Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:48:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240022.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_SRR6240022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:48:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,430,403
Mapped reads	1,013,996 / 70.89%
Unmapped reads	416,407 / 29.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,277 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	137,324 / 9.6%
Duplication rate	10.51%
Clipped reads	594,395 / 41.55%

2.2. ACGT Content

Number/percentage of A's	17,677,926 / 27.62%
Number/percentage of C's	11,465,380 / 17.91%
Number/percentage of T's	20,530,205 / 32.07%
Number/percentage of G's	14,299,608 / 22.34%
Number/percentage of N's	42,144 / 0.07%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2732

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

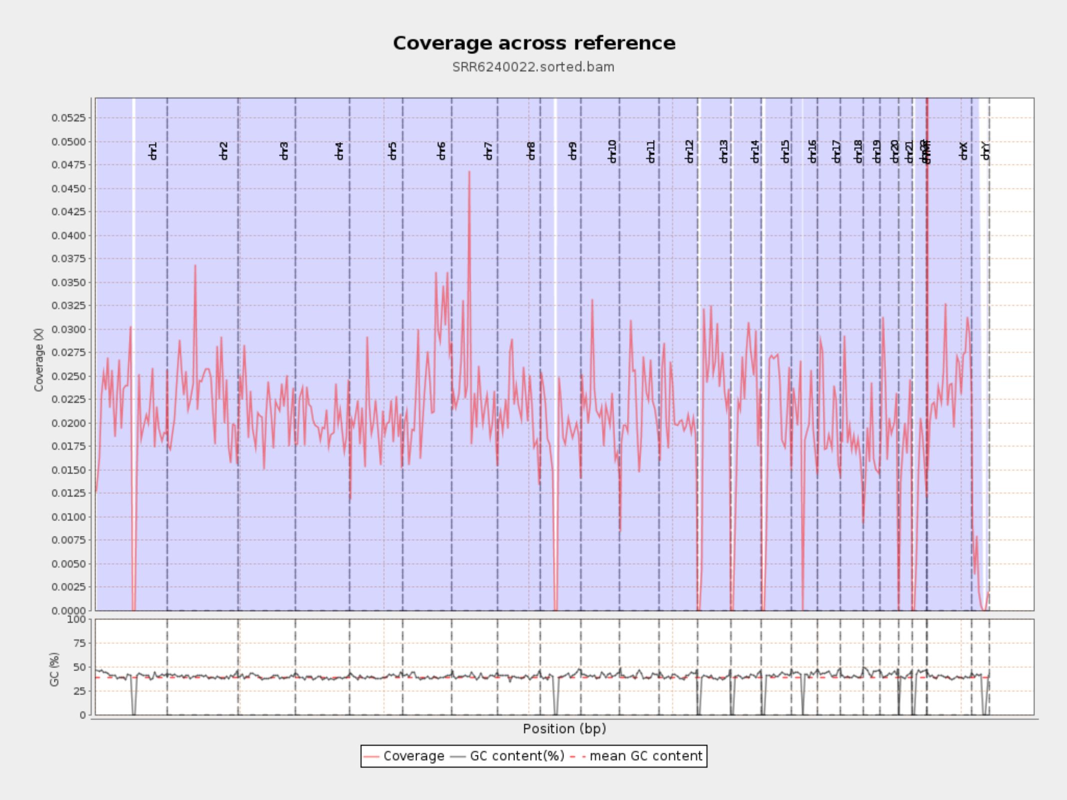
General error rate	0.9%
Mismatches	565,003
Insertions	4,489
Mapped reads with at least one insertion	0.44%
Deletions	15,348
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.07%

2.6. Chromosome stats

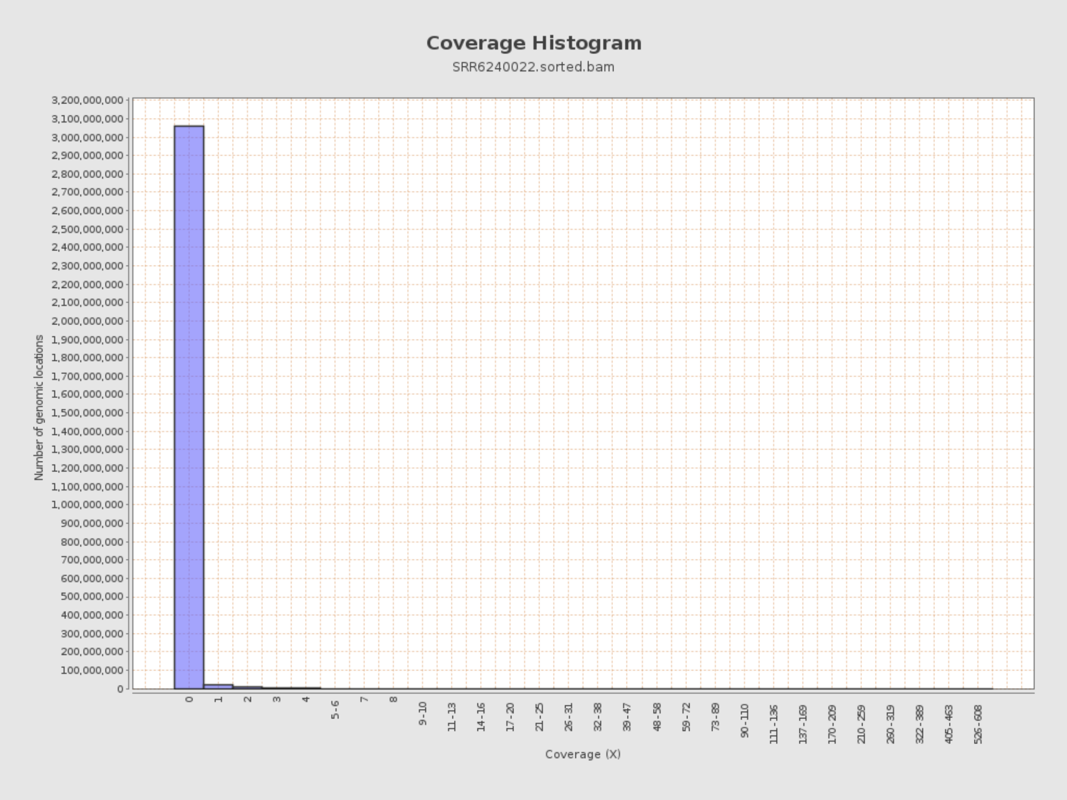
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5050912	0.0203	0.3487
chr2	243199373	5586226	0.023	0.2926
chr3	198022430	4250786	0.0215	0.2259
chr4	191154276	3865452	0.0202	0.2246
chr5	180915260	3671135	0.0203	0.2218
chr6	171115067	4256134	0.0249	0.2563
chr7	159138663	3761440	0.0236	0.3603

chr8	146364022	3185313	0.0218	0.4174
chr9	141213431	2520926	0.0179	0.2529
chr10	135534747	2898816	0.0214	0.2588
chr11	135006516	2936229	0.0217	0.2444
chr12	133851895	2790761	0.0208	0.2279
chr13	115169878	2521755	0.0219	0.2311
chr14	107349540	2217840	0.0207	0.231
chr15	102531392	1992819	0.0194	0.2292
chr16	90354753	1701988	0.0188	0.214
chr17	81195210	1653769	0.0204	0.2231
chr18	78077248	1468208	0.0188	0.422
chr19	59128983	984188	0.0166	0.2739
chr20	63025520	1341154	0.0213	0.2323
chr21	48129895	809529	0.0168	0.2025
chr22	51304566	586969	0.0114	0.1594
chrMT	16571	26506	1.5995	2.1045
chrX	155270560	3789395	0.0244	0.2507
chrY	59373566	172903	0.0029	0.0872

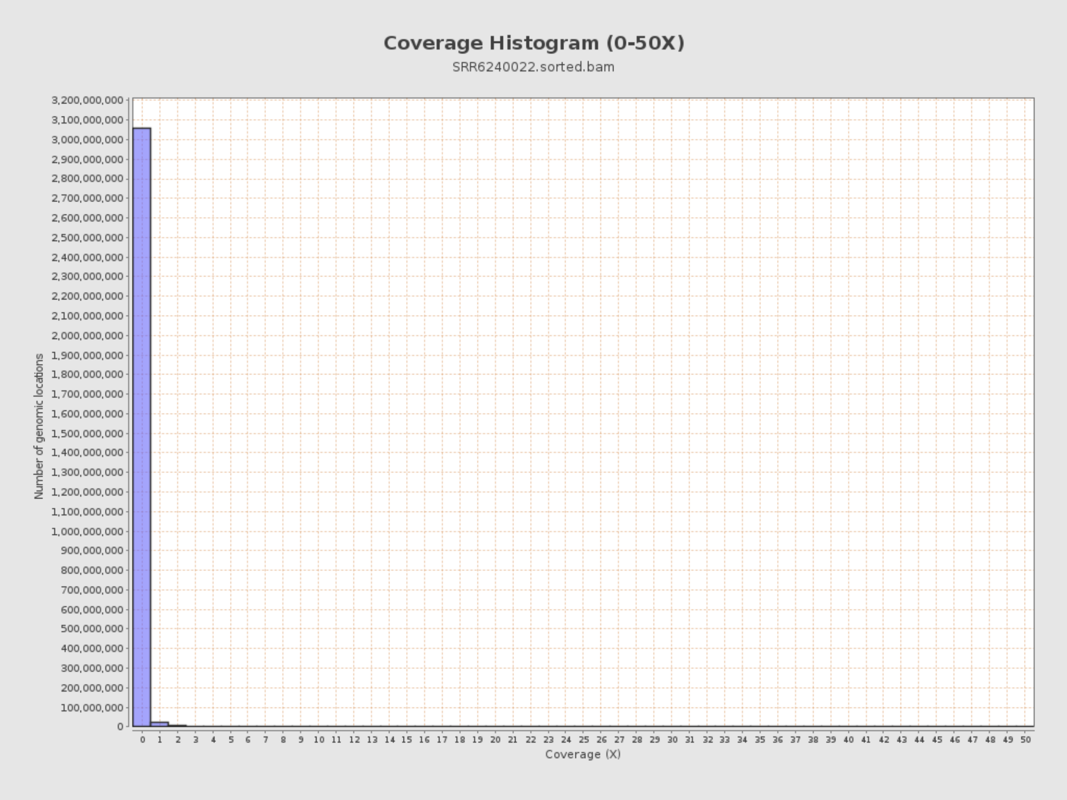
3. Results : Coverage across reference



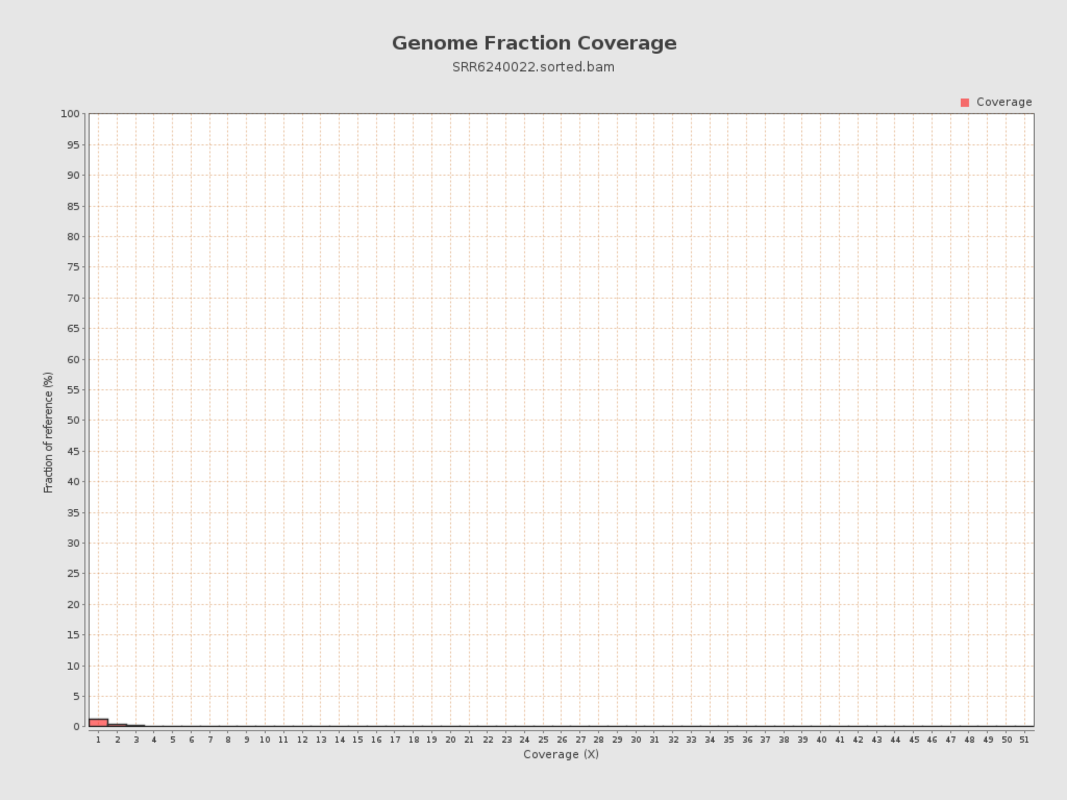
4. Results : Coverage Histogram



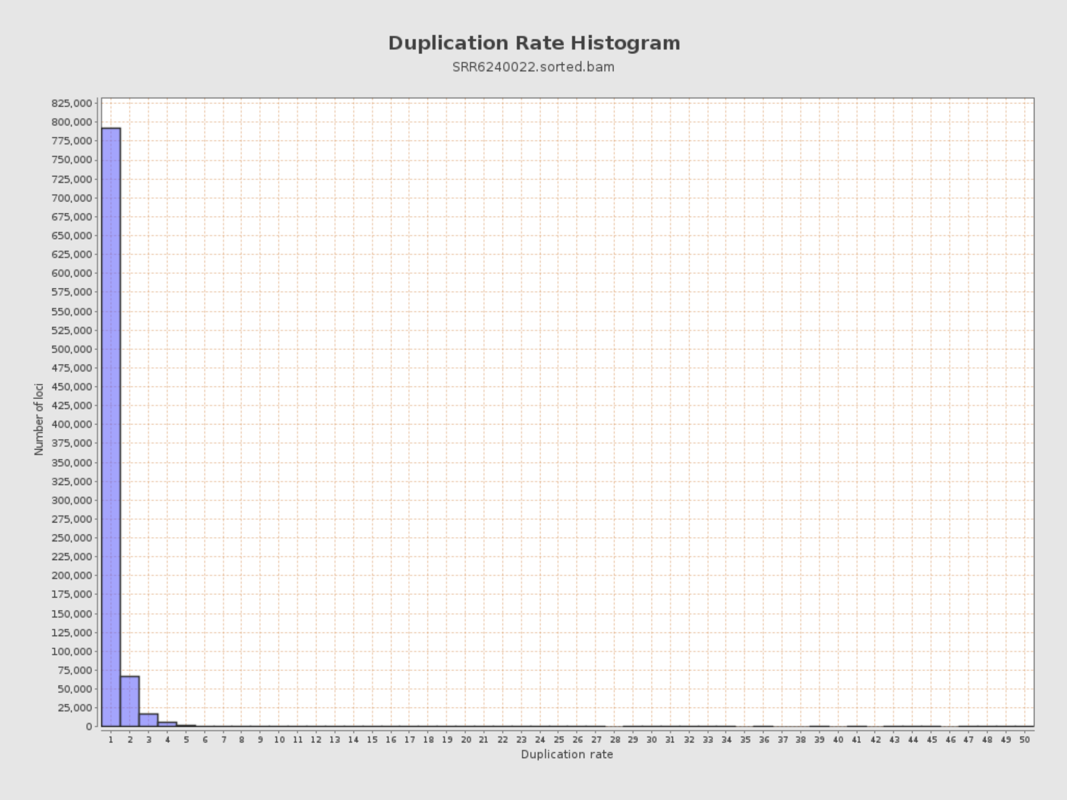
5. Results : Coverage Histogram (0-50X)



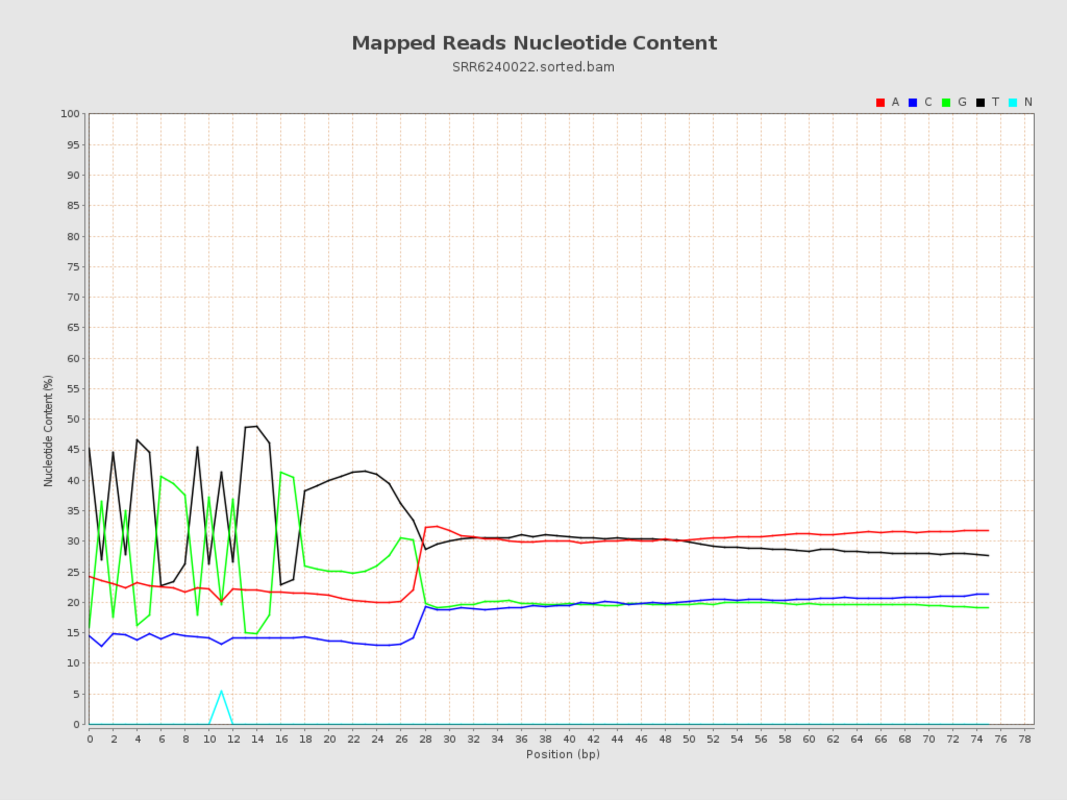
6. Results : Genome Fraction Coverage



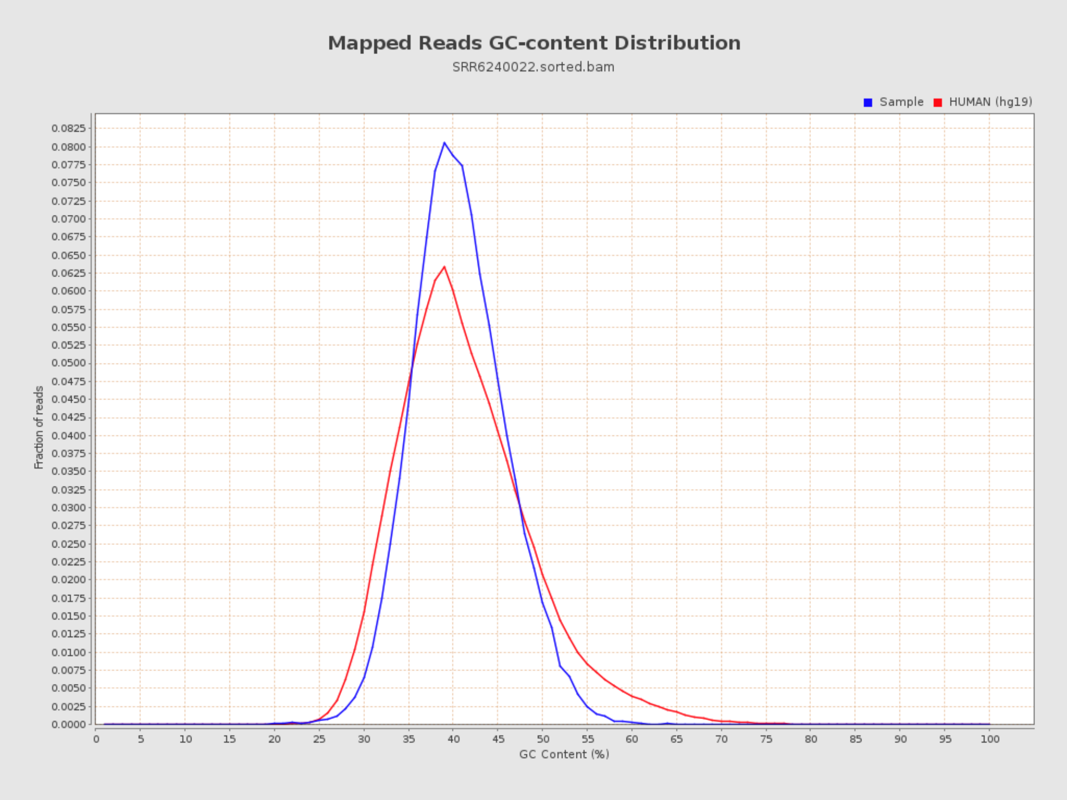
7. Results : Duplication Rate Histogram



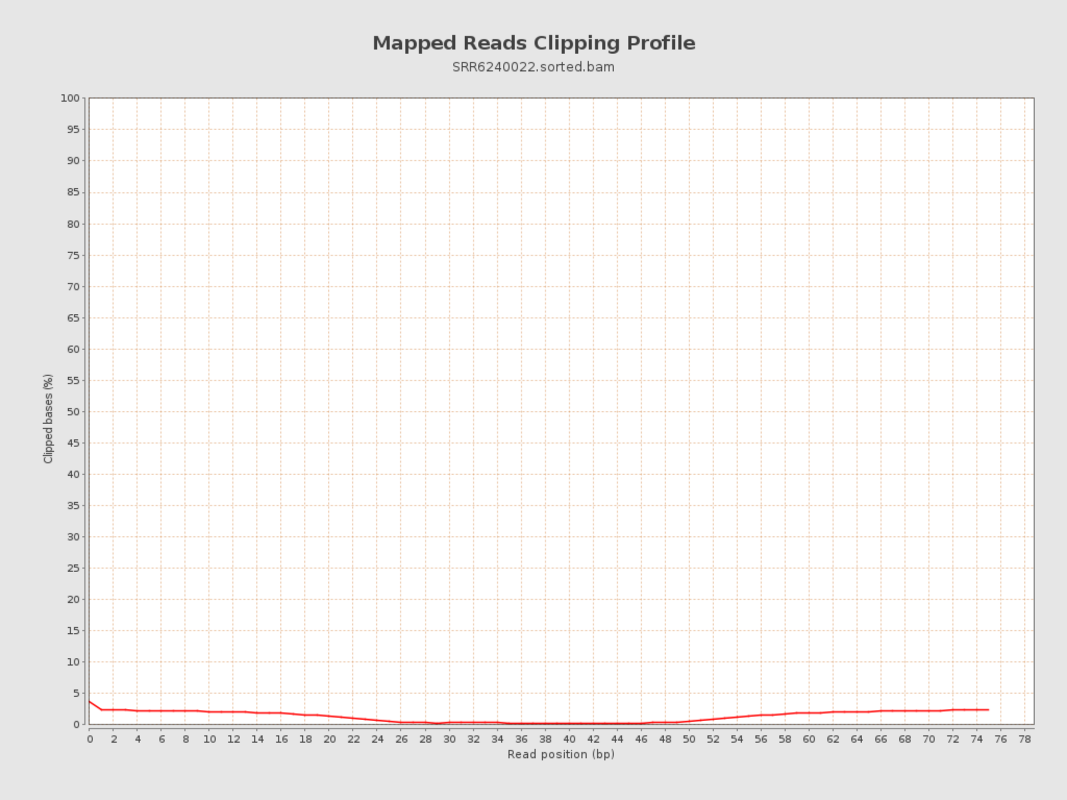
8. Results : Mapped Reads Nucleotide Content



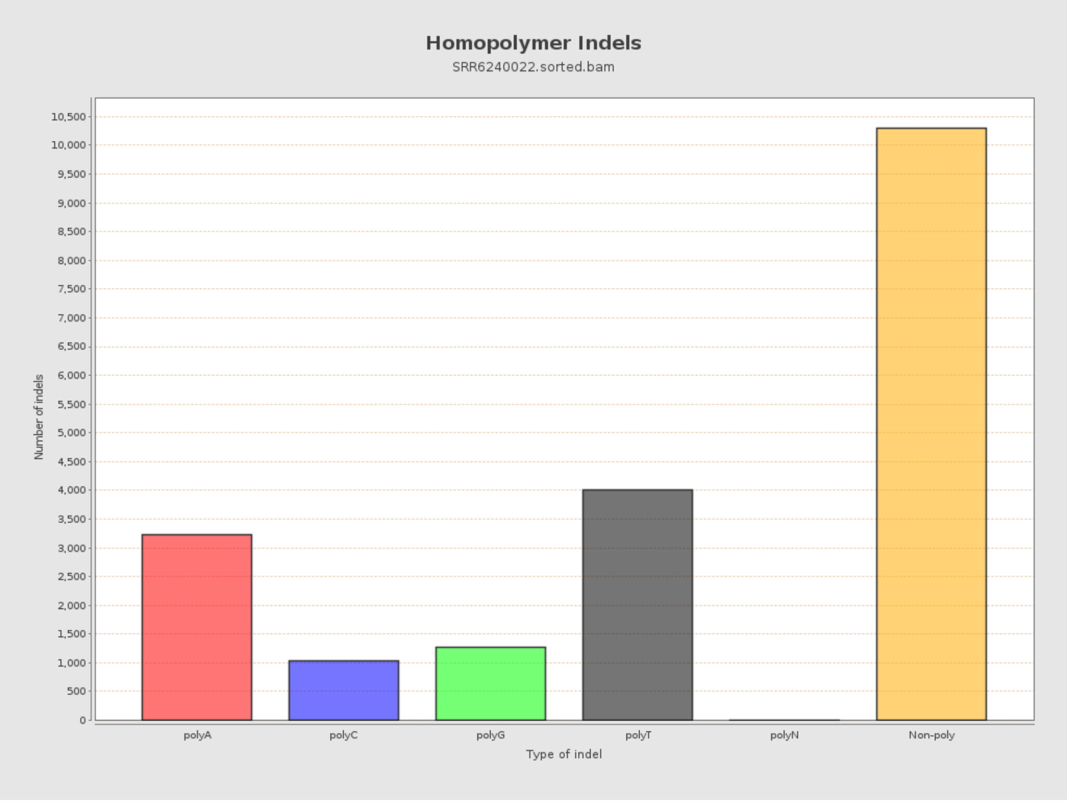
9. Results : Mapped Reads GC-content Distribution



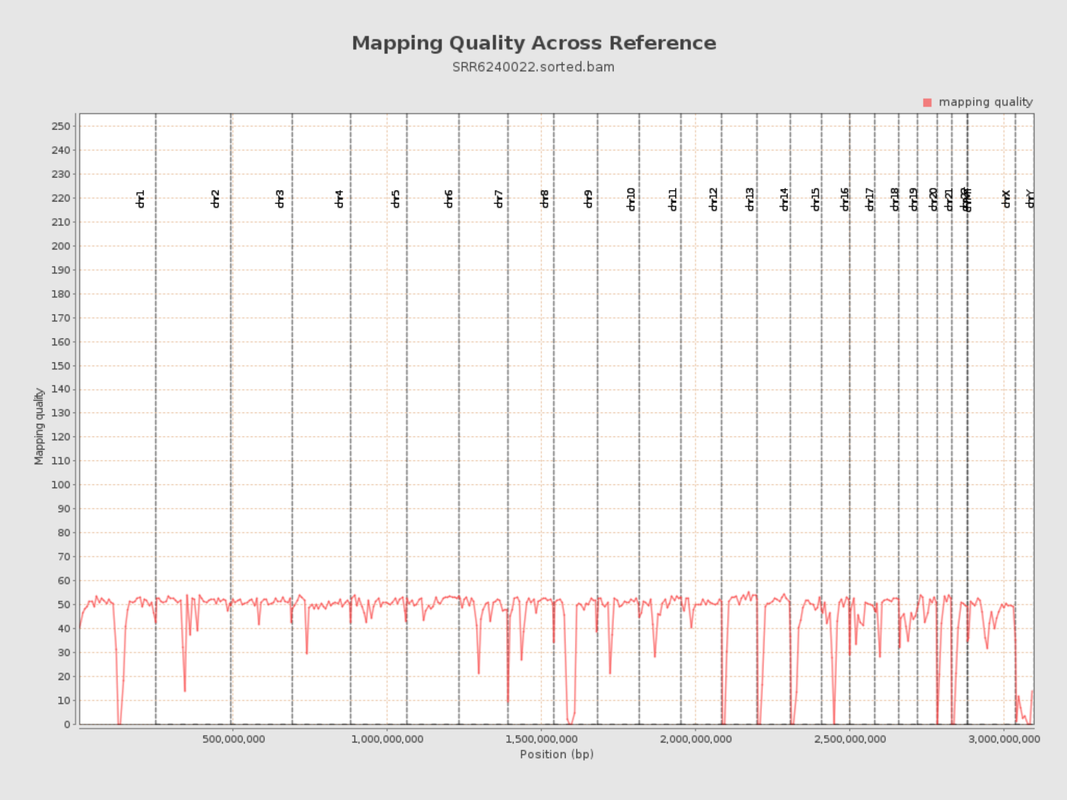
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram