Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:21:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080742.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_SRR3080742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:21:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,133,359
Mapped reads	6,618,413 / 81.37%
Unmapped reads	1,514,946 / 18.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,831 / 0.53%
Read min/max/mean length	30 / 66 / 66.17
Duplicated reads (estimated)	1,276,877 / 15.7%
Duplication rate	13.08%
Clipped reads	874,705 / 10.75%

2.2. ACGT Content

Number/percentage of A's	133,771,505 / 31.49%
Number/percentage of C's	84,687,126 / 19.94%
Number/percentage of T's	109,259,644 / 25.72%
Number/percentage of G's	96,065,672 / 22.62%
Number/percentage of N's	978,051 / 0.23%
GC Percentage	42.55%

2.3. Coverage

Mean	0.1373

Standard Deviation	0.8303

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

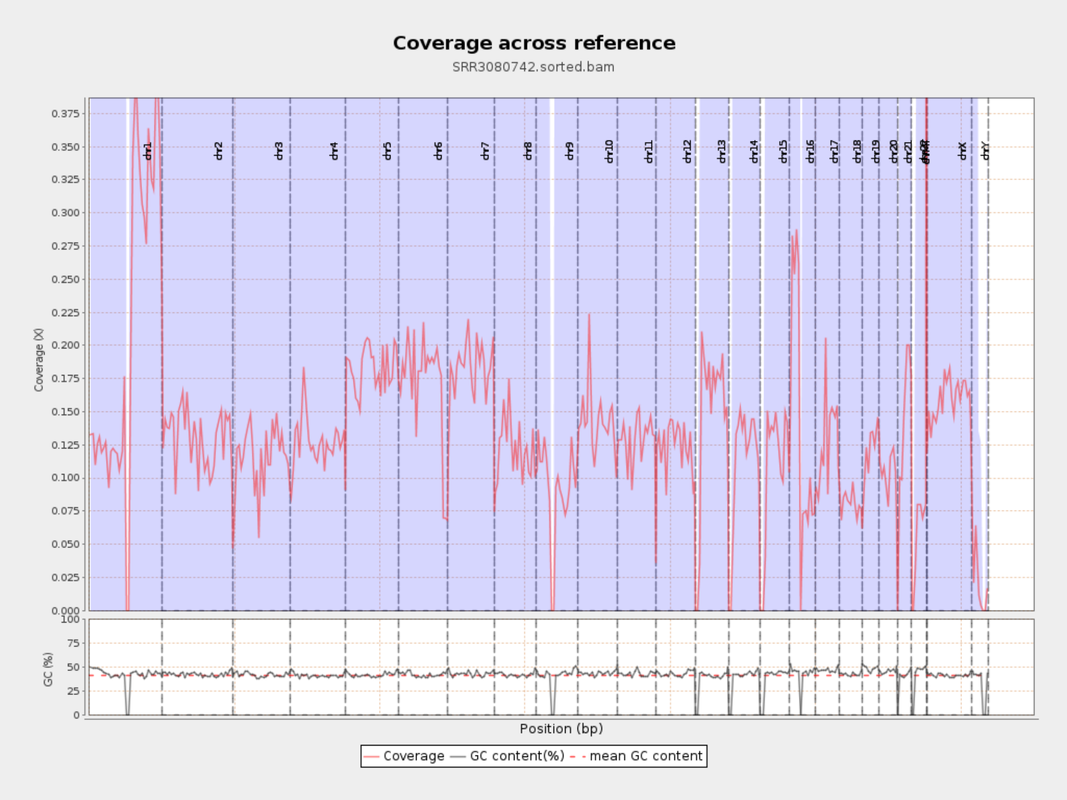
General error rate	0.99%
Mismatches	4,153,231
Insertions	29,581
Mapped reads with at least one insertion	0.44%
Deletions	73,433
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.29%

2.6. Chromosome stats

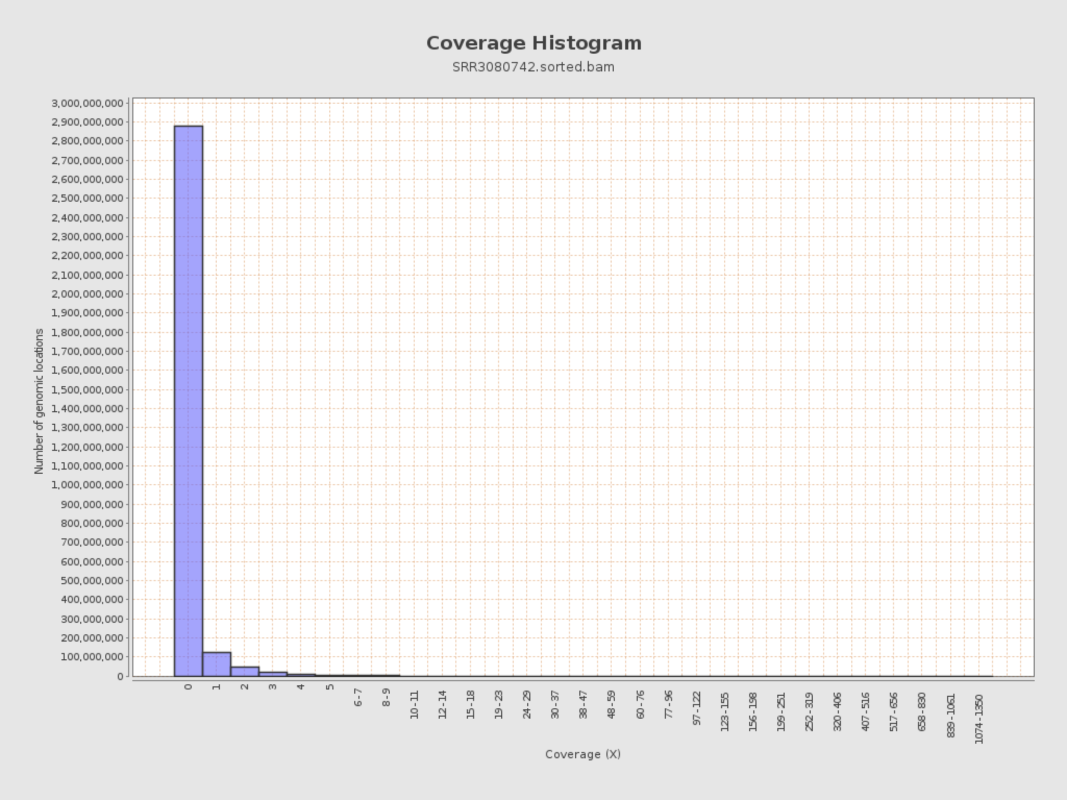
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	51672390	0.2073	1.2506
chr2	243199373	31955510	0.1314	0.7376
chr3	198022430	22782784	0.1151	0.6142
chr4	191154276	24322663	0.1272	0.6998
chr5	180915260	33081763	0.1829	0.7903
chr6	171115067	29382803	0.1717	0.8703
chr7	159138663	29266015	0.1839	1.0883

chr8	146364022	17805963	0.1217	1.0424
chr9	141213431	12880067	0.0912	0.5888
chr10	135534747	19379357	0.143	0.973
chr11	135006516	17470273	0.1294	0.7512
chr12	133851895	16673837	0.1246	0.6457
chr13	115169878	16794825	0.1458	0.7217
chr14	107349540	12058753	0.1123	0.6336
chr15	102531392	10859408	0.1059	0.5876
chr16	90354753	12715050	0.1407	0.747
chr17	81195210	10469516	0.1289	0.6874
chr18	78077248	6372491	0.0816	0.7963
chr19	59128983	7128518	0.1206	1.3474
chr20	63025520	6479810	0.1028	0.5954
chr21	48129895	6647931	0.1381	0.7449
chr22	51304566	2780854	0.0542	0.4375
chrMT	16571	28142	1.6983	2.2042
chrX	155270560	24701297	0.1591	0.7373
chrY	59373566	1189916	0.02	0.4583

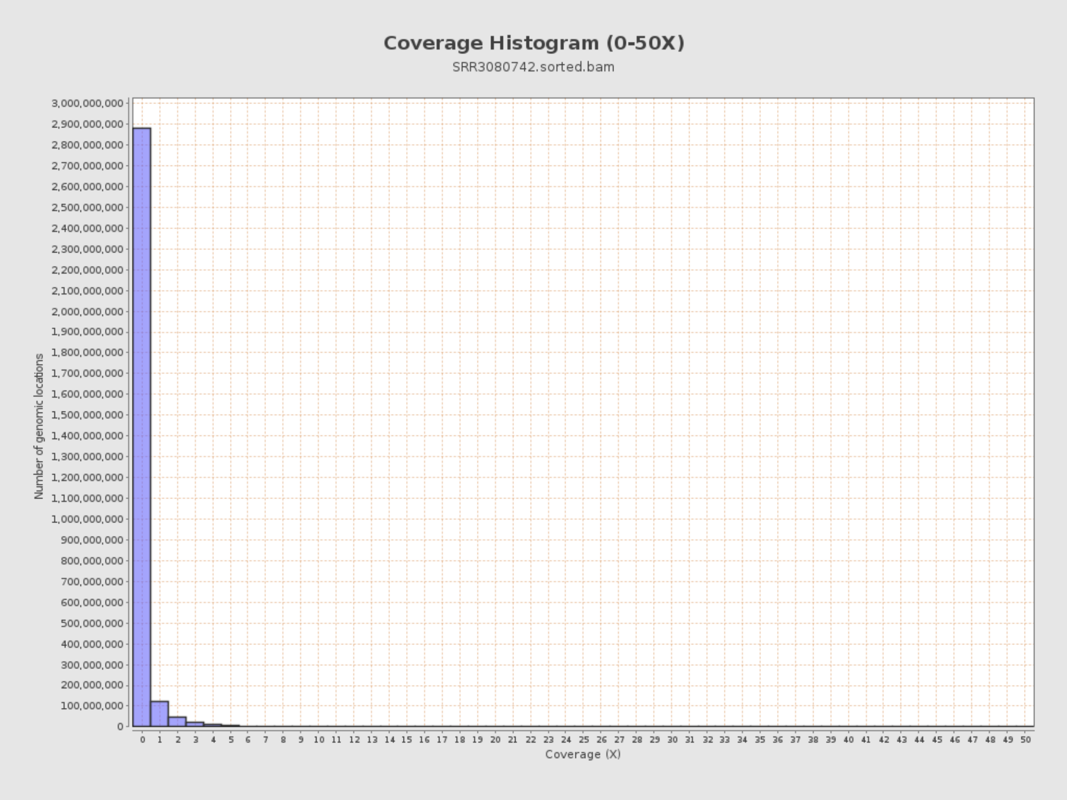
3. Results : Coverage across reference



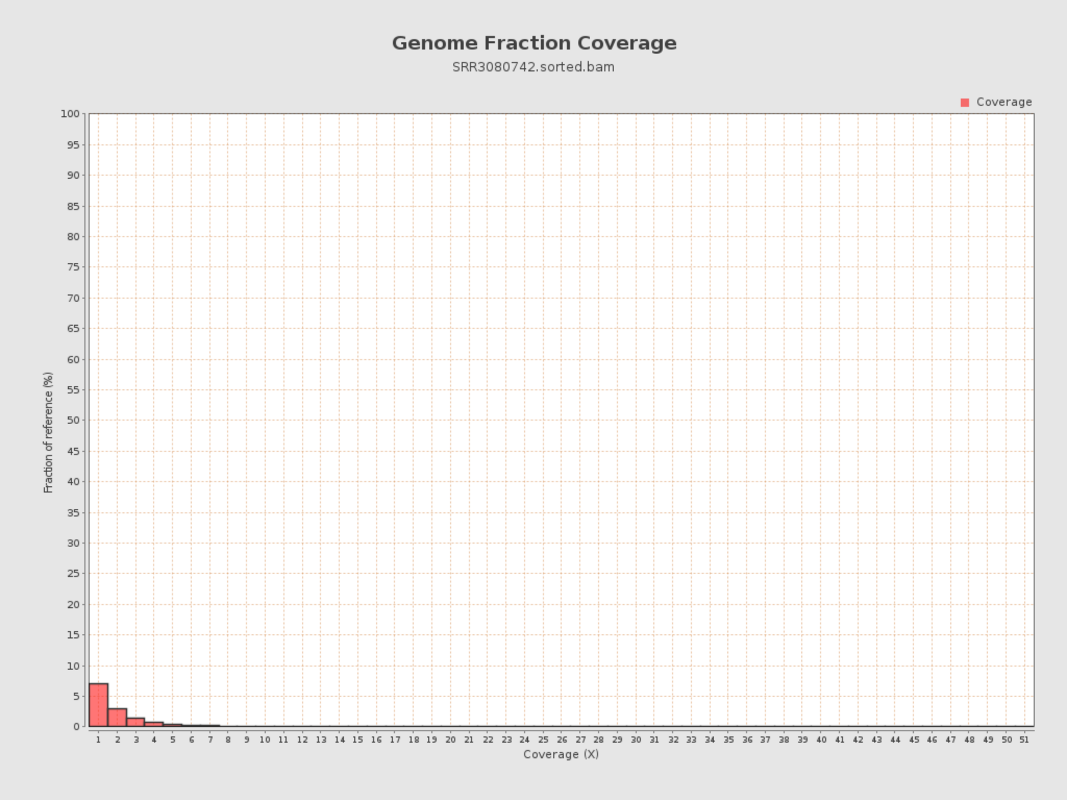
4. Results : Coverage Histogram



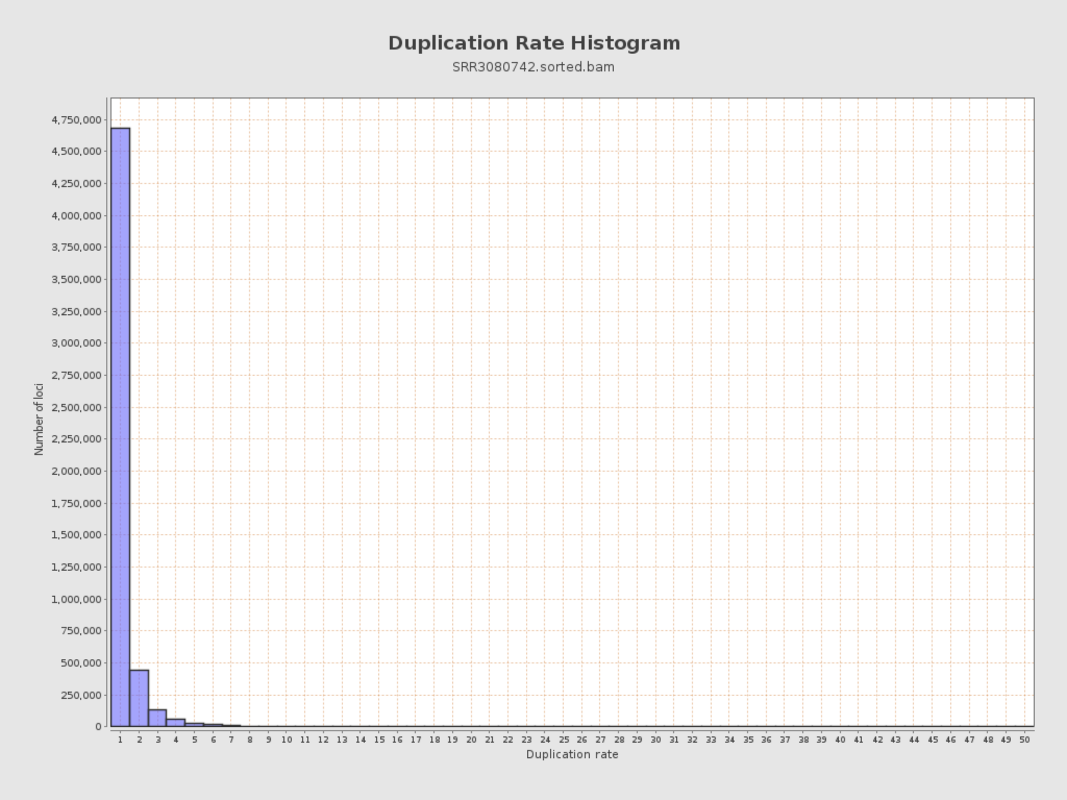
5. Results : Coverage Histogram (0-50X)



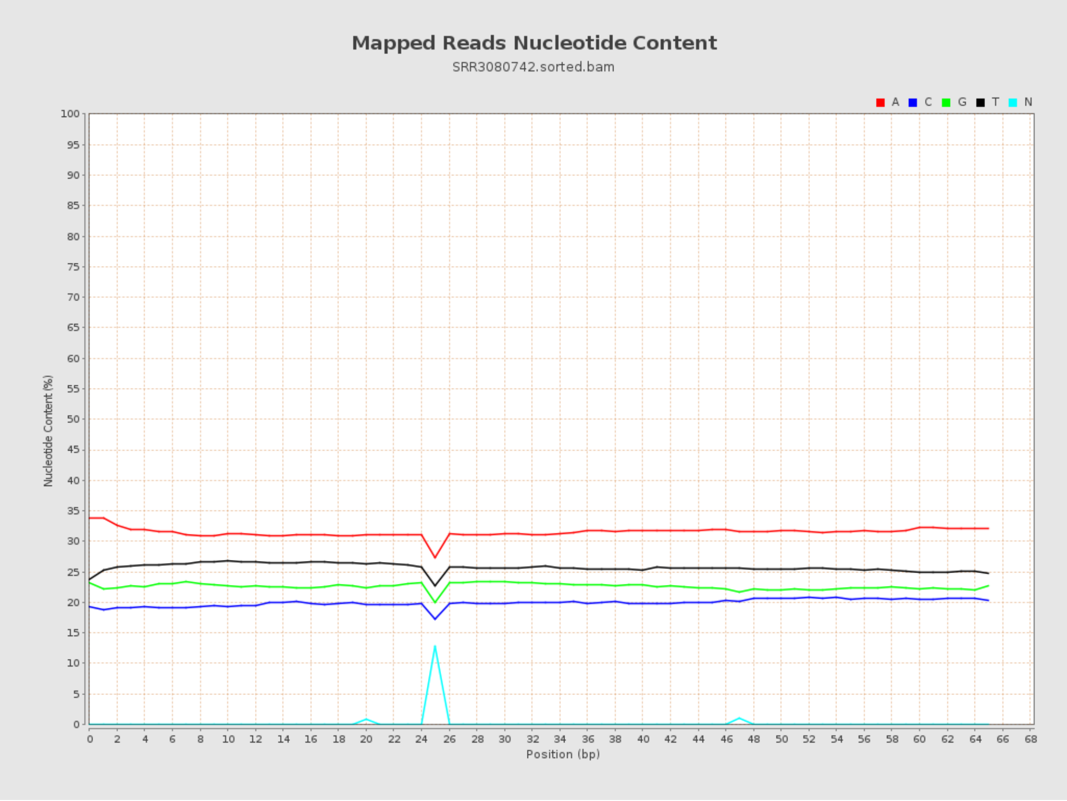
6. Results : Genome Fraction Coverage



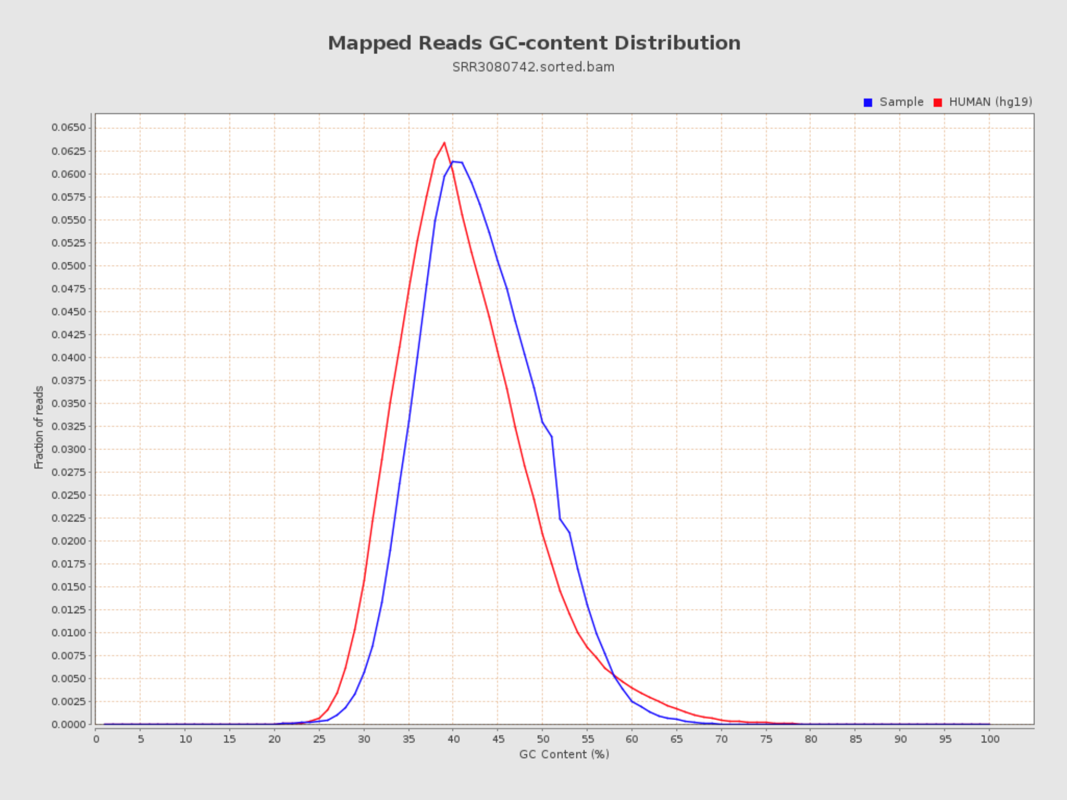
7. Results : Duplication Rate Histogram



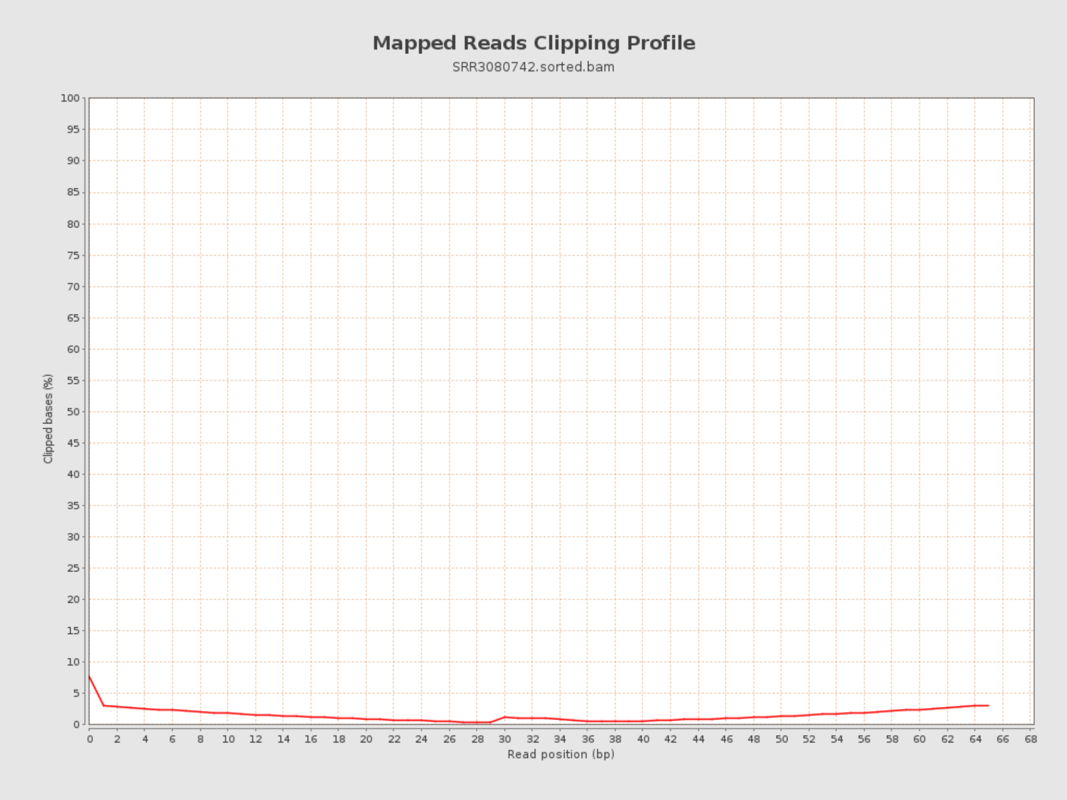
8. Results : Mapped Reads Nucleotide Content



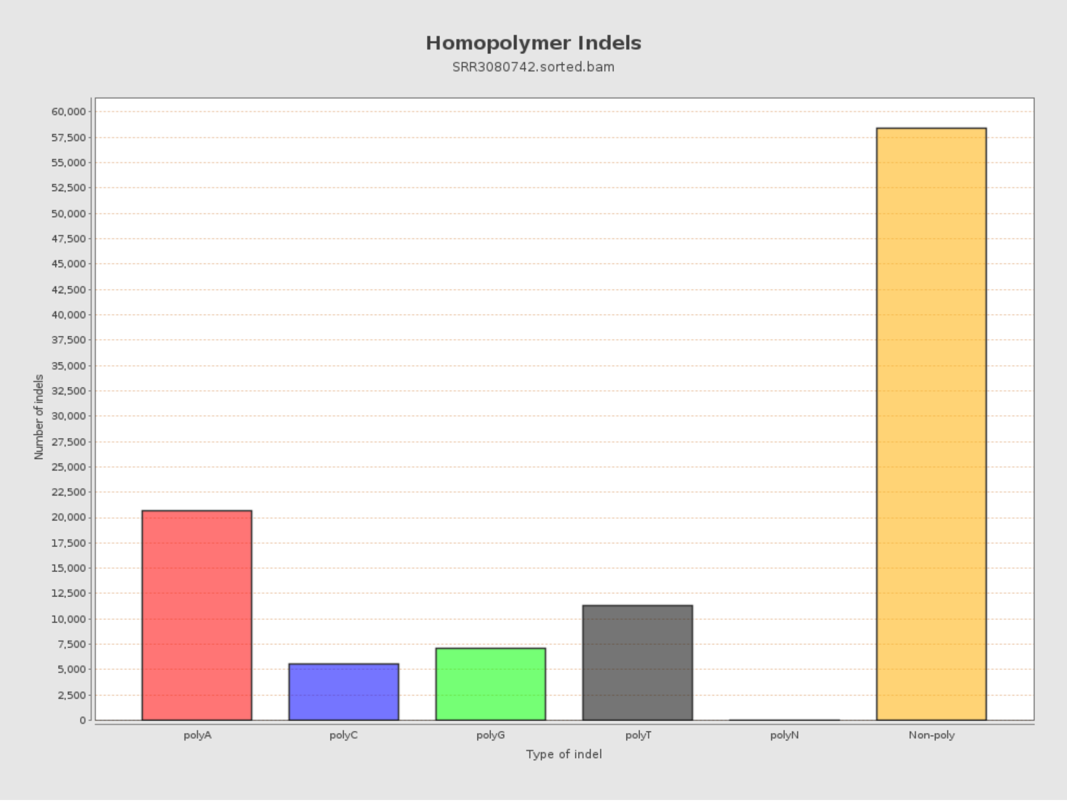
9. Results : Mapped Reads GC-content Distribution



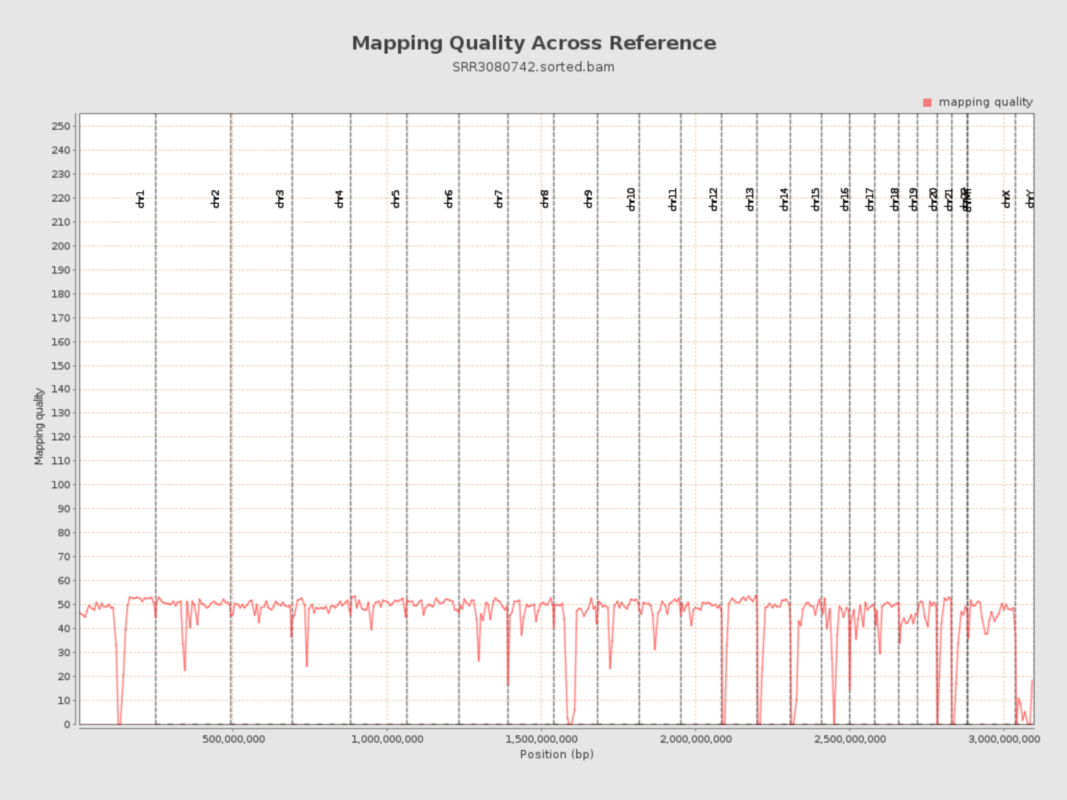
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram