Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:14:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008761.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_SRR6008761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:14:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,298,194
Mapped reads	840,715 / 64.76%
Unmapped reads	457,479 / 35.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,070 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	39,132 / 3.01%
Duplication rate	3.24%
Clipped reads	552,227 / 42.54%

2.2. ACGT Content

Number/percentage of A's	14,078,022 / 27.19%
Number/percentage of C's	8,888,121 / 17.17%
Number/percentage of T's	16,219,874 / 31.33%
Number/percentage of G's	12,582,027 / 24.3%
Number/percentage of N's	2,269 / 0%
GC Percentage	41.47%

2.3. Coverage

Mean	0.0167

Standard Deviation	0.1962

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Mismatches and indels

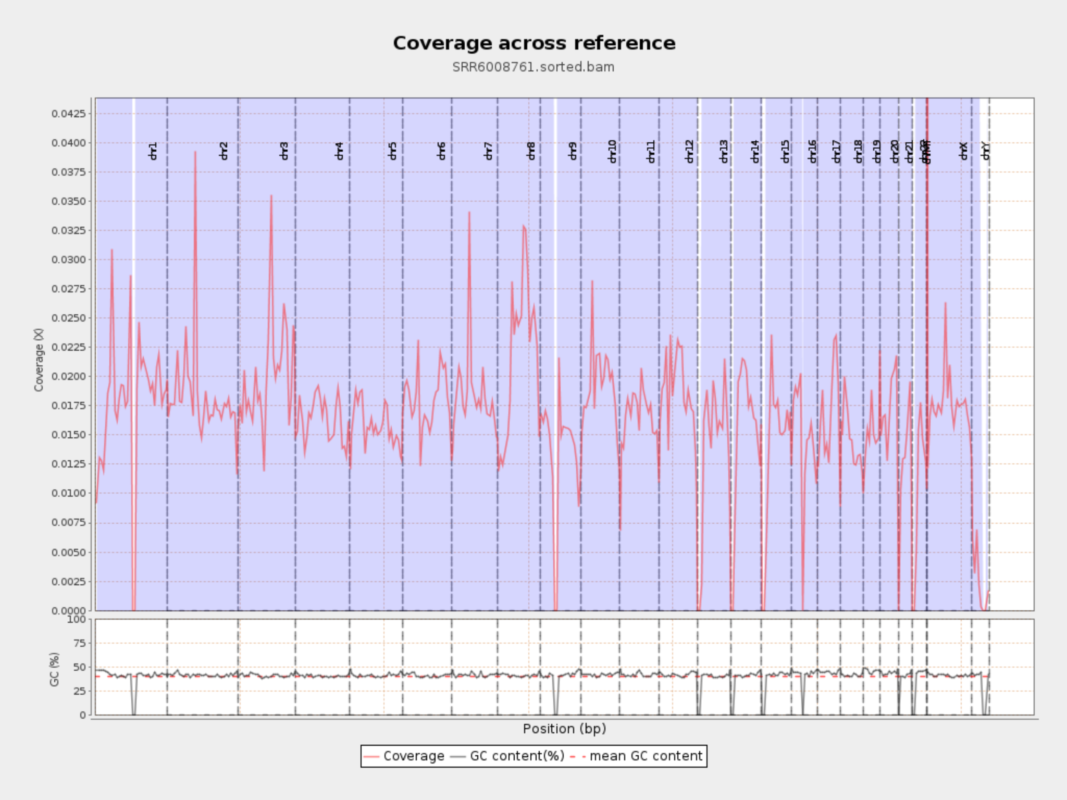
General error rate	0.97%
Mismatches	497,350
Insertions	4,111
Mapped reads with at least one insertion	0.49%
Deletions	19,149
Mapped reads with at least one deletion	2.25%
Homopolymer indels	48.08%

2.6. Chromosome stats

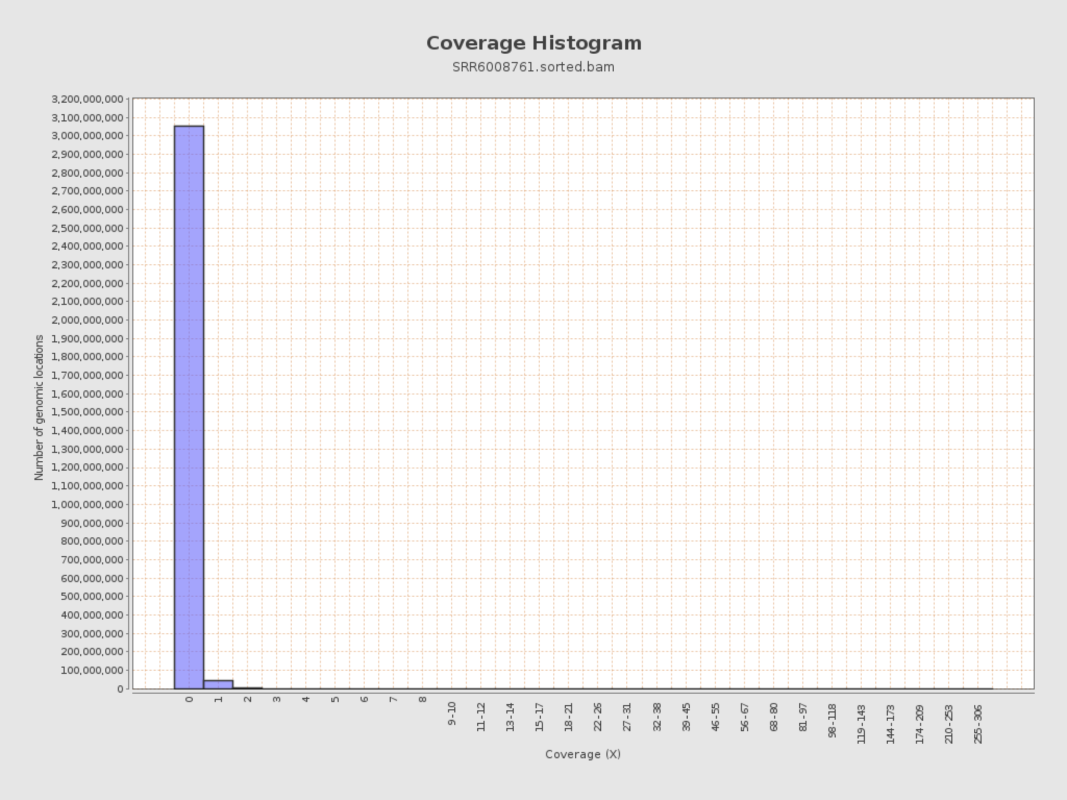
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4404474	0.0177	0.2574
chr2	243199373	4473269	0.0184	0.2618
chr3	198022430	3947668	0.0199	0.1656
chr4	191154276	3116568	0.0163	0.1483
chr5	180915260	2878833	0.0159	0.1463
chr6	171115067	3071957	0.018	0.1751
chr7	159138663	2950230	0.0185	0.3123

chr8	146364022	3217206	0.022	0.2134
chr9	141213431	1900646	0.0135	0.1952
chr10	135534747	2600554	0.0192	0.1861
chr11	135006516	2250547	0.0167	0.1809
chr12	133851895	2519109	0.0188	0.1623
chr13	115169878	1596335	0.0139	0.1413
chr14	107349540	1612633	0.015	0.1479
chr15	102531392	1414253	0.0138	0.1408
chr16	90354753	1287038	0.0142	0.1451
chr17	81195210	1369990	0.0169	0.1703
chr18	78077248	1144207	0.0147	0.2778
chr19	59128983	897773	0.0152	0.1848
chr20	63025520	1086285	0.0172	0.1539
chr21	48129895	614802	0.0128	0.1368
chr22	51304566	530016	0.0103	0.1195
chrMT	16571	25931	1.5648	2.1003
chrX	155270560	2746333	0.0177	0.1703
chrY	59373566	142976	0.0024	0.0617

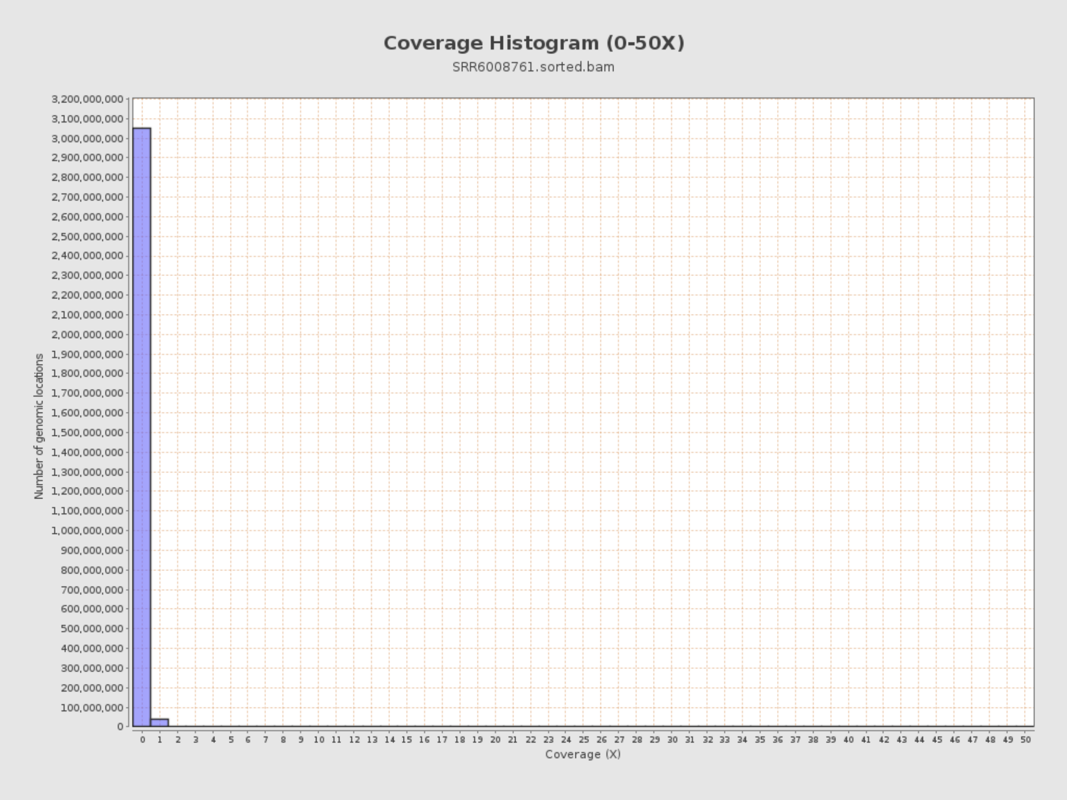
3. Results : Coverage across reference



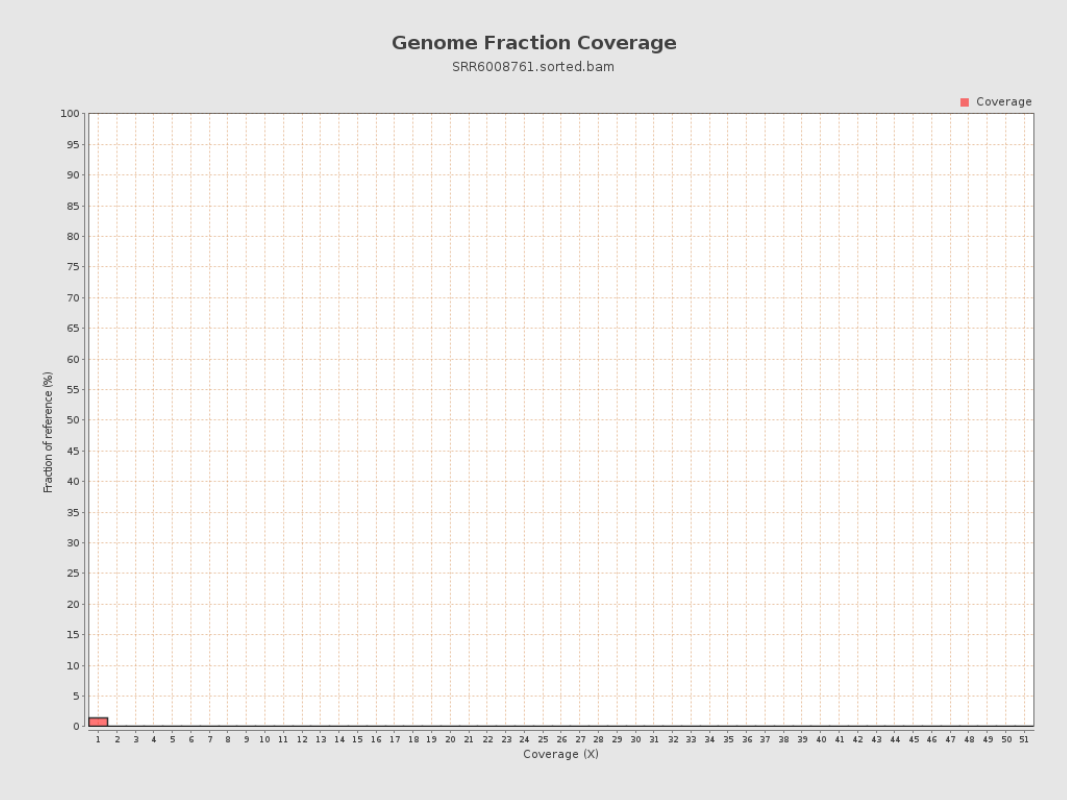
4. Results : Coverage Histogram



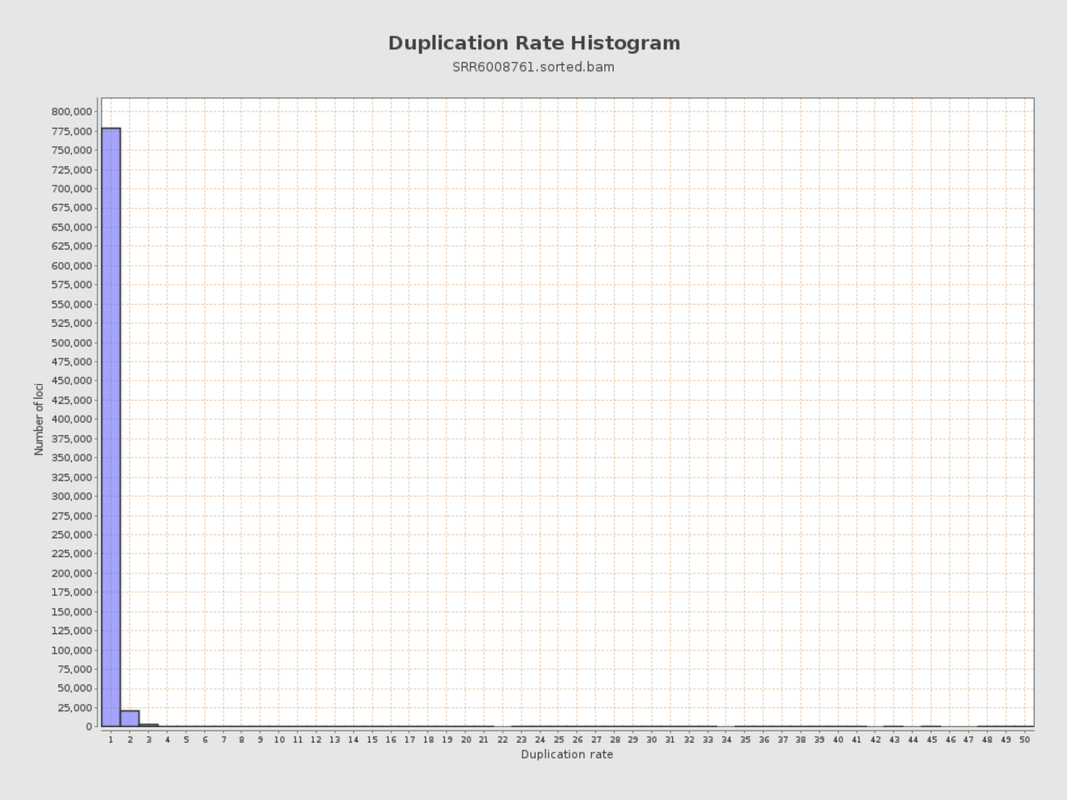
5. Results : Coverage Histogram (0-50X)



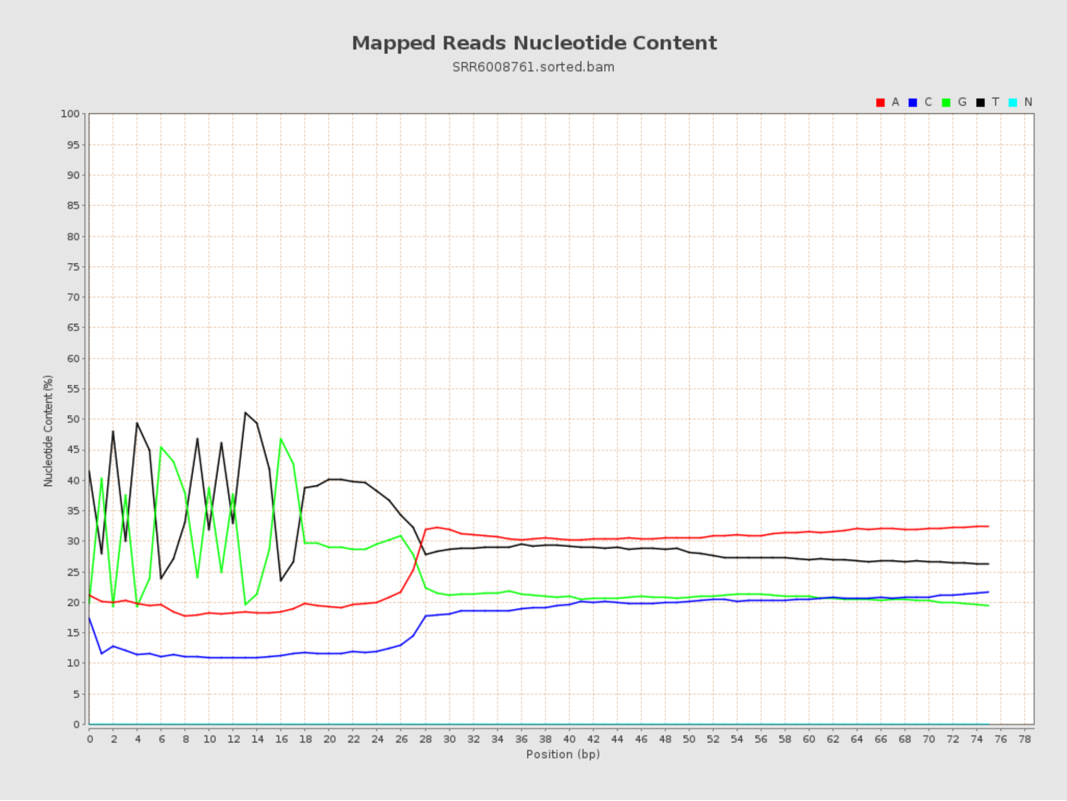
6. Results : Genome Fraction Coverage



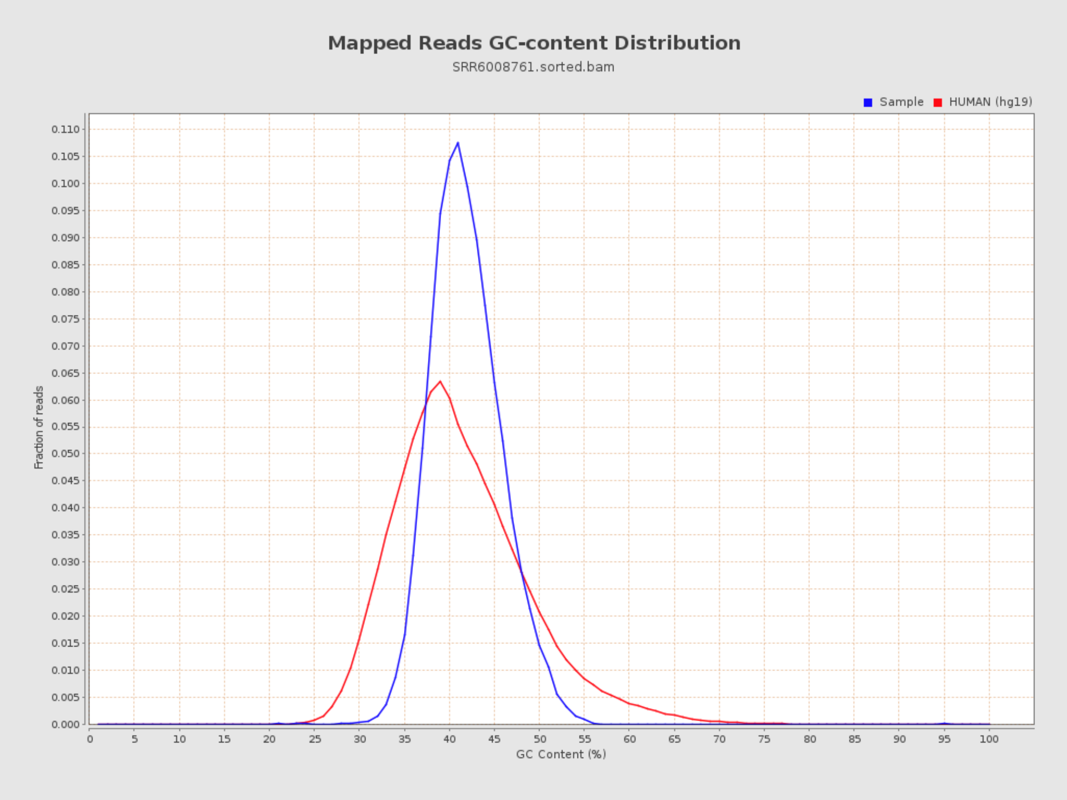
7. Results : Duplication Rate Histogram



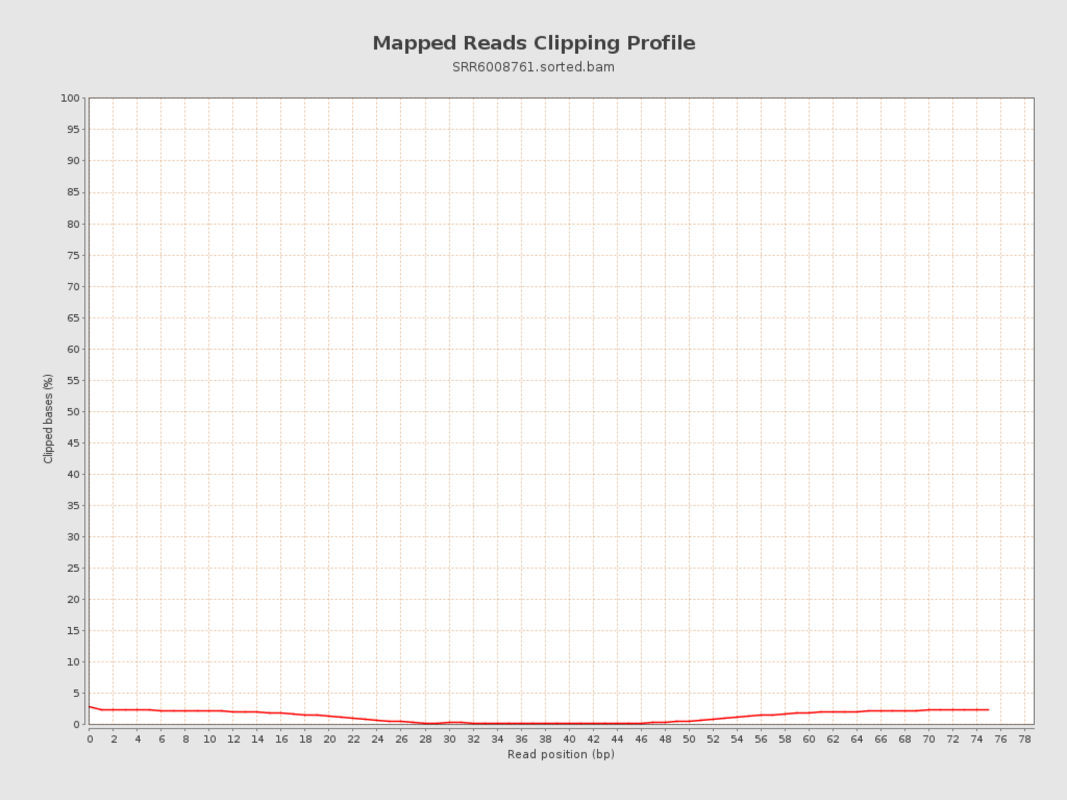
8. Results : Mapped Reads Nucleotide Content



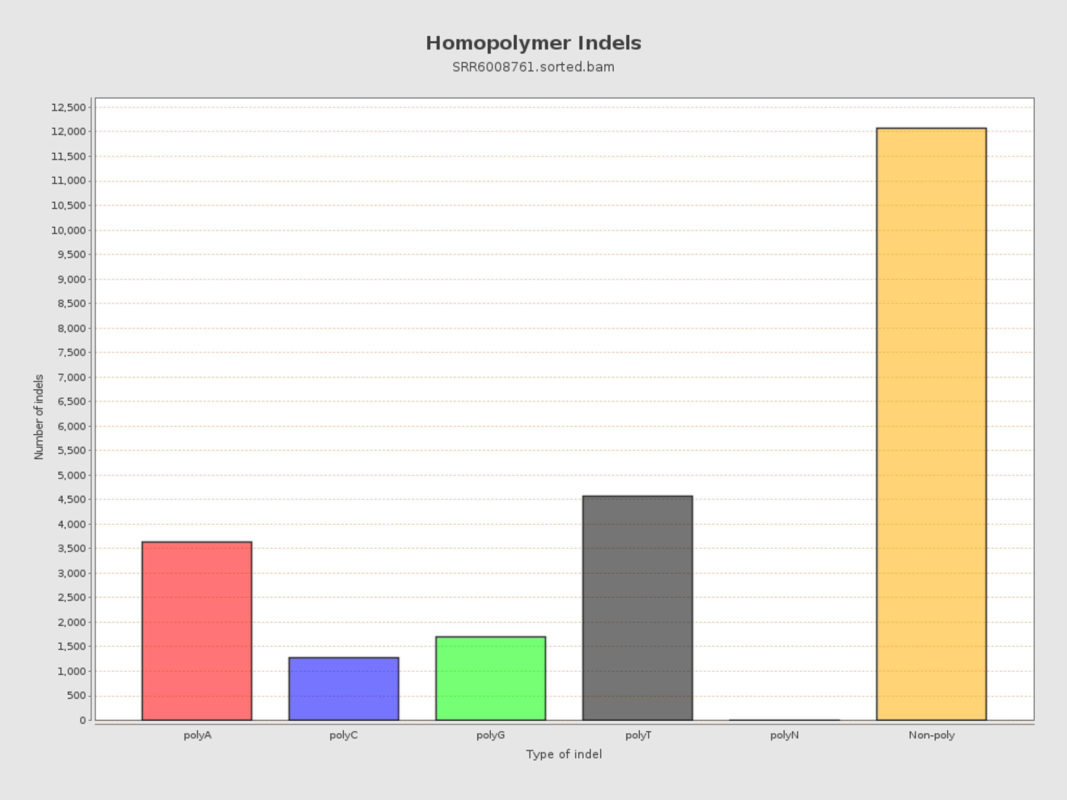
9. Results : Mapped Reads GC-content Distribution



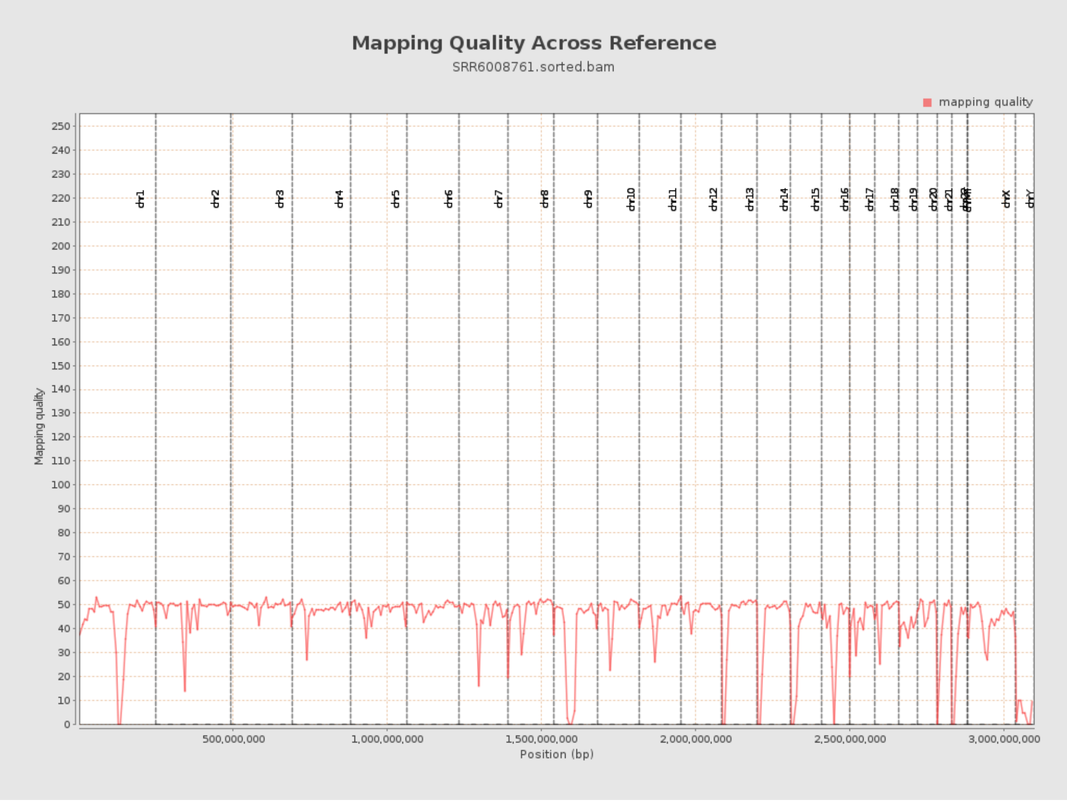
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram