

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:13:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068119.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_SRR6068119 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068119.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:13:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068119.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,851,811
Mapped reads	709,938 / 24.89%
Unmapped reads	2,141,873 / 75.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,767 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	110,041 / 3.86%
Duplication rate	10.94%
Clipped reads	427,753 / 15%

2.2. ACGT Content

Number/percentage of A's	11,595,558 / 26.19%
Number/percentage of C's	7,868,642 / 17.77%
Number/percentage of T's	14,308,112 / 32.31%
Number/percentage of G's	10,467,802 / 23.64%
Number/percentage of N's	43,066 / 0.1%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.2643
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2.4. Mapping Quality

Mean Mapping Quality	44.94
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2.5. Mismatches and indels

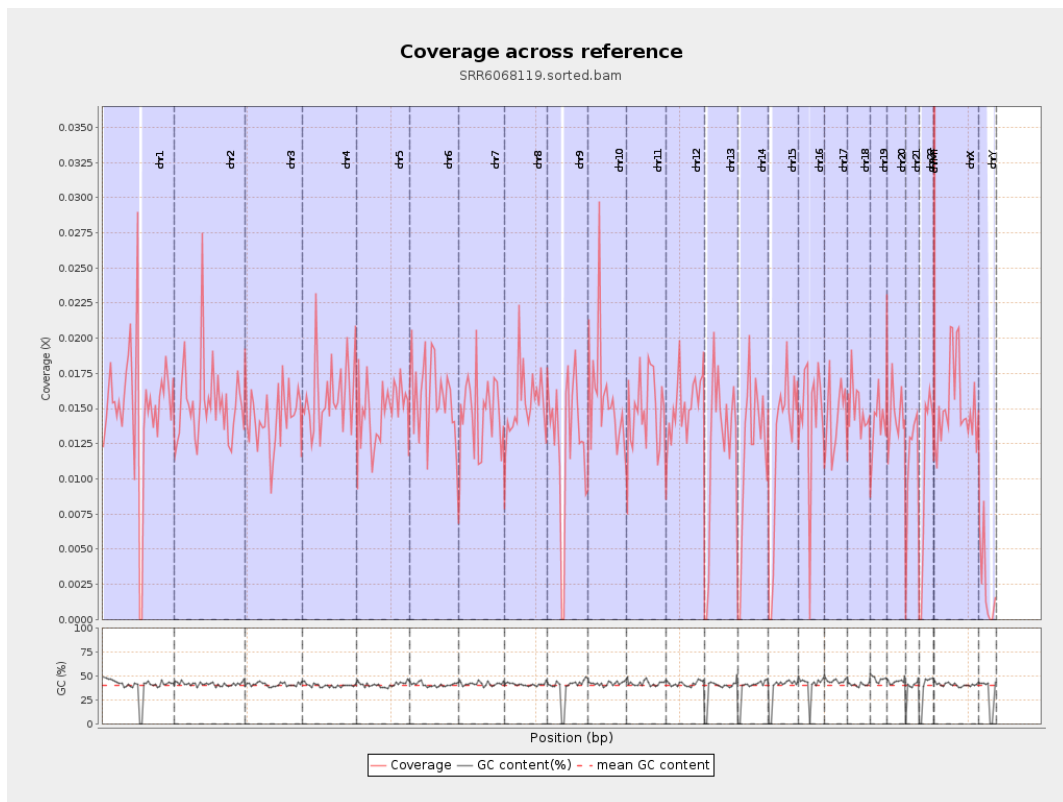
General error rate	0.99%
Mismatches	433,752
Insertions	3,268
Mapped reads with at least one insertion	0.46%
Deletions	10,307
Mapped reads with at least one deletion	1.44%
Homopolymer indels	46.69%

2.6. Chromosome stats

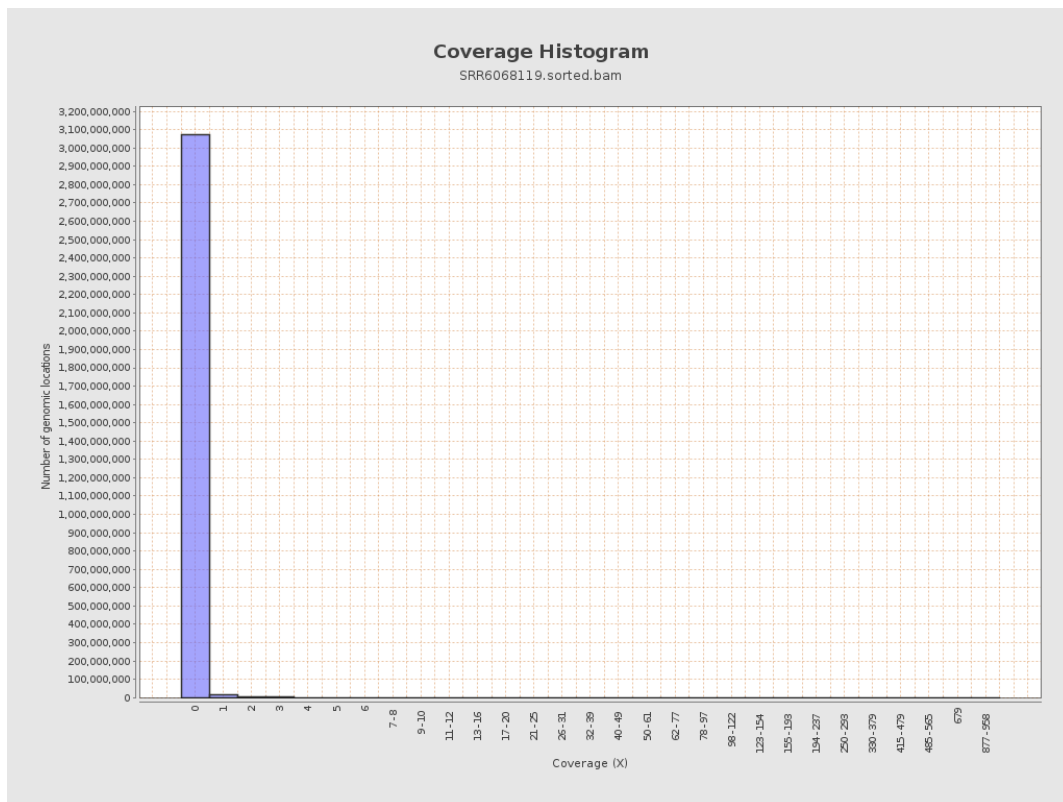
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3745858	0.015	0.3044
chr2	243199373	3733627	0.0154	0.2829
chr3	198022430	2836412	0.0143	0.2118
chr4	191154276	3050742	0.016	0.4529
chr5	180915260	2703419	0.0149	0.2199
chr6	171115067	2689290	0.0157	0.2429
chr7	159138663	2341102	0.0147	0.2315

chr8	146364022	2249012	0.0154	0.2331
chr9	141213431	1789285	0.0127	0.2121
chr10	135534747	2135644	0.0158	0.2501
chr11	135006516	2012435	0.0149	0.2243
chr12	133851895	2048800	0.0153	0.2208
chr13	115169878	1409369	0.0122	0.2013
chr14	107349540	1293012	0.012	0.2161
chr15	102531392	1268510	0.0124	0.4246
chr16	90354753	1298333	0.0144	0.2162
chr17	81195210	1161289	0.0143	0.2096
chr18	78077248	1170563	0.015	0.2844
chr19	59128983	841019	0.0142	0.2555
chr20	63025520	910671	0.0144	0.2056
chr21	48129895	541491	0.0113	0.1789
chr22	51304566	540503	0.0105	0.173
chrMT	16571	12187	0.7354	2.4613
chrX	155270560	2374119	0.0153	0.2283
chrY	59373566	142994	0.0024	0.1881

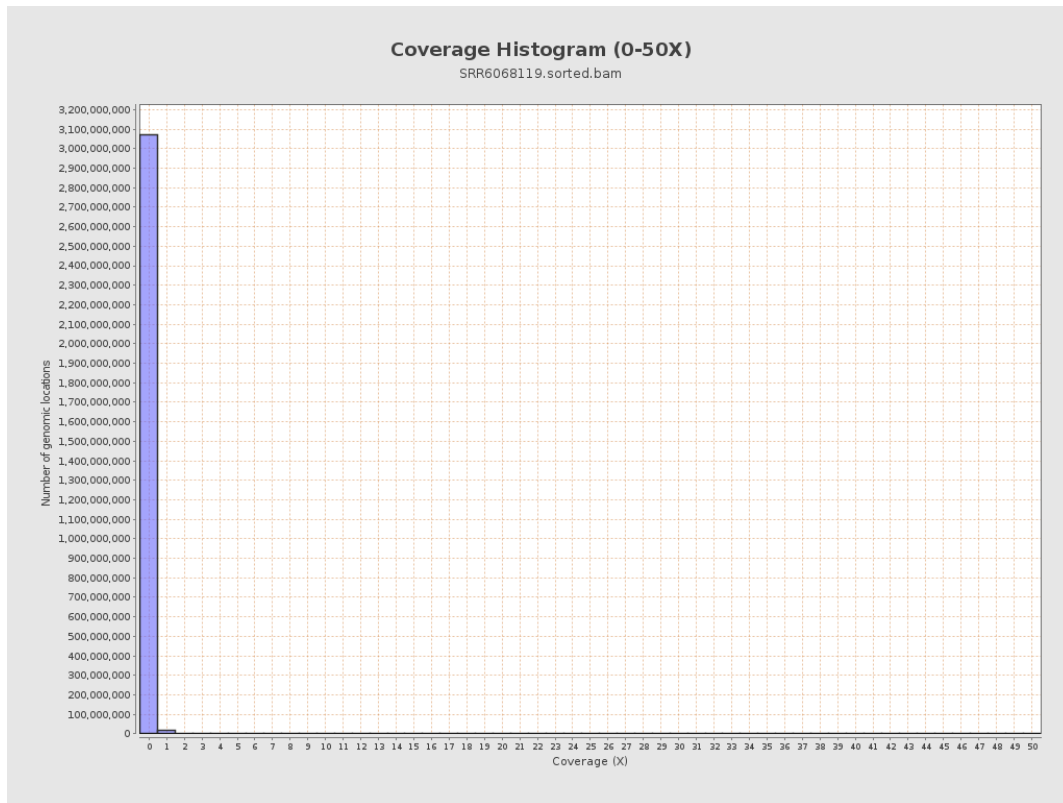
3. Results : Coverage across reference



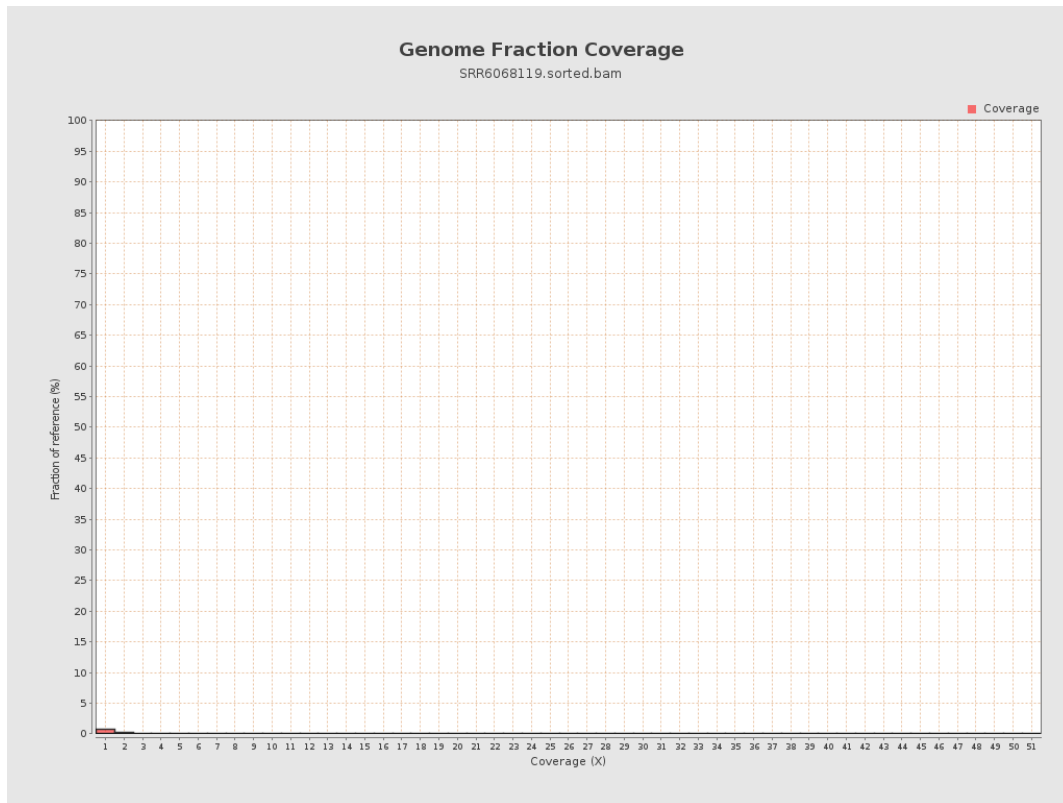
4. Results : Coverage Histogram



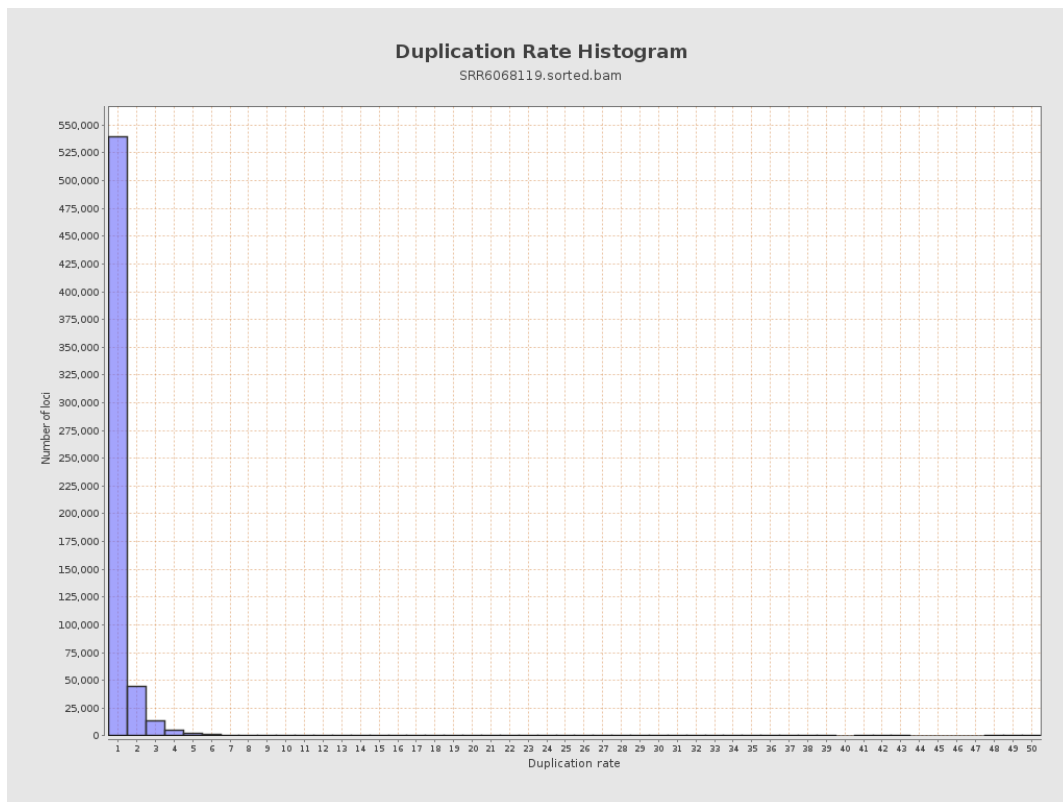
5. Results : Coverage Histogram (0-50X)



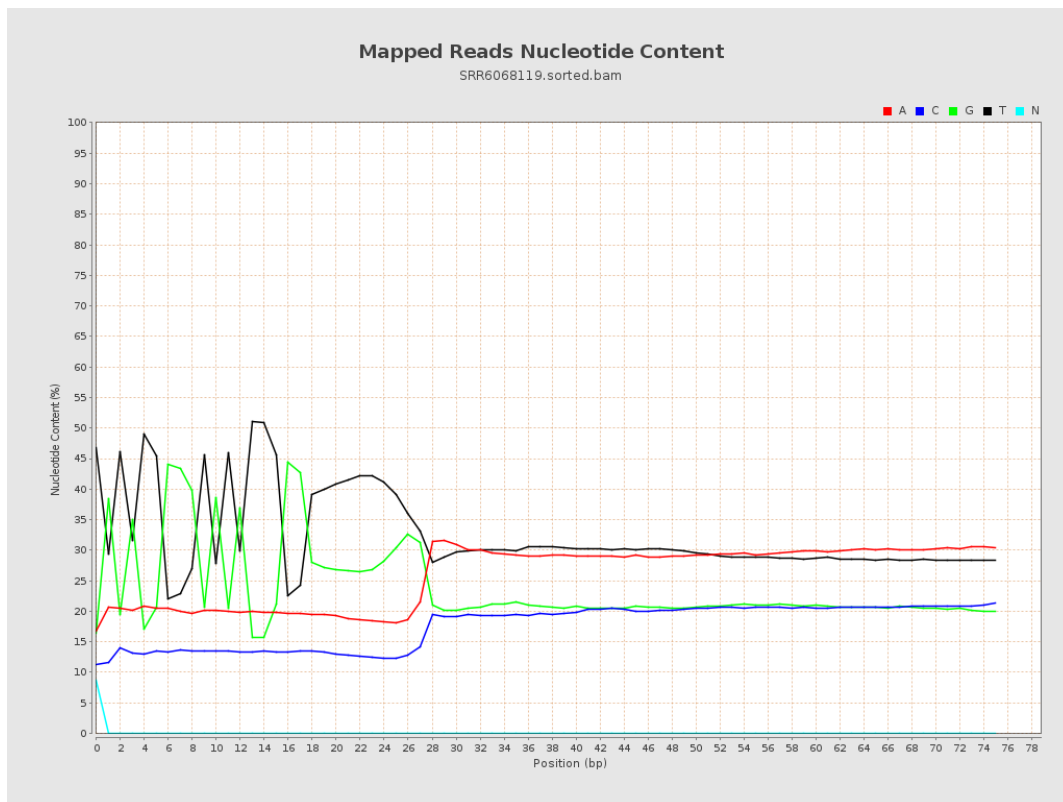
6. Results : Genome Fraction Coverage



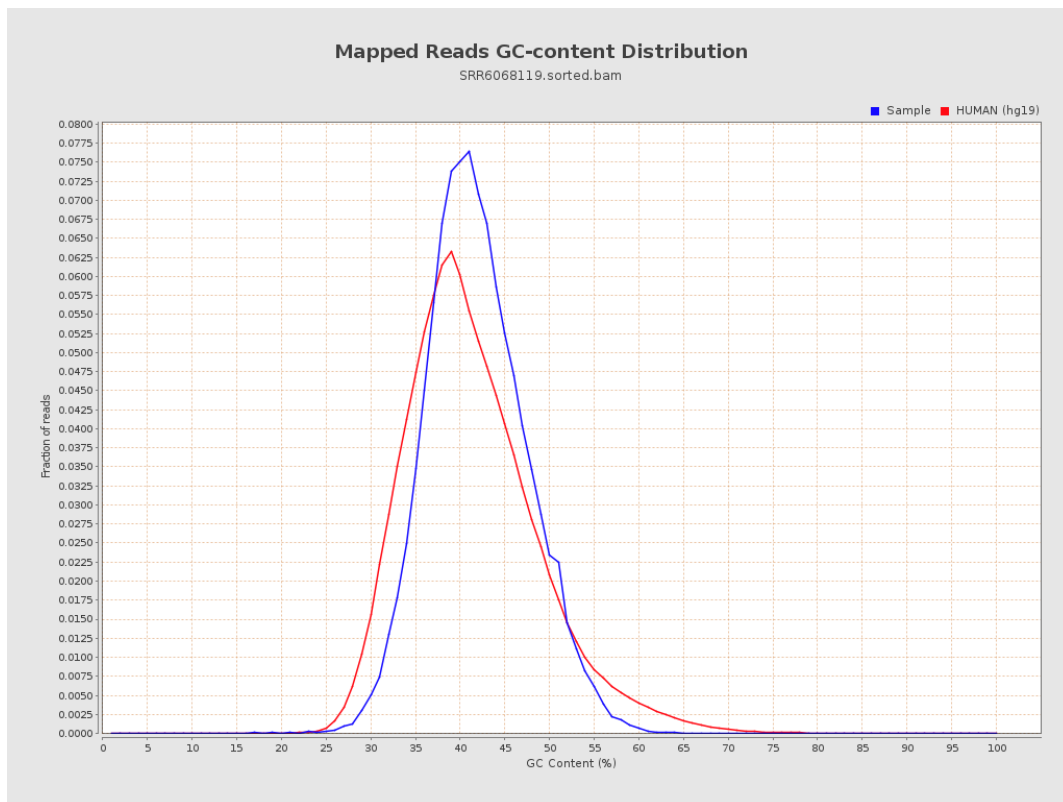
7. Results : Duplication Rate Histogram



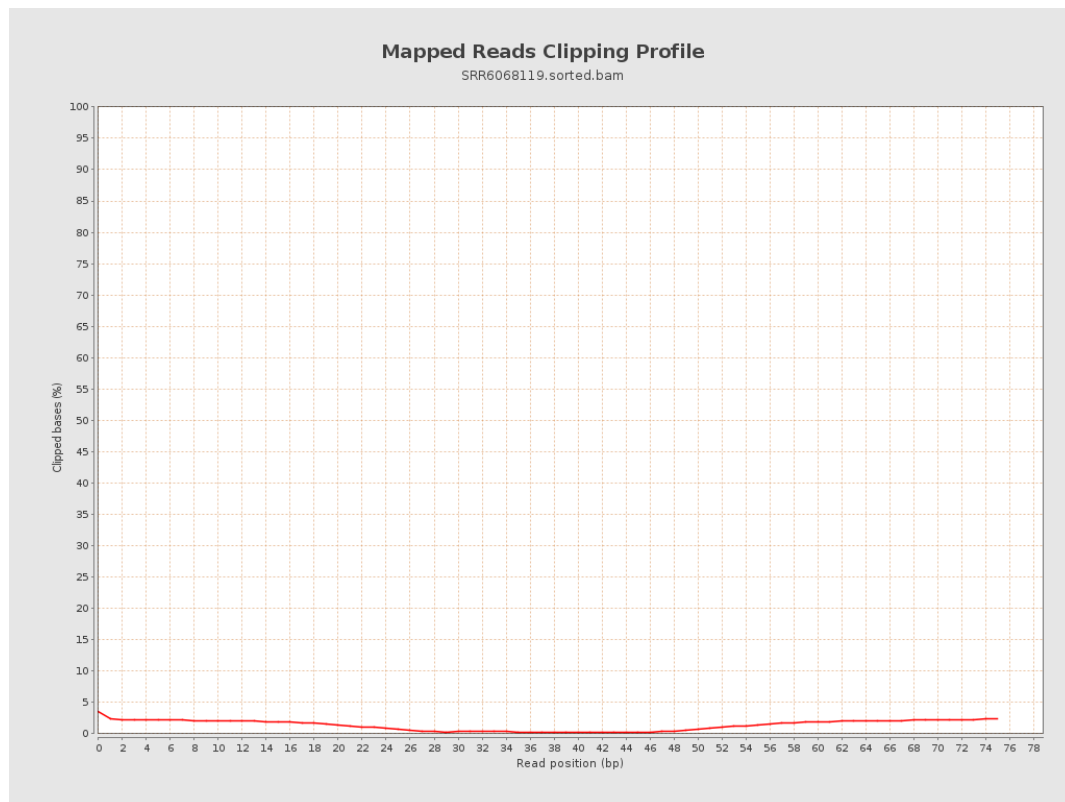
8. Results : Mapped Reads Nucleotide Content



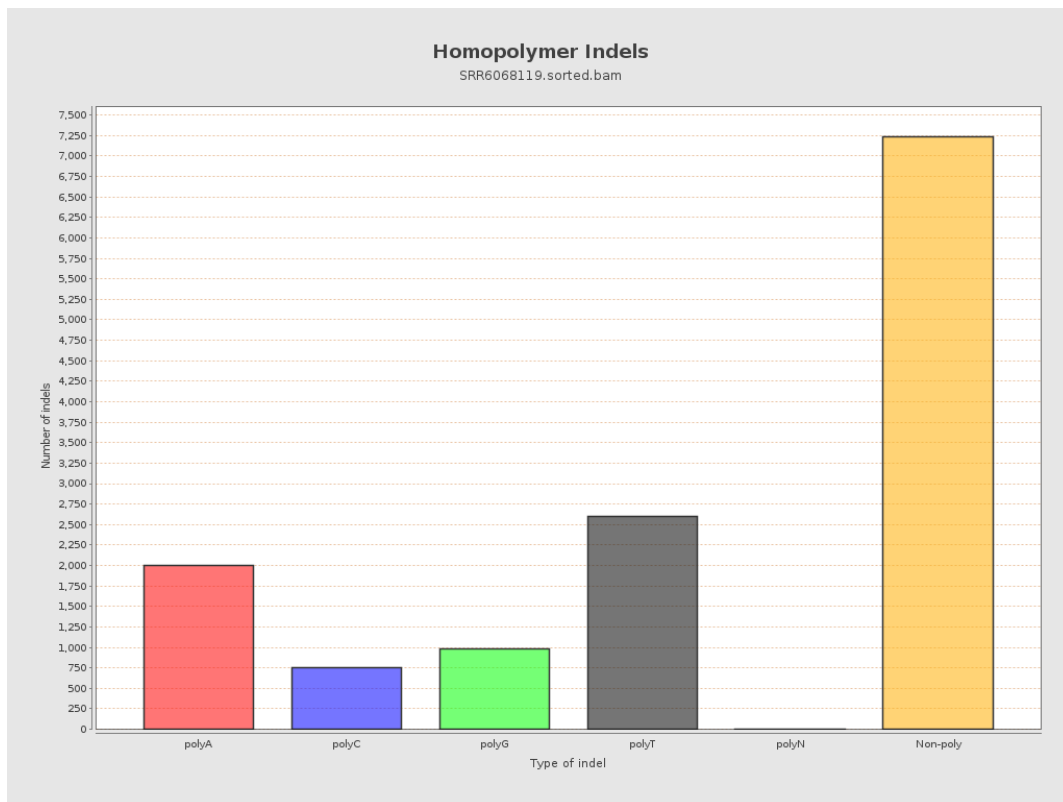
9. Results : Mapped Reads GC-content Distribution



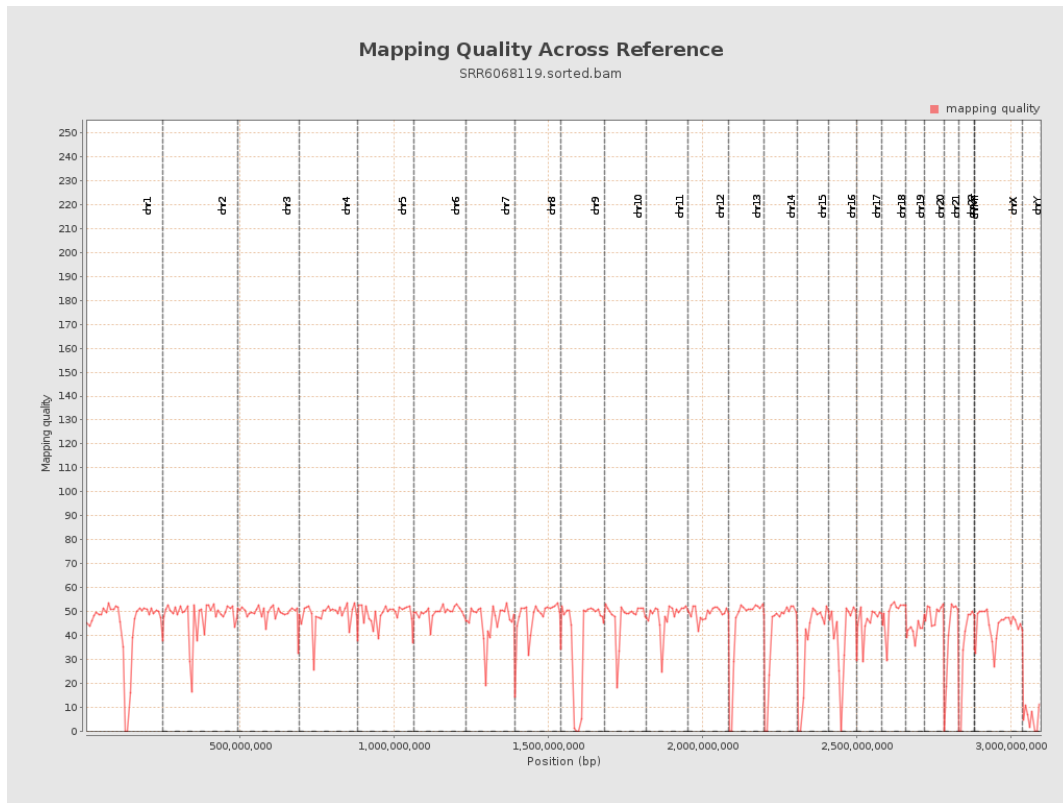
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

