Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:25:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240183.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_SRR6240183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240183.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:25:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,322,394
Mapped reads	1,031,648 / 78.01%
Unmapped reads	290,746 / 21.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,902 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	102,375 / 7.74%
Duplication rate	8%
Clipped reads	508,094 / 38.42%

2.2. ACGT Content

Number/percentage of A's	19,216,923 / 28.29%
Number/percentage of C's	12,561,829 / 18.49%
Number/percentage of T's	21,519,195 / 31.68%
Number/percentage of G's	14,592,222 / 21.48%
Number/percentage of N's	45,510 / 0.07%
GC Percentage	39.97%

2.3. Coverage

Mean	0.022

Standard Deviation	0.2724

2.4. Mapping Quality

Mean Mapping Quality	46.7

2.5. Mismatches and indels

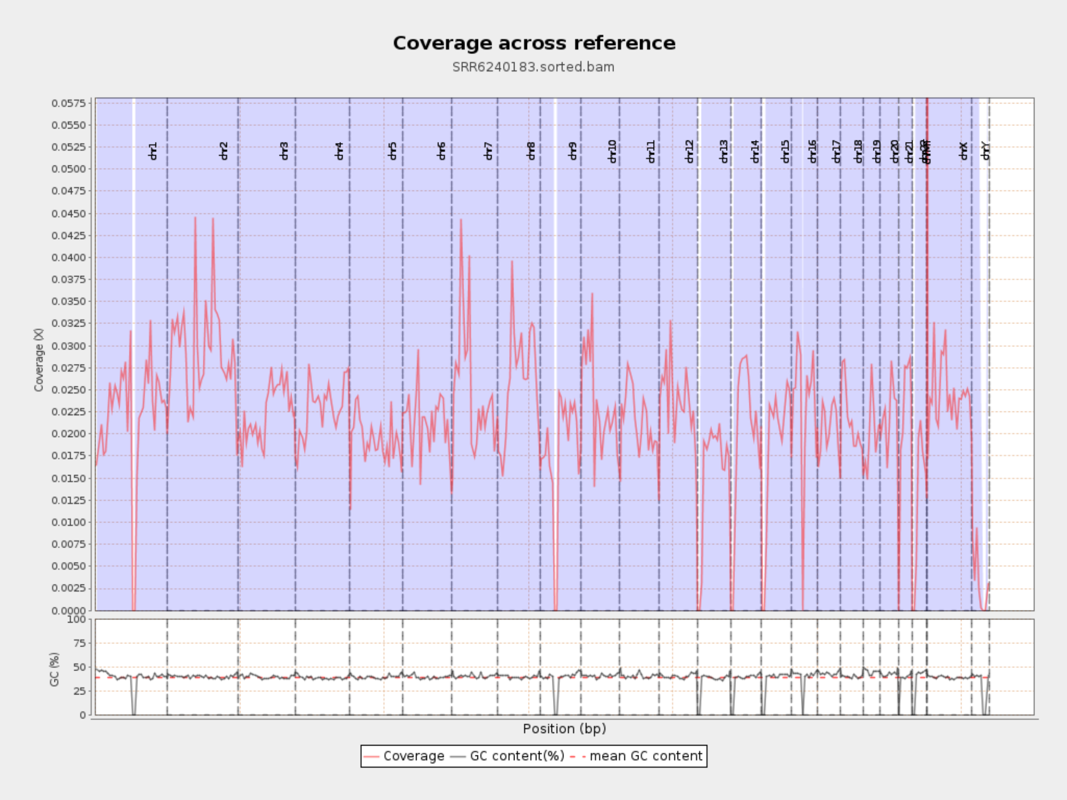
General error rate	0.92%
Mismatches	615,055
Insertions	4,802
Mapped reads with at least one insertion	0.46%
Deletions	18,277
Mapped reads with at least one deletion	1.75%
Homopolymer indels	48.29%

2.6. Chromosome stats

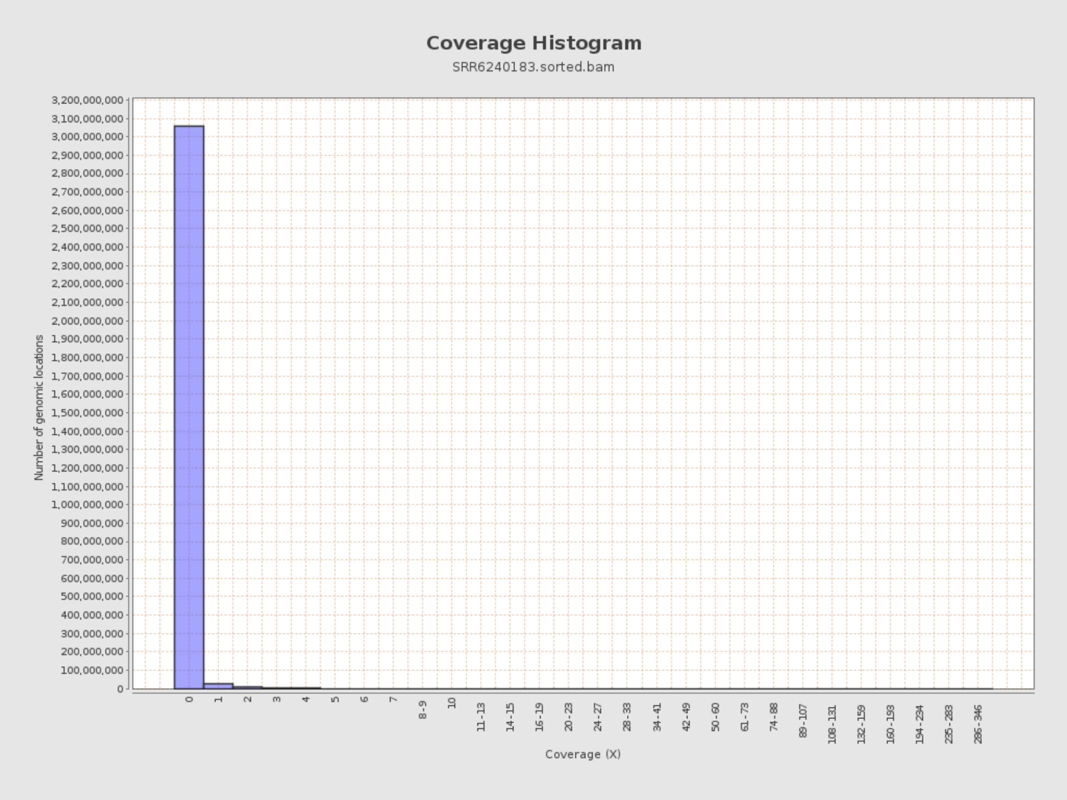
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5495616	0.022	0.368
chr2	243199373	7197793	0.0296	0.3182
chr3	198022430	4432667	0.0224	0.2364
chr4	191154276	4379040	0.0229	0.2403
chr5	180915260	3529282	0.0195	0.2165
chr6	171115067	3657628	0.0214	0.249
chr7	159138663	4006882	0.0252	0.3577

chr8	146364022	3847398	0.0263	0.3304
chr9	141213431	2538638	0.018	0.2446
chr10	135534747	3191070	0.0235	0.2708
chr11	135006516	2911803	0.0216	0.2711
chr12	133851895	3210186	0.024	0.2418
chr13	115169878	1790512	0.0155	0.1944
chr14	107349540	2151797	0.02	0.229
chr15	102531392	1892041	0.0185	0.2141
chr16	90354753	2054424	0.0227	0.2393
chr17	81195210	1660517	0.0205	0.2322
chr18	78077248	1705626	0.0218	0.3619
chr19	59128983	1188298	0.0201	0.287
chr20	63025520	1383507	0.022	0.2344
chr21	48129895	1065890	0.0221	0.2364
chr22	51304566	647491	0.0126	0.1748
chrMT	16571	28160	1.6994	2.1874
chrX	155270560	3814272	0.0246	0.2542
chrY	59373566	186968	0.0031	0.0825

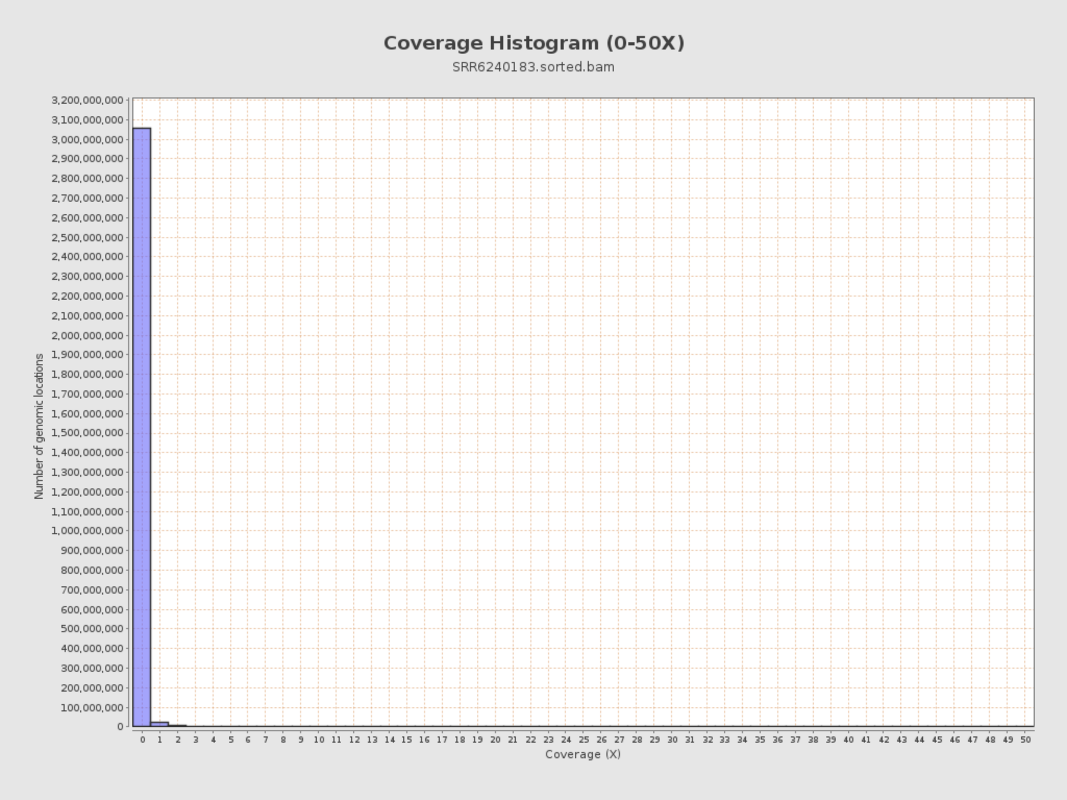
3. Results : Coverage across reference



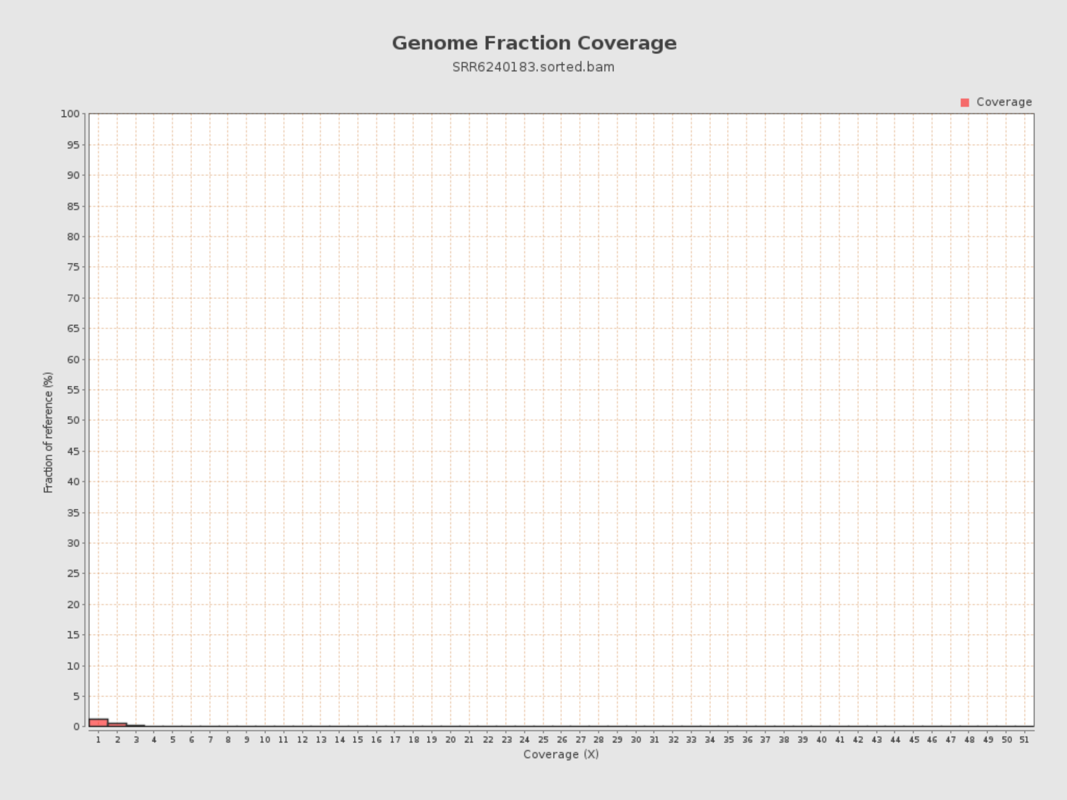
4. Results : Coverage Histogram



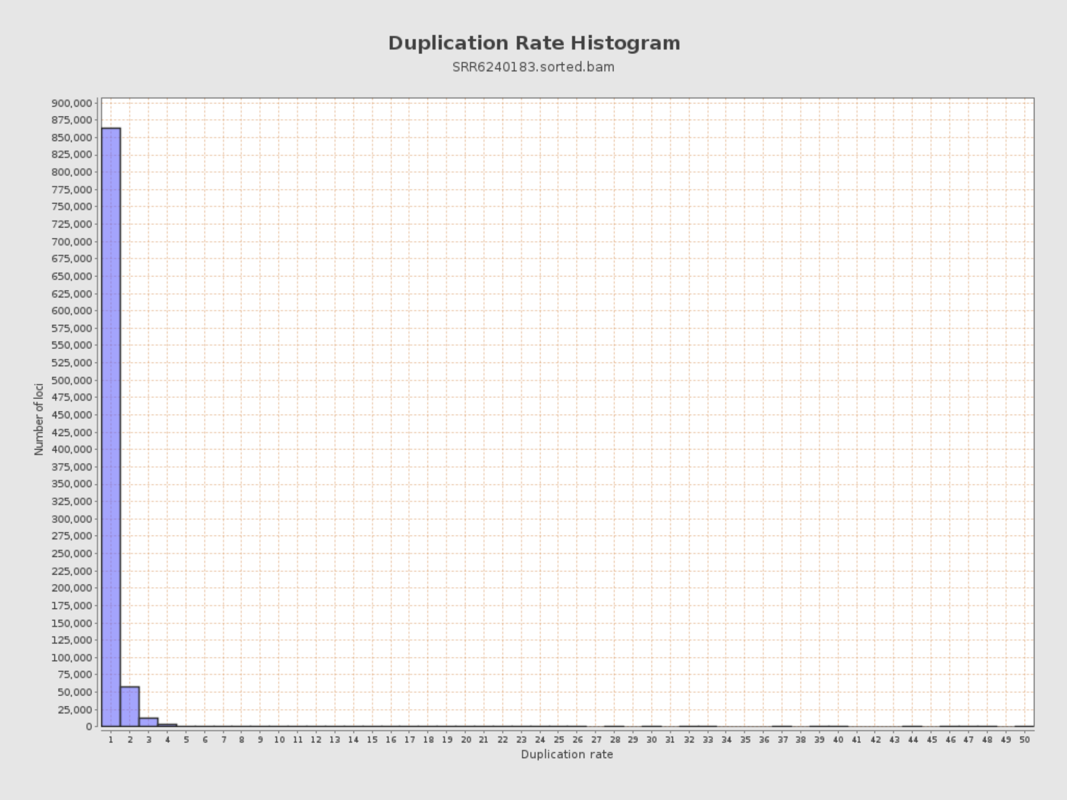
5. Results : Coverage Histogram (0-50X)



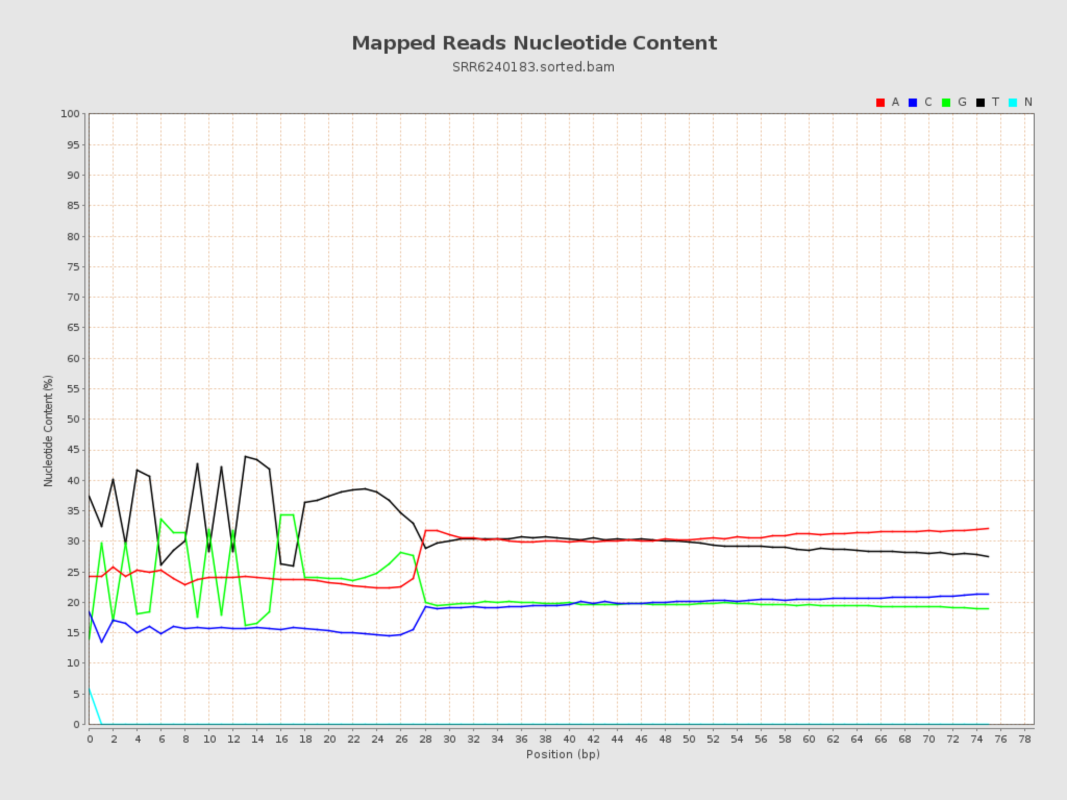
6. Results : Genome Fraction Coverage



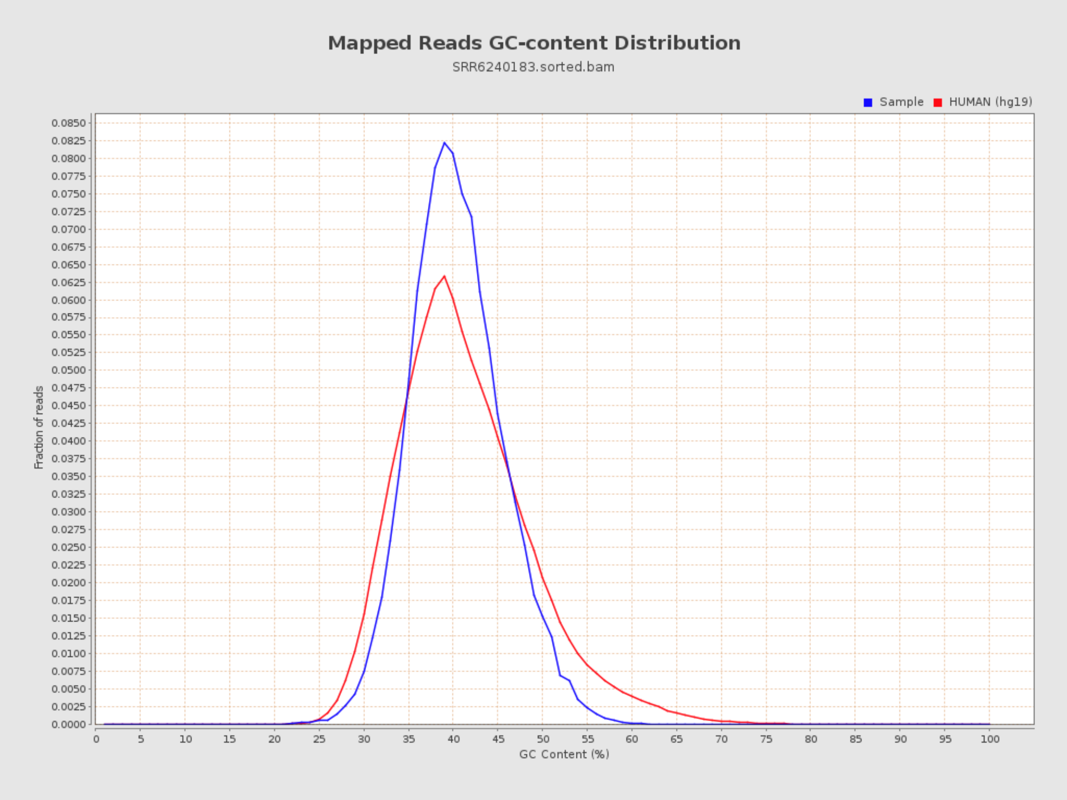
7. Results : Duplication Rate Histogram



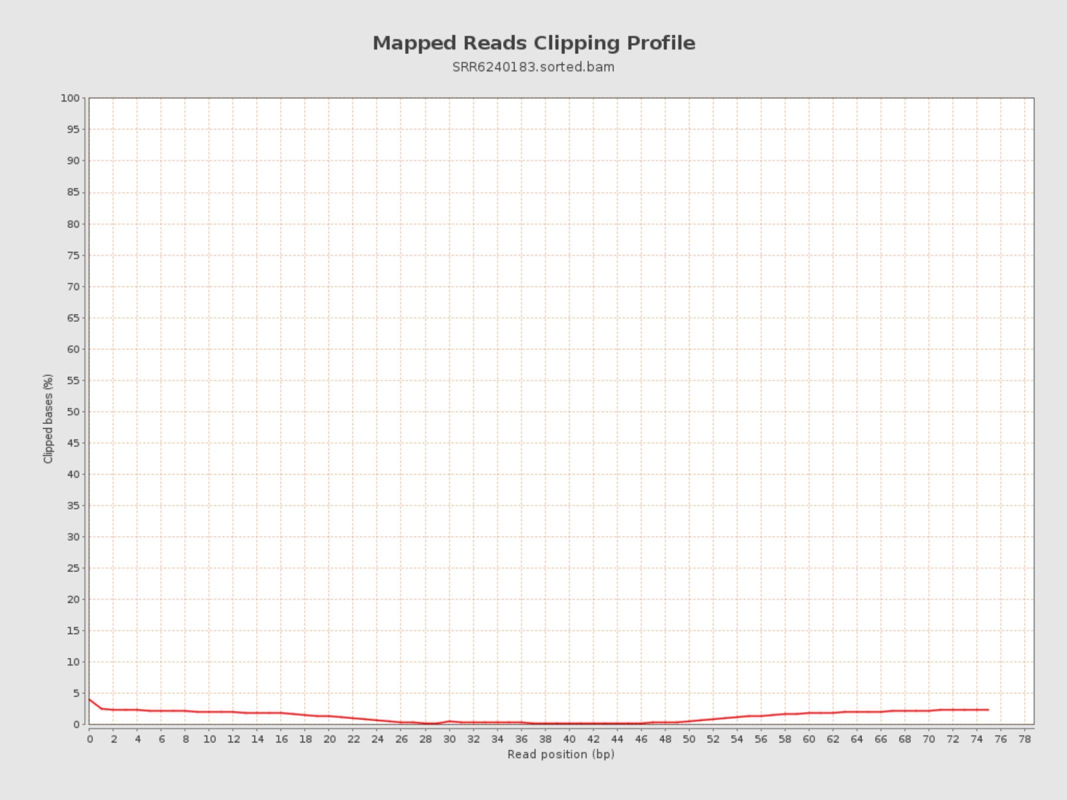
8. Results : Mapped Reads Nucleotide Content



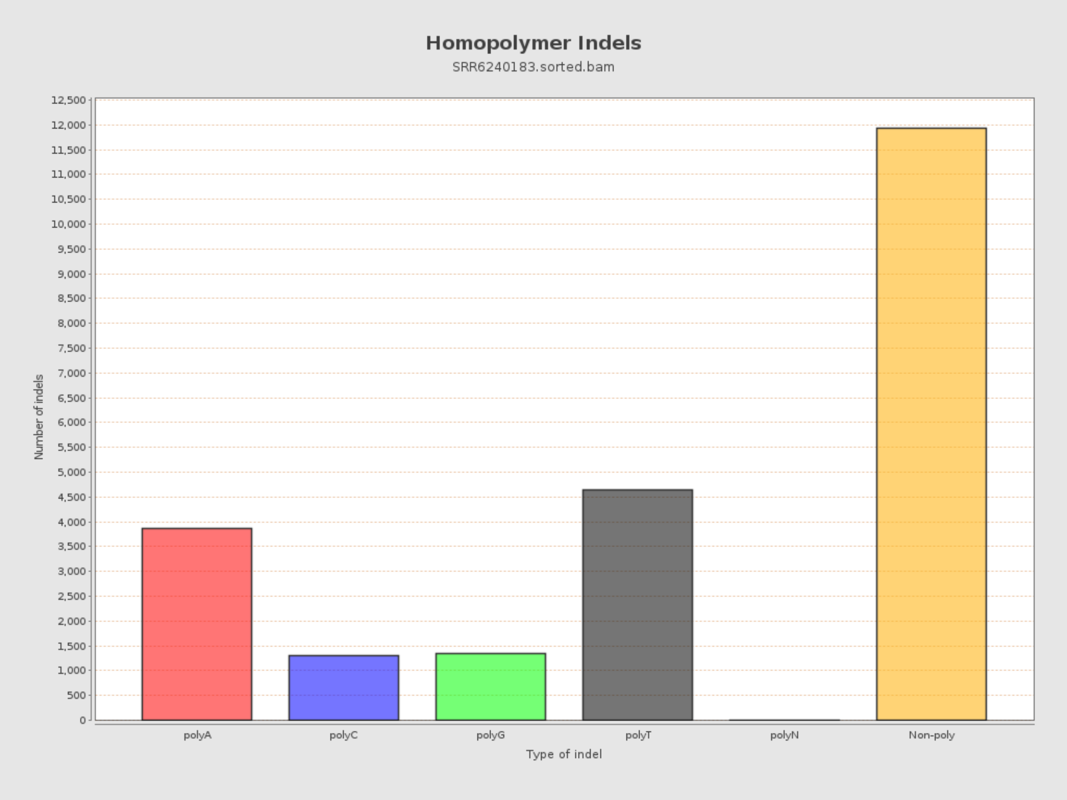
9. Results : Mapped Reads GC-content Distribution



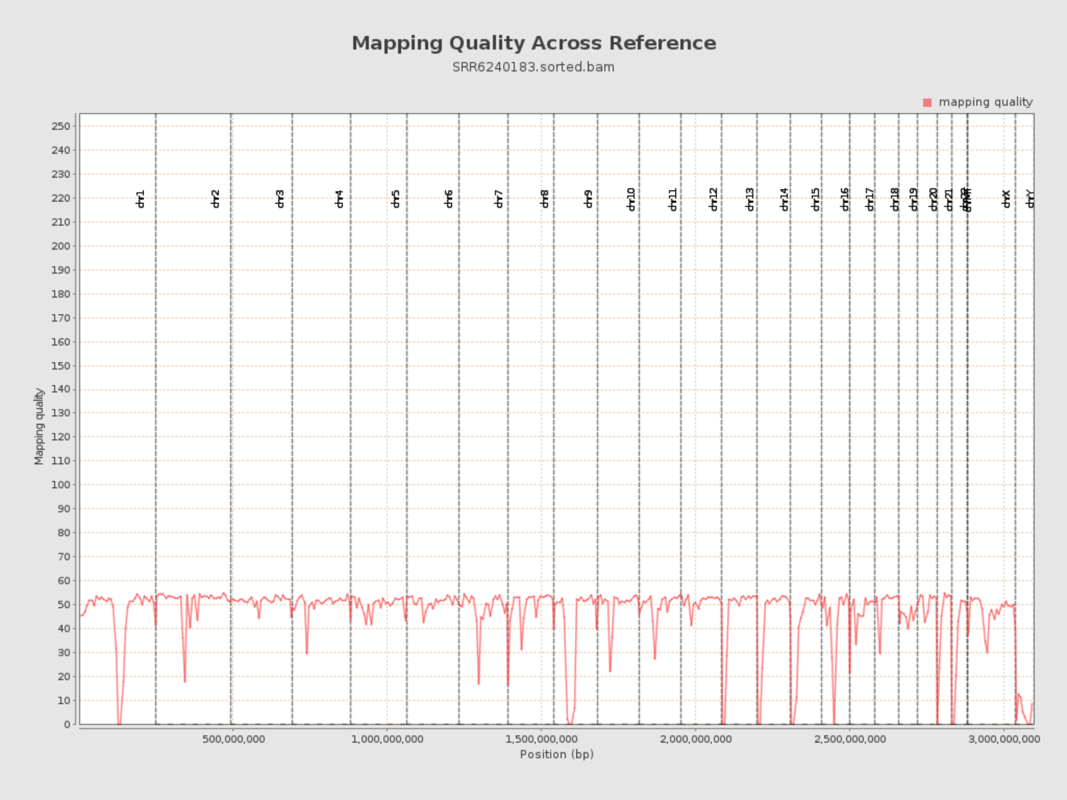
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram