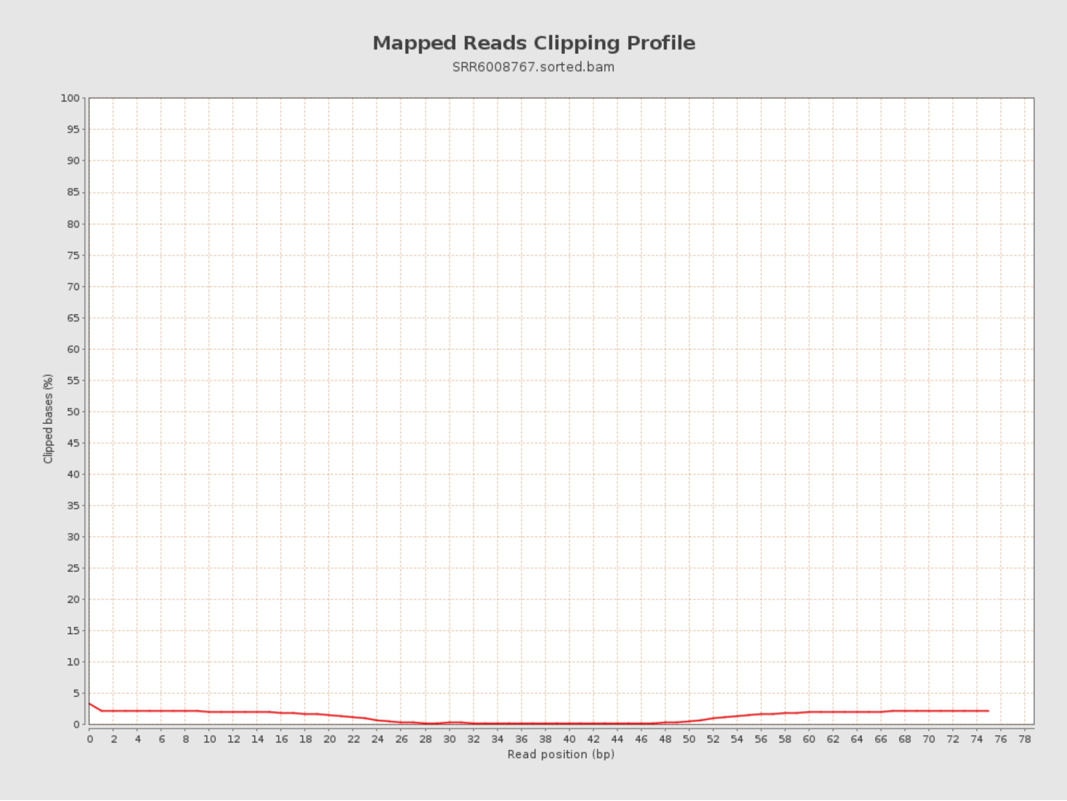
8. Results : Mapped Reads Nucleotide Content



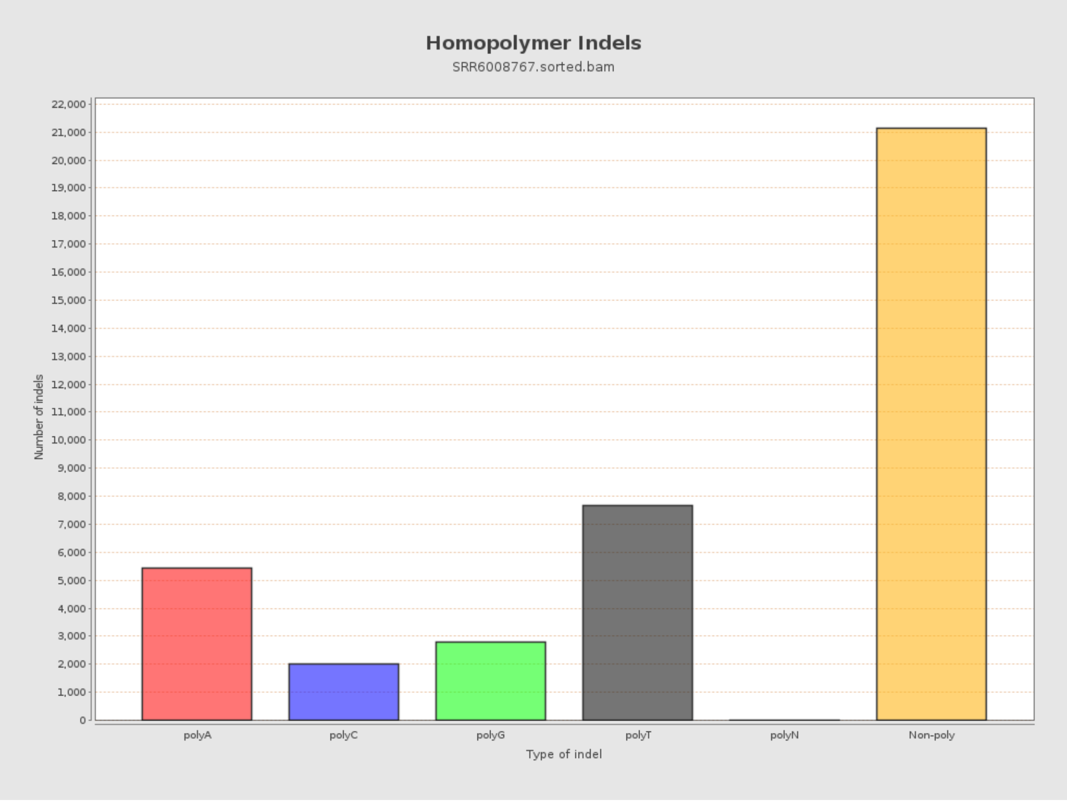
9. Results : Mapped Reads GC-content Distribution



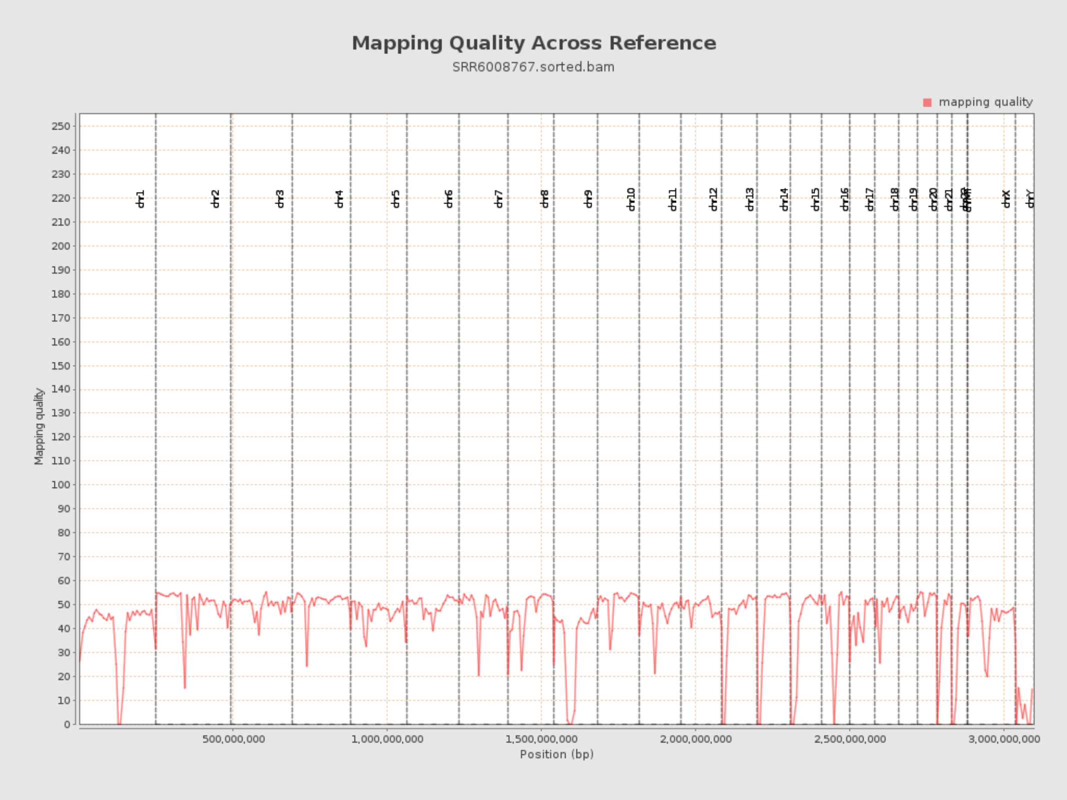
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram