

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:13:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080902.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_SRR3080902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080902.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:13:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,079,673
Mapped reads	3,710,284 / 90.95%
Unmapped reads	369,389 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,822 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	167,498 / 4.11%
Duplication rate	3.6%
Clipped reads	1,345,965 / 32.99%

2.2. ACGT Content

Number/percentage of A's	73,339,907 / 28.78%
Number/percentage of C's	45,311,001 / 17.78%
Number/percentage of T's	81,285,032 / 31.89%
Number/percentage of G's	53,721,250 / 21.08%
Number/percentage of N's	1,216,401 / 0.48%
GC Percentage	38.86%

2.3. Coverage

Mean	0.0824

Standard Deviation	0.5322
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2.4. Mapping Quality

Mean Mapping Quality	47.8
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2.5. Mismatches and indels

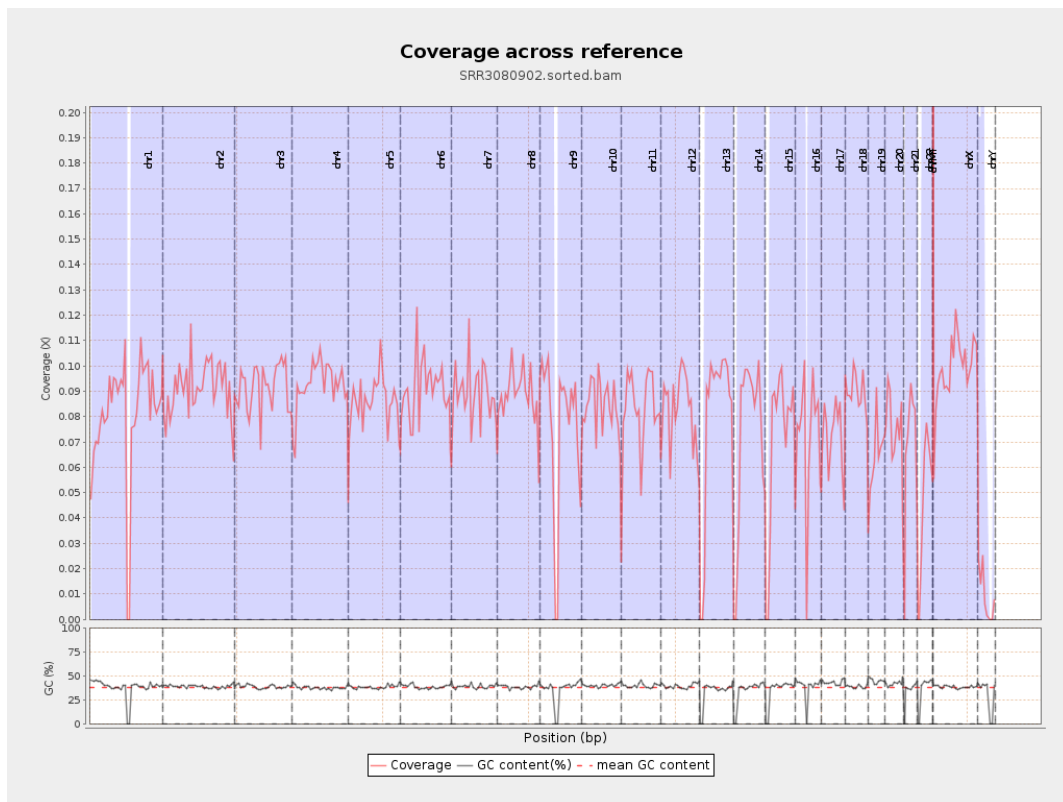
General error rate	1.14%
Mismatches	2,865,436
Insertions	19,215
Mapped reads with at least one insertion	0.51%
Deletions	57,653
Mapped reads with at least one deletion	1.54%
Homopolymer indels	50.27%

2.6. Chromosome stats

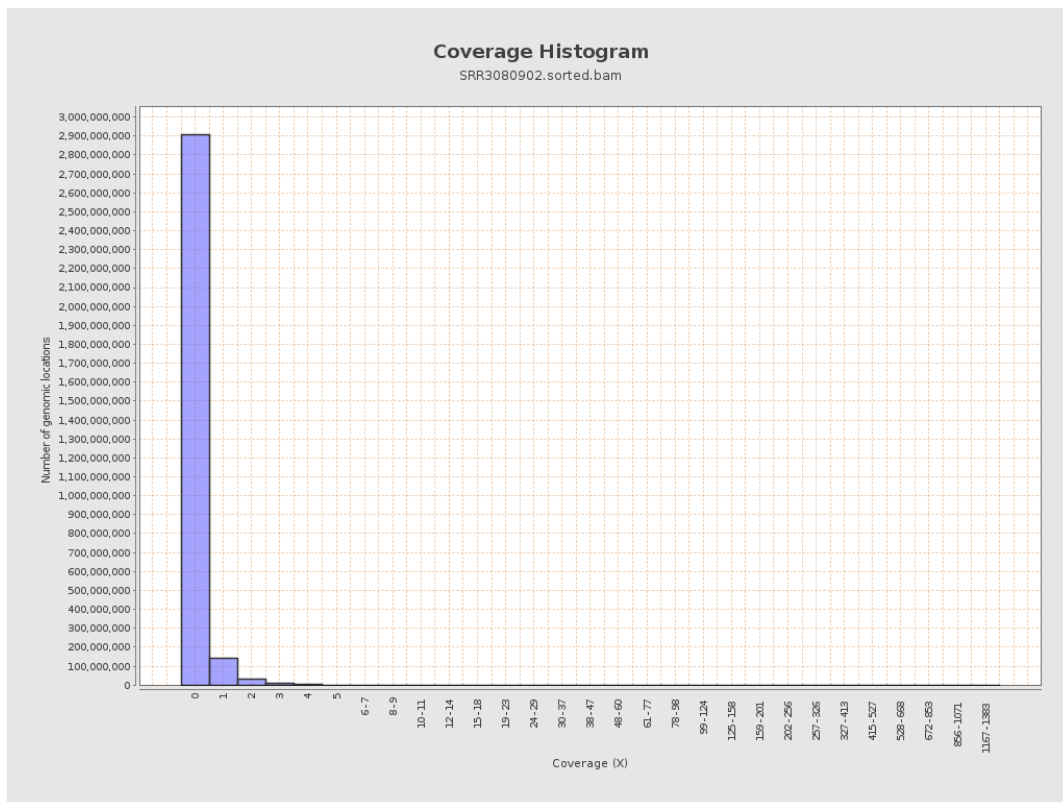
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20157797	0.0809	0.7871
chr2	243199373	22149225	0.0911	0.533
chr3	198022430	18150095	0.0917	0.3896
chr4	191154276	17748553	0.0928	0.4026
chr5	180915260	15494739	0.0856	0.378
chr6	171115067	15590205	0.0911	0.4705
chr7	159138663	14165543	0.089	0.7553

chr8	146364022	12941955	0.0884	0.9272
chr9	141213431	10800791	0.0765	0.5057
chr10	135534747	11428756	0.0843	0.462
chr11	135006516	11291440	0.0836	0.4826
chr12	133851895	11106288	0.083	0.3764
chr13	115169878	9080577	0.0788	0.3617
chr14	107349540	7968194	0.0742	0.3796
chr15	102531392	7184583	0.0701	0.3401
chr16	90354753	6362622	0.0704	0.3674
chr17	81195210	5953487	0.0733	0.4098
chr18	78077248	7035236	0.0901	0.884
chr19	59128983	3843259	0.065	0.5528
chr20	63025520	4832567	0.0767	0.368
chr21	48129895	3283150	0.0682	0.3623
chr22	51304566	2433349	0.0474	0.2793
chrMT	16571	11832	0.714	1.1002
chrX	155270560	15408392	0.0992	0.4263
chrY	59373566	545057	0.0092	0.1612

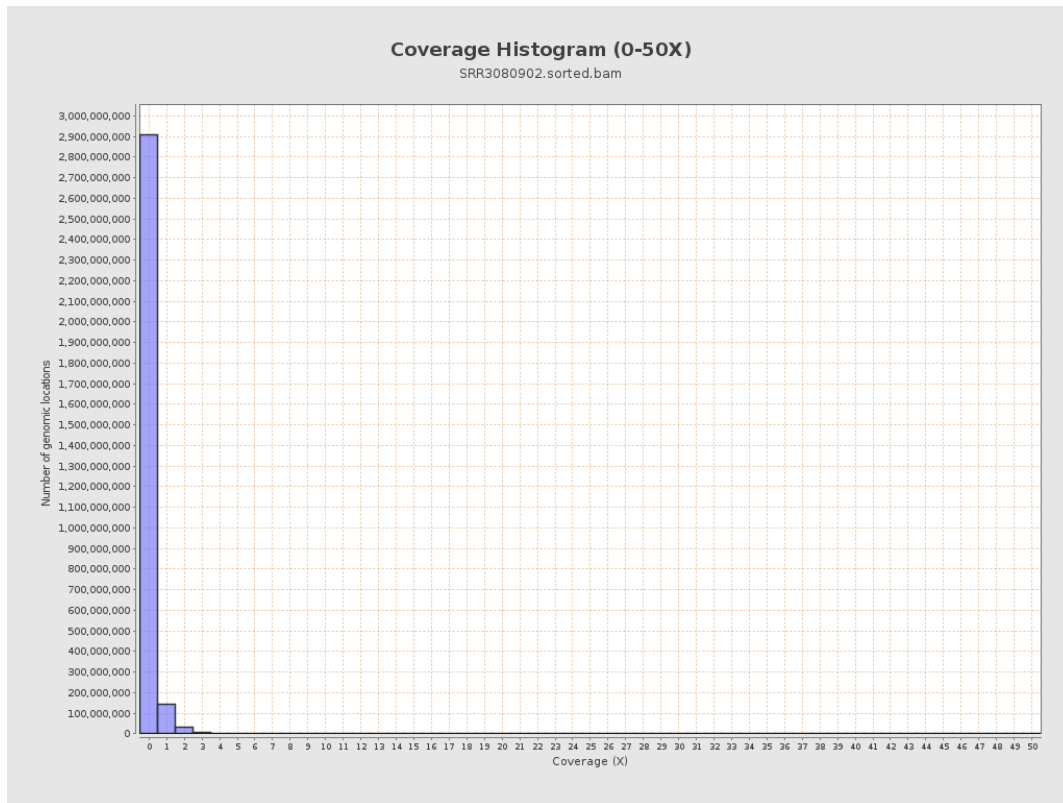
3. Results : Coverage across reference



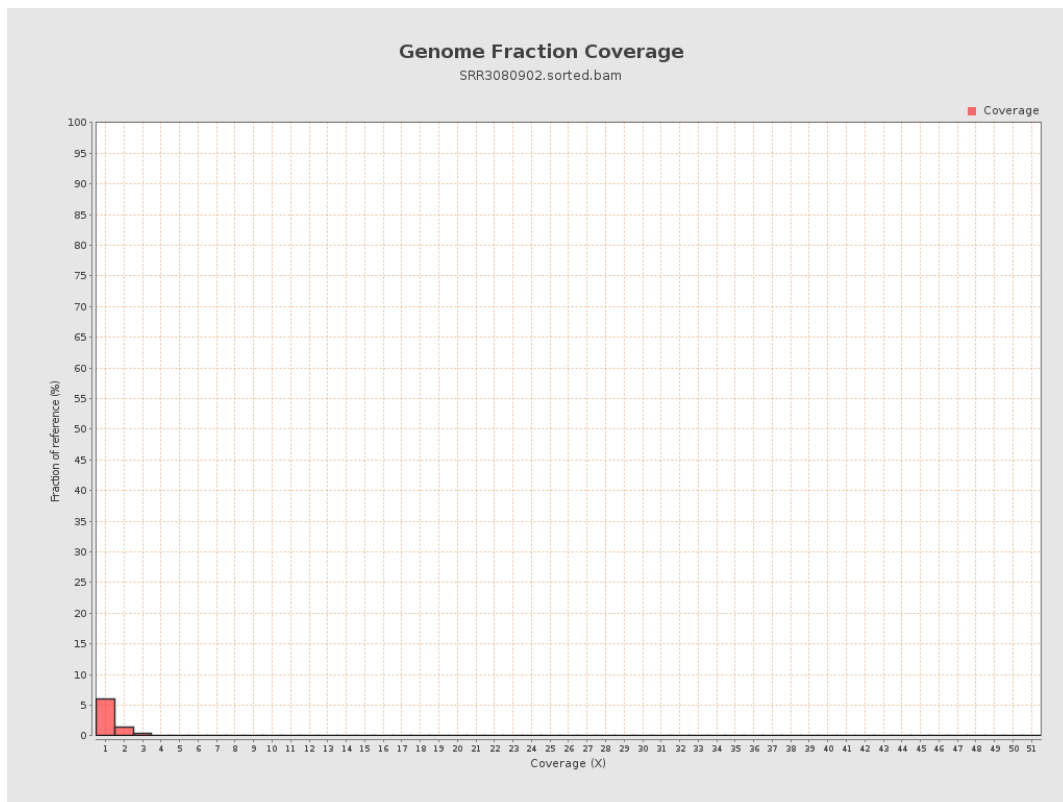
4. Results : Coverage Histogram



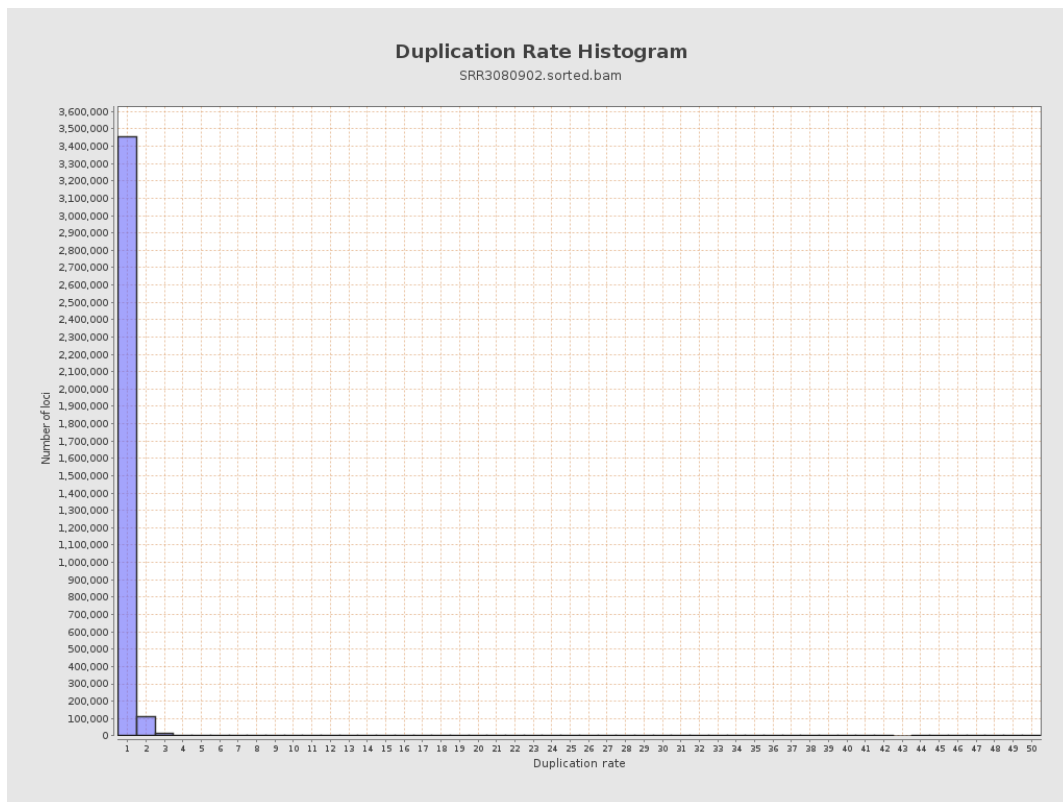
5. Results : Coverage Histogram (0-50X)



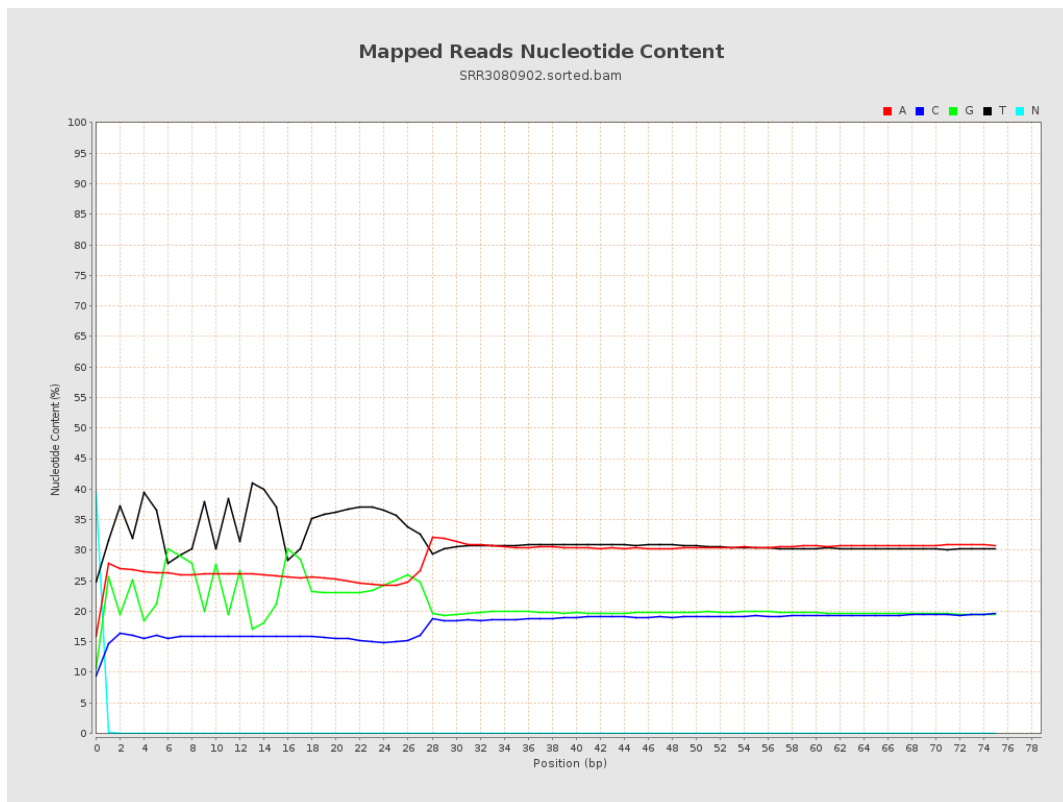
6. Results : Genome Fraction Coverage



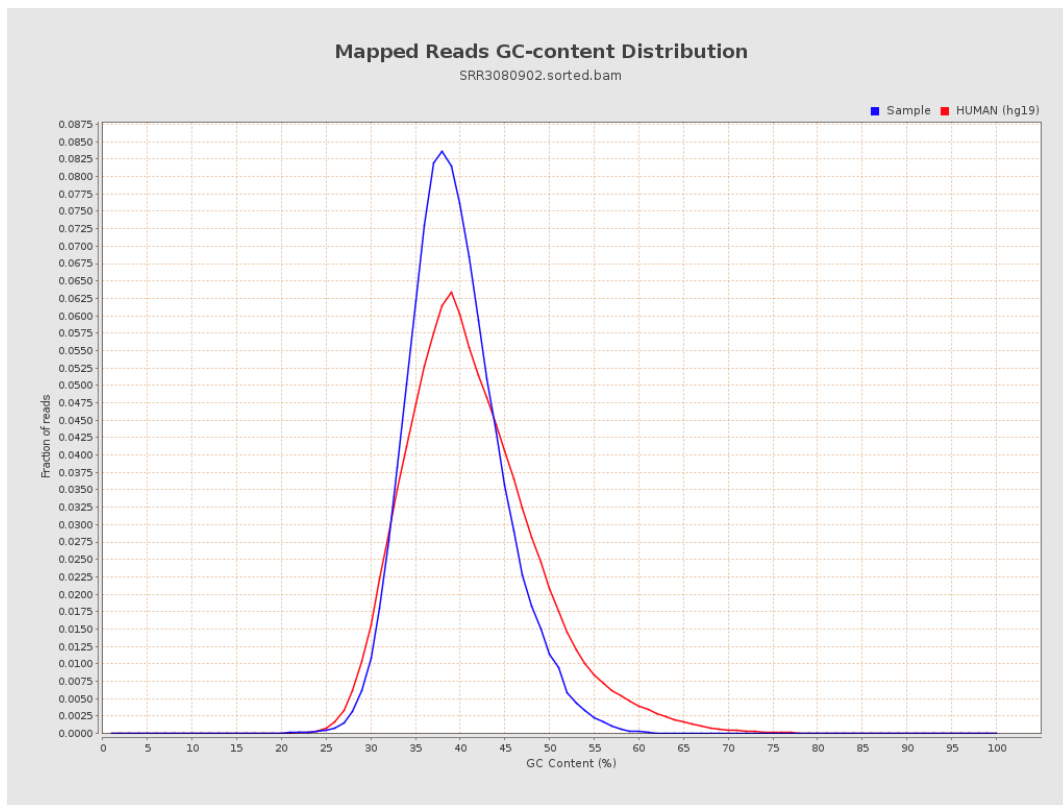
7. Results : Duplication Rate Histogram



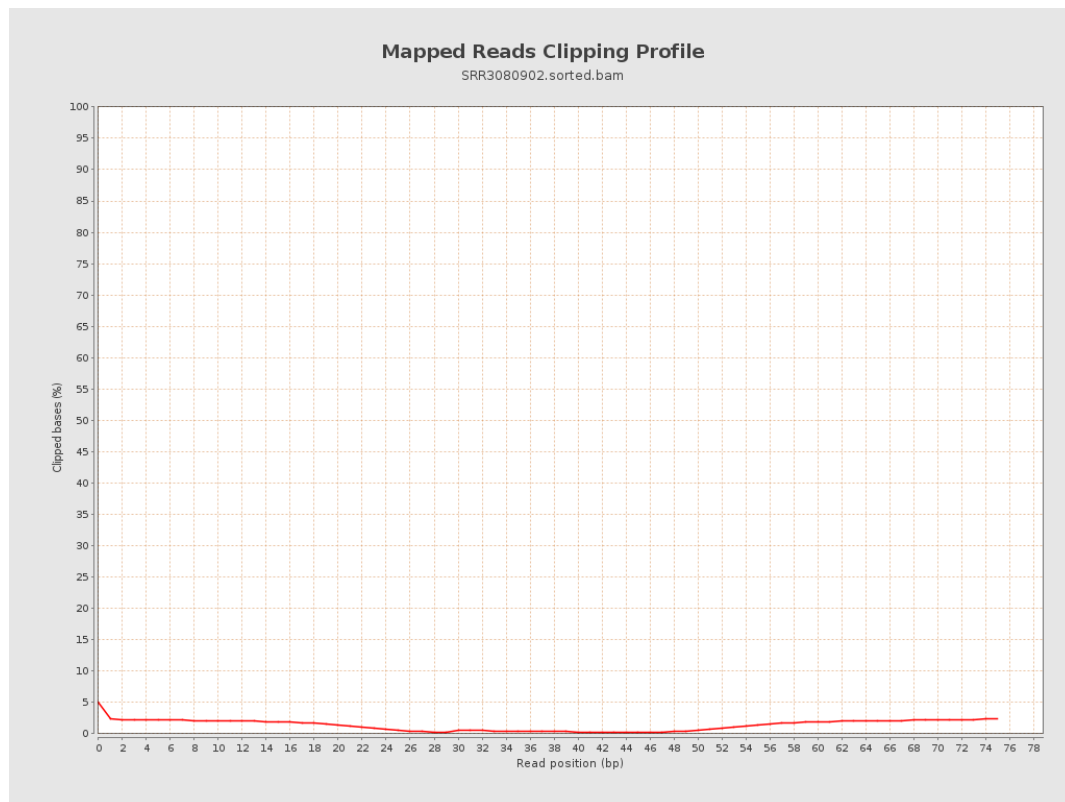
8. Results : Mapped Reads Nucleotide Content



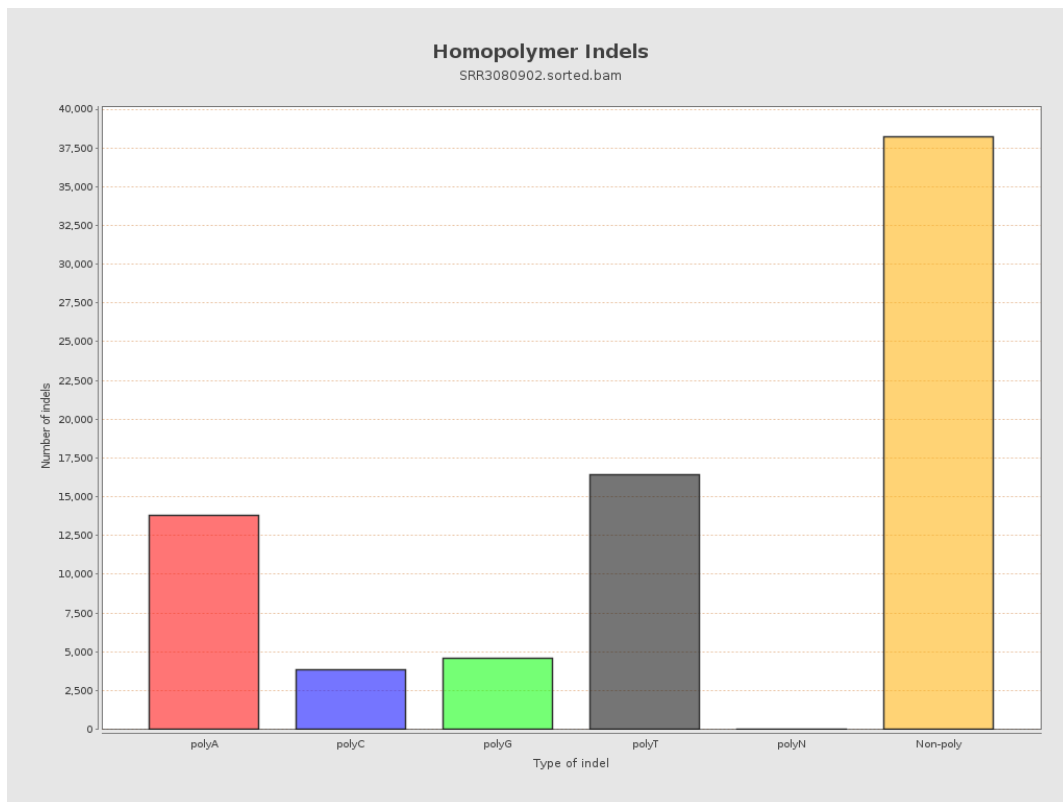
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

