

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:08:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082677.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_SRR3082677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:08:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,387,762
Mapped reads	3,118,008 / 92.04%
Unmapped reads	269,754 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,185 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	137,955 / 4.07%
Duplication rate	3.19%
Clipped reads	1,493,081 / 44.07%

2.2. ACGT Content

Number/percentage of A's	56,648,724 / 27.47%
Number/percentage of C's	35,301,587 / 17.12%
Number/percentage of T's	68,769,220 / 33.35%
Number/percentage of G's	45,432,711 / 22.03%
Number/percentage of N's	55,469 / 0.03%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0666

Standard Deviation	0.5584
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2.4. Mapping Quality

Mean Mapping Quality	45.75
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2.5. Mismatches and indels

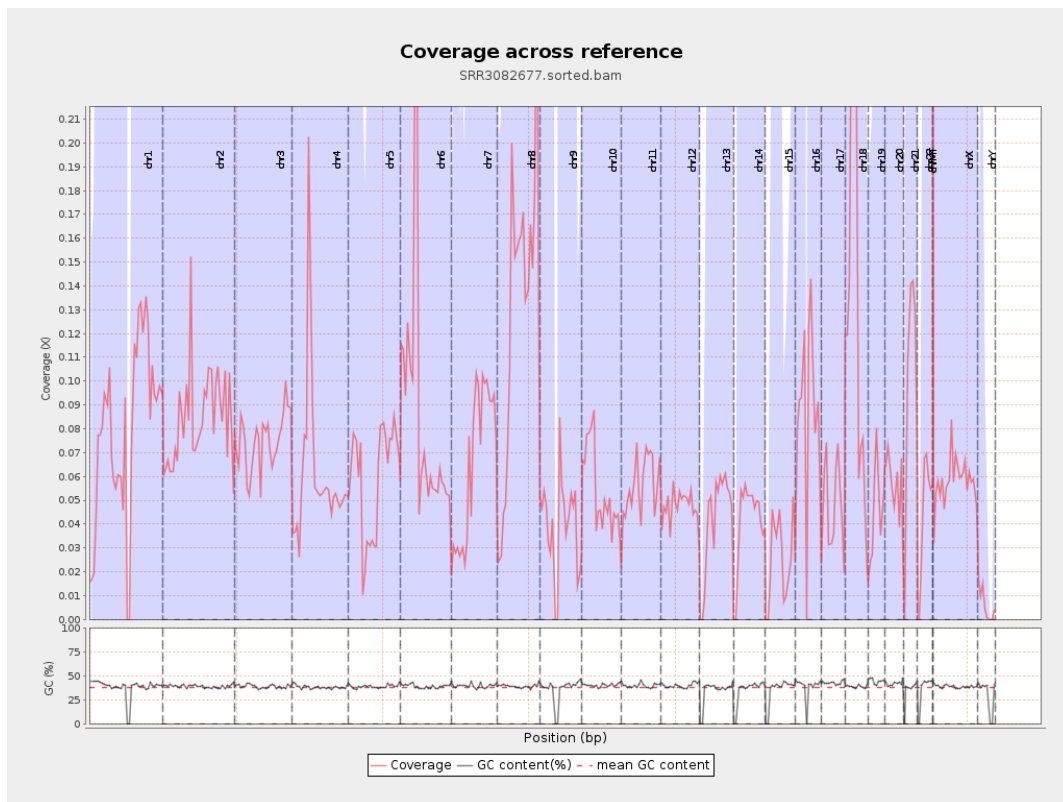
General error rate	0.93%
Mismatches	1,894,642
Insertions	18,632
Mapped reads with at least one insertion	0.59%
Deletions	49,153
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.05%

2.6. Chromosome stats

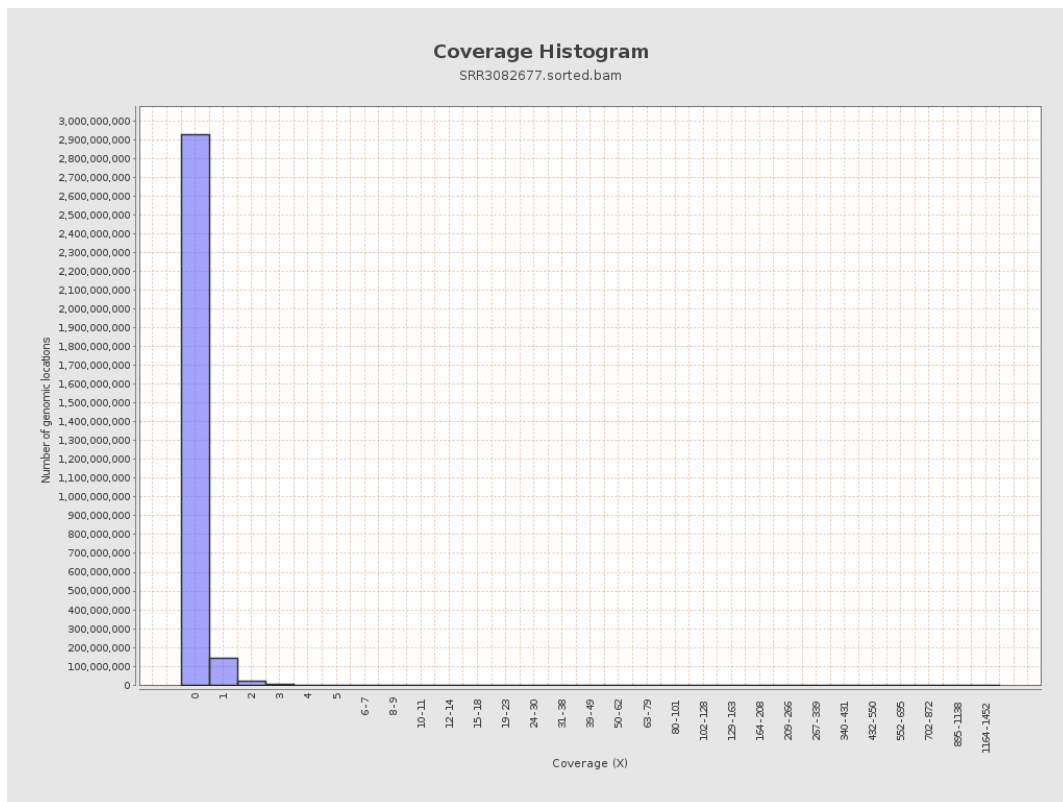
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19938533	0.08	0.7743
chr2	243199373	20581169	0.0846	0.907
chr3	198022430	14825587	0.0749	0.3234
chr4	191154276	11887769	0.0622	0.2995
chr5	180915260	10592903	0.0586	0.2834
chr6	171115067	14778272	0.0864	0.6834
chr7	159138663	10386826	0.0653	0.6007

chr8	146364022	19204535	0.1312	0.7192
chr9	141213431	5574053	0.0395	0.6269
chr10	135534747	7303789	0.0539	0.4294
chr11	135006516	7626603	0.0565	0.4481
chr12	133851895	6360676	0.0475	0.2695
chr13	115169878	4826489	0.0419	0.2336
chr14	107349540	4471430	0.0417	0.3344
chr15	102531392	2629989	0.0257	0.1849
chr16	90354753	7709423	0.0853	0.3834
chr17	81195210	3998634	0.0492	0.3981
chr18	78077248	10905388	0.1397	1.2298
chr19	59128983	2782704	0.0471	0.6521
chr20	63025520	3631007	0.0576	0.3114
chr21	48129895	4683190	0.0973	0.3827
chr22	51304566	2233182	0.0435	0.2404
chrMT	16571	5089	0.3071	0.6139
chrX	155270560	8994801	0.0579	0.3833
chrY	59373566	355280	0.006	0.1233

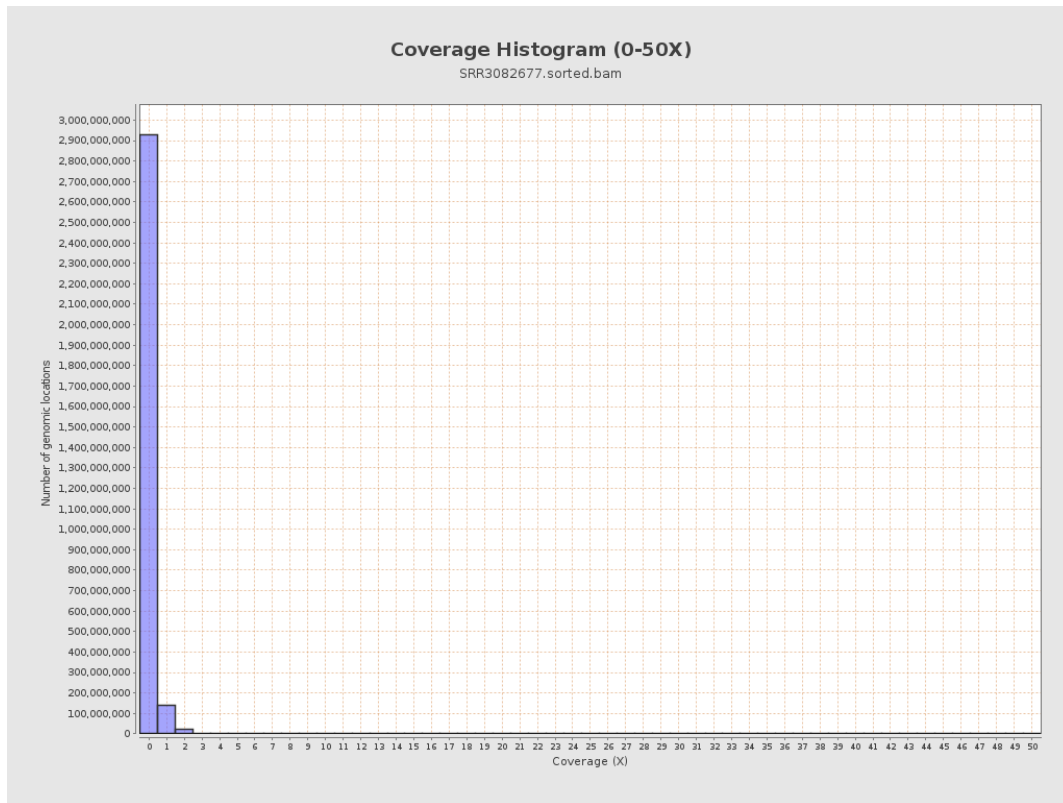
3. Results : Coverage across reference



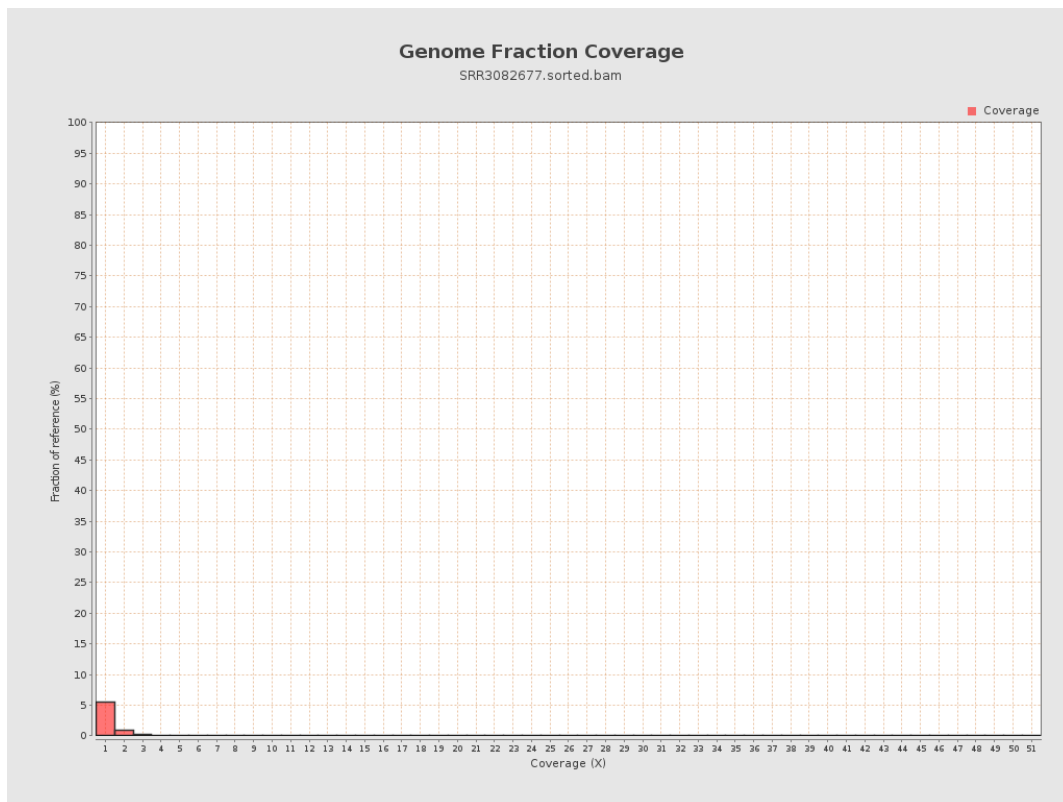
4. Results : Coverage Histogram



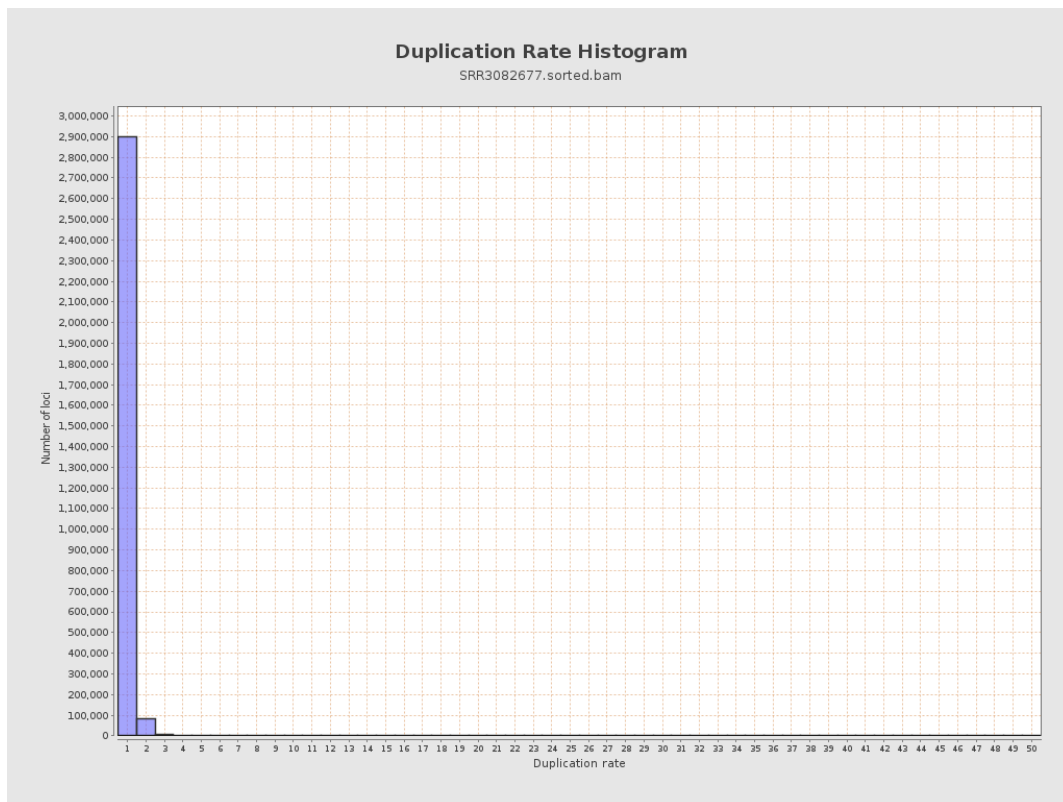
5. Results : Coverage Histogram (0-50X)



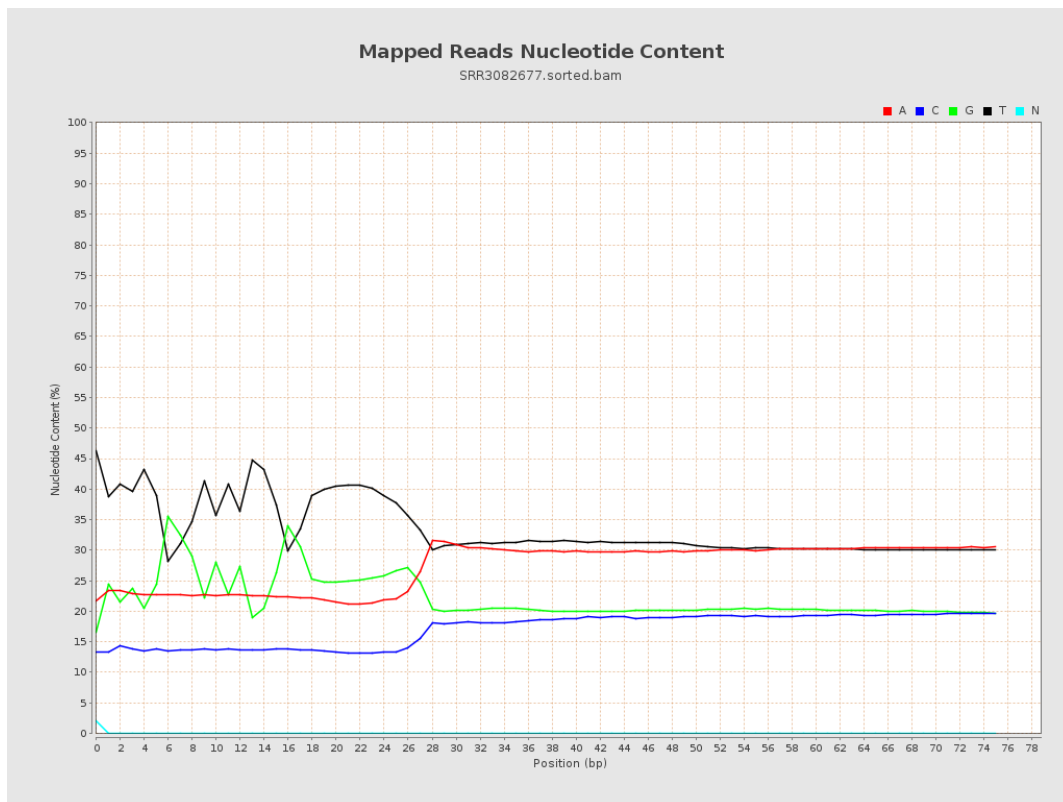
6. Results : Genome Fraction Coverage



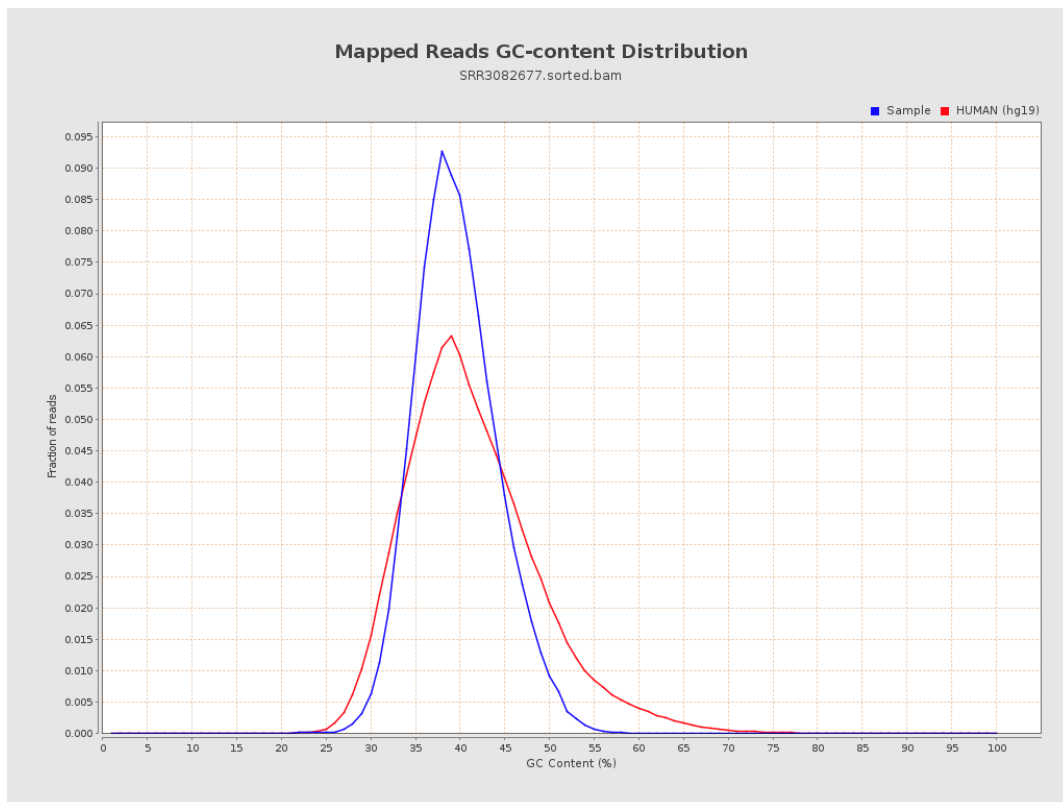
7. Results : Duplication Rate Histogram



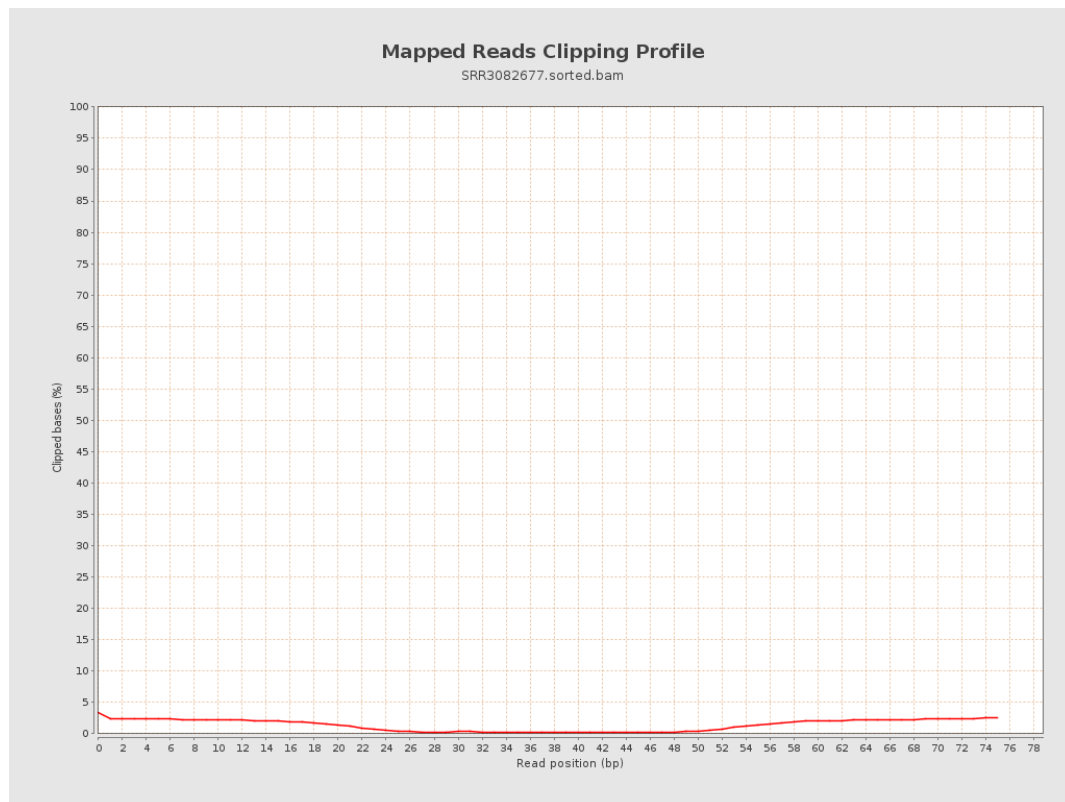
8. Results : Mapped Reads Nucleotide Content



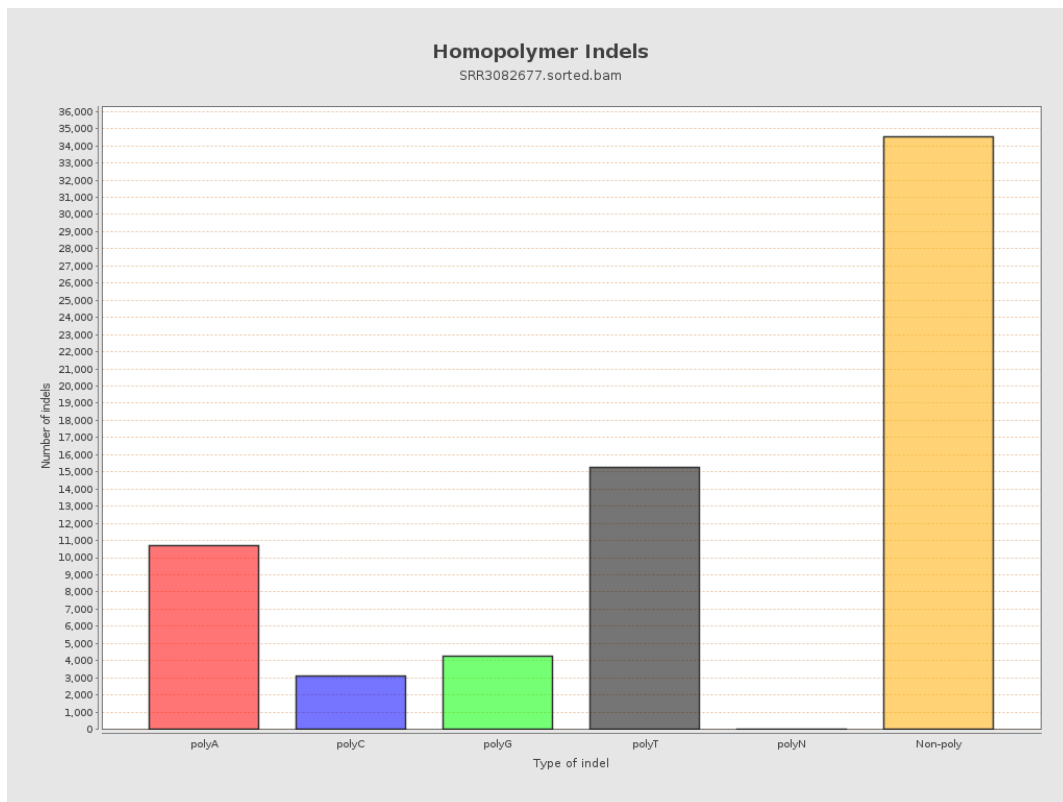
9. Results : Mapped Reads GC-content Distribution



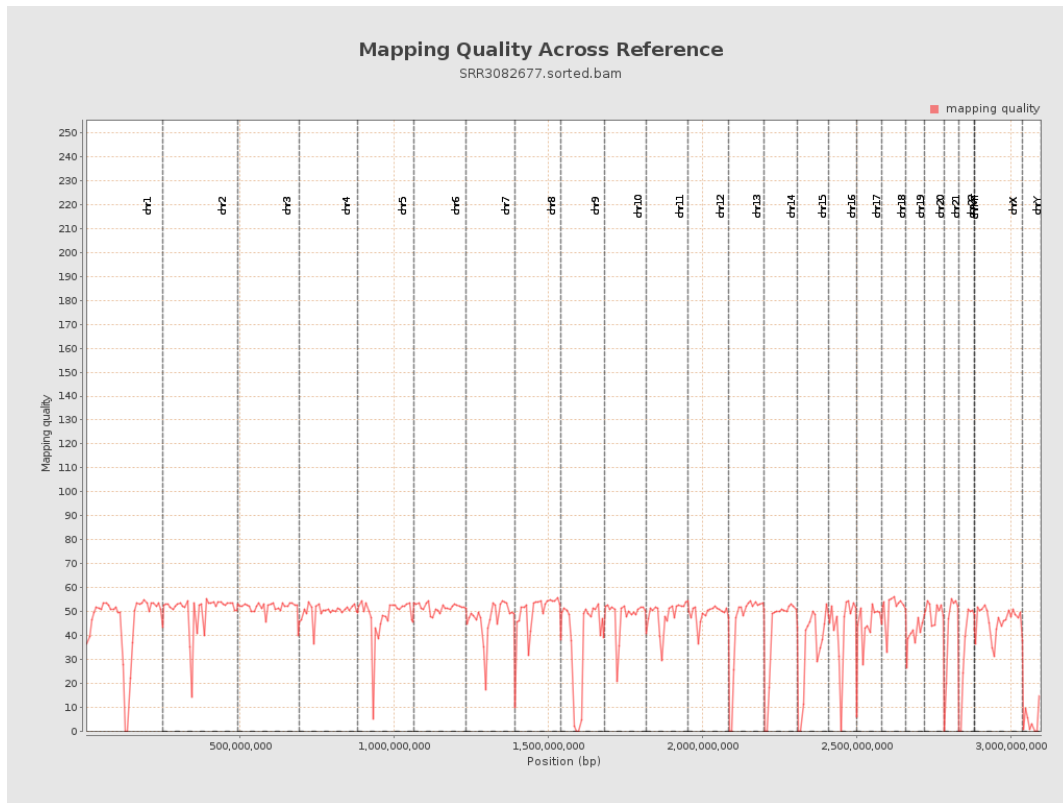
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

