

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 09:15:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240266.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_SRR6240266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 09:15:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,633,231
Mapped reads	1,278,025 / 78.25%
Unmapped reads	355,206 / 21.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,157 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	153,368 / 9.39%
Duplication rate	10.05%
Clipped reads	873,241 / 53.47%

2.2. ACGT Content

Number/percentage of A's	20,932,874 / 26.91%
Number/percentage of C's	13,450,331 / 17.29%
Number/percentage of T's	25,565,549 / 32.87%
Number/percentage of G's	17,813,843 / 22.9%
Number/percentage of N's	18,781 / 0.02%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2662
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2.4. Mapping Quality

Mean Mapping Quality	45.1
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2.5. Mismatches and indels

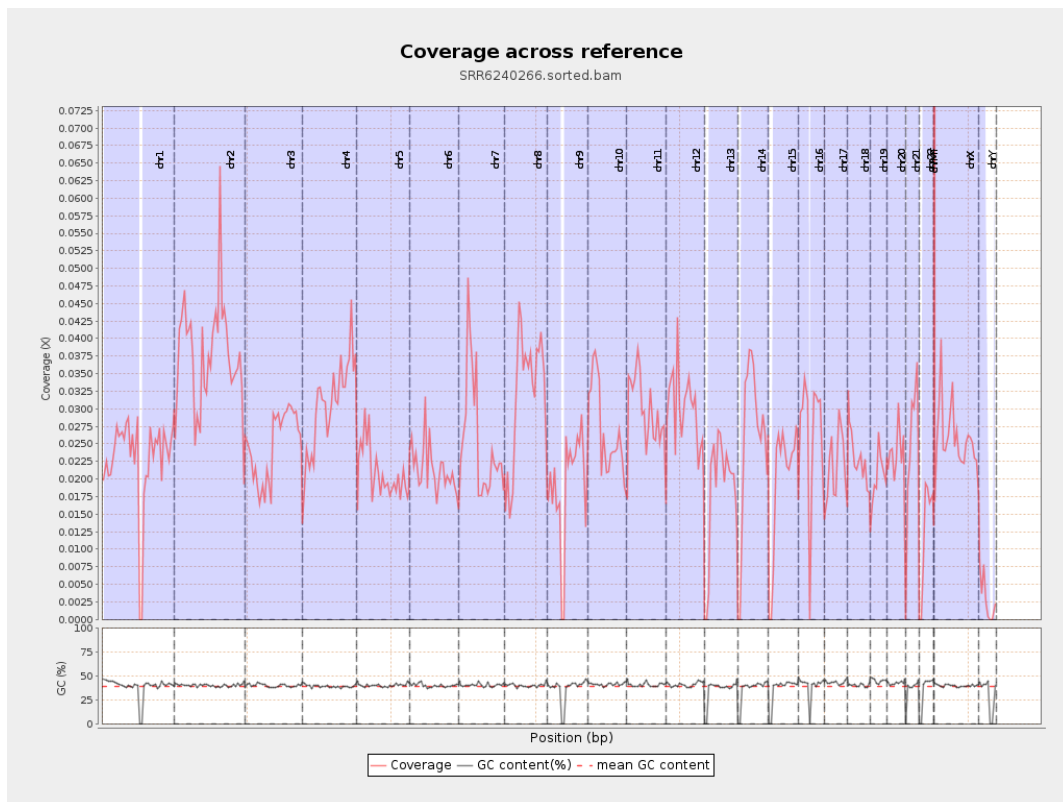
General error rate	0.93%
Mismatches	711,491
Insertions	5,430
Mapped reads with at least one insertion	0.42%
Deletions	23,240
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.22%

2.6. Chromosome stats

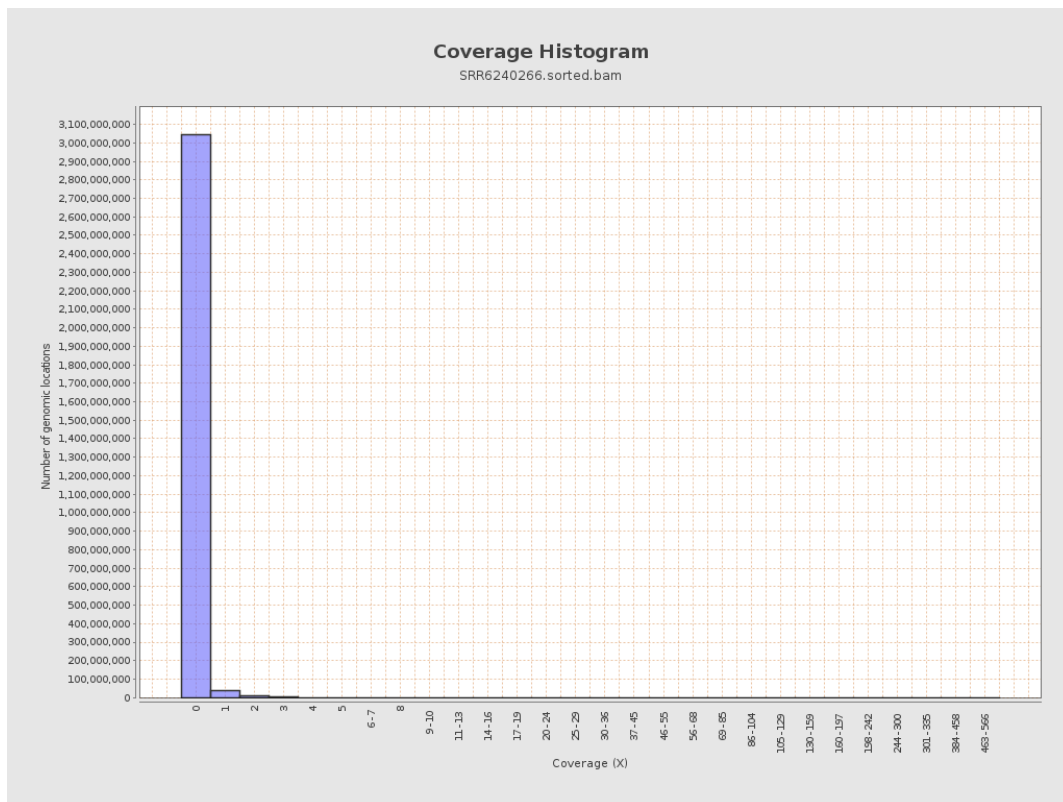
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5692479	0.0228	0.3157
chr2	243199373	9180849	0.0378	0.381
chr3	198022430	4900602	0.0247	0.2162
chr4	191154276	5820288	0.0304	0.2479
chr5	180915260	3789022	0.0209	0.1979
chr6	171115067	3683363	0.0215	0.2267
chr7	159138663	4059397	0.0255	0.3503

chr8	146364022	4700509	0.0321	0.381
chr9	141213431	2686320	0.019	0.2206
chr10	135534747	3652781	0.027	0.2498
chr11	135006516	4035621	0.0299	0.2818
chr12	133851895	4049663	0.0303	0.2396
chr13	115169878	2110077	0.0183	0.1836
chr14	107349540	2777933	0.0259	0.2228
chr15	102531392	2022658	0.0197	0.2047
chr16	90354753	2332355	0.0258	0.2183
chr17	81195210	1768949	0.0218	0.211
chr18	78077248	1795457	0.023	0.3189
chr19	59128983	1208436	0.0204	0.2437
chr20	63025520	1476232	0.0234	0.2093
chr21	48129895	1200175	0.0249	0.2187
chr22	51304566	651606	0.0127	0.1482
chrMT	16571	30984	1.8698	2.948
chrX	155270560	4023268	0.0259	0.2295
chrY	59373566	171701	0.0029	0.0701

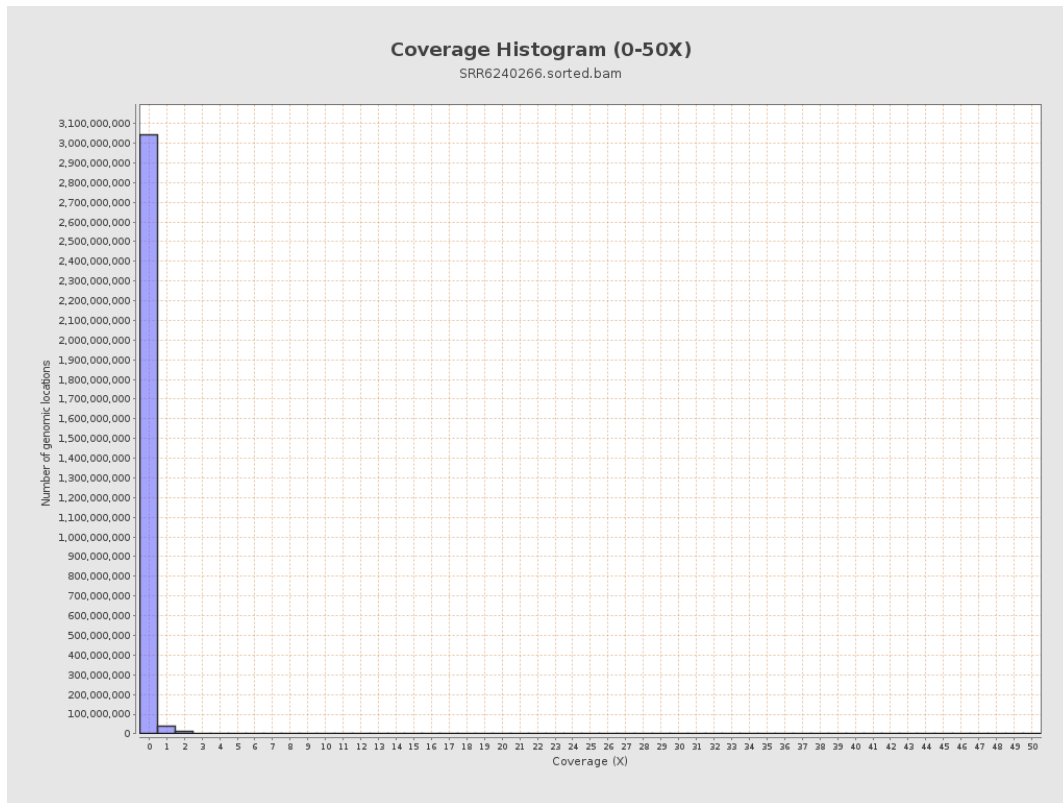
3. Results : Coverage across reference



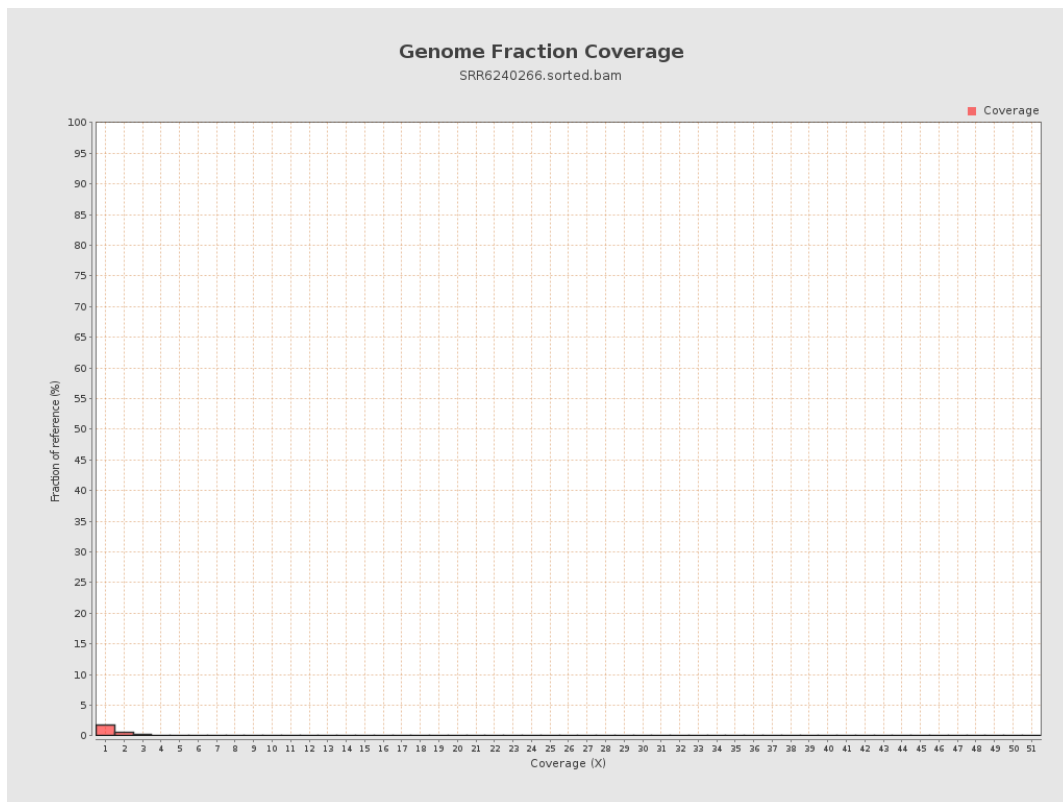
4. Results : Coverage Histogram



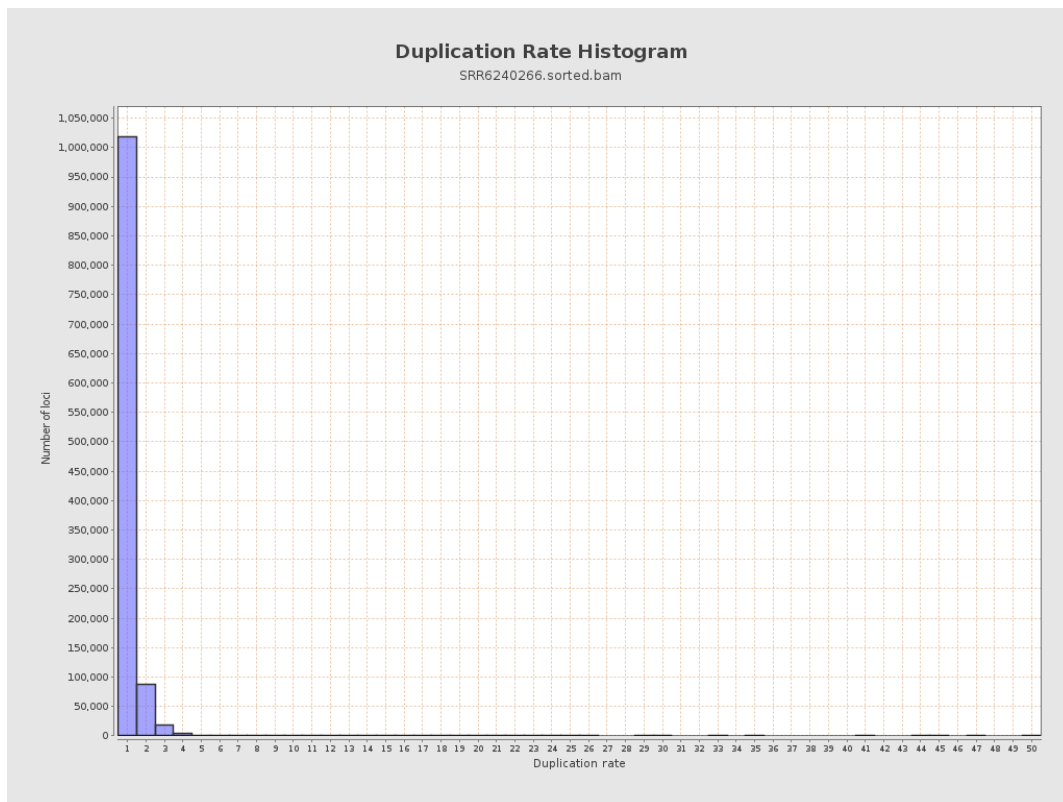
5. Results : Coverage Histogram (0-50X)



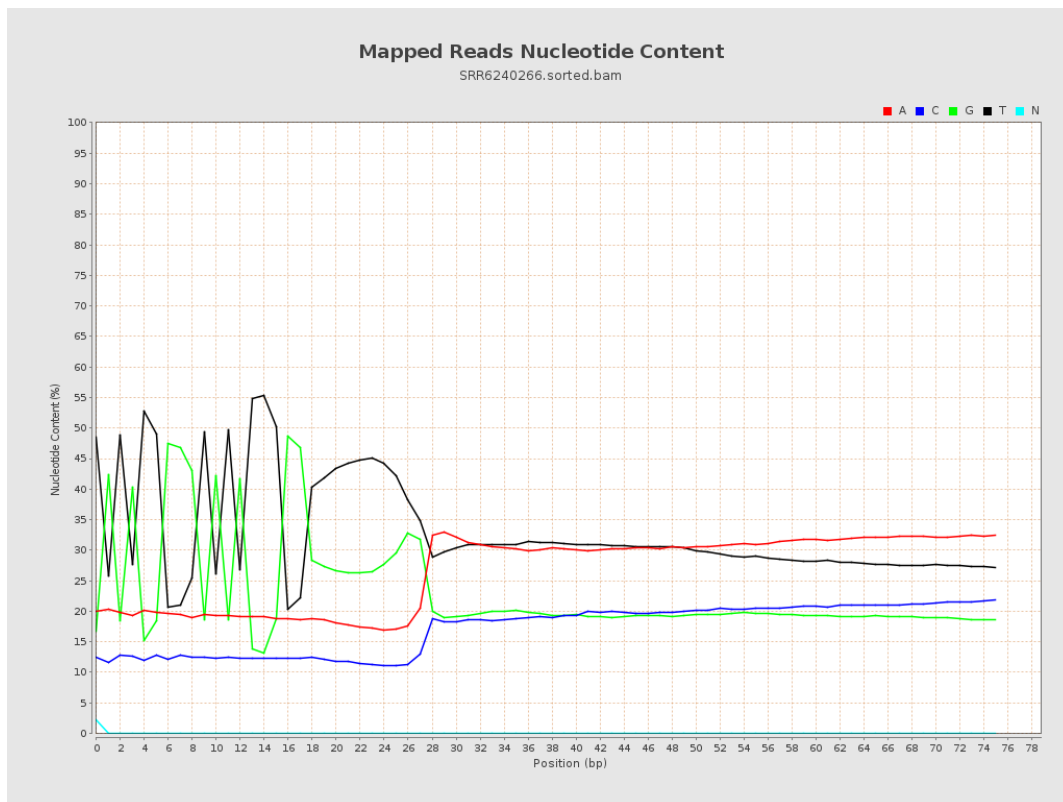
6. Results : Genome Fraction Coverage



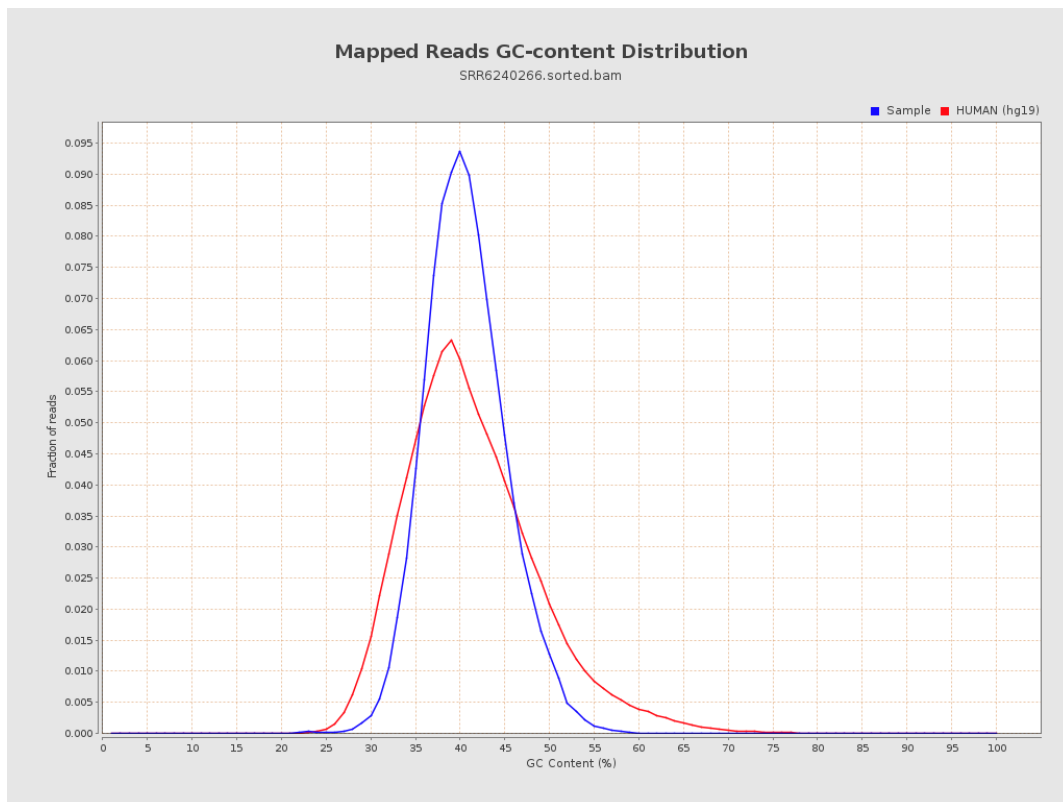
7. Results : Duplication Rate Histogram



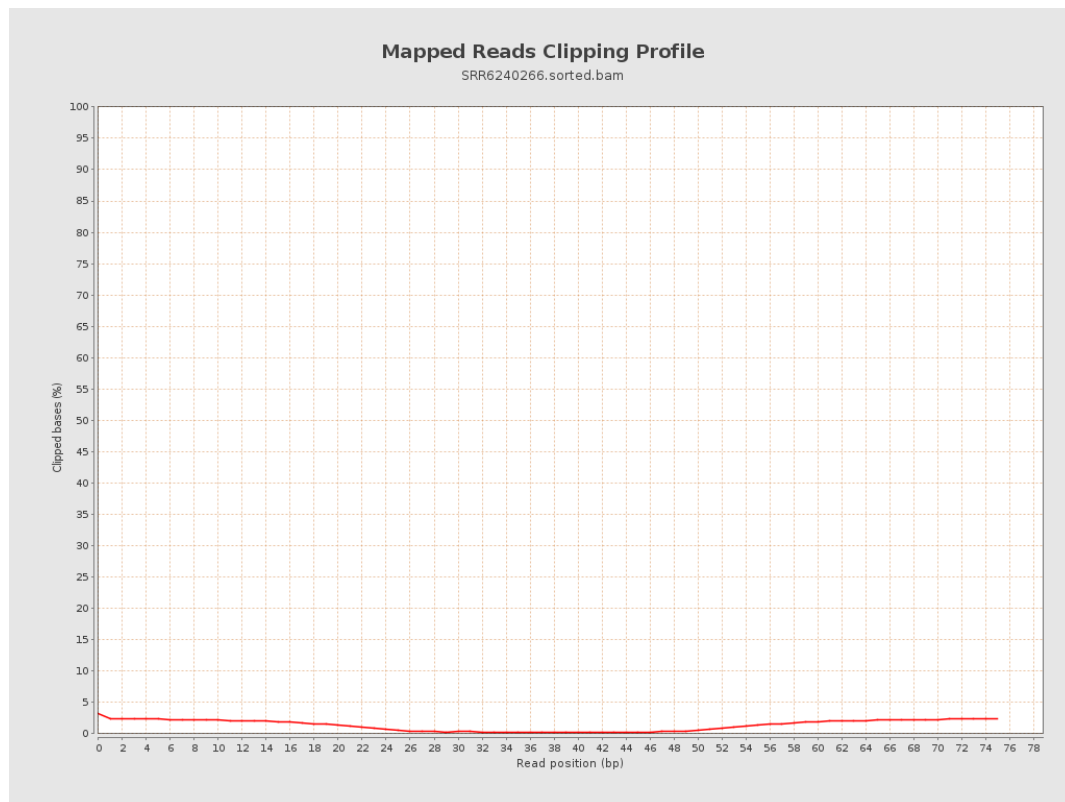
8. Results : Mapped Reads Nucleotide Content



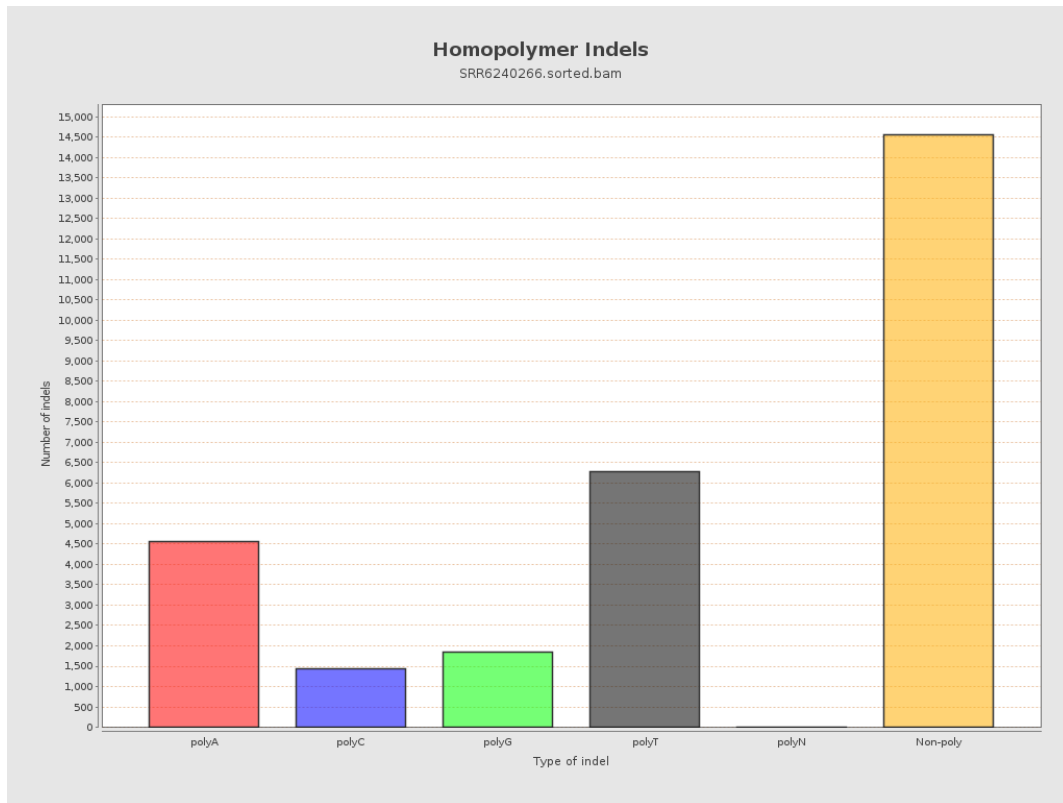
9. Results : Mapped Reads GC-content Distribution



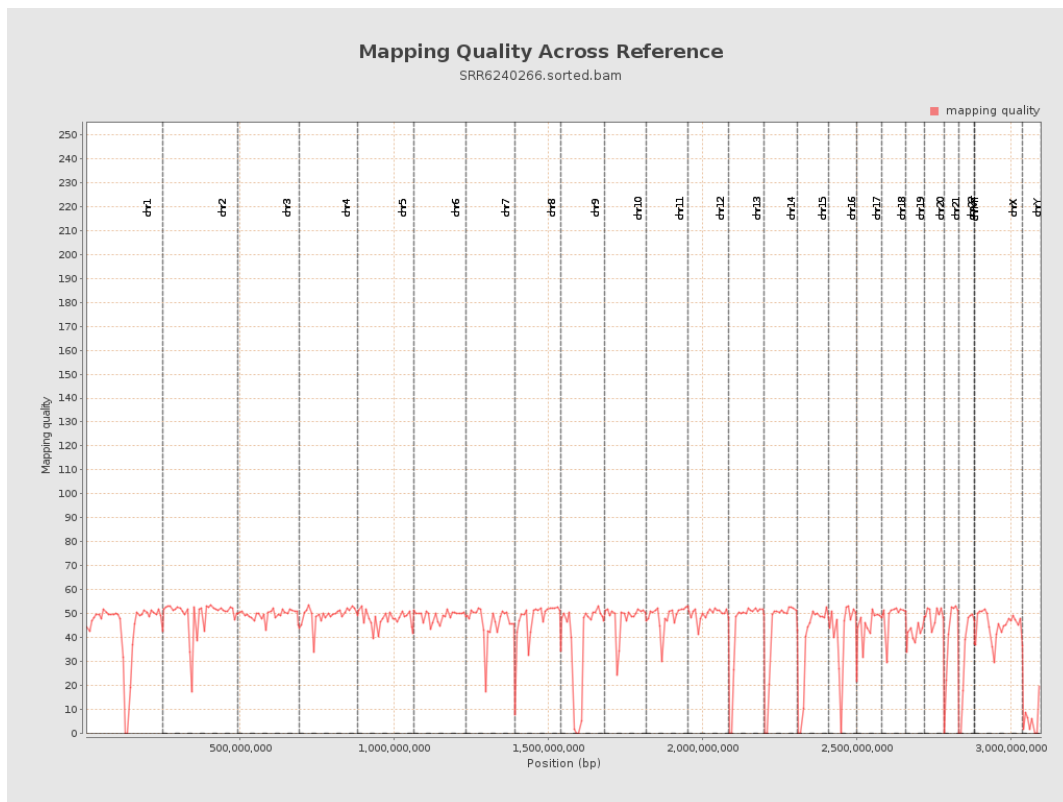
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

