

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:44:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004032.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_SRR6004032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:44:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,362,043
Mapped reads	2,124,449 / 89.94%
Unmapped reads	237,594 / 10.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,784 / 1.18%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	120,793 / 5.11%
Duplication rate	4.29%
Clipped reads	973,421 / 41.21%

2.2. ACGT Content

Number/percentage of A's	40,592,684 / 28.63%
Number/percentage of C's	26,491,396 / 18.68%
Number/percentage of T's	44,641,418 / 31.49%
Number/percentage of G's	30,043,798 / 21.19%
Number/percentage of N's	10,628 / 0.01%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.4511
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2.4. Mapping Quality

Mean Mapping Quality	40.05
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2.5. Mismatches and indels

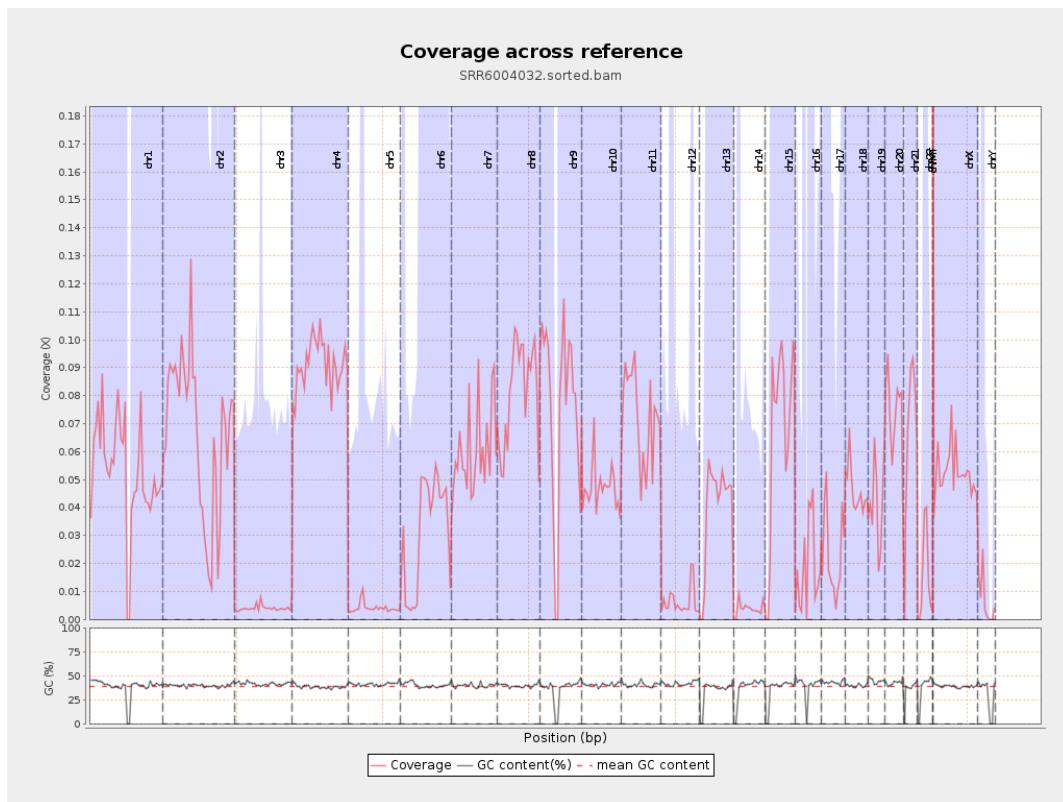
General error rate	0.94%
Mismatches	1,313,685
Insertions	11,257
Mapped reads with at least one insertion	0.53%
Deletions	47,466
Mapped reads with at least one deletion	2.2%
Homopolymer indels	44.36%

2.6. Chromosome stats

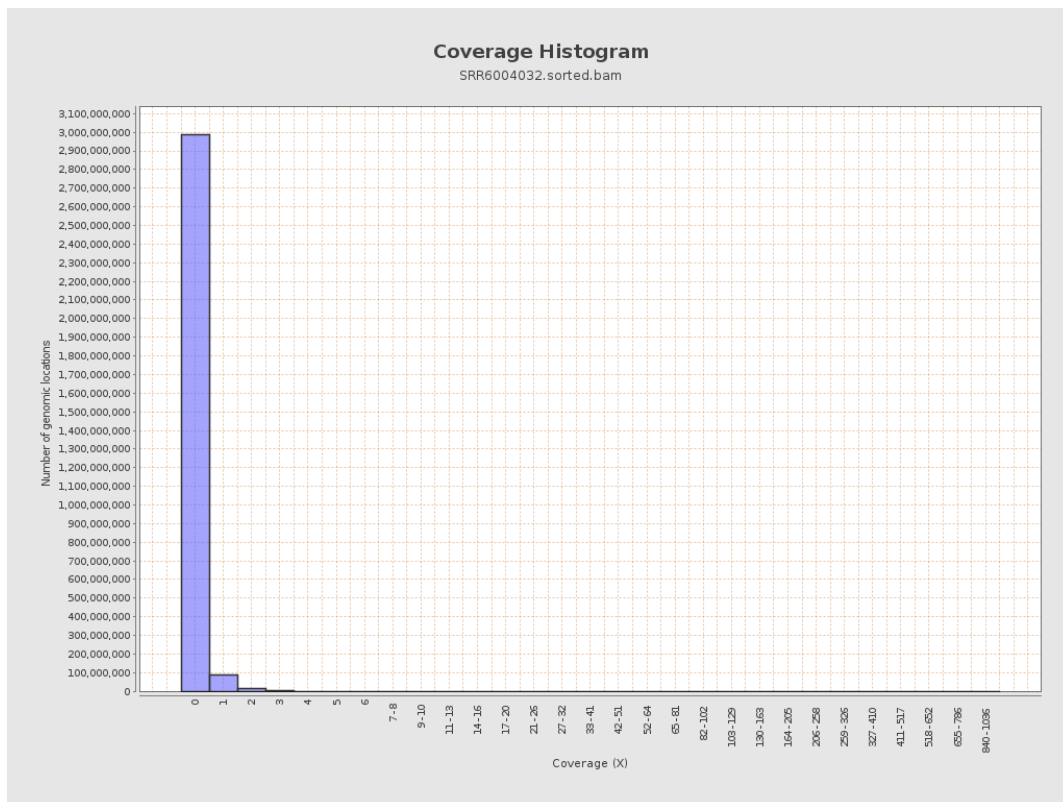
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13273260	0.0533	0.7276
chr2	243199373	16161033	0.0665	0.53
chr3	198022430	799364	0.004	0.0891
chr4	191154276	17461798	0.0913	0.3986
chr5	180915260	752248	0.0042	0.1041
chr6	171115067	5343641	0.0312	0.2187
chr7	159138663	9614375	0.0604	0.5593

chr8	146364022	11942855	0.0816	0.7142
chr9	141213431	10721326	0.0759	0.5661
chr10	135534747	6357170	0.0469	0.3936
chr11	135006516	9747747	0.0722	0.5508
chr12	133851895	855706	0.0064	0.1422
chr13	115169878	4617295	0.0401	0.2437
chr14	107349540	412911	0.0038	0.2093
chr15	102531392	6863891	0.0669	0.3178
chr16	90354753	1725695	0.0191	0.2825
chr17	81195210	1852365	0.0228	0.2592
chr18	78077248	3637765	0.0466	0.9371
chr19	59128983	2482128	0.042	0.4369
chr20	63025520	4735408	0.0751	0.3523
chr21	48129895	3175095	0.066	0.3674
chr22	51304566	778823	0.0152	0.15
chrMT	16571	8804	0.5313	0.7631
chrX	155270560	8130316	0.0524	0.3417
chrY	59373566	408301	0.0069	0.2107

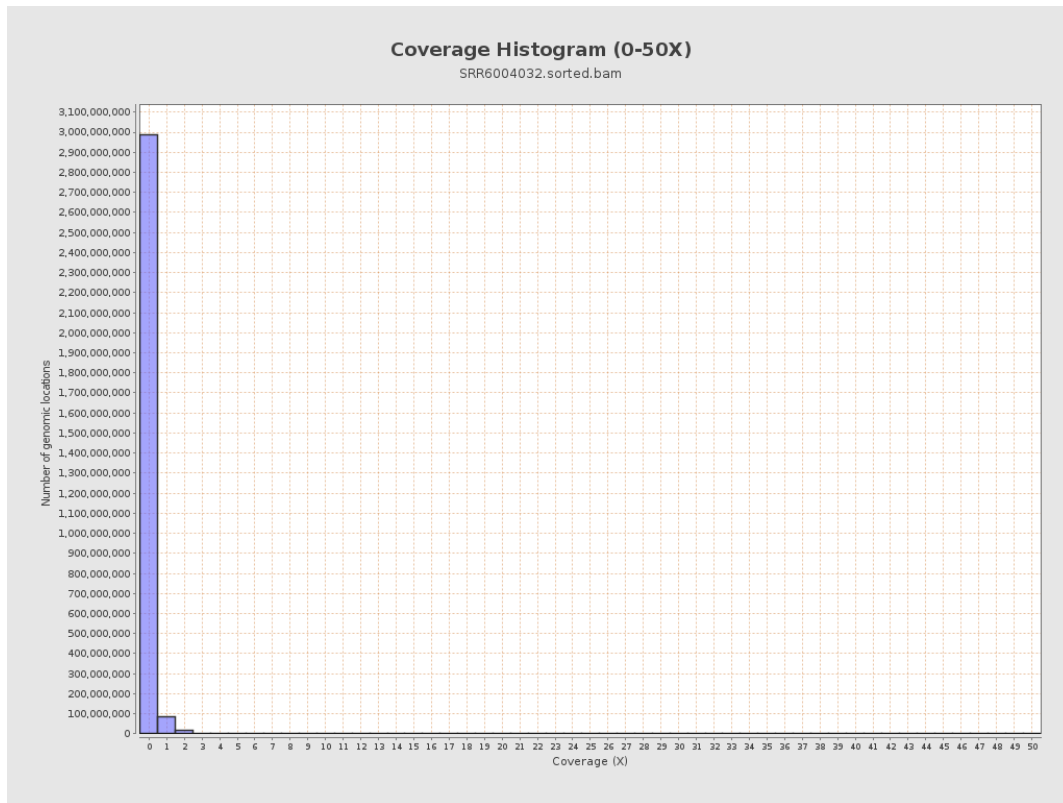
3. Results : Coverage across reference



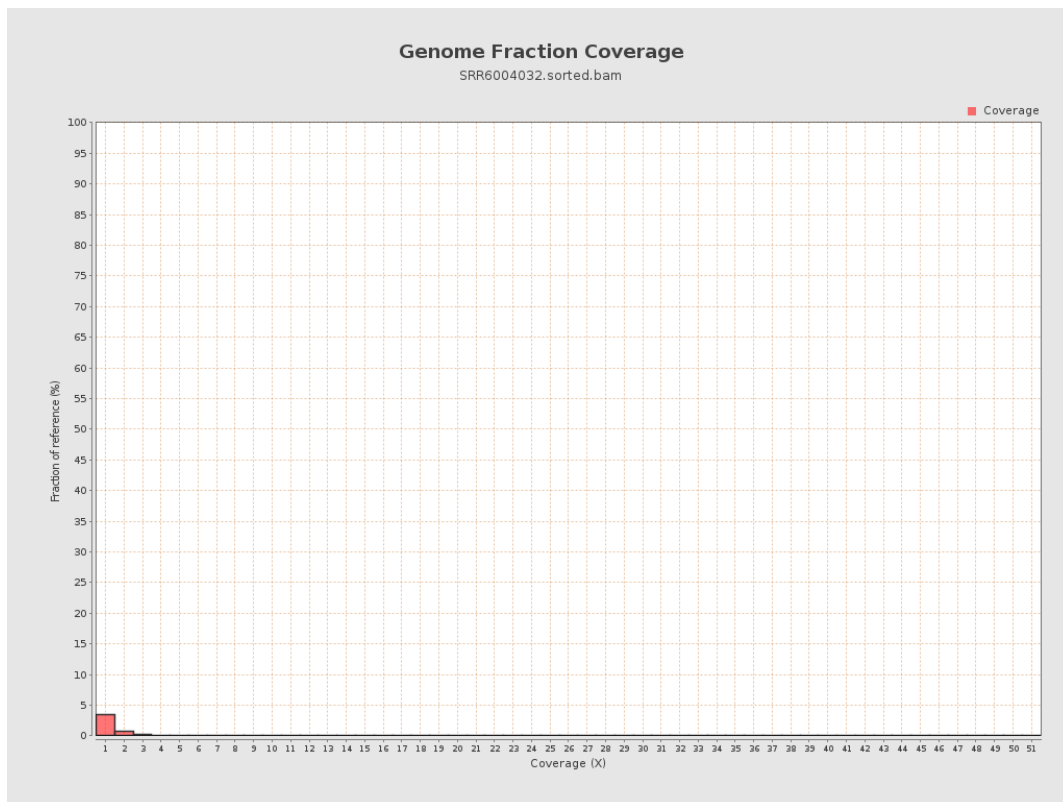
4. Results : Coverage Histogram



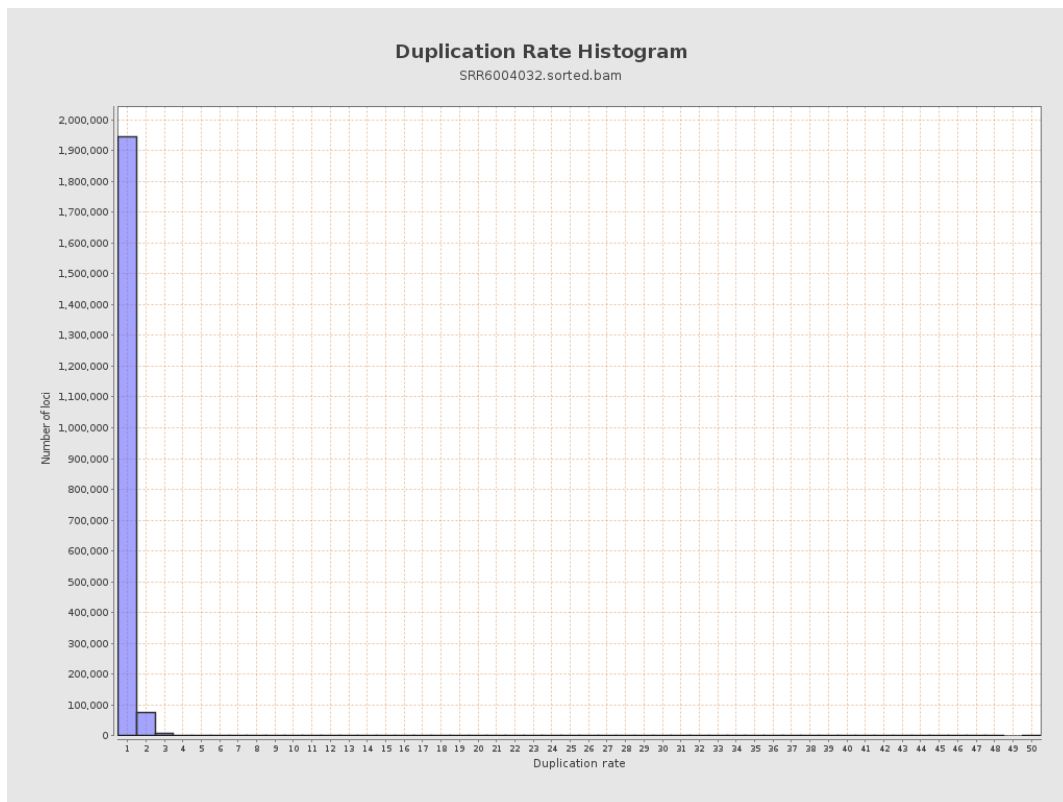
5. Results : Coverage Histogram (0-50X)



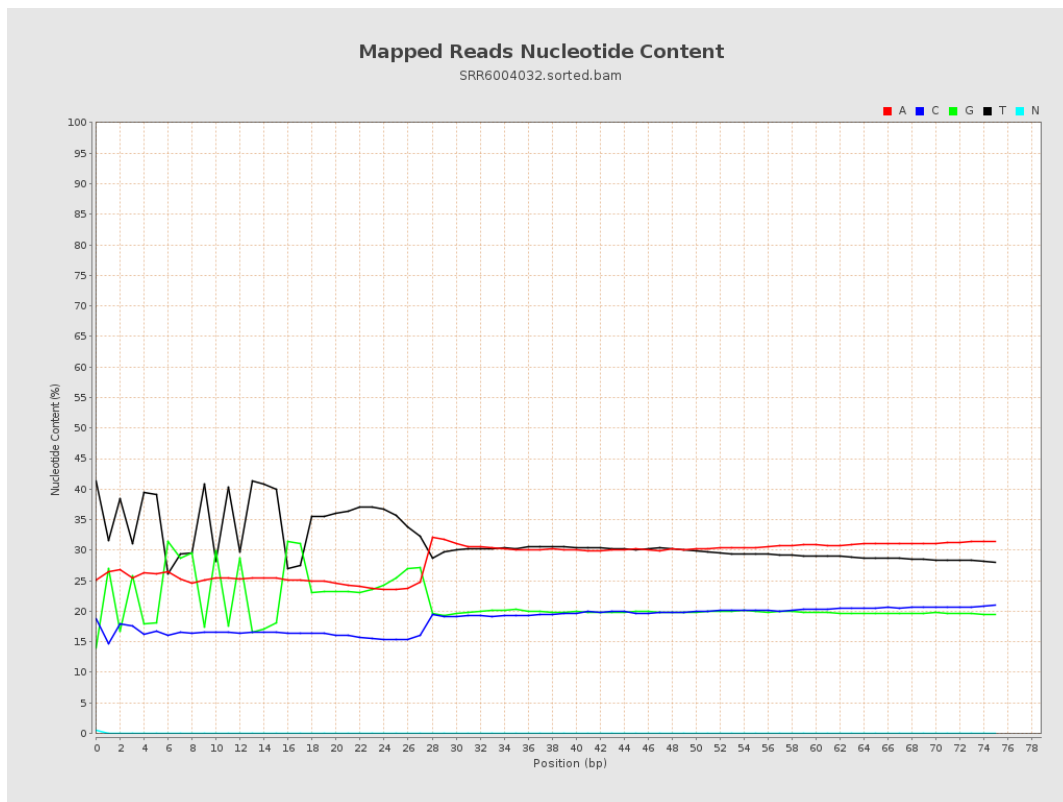
6. Results : Genome Fraction Coverage



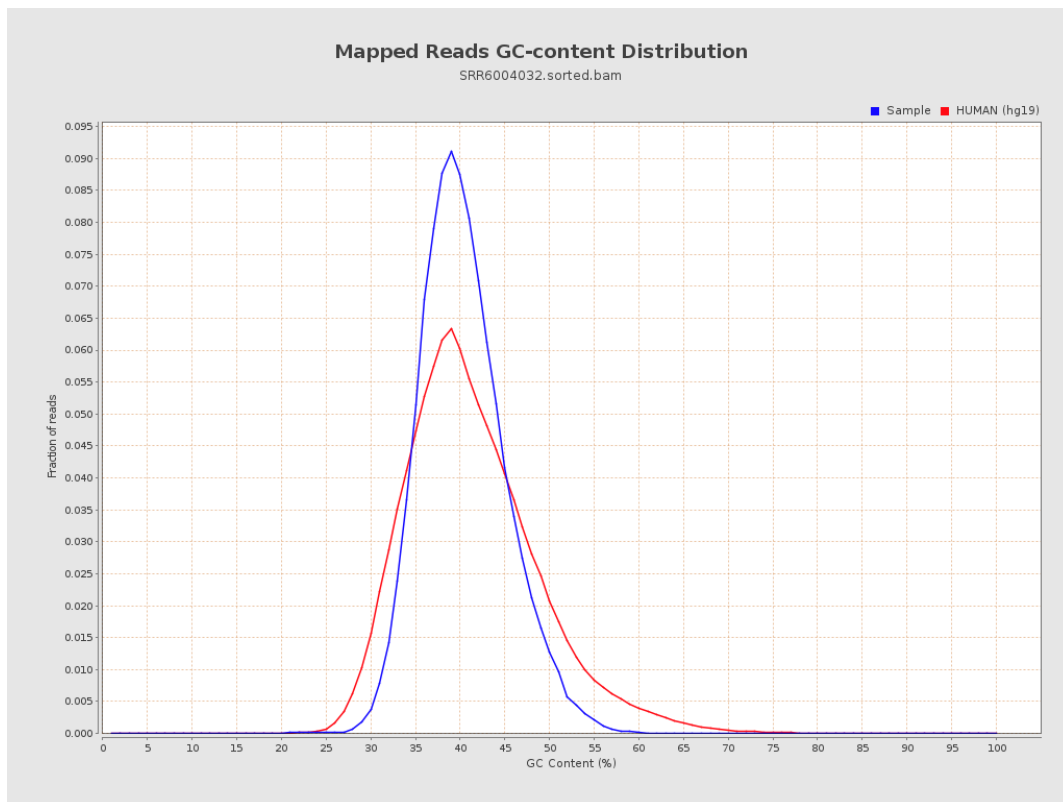
7. Results : Duplication Rate Histogram



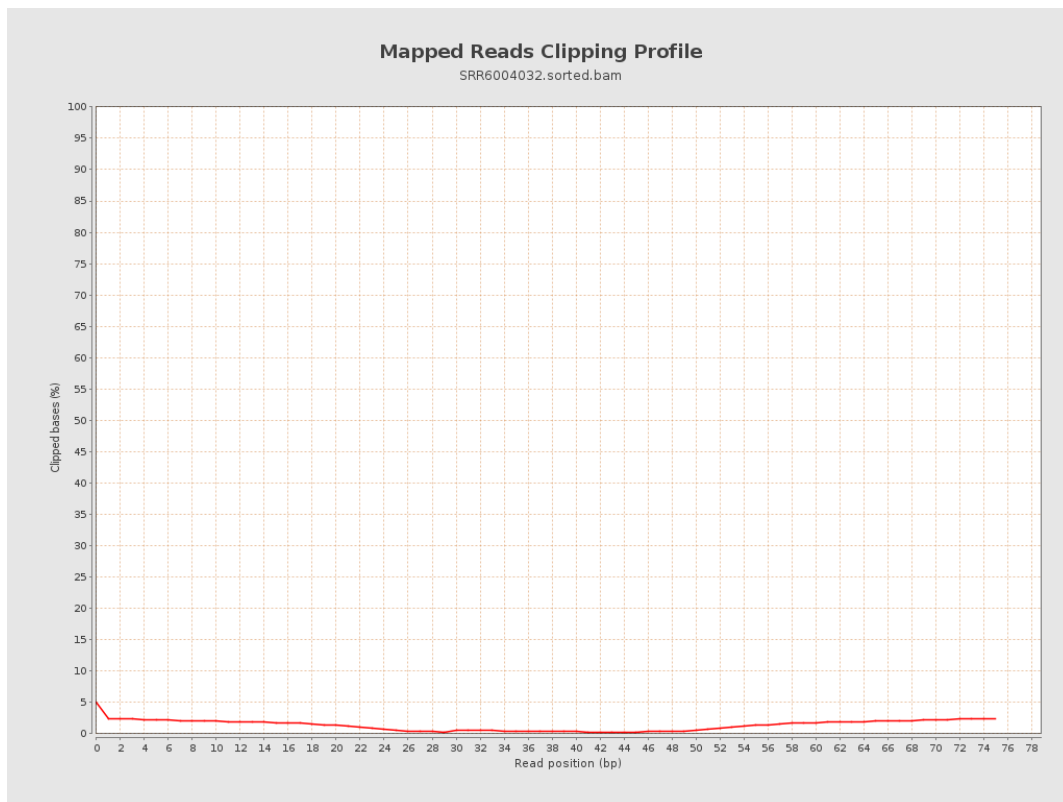
8. Results : Mapped Reads Nucleotide Content



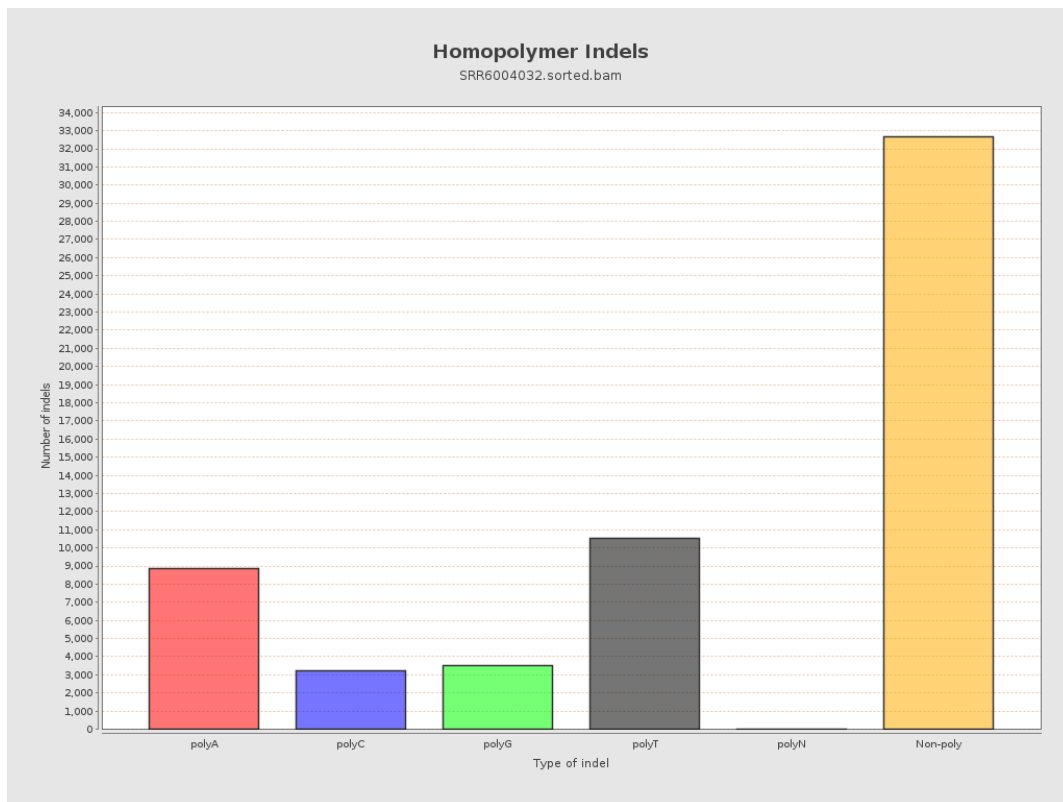
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

