Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:56:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240259.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_SRR6240259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:56:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,053
Mapped reads	1,159,252 / 82.27%
Unmapped reads	249,801 / 17.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,653 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	59,625 / 4.23%
Duplication rate	4.38%
Clipped reads	708,662 / 50.29%

2.2. ACGT Content

Number/percentage of A's	20,052,243 / 27.67%
Number/percentage of C's	12,896,968 / 17.8%
Number/percentage of T's	23,323,864 / 32.18%
Number/percentage of G's	16,181,497 / 22.33%
Number/percentage of N's	18,949 / 0.03%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.2289

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

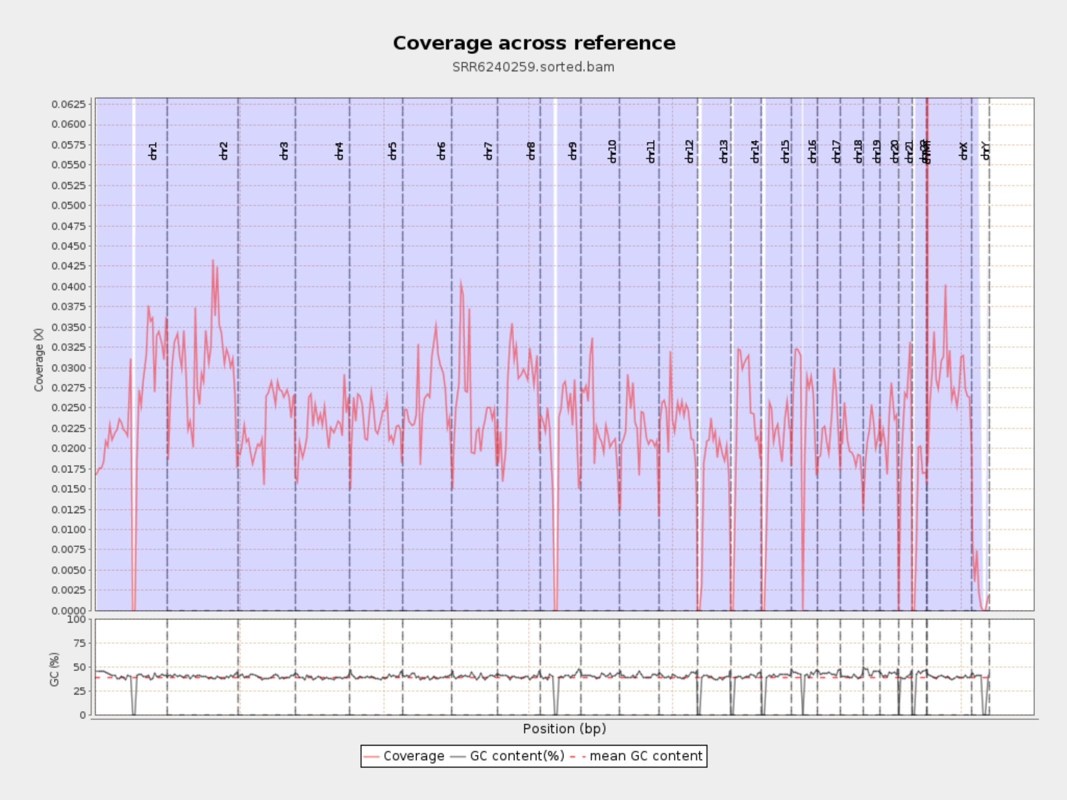
General error rate	0.85%
Mismatches	609,859
Insertions	5,157
Mapped reads with at least one insertion	0.44%
Deletions	19,958
Mapped reads with at least one deletion	1.7%
Homopolymer indels	48.38%

2.6. Chromosome stats

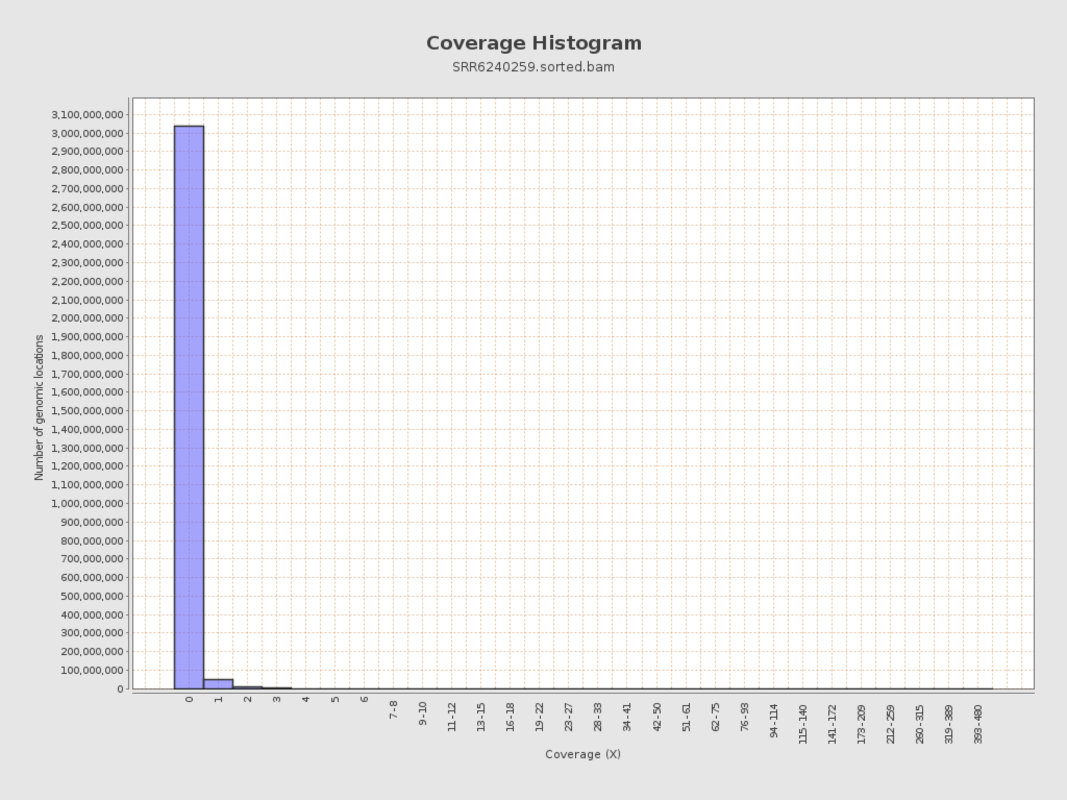
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6091254	0.0244	0.3392
chr2	243199373	7434820	0.0306	0.2701
chr3	198022430	4642208	0.0234	0.1782
chr4	191154276	4352841	0.0228	0.1785
chr5	180915260	4243779	0.0235	0.1789
chr6	171115067	4516982	0.0264	0.2144
chr7	159138663	4004268	0.0252	0.2852

chr8	146364022	4047402	0.0277	0.3451
chr9	141213431	2960231	0.021	0.2053
chr10	135534747	3128839	0.0231	0.2081
chr11	135006516	3004754	0.0223	0.2057
chr12	133851895	3182486	0.0238	0.1813
chr13	115169878	1918920	0.0167	0.1502
chr14	107349540	2422240	0.0226	0.1803
chr15	102531392	1899535	0.0185	0.1613
chr16	90354753	2197675	0.0243	0.1848
chr17	81195210	1823908	0.0225	0.1832
chr18	78077248	1560498	0.02	0.3204
chr19	59128983	1261754	0.0213	0.2341
chr20	63025520	1399934	0.0222	0.1767
chr21	48129895	1086501	0.0226	0.18
chr22	51304566	668123	0.013	0.1313
chrMT	16571	24745	1.4933	1.792
chrX	155270560	4471036	0.0288	0.2087
chrY	59373566	162781	0.0027	0.0633

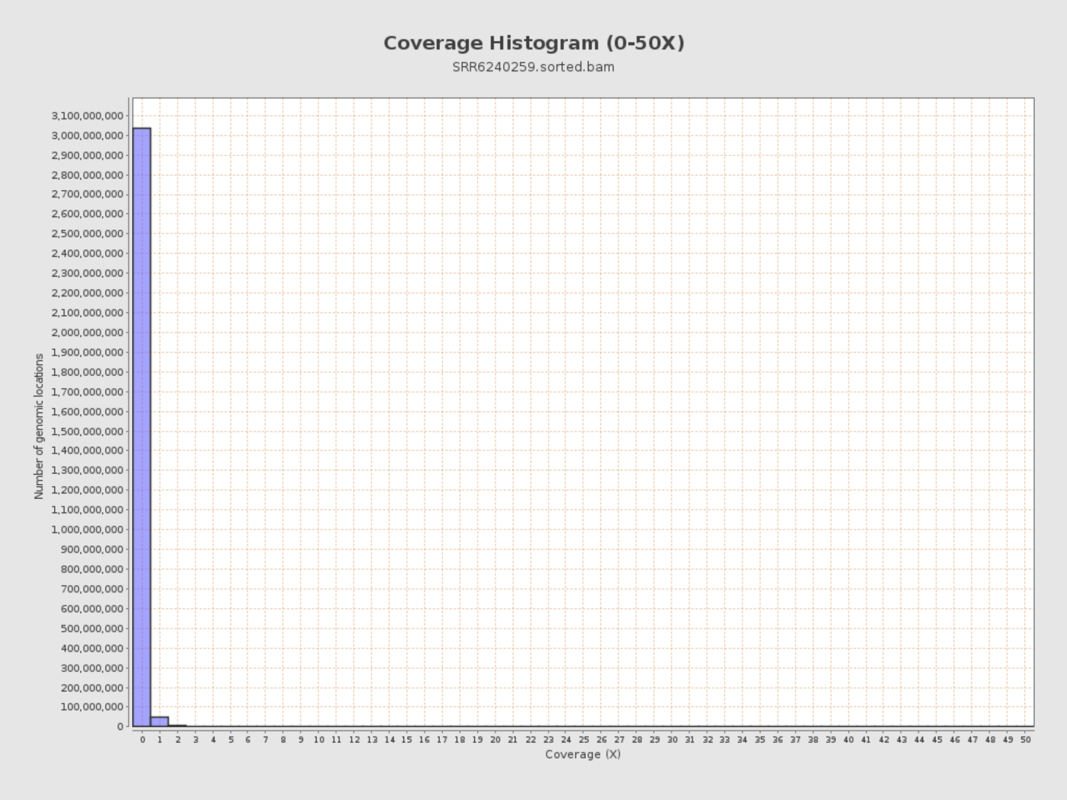
3. Results : Coverage across reference



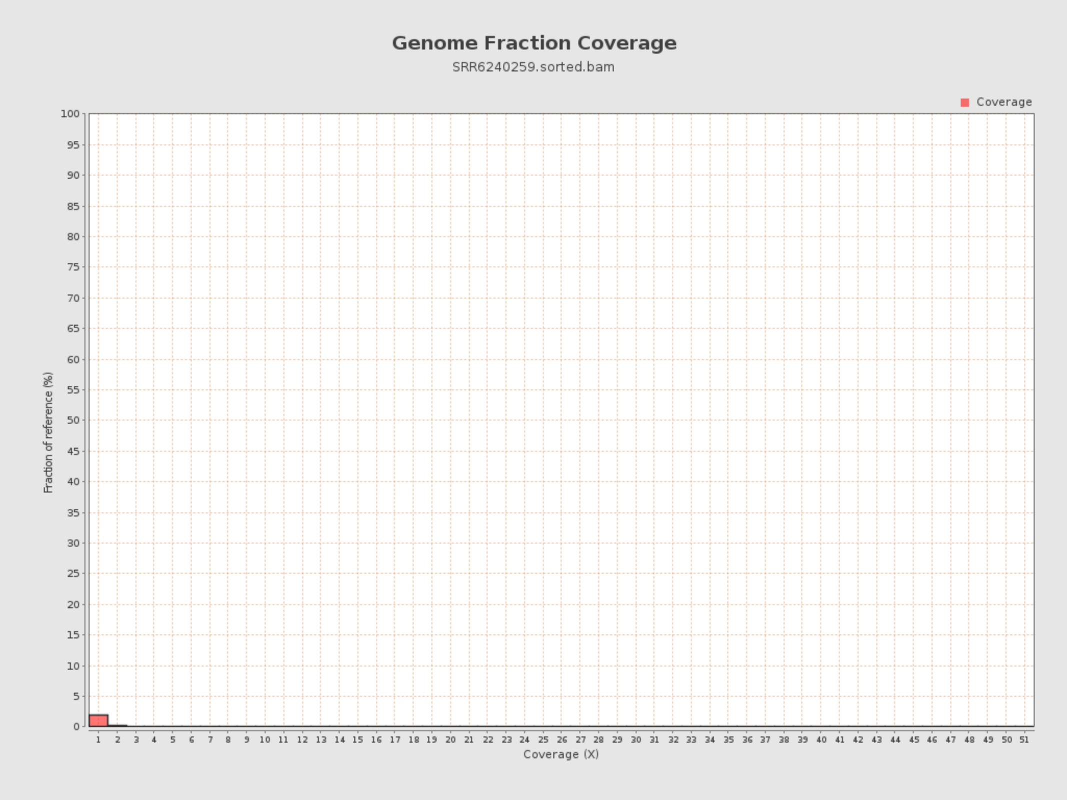
4. Results : Coverage Histogram



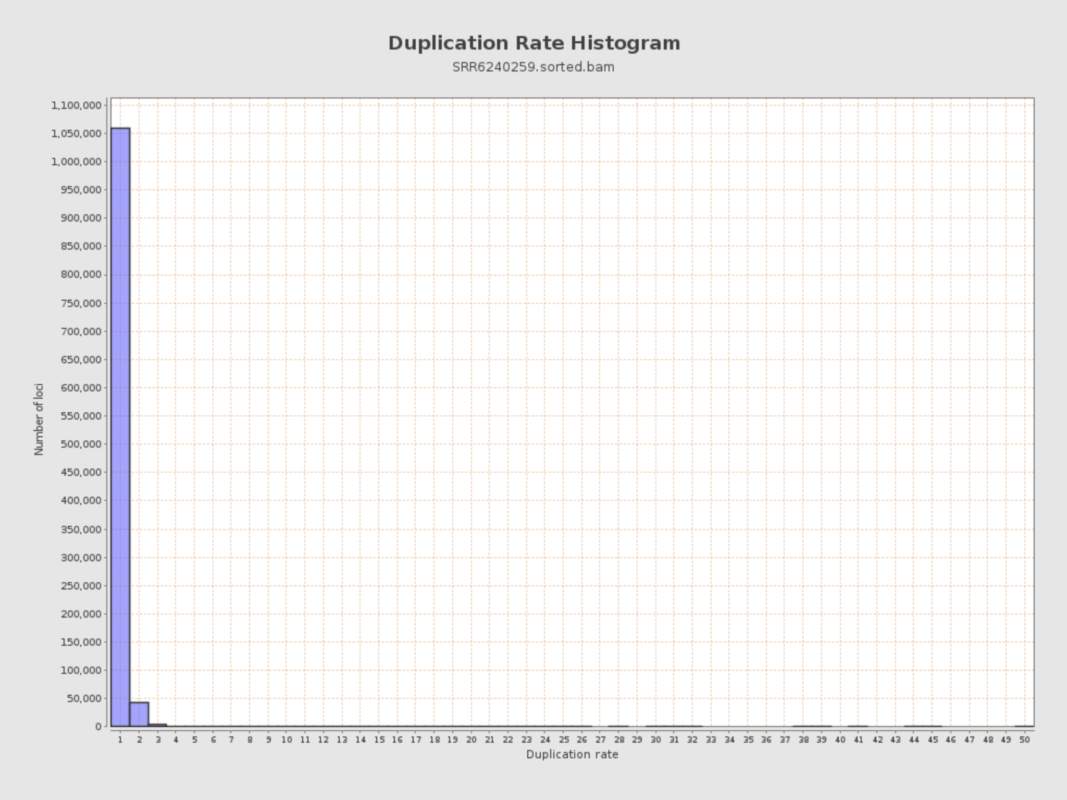
5. Results : Coverage Histogram (0-50X)



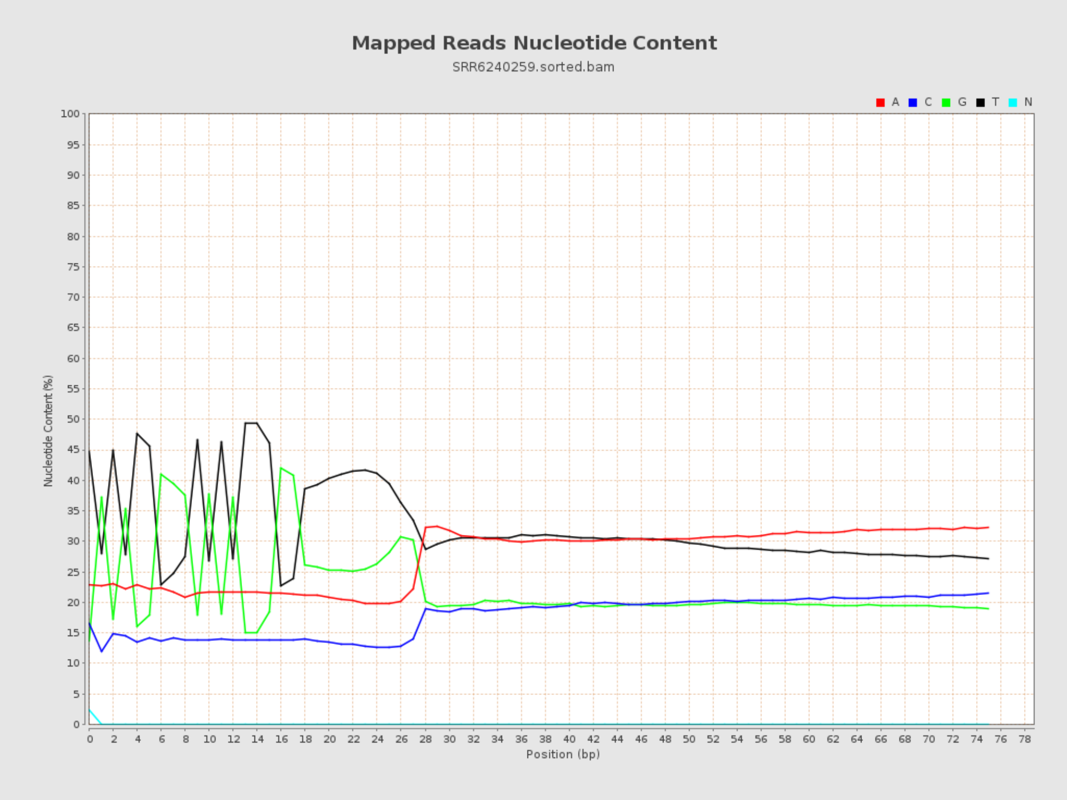
6. Results : Genome Fraction Coverage



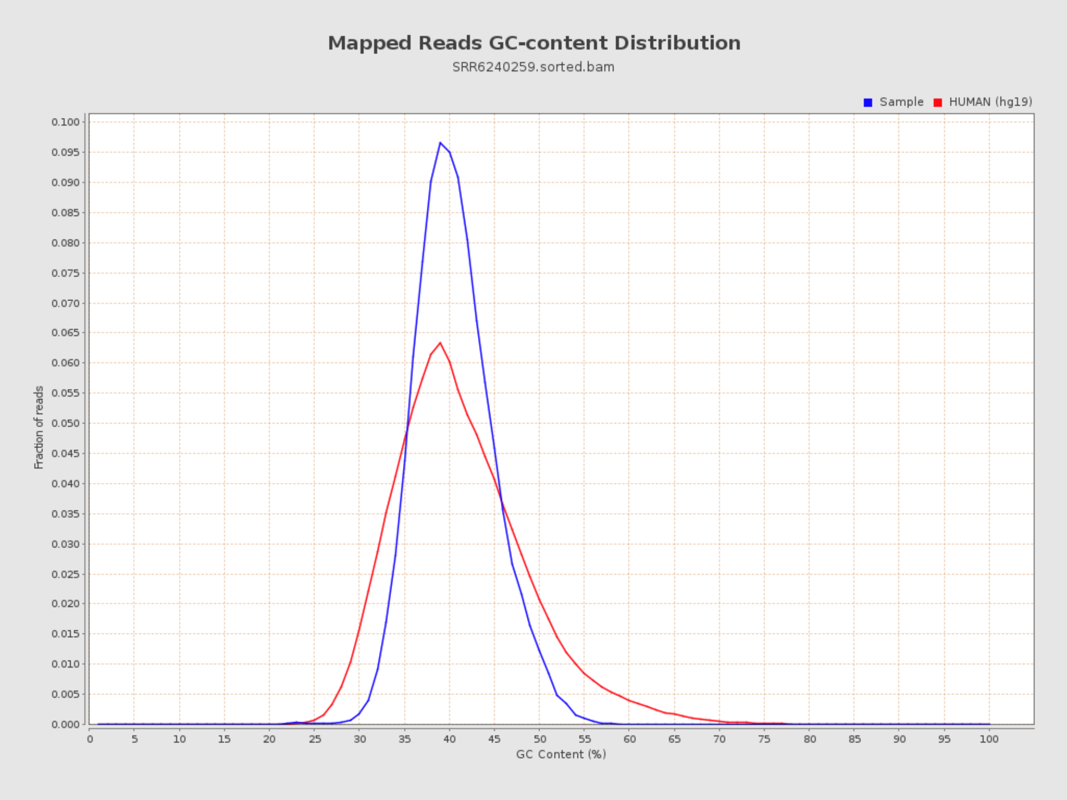
7. Results : Duplication Rate Histogram



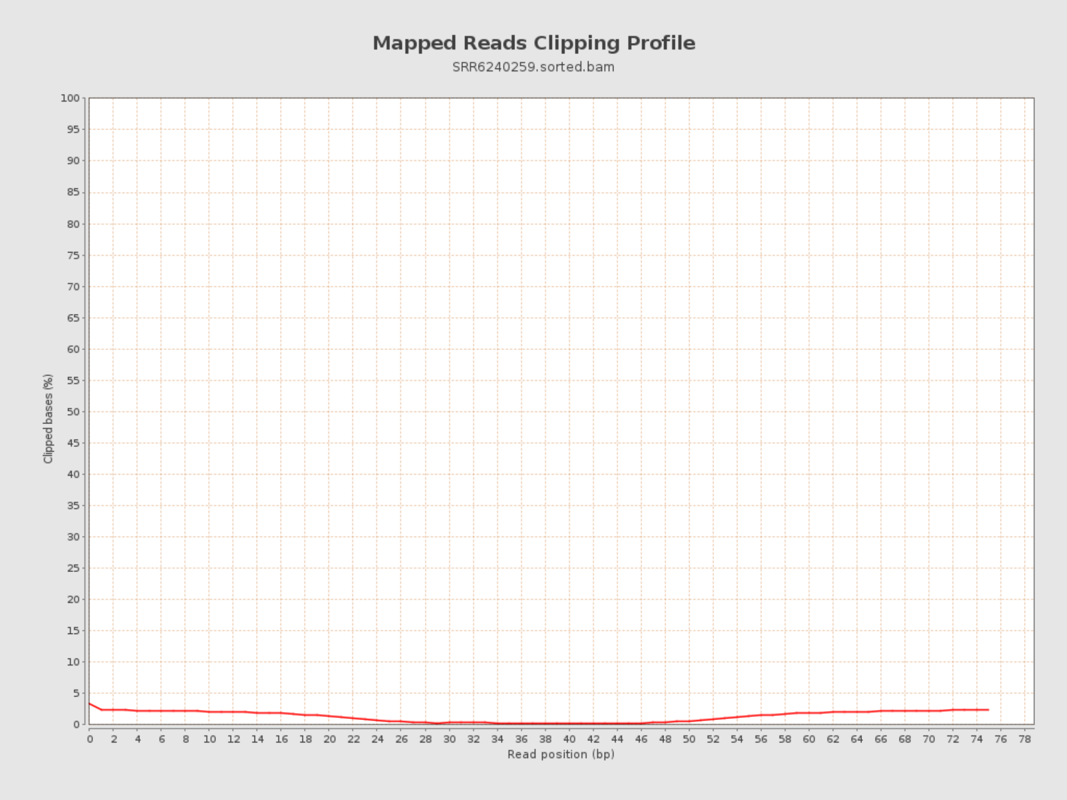
8. Results : Mapped Reads Nucleotide Content



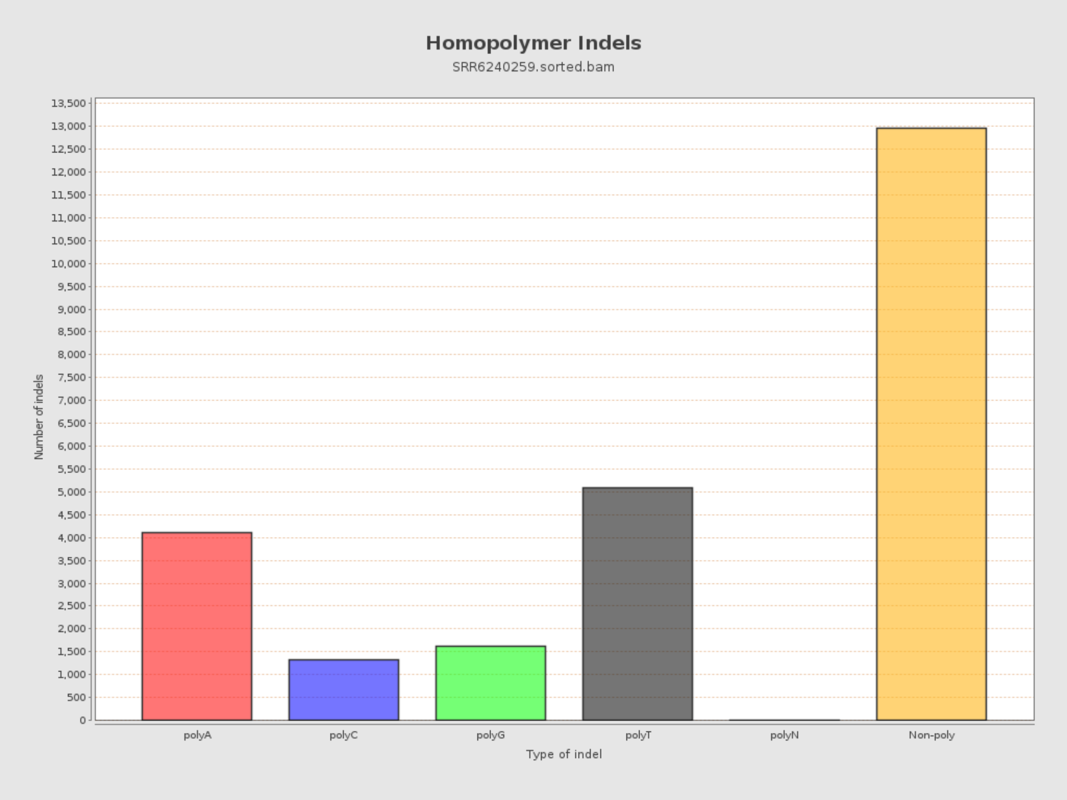
9. Results : Mapped Reads GC-content Distribution



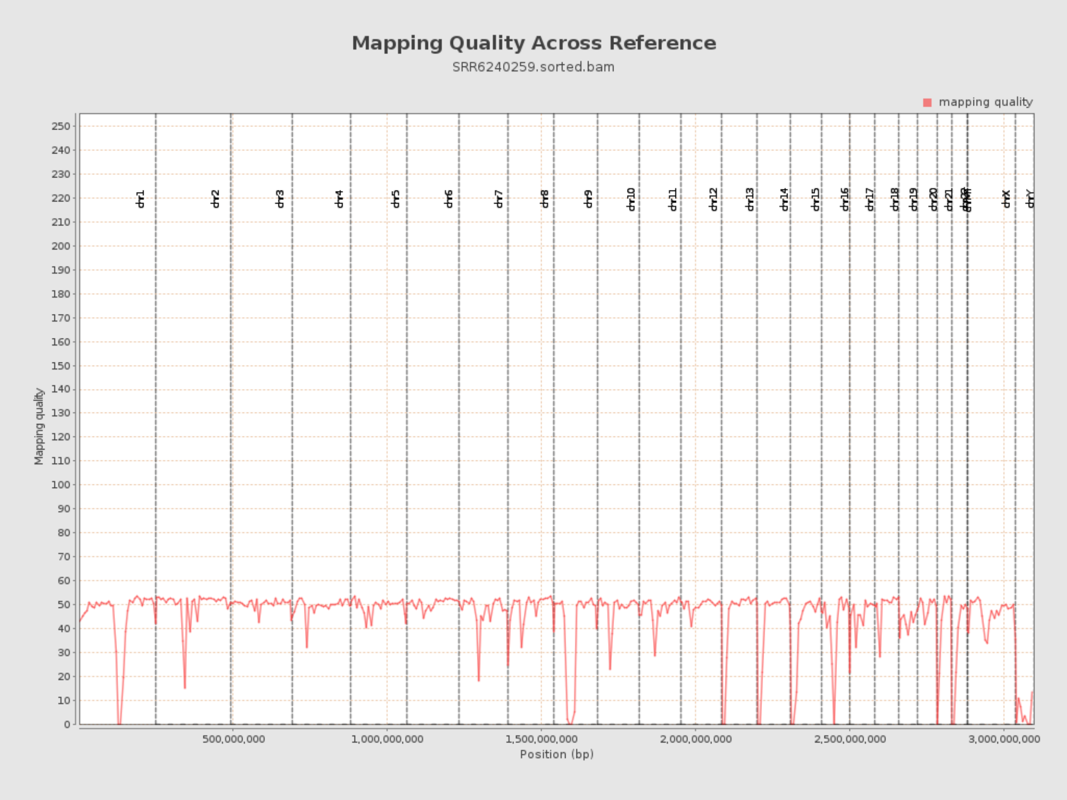
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram