

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:20:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708526.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_SRR1708526 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708526.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:20:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708526.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,189,154
Mapped reads	2,068,241 / 64.85%
Unmapped reads	1,120,913 / 35.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	602 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	90,829 / 2.85%
Duplication rate	3.23%
Clipped reads	473,740 / 14.85%

2.2. ACGT Content

Number/percentage of A's	27,608,604 / 28.15%
Number/percentage of C's	18,469,437 / 18.83%
Number/percentage of T's	31,045,968 / 31.65%
Number/percentage of G's	20,966,041 / 21.37%
Number/percentage of N's	1,292 / 0%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0317

Standard Deviation	0.2979
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2.4. Mapping Quality

Mean Mapping Quality	39.42
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2.5. Mismatches and indels

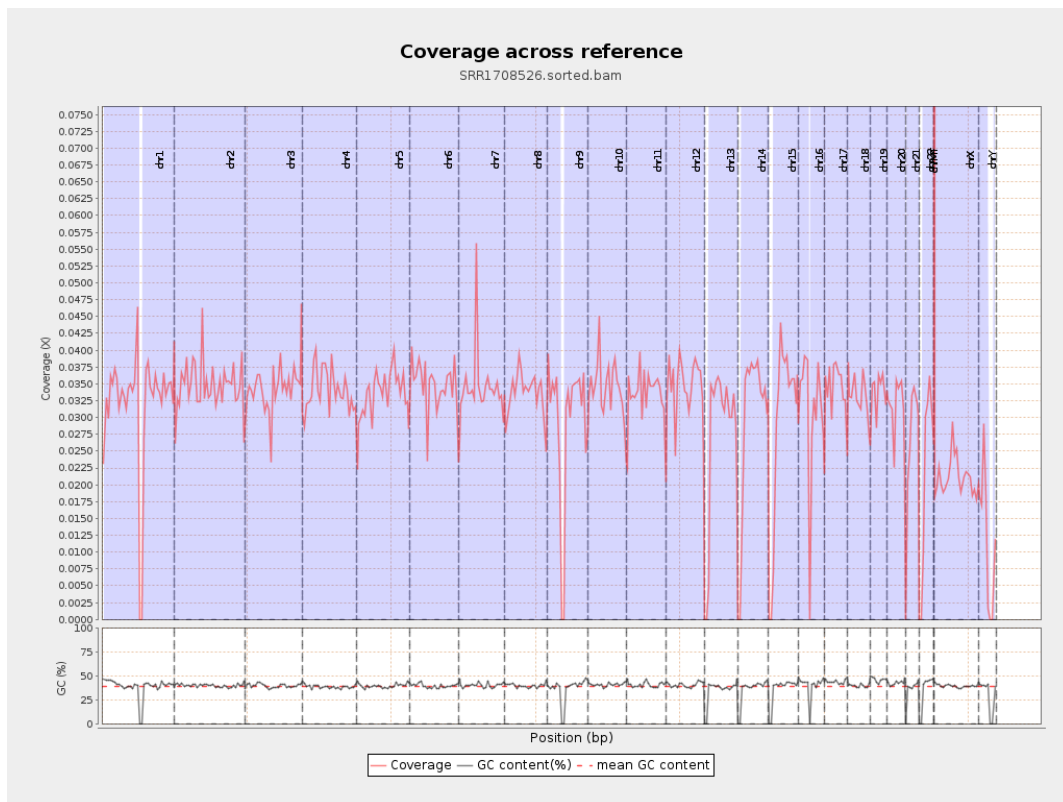
General error rate	0.53%
Mismatches	512,003
Insertions	5,495
Mapped reads with at least one insertion	0.26%
Deletions	15,388
Mapped reads with at least one deletion	0.74%
Homopolymer indels	48.47%

2.6. Chromosome stats

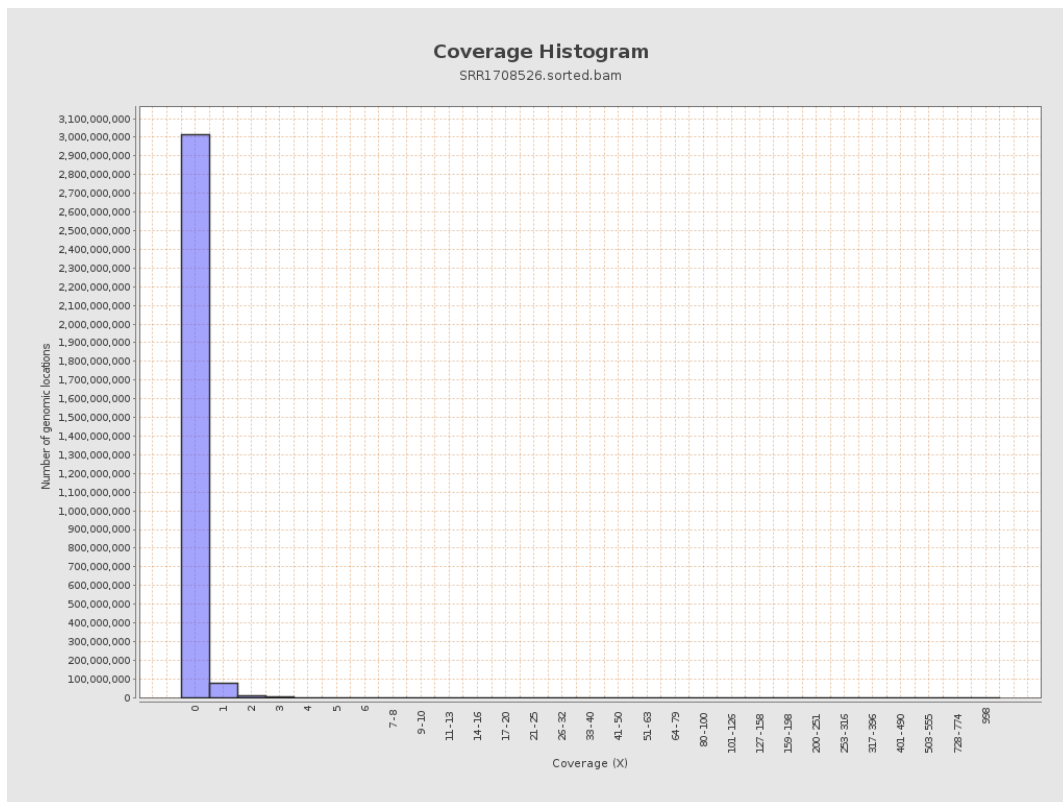
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7990807	0.0321	0.3919
chr2	243199373	8473522	0.0348	0.4807
chr3	198022430	6771175	0.0342	0.2218
chr4	191154276	6499443	0.034	0.2235
chr5	180915260	6128254	0.0339	0.2156
chr6	171115067	5921902	0.0346	0.3308
chr7	159138663	5490980	0.0345	0.3684

chr8	146364022	4909424	0.0335	0.3737
chr9	141213431	4140873	0.0293	0.2503
chr10	135534747	4674212	0.0345	0.258
chr11	135006516	4579495	0.0339	0.2818
chr12	133851895	4661078	0.0348	0.2258
chr13	115169878	3133475	0.0272	0.2587
chr14	107349540	3176079	0.0296	0.2076
chr15	102531392	2964393	0.0289	0.21
chr16	90354753	2766064	0.0306	0.2141
chr17	81195210	2801198	0.0345	0.2449
chr18	78077248	2603200	0.0333	0.3542
chr19	59128983	1992170	0.0337	0.3231
chr20	63025520	1973469	0.0313	0.2147
chr21	48129895	1276785	0.0265	0.2096
chr22	51304566	1115704	0.0217	0.1779
chrMT	16571	76982	4.6456	4.889
chrX	155270560	3294101	0.0212	0.195
chrY	59373566	699926	0.0118	0.1393

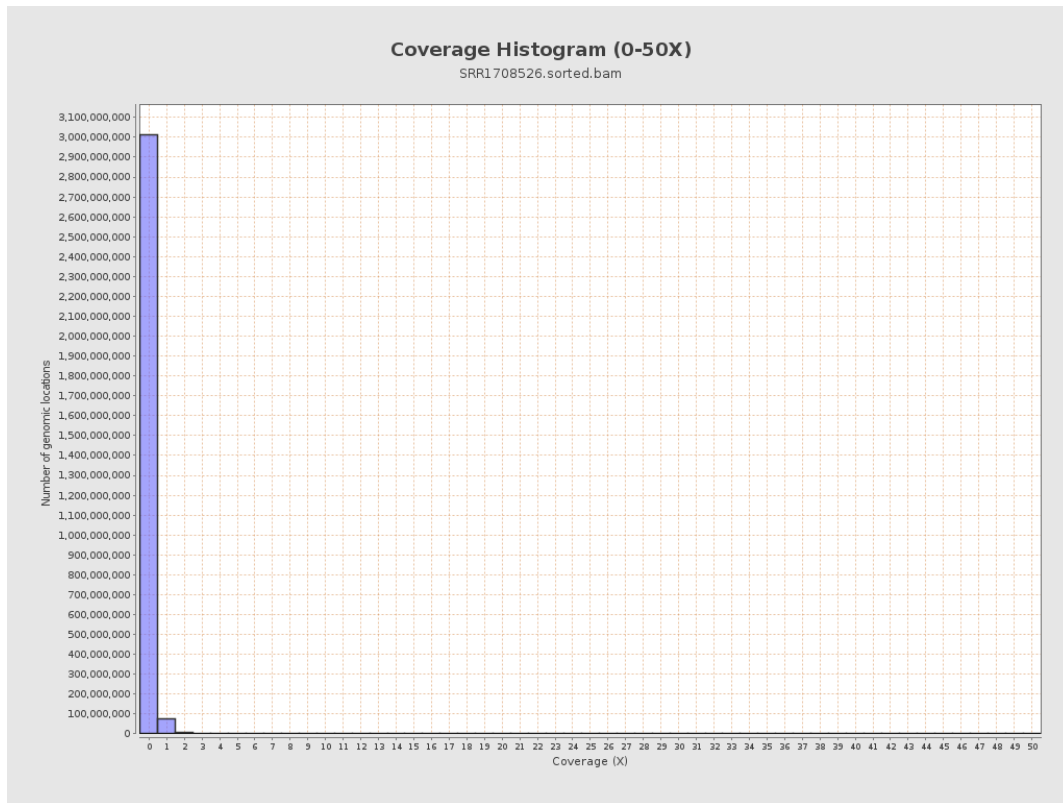
3. Results : Coverage across reference



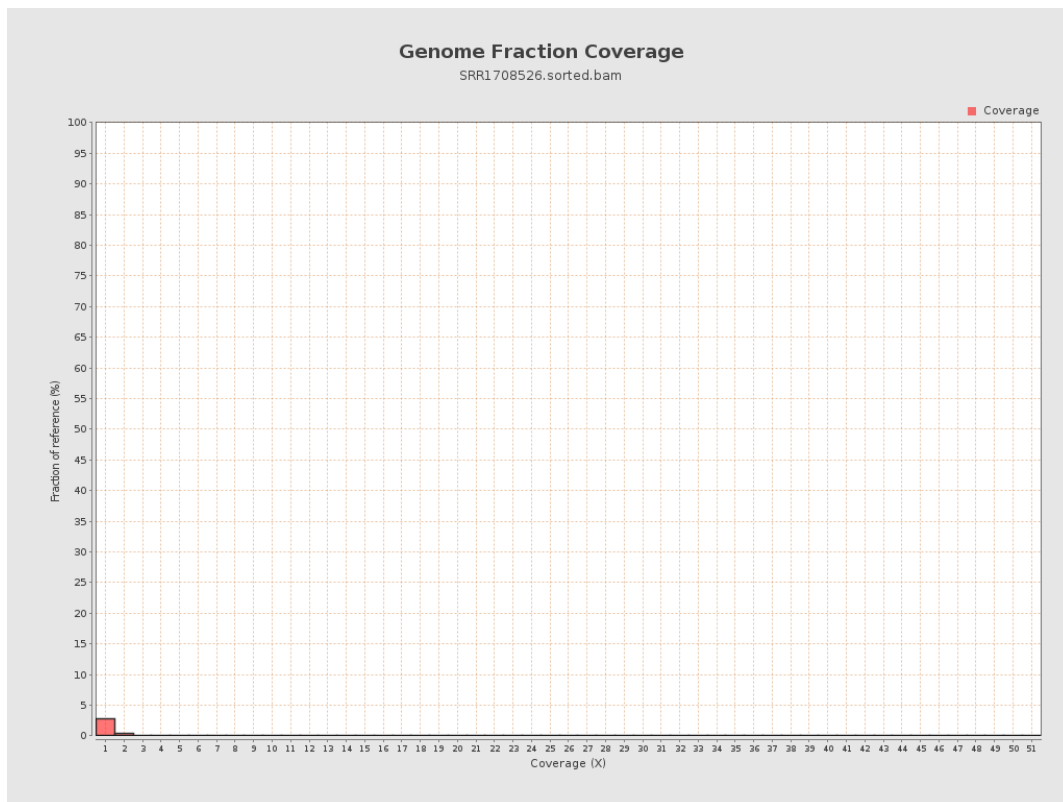
4. Results : Coverage Histogram



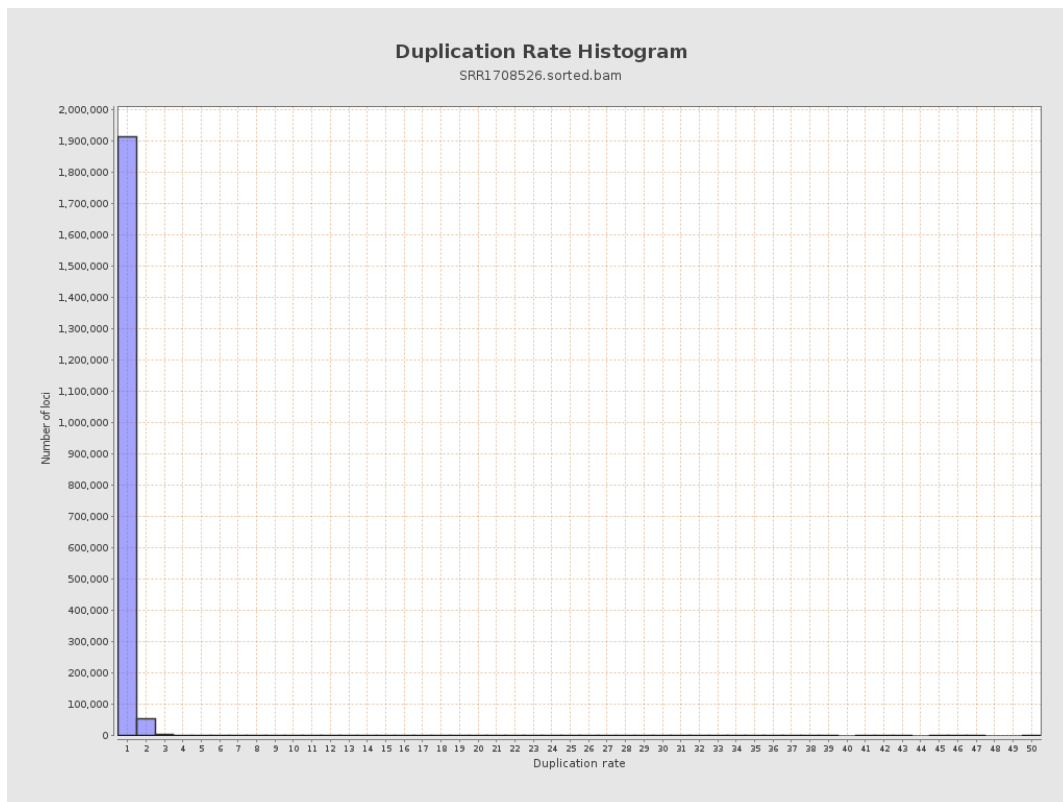
5. Results : Coverage Histogram (0-50X)



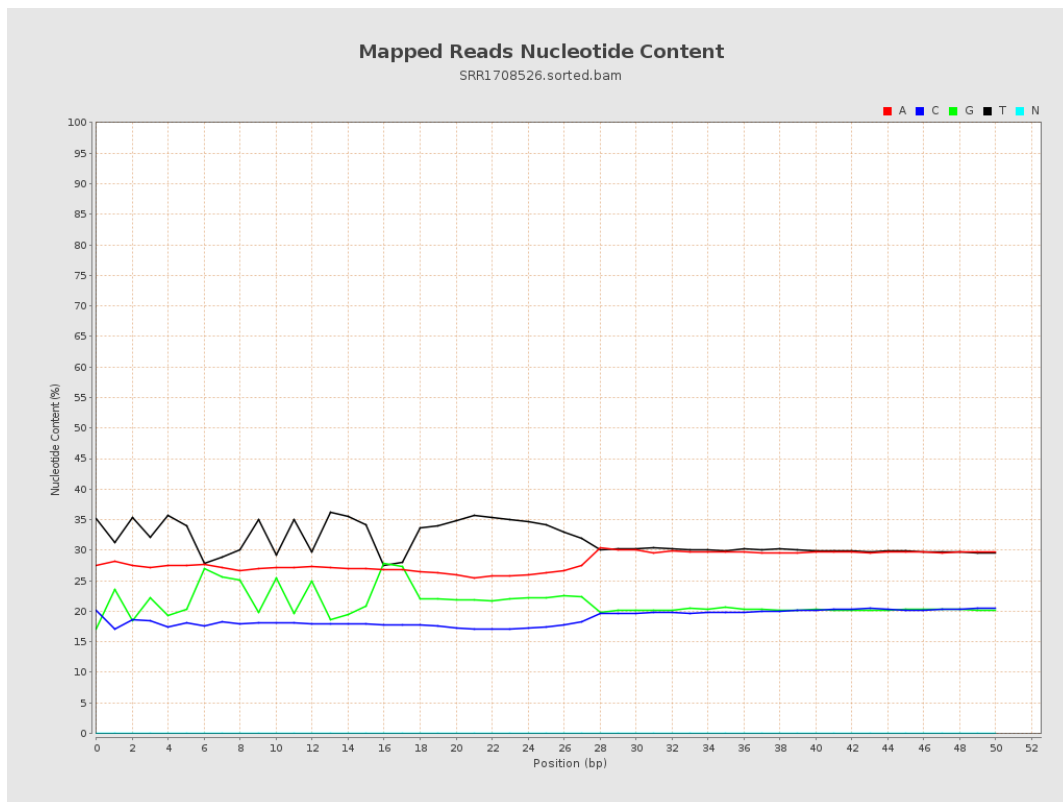
6. Results : Genome Fraction Coverage



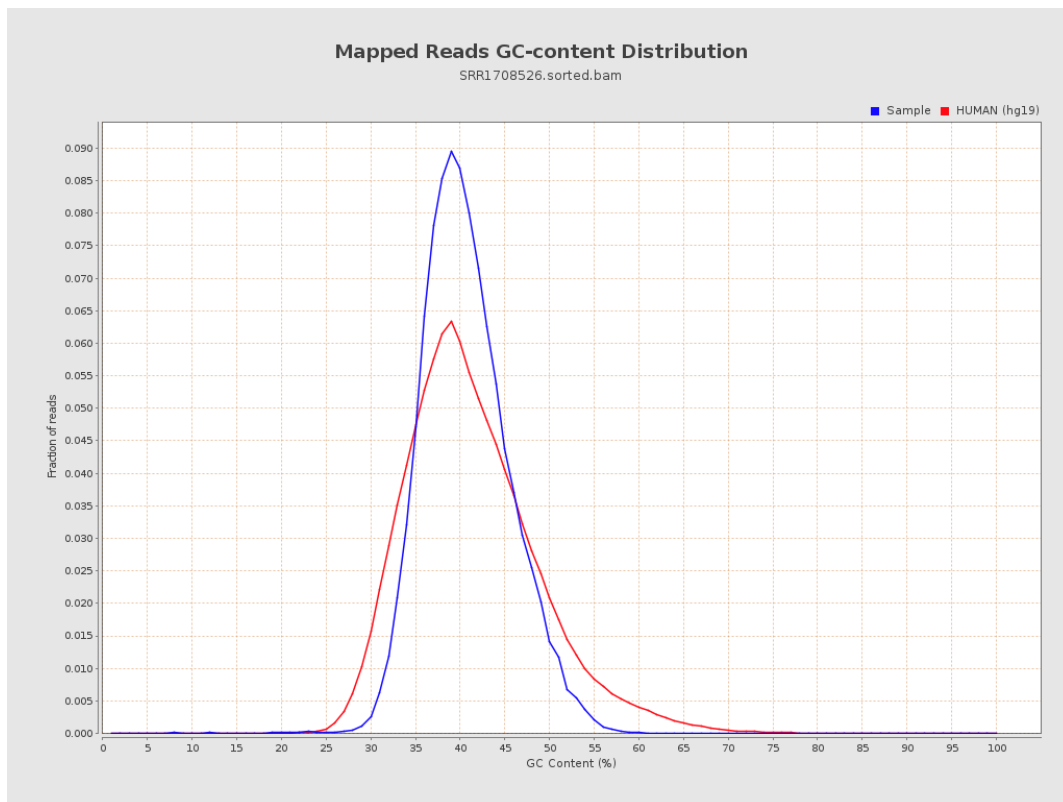
7. Results : Duplication Rate Histogram



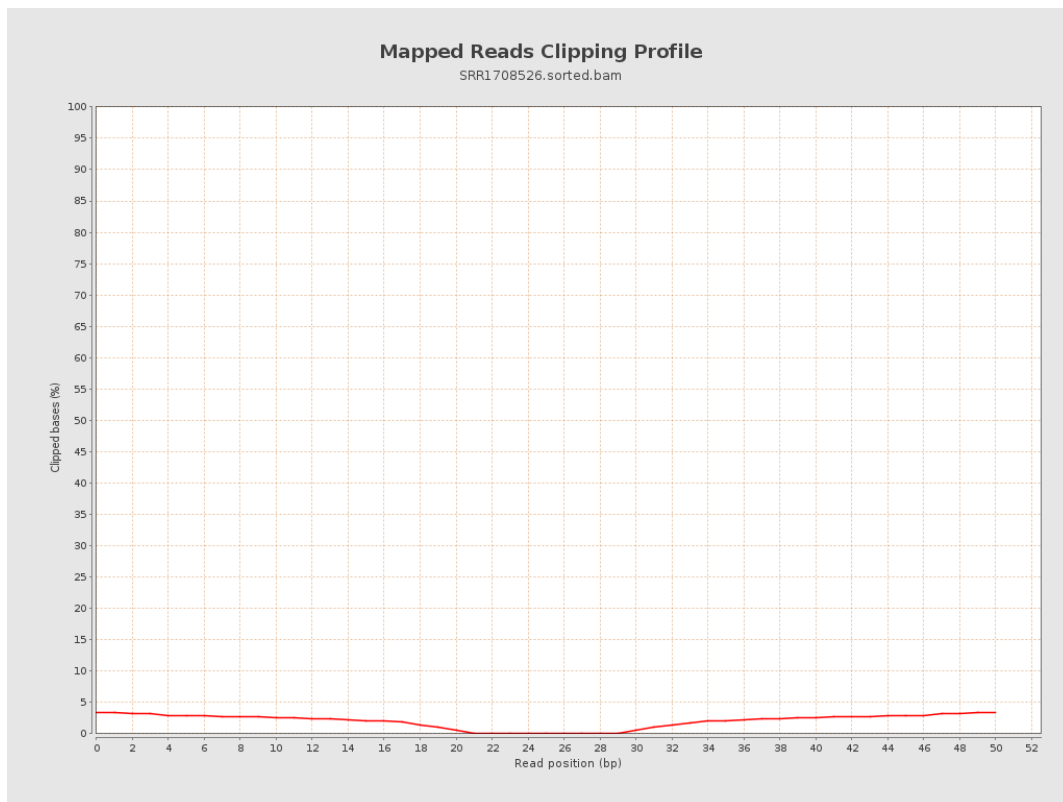
8. Results : Mapped Reads Nucleotide Content



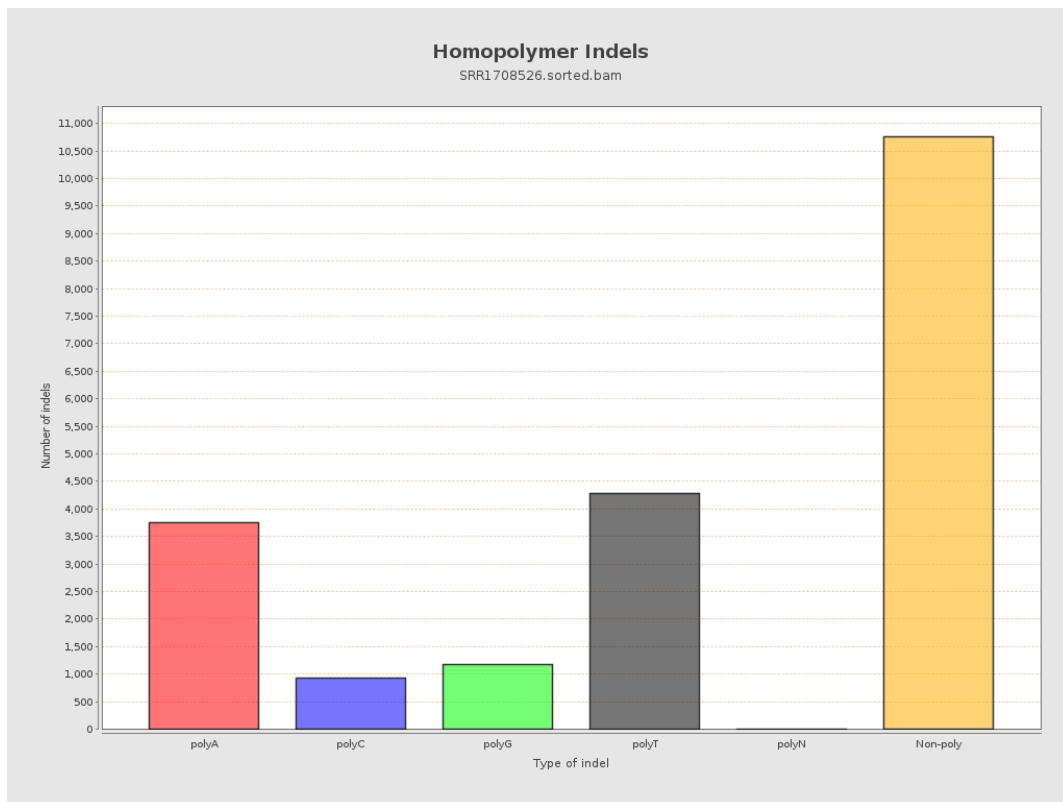
9. Results : Mapped Reads GC-content Distribution



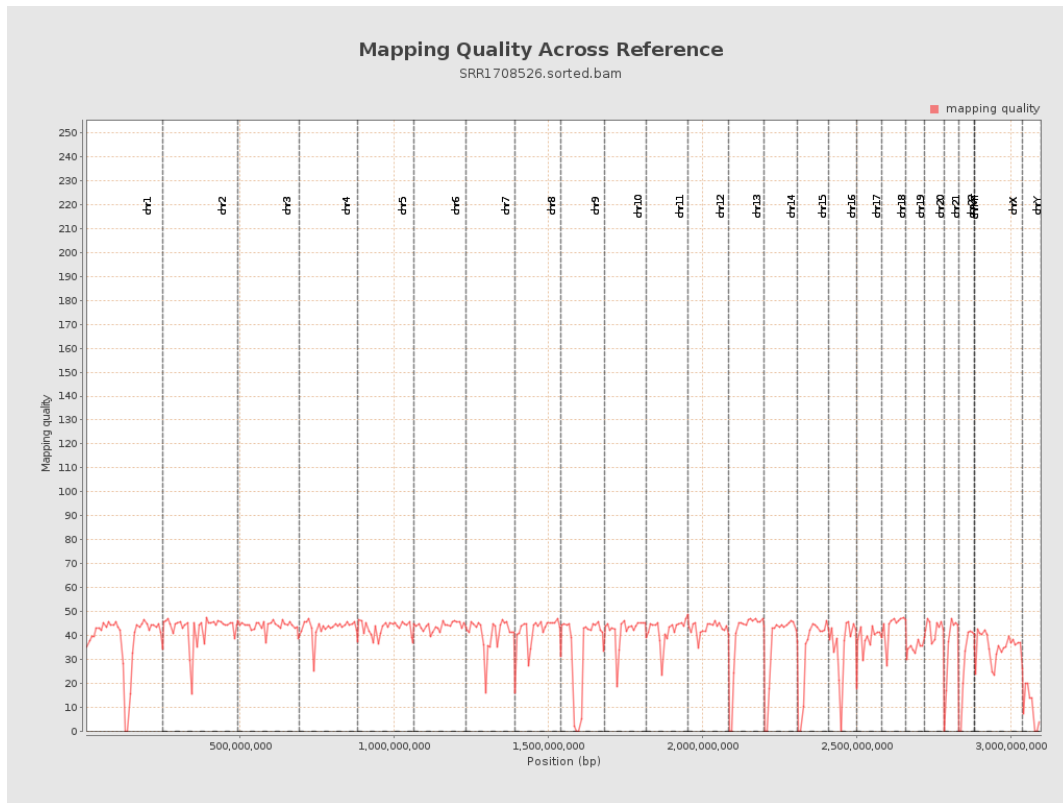
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

