

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:19:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084887.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_SRR3084887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084887.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:19:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,551,038
Mapped reads	2,249,373 / 88.17%
Unmapped reads	301,665 / 11.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,419 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	95,592 / 3.75%
Duplication rate	3.26%
Clipped reads	775,352 / 30.39%

2.2. ACGT Content

Number/percentage of A's	45,347,340 / 29.14%
Number/percentage of C's	28,445,674 / 18.28%
Number/percentage of T's	49,473,957 / 31.79%
Number/percentage of G's	32,337,253 / 20.78%
Number/percentage of N's	24,474 / 0.02%
GC Percentage	39.06%

2.3. Coverage

Mean	0.0503

Standard Deviation	0.4922
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2.4. Mapping Quality

Mean Mapping Quality	46.5
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2.5. Mismatches and indels

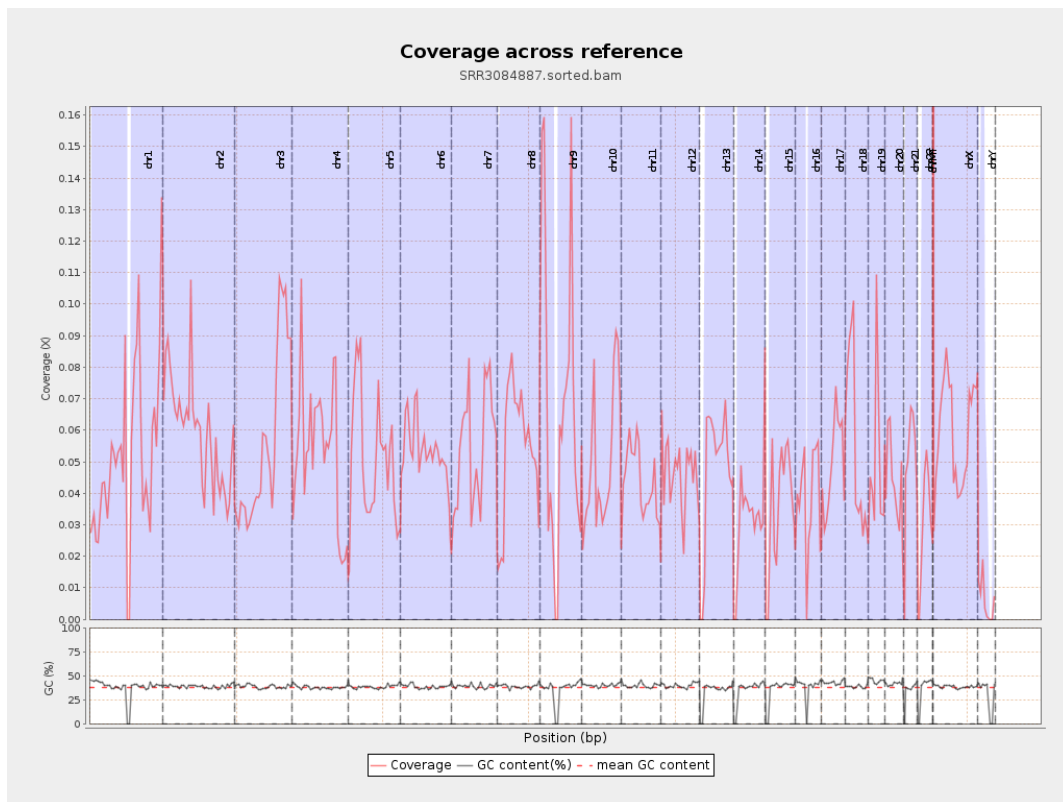
General error rate	0.89%
Mismatches	1,358,081
Insertions	12,961
Mapped reads with at least one insertion	0.57%
Deletions	35,797
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.66%

2.6. Chromosome stats

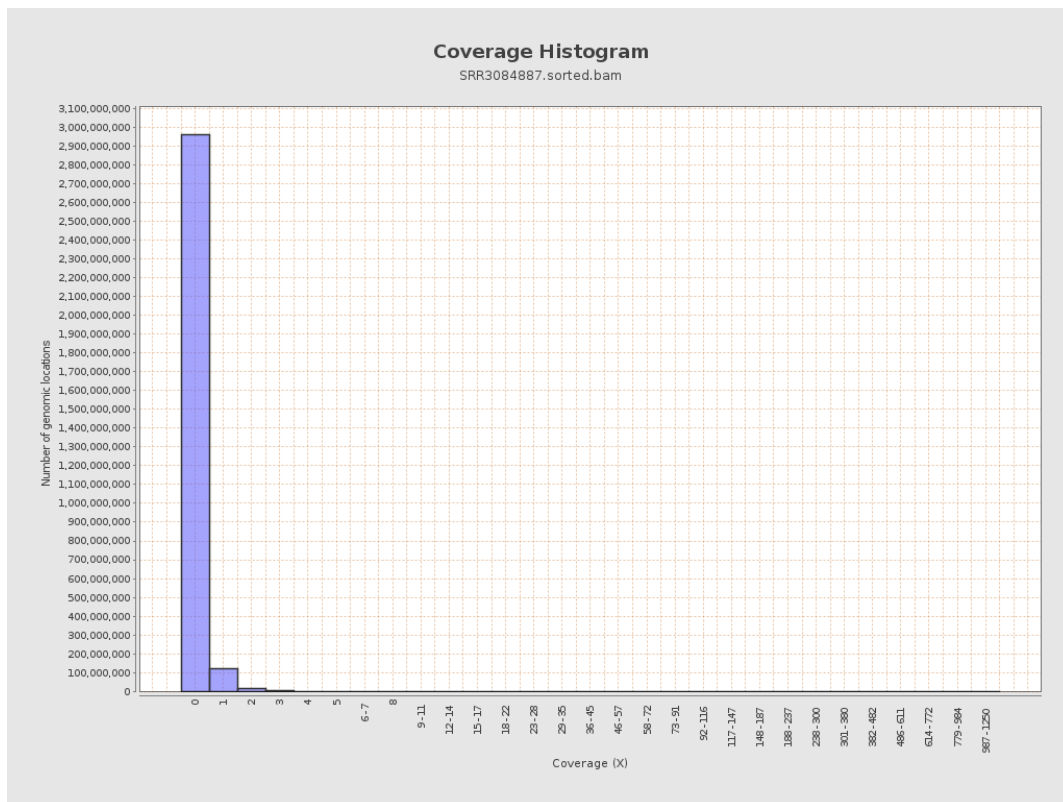
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12968663	0.052	1.0809
chr2	243199373	14436000	0.0594	0.5021
chr3	198022430	11043117	0.0558	0.2632
chr4	191154276	10213874	0.0534	0.2726
chr5	180915260	9131573	0.0505	0.2638
chr6	171115067	9164211	0.0536	0.2634
chr7	159138663	8589118	0.054	0.4352

chr8	146364022	8064013	0.0551	0.8385
chr9	141213431	9437279	0.0668	0.4706
chr10	135534747	6736995	0.0497	0.3783
chr11	135006516	5973081	0.0442	0.3499
chr12	133851895	6250631	0.0467	0.2444
chr13	115169878	5441630	0.0472	0.2386
chr14	107349540	3271676	0.0305	0.2154
chr15	102531392	3656821	0.0357	0.2097
chr16	90354753	3338183	0.0369	0.2691
chr17	81195210	4073399	0.0502	0.263
chr18	78077248	4464022	0.0572	0.8995
chr19	59128983	2991329	0.0506	0.5625
chr20	63025520	2795463	0.0444	0.2532
chr21	48129895	2403387	0.0499	0.2668
chr22	51304566	1546964	0.0302	0.1893
chrMT	16571	124780	7.53	4.572
chrX	155270560	9211175	0.0593	0.308
chrY	59373566	364656	0.0061	0.1441

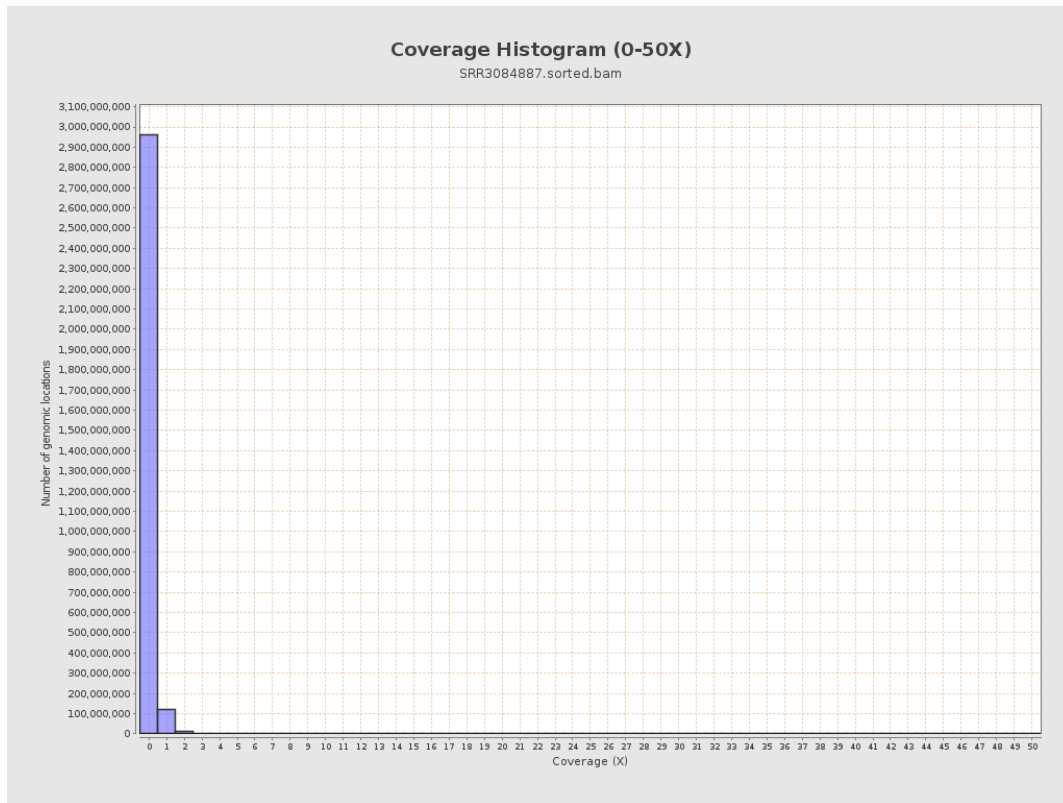
3. Results : Coverage across reference



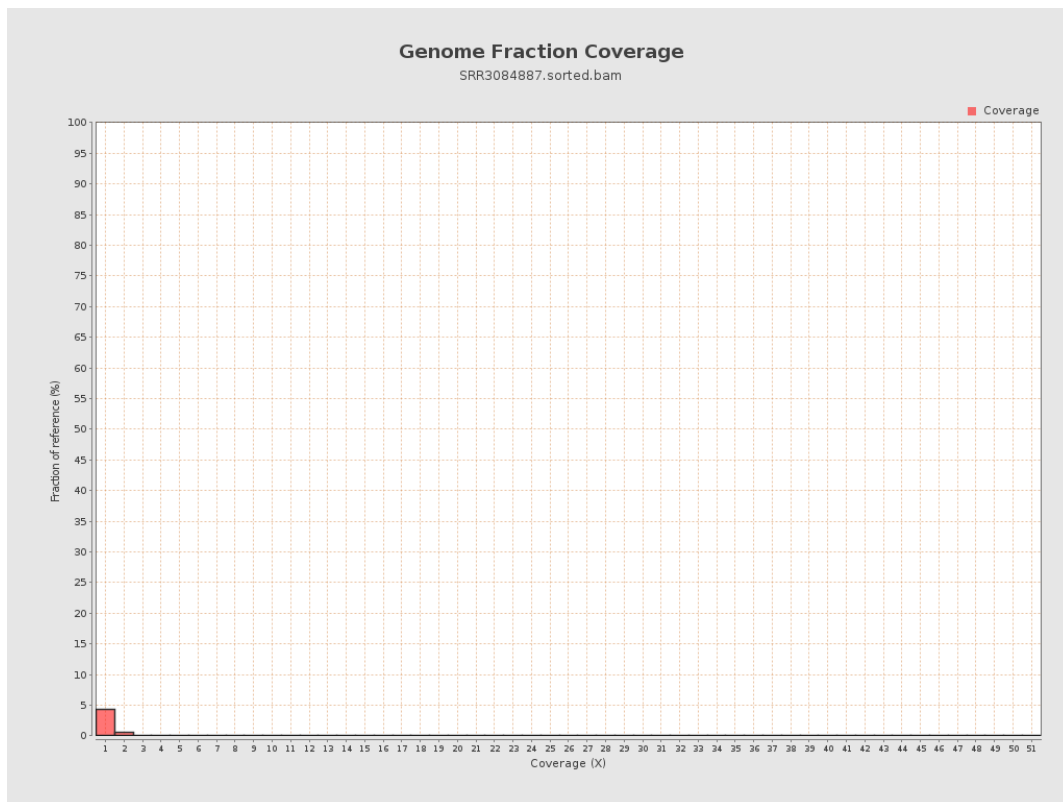
4. Results : Coverage Histogram



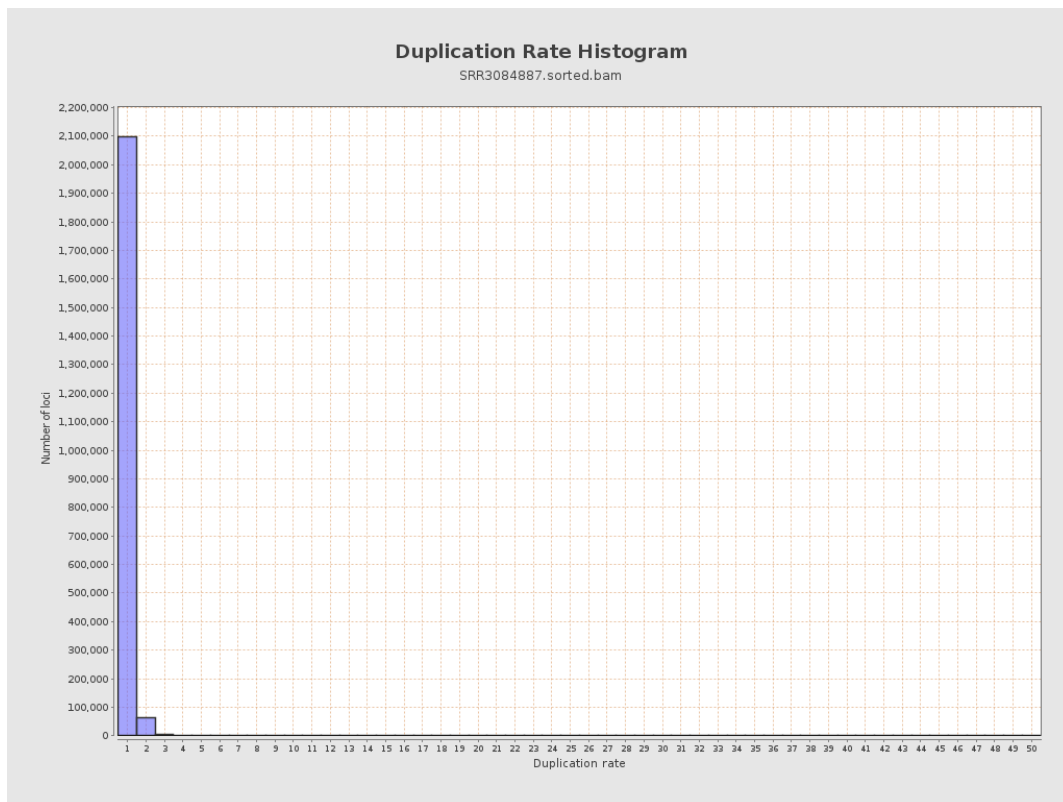
5. Results : Coverage Histogram (0-50X)



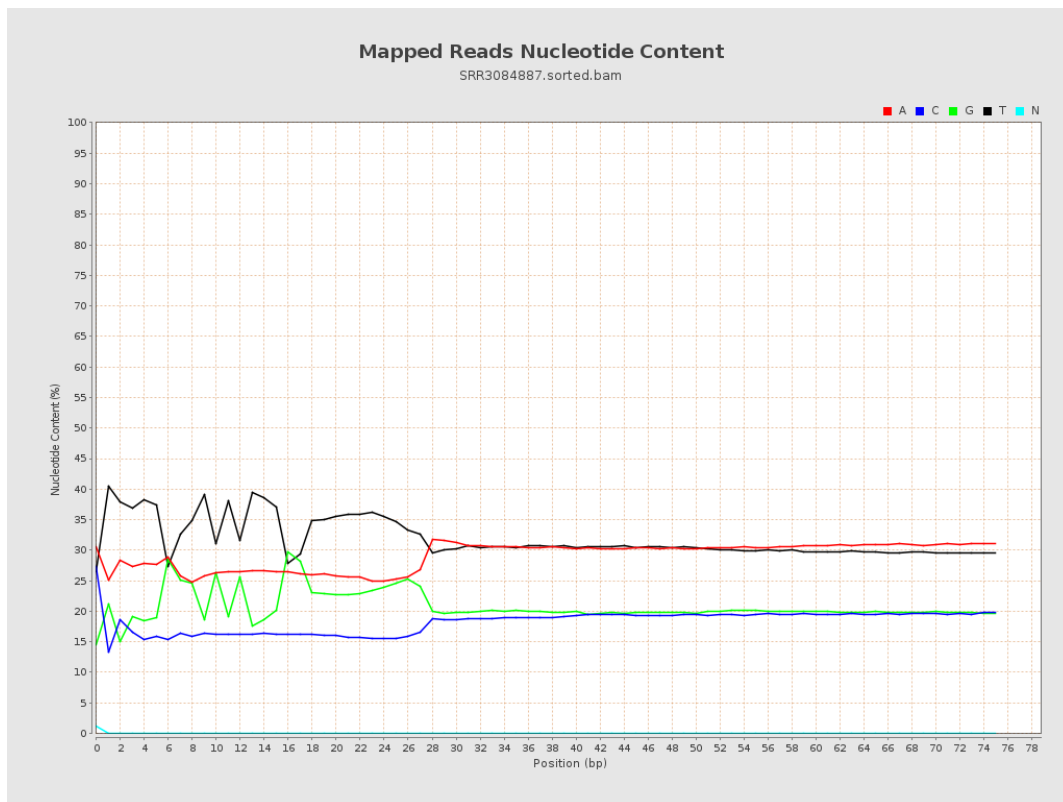
6. Results : Genome Fraction Coverage



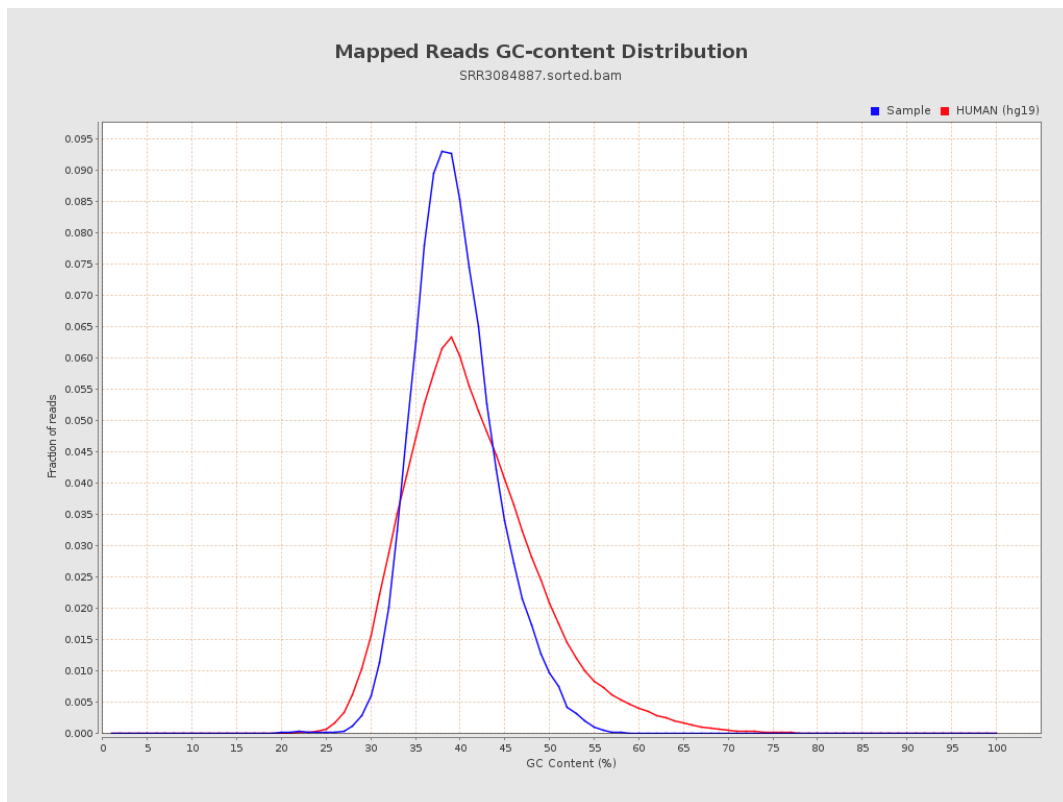
7. Results : Duplication Rate Histogram



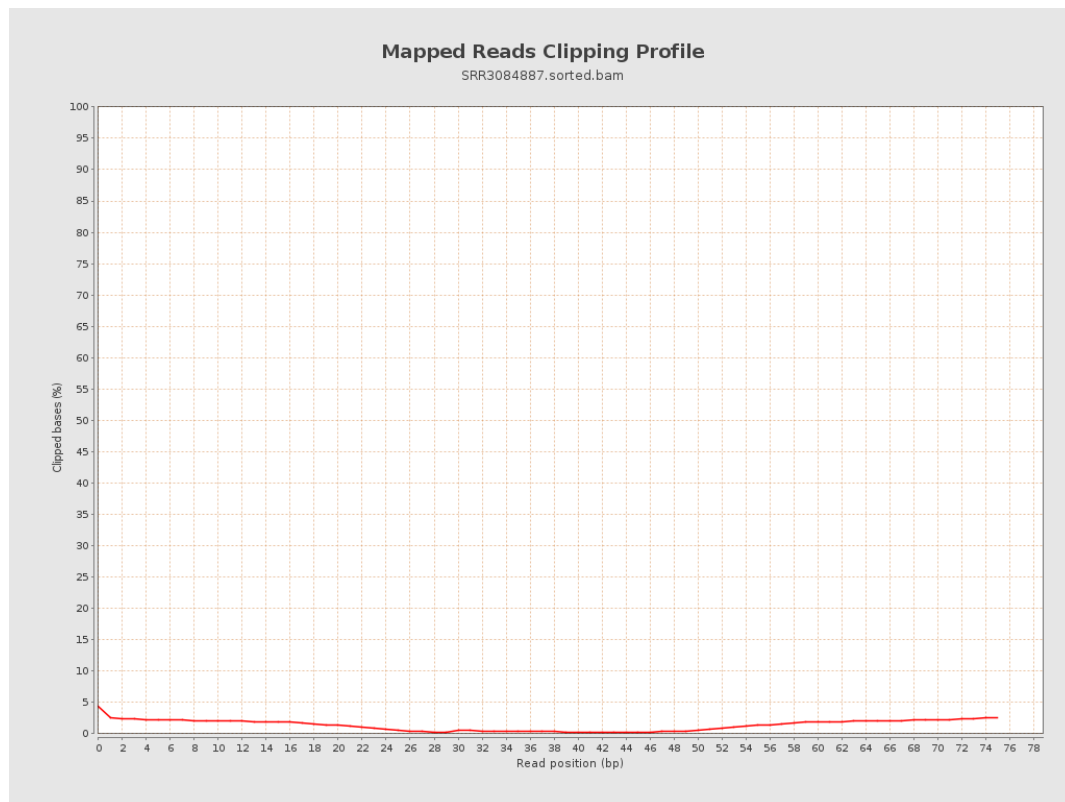
8. Results : Mapped Reads Nucleotide Content



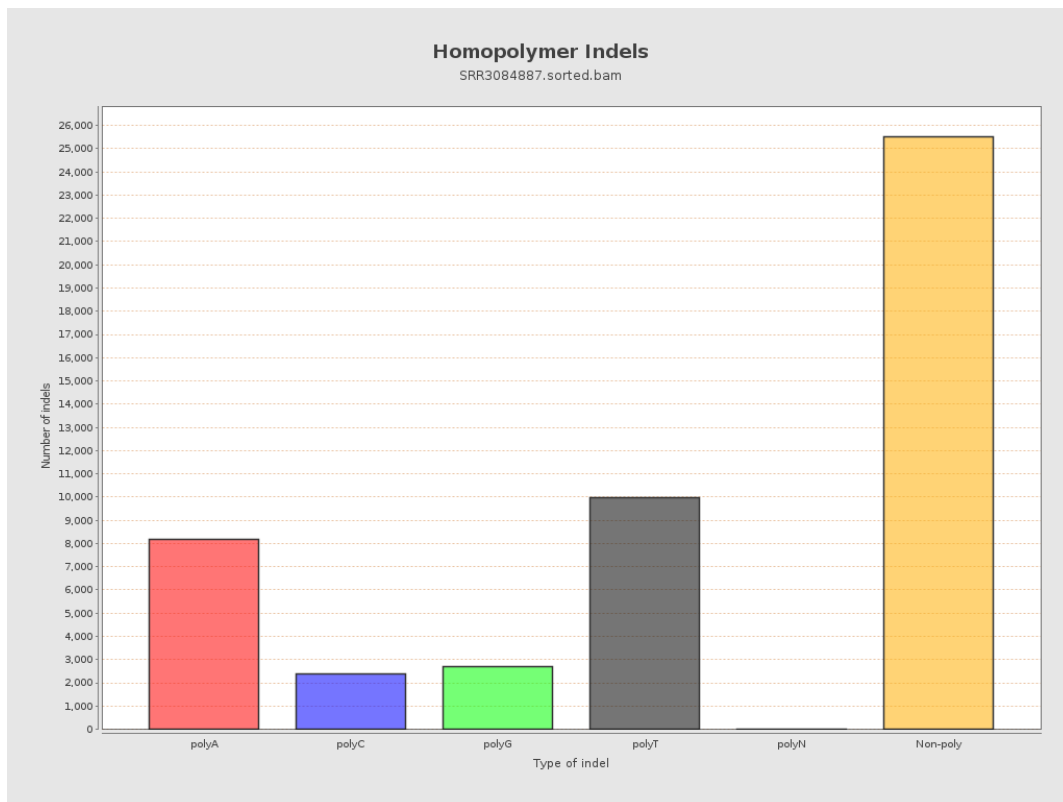
9. Results : Mapped Reads GC-content Distribution



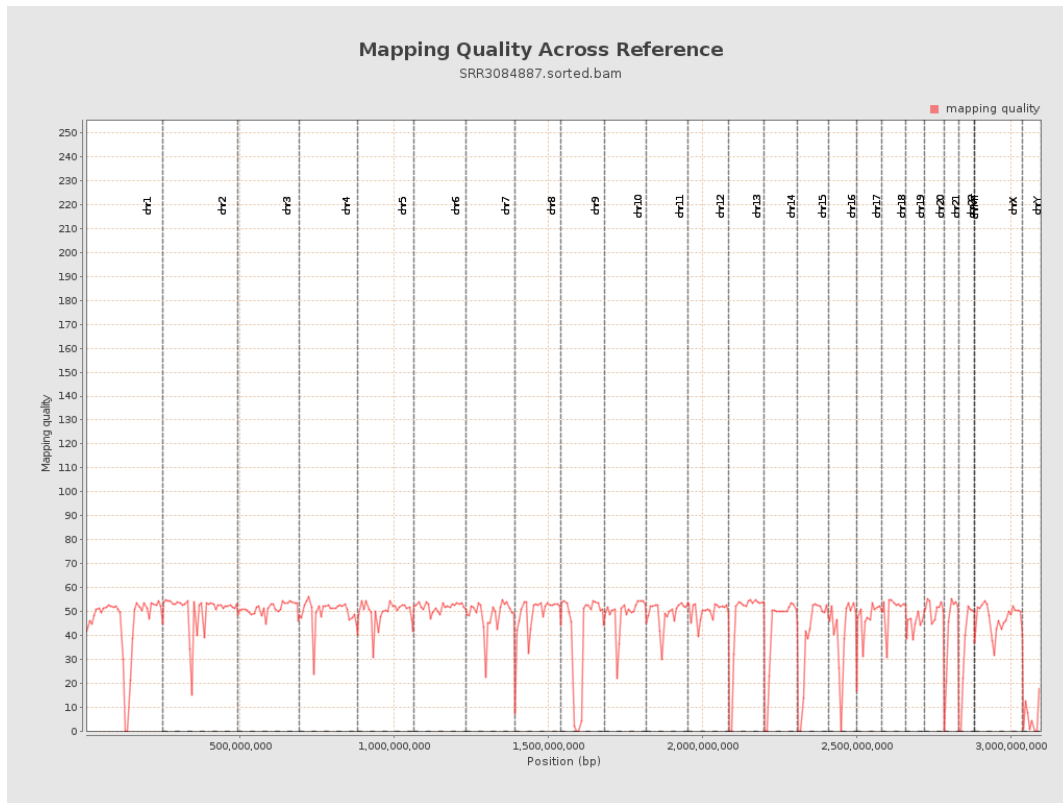
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

