Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:19:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008781.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_SRR6008781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:19:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,363,162
Mapped reads	1,122,236 / 82.33%
Unmapped reads	240,926 / 17.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,929 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	49,375 / 3.62%
Duplication rate	3.61%
Clipped reads	516,021 / 37.85%

2.2. ACGT Content

Number/percentage of A's	19,828,197 / 26.78%
Number/percentage of C's	14,365,618 / 19.4%
Number/percentage of T's	22,758,291 / 30.74%
Number/percentage of G's	16,979,495 / 22.93%
Number/percentage of N's	107,030 / 0.14%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2397

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

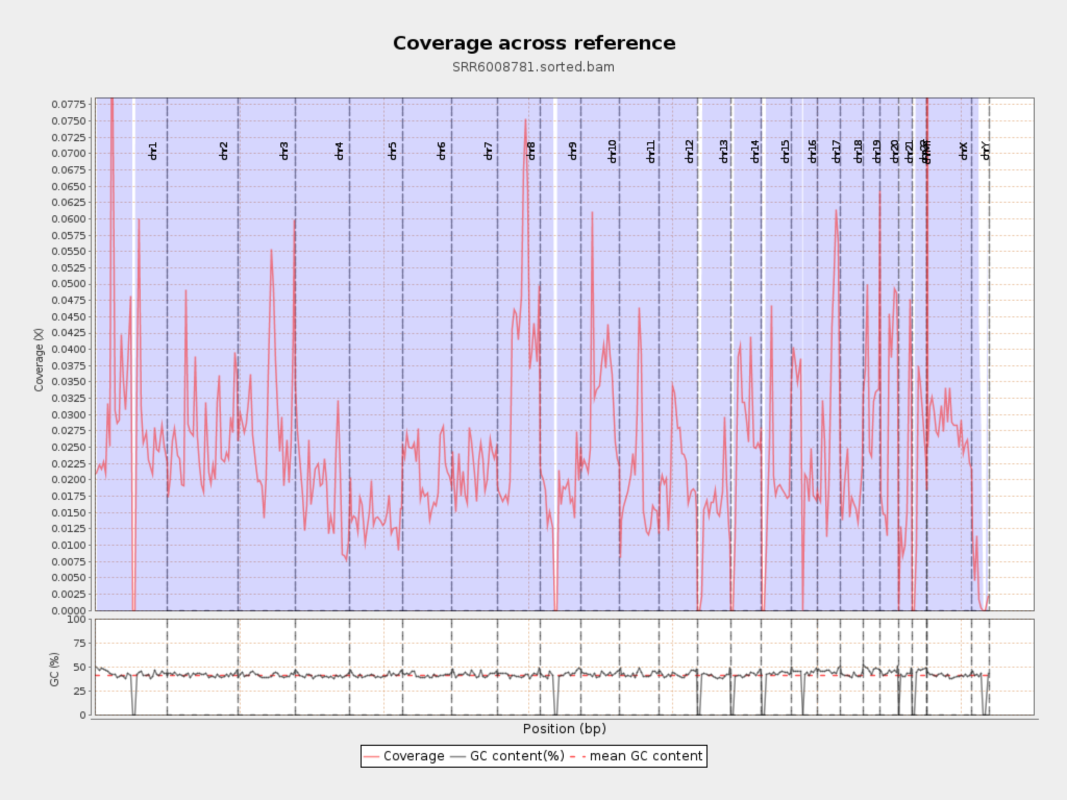
General error rate	0.86%
Mismatches	626,635
Insertions	5,373
Mapped reads with at least one insertion	0.47%
Deletions	22,072
Mapped reads with at least one deletion	1.95%
Homopolymer indels	45.06%

2.6. Chromosome stats

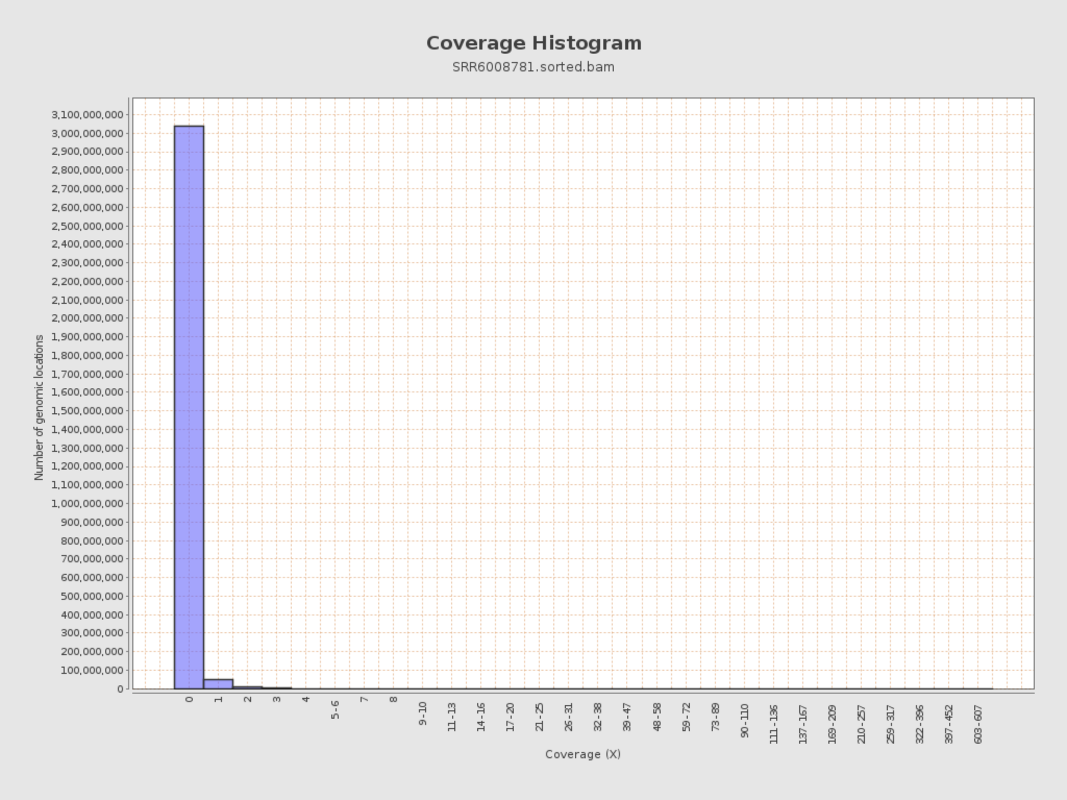
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7353852	0.0295	0.3783
chr2	243199373	6392583	0.0263	0.33
chr3	198022430	5777118	0.0292	0.21
chr4	191154276	3574668	0.0187	0.1683
chr5	180915260	2543664	0.0141	0.1402
chr6	171115067	3659441	0.0214	0.1923
chr7	159138663	3459707	0.0217	0.2231

chr8	146364022	5733932	0.0392	0.2926
chr9	141213431	2294832	0.0163	0.1764
chr10	135534747	4413443	0.0326	0.3321
chr11	135006516	2700360	0.02	0.187
chr12	133851895	2945559	0.022	0.1776
chr13	115169878	1646386	0.0143	0.1429
chr14	107349540	2747330	0.0256	0.1943
chr15	102531392	1847061	0.018	0.1607
chr16	90354753	2258418	0.025	0.2297
chr17	81195210	2680908	0.033	0.233
chr18	78077248	1346631	0.0172	0.2643
chr19	59128983	2043297	0.0346	0.2954
chr20	63025520	1961748	0.0311	0.2152
chr21	48129895	913015	0.019	0.1731
chr22	51304566	1081124	0.0211	0.1738
chrMT	16571	86772	5.2364	3.9282
chrX	155270560	4399319	0.0283	0.2071
chrY	59373566	216697	0.0036	0.1097

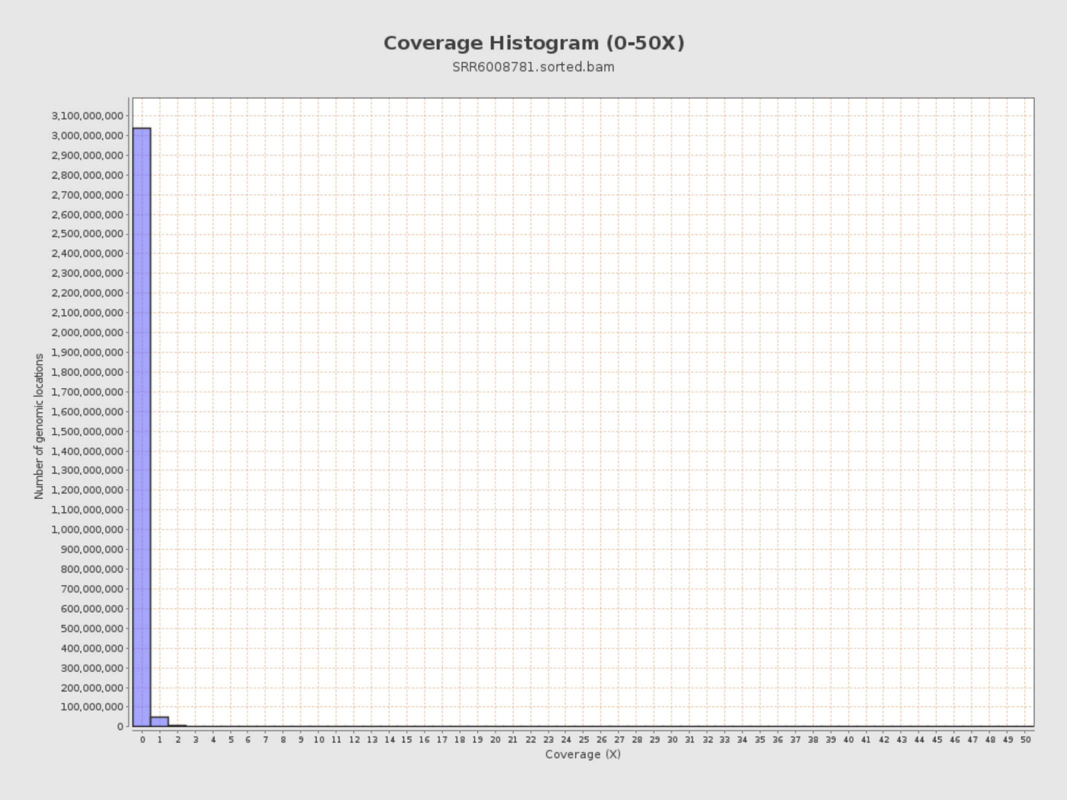
3. Results : Coverage across reference



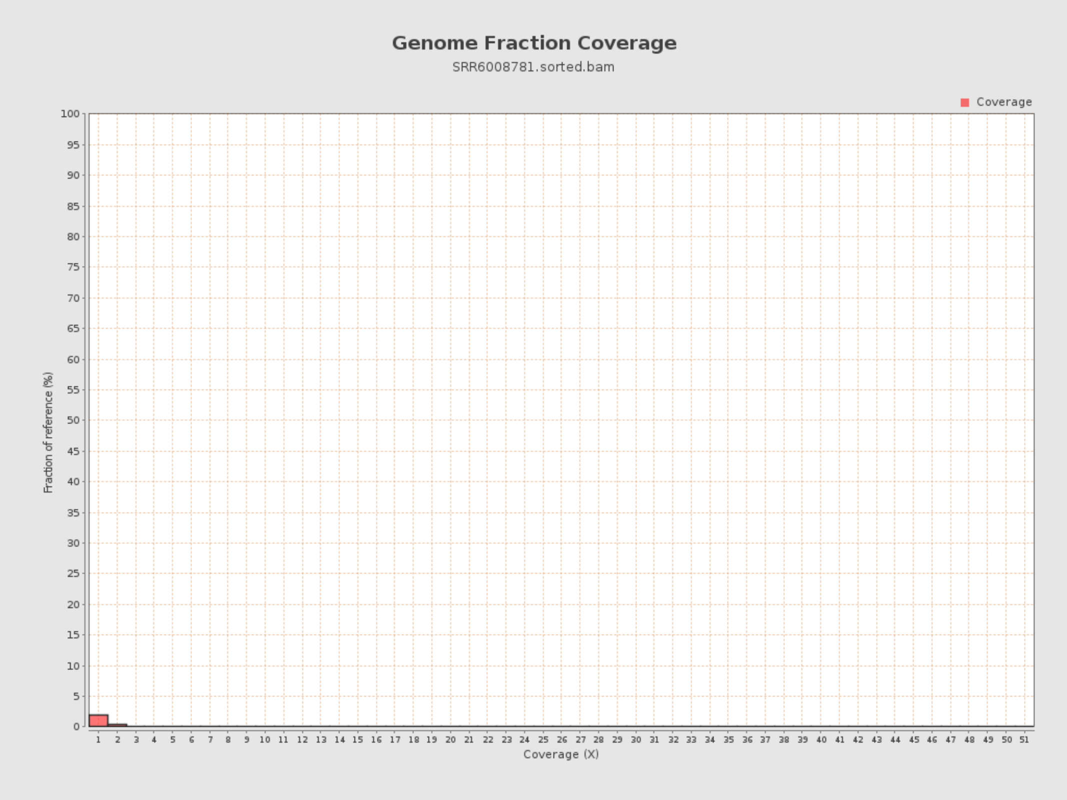
4. Results : Coverage Histogram



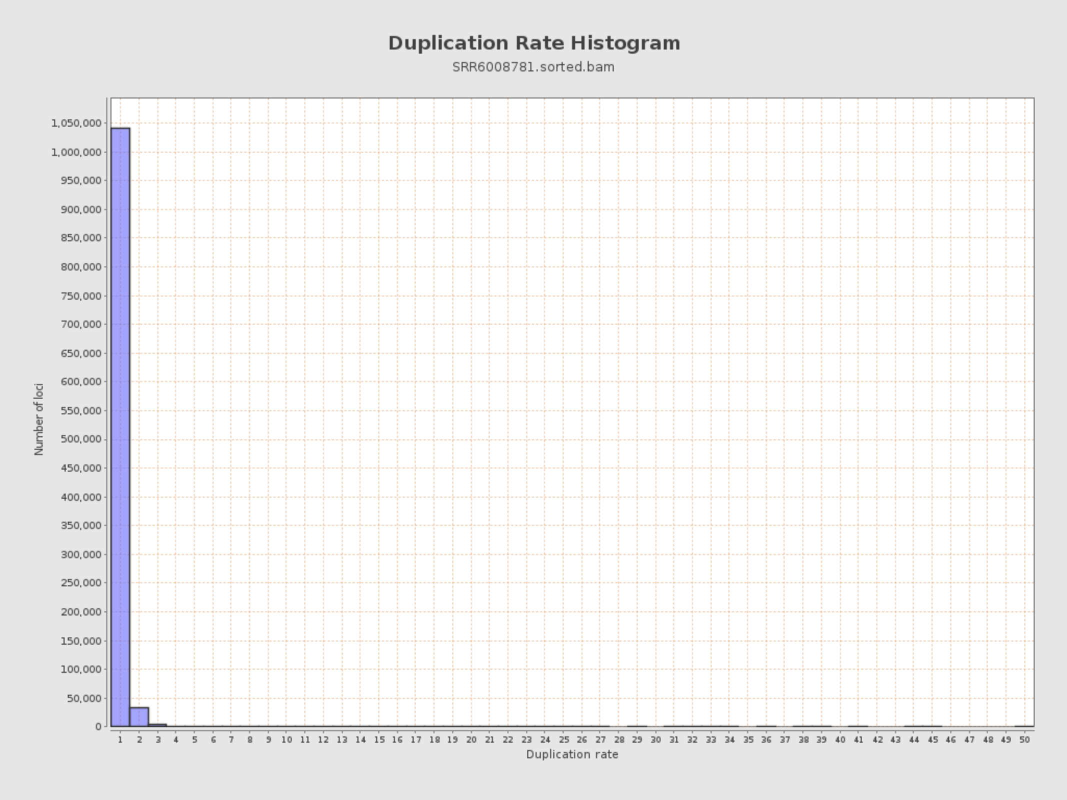
5. Results : Coverage Histogram (0-50X)



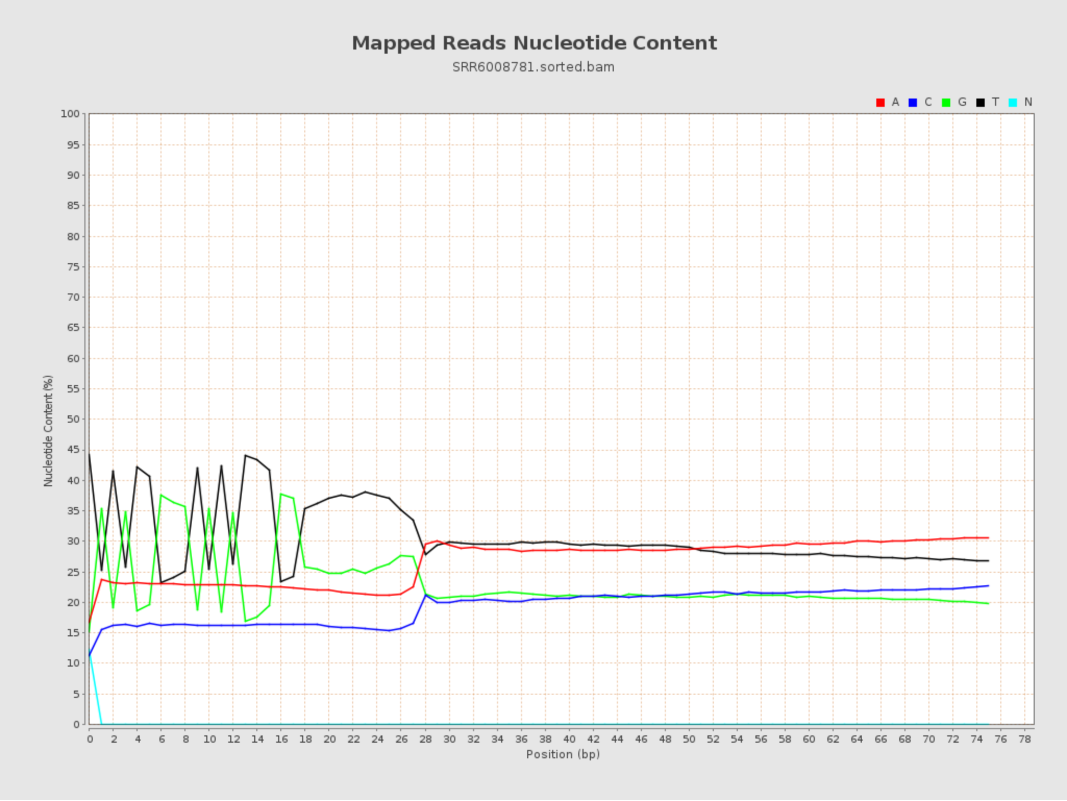
6. Results : Genome Fraction Coverage



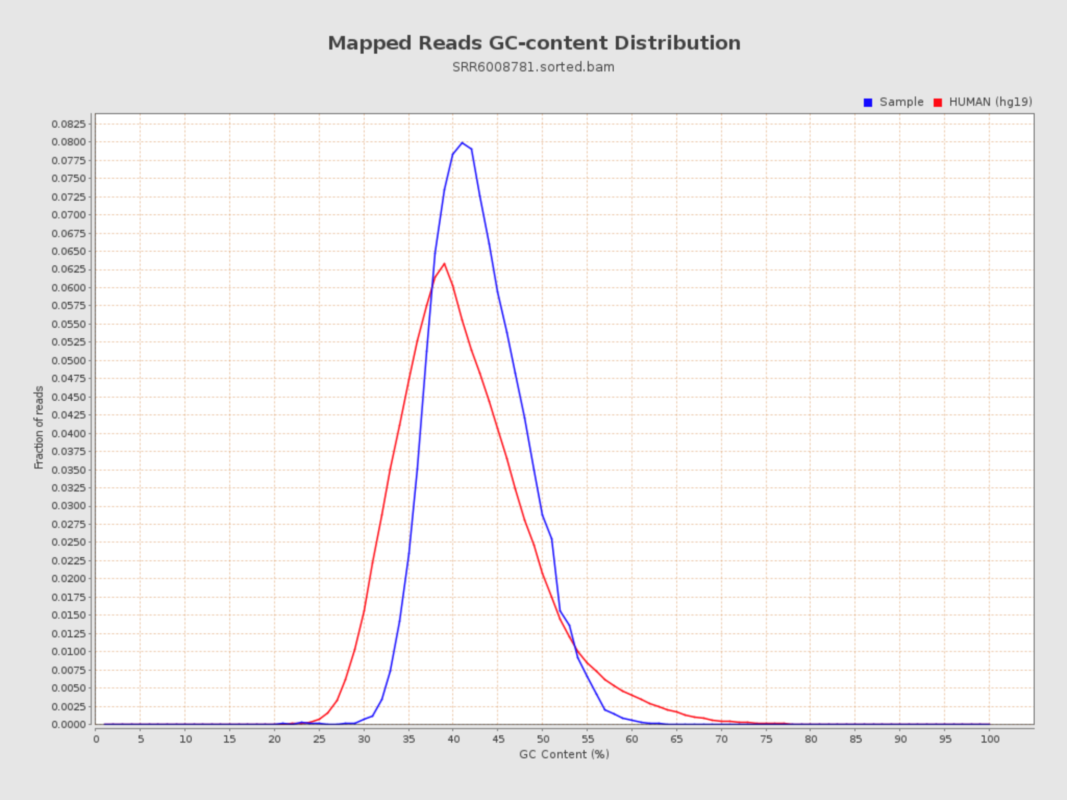
7. Results : Duplication Rate Histogram



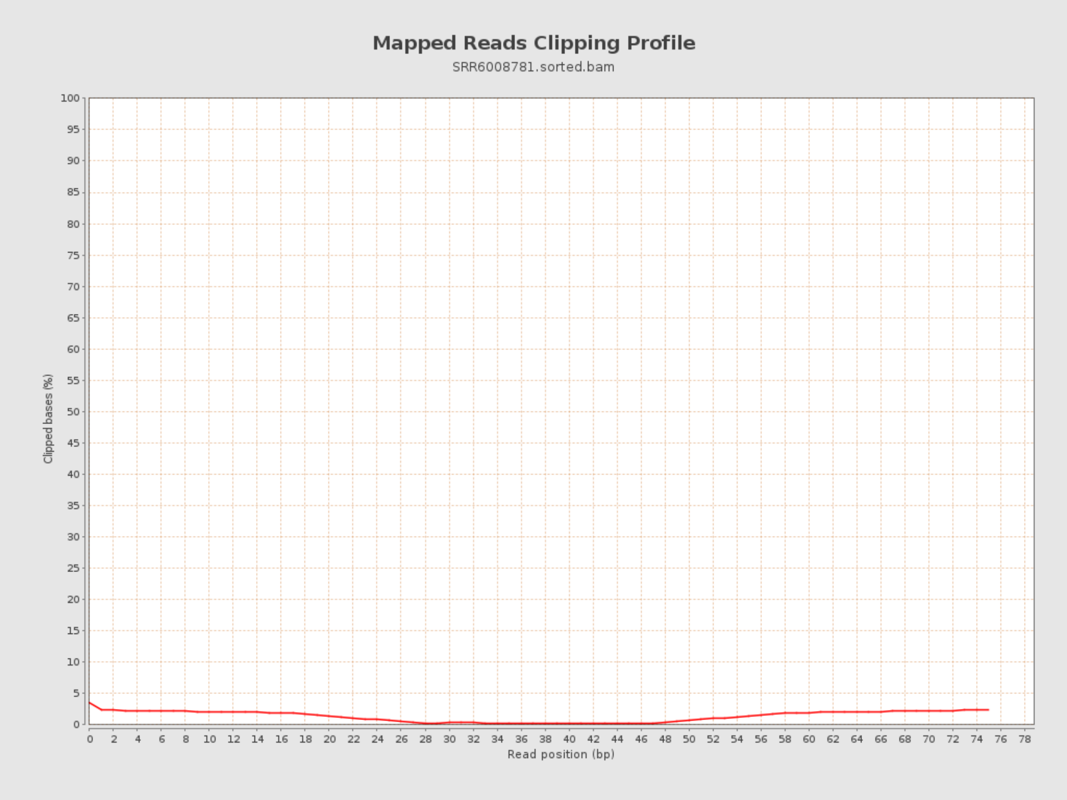
8. Results : Mapped Reads Nucleotide Content



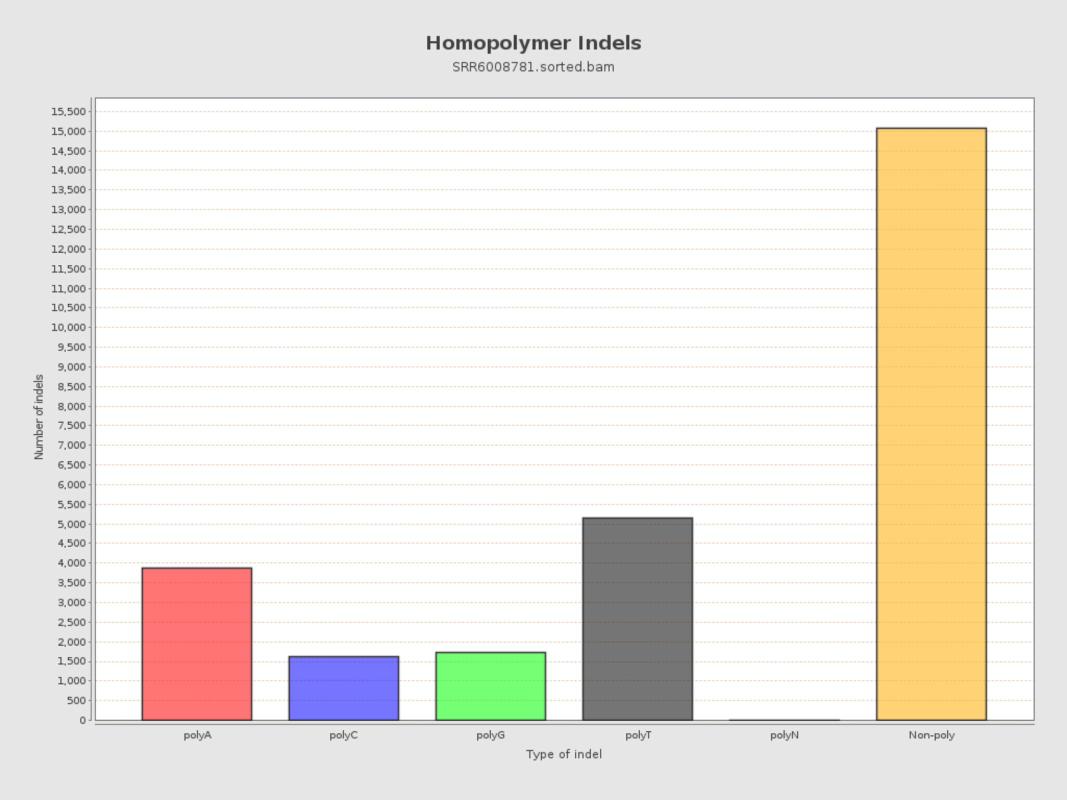
9. Results : Mapped Reads GC-content Distribution



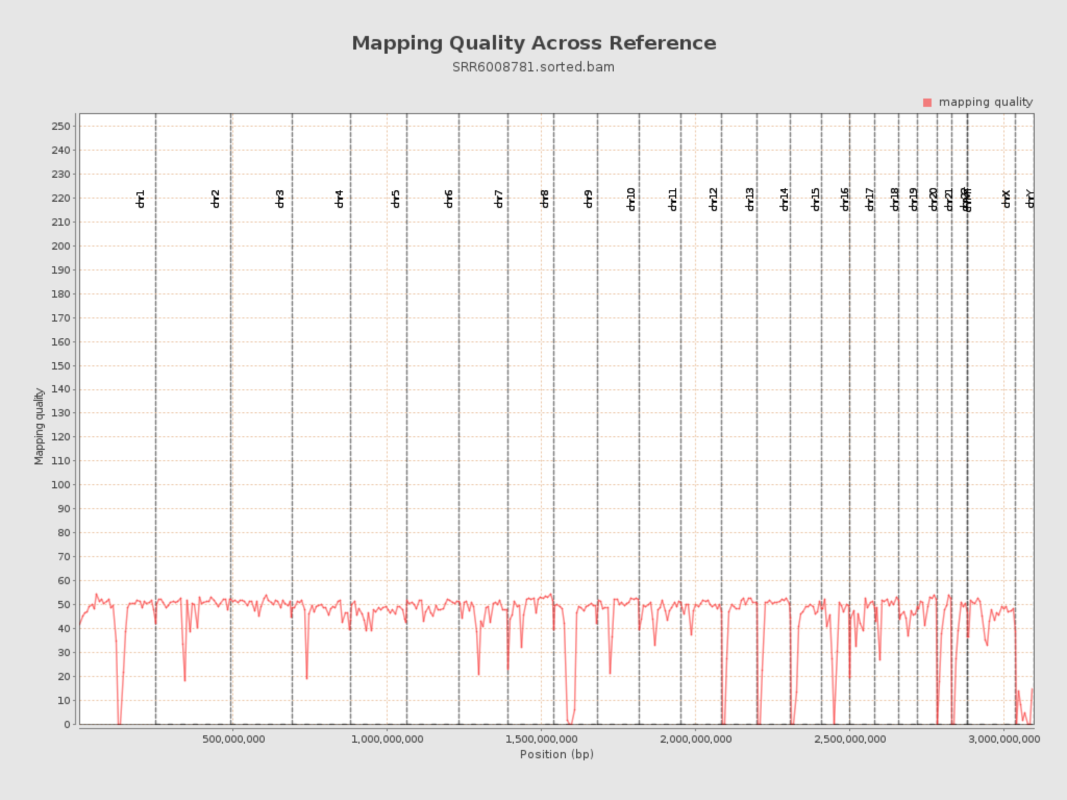
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram