Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:47:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234084.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_SRR6234084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:47:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	954,563
Mapped reads	706,809 / 74.05%
Unmapped reads	247,754 / 25.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,186 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	21,490 / 2.25%
Duplication rate	2.41%
Clipped reads	342,395 / 35.87%

2.2. ACGT Content

Number/percentage of A's	12,923,858 / 28.09%
Number/percentage of C's	7,841,052 / 17.04%
Number/percentage of T's	15,147,939 / 32.92%
Number/percentage of G's	10,094,936 / 21.94%
Number/percentage of N's	7,136 / 0.02%
GC Percentage	38.98%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.1815

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

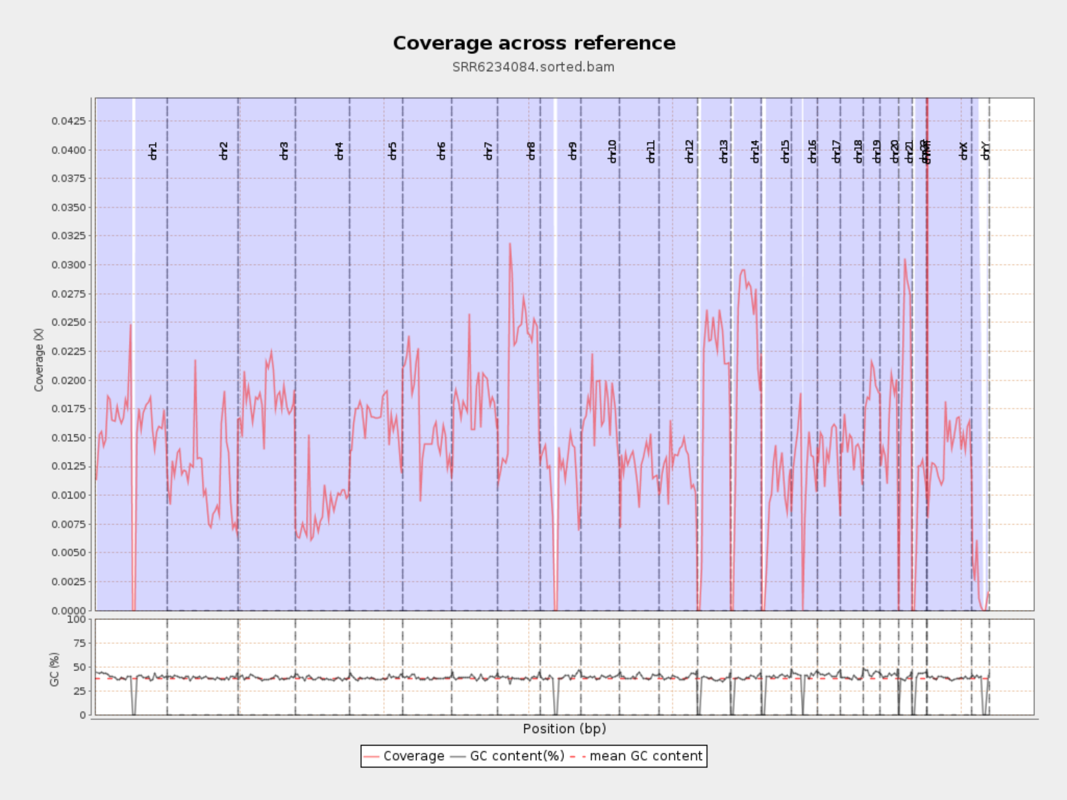
General error rate	0.88%
Mismatches	397,440
Insertions	3,600
Mapped reads with at least one insertion	0.5%
Deletions	15,148
Mapped reads with at least one deletion	2.11%
Homopolymer indels	45.3%

2.6. Chromosome stats

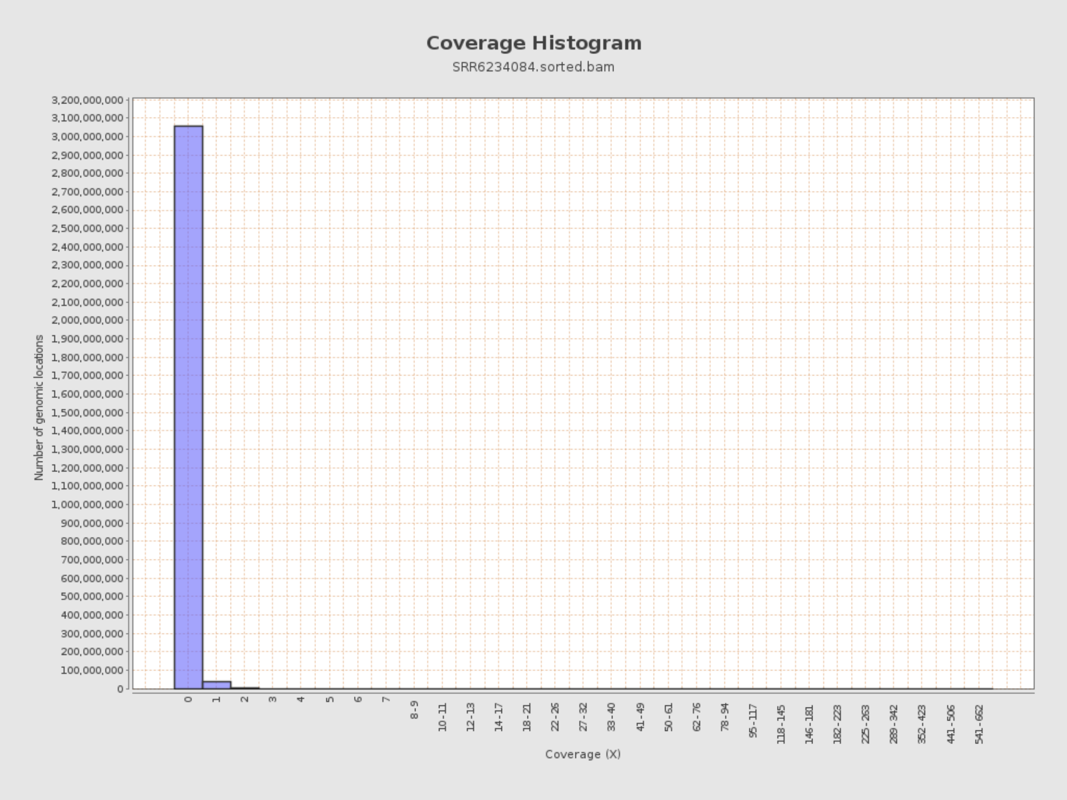
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3880975	0.0156	0.2394
chr2	243199373	2829231	0.0116	0.1642
chr3	198022430	3640482	0.0184	0.1476
chr4	191154276	1658953	0.0087	0.1029
chr5	180915260	2998805	0.0166	0.1387
chr6	171115067	2843091	0.0166	0.1459
chr7	159138663	2916567	0.0183	0.2024

chr8	146364022	3155110	0.0216	0.4351
chr9	141213431	1581849	0.0112	0.1307
chr10	135534747	2361773	0.0174	0.1555
chr11	135006516	1699551	0.0126	0.1808
chr12	133851895	1687753	0.0126	0.1213
chr13	115169878	2247489	0.0195	0.1511
chr14	107349540	2361824	0.022	0.1625
chr15	102531392	935842	0.0091	0.1036
chr16	90354753	1085748	0.012	0.1235
chr17	81195210	1116221	0.0137	0.1287
chr18	78077248	1106770	0.0142	0.2252
chr19	59128983	1123457	0.019	0.1779
chr20	63025520	996452	0.0158	0.1417
chr21	48129895	1053796	0.0219	0.1621
chr22	51304566	439719	0.0086	0.0984
chrMT	16571	37605	2.2693	2.3043
chrX	155270560	2169342	0.014	0.1348
chrY	59373566	112797	0.0019	0.0525

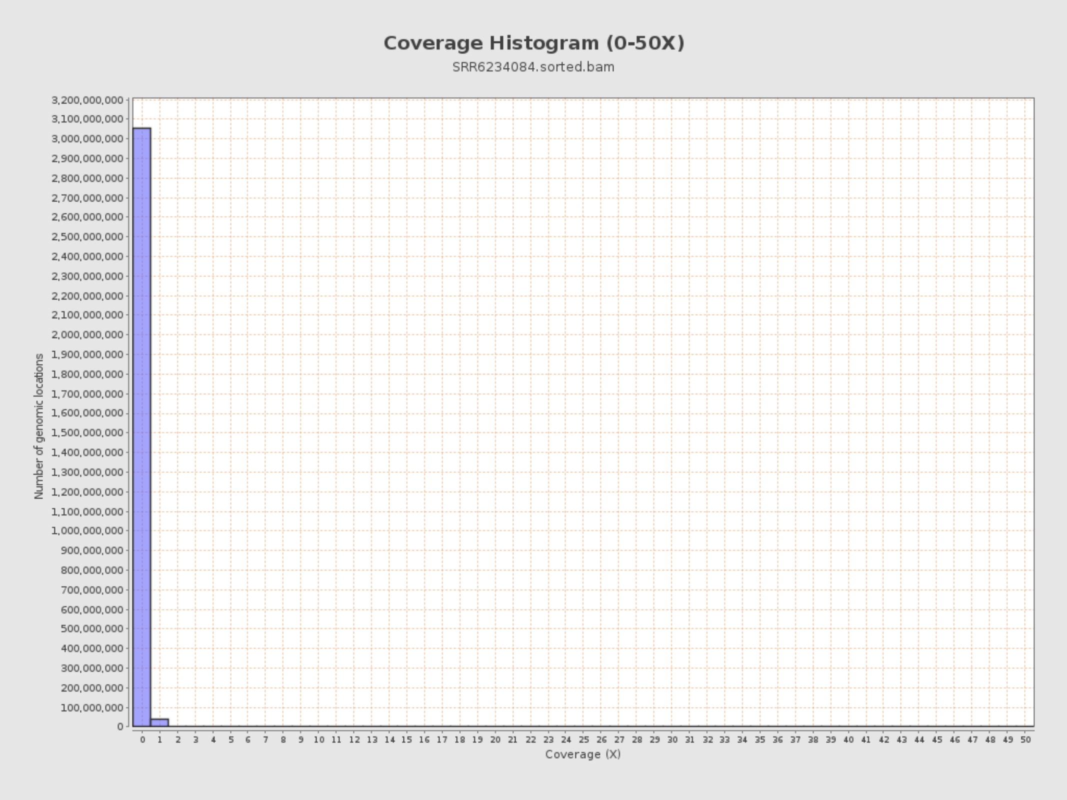
3. Results : Coverage across reference



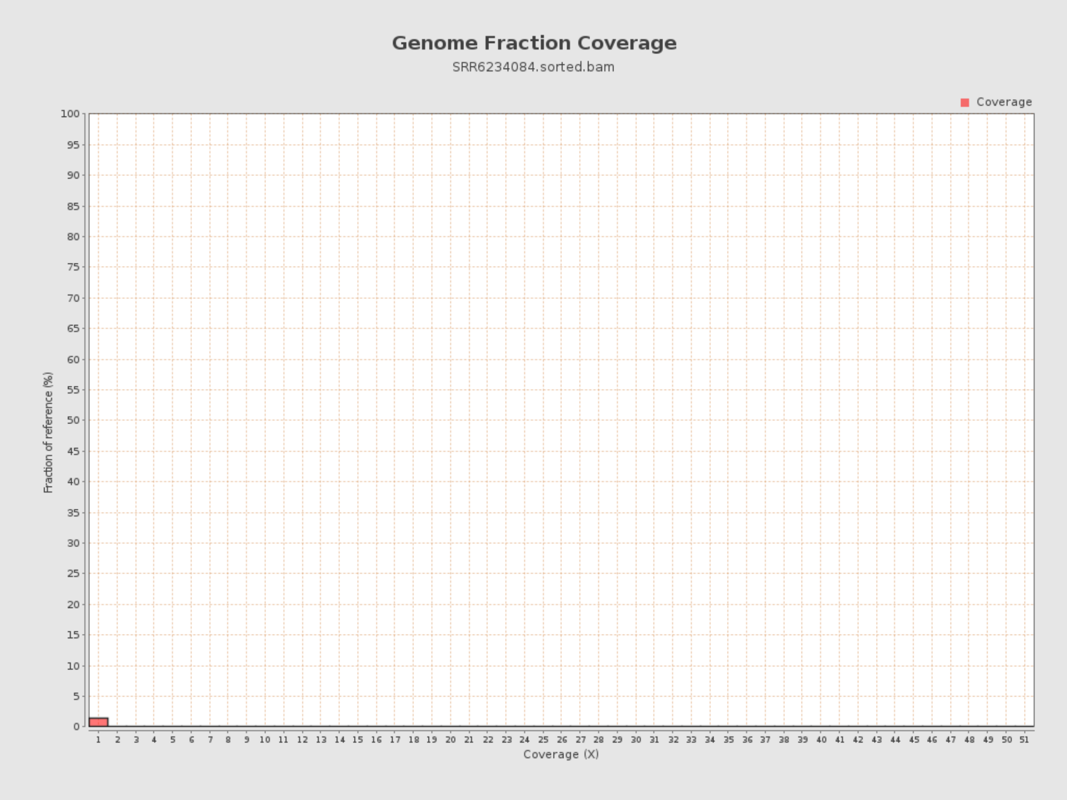
4. Results : Coverage Histogram



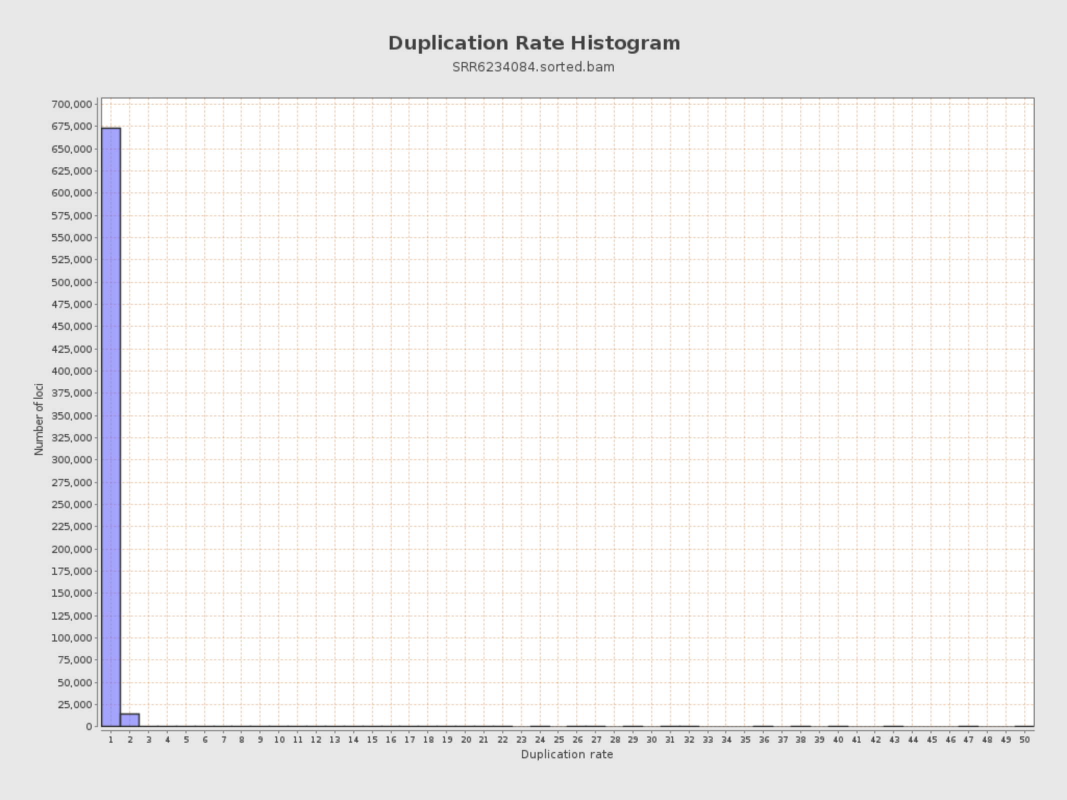
5. Results : Coverage Histogram (0-50X)



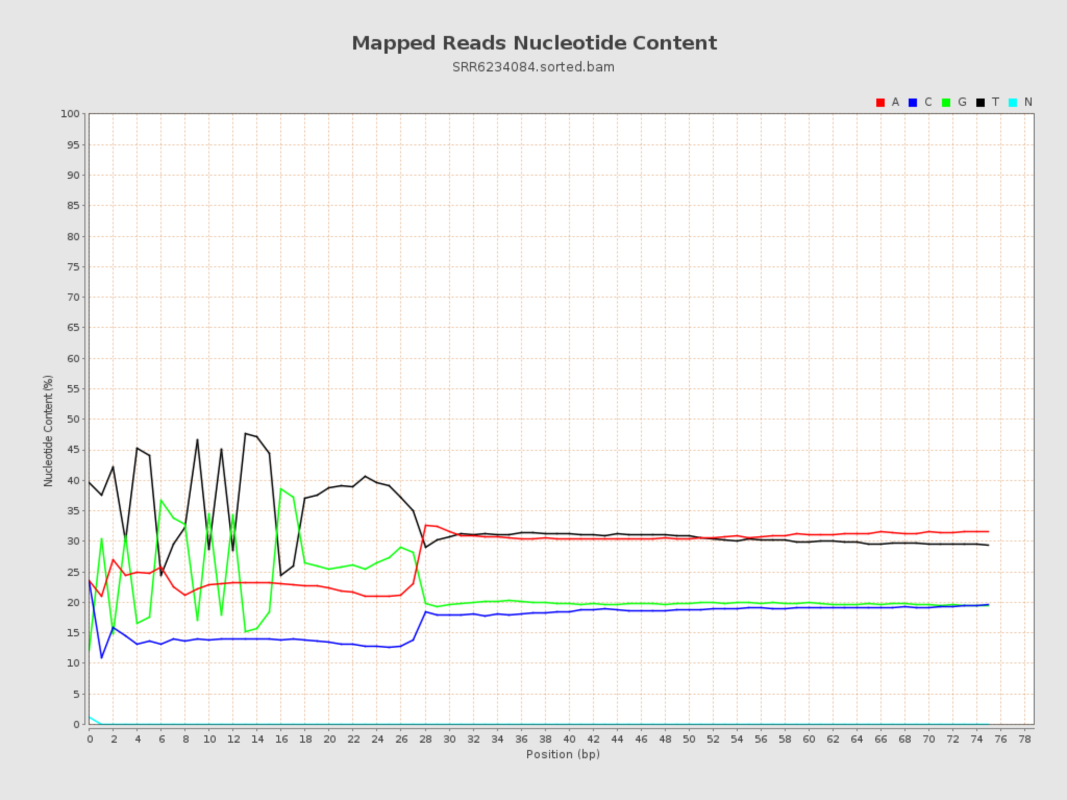
6. Results : Genome Fraction Coverage



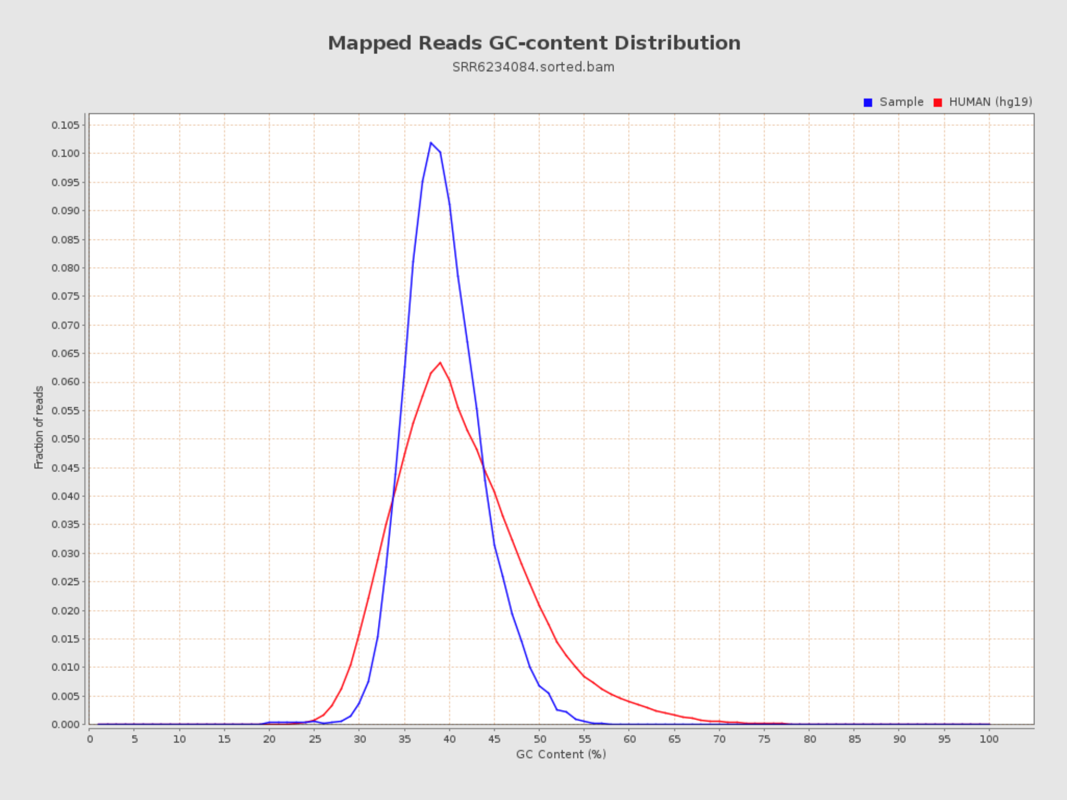
7. Results : Duplication Rate Histogram



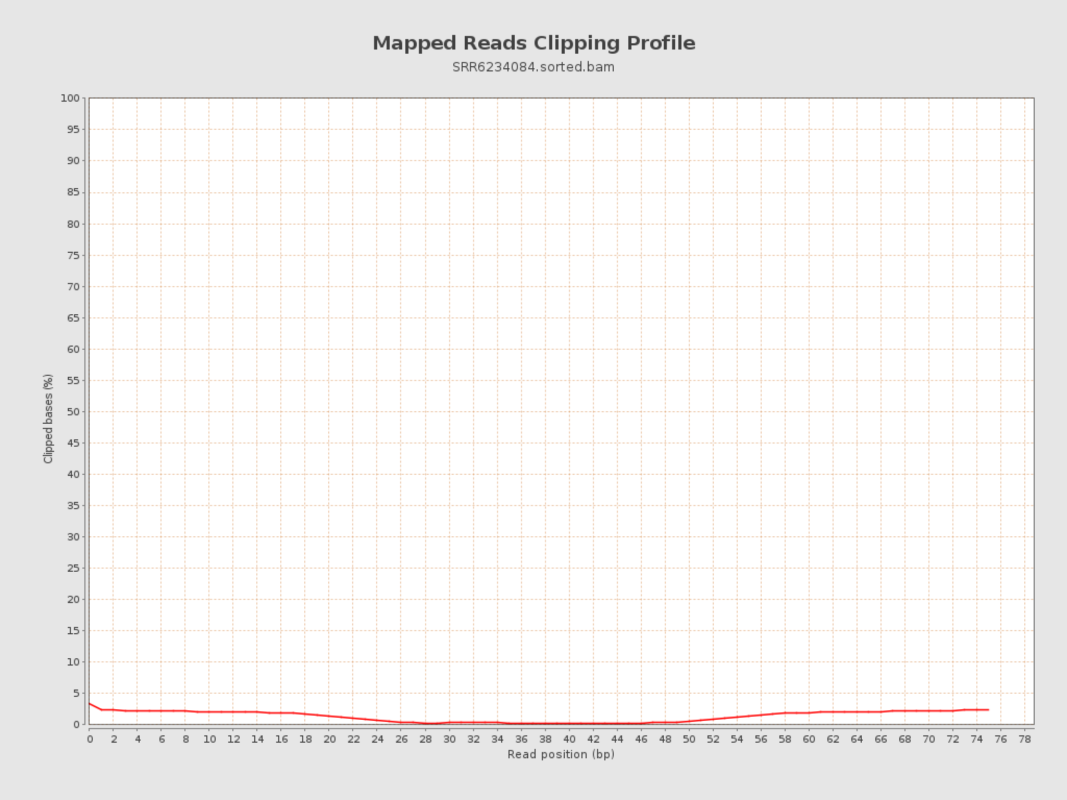
8. Results : Mapped Reads Nucleotide Content



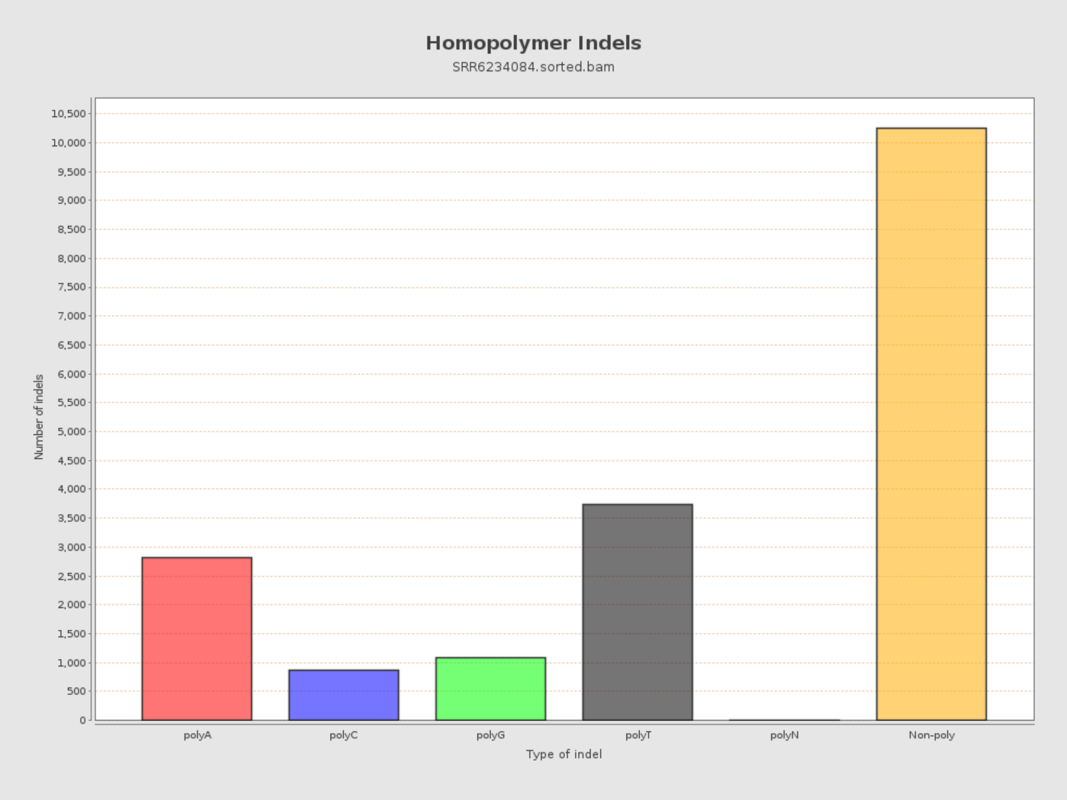
9. Results : Mapped Reads GC-content Distribution



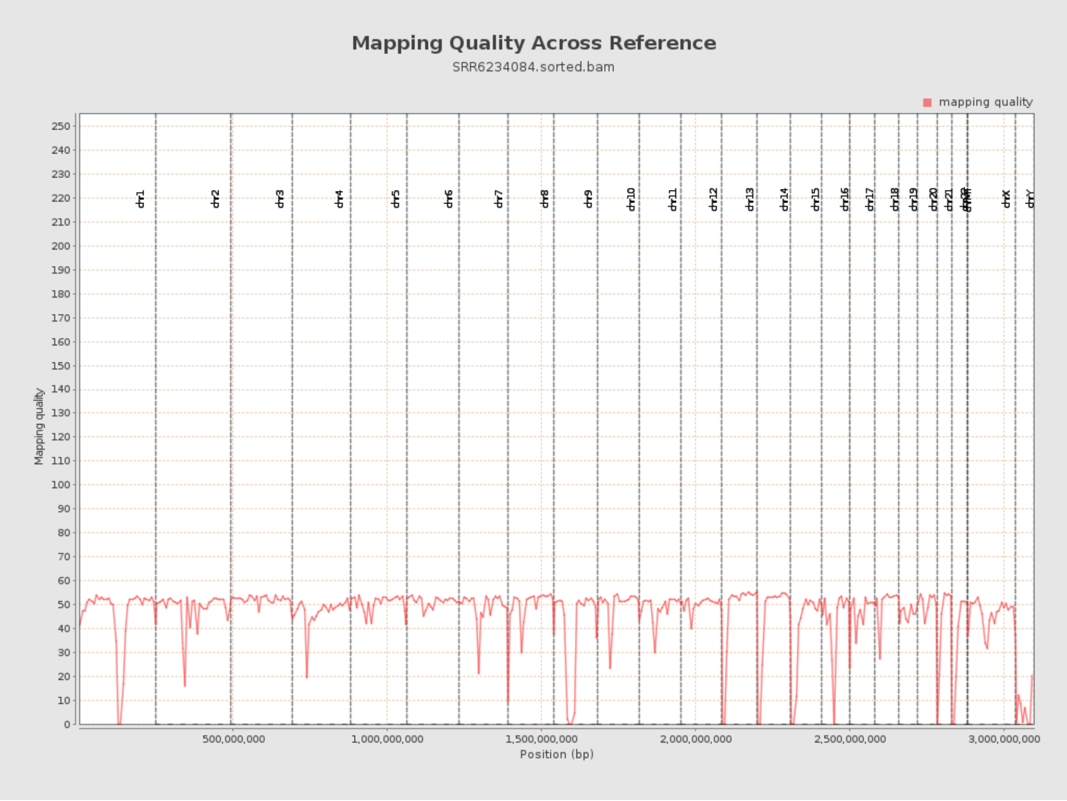
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram