Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:51:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240045.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_SRR6240045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:51:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,349,901
Mapped reads	1,151,429 / 85.3%
Unmapped reads	198,472 / 14.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,922 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	30,429 / 2.25%
Duplication rate	1.94%
Clipped reads	562,159 / 41.64%

2.2. ACGT Content

Number/percentage of A's	21,121,133 / 28.01%
Number/percentage of C's	13,802,985 / 18.31%
Number/percentage of T's	23,168,045 / 30.73%
Number/percentage of G's	17,249,068 / 22.88%
Number/percentage of N's	51,653 / 0.07%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2394

2.4. Mapping Quality

Mean Mapping Quality	43.34

2.5. Mismatches and indels

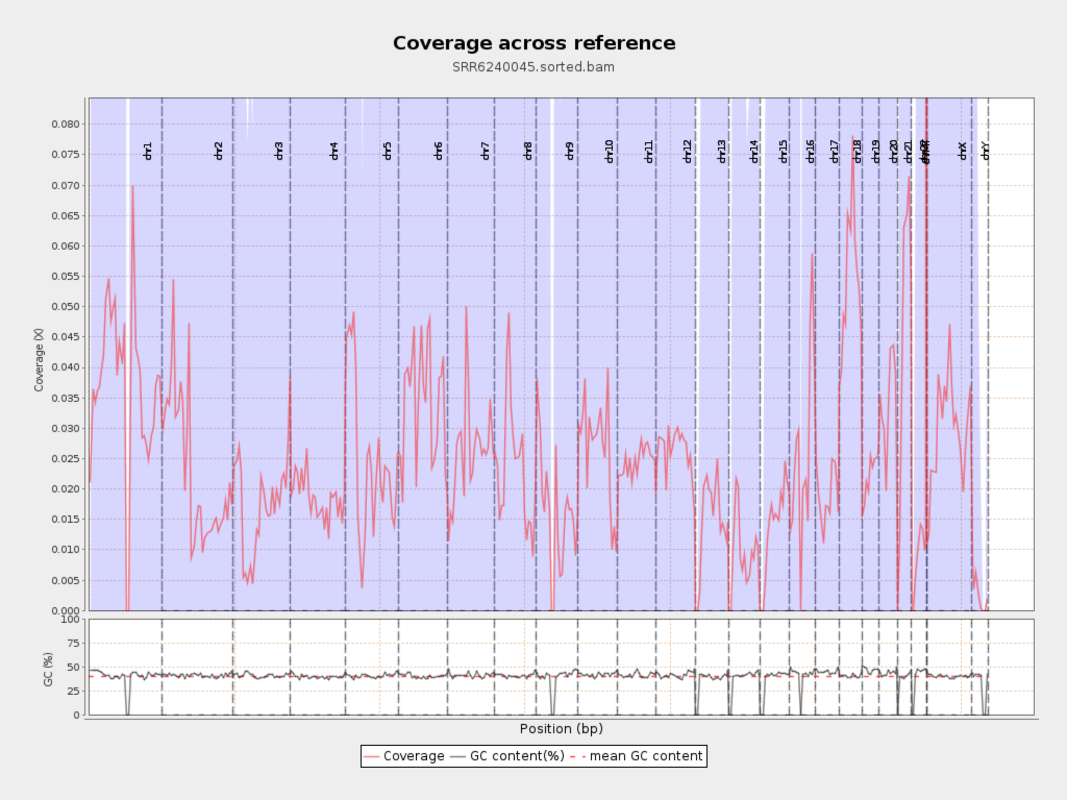
General error rate	0.95%
Mismatches	710,393
Insertions	5,374
Mapped reads with at least one insertion	0.46%
Deletions	17,928
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.2%

2.6. Chromosome stats

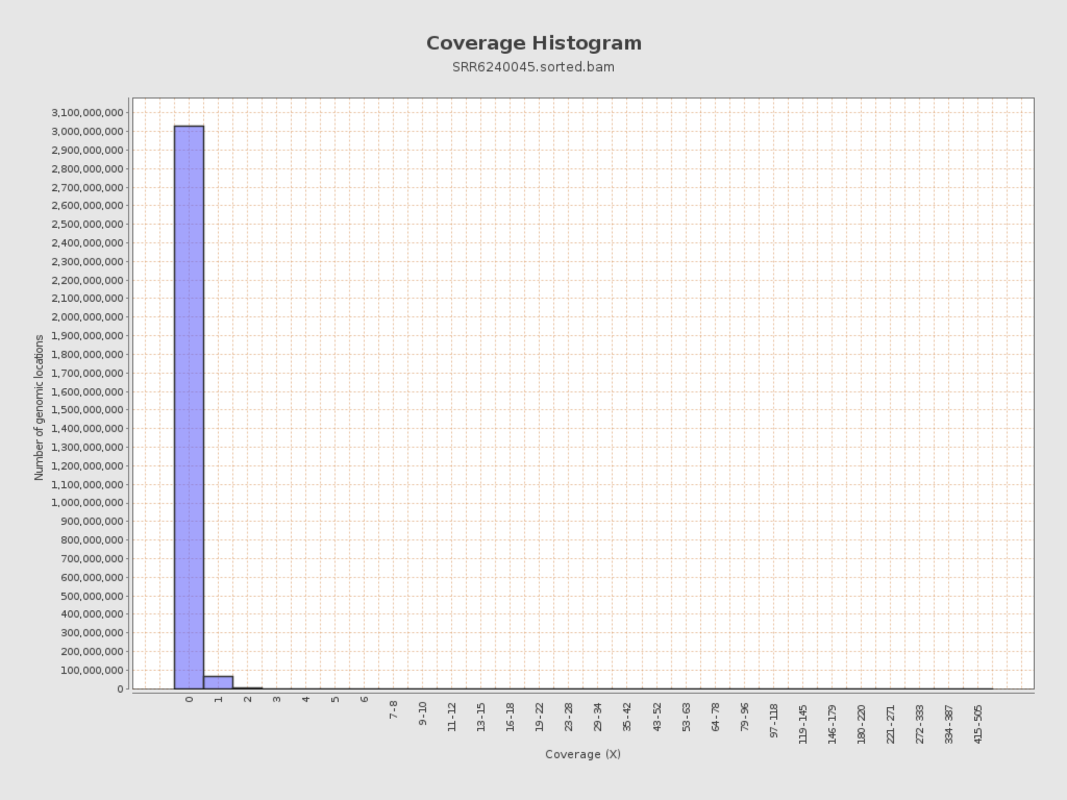
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9229781	0.037	0.3744
chr2	243199373	5567319	0.0229	0.2828
chr3	198022430	3340934	0.0169	0.1379
chr4	191154276	3535127	0.0185	0.1458
chr5	180915260	4428648	0.0245	0.1673
chr6	171115067	5852578	0.0342	0.2473
chr7	159138663	4219514	0.0265	0.3115

chr8	146364022	3402238	0.0232	0.3624
chr9	141213431	2232994	0.0158	0.2215
chr10	135534747	3632970	0.0268	0.2102
chr11	135006516	3290765	0.0244	0.1987
chr12	133851895	3532563	0.0264	0.1741
chr13	115169878	1661056	0.0144	0.1268
chr14	107349540	993443	0.0093	0.1302
chr15	102531392	1428048	0.0139	0.13
chr16	90354753	2397342	0.0265	0.1916
chr17	81195210	1527611	0.0188	0.1478
chr18	78077248	4307501	0.0552	0.4512
chr19	59128983	1323497	0.0224	0.2581
chr20	63025520	2139976	0.034	0.2054
chr21	48129895	2187427	0.0454	0.2332
chr22	51304566	424985	0.0083	0.0953
chrMT	16571	8920	0.5383	0.8358
chrX	155270560	4603644	0.0296	0.1988
chrY	59373566	154732	0.0026	0.0607

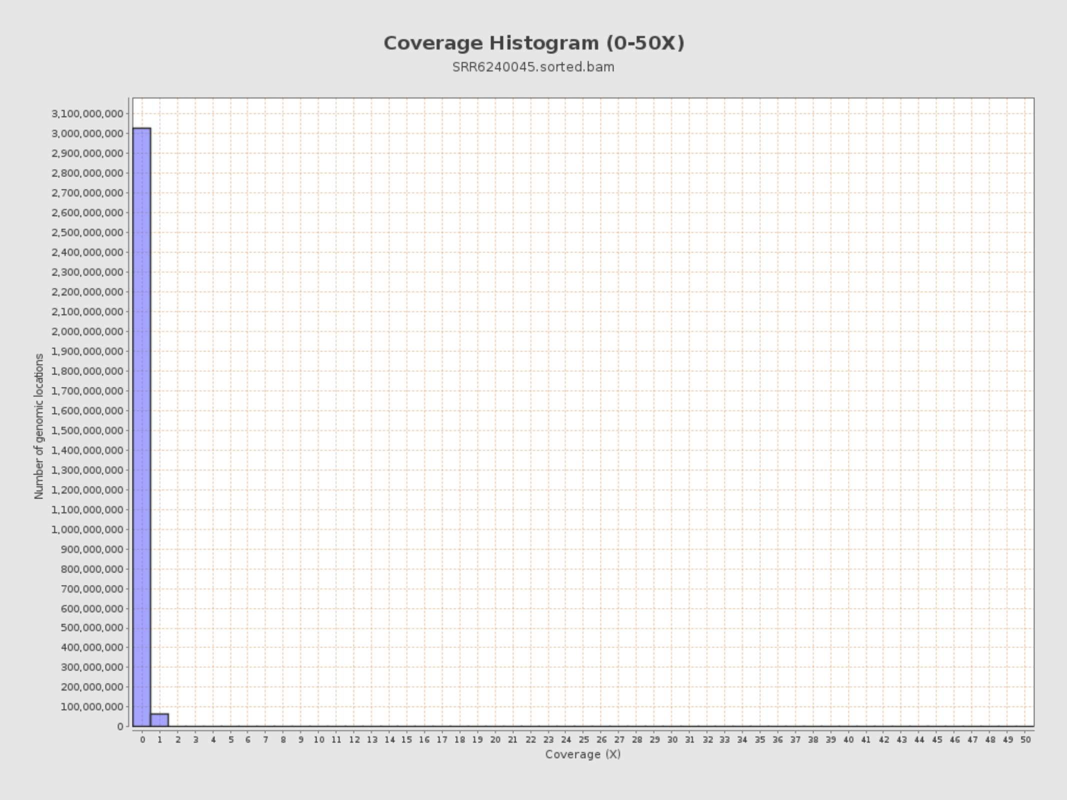
3. Results : Coverage across reference



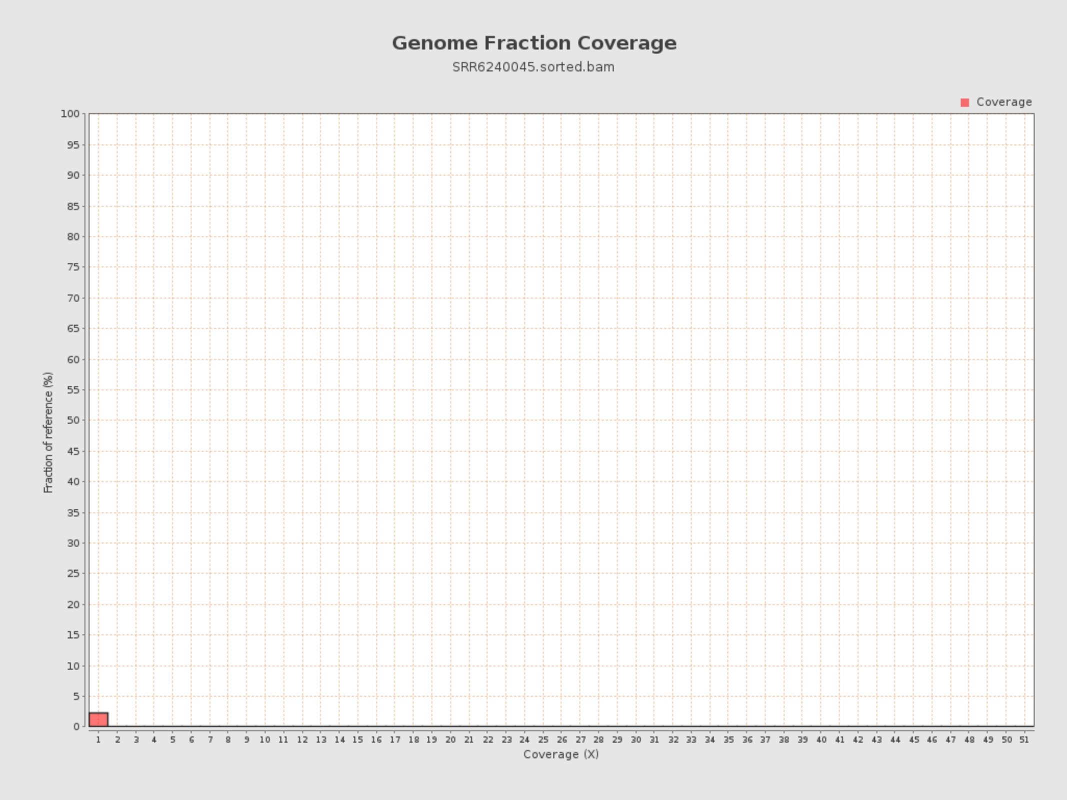
4. Results : Coverage Histogram



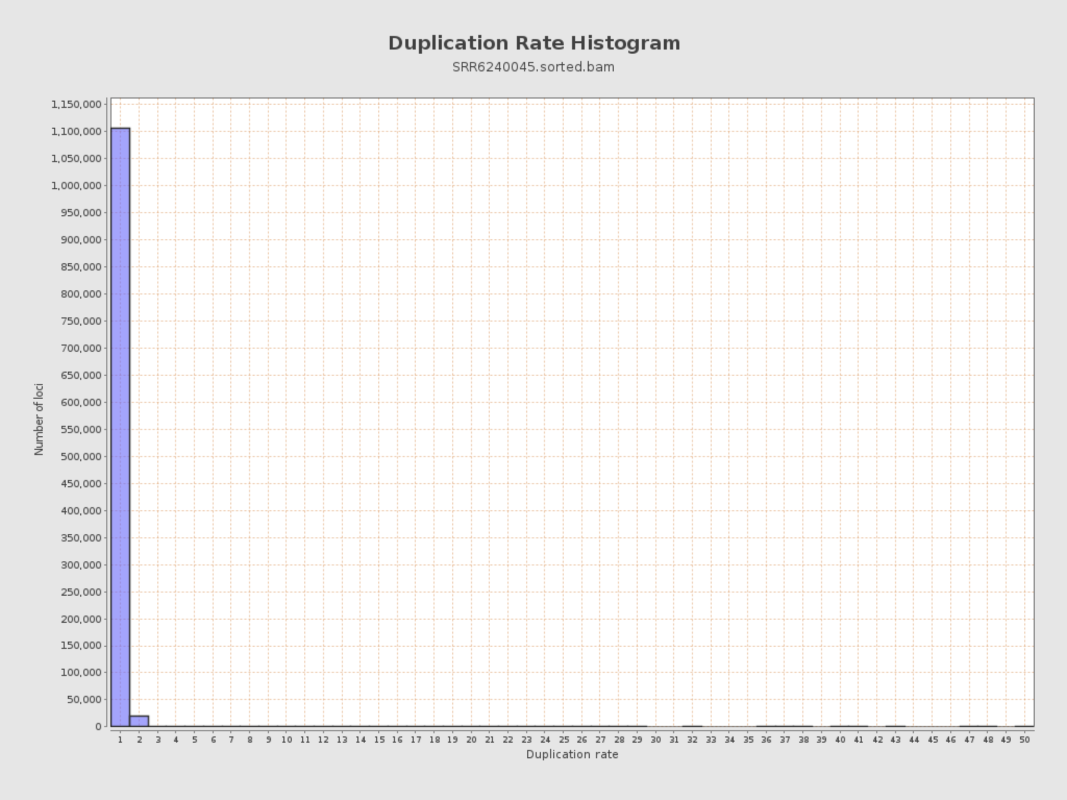
5. Results : Coverage Histogram (0-50X)



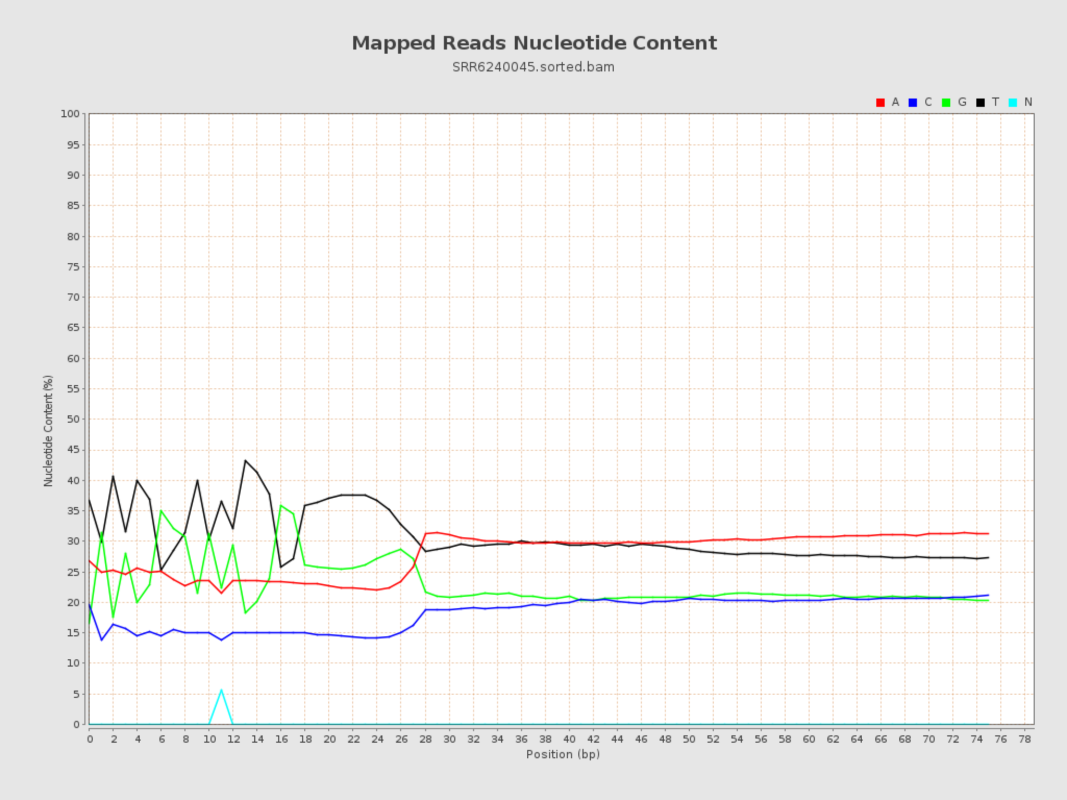
6. Results : Genome Fraction Coverage



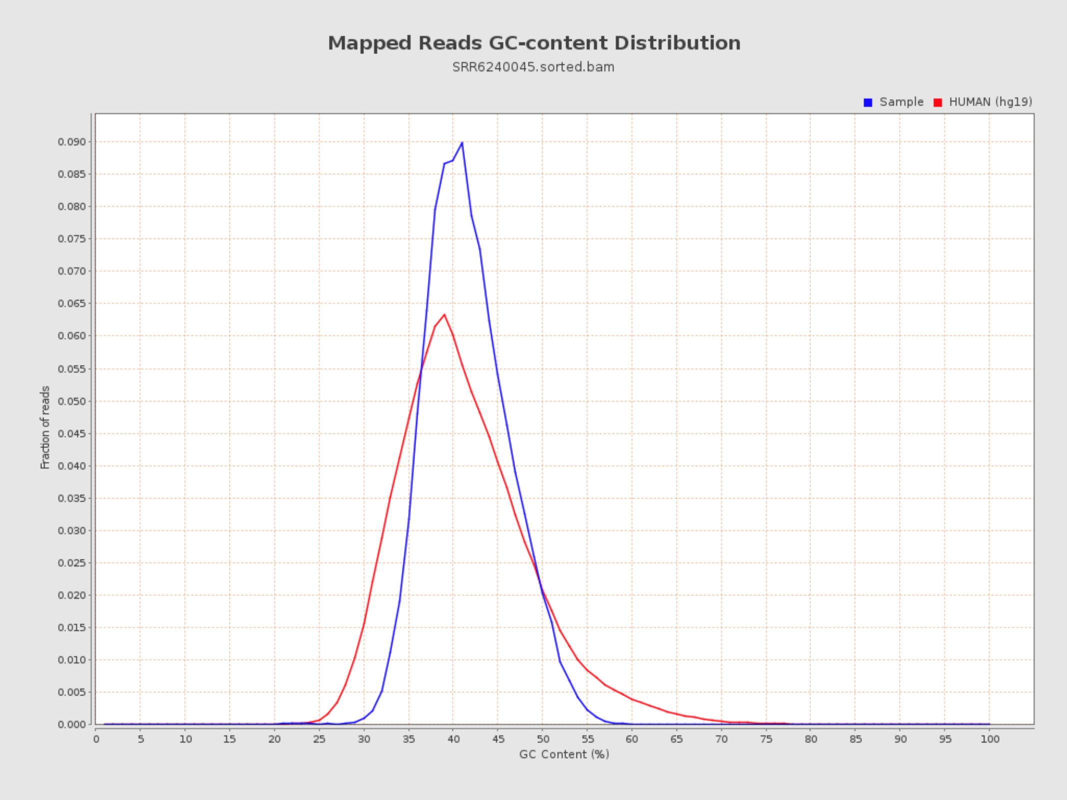
7. Results : Duplication Rate Histogram



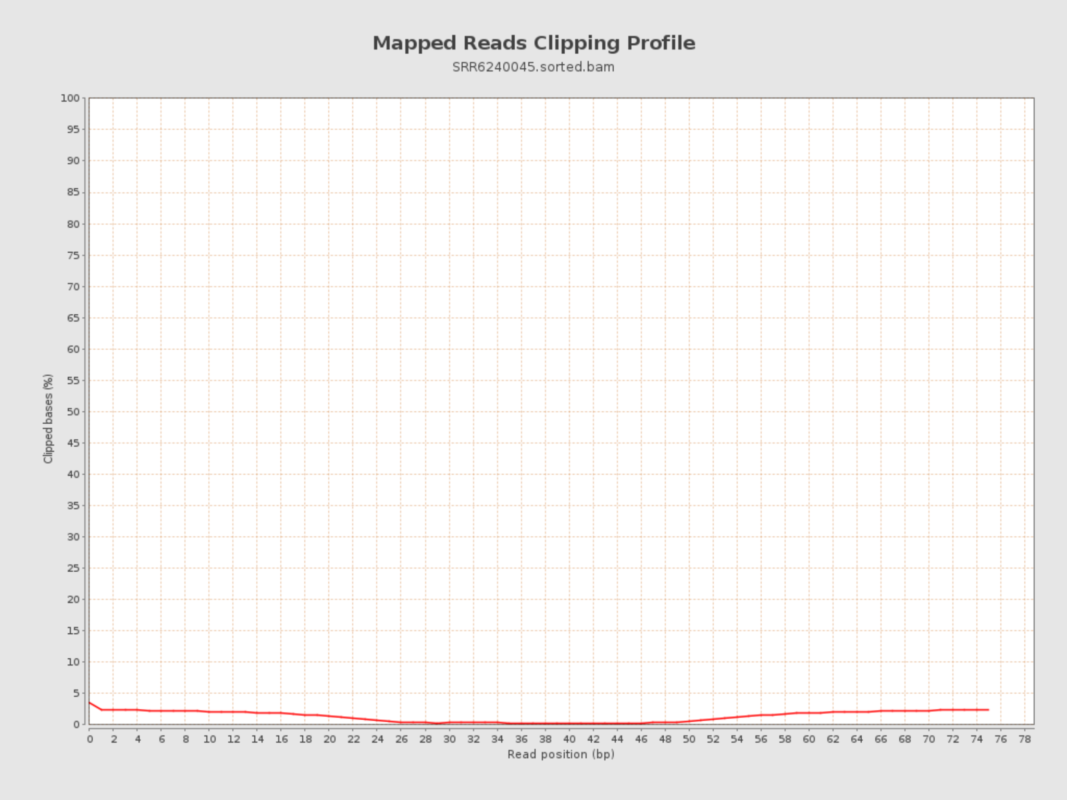
8. Results : Mapped Reads Nucleotide Content



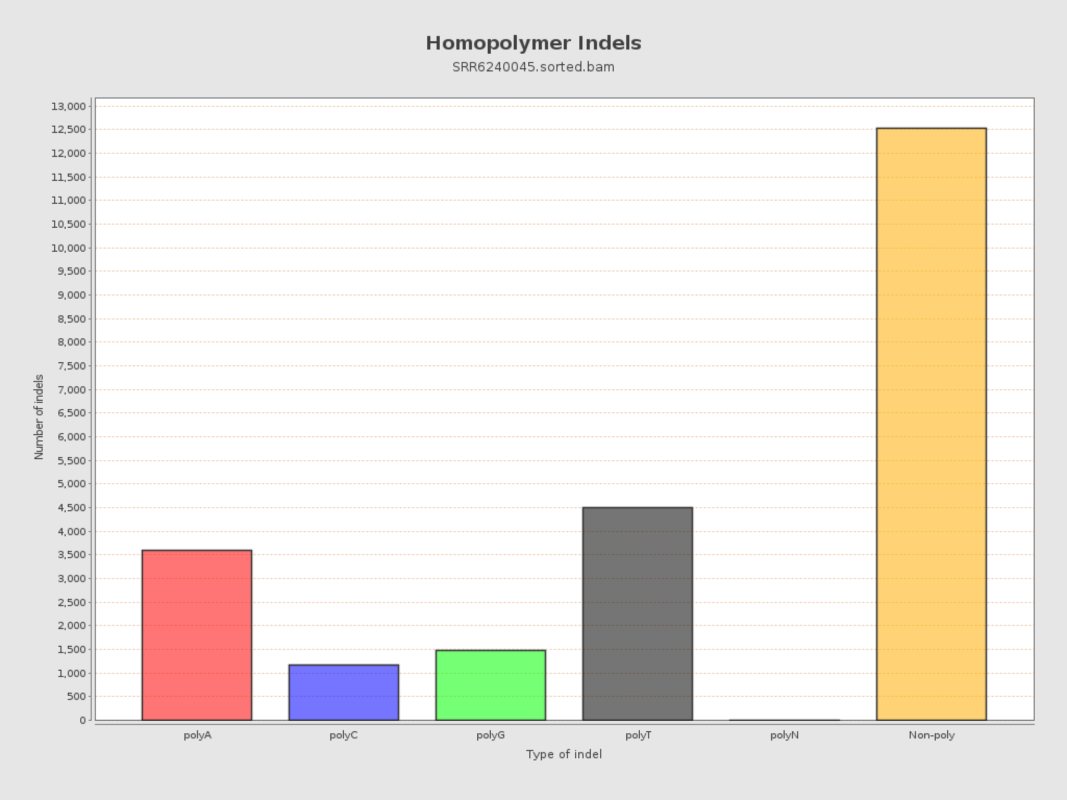
9. Results : Mapped Reads GC-content Distribution



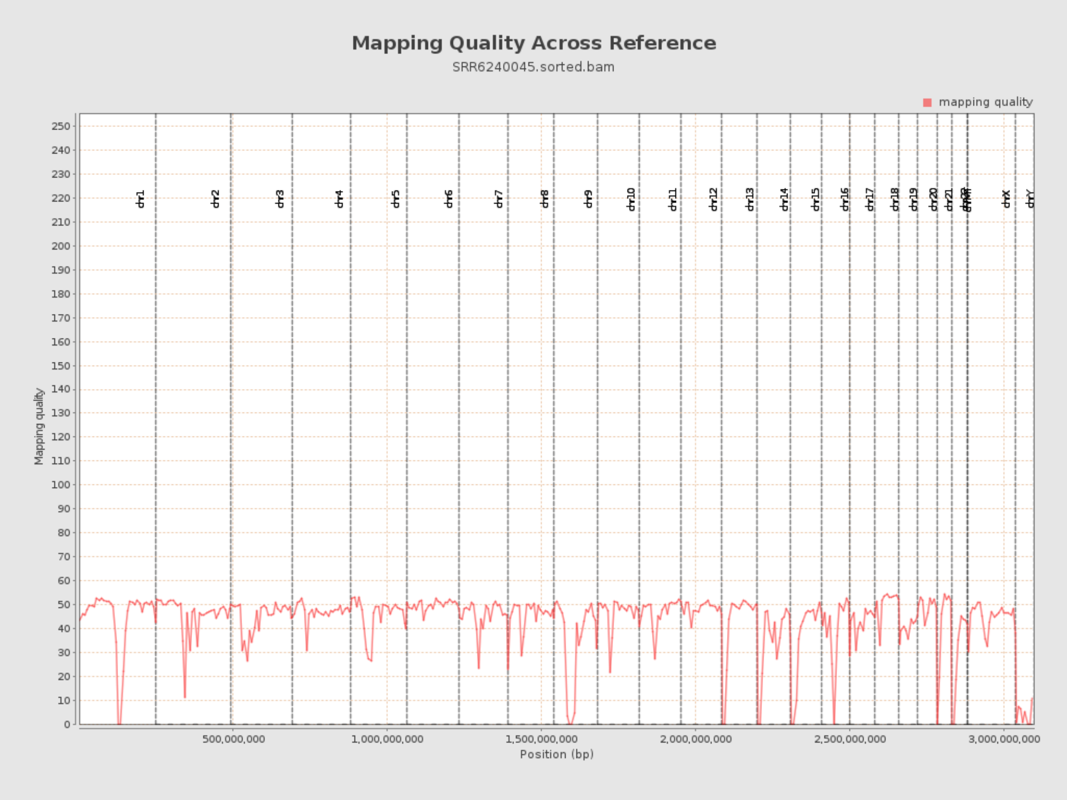
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram