Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:15:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240203.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_SRR6240203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:15:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,412,521
Mapped reads	1,101,010 / 77.95%
Unmapped reads	311,511 / 22.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,976 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	50,096 / 3.55%
Duplication rate	3.56%
Clipped reads	775,546 / 54.91%

2.2. ACGT Content

Number/percentage of A's	17,688,632 / 26.6%
Number/percentage of C's	11,208,420 / 16.86%
Number/percentage of T's	21,233,682 / 31.93%
Number/percentage of G's	16,352,863 / 24.59%
Number/percentage of N's	14,409 / 0.02%
GC Percentage	41.45%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2356

2.4. Mapping Quality

Mean Mapping Quality	42.37

2.5. Mismatches and indels

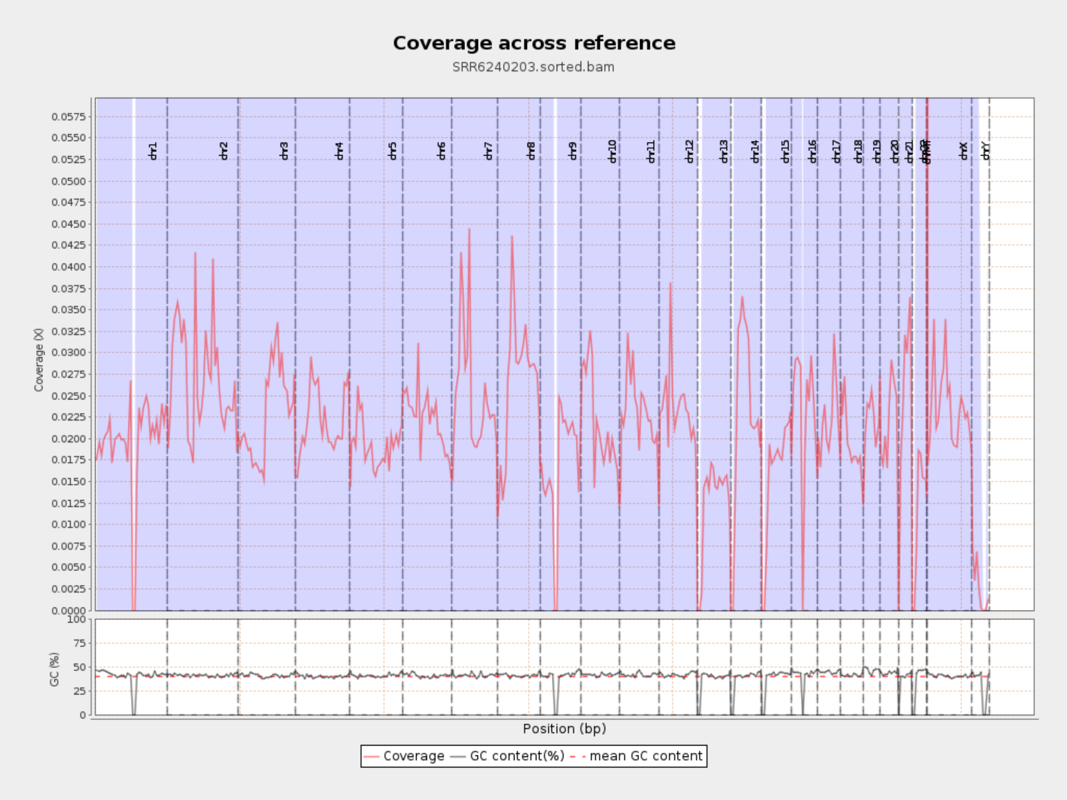
General error rate	1.03%
Mismatches	677,409
Insertions	4,894
Mapped reads with at least one insertion	0.44%
Deletions	22,417
Mapped reads with at least one deletion	2.01%
Homopolymer indels	49.23%

2.6. Chromosome stats

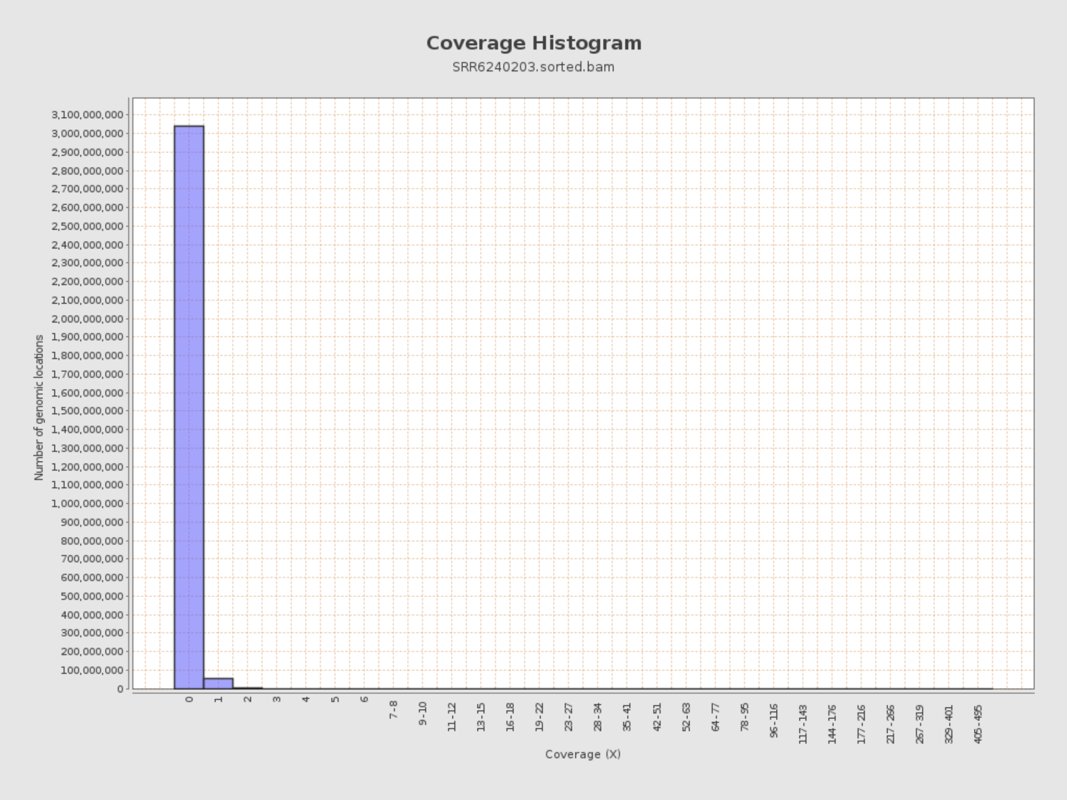
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4888019	0.0196	0.3004
chr2	243199373	6596742	0.0271	0.2999
chr3	198022430	4535026	0.0229	0.1721
chr4	191154276	4212421	0.022	0.1753
chr5	180915260	3492281	0.0193	0.1586
chr6	171115067	3830565	0.0224	0.2022
chr7	159138663	4036784	0.0254	0.418

chr8	146364022	3956480	0.027	0.3429
chr9	141213431	2356688	0.0167	0.2188
chr10	135534747	2983739	0.022	0.1956
chr11	135006516	3150973	0.0233	0.2305
chr12	133851895	3178992	0.0238	0.1748
chr13	115169878	1435240	0.0125	0.1244
chr14	107349540	2498593	0.0233	0.18
chr15	102531392	1595865	0.0156	0.1774
chr16	90354753	2075469	0.023	0.1728
chr17	81195210	1805384	0.0222	0.1838
chr18	78077248	1527288	0.0196	0.3157
chr19	59128983	1312225	0.0222	0.2444
chr20	63025520	1375823	0.0218	0.1727
chr21	48129895	1214571	0.0252	0.1862
chr22	51304566	600048	0.0117	0.1192
chrMT	16571	26163	1.5788	2.278
chrX	155270560	3699936	0.0238	0.1957
chrY	59373566	151585	0.0026	0.0615

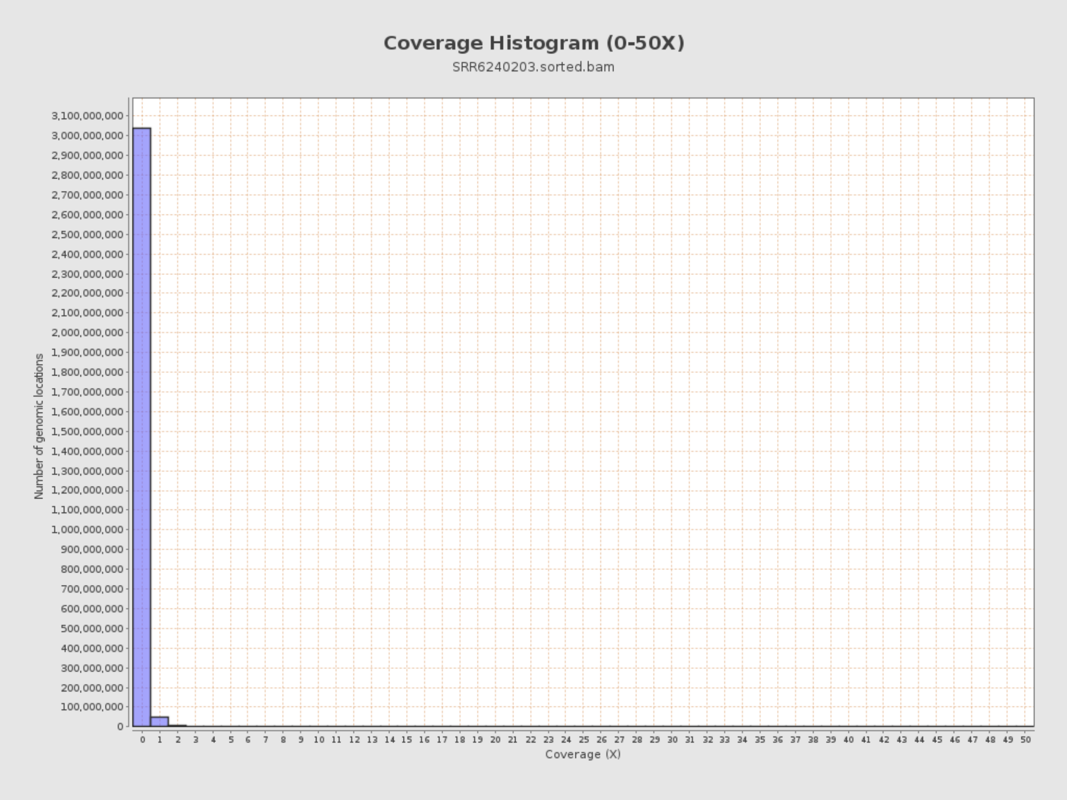
3. Results : Coverage across reference



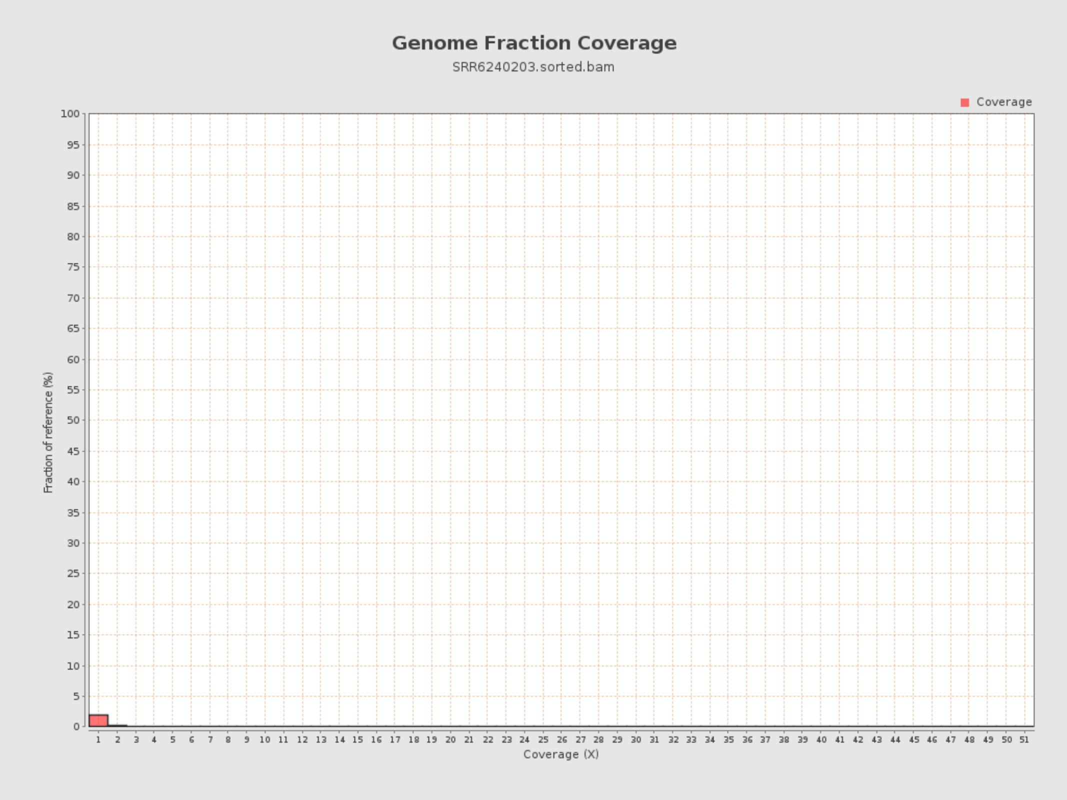
4. Results : Coverage Histogram



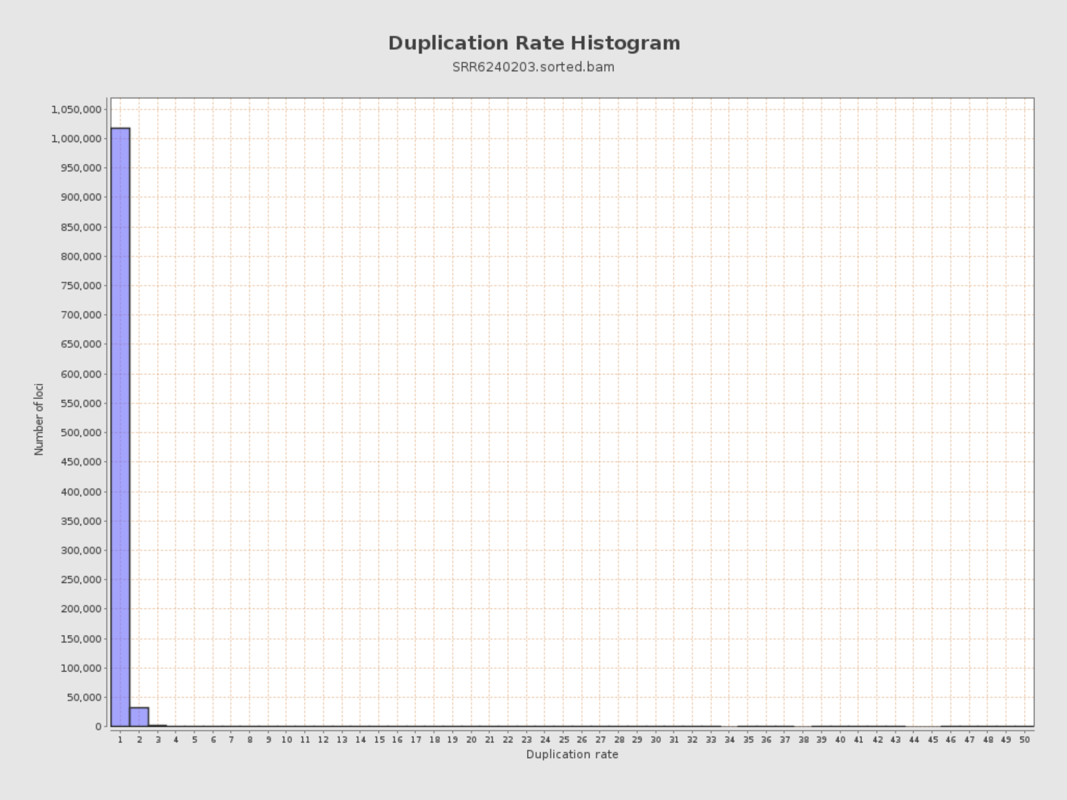
5. Results : Coverage Histogram (0-50X)



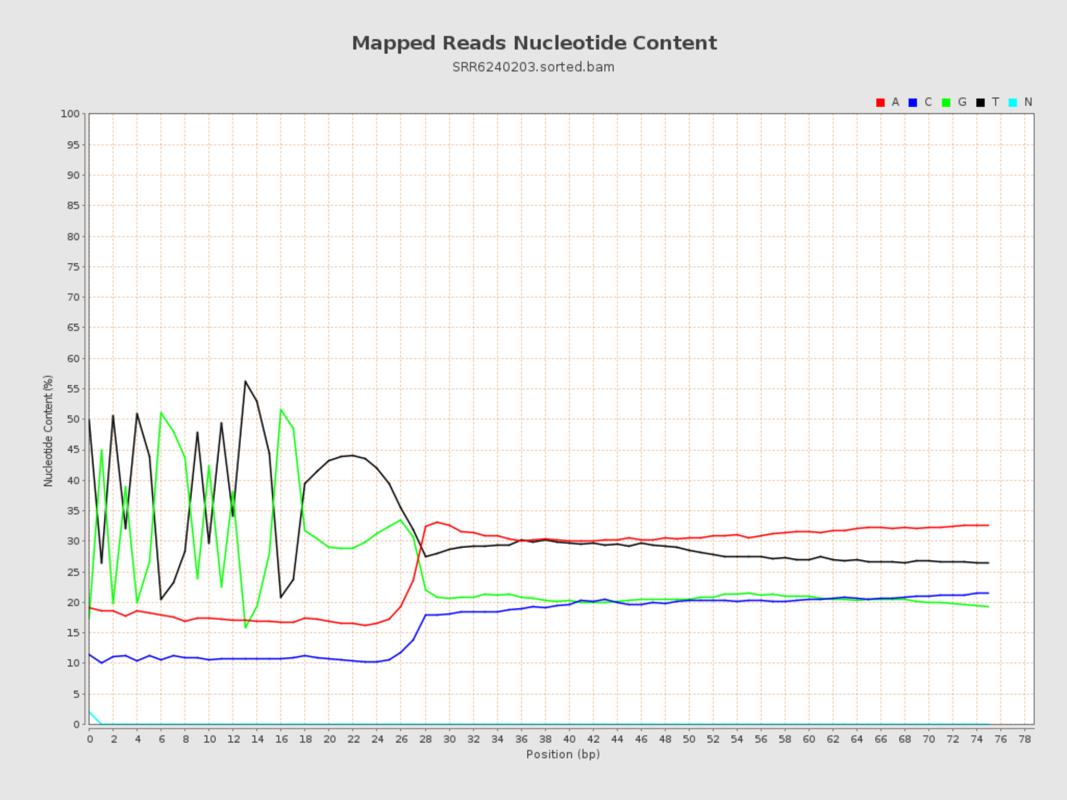
6. Results : Genome Fraction Coverage



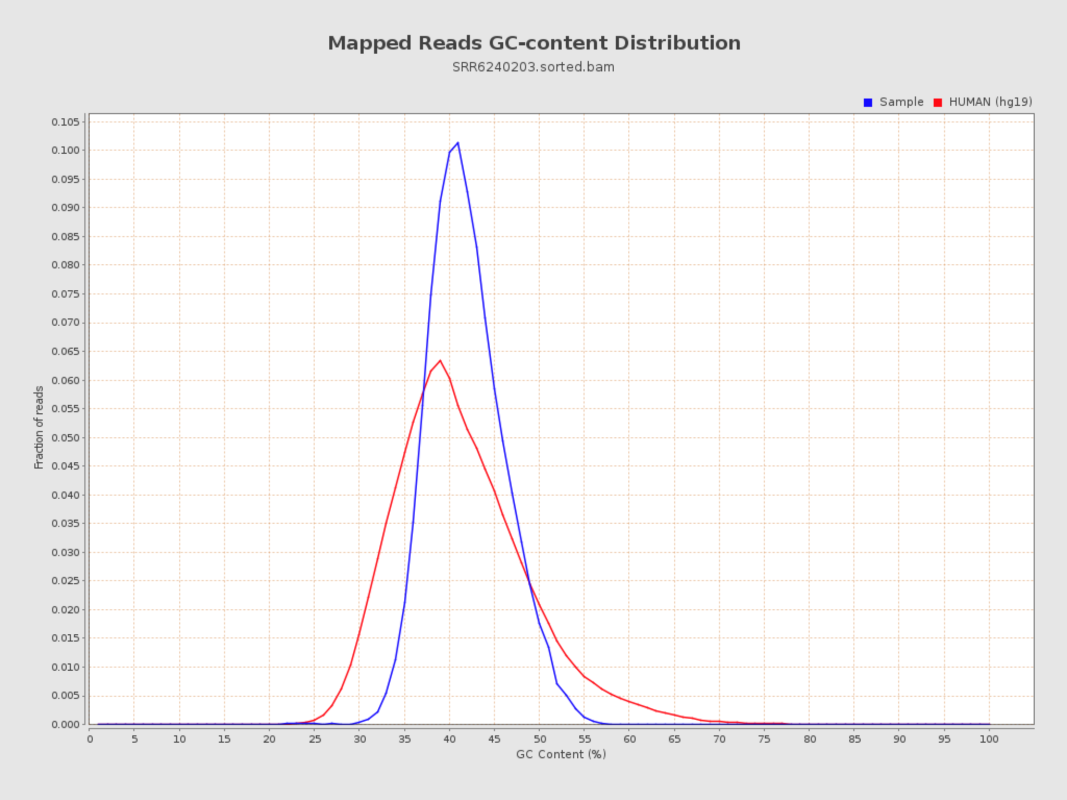
7. Results : Duplication Rate Histogram



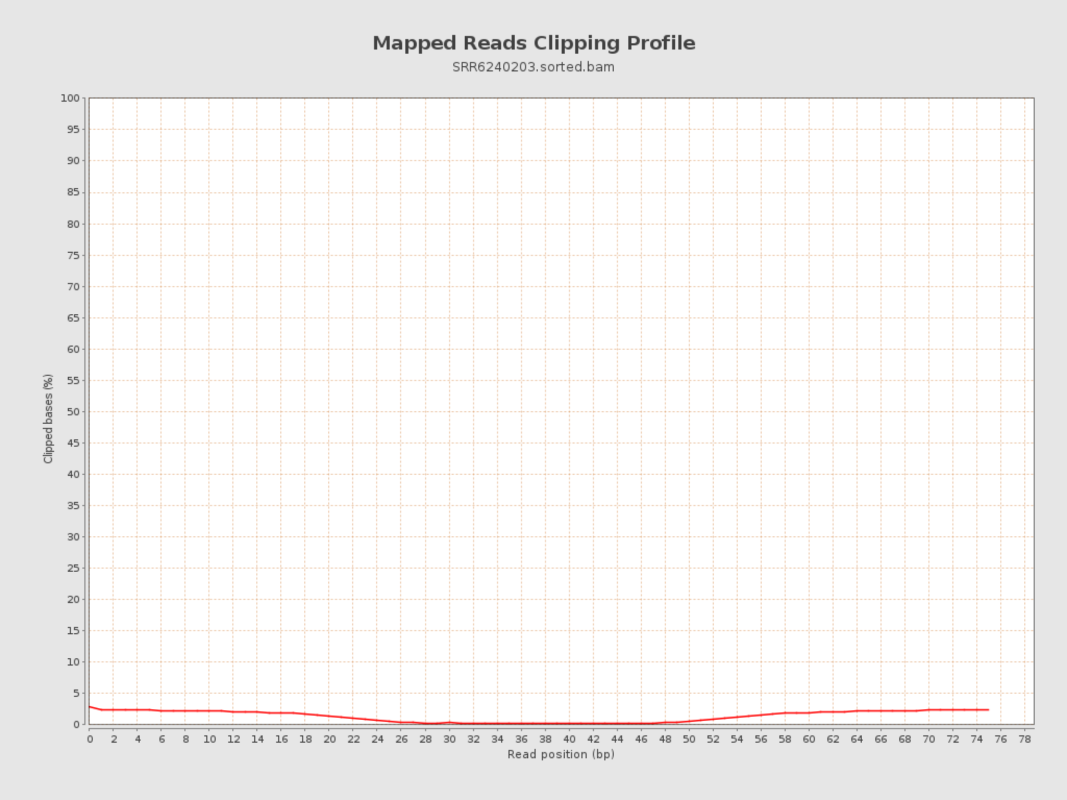
8. Results : Mapped Reads Nucleotide Content



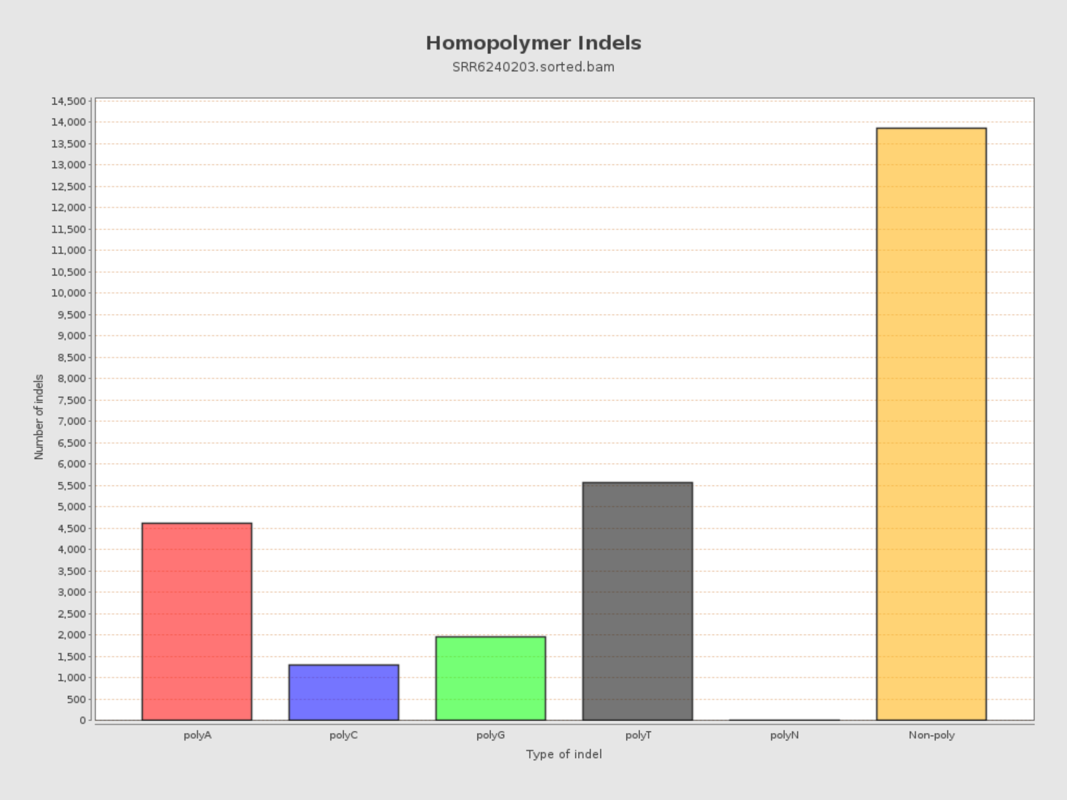
9. Results : Mapped Reads GC-content Distribution



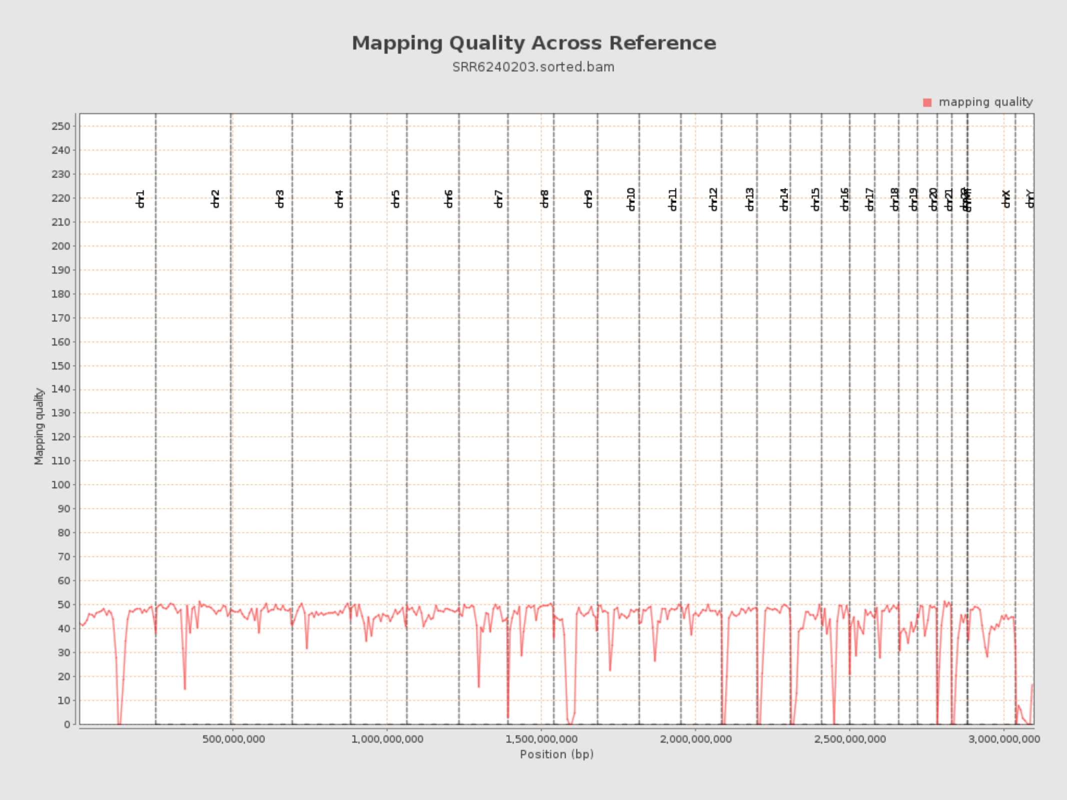
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram