

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:31:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818923.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_SRR1818923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818923.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:31:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,508,104
Mapped reads	1,489,015 / 98.73%
Unmapped reads	19,089 / 1.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,185 / 1.47%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	393,414 / 26.09%
Duplication rate	22.58%
Clipped reads	1,508,459 / 100.02%

2.2. ACGT Content

Number/percentage of A's	40,241,562 / 29.22%
Number/percentage of C's	30,354,513 / 22.04%
Number/percentage of T's	38,307,012 / 27.81%
Number/percentage of G's	28,828,117 / 20.93%
Number/percentage of N's	2,137 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.5661
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2.4. Mapping Quality

Mean Mapping Quality	49.18
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2.5. Mismatches and indels

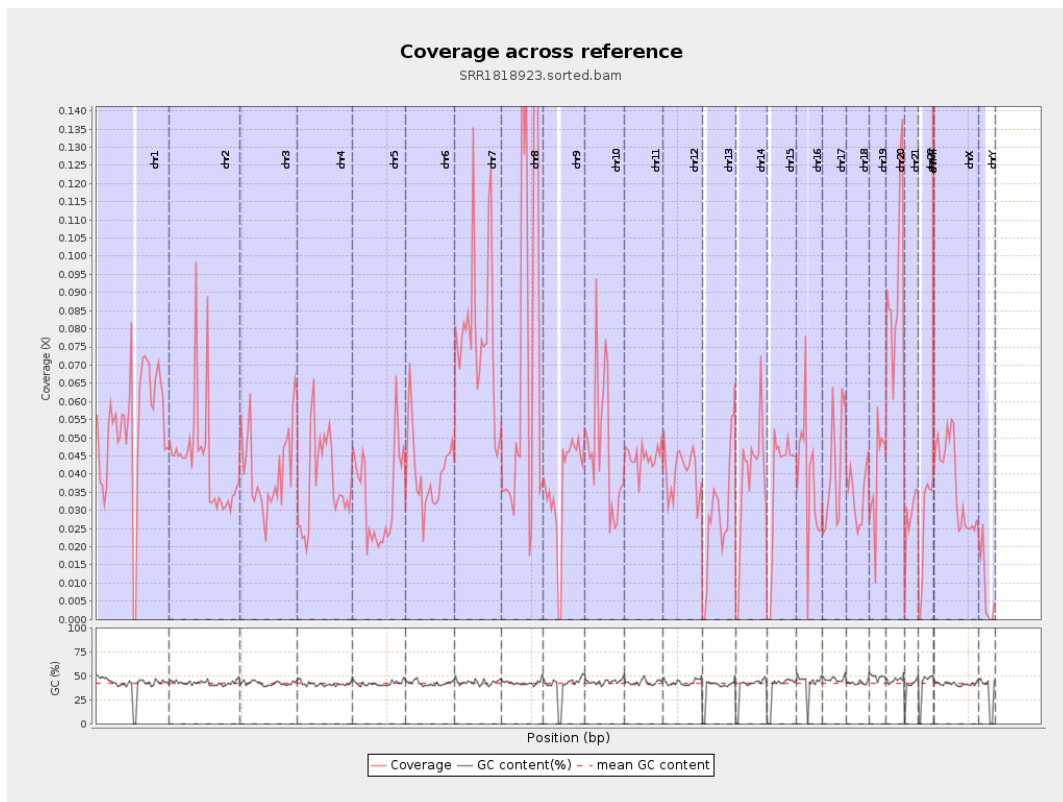
General error rate	0.63%
Mismatches	824,643
Insertions	17,886
Mapped reads with at least one insertion	1.16%
Deletions	45,100
Mapped reads with at least one deletion	2.96%
Homopolymer indels	42.06%

2.6. Chromosome stats

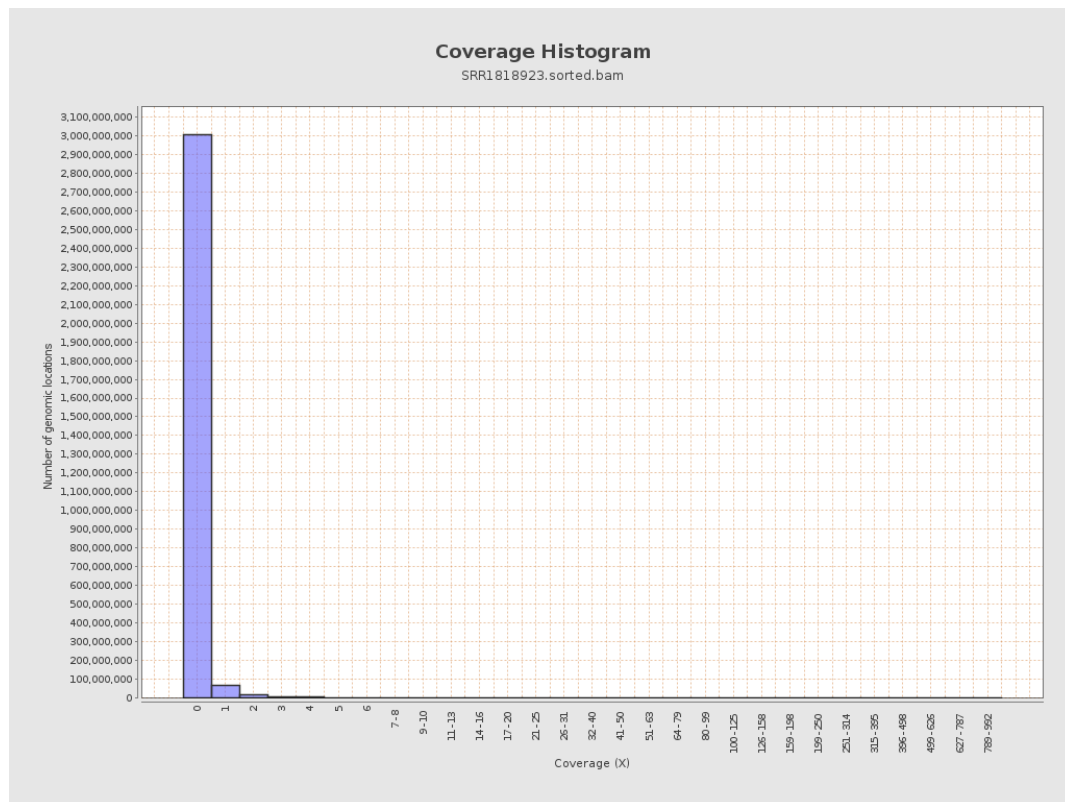
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13193529	0.0529	0.7925
chr2	243199373	10595934	0.0436	0.9118
chr3	198022430	8249201	0.0417	0.2867
chr4	191154276	7159385	0.0375	0.3436
chr5	180915260	6126321	0.0339	0.269
chr6	171115067	6908527	0.0404	0.3087
chr7	159138663	12519780	0.0787	1.243

chr8	146364022	11827758	0.0808	0.4827
chr9	141213431	5181134	0.0367	0.4385
chr10	135534747	6380537	0.0471	0.6397
chr11	135006516	6042791	0.0448	0.3374
chr12	133851895	5467626	0.0408	0.2894
chr13	115169878	3346876	0.0291	0.2382
chr14	107349540	4111142	0.0383	0.2927
chr15	102531392	3877695	0.0378	0.2713
chr16	90354753	3429387	0.038	0.595
chr17	81195210	3416546	0.0421	0.3515
chr18	78077248	2693171	0.0345	0.4873
chr19	59128983	2334465	0.0395	0.6764
chr20	63025520	5855056	0.0929	0.4651
chr21	48129895	1358052	0.0282	0.272
chr22	51304566	1278166	0.0249	0.2446
chrMT	16571	180970	10.9209	7.4272
chrX	155270560	5798192	0.0373	0.3077
chrY	59373566	487557	0.0082	0.6663

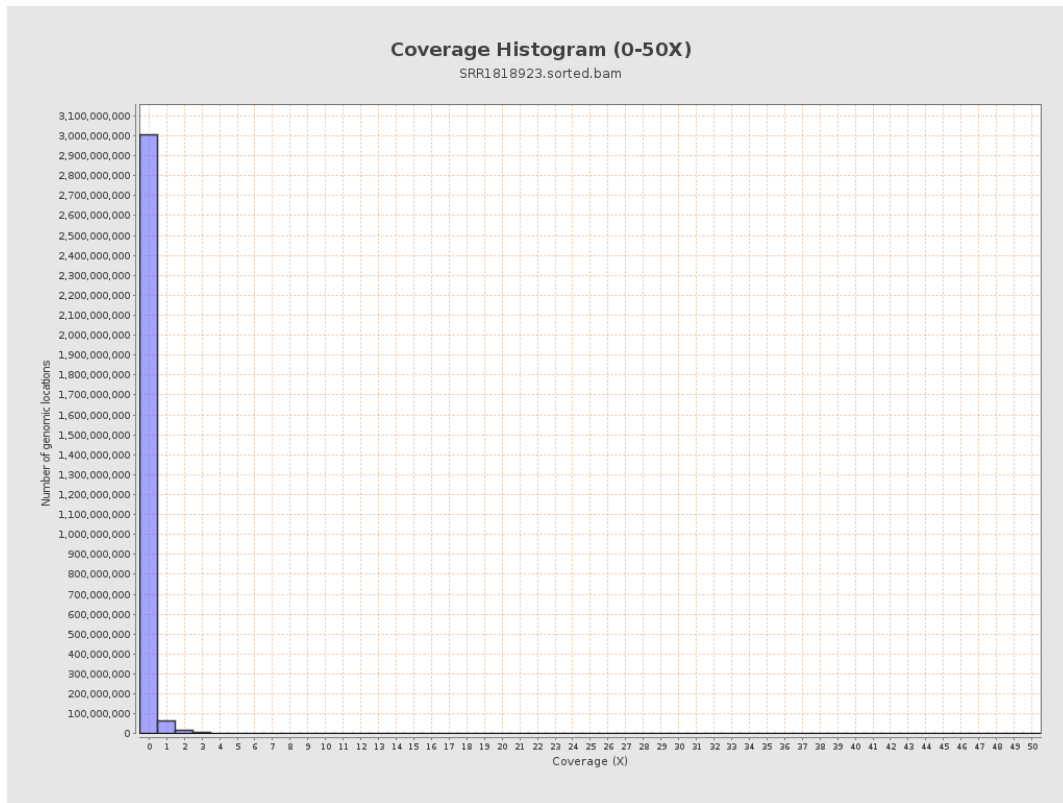
3. Results : Coverage across reference



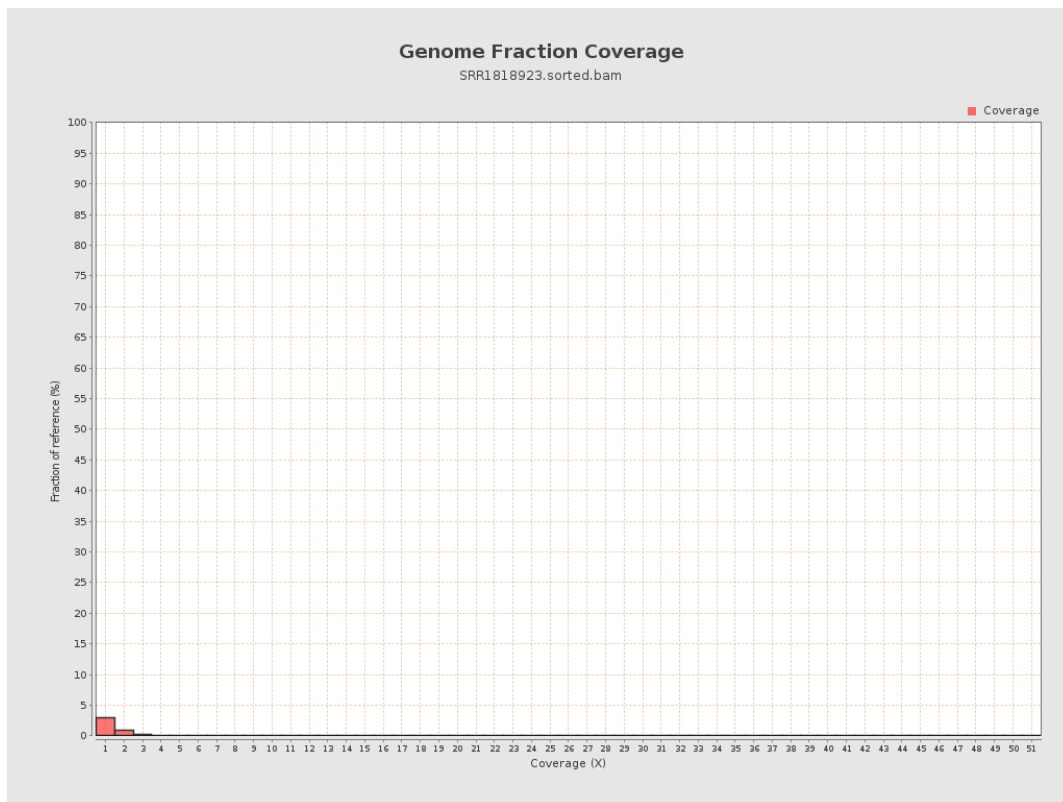
4. Results : Coverage Histogram



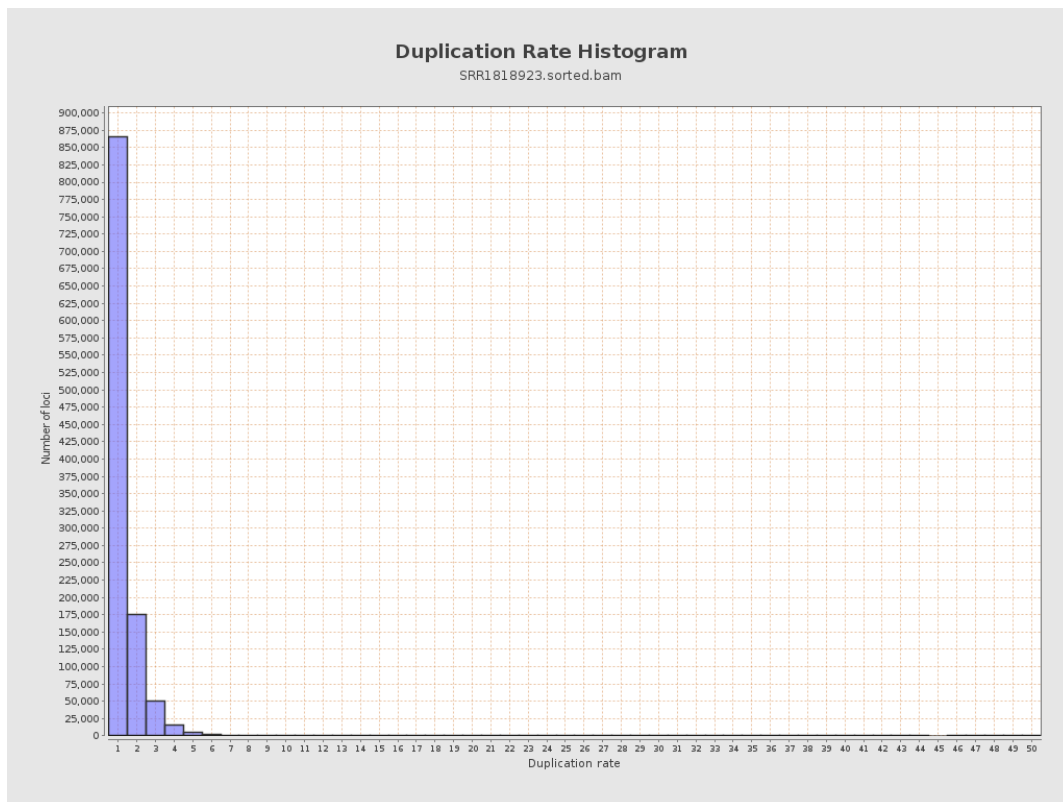
5. Results : Coverage Histogram (0-50X)



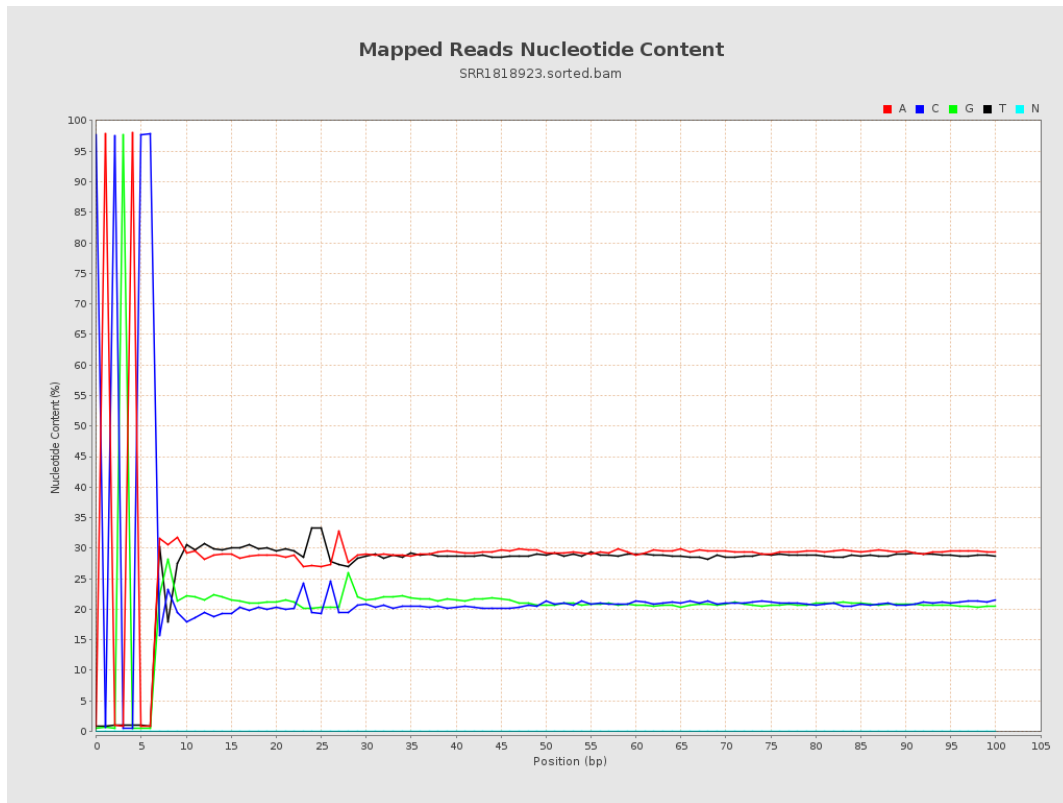
6. Results : Genome Fraction Coverage



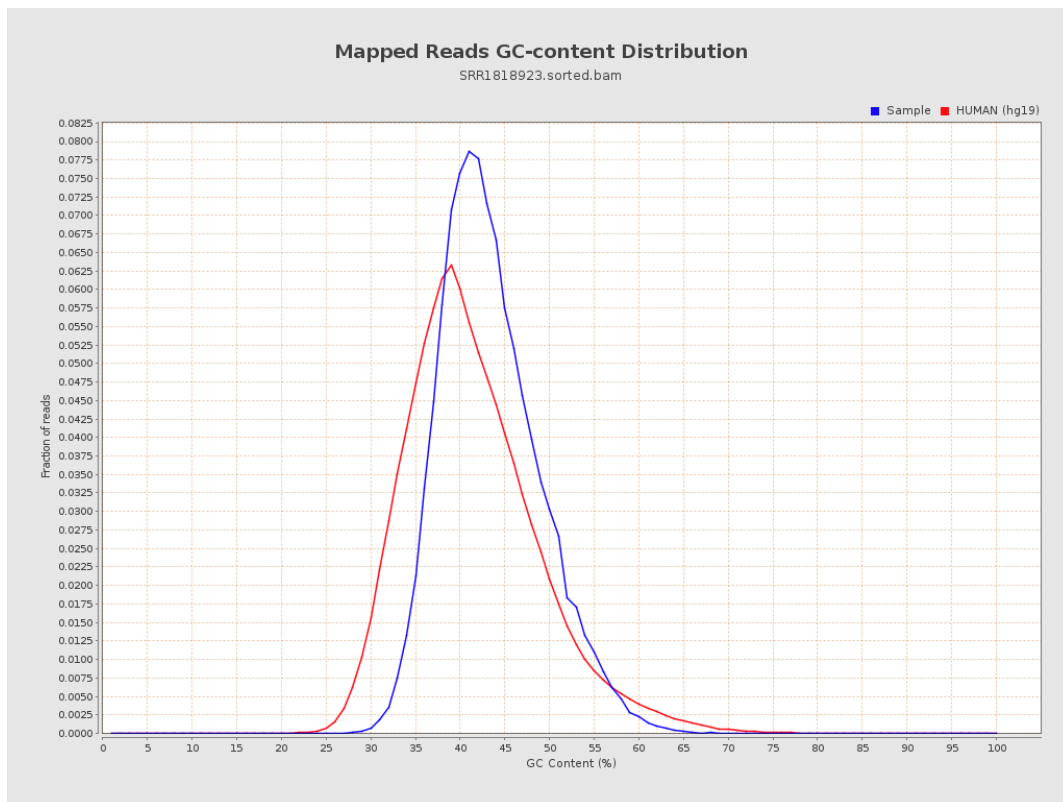
7. Results : Duplication Rate Histogram



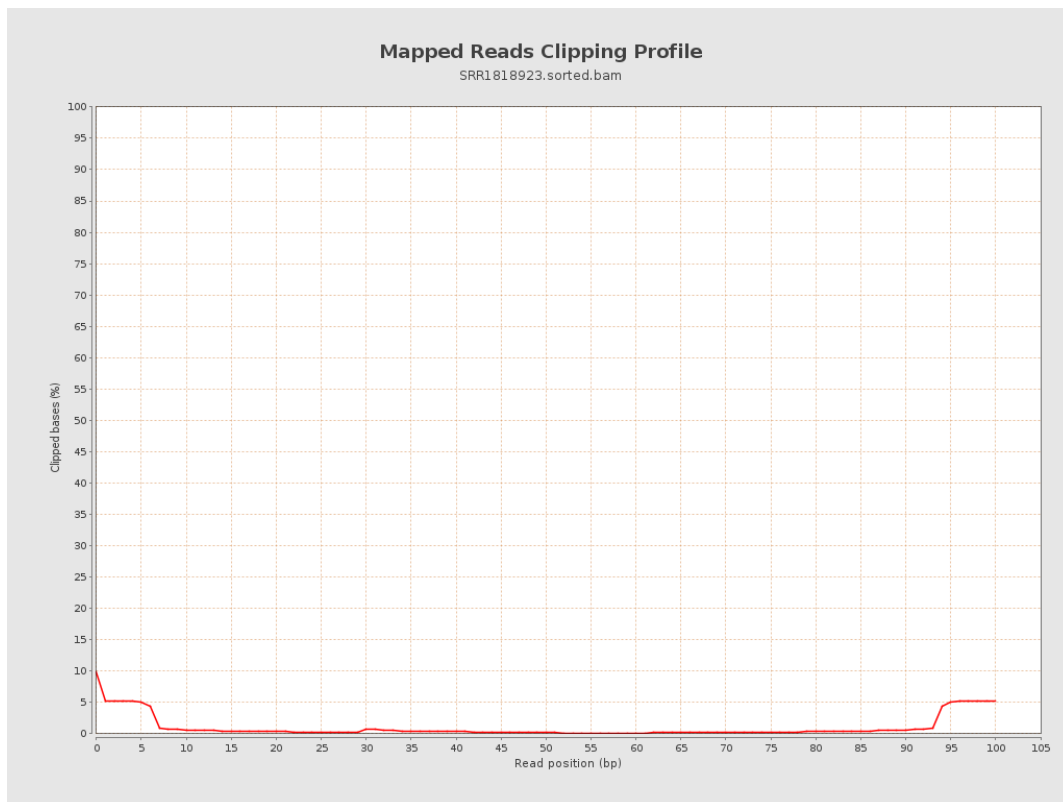
8. Results : Mapped Reads Nucleotide Content



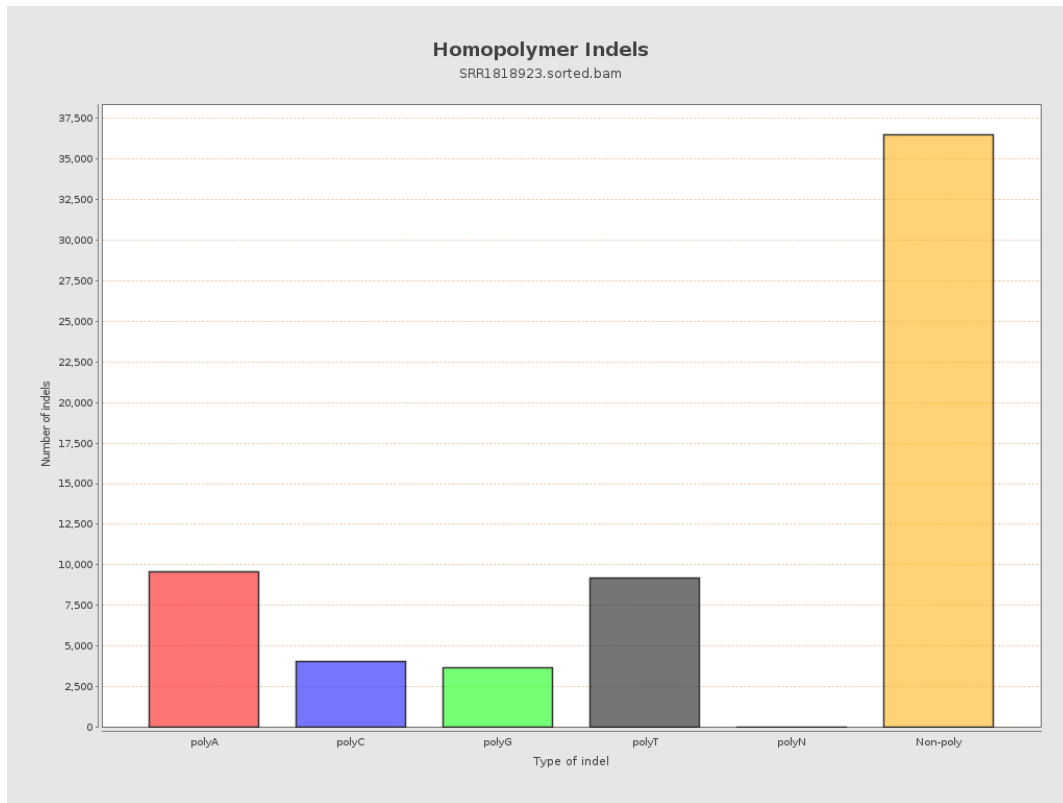
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

