Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:41:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080654.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_SRR3080654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080654.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:41:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,512,226
Mapped reads	1,376,165 / 91%
Unmapped reads	136,061 / 9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,953 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	50,290 / 3.33%
Duplication rate	3.13%
Clipped reads	641,652 / 42.43%

2.2. ACGT Content

Number/percentage of A's	24,371,418 / 26.77%
Number/percentage of C's	17,070,798 / 18.75%
Number/percentage of T's	28,497,541 / 31.31%
Number/percentage of G's	21,081,983 / 23.16%
Number/percentage of N's	3,849 / 0%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0294

Standard Deviation	0.2388

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

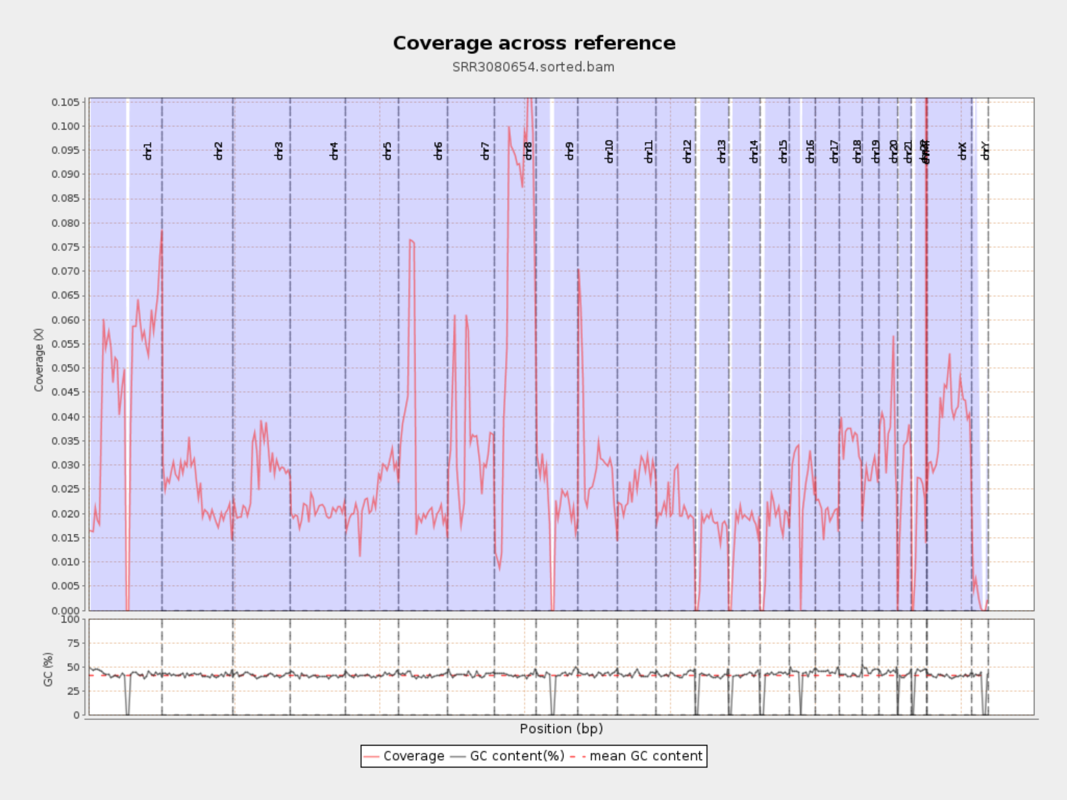
General error rate	0.69%
Mismatches	620,200
Insertions	6,918
Mapped reads with at least one insertion	0.5%
Deletions	21,178
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.89%

2.6. Chromosome stats

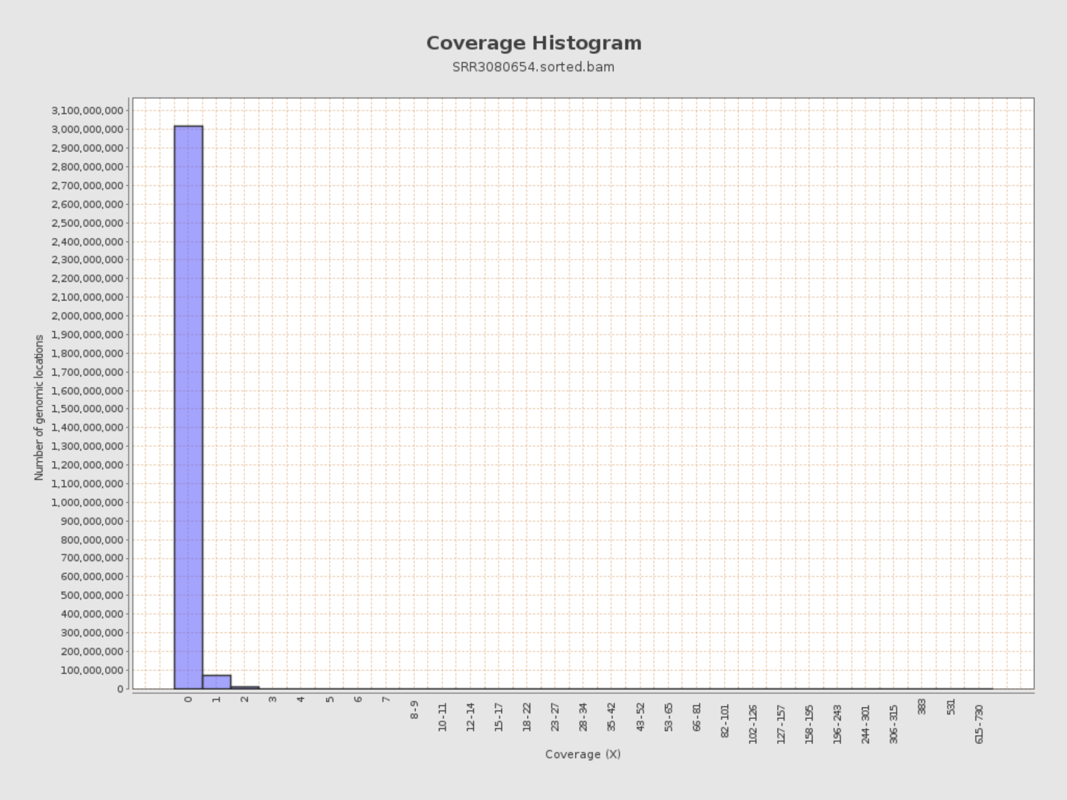
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11462349	0.046	0.2812
chr2	243199373	6000865	0.0247	0.3612
chr3	198022430	5567041	0.0281	0.1866
chr4	191154276	3922452	0.0205	0.1626
chr5	180915260	4321218	0.0239	0.1723
chr6	171115067	5286430	0.0309	0.2377
chr7	159138663	5660752	0.0356	0.4118

chr8	146364022	10596034	0.0724	0.3283
chr9	141213431	2982554	0.0211	0.1959
chr10	135534747	4448953	0.0328	0.2101
chr11	135006516	3530175	0.0261	0.1985
chr12	133851895	2850534	0.0213	0.1626
chr13	115169878	1756932	0.0153	0.1375
chr14	107349540	1704793	0.0159	0.1438
chr15	102531392	1650331	0.0161	0.1506
chr16	90354753	2378156	0.0263	0.1829
chr17	81195210	1630951	0.0201	0.1615
chr18	78077248	2780865	0.0356	0.2696
chr19	59128983	1635139	0.0277	0.2135
chr20	63025520	2370708	0.0376	0.2189
chr21	48129895	1304536	0.0271	0.1878
chr22	51304566	897592	0.0175	0.1475
chrMT	16571	14945	0.9019	1.1327
chrX	155270560	6123089	0.0394	0.2289
chrY	59373566	182195	0.0031	0.0659

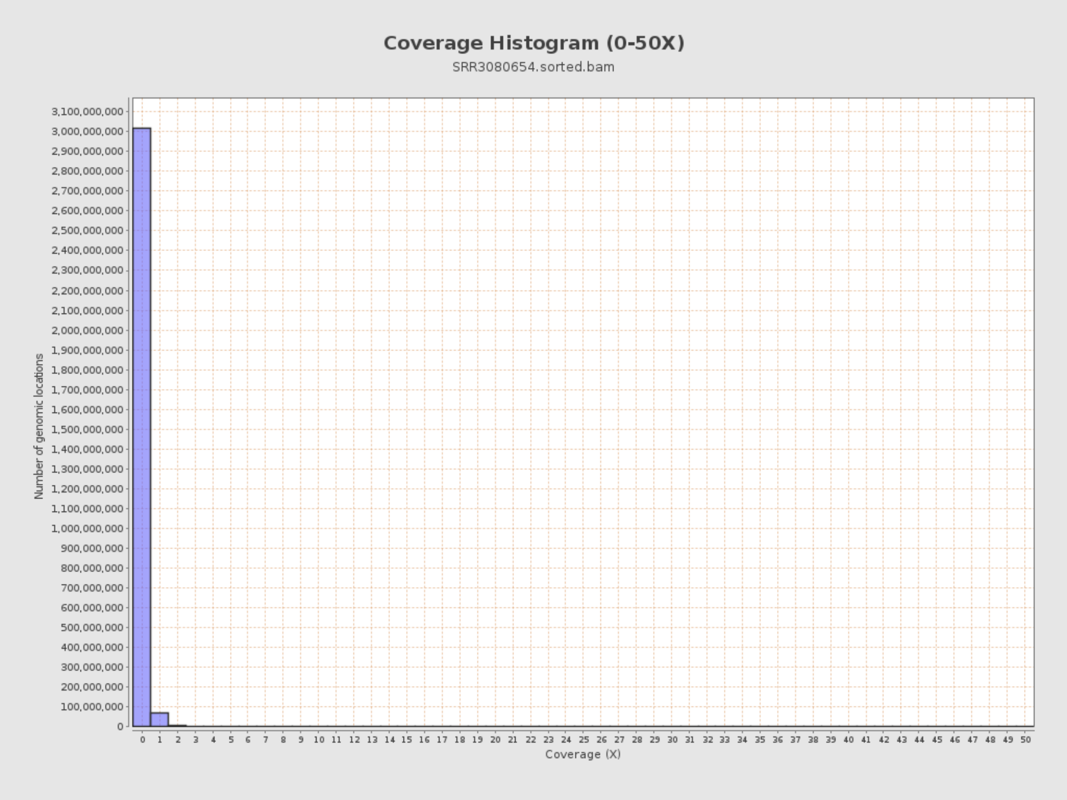
3. Results : Coverage across reference



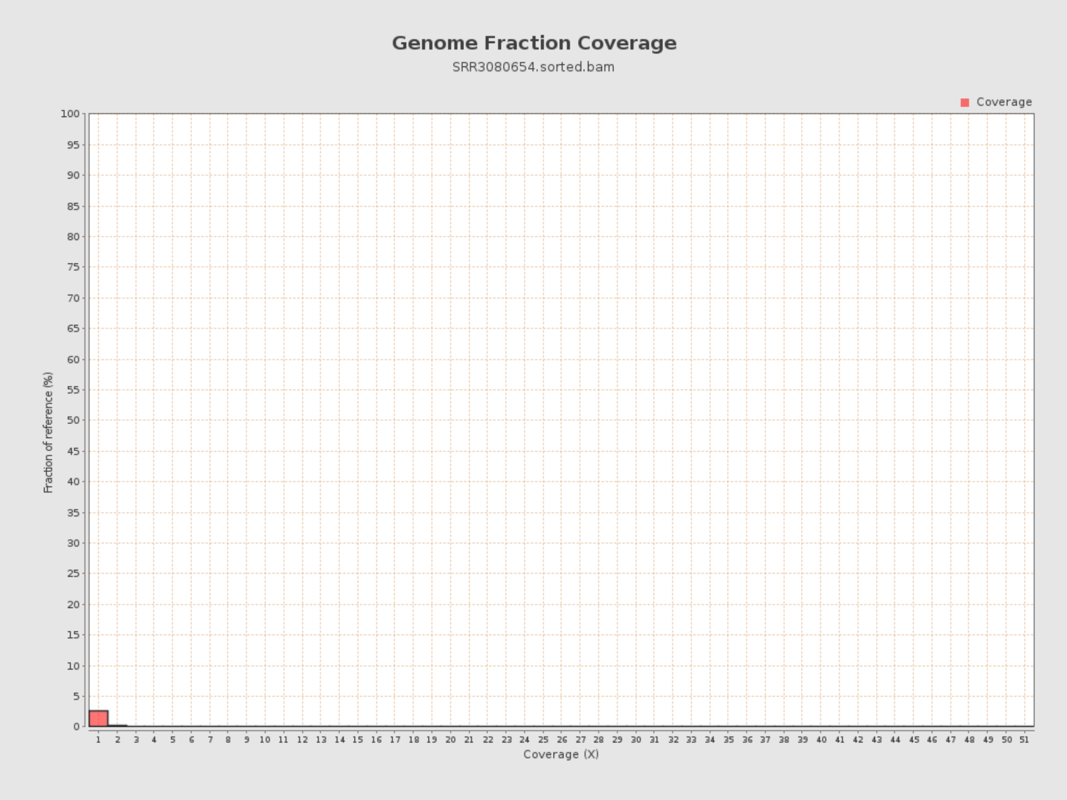
4. Results : Coverage Histogram



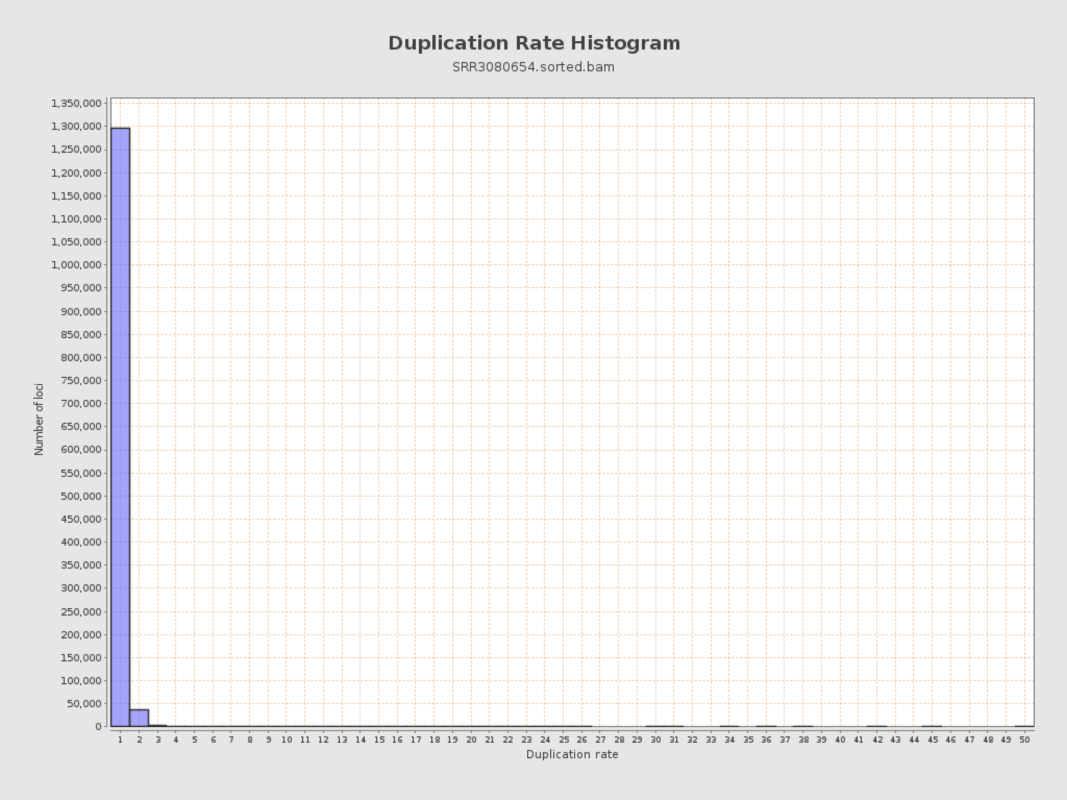
5. Results : Coverage Histogram (0-50X)



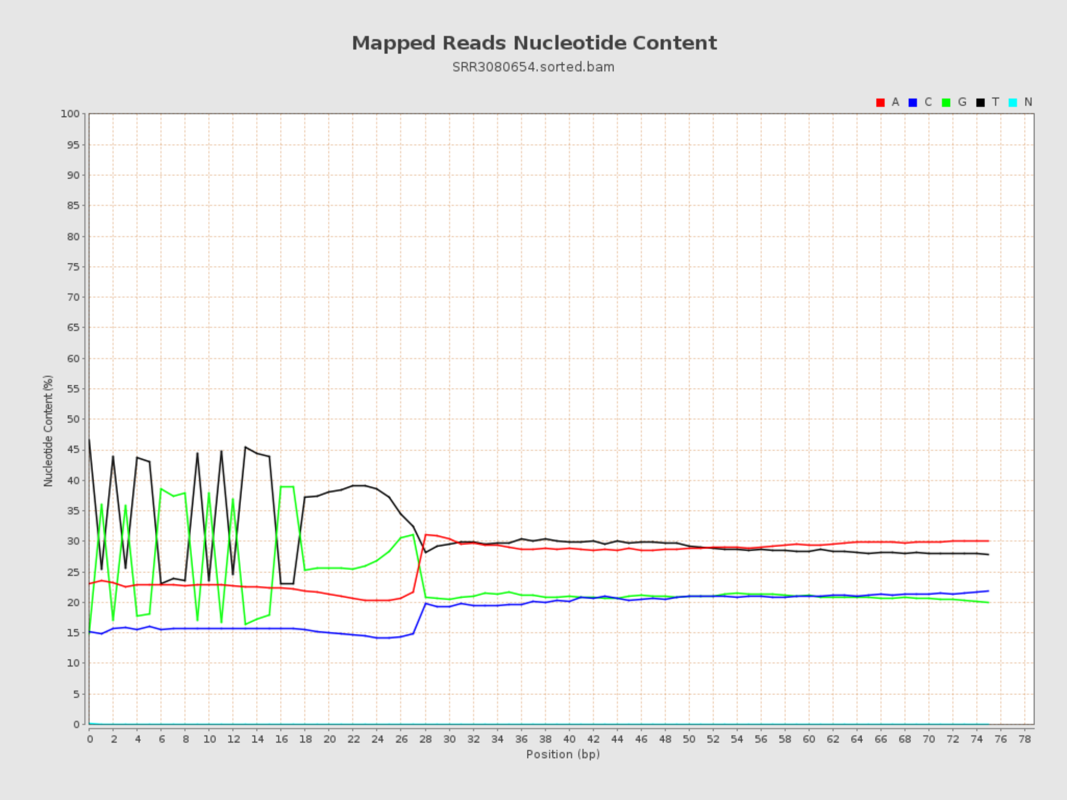
6. Results : Genome Fraction Coverage



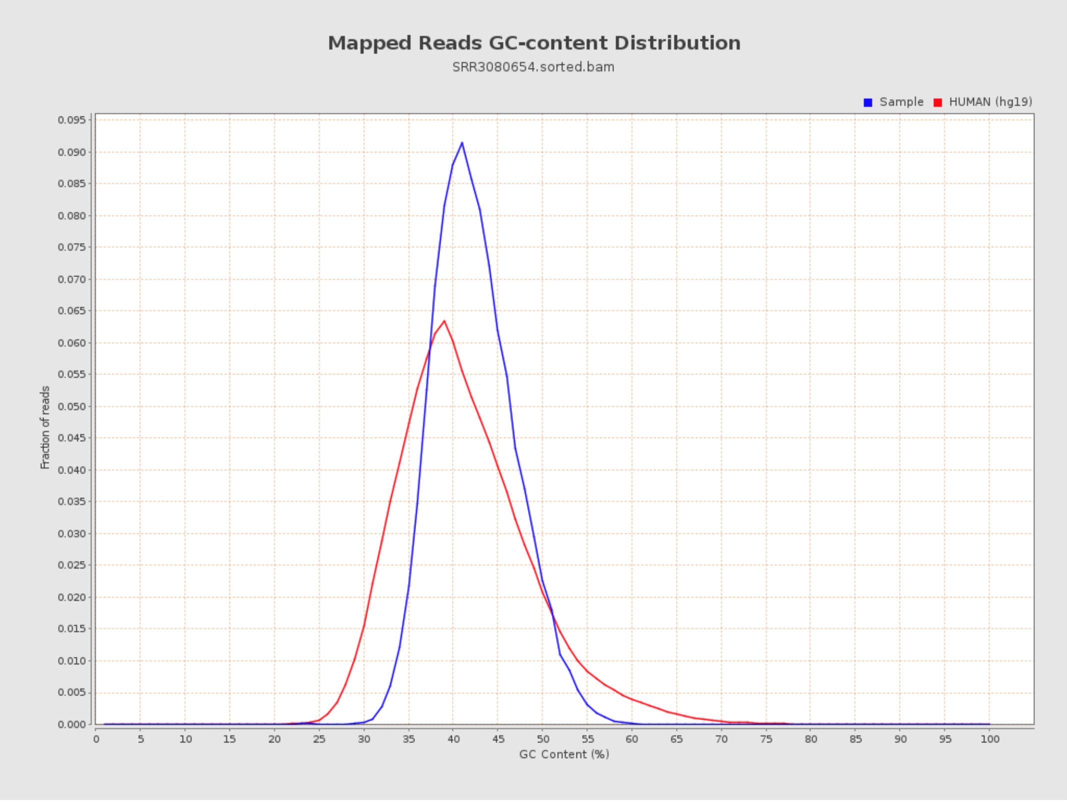
7. Results : Duplication Rate Histogram



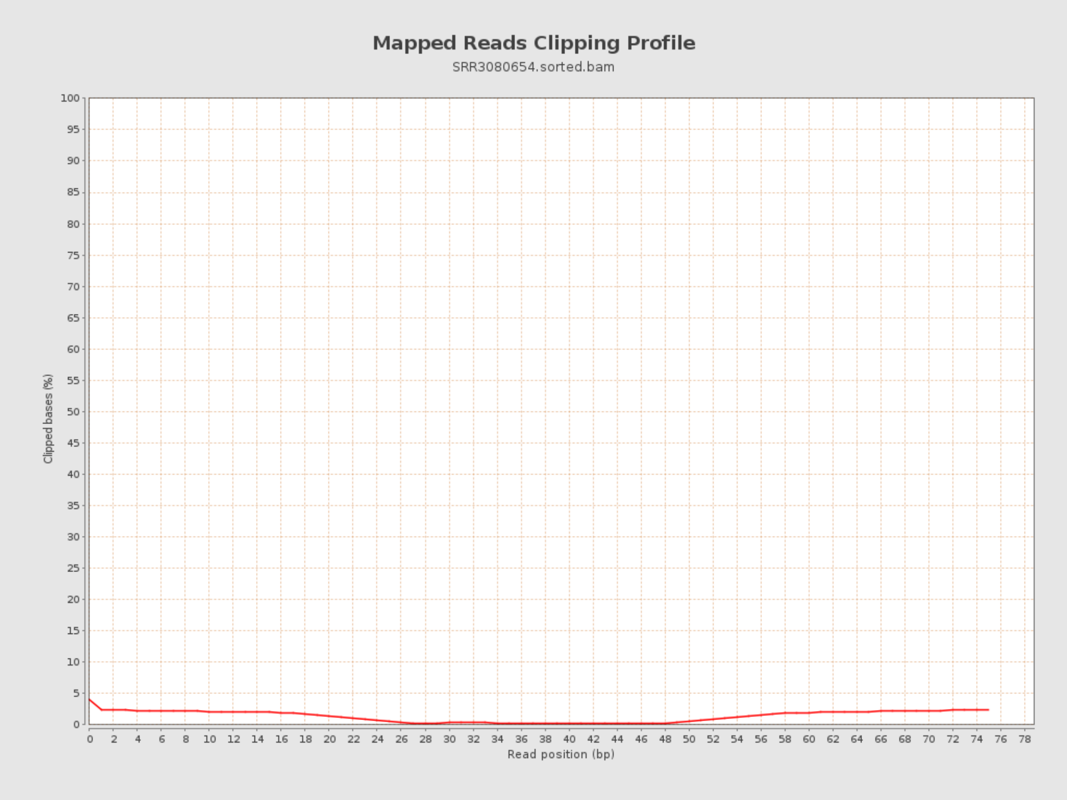
8. Results : Mapped Reads Nucleotide Content



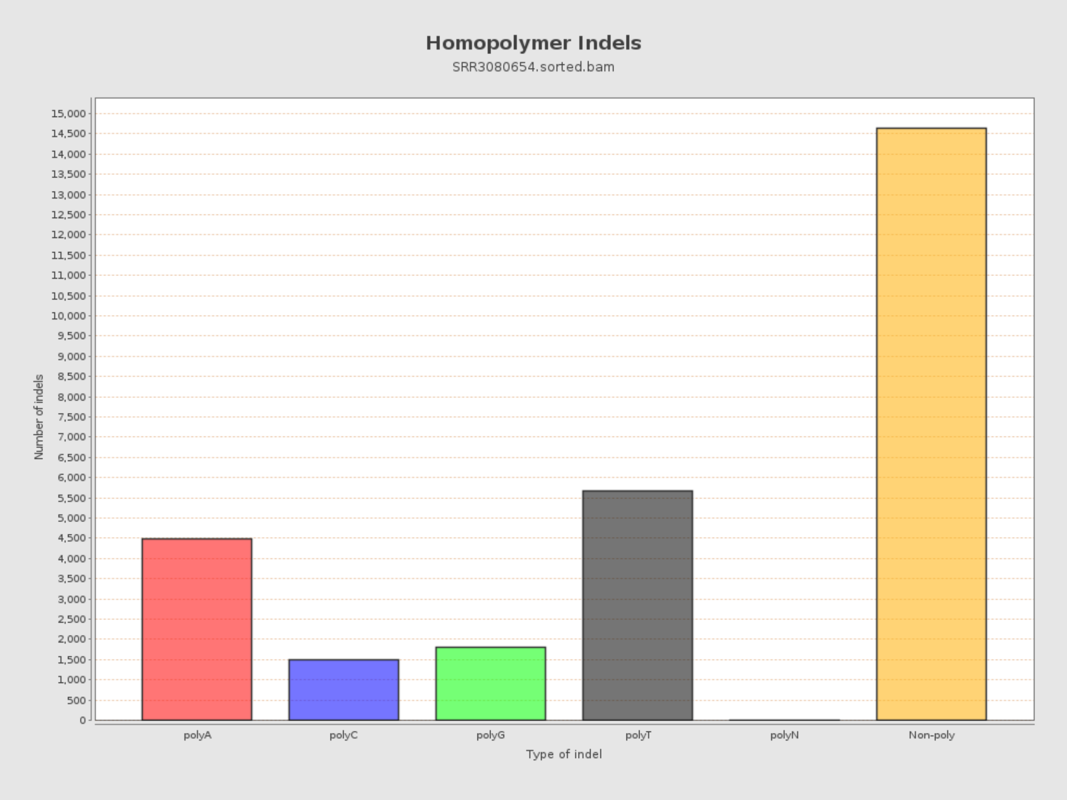
9. Results : Mapped Reads GC-content Distribution



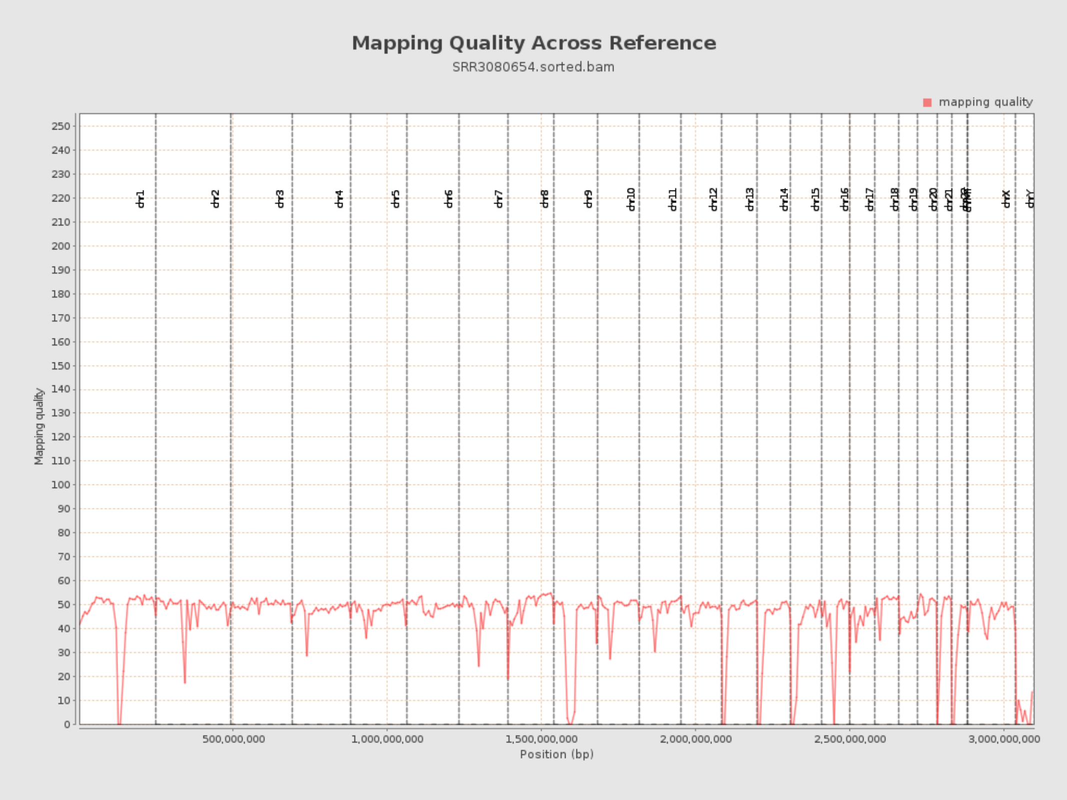
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram