

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:33:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867833.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_SRR9867833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:33:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,378,844
Mapped reads	1,272,075 / 92.26%
Unmapped reads	106,769 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,694 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	48,466 / 3.51%
Duplication rate	2.84%
Clipped reads	1,274,351 / 92.42%

2.2. ACGT Content

Number/percentage of A's	18,805,606 / 25.04%
Number/percentage of C's	14,077,077 / 18.74%
Number/percentage of T's	24,004,320 / 31.96%
Number/percentage of G's	18,212,274 / 24.25%
Number/percentage of N's	9,881 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2438
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2.4. Mapping Quality

Mean Mapping Quality	45.84
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2.5. Mismatches and indels

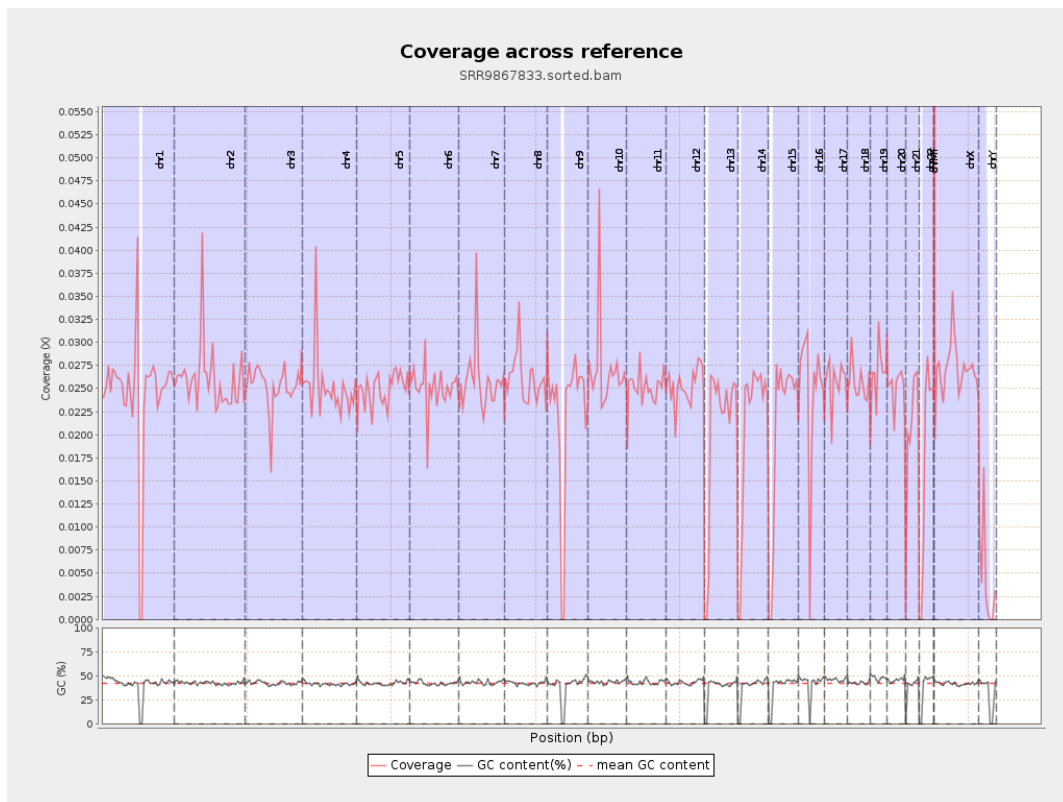
General error rate	0.51%
Mismatches	375,065
Insertions	5,490
Mapped reads with at least one insertion	0.43%
Deletions	14,203
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.08%

2.6. Chromosome stats

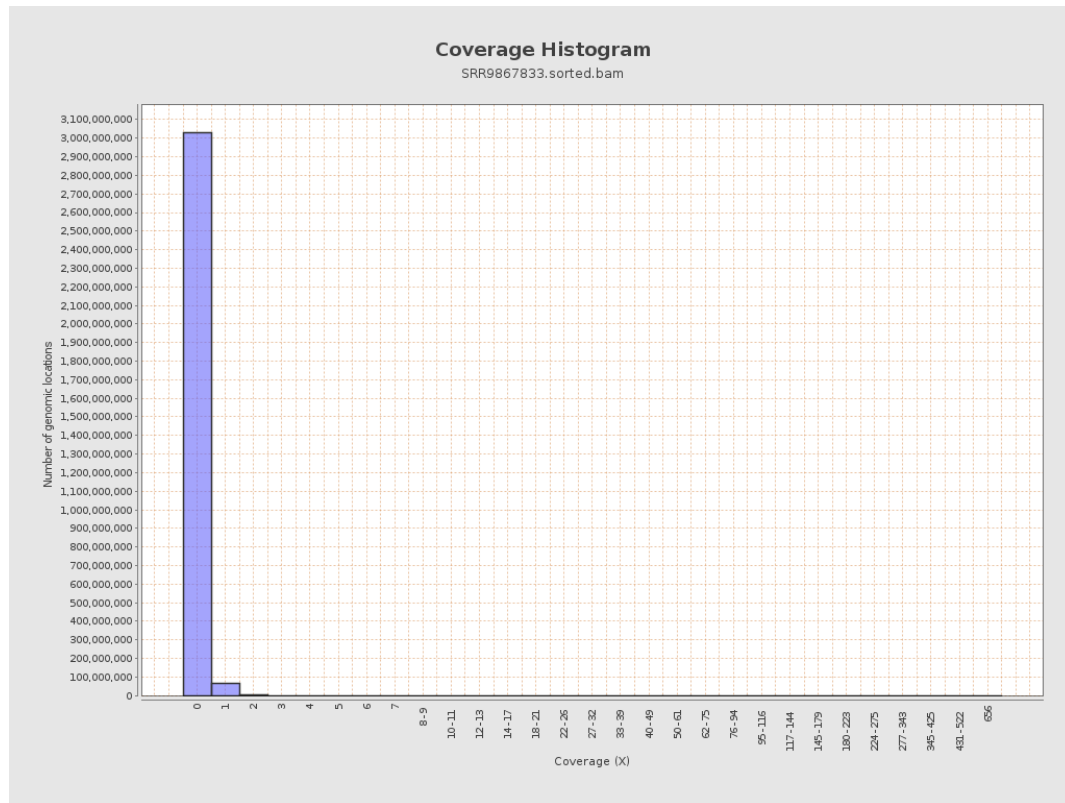
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6066415	0.0243	0.4169
chr2	243199373	6331655	0.026	0.334
chr3	198022430	5001652	0.0253	0.1714
chr4	191154276	4809374	0.0252	0.1908
chr5	180915260	4543347	0.0251	0.1713
chr6	171115067	4299782	0.0251	0.1892
chr7	159138663	4119852	0.0259	0.2773

chr8	146364022	3821991	0.0261	0.2746
chr9	141213431	3132596	0.0222	0.2056
chr10	135534747	3674087	0.0271	0.2539
chr11	135006516	3407754	0.0252	0.2191
chr12	133851895	3385127	0.0253	0.1732
chr13	115169878	2339187	0.0203	0.1537
chr14	107349540	2236558	0.0208	0.158
chr15	102531392	2129851	0.0208	0.156
chr16	90354753	2202721	0.0244	0.1779
chr17	81195210	2088578	0.0257	0.1824
chr18	78077248	2003144	0.0257	0.3551
chr19	59128983	1589513	0.0269	0.308
chr20	63025520	1577975	0.025	0.1723
chr21	48129895	995313	0.0207	0.1743
chr22	51304566	902526	0.0176	0.1436
chrMT	16571	5862	0.3538	0.6721
chrX	155270560	4212868	0.0271	0.1923
chrY	59373566	254215	0.0043	0.1711

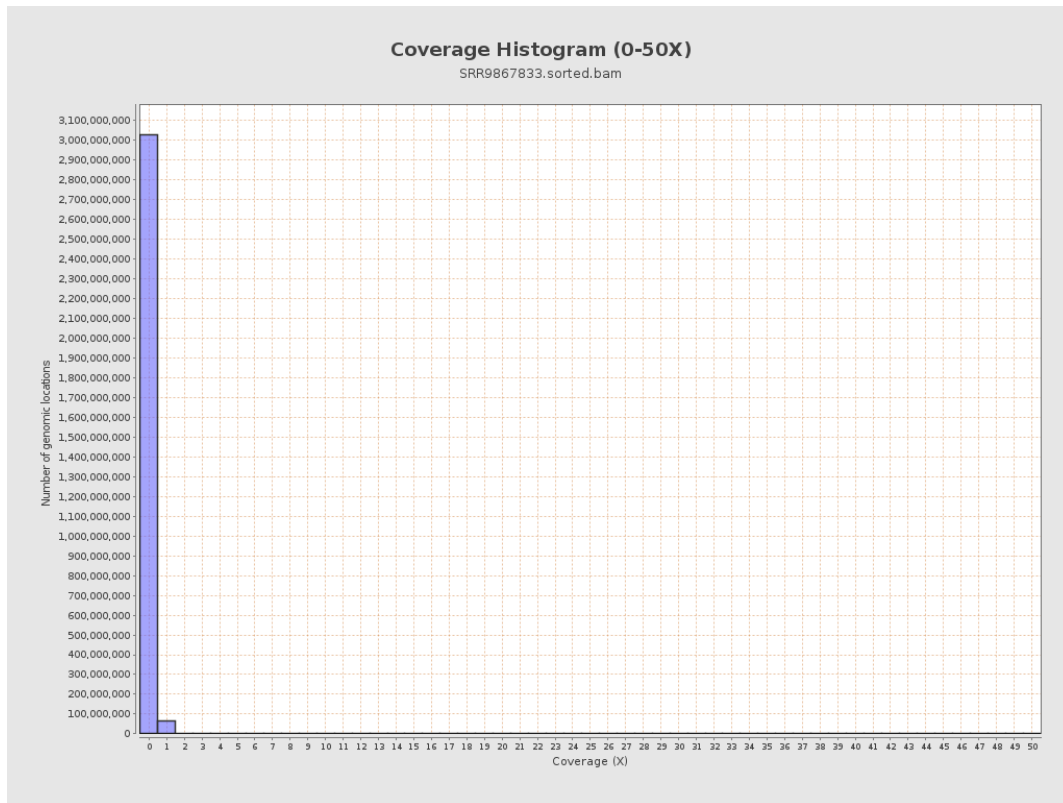
3. Results : Coverage across reference



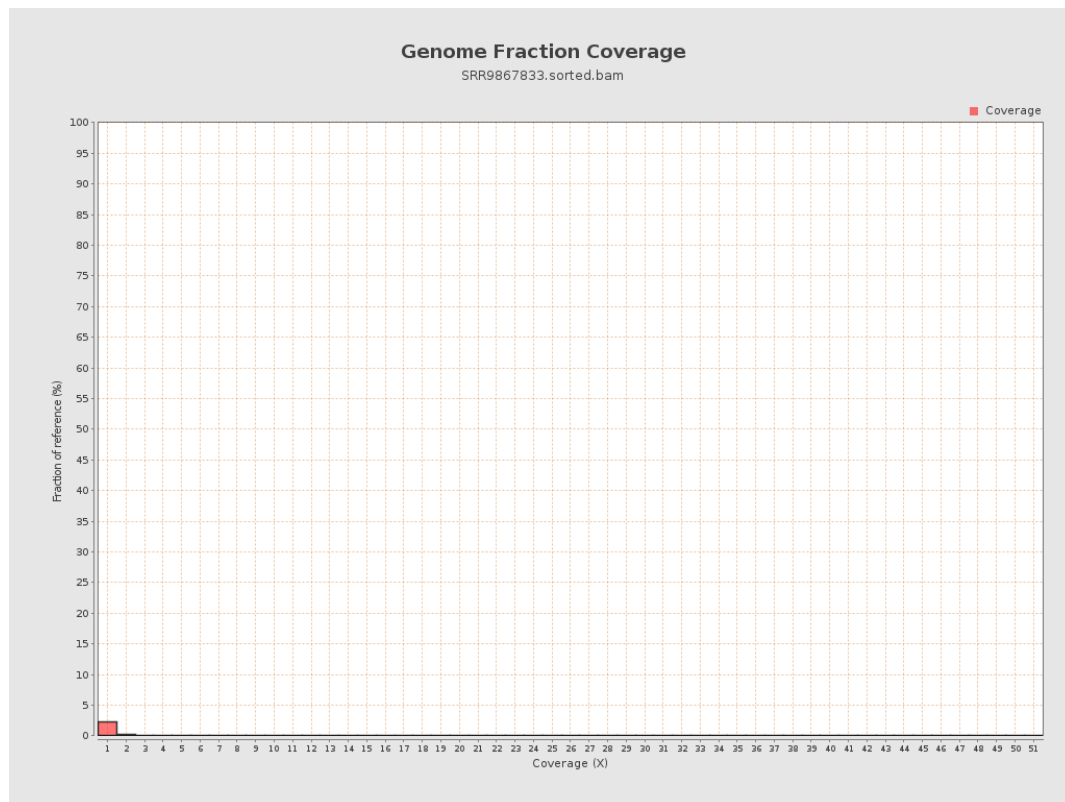
4. Results : Coverage Histogram



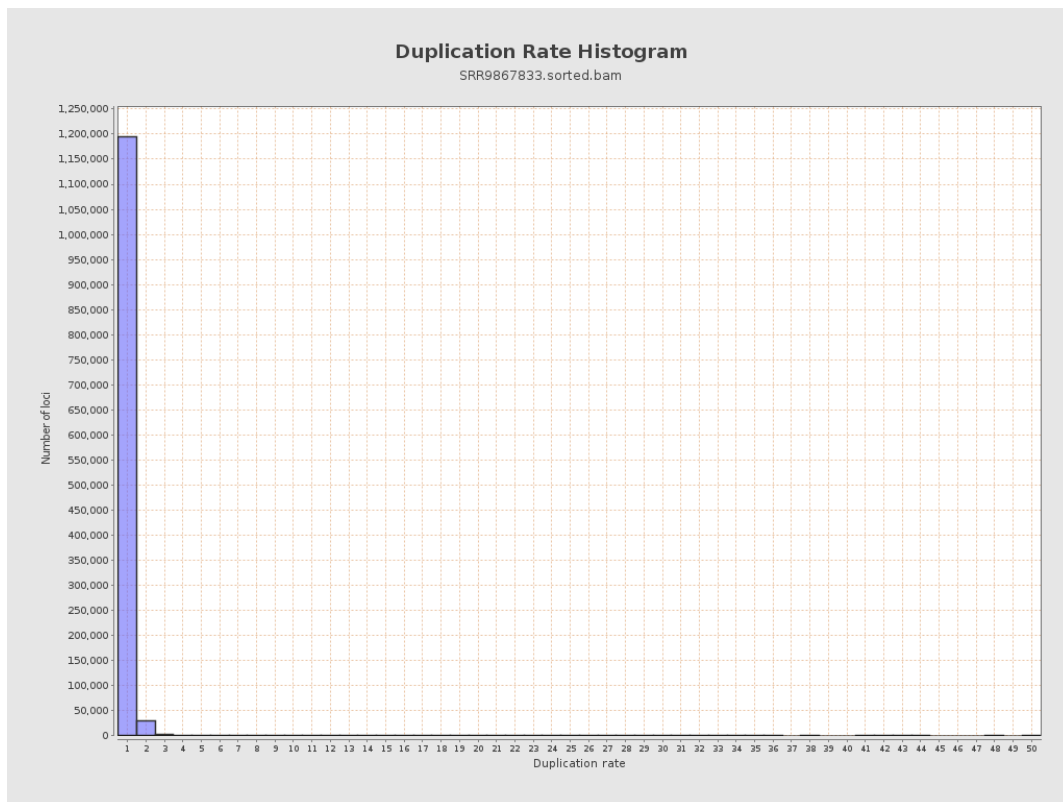
5. Results : Coverage Histogram (0-50X)



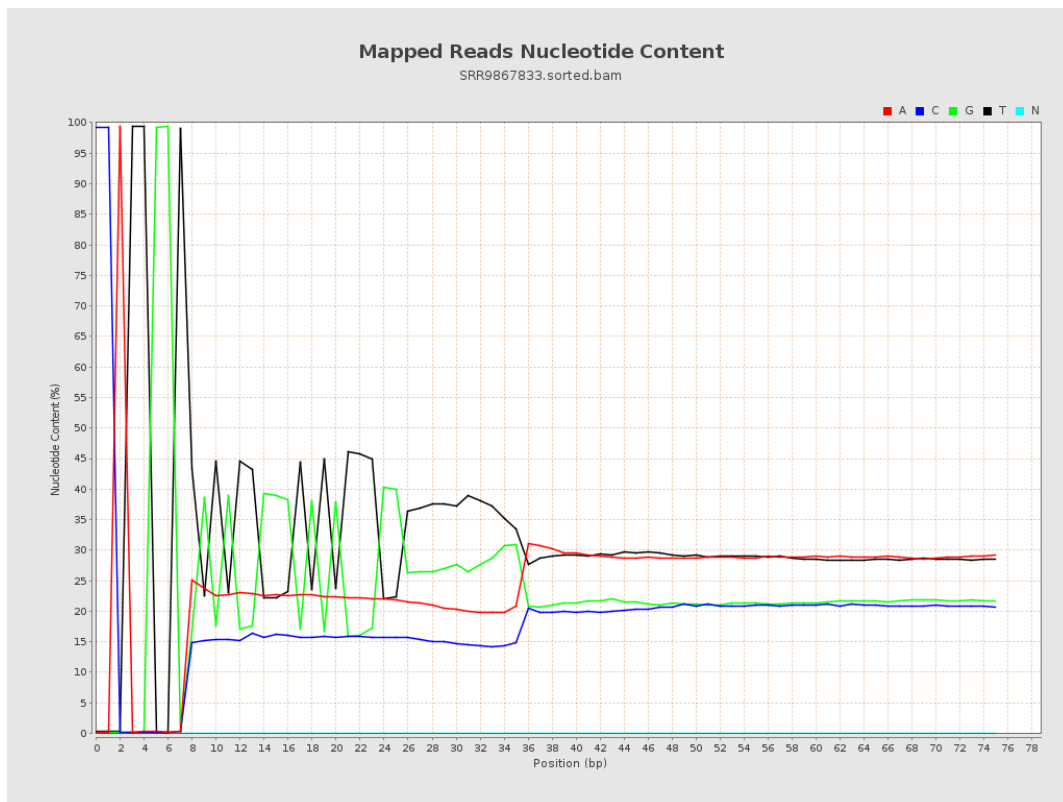
6. Results : Genome Fraction Coverage



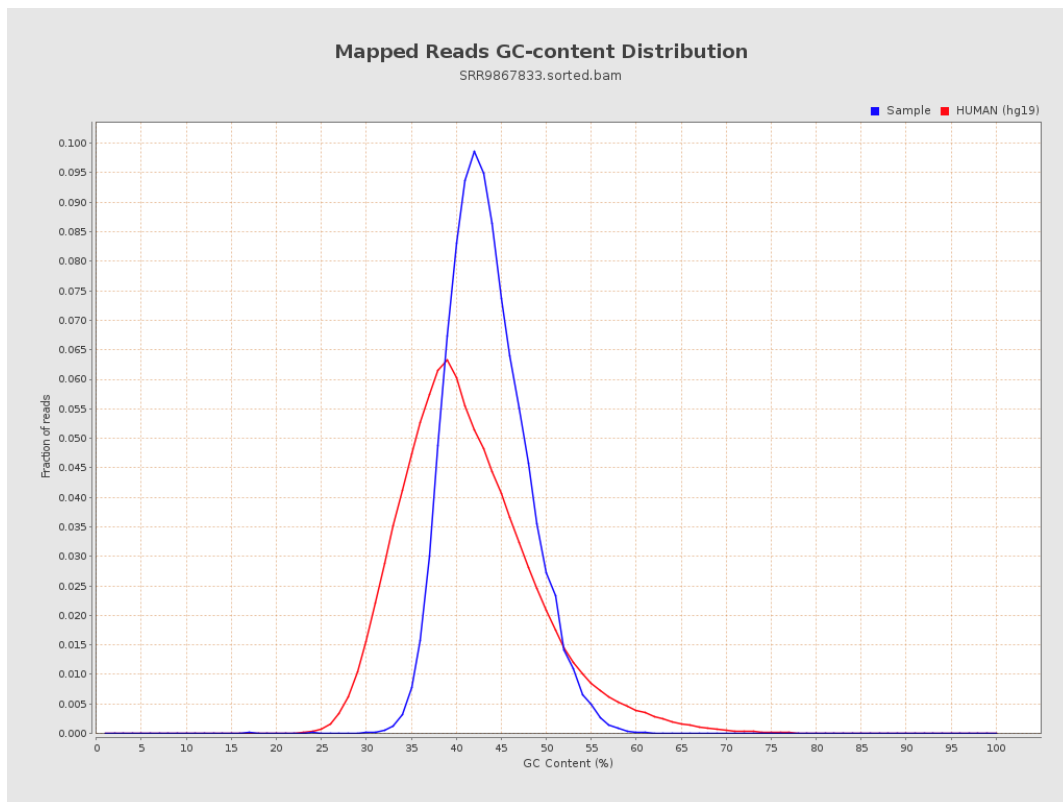
7. Results : Duplication Rate Histogram



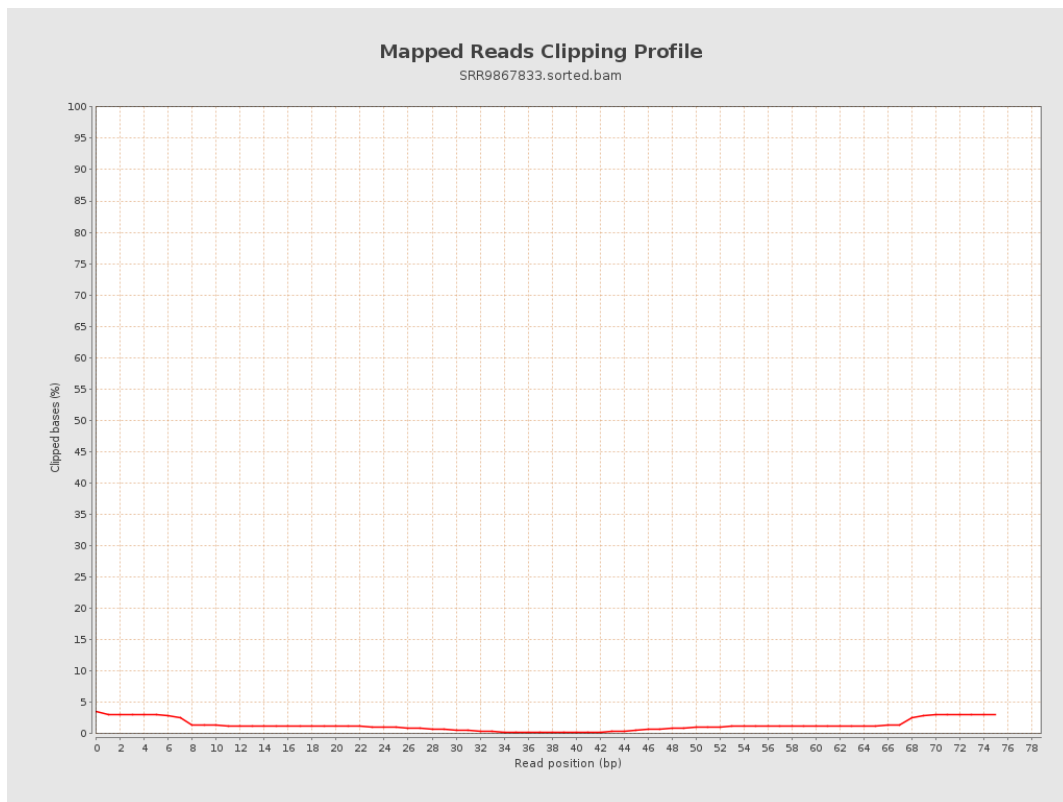
8. Results : Mapped Reads Nucleotide Content



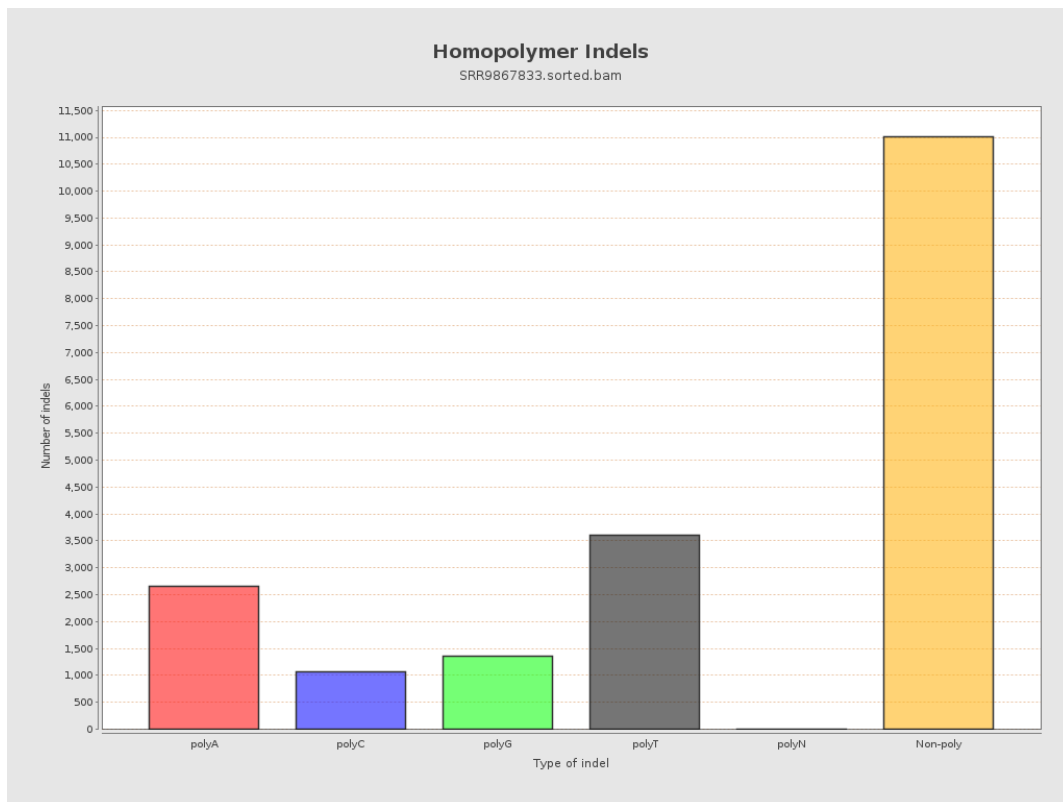
9. Results : Mapped Reads GC-content Distribution



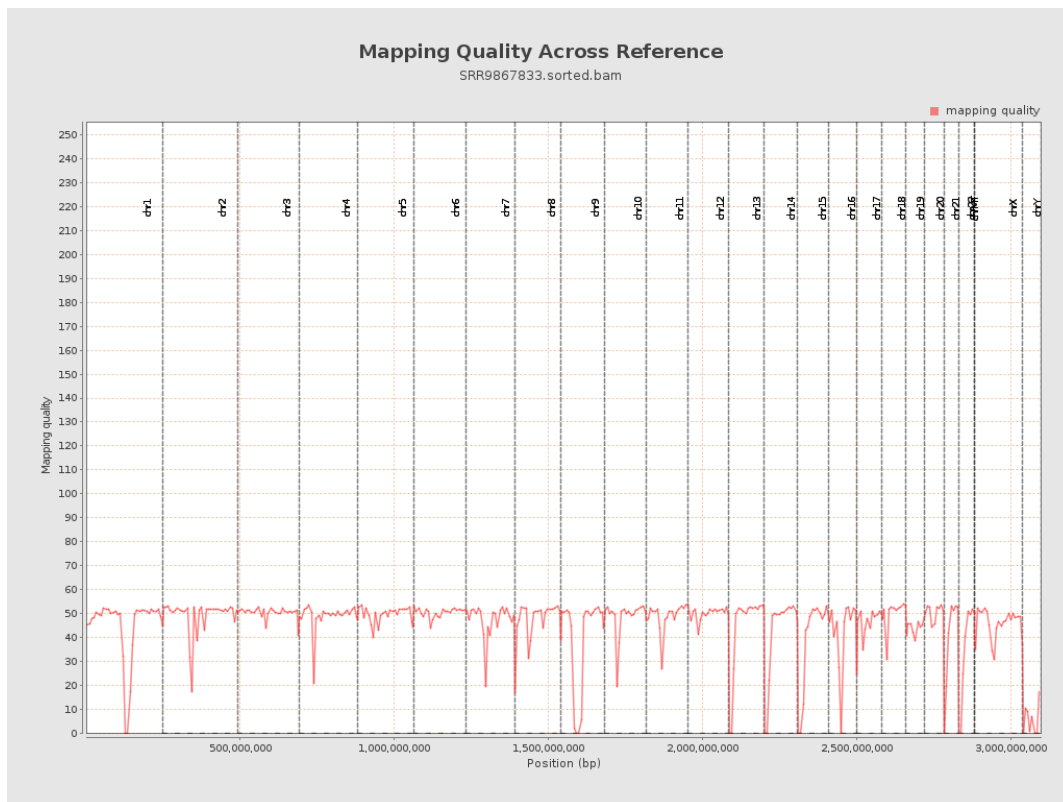
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

