Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:05:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084257.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_SRR3084257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:05:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,242,562
Mapped reads	1,001,874 / 80.63%
Unmapped reads	240,688 / 19.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,734 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	17,297 / 1.39%
Duplication rate	1.43%
Clipped reads	355,957 / 28.65%

2.2. ACGT Content

Number/percentage of A's	21,420,244 / 30.98%
Number/percentage of C's	12,551,656 / 18.15%
Number/percentage of T's	20,783,070 / 30.06%
Number/percentage of G's	14,380,764 / 20.8%
Number/percentage of N's	810 / 0%
GC Percentage	38.96%

2.3. Coverage

Mean	0.0223

Standard Deviation	0.1912

2.4. Mapping Quality

Mean Mapping Quality	47.76

2.5. Mismatches and indels

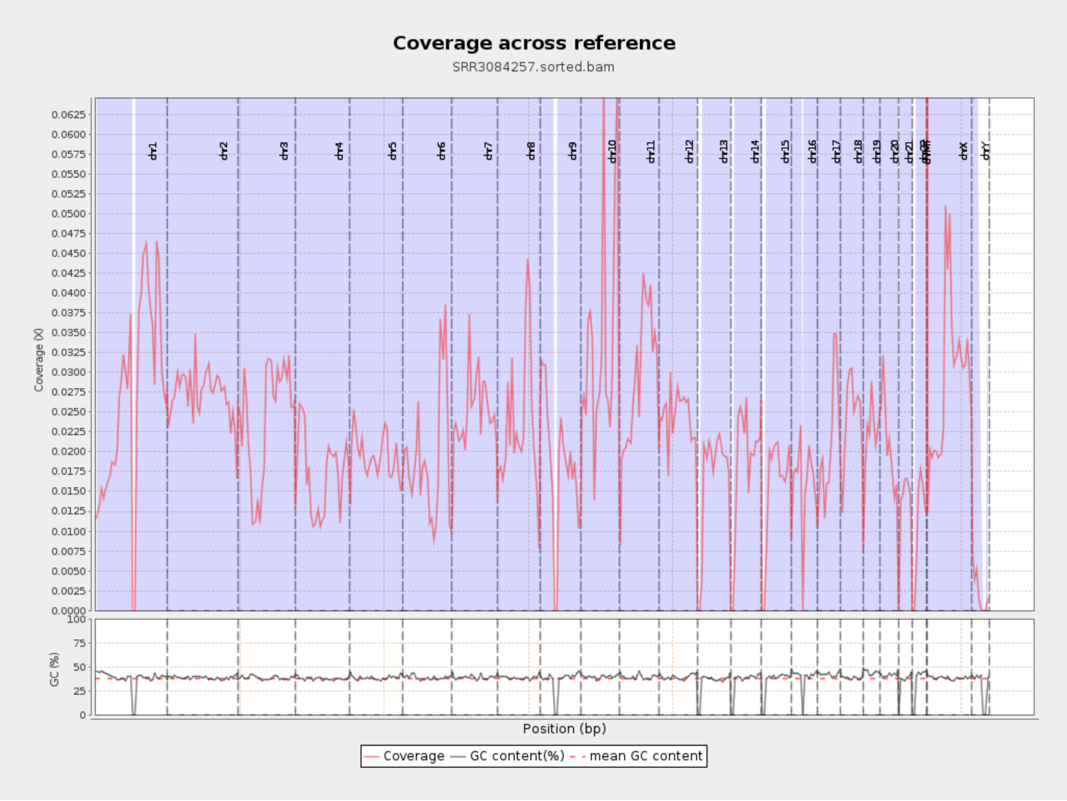
General error rate	0.9%
Mismatches	614,165
Insertions	5,395
Mapped reads with at least one insertion	0.53%
Deletions	15,501
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.85%

2.6. Chromosome stats

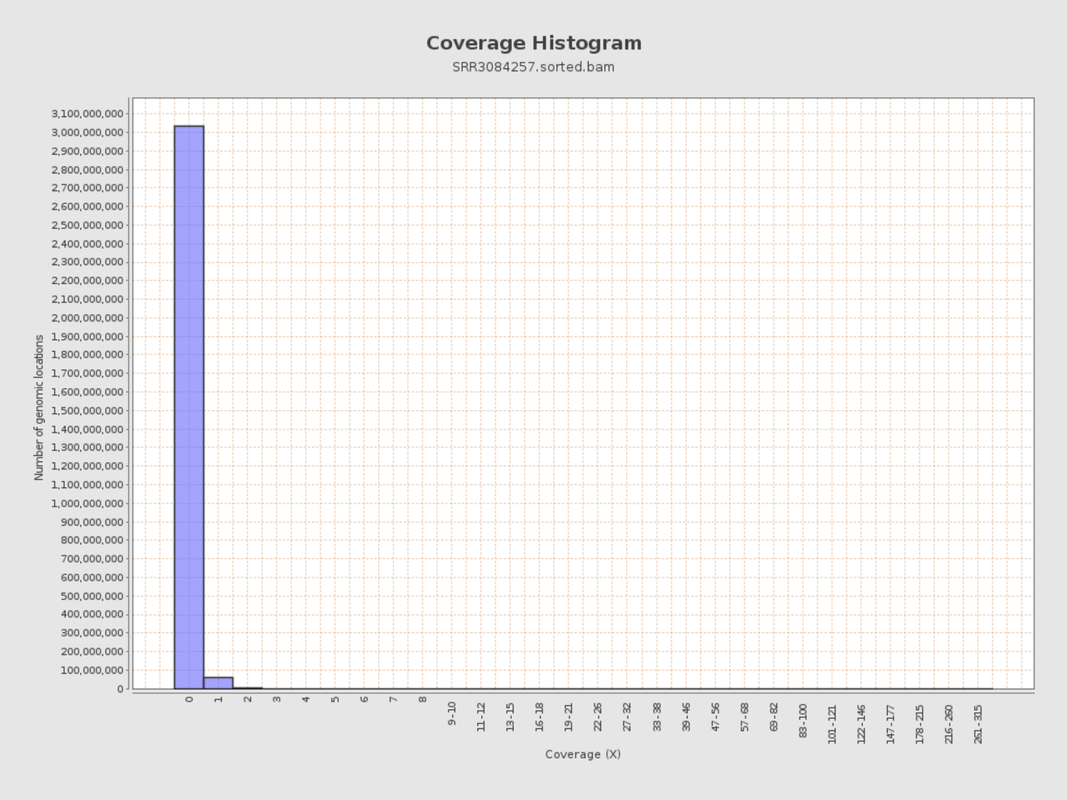
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6673844	0.0268	0.3012
chr2	243199373	6634568	0.0273	0.2018
chr3	198022430	4777934	0.0241	0.1653
chr4	191154276	3255466	0.017	0.1381
chr5	180915260	3535354	0.0195	0.1471
chr6	171115067	3266657	0.0191	0.1546
chr7	159138663	3992301	0.0251	0.2465

chr8	146364022	3477313	0.0238	0.2123
chr9	141213431	2633855	0.0187	0.1595
chr10	135534747	4544638	0.0335	0.2439
chr11	135006516	3999141	0.0296	0.2002
chr12	133851895	3275603	0.0245	0.1644
chr13	115169878	1885421	0.0164	0.1339
chr14	107349540	1967097	0.0183	0.1443
chr15	102531392	1584680	0.0155	0.1308
chr16	90354753	1414084	0.0157	0.1383
chr17	81195210	1730308	0.0213	0.1602
chr18	78077248	1900388	0.0243	0.2517
chr19	59128983	1325137	0.0224	0.2116
chr20	63025520	1316093	0.0209	0.1526
chr21	48129895	648411	0.0135	0.1243
chr22	51304566	544515	0.0106	0.108
chrMT	16571	52935	3.1944	2.7392
chrX	155270560	4593387	0.0296	0.193
chrY	59373566	131691	0.0022	0.0553

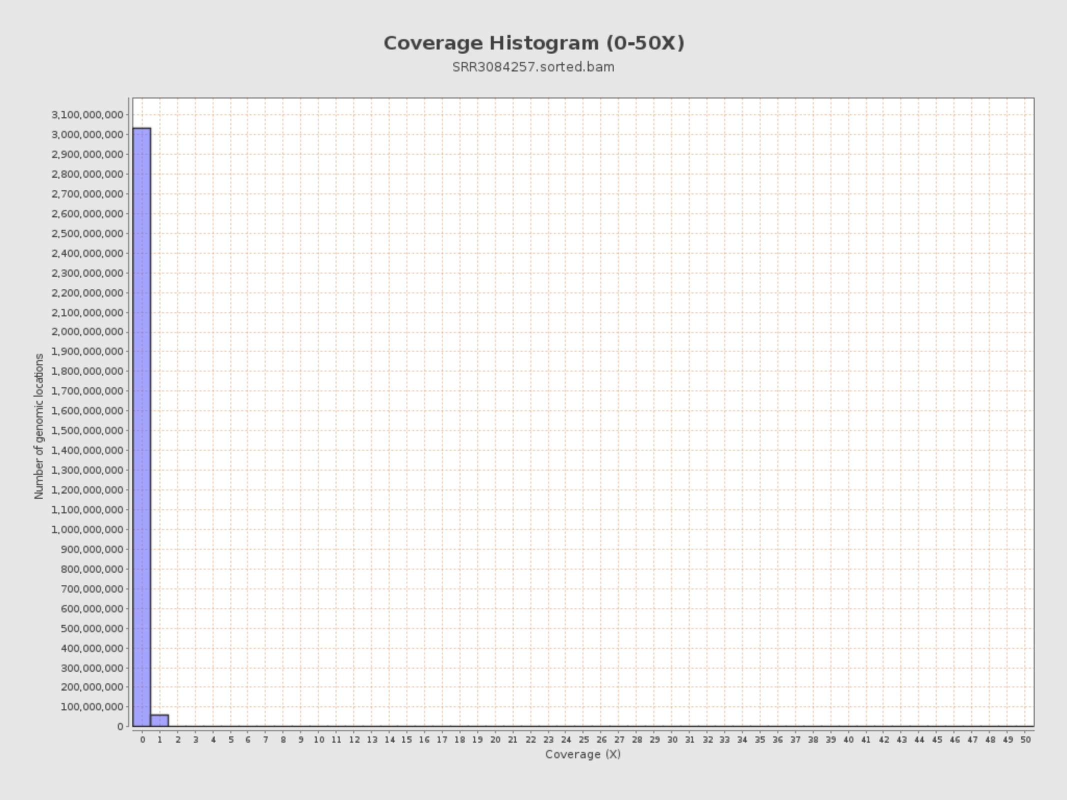
3. Results : Coverage across reference



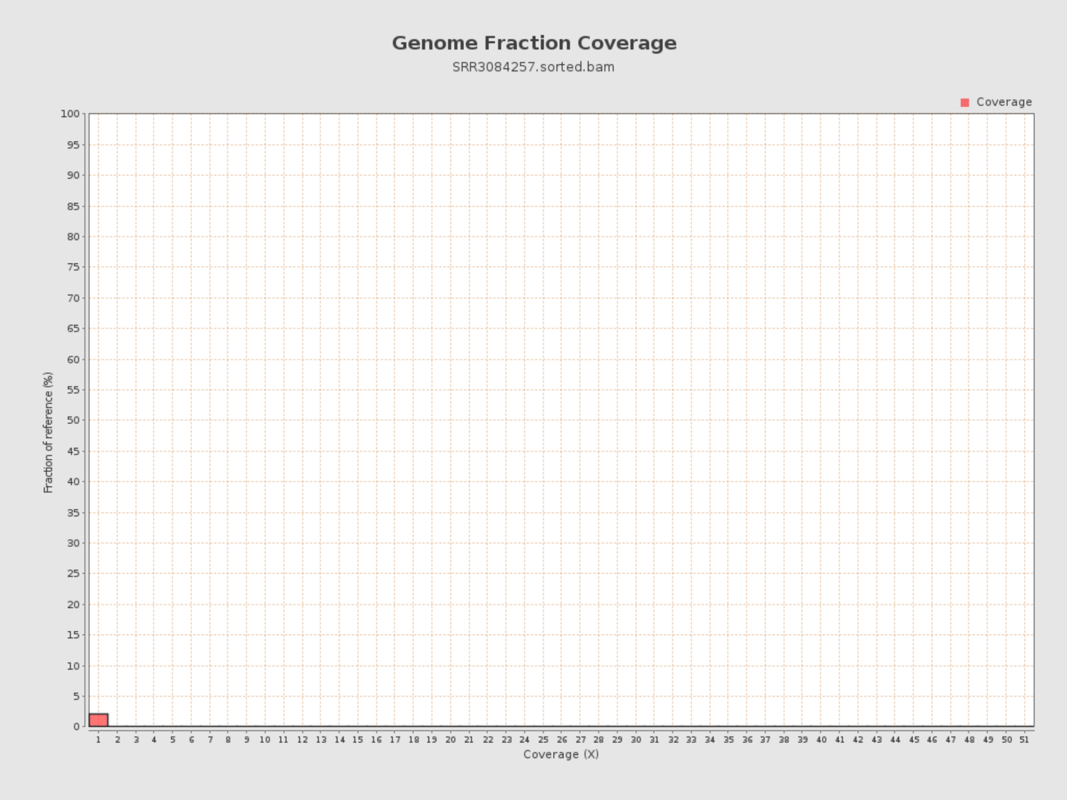
4. Results : Coverage Histogram



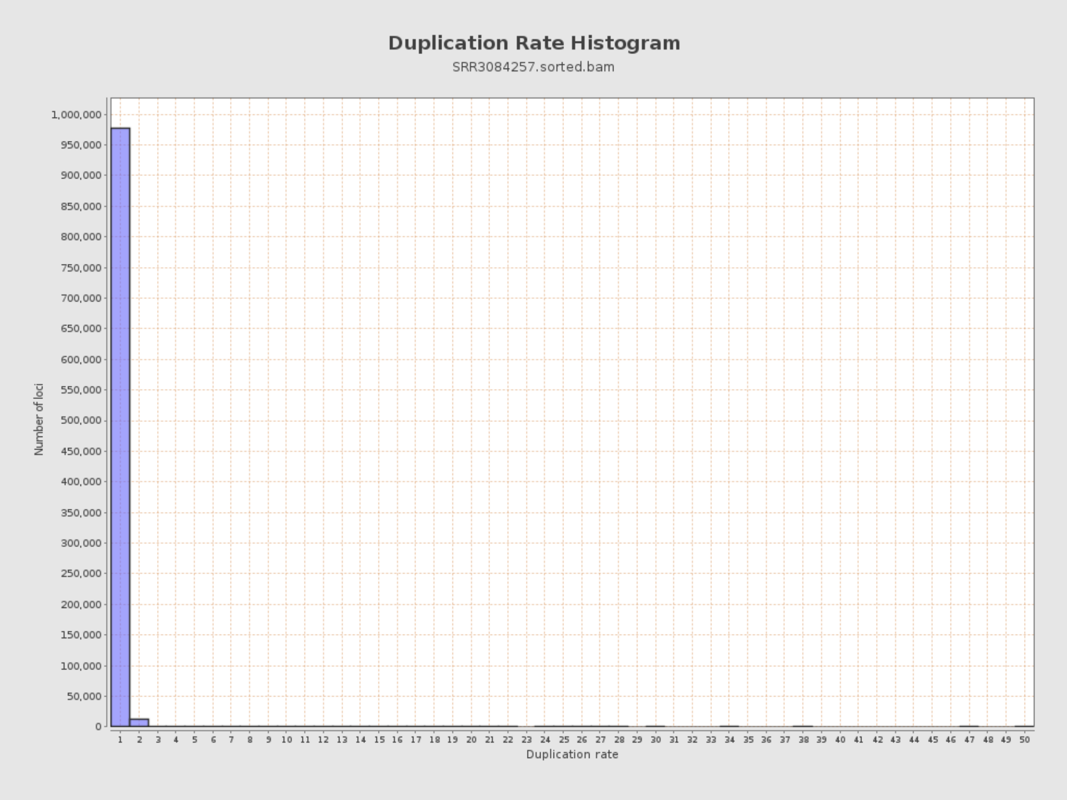
5. Results : Coverage Histogram (0-50X)



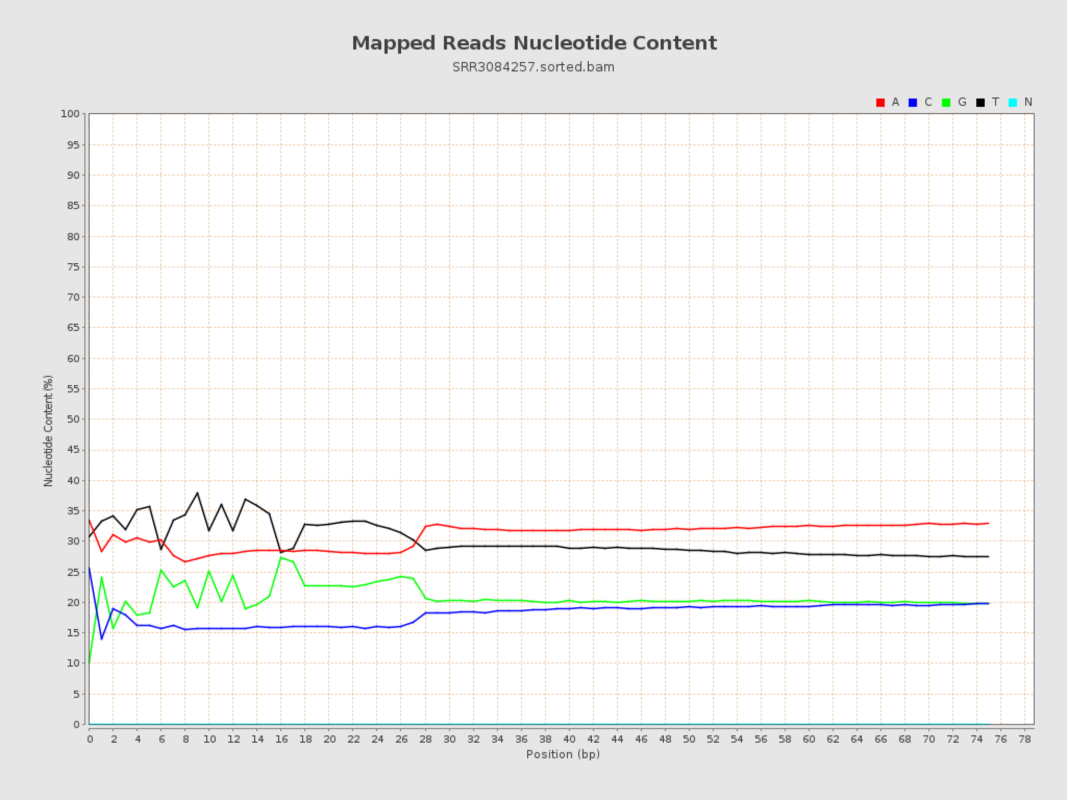
6. Results : Genome Fraction Coverage



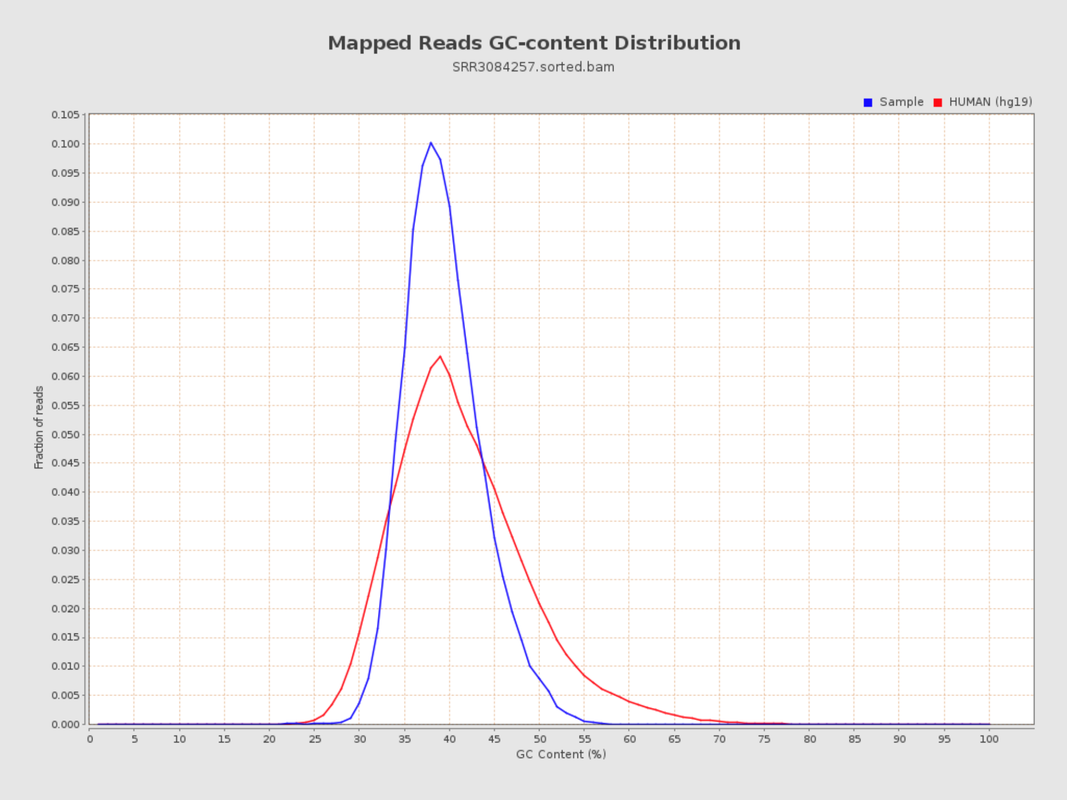
7. Results : Duplication Rate Histogram



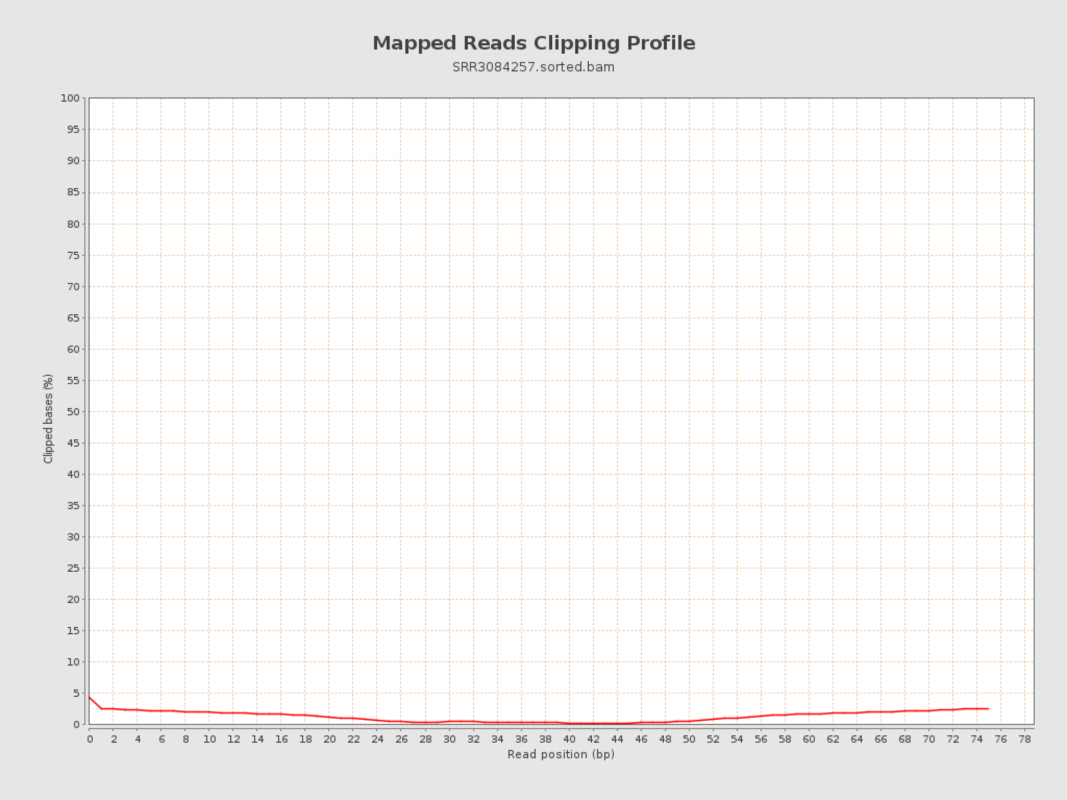
8. Results : Mapped Reads Nucleotide Content



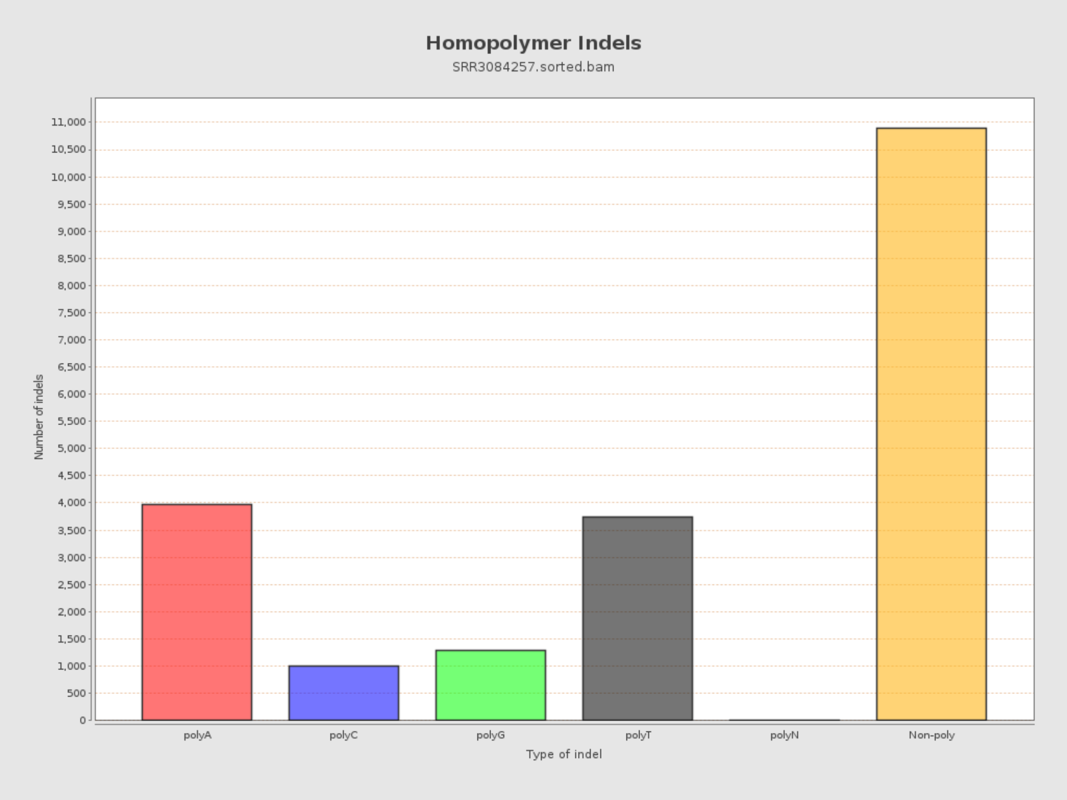
9. Results : Mapped Reads GC-content Distribution



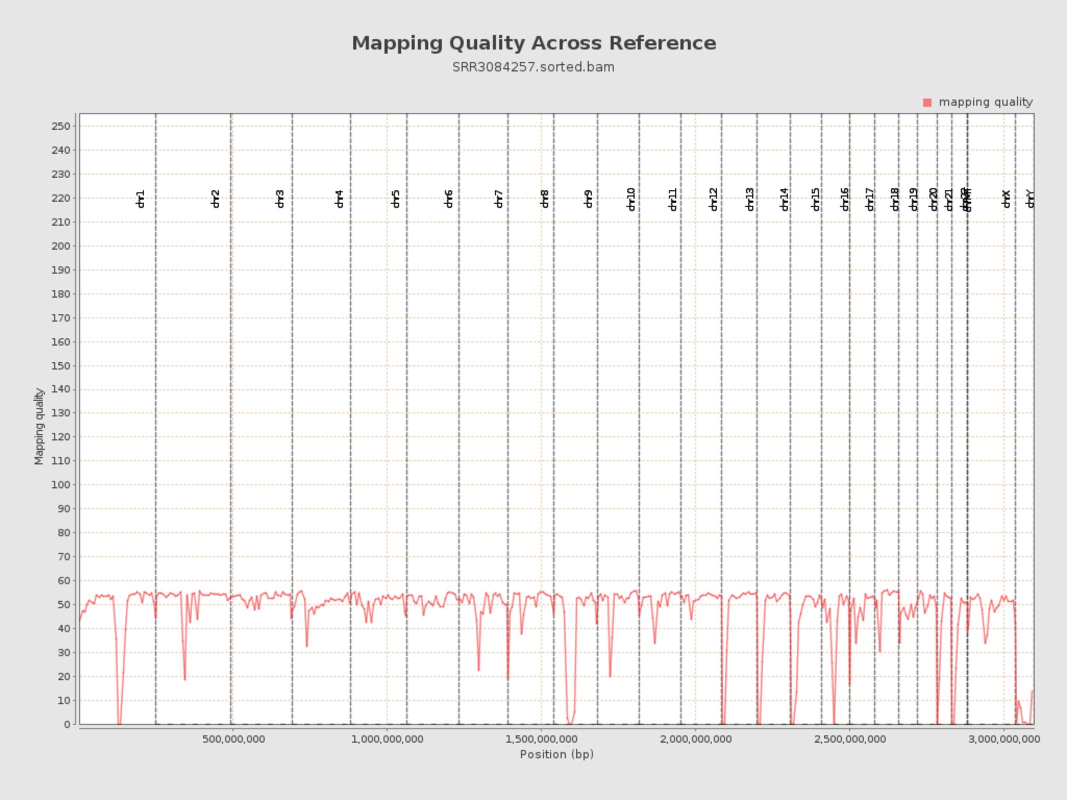
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram