Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:21:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008782.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_SRR6008782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:21:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,197,972
Mapped reads	1,058,121 / 88.33%
Unmapped reads	139,851 / 11.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,079 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	41,776 / 3.49%
Duplication rate	3.28%
Clipped reads	497,957 / 41.57%

2.2. ACGT Content

Number/percentage of A's	18,591,007 / 26.71%
Number/percentage of C's	13,457,918 / 19.33%
Number/percentage of T's	21,465,102 / 30.83%
Number/percentage of G's	15,984,998 / 22.96%
Number/percentage of N's	113,854 / 0.16%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2216

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

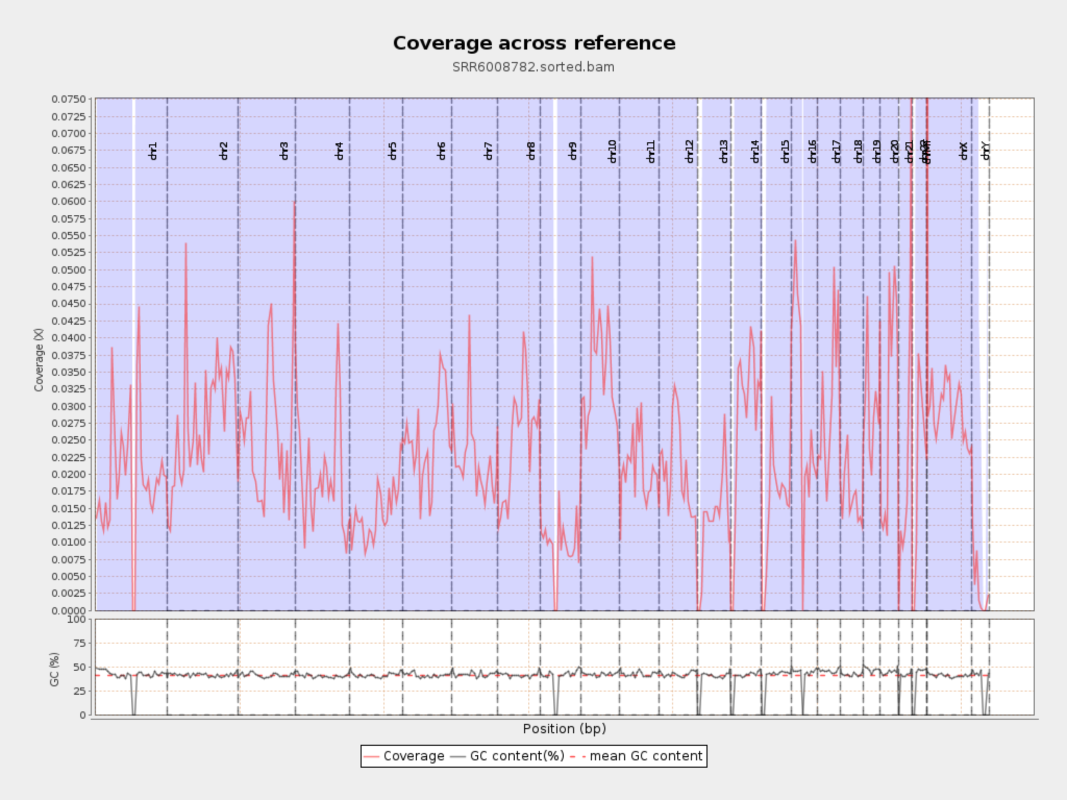
General error rate	0.82%
Mismatches	562,777
Insertions	4,834
Mapped reads with at least one insertion	0.45%
Deletions	16,997
Mapped reads with at least one deletion	1.59%
Homopolymer indels	45.25%

2.6. Chromosome stats

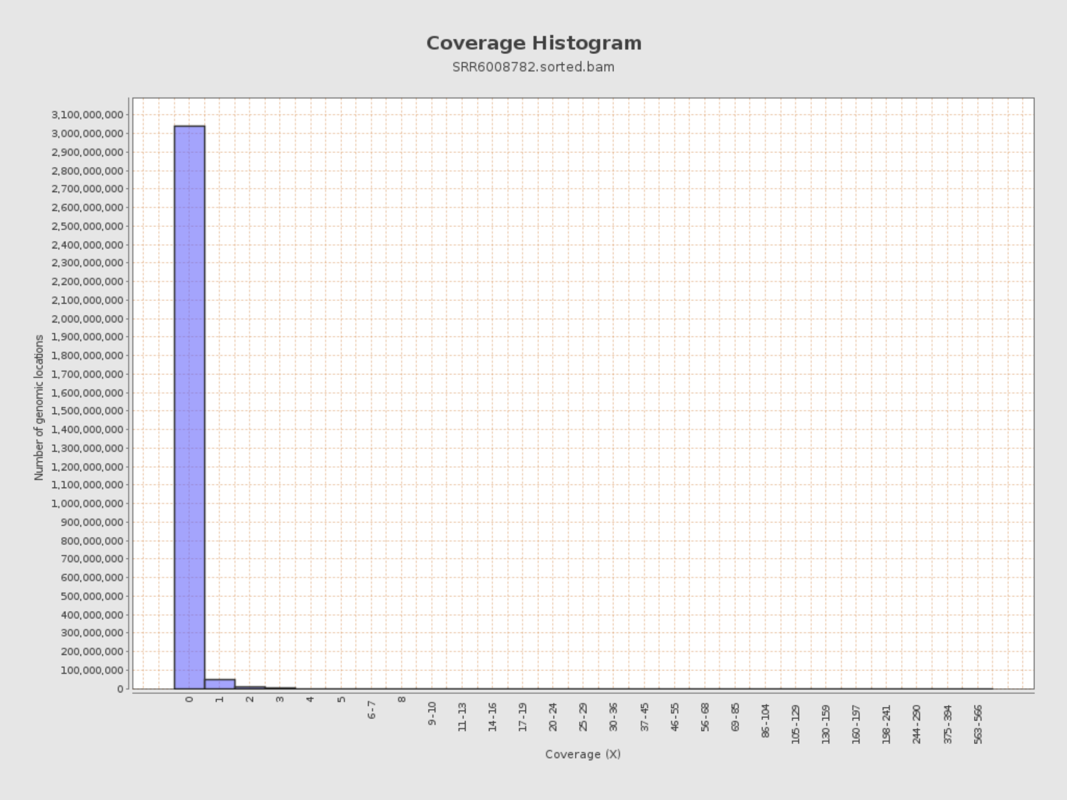
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4887788	0.0196	0.2615
chr2	243199373	6838611	0.0281	0.3115
chr3	198022430	5093760	0.0257	0.1905
chr4	191154276	3890306	0.0204	0.1726
chr5	180915260	2563263	0.0142	0.1382
chr6	171115067	4306326	0.0252	0.2007
chr7	159138663	3518176	0.0221	0.3167

chr8	146364022	3695309	0.0252	0.2502
chr9	141213431	1336428	0.0095	0.1357
chr10	135534747	4691734	0.0346	0.2738
chr11	135006516	2848602	0.0211	0.2194
chr12	133851895	2742768	0.0205	0.1679
chr13	115169878	1528855	0.0133	0.1345
chr14	107349540	3015981	0.0281	0.1981
chr15	102531392	1584448	0.0155	0.1446
chr16	90354753	2642557	0.0292	0.2209
chr17	81195210	2447248	0.0301	0.2232
chr18	78077248	1282985	0.0164	0.2535
chr19	59128983	1775056	0.03	0.2542
chr20	63025520	1900639	0.0302	0.2083
chr21	48129895	1105412	0.023	0.186
chr22	51304566	1088260	0.0212	0.1709
chrMT	16571	108315	6.5364	4.7308
chrX	155270560	4554709	0.0293	0.2081
chrY	59373566	195750	0.0033	0.0844

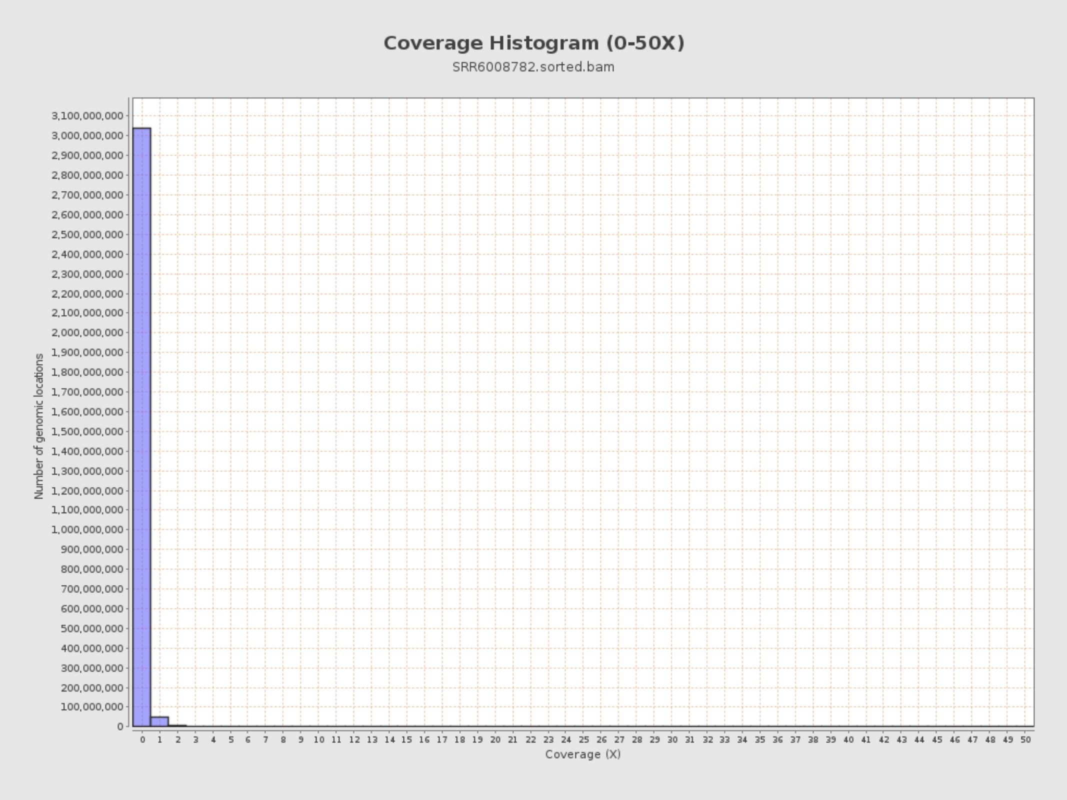
3. Results : Coverage across reference



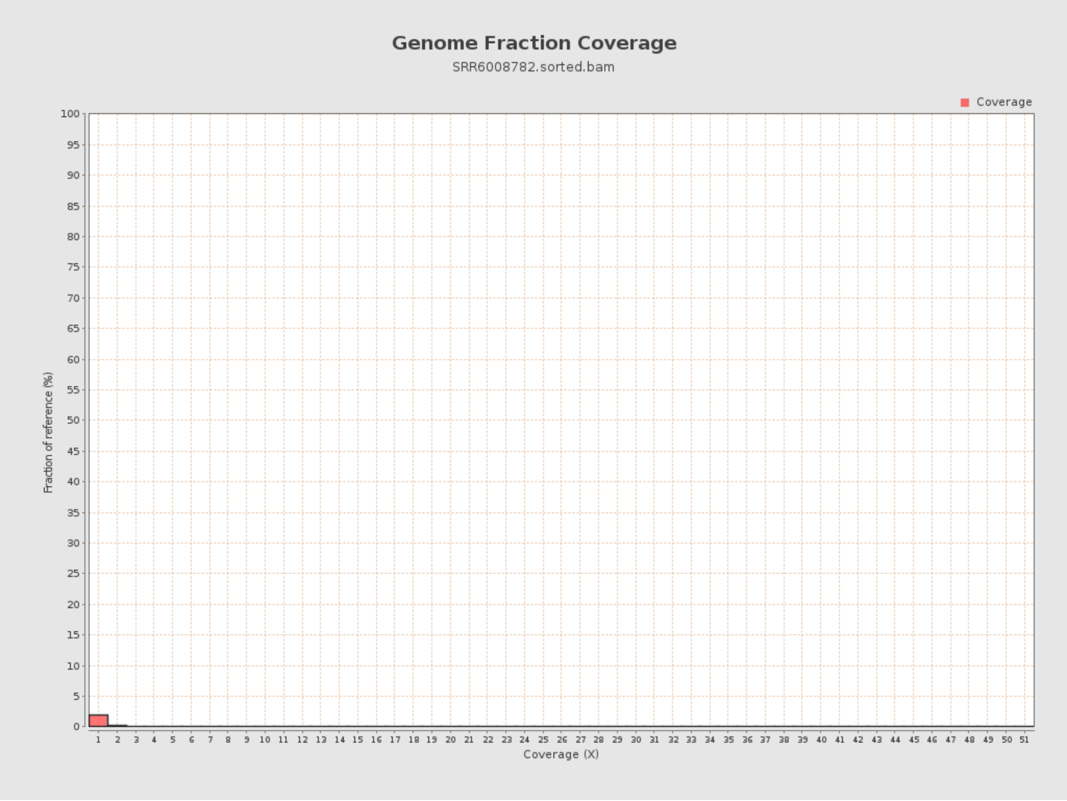
4. Results : Coverage Histogram



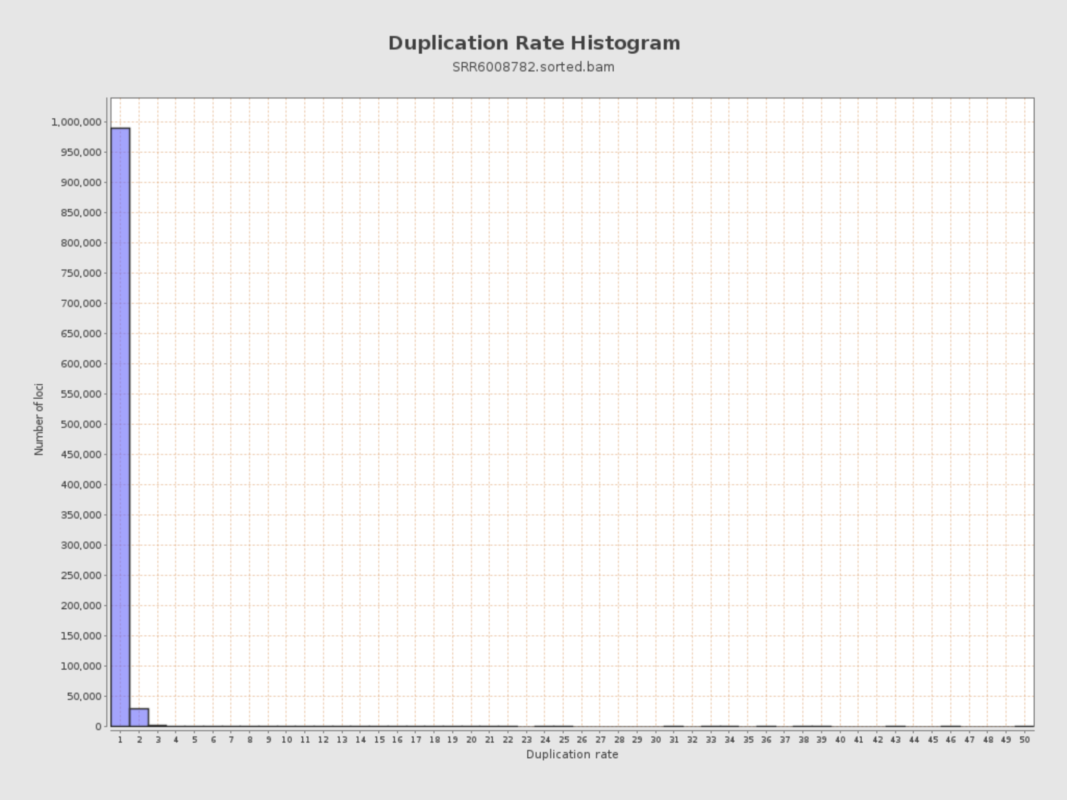
5. Results : Coverage Histogram (0-50X)



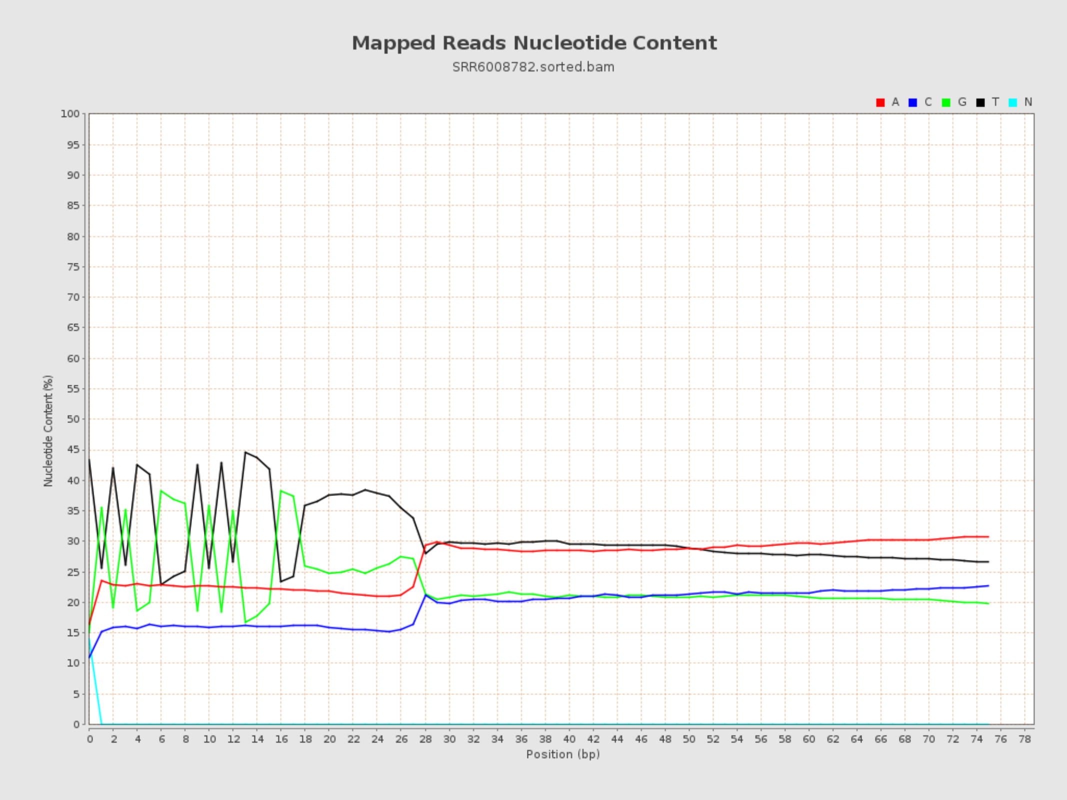
6. Results : Genome Fraction Coverage



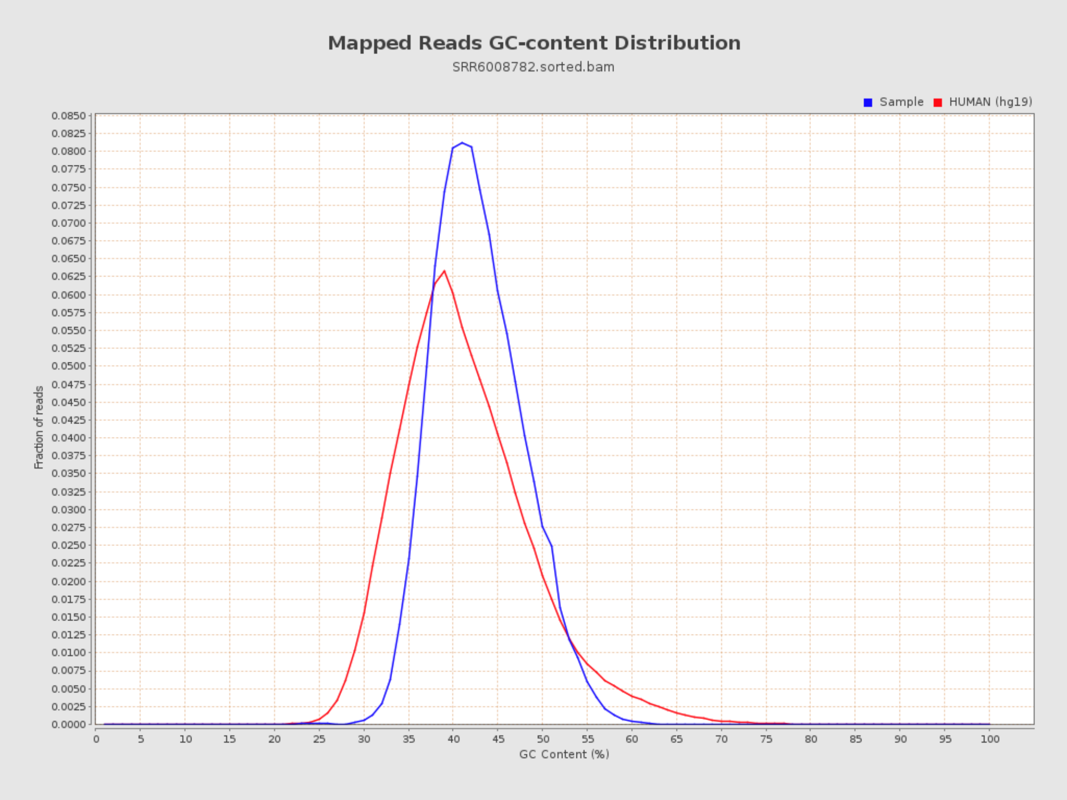
7. Results : Duplication Rate Histogram



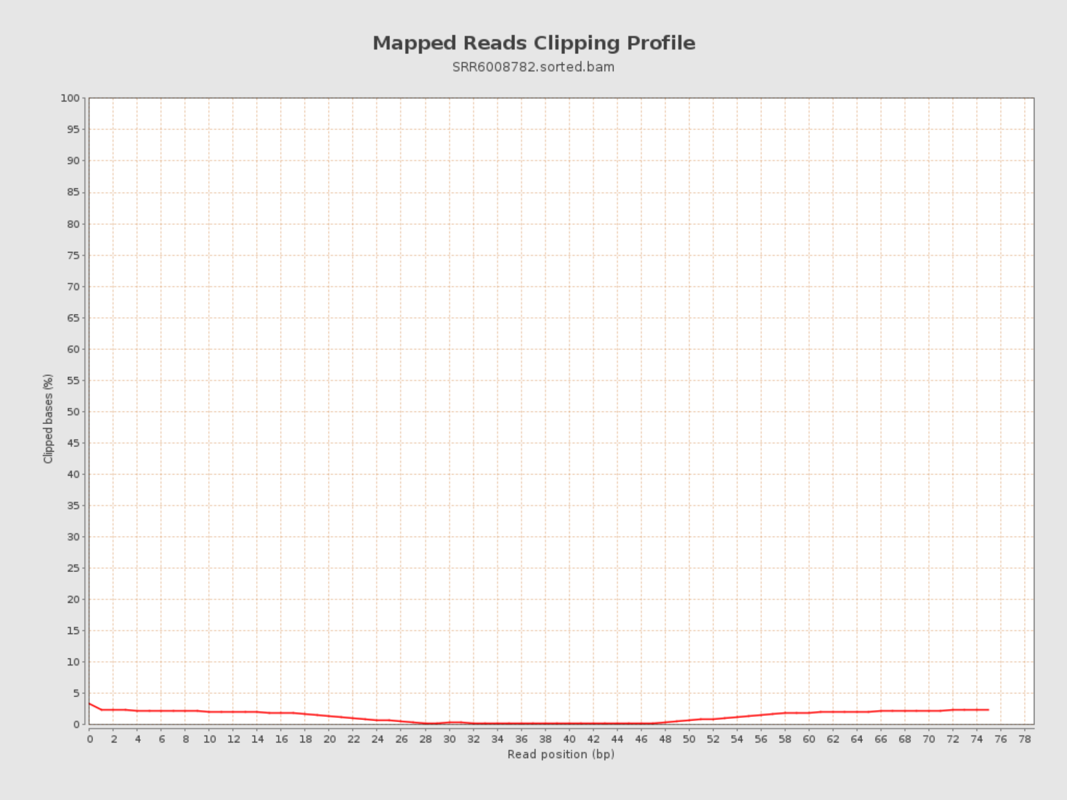
8. Results : Mapped Reads Nucleotide Content



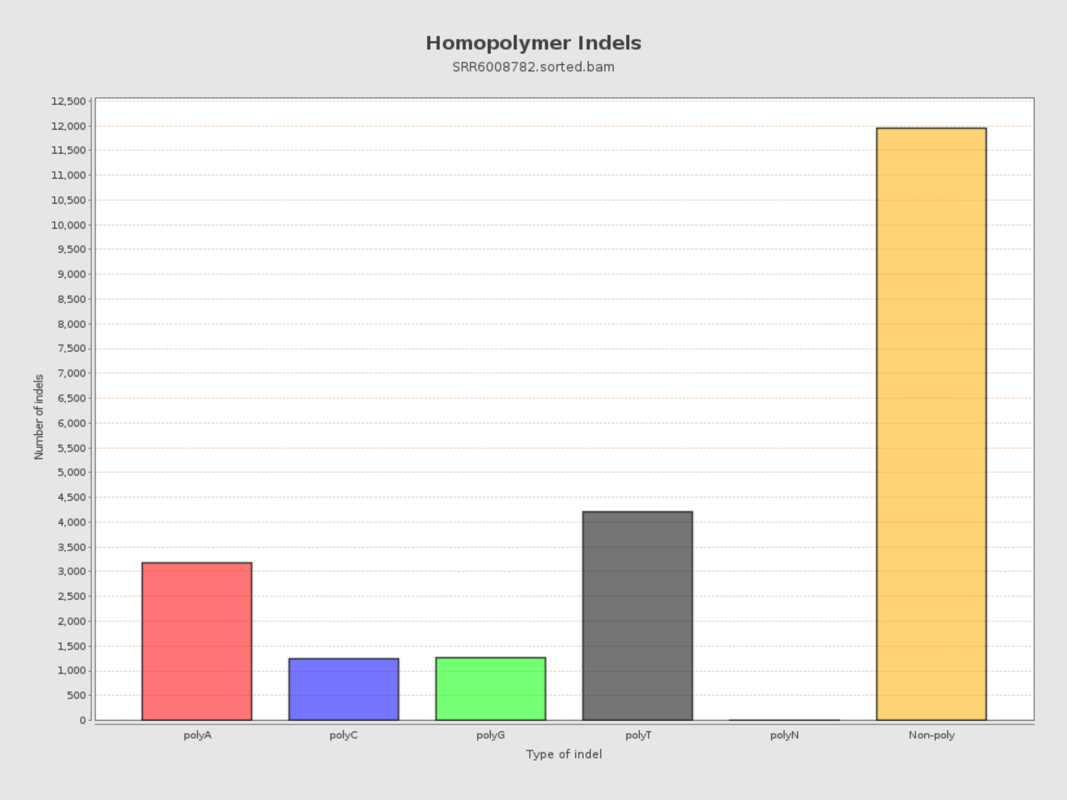
9. Results : Mapped Reads GC-content Distribution



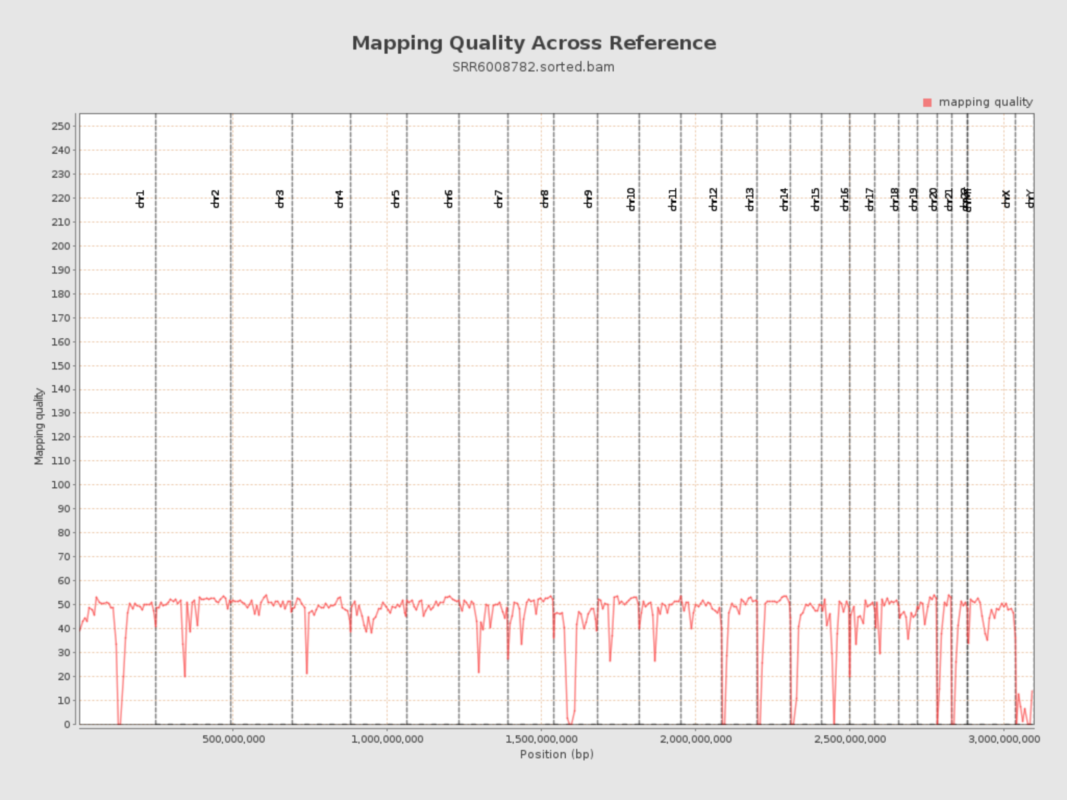
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram