

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 05:33:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212161.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_SRR3212161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 05:32:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,000,938
Mapped reads	1,795,124 / 89.71%
Unmapped reads	205,814 / 10.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,176 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	68,700 / 3.43%
Duplication rate	3.15%
Clipped reads	961,934 / 48.07%

2.2. ACGT Content

Number/percentage of A's	33,826,380 / 28.95%
Number/percentage of C's	22,259,664 / 19.05%
Number/percentage of T's	36,025,159 / 30.83%
Number/percentage of G's	24,731,547 / 21.17%
Number/percentage of N's	7,536 / 0.01%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.3127
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.42
----------------------	-------

2.5. Mismatches and indels

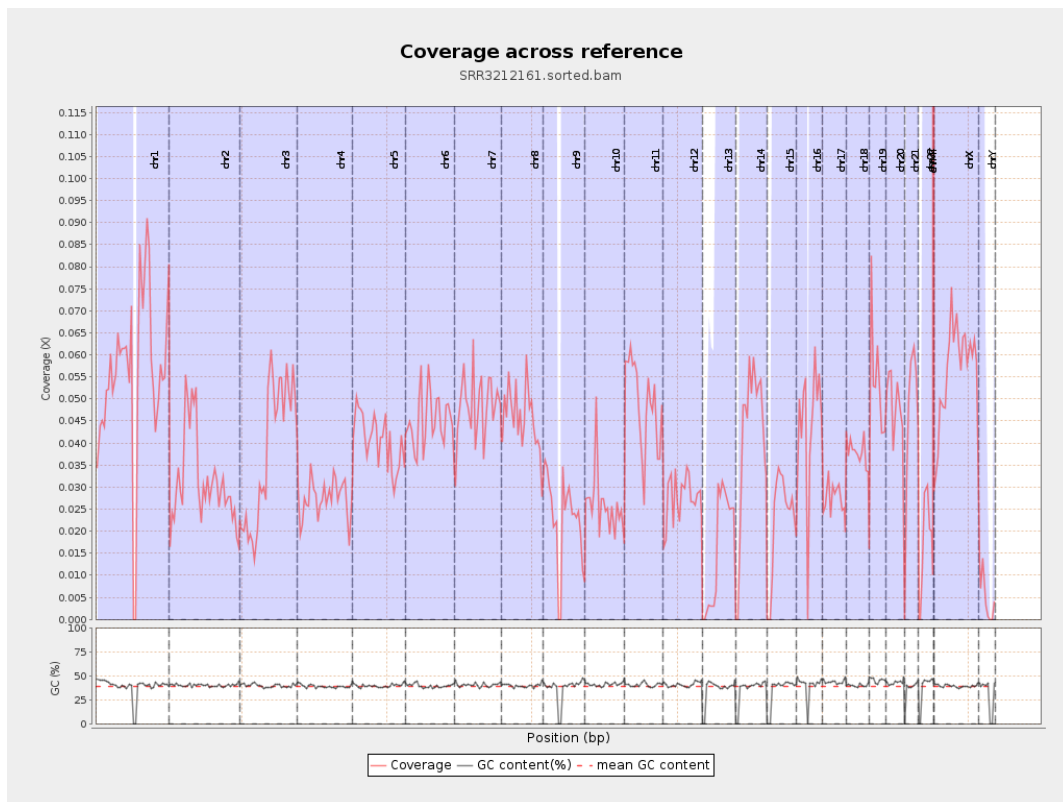
General error rate	0.91%
Mismatches	1,045,230
Insertions	8,632
Mapped reads with at least one insertion	0.48%
Deletions	27,543
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.9%

2.6. Chromosome stats

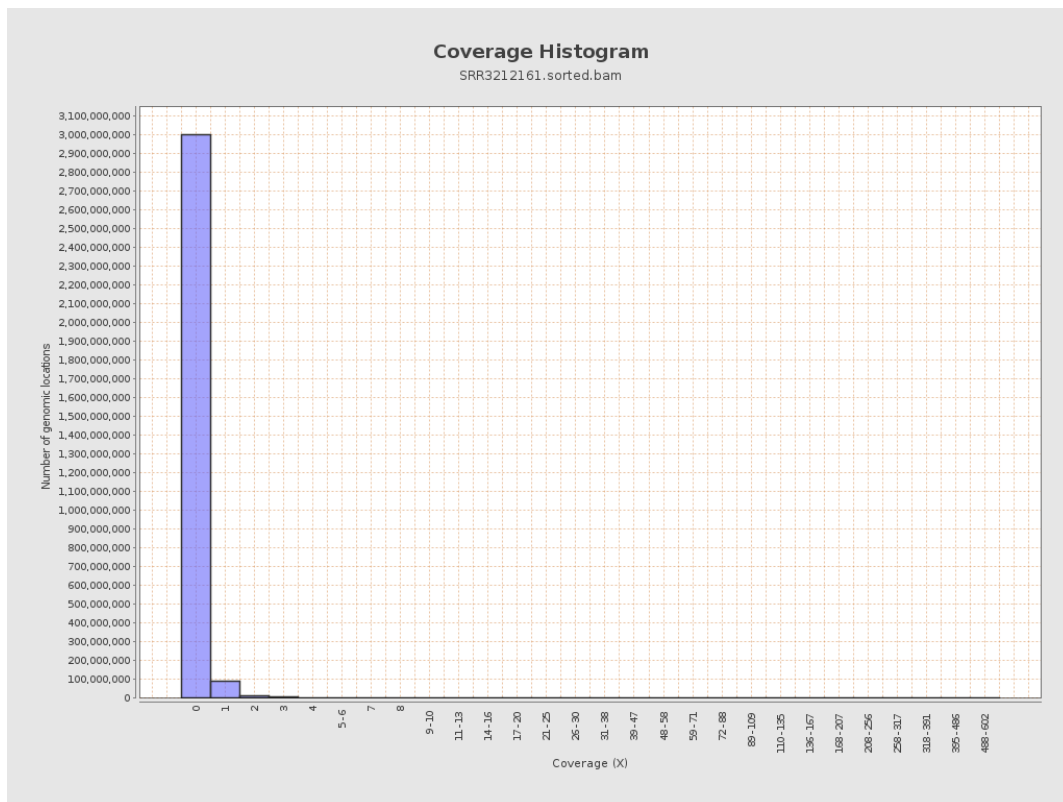
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13877049	0.0557	0.5942
chr2	243199373	7688988	0.0316	0.3098
chr3	198022430	7501159	0.0379	0.2256
chr4	191154276	5210787	0.0273	0.1956
chr5	180915260	7324559	0.0405	0.2318
chr6	171115067	7715678	0.0451	0.2581
chr7	159138663	7748168	0.0487	0.3921

chr8	146364022	6665786	0.0455	0.4114
chr9	141213431	3256436	0.0231	0.2245
chr10	135534747	3538530	0.0261	0.2841
chr11	135006516	6515950	0.0483	0.3342
chr12	133851895	3678172	0.0275	0.1912
chr13	115169878	1883246	0.0164	0.1482
chr14	107349540	4453859	0.0415	0.2397
chr15	102531392	2340059	0.0228	0.1805
chr16	90354753	4012030	0.0444	0.2486
chr17	81195210	2211757	0.0272	0.2125
chr18	78077248	2966539	0.038	0.3775
chr19	59128983	3143545	0.0532	0.4296
chr20	63025520	3011700	0.0478	0.2539
chr21	48129895	2217712	0.0461	0.2529
chr22	51304566	882367	0.0172	0.1476
chrMT	16571	17970	1.0844	1.1781
chrX	155270560	8742280	0.0563	0.2881
chrY	59373566	291341	0.0049	0.0919

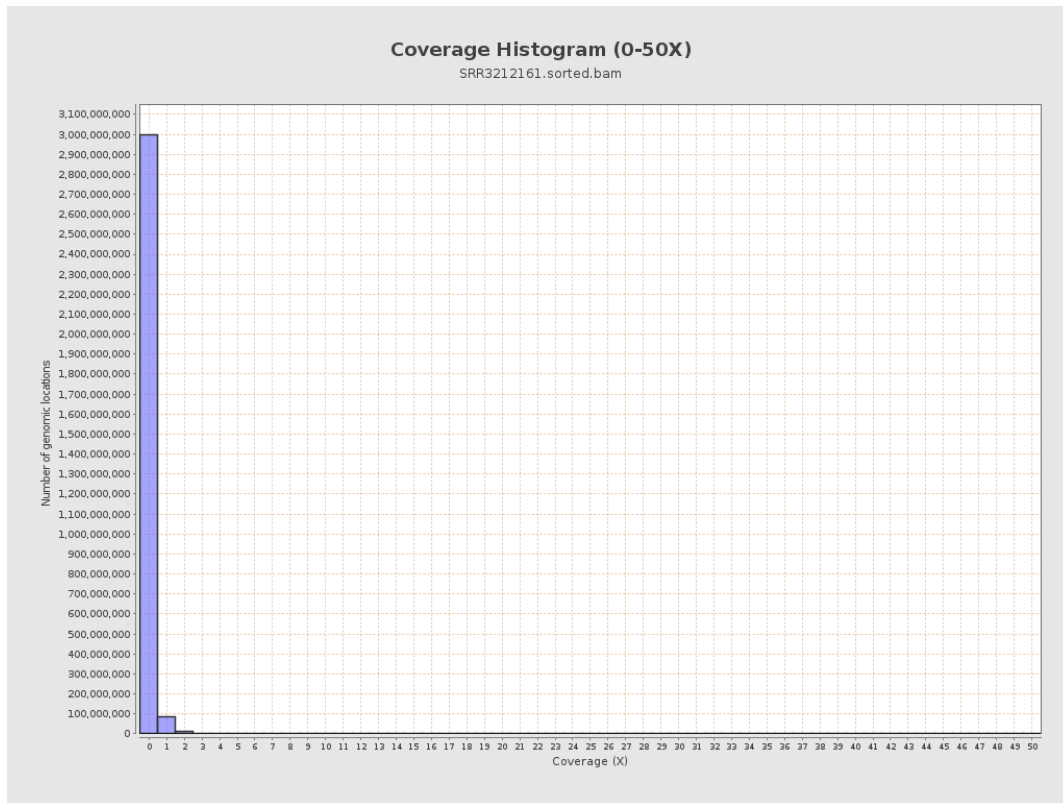
3. Results : Coverage across reference



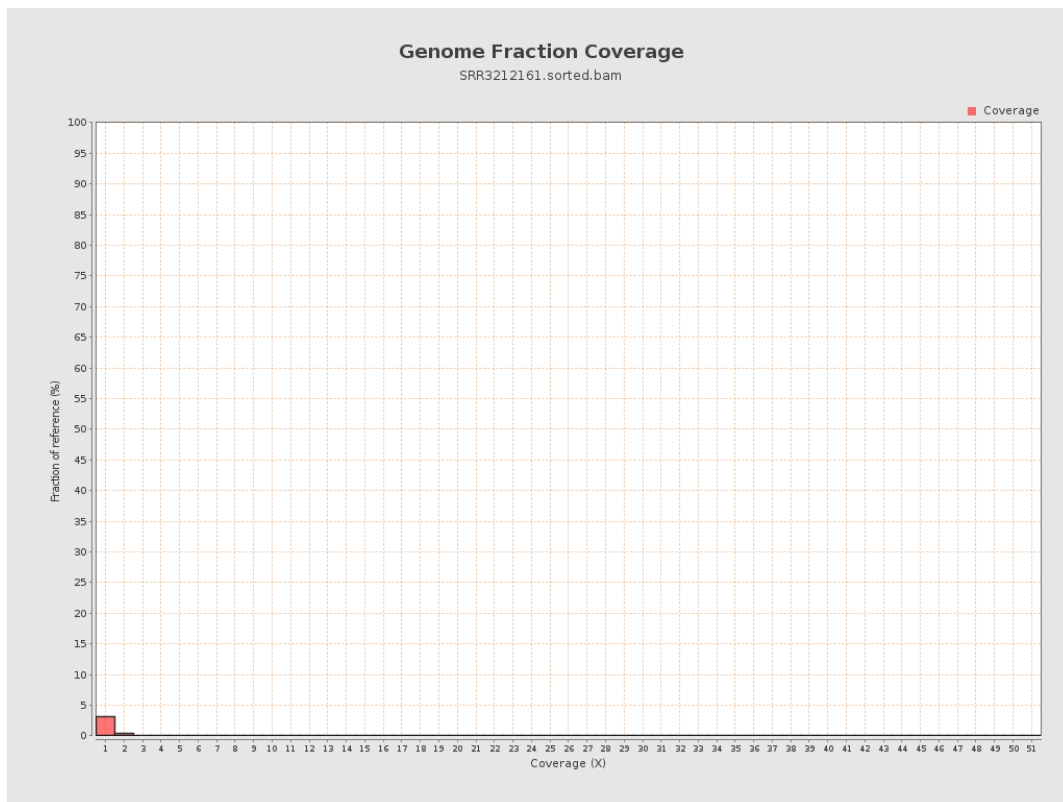
4. Results : Coverage Histogram



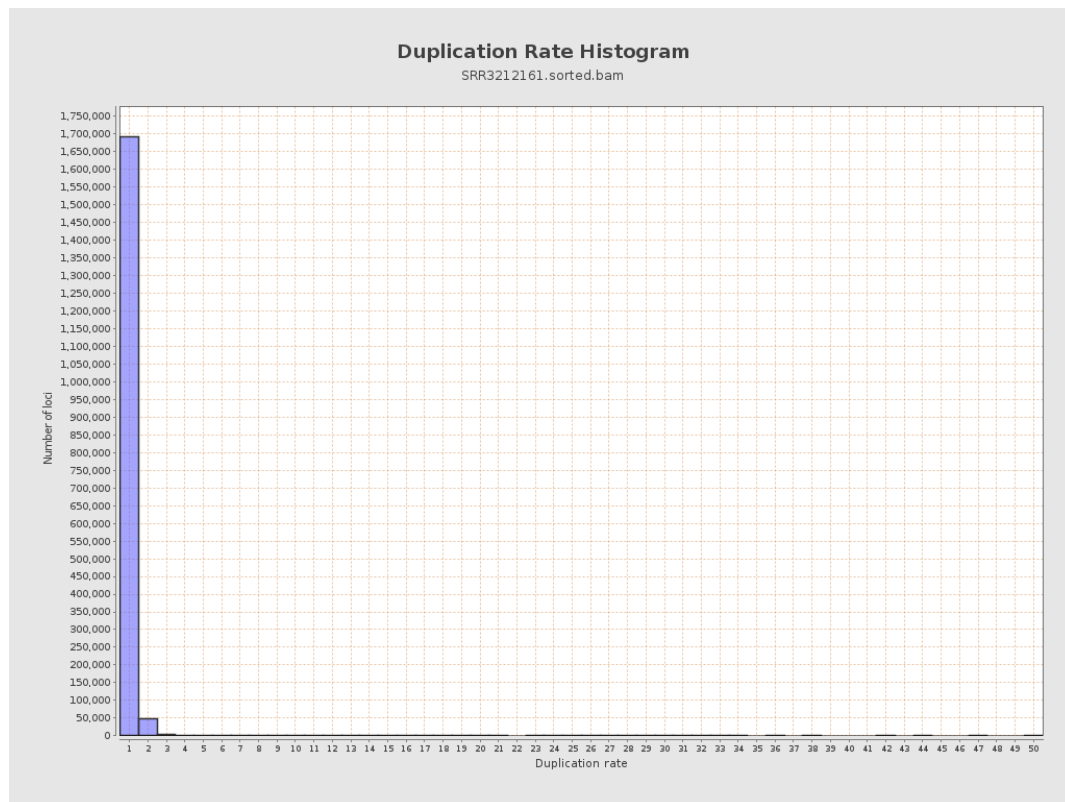
5. Results : Coverage Histogram (0-50X)



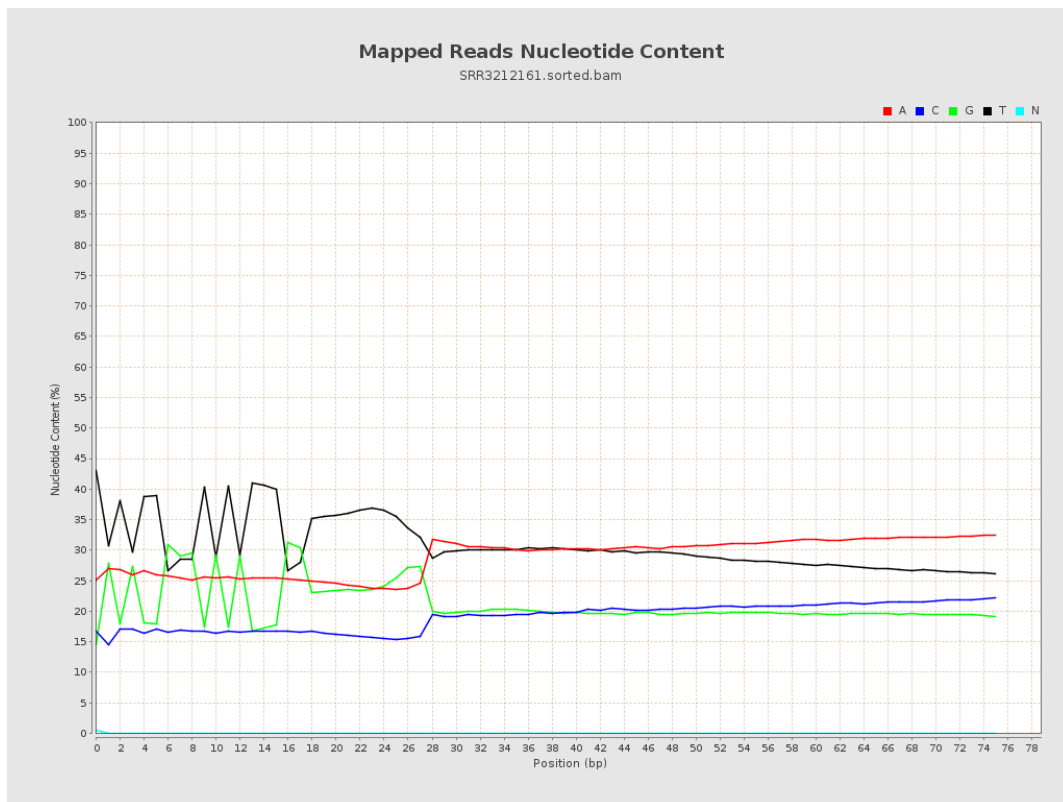
6. Results : Genome Fraction Coverage



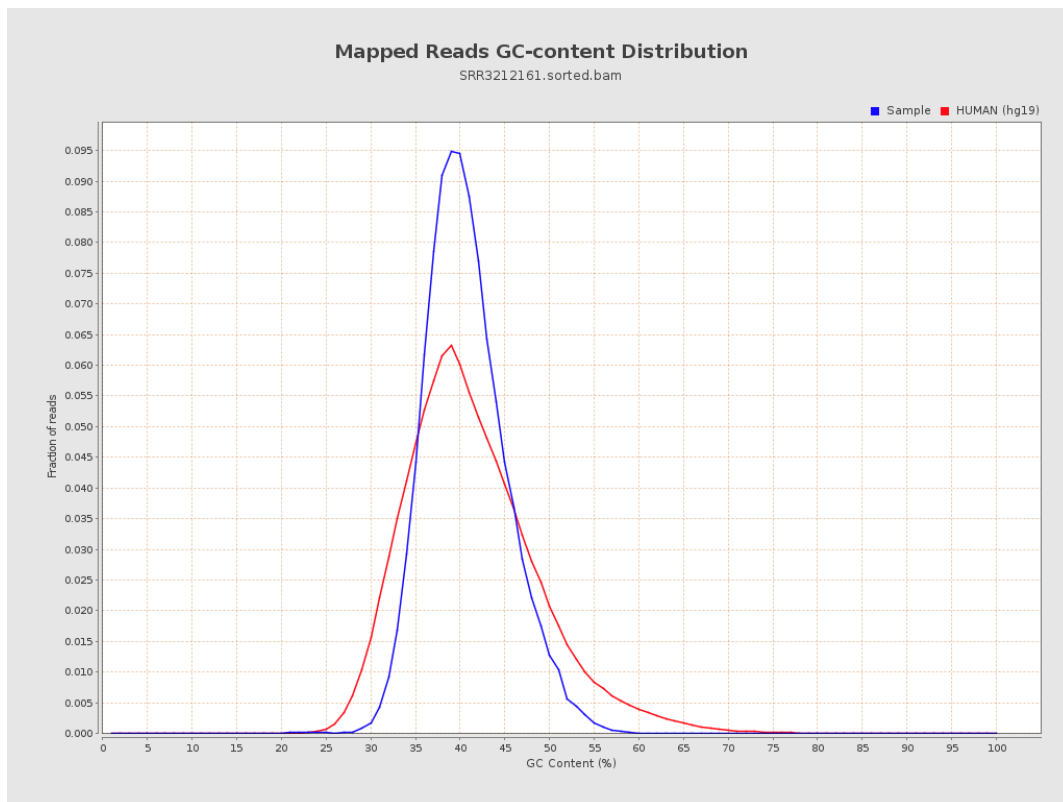
7. Results : Duplication Rate Histogram



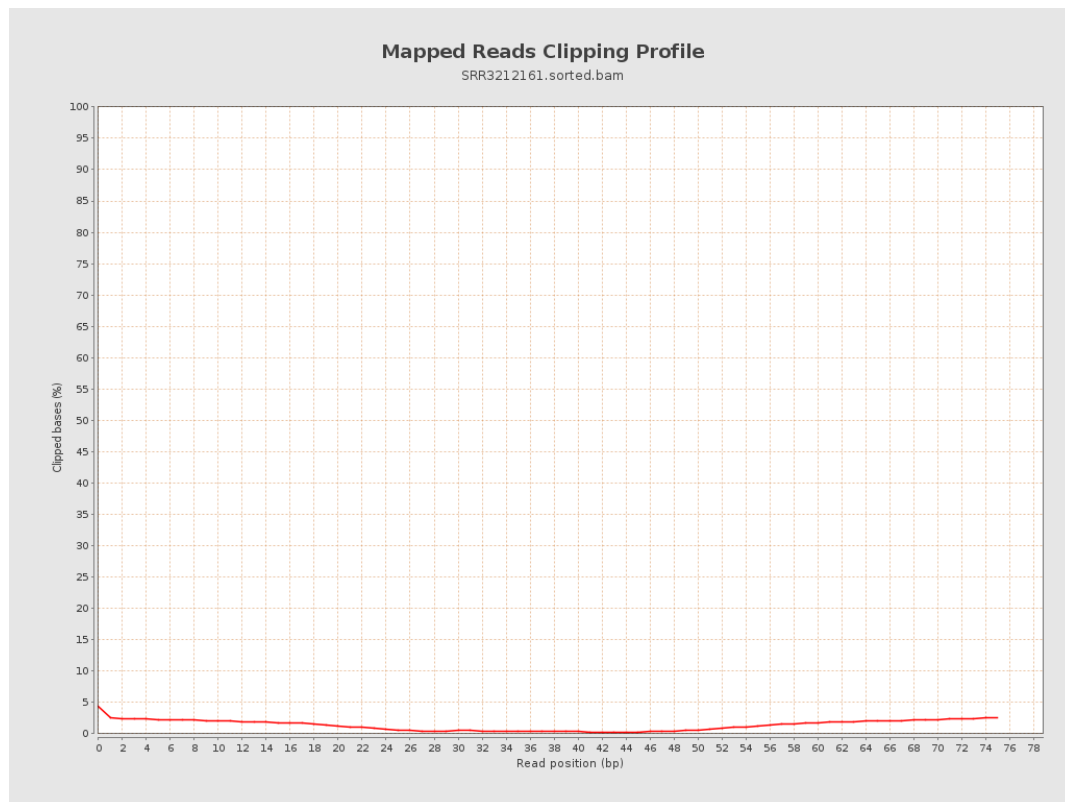
8. Results : Mapped Reads Nucleotide Content



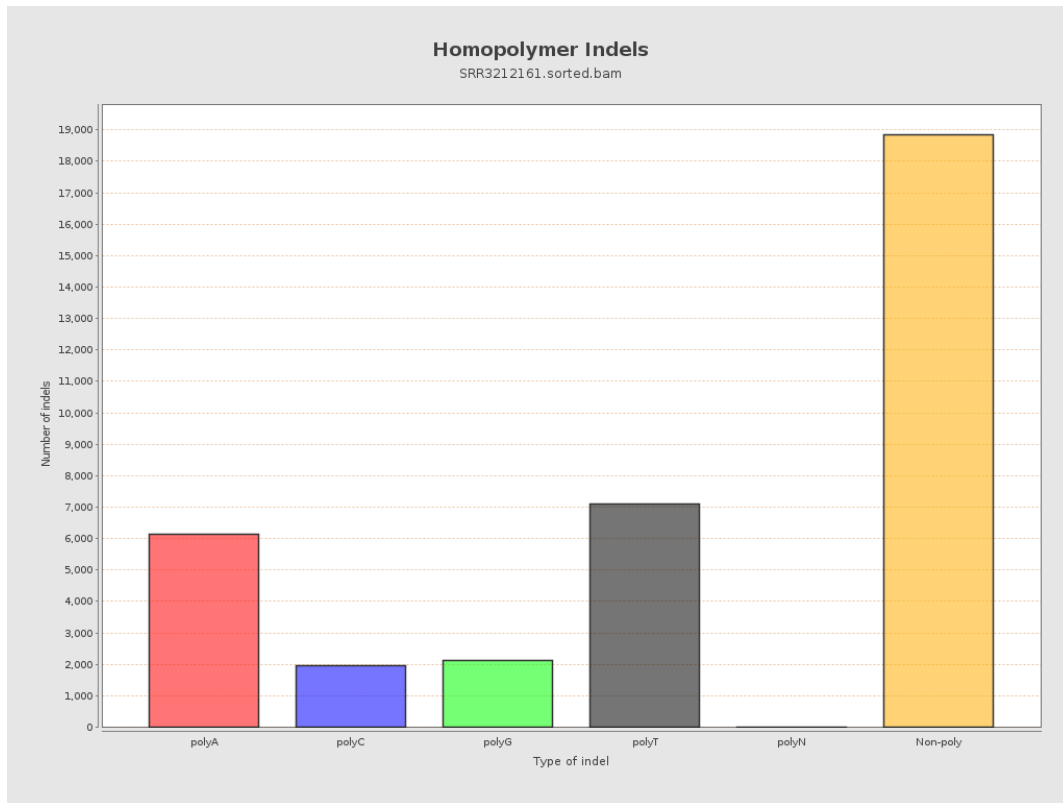
9. Results : Mapped Reads GC-content Distribution



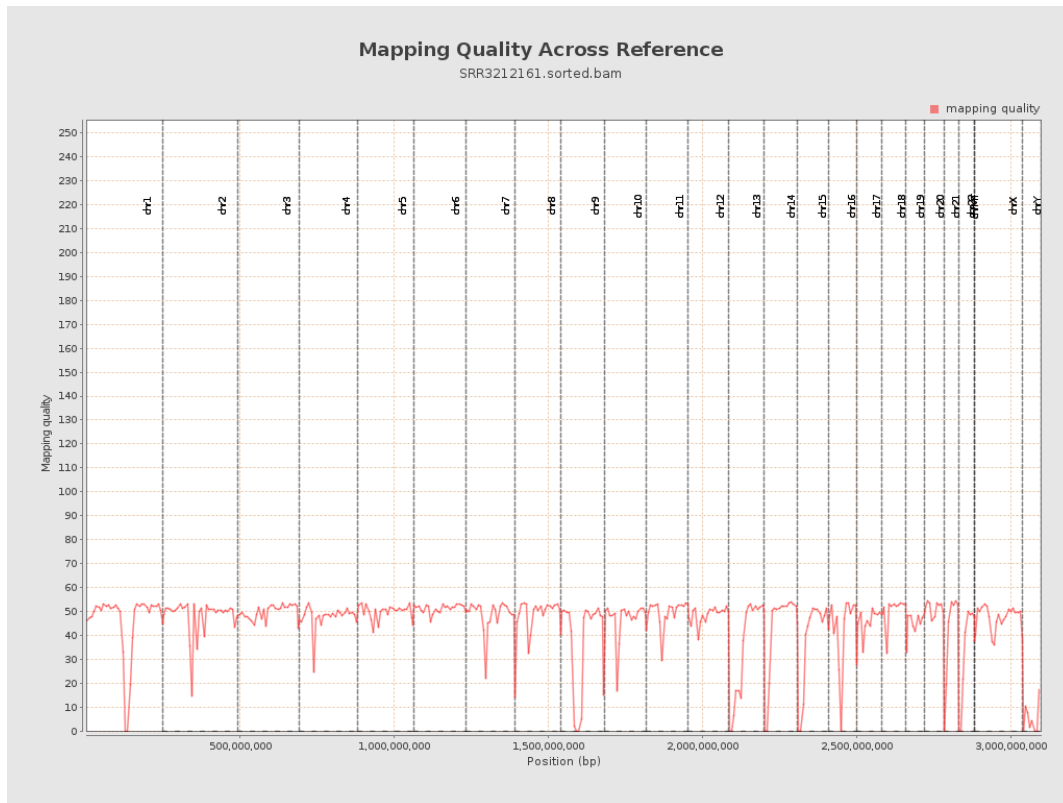
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

