

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:34:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818924.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_SRR1818924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818924.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:34:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	651,161
Mapped reads	623,239 / 95.71%
Unmapped reads	27,922 / 4.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,709 / 1.34%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	106,590 / 16.37%
Duplication rate	14.81%
Clipped reads	624,156 / 95.85%

2.2. ACGT Content

Number/percentage of A's	16,936,430 / 29.38%
Number/percentage of C's	11,953,582 / 20.74%
Number/percentage of T's	16,583,210 / 28.77%
Number/percentage of G's	12,171,661 / 21.11%
Number/percentage of N's	2,593 / 0%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.2474
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2.4. Mapping Quality

Mean Mapping Quality	49.17
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2.5. Mismatches and indels

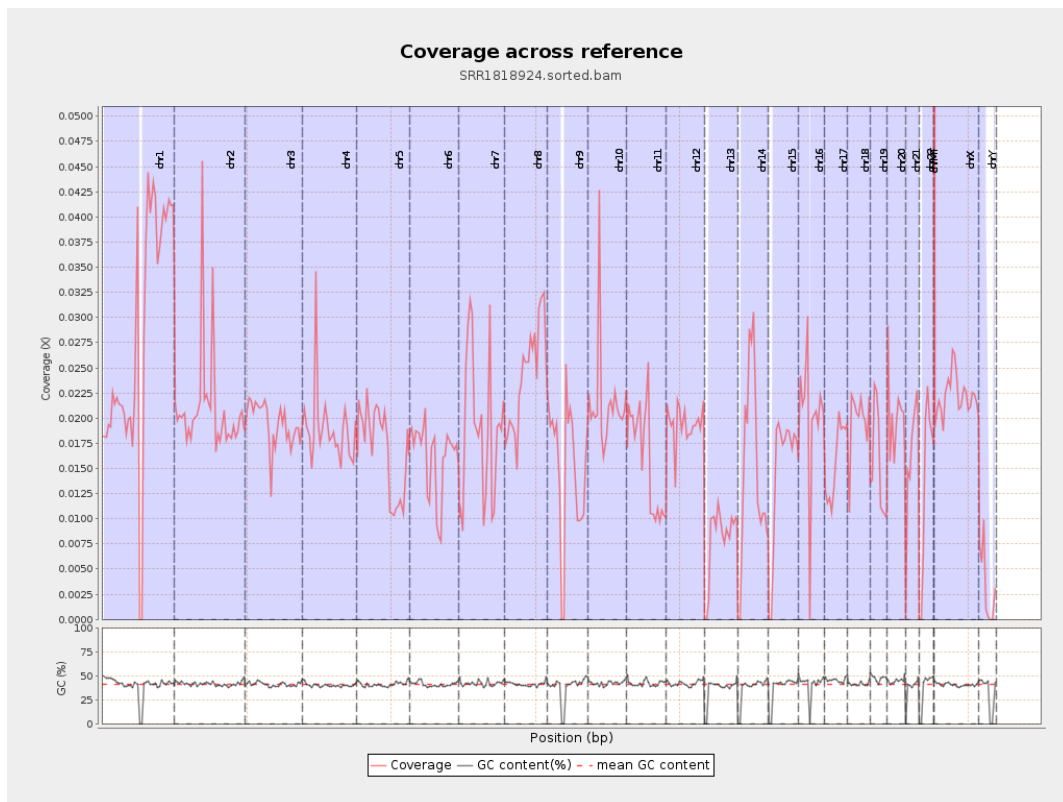
General error rate	0.72%
Mismatches	394,857
Insertions	7,912
Mapped reads with at least one insertion	1.23%
Deletions	17,824
Mapped reads with at least one deletion	2.8%
Homopolymer indels	43.01%

2.6. Chromosome stats

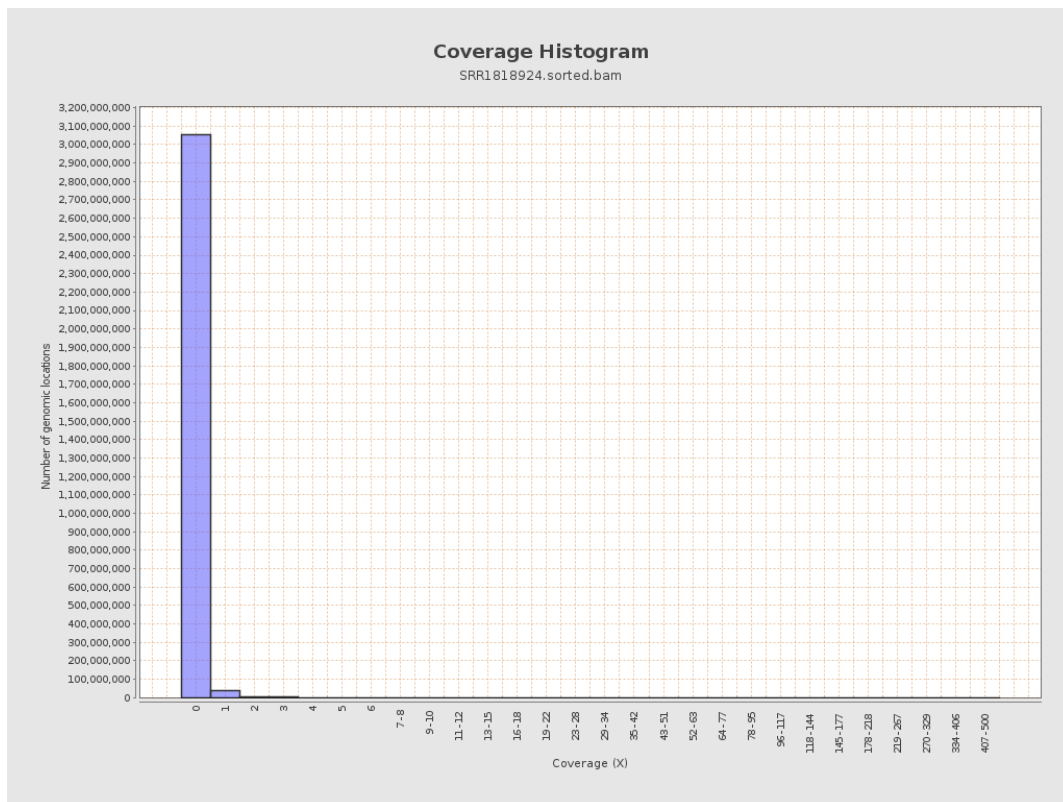
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6983818	0.028	0.4573
chr2	243199373	5086552	0.0209	0.3276
chr3	198022430	3852207	0.0195	0.1736
chr4	191154276	3617326	0.0189	0.1917
chr5	180915260	3052098	0.0169	0.1633
chr6	171115067	2744055	0.016	0.1647
chr7	159138663	3014814	0.0189	0.2182

chr8	146364022	3532358	0.0241	0.2197
chr9	141213431	2107968	0.0149	0.251
chr10	135534747	2930340	0.0216	0.2988
chr11	135006516	2188842	0.0162	0.182
chr12	133851895	2598262	0.0194	0.1761
chr13	115169878	918599	0.008	0.1094
chr14	107349540	1621552	0.0151	0.1598
chr15	102531392	1517056	0.0148	0.1514
chr16	90354753	1793021	0.0198	0.2477
chr17	81195210	1264898	0.0156	0.1668
chr18	78077248	1513462	0.0194	0.3083
chr19	59128983	928096	0.0157	0.3935
chr20	63025520	1259712	0.02	0.1816
chr21	48129895	790068	0.0164	0.1721
chr22	51304566	713570	0.0139	0.1527
chrMT	16571	6360	0.3838	0.8235
chrX	155270560	3451803	0.0222	0.2069
chrY	59373566	193412	0.0033	0.1915

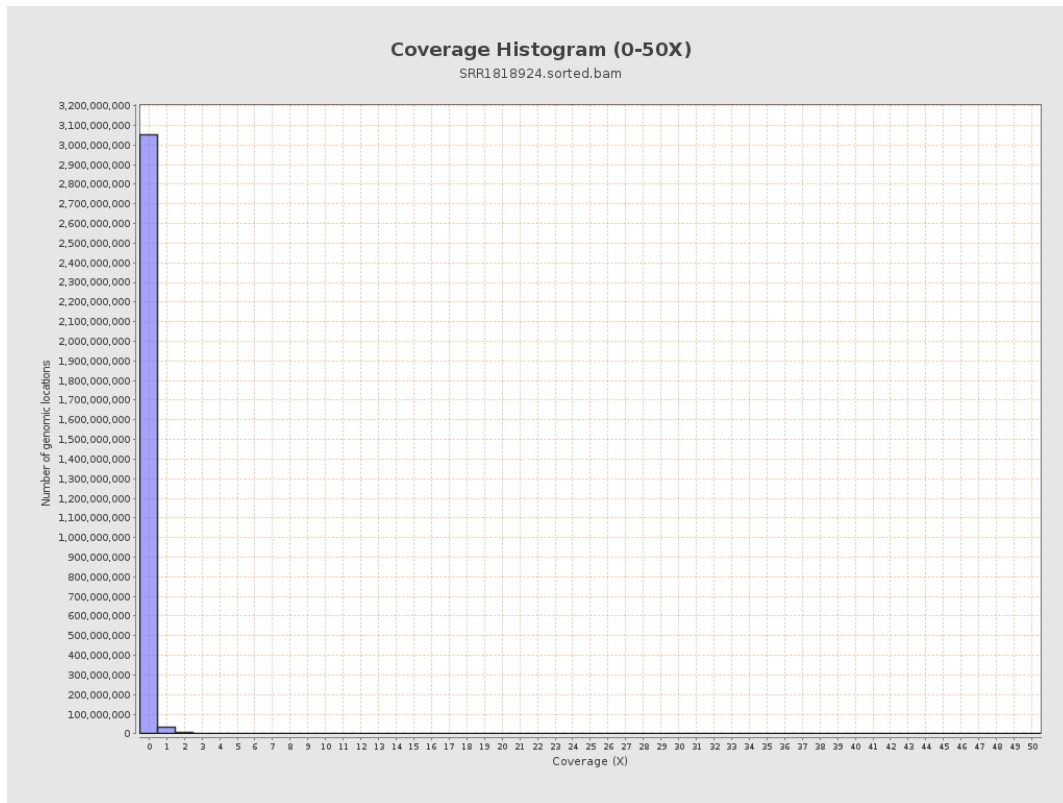
3. Results : Coverage across reference



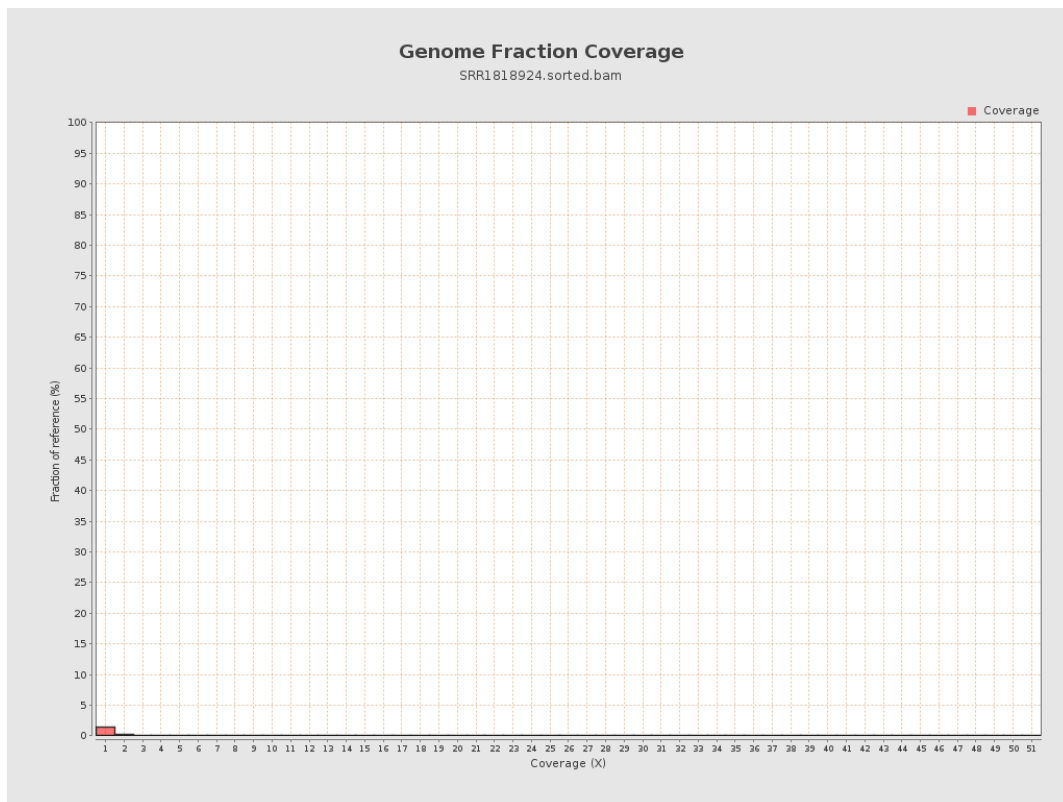
4. Results : Coverage Histogram



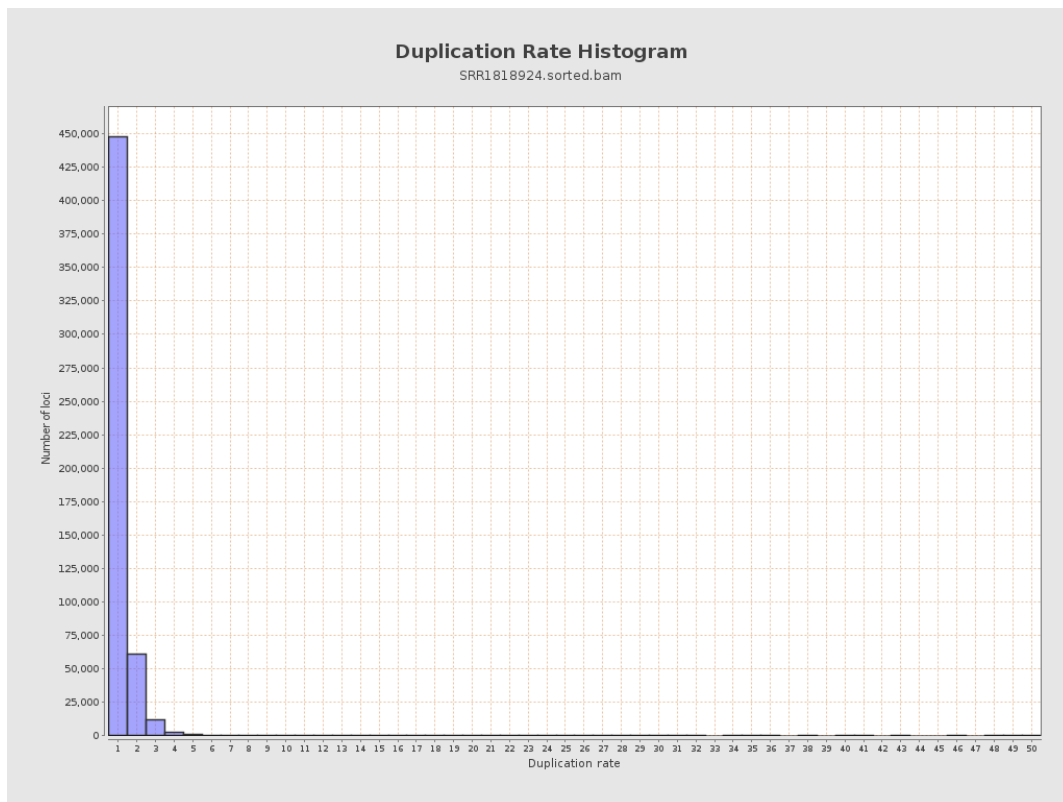
5. Results : Coverage Histogram (0-50X)



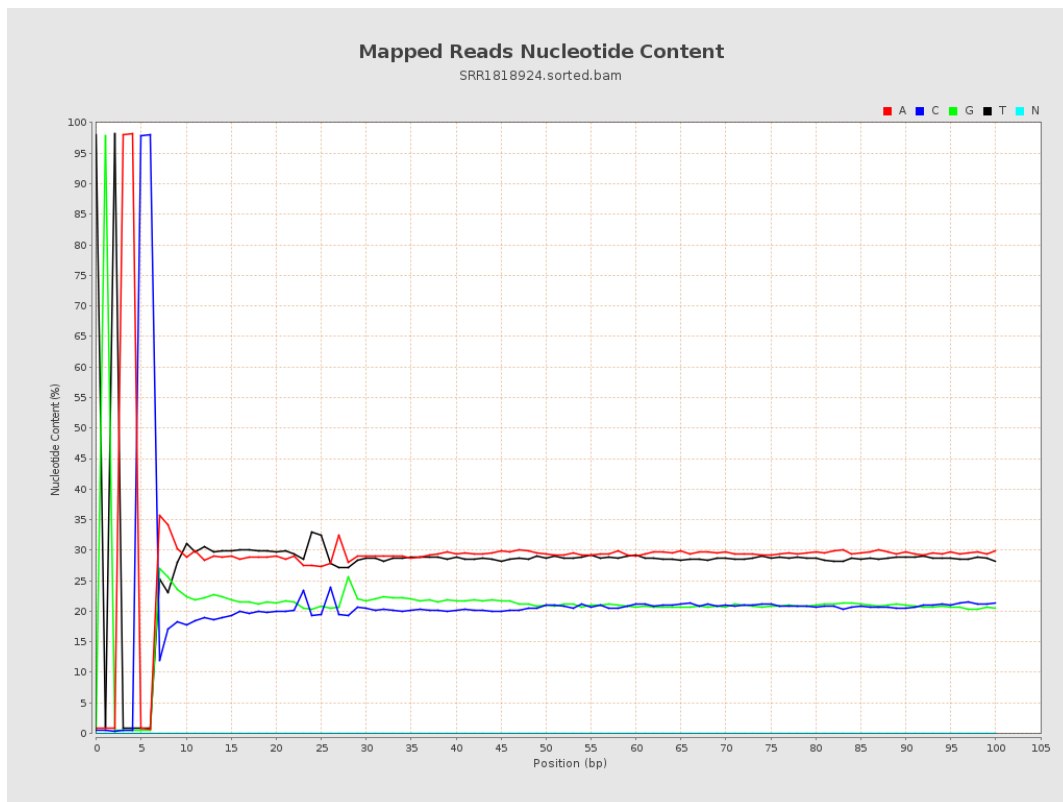
6. Results : Genome Fraction Coverage



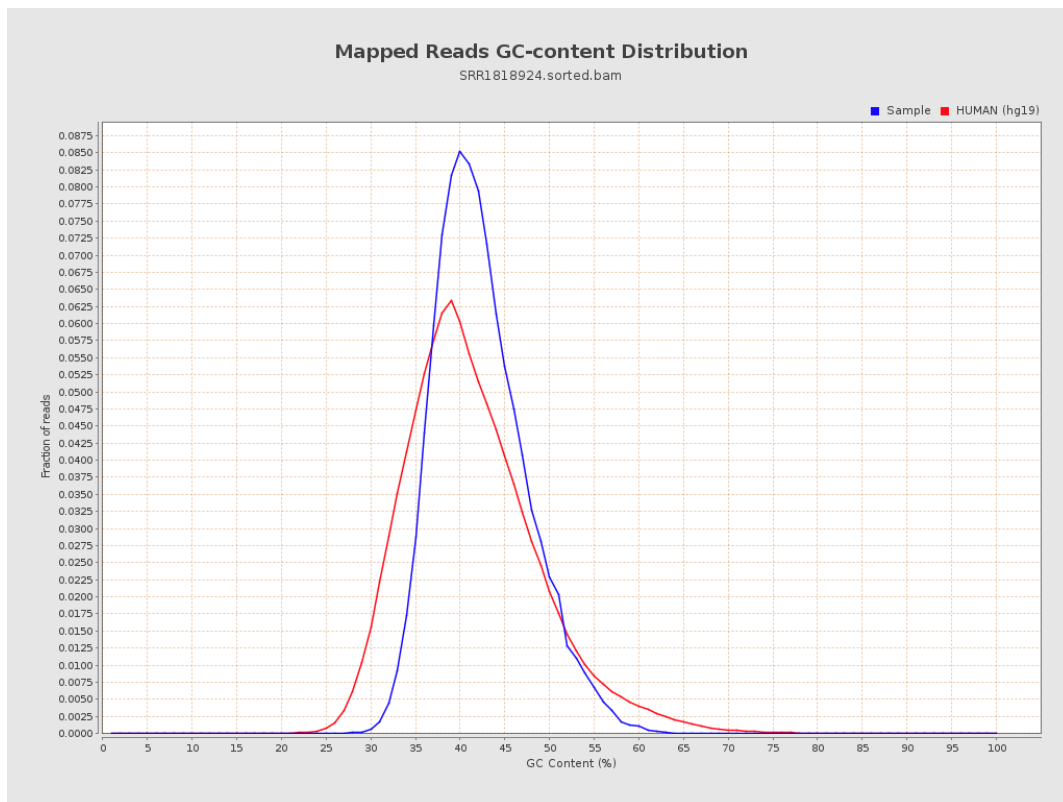
7. Results : Duplication Rate Histogram



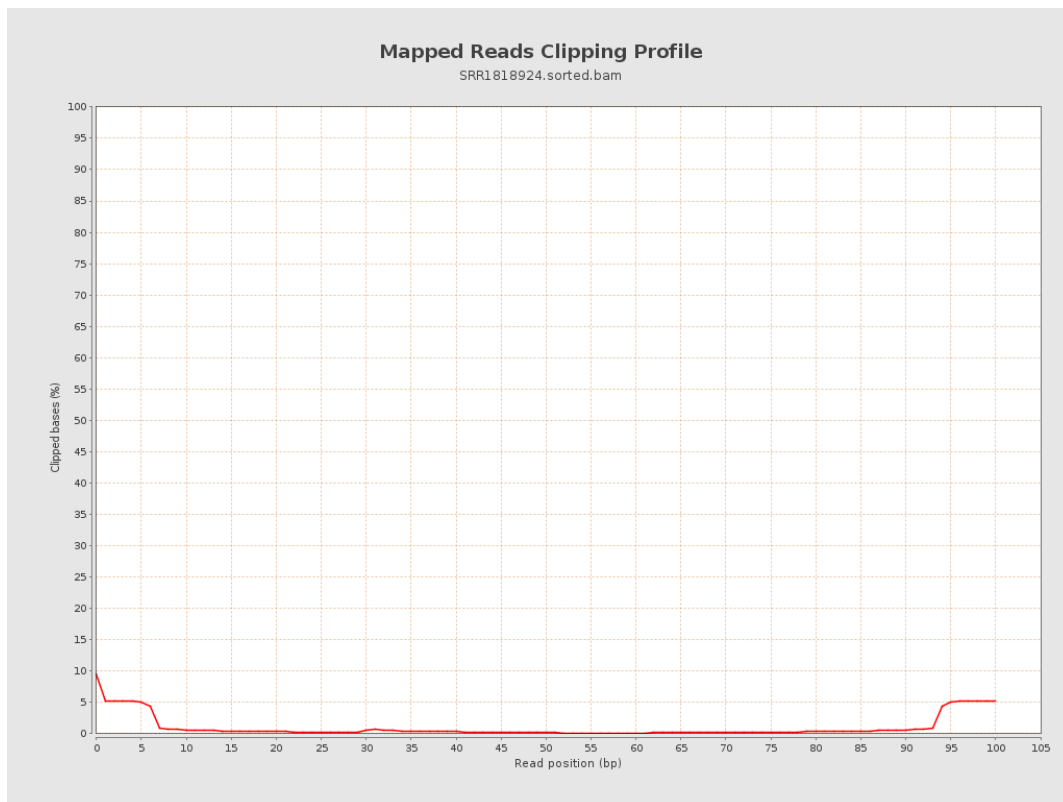
8. Results : Mapped Reads Nucleotide Content



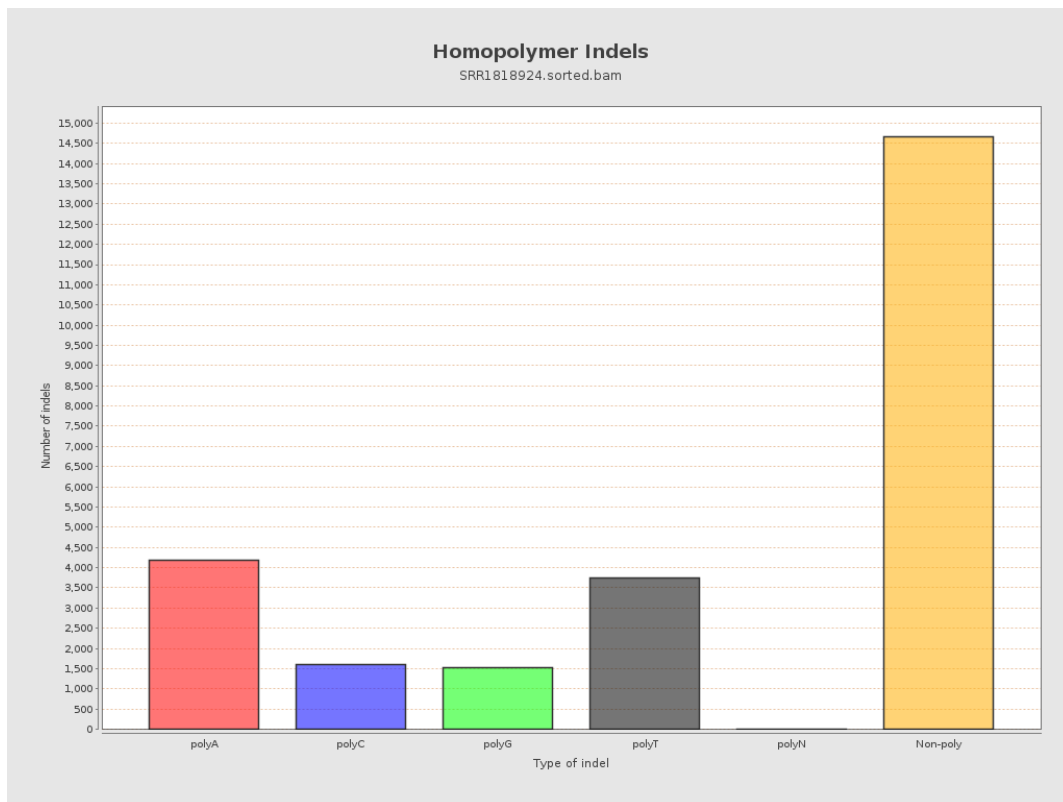
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

