

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:40:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080986.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_SRR3080986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:40:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,578,993
Mapped reads	2,937,856 / 82.09%
Unmapped reads	641,137 / 17.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,510 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	215,813 / 6.03%
Duplication rate	6.12%
Clipped reads	1,200,431 / 33.54%

2.2. ACGT Content

Number/percentage of A's	55,772,385 / 28.27%
Number/percentage of C's	34,275,304 / 17.37%
Number/percentage of T's	65,056,065 / 32.97%
Number/percentage of G's	41,815,218 / 21.19%
Number/percentage of N's	393,962 / 0.2%
GC Percentage	38.56%

2.3. Coverage

Mean	0.0638

Standard Deviation	0.4484
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2.4. Mapping Quality

Mean Mapping Quality	47.55
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2.5. Mismatches and indels

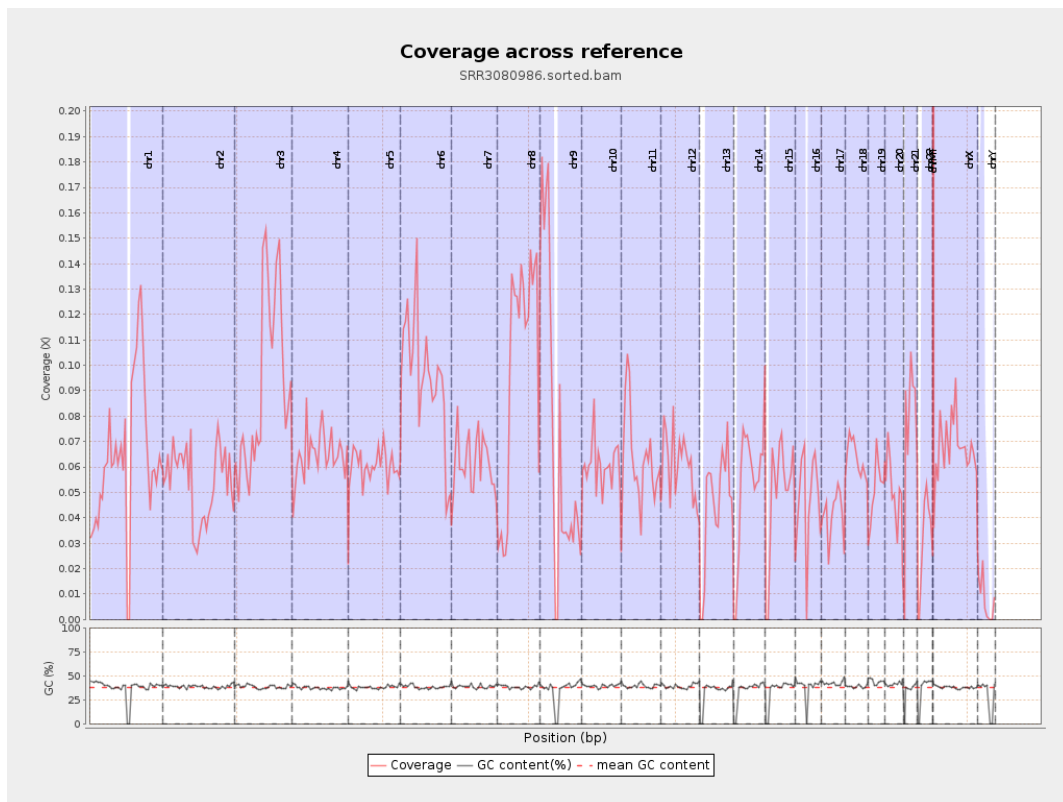
General error rate	0.98%
Mismatches	1,900,402
Insertions	14,701
Mapped reads with at least one insertion	0.5%
Deletions	39,550
Mapped reads with at least one deletion	1.33%
Homopolymer indels	49.58%

2.6. Chromosome stats

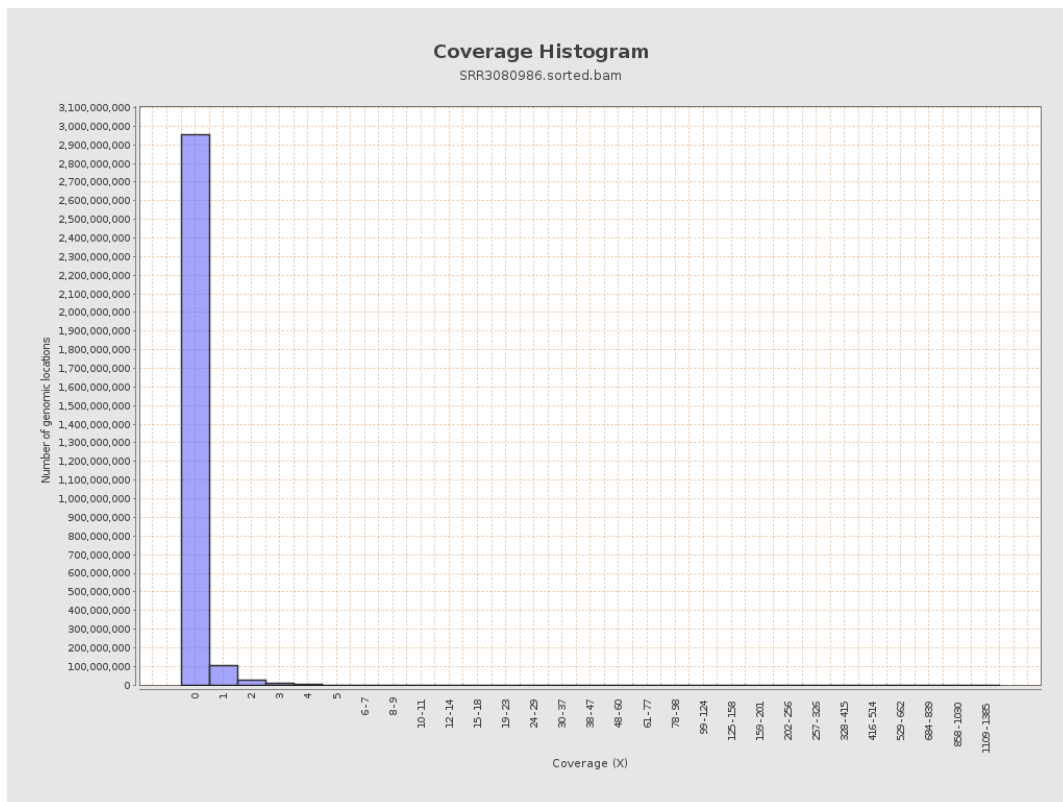
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15933514	0.0639	0.5634
chr2	243199373	13162579	0.0541	0.3908
chr3	198022430	18036379	0.0911	0.4042
chr4	191154276	12435845	0.0651	0.3509
chr5	180915260	10933010	0.0604	0.3264
chr6	171115067	16528270	0.0966	0.513
chr7	159138663	9797402	0.0616	0.3969

chr8	146364022	14479161	0.0989	0.9358
chr9	141213431	10175550	0.0721	0.5079
chr10	135534747	8227095	0.0607	0.3999
chr11	135006516	8582181	0.0636	0.3831
chr12	133851895	8090514	0.0604	0.3321
chr13	115169878	5162464	0.0448	0.2787
chr14	107349540	5676391	0.0529	0.329
chr15	102531392	5058593	0.0493	0.2935
chr16	90354753	4182216	0.0463	0.3092
chr17	81195210	3423096	0.0422	0.2786
chr18	78077248	4963648	0.0636	0.7463
chr19	59128983	3079655	0.0521	0.4514
chr20	63025520	3190436	0.0506	0.3093
chr21	48129895	3742625	0.0778	0.4049
chr22	51304566	1611721	0.0314	0.2304
chrMT	16571	32543	1.9639	1.9958
chrX	155270560	10420509	0.0671	0.3671
chrY	59373566	456973	0.0077	0.1555

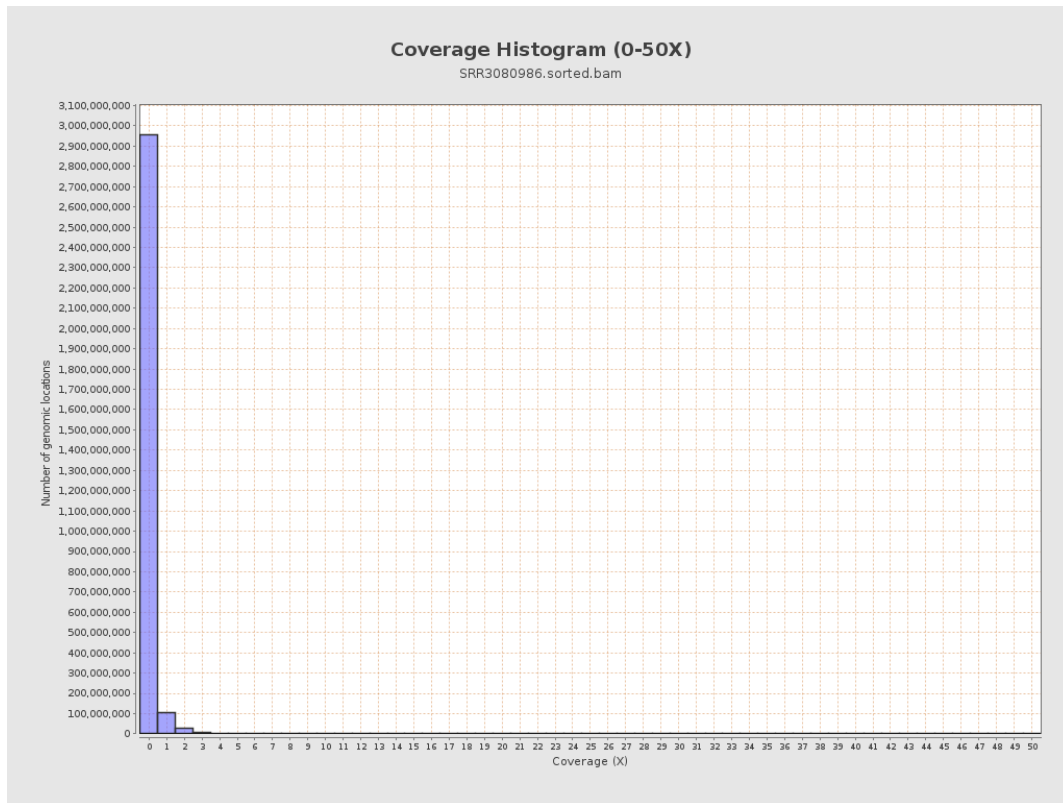
3. Results : Coverage across reference



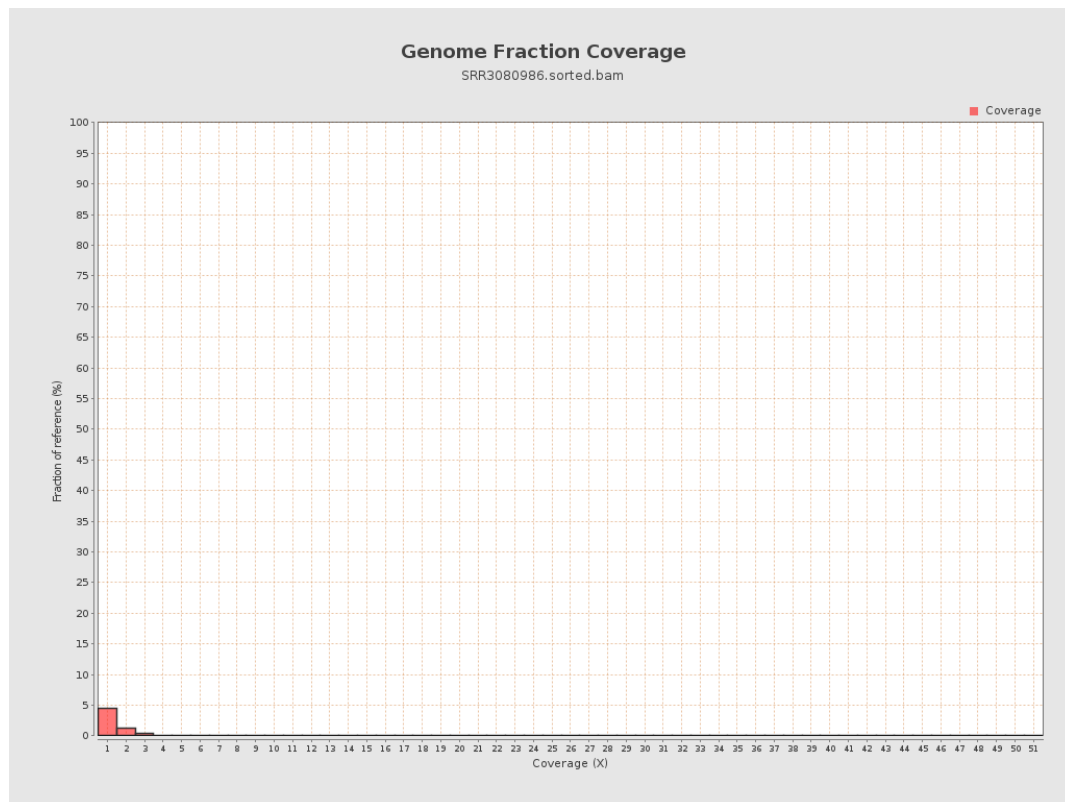
4. Results : Coverage Histogram



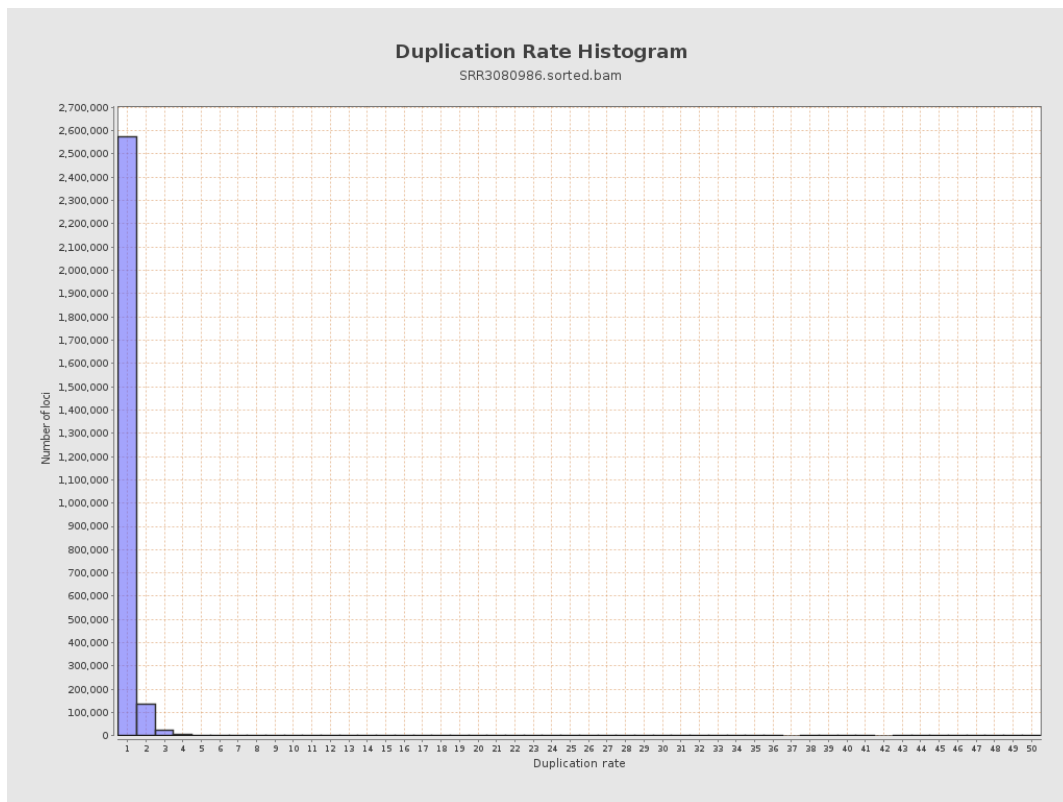
5. Results : Coverage Histogram (0-50X)



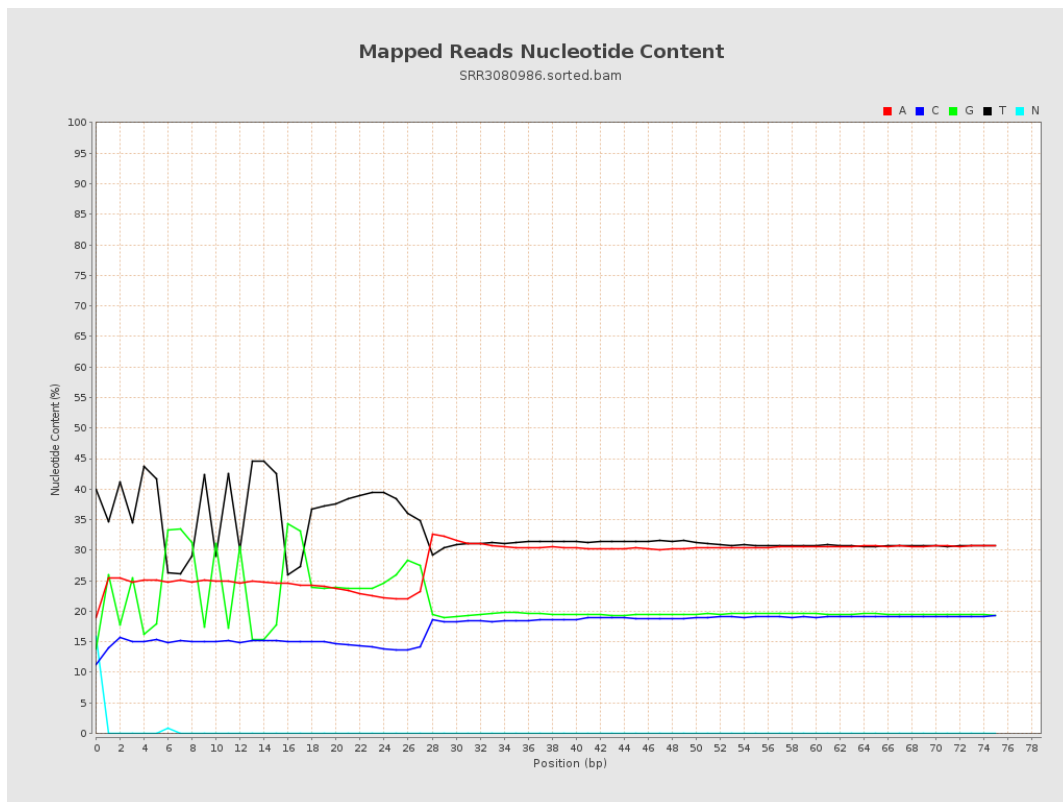
6. Results : Genome Fraction Coverage



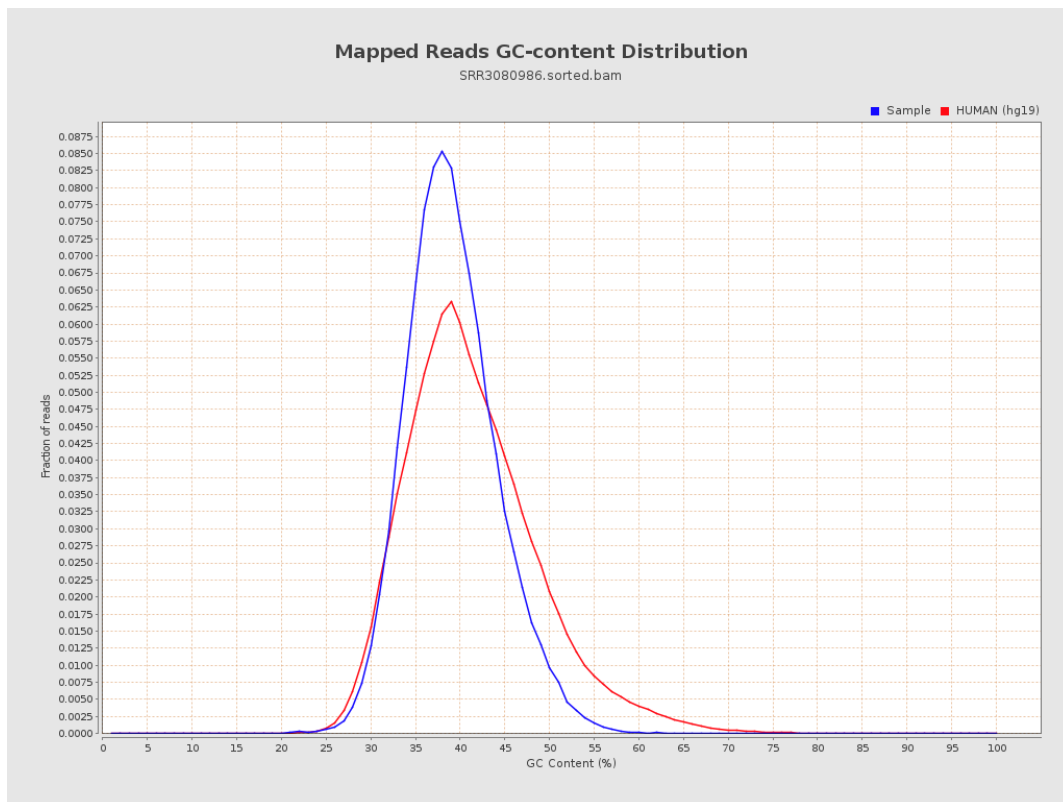
7. Results : Duplication Rate Histogram



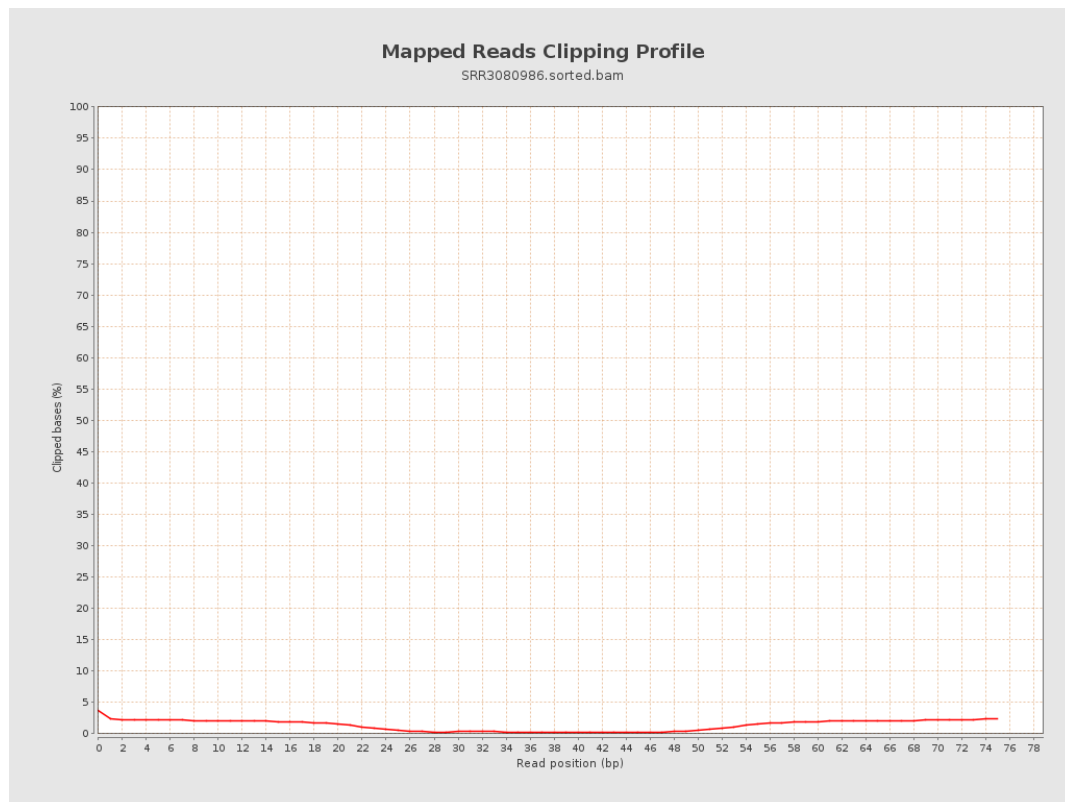
8. Results : Mapped Reads Nucleotide Content



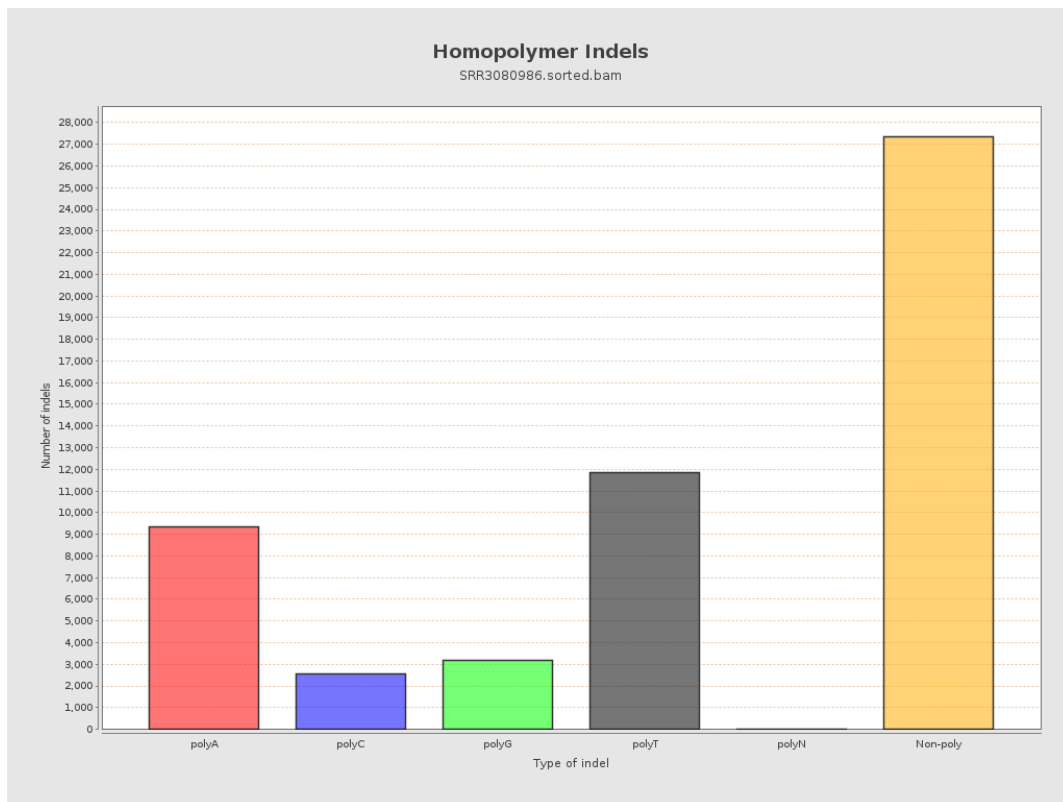
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

