

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:33:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080713.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_SRR3080713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:33:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,858,384
Mapped reads	1,691,830 / 91.04%
Unmapped reads	166,554 / 8.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,902 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	88,505 / 4.76%
Duplication rate	4.51%
Clipped reads	661,224 / 35.58%

2.2. ACGT Content

Number/percentage of A's	32,287,330 / 28.1%
Number/percentage of C's	21,199,776 / 18.45%
Number/percentage of T's	36,626,044 / 31.88%
Number/percentage of G's	24,773,115 / 21.56%
Number/percentage of N's	1,834 / 0%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0371

Standard Deviation	0.3147
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2.4. Mapping Quality

Mean Mapping Quality	46.43
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2.5. Mismatches and indels

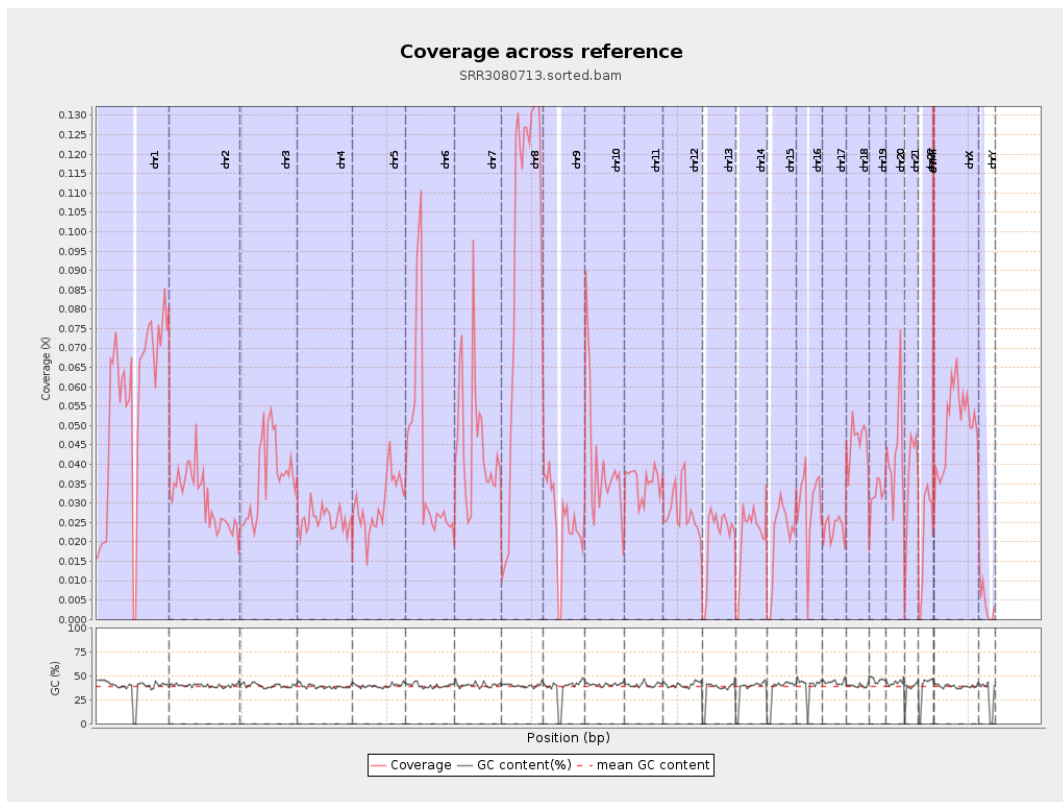
General error rate	0.77%
Mismatches	871,400
Insertions	7,928
Mapped reads with at least one insertion	0.47%
Deletions	23,965
Mapped reads with at least one deletion	1.4%
Homopolymer indels	48.19%

2.6. Chromosome stats

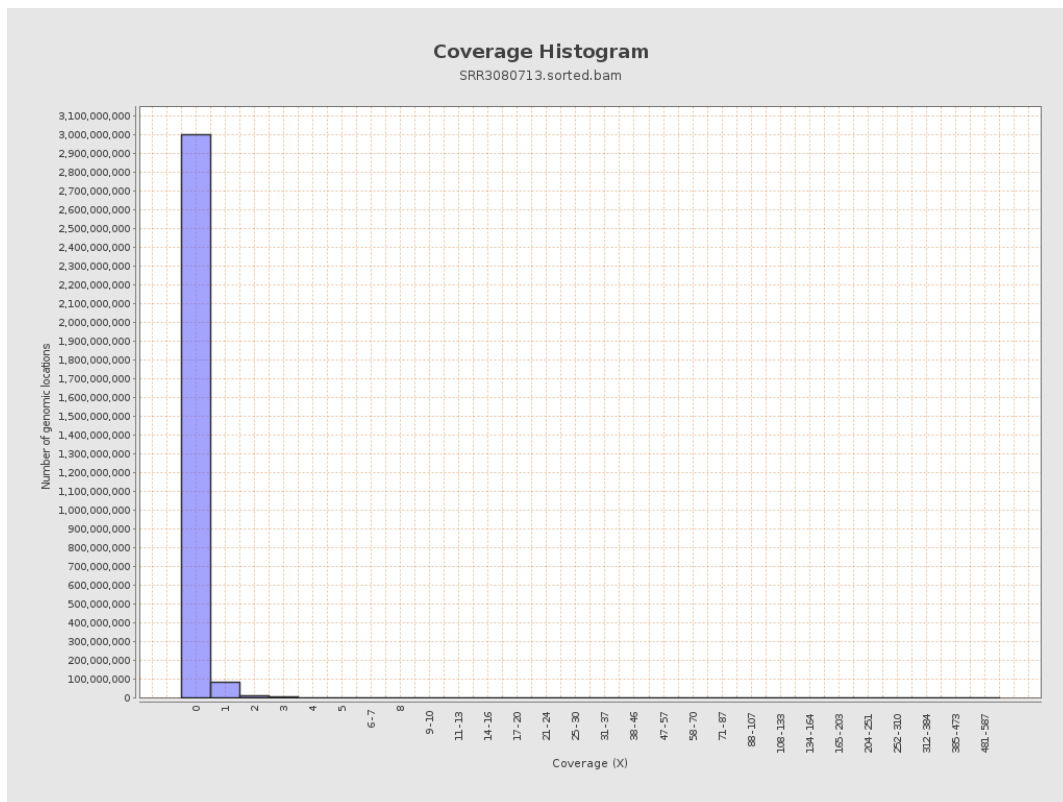
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13764104	0.0552	0.4514
chr2	243199373	7487567	0.0308	0.2947
chr3	198022430	7234735	0.0365	0.2207
chr4	191154276	4901912	0.0256	0.1886
chr5	180915260	5413119	0.0299	0.1991
chr6	171115067	7012764	0.041	0.2836
chr7	159138663	7296136	0.0458	0.7398

chr8	146364022	13878009	0.0948	0.4499
chr9	141213431	3517449	0.0249	0.2101
chr10	135534747	5501296	0.0406	0.2886
chr11	135006516	4754474	0.0352	0.2274
chr12	133851895	3728485	0.0279	0.1937
chr13	115169878	2412732	0.0209	0.1668
chr14	107349540	2246105	0.0209	0.1728
chr15	102531392	2160424	0.0211	0.1666
chr16	90354753	2693872	0.0298	0.2067
chr17	81195210	1870568	0.023	0.1808
chr18	78077248	3598769	0.0461	0.3479
chr19	59128983	1927066	0.0326	0.3124
chr20	63025520	2683408	0.0426	0.2429
chr21	48129895	1730582	0.036	0.225
chr22	51304566	1101281	0.0215	0.168
chrMT	16571	16696	1.0075	1.2543
chrX	155270560	7751945	0.0499	0.2672
chrY	59373566	246927	0.0042	0.0883

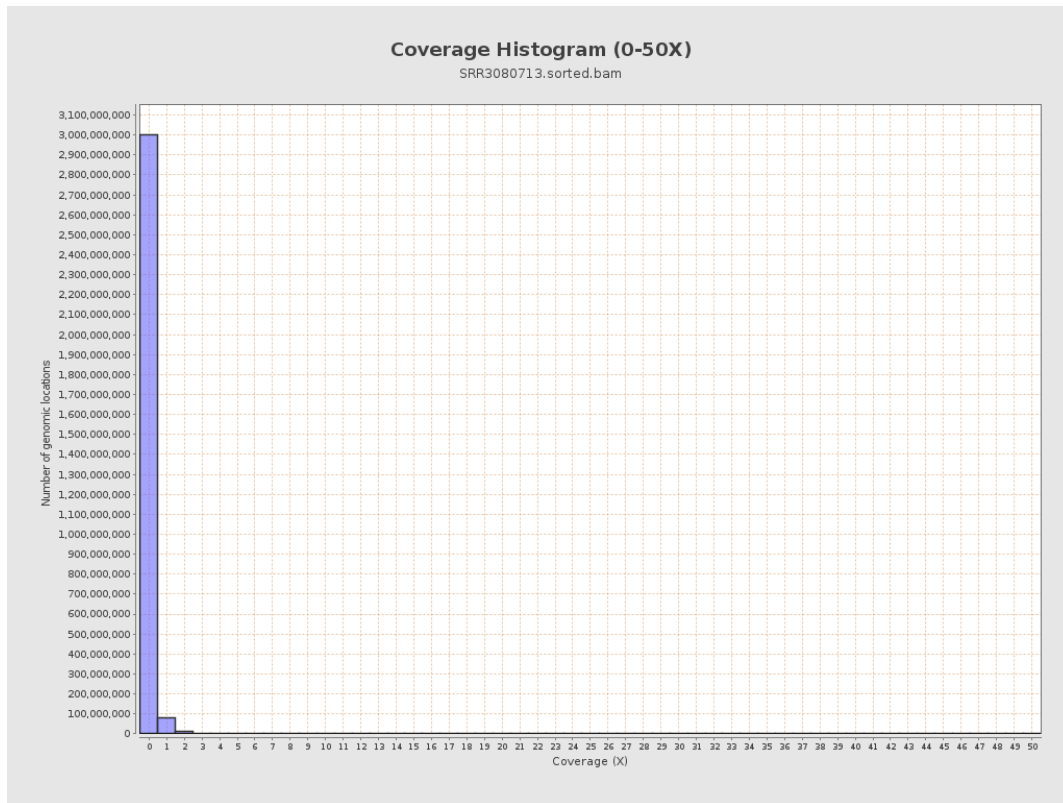
3. Results : Coverage across reference



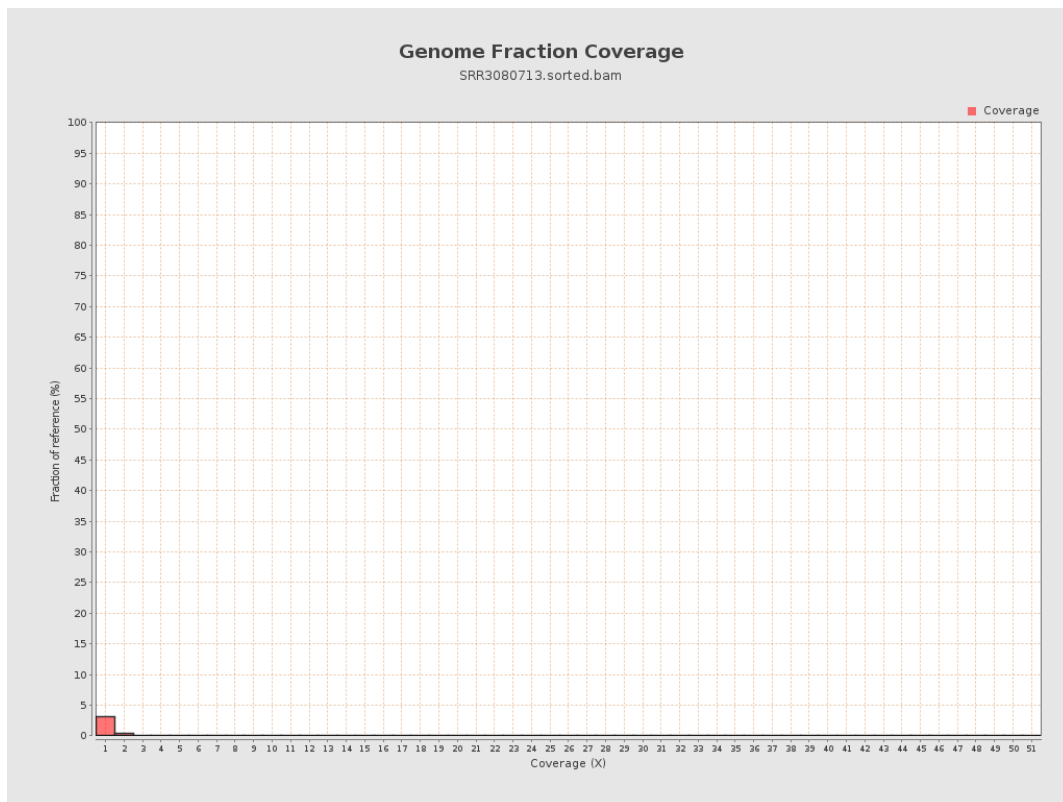
4. Results : Coverage Histogram



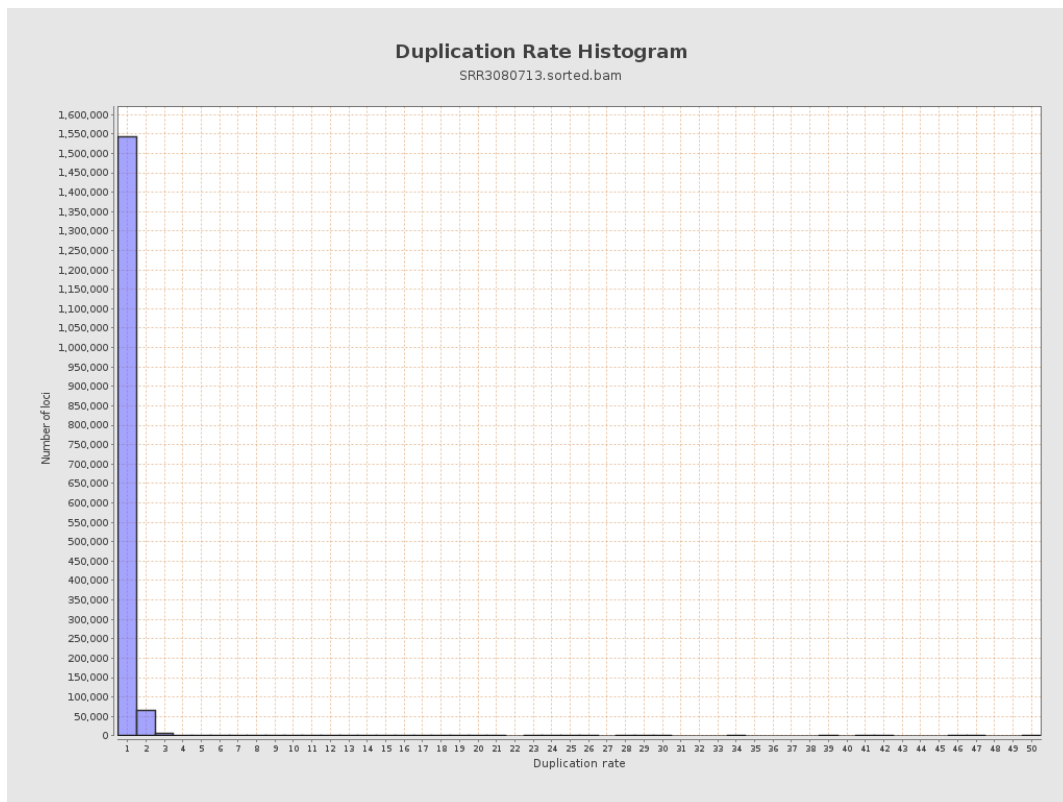
5. Results : Coverage Histogram (0-50X)



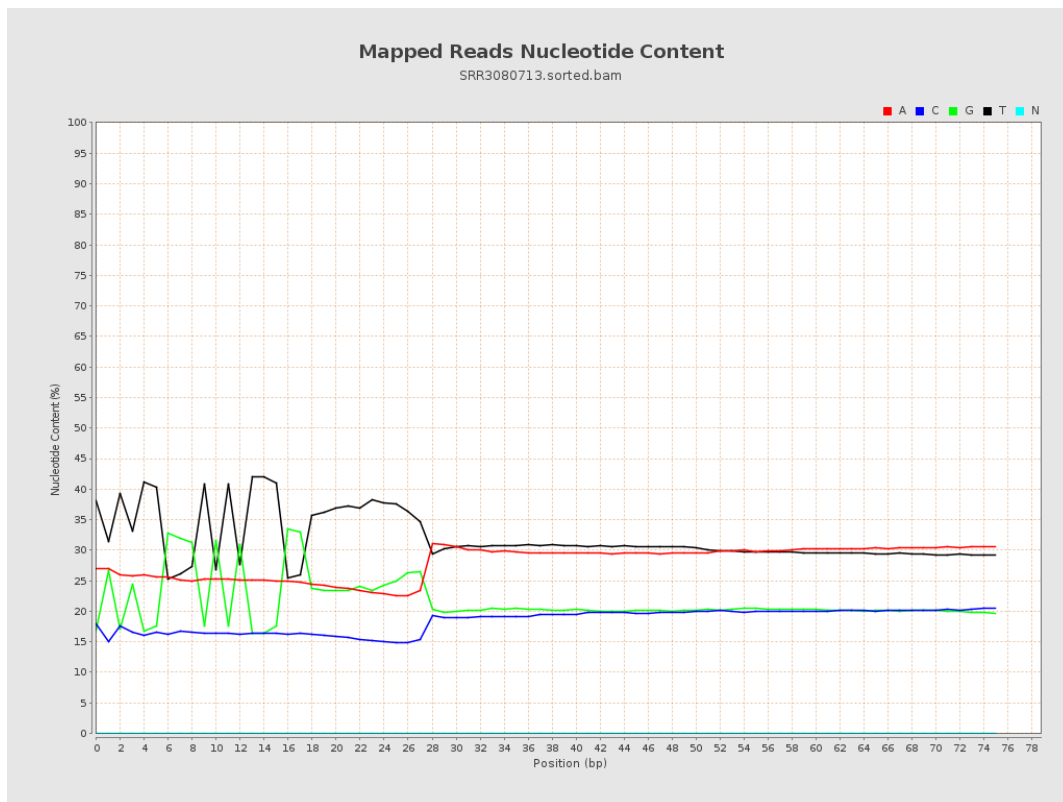
6. Results : Genome Fraction Coverage



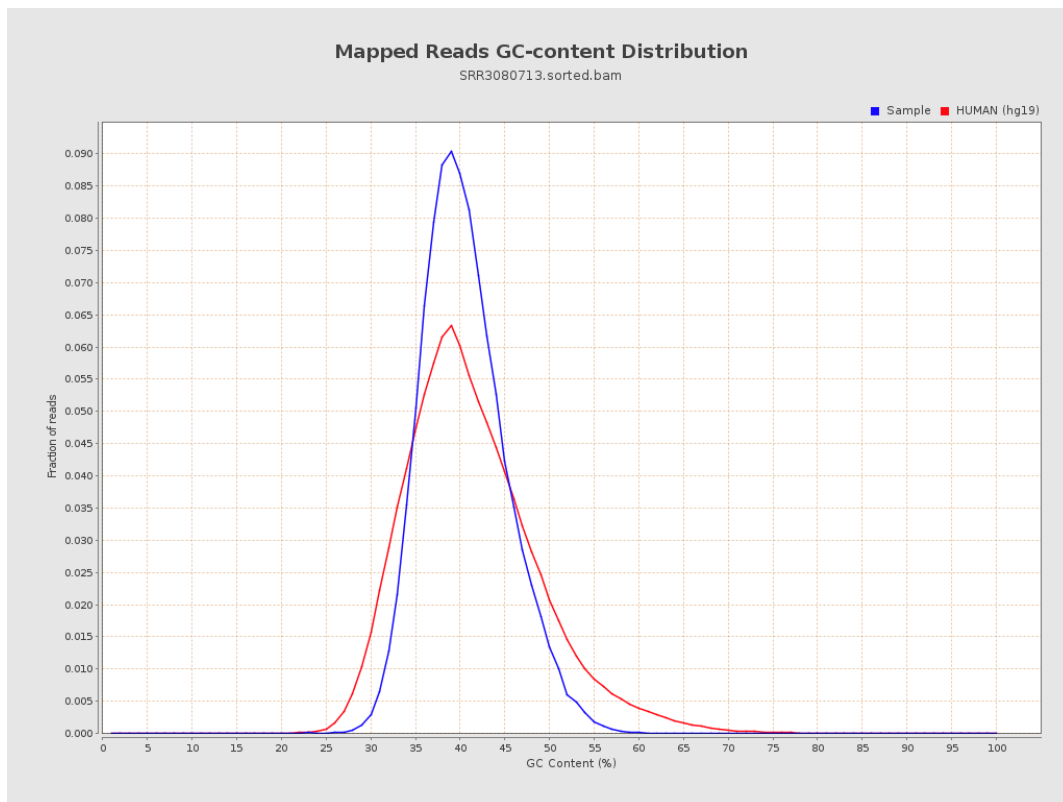
7. Results : Duplication Rate Histogram



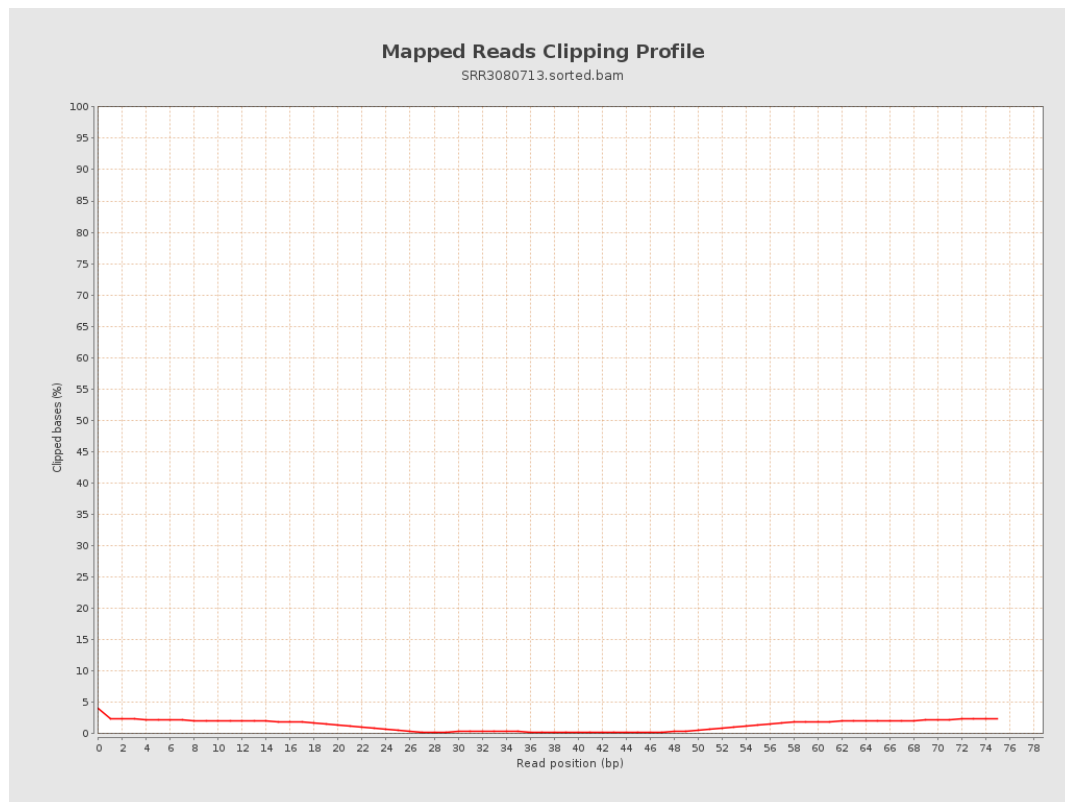
8. Results : Mapped Reads Nucleotide Content



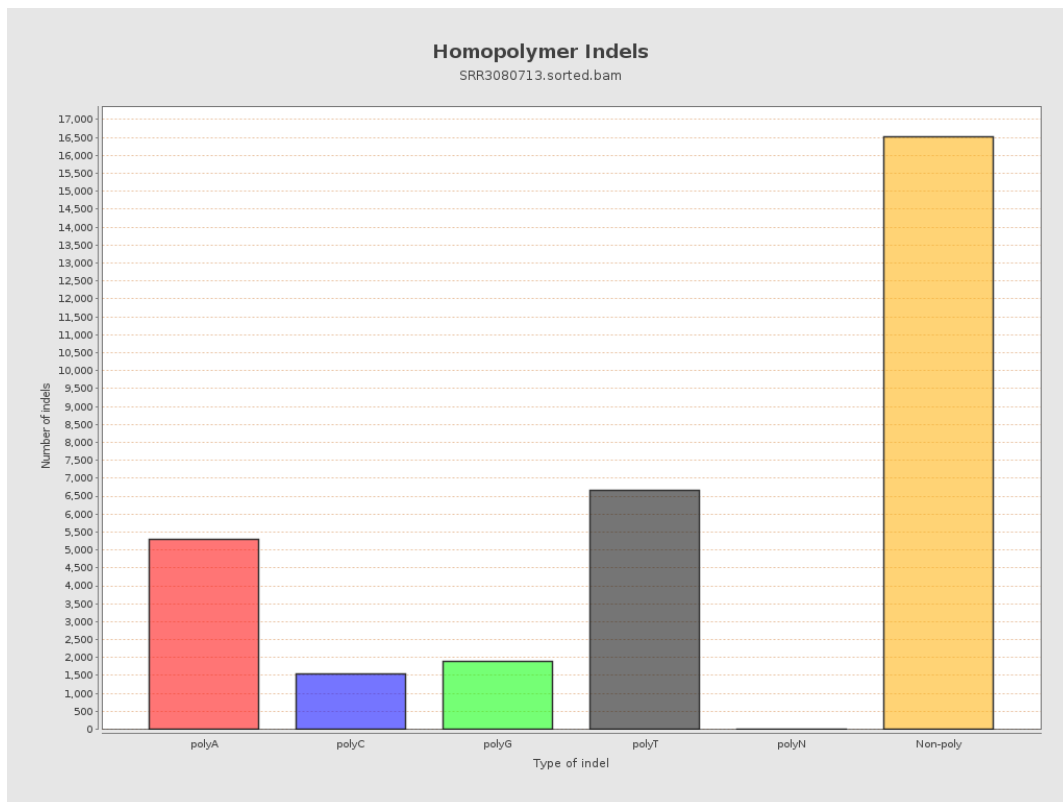
9. Results : Mapped Reads GC-content Distribution



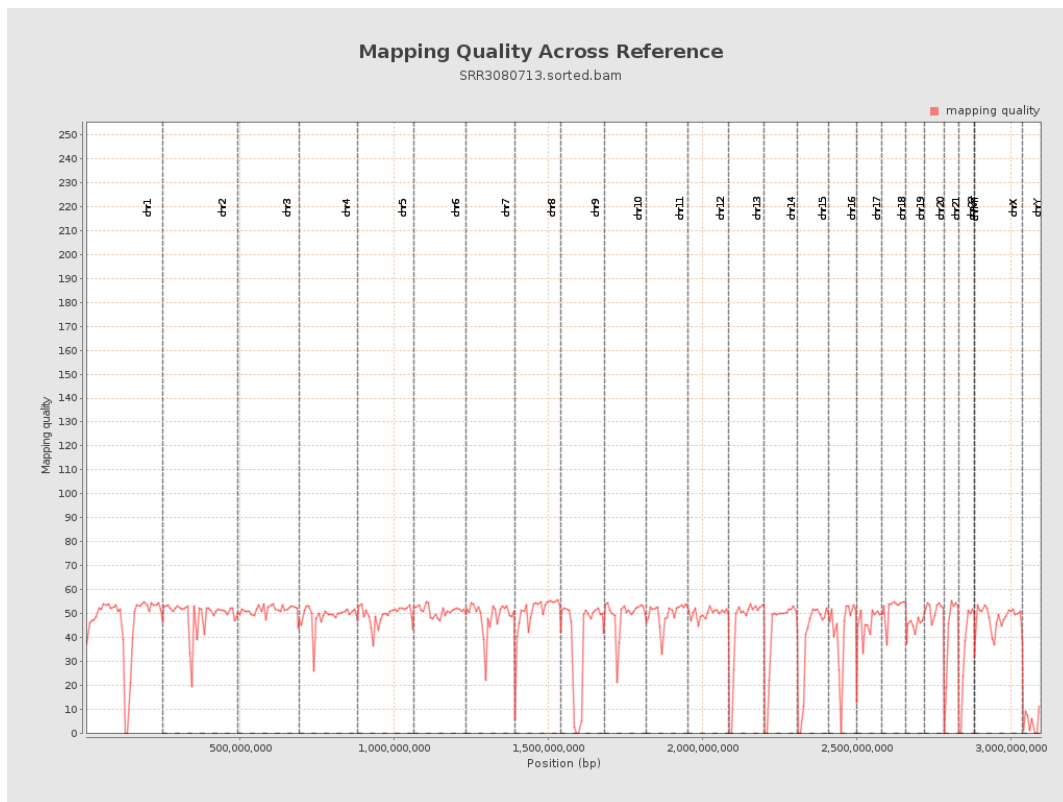
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

