Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:32:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240016.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_SRR6240016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240016.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:32:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,706,041
Mapped reads	1,401,984 / 82.18%
Unmapped reads	304,057 / 17.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,066 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	121,628 / 7.13%
Duplication rate	7.24%
Clipped reads	825,120 / 48.36%

2.2. ACGT Content

Number/percentage of A's	24,403,539 / 27.6%
Number/percentage of C's	15,621,041 / 17.66%
Number/percentage of T's	28,588,650 / 32.33%
Number/percentage of G's	19,756,612 / 22.34%
Number/percentage of N's	61,600 / 0.07%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.304

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

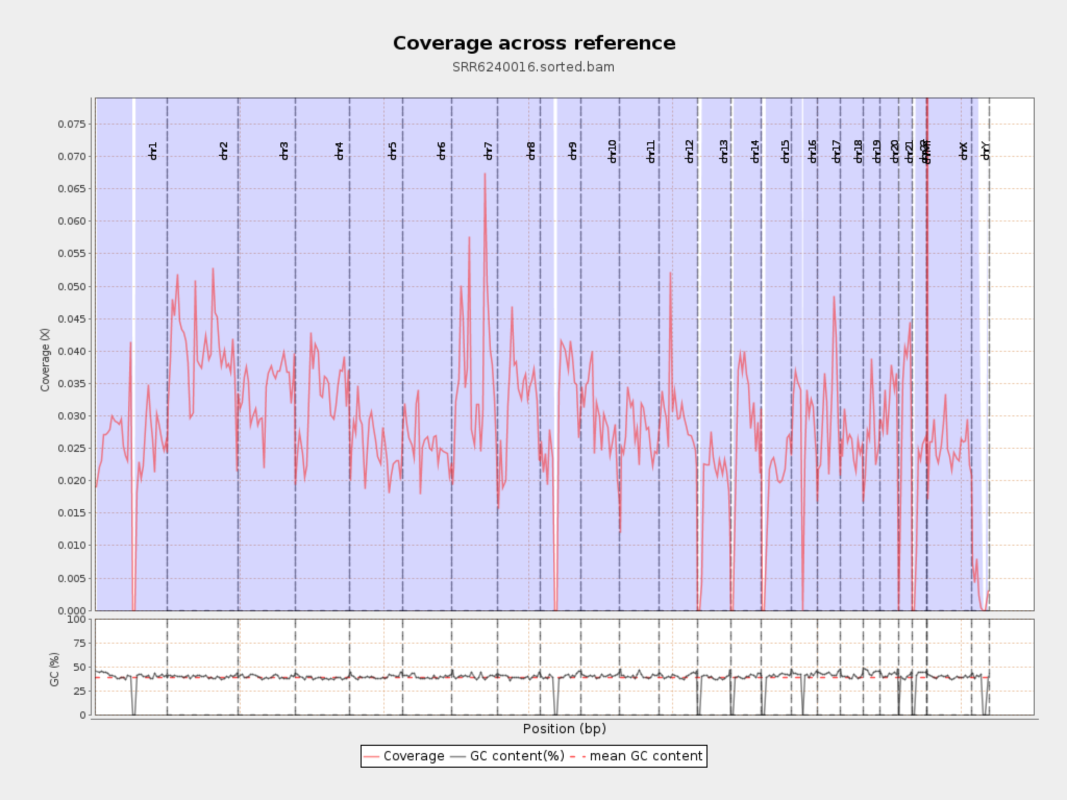
General error rate	0.94%
Mismatches	819,158
Insertions	6,273
Mapped reads with at least one insertion	0.44%
Deletions	25,415
Mapped reads with at least one deletion	1.79%
Homopolymer indels	48.52%

2.6. Chromosome stats

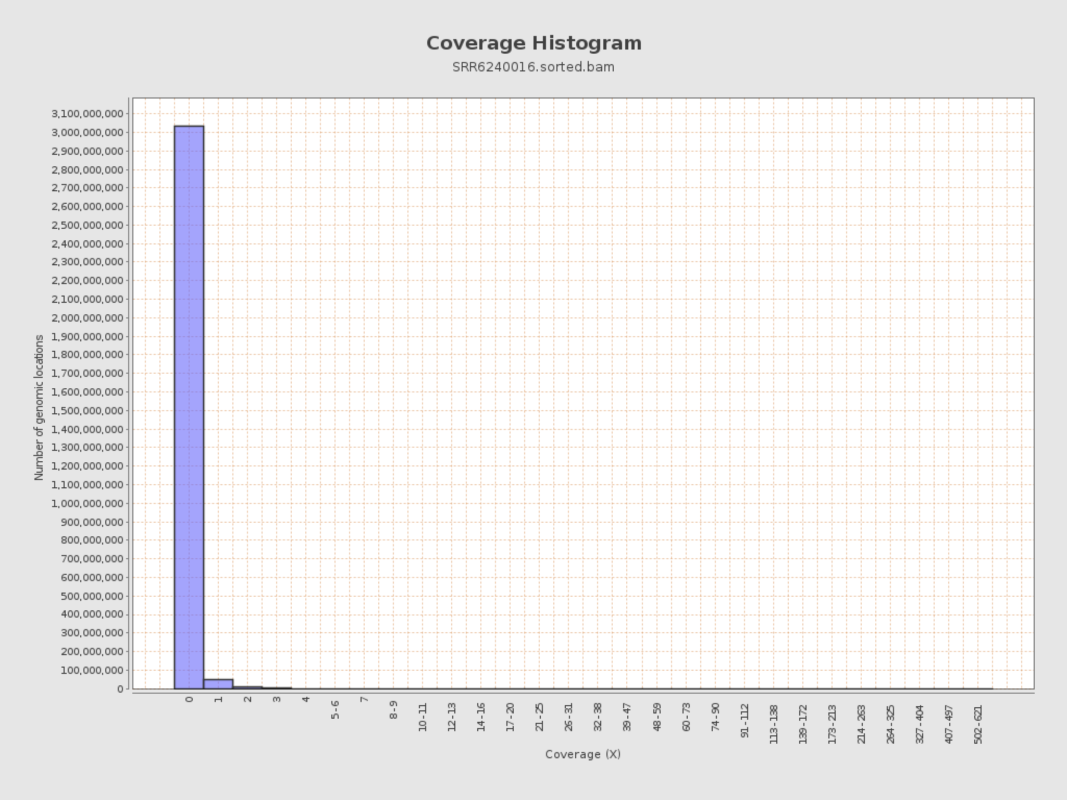
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6210305	0.0249	0.4507
chr2	243199373	9841150	0.0405	0.377
chr3	198022430	6706521	0.0339	0.2425
chr4	191154276	6234760	0.0326	0.2415
chr5	180915260	4583138	0.0253	0.2295
chr6	171115067	4427240	0.0259	0.2301
chr7	159138663	5816116	0.0365	0.5117

chr8	146364022	4686065	0.032	0.4347
chr9	141213431	4025893	0.0285	0.2678
chr10	135534747	4007833	0.0296	0.2736
chr11	135006516	3659320	0.0271	0.2461
chr12	133851895	4073148	0.0304	0.2302
chr13	115169878	2137508	0.0186	0.1802
chr14	107349540	2929810	0.0273	0.2259
chr15	102531392	1893177	0.0185	0.1764
chr16	90354753	2560645	0.0283	0.2219
chr17	81195210	2531143	0.0312	0.2391
chr18	78077248	1994241	0.0255	0.373
chr19	59128983	1608870	0.0272	0.3374
chr20	63025520	2008081	0.0319	0.2361
chr21	48129895	1520058	0.0316	0.2388
chr22	51304566	890826	0.0174	0.1662
chrMT	16571	28203	1.7019	2.0989
chrX	155270560	3922975	0.0253	0.2162
chrY	59373566	177446	0.003	0.0705

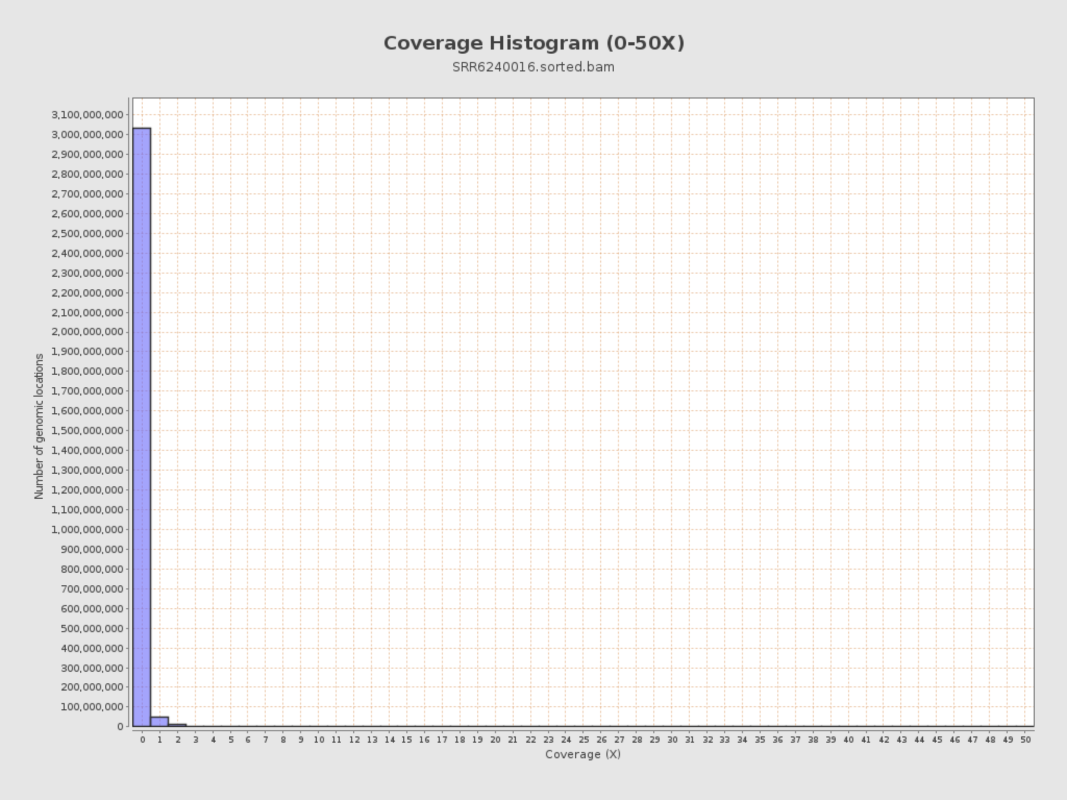
3. Results : Coverage across reference



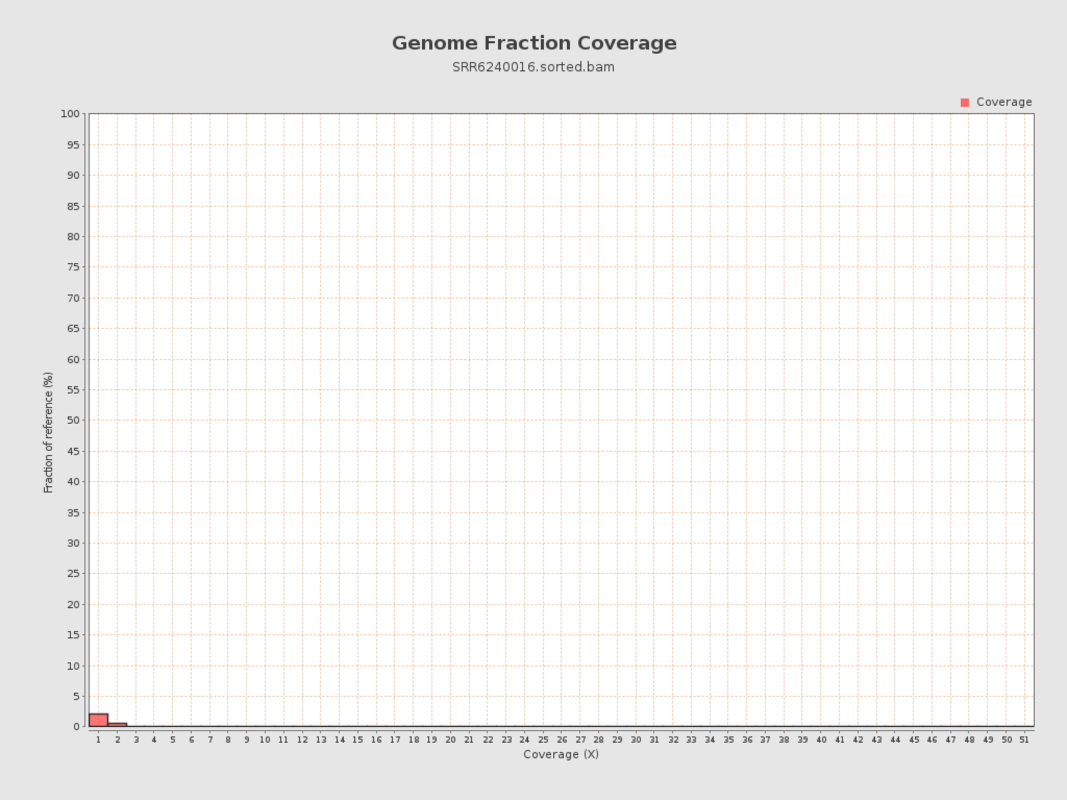
4. Results : Coverage Histogram



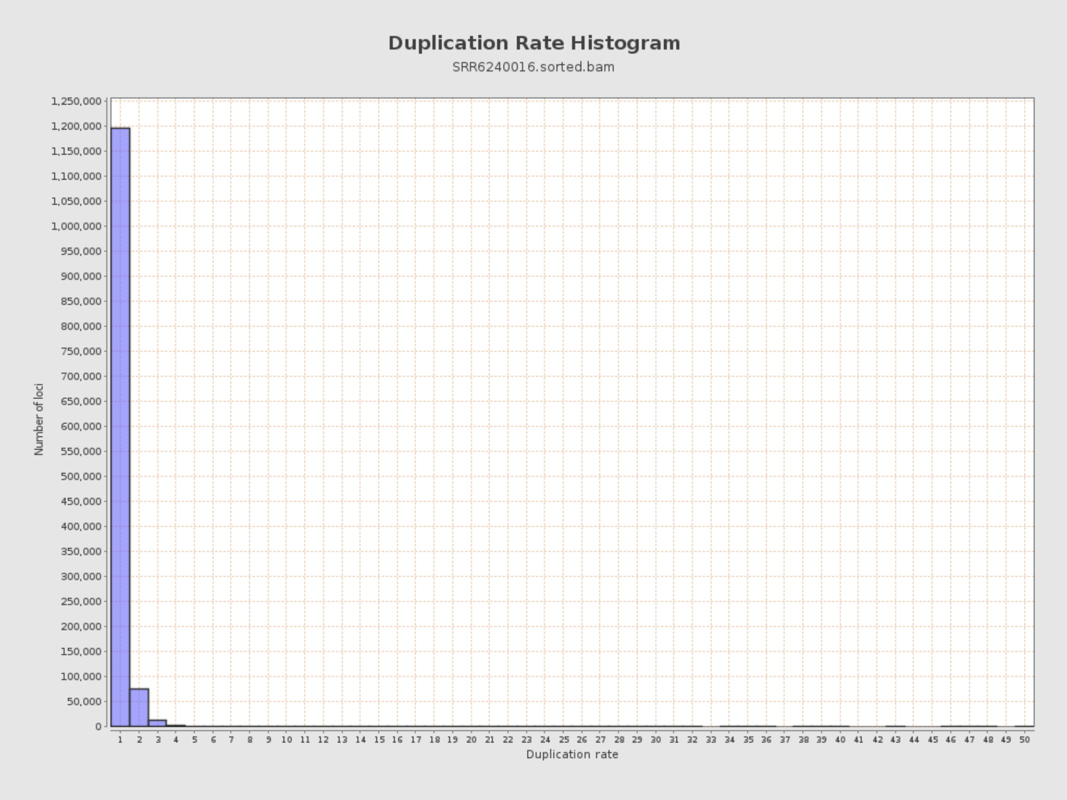
5. Results : Coverage Histogram (0-50X)



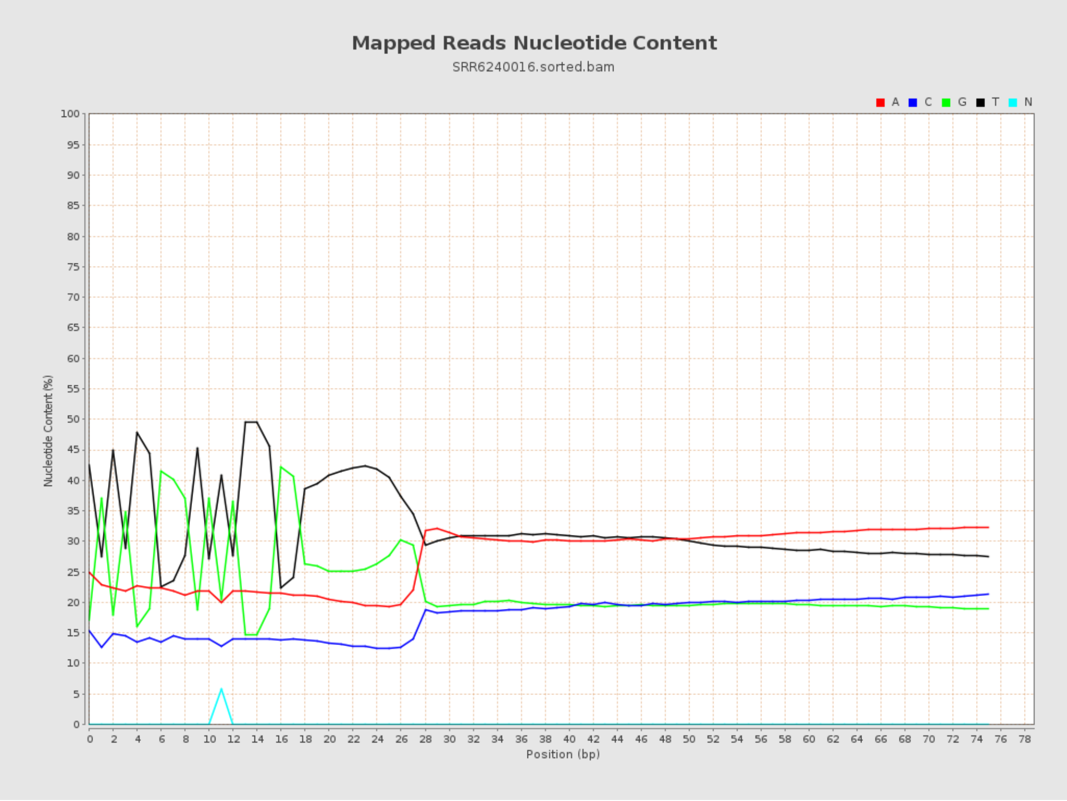
6. Results : Genome Fraction Coverage



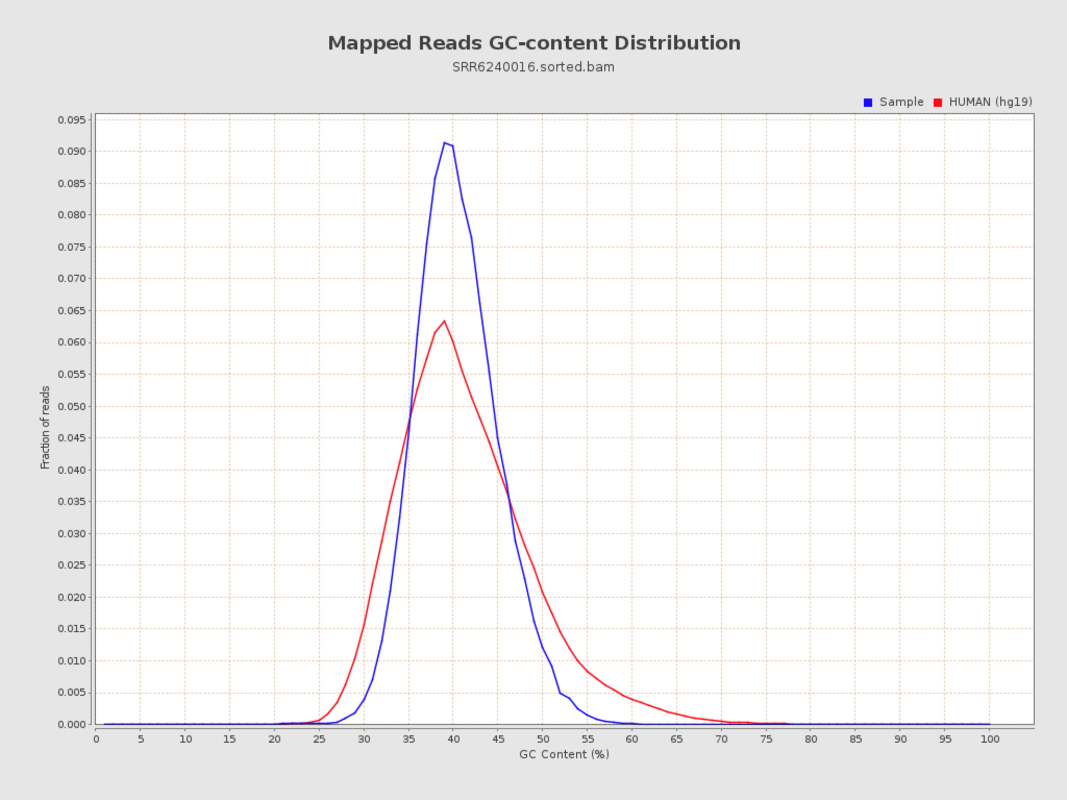
7. Results : Duplication Rate Histogram



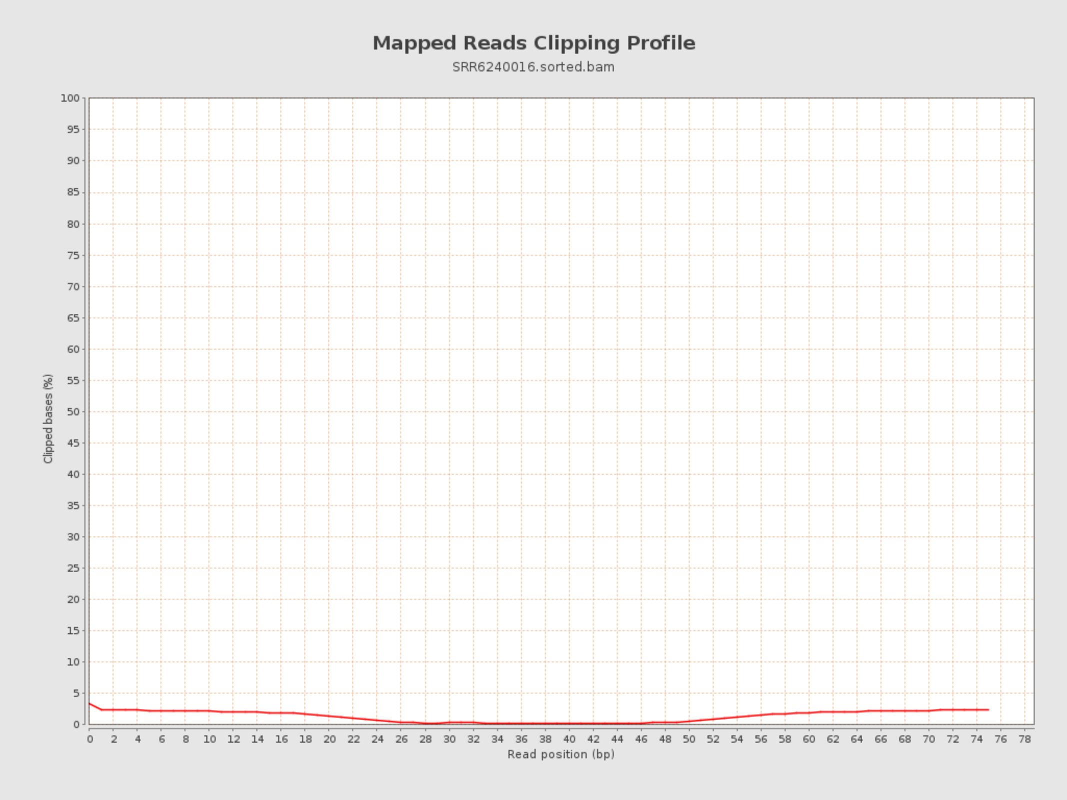
8. Results : Mapped Reads Nucleotide Content



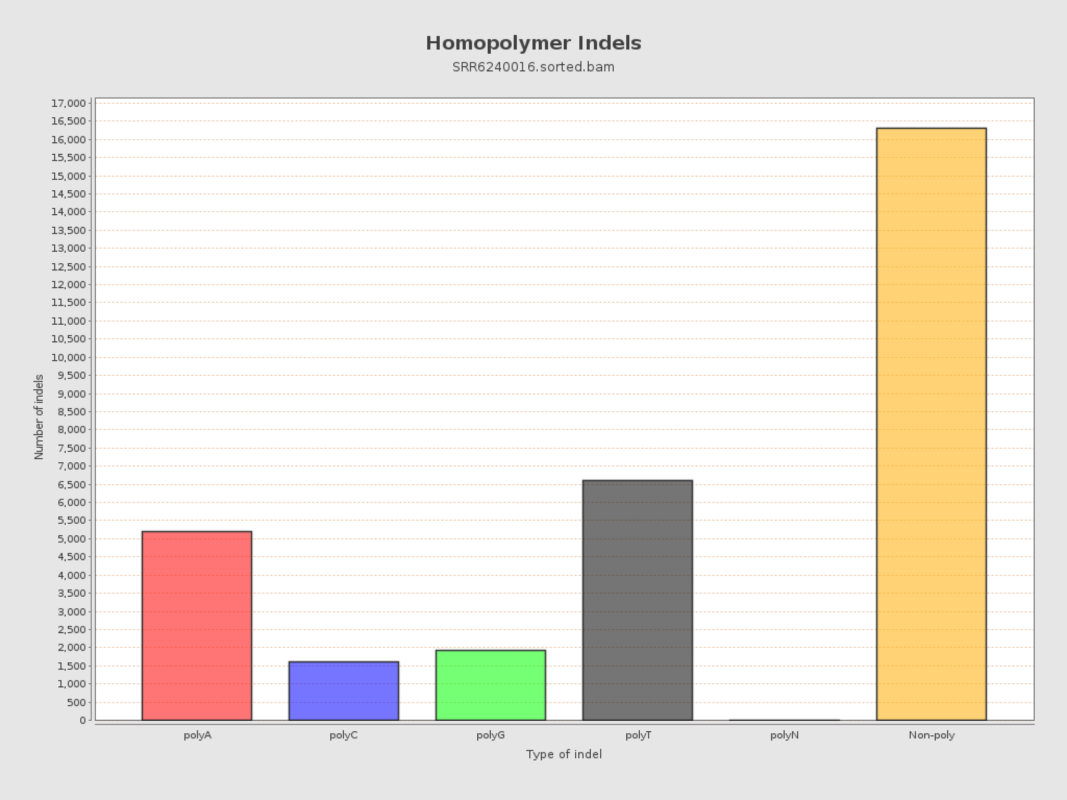
9. Results : Mapped Reads GC-content Distribution



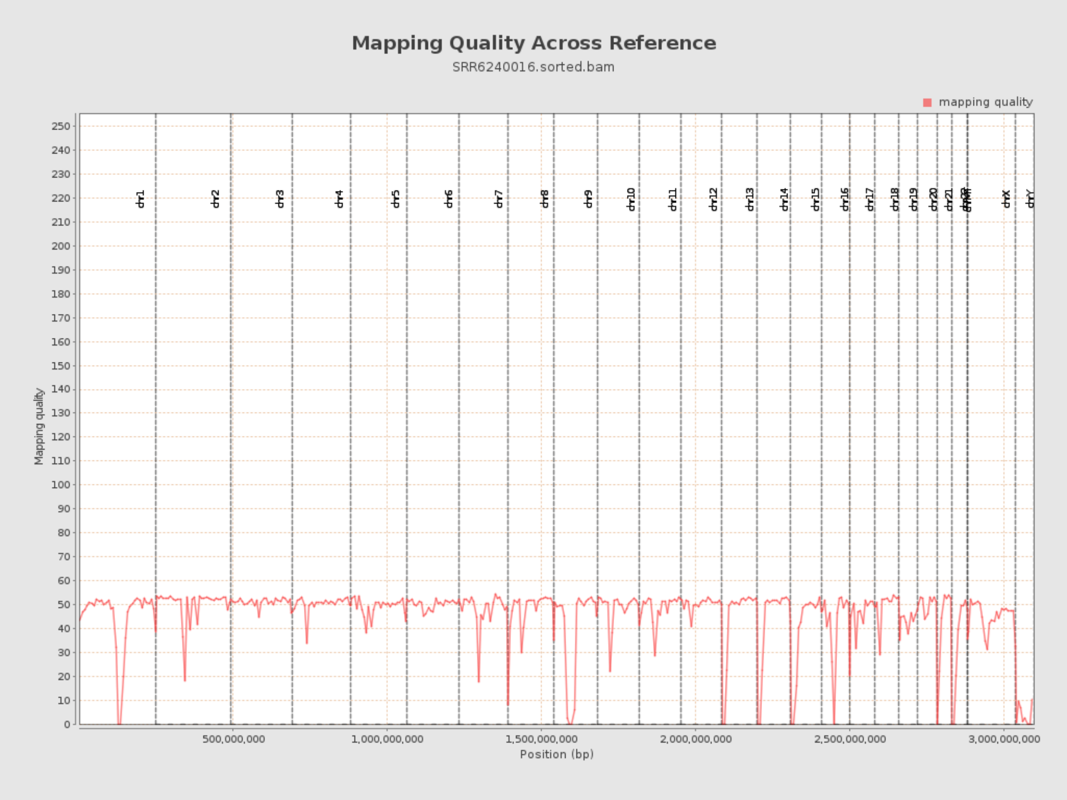
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram