

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:55:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819048.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_SRR1819048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:55:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	635,854
Mapped reads	576,558 / 90.67%
Unmapped reads	59,296 / 9.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,157 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	8,617 / 1.36%
Duplication rate	1.16%
Clipped reads	577,408 / 90.81%

2.2. ACGT Content

Number/percentage of A's	7,931,808 / 24.18%
Number/percentage of C's	6,610,186 / 20.15%
Number/percentage of T's	10,033,176 / 30.59%
Number/percentage of G's	8,227,432 / 25.08%
Number/percentage of N's	798 / 0%
GC Percentage	45.23%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.117
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2.4. Mapping Quality

Mean Mapping Quality	43.9
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2.5. Mismatches and indels

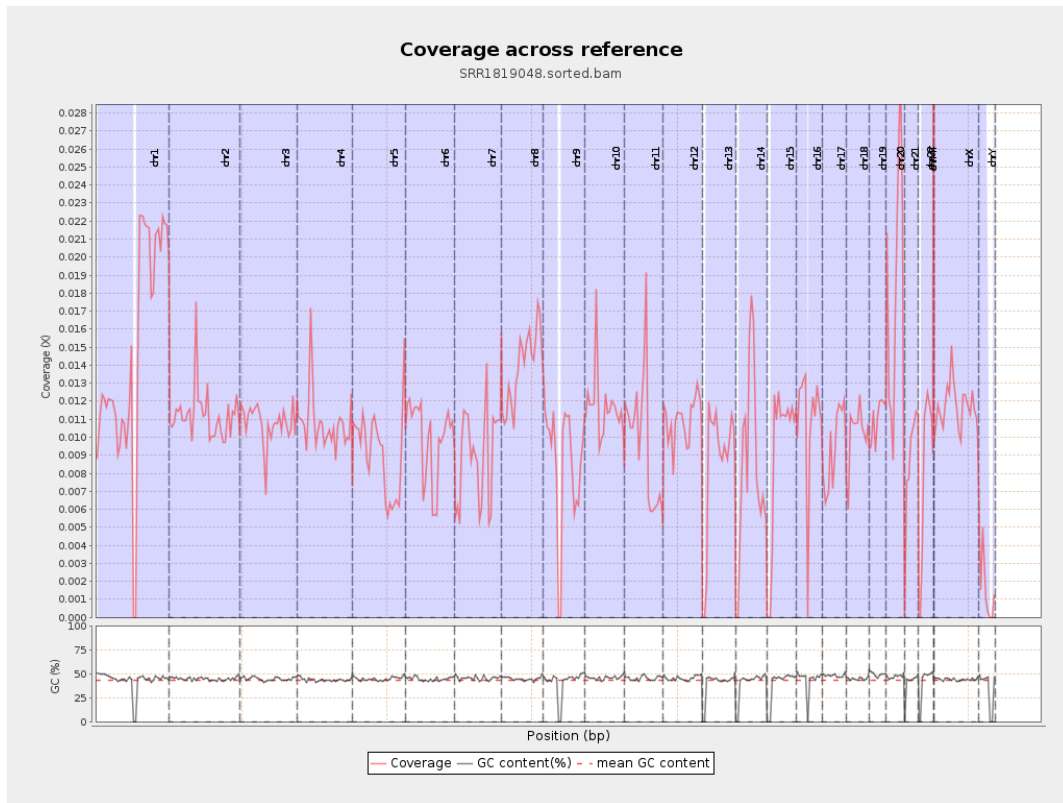
General error rate	0.5%
Mismatches	161,563
Insertions	2,078
Mapped reads with at least one insertion	0.36%
Deletions	5,277
Mapped reads with at least one deletion	0.91%
Homopolymer indels	40.57%

2.6. Chromosome stats

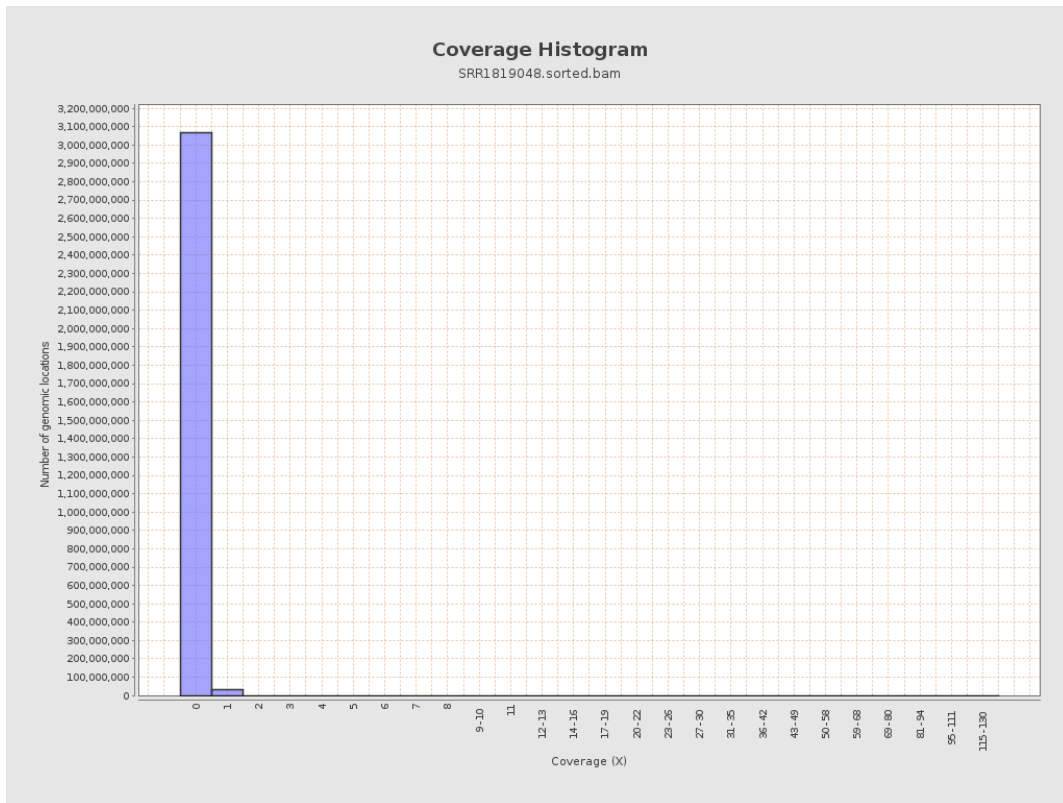
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3659452	0.0147	0.1519
chr2	243199373	2733489	0.0112	0.1268
chr3	198022430	2128426	0.0107	0.1072
chr4	191154276	2051473	0.0107	0.1112
chr5	180915260	1645878	0.0091	0.0989
chr6	171115067	1694041	0.0099	0.1062
chr7	159138663	1423250	0.0089	0.1089

chr8	146364022	2039553	0.0139	0.1279
chr9	141213431	1184765	0.0084	0.1086
chr10	135534747	1581526	0.0117	0.1276
chr11	135006516	1310080	0.0097	0.1201
chr12	133851895	1465930	0.011	0.1087
chr13	115169878	982556	0.0085	0.0955
chr14	107349540	899622	0.0084	0.0958
chr15	102531392	949432	0.0093	0.0996
chr16	90354753	989638	0.011	0.1115
chr17	81195210	770475	0.0095	0.1022
chr18	78077248	796072	0.0102	0.1692
chr19	59128983	649409	0.011	0.1246
chr20	63025520	1115136	0.0177	0.1399
chr21	48129895	422050	0.0088	0.1026
chr22	51304566	408364	0.008	0.0925
chrMT	16571	813	0.0491	0.2418
chrX	155270560	1818889	0.0117	0.1179
chrY	59373566	92113	0.0016	0.048

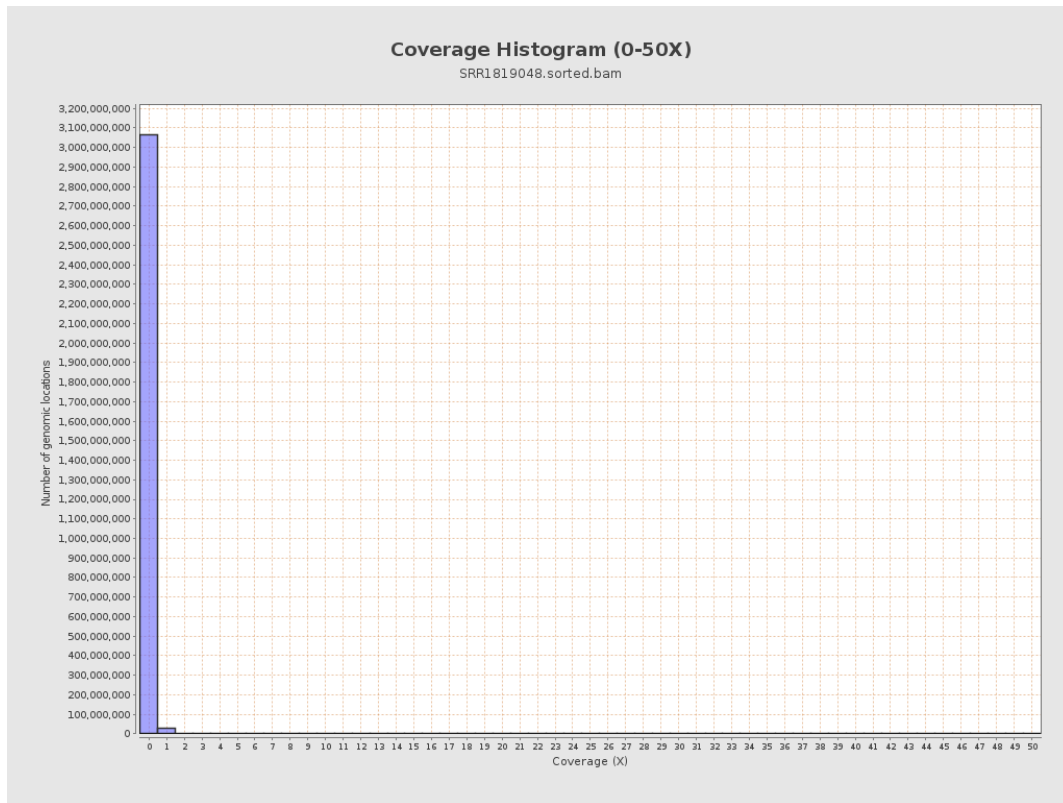
3. Results : Coverage across reference



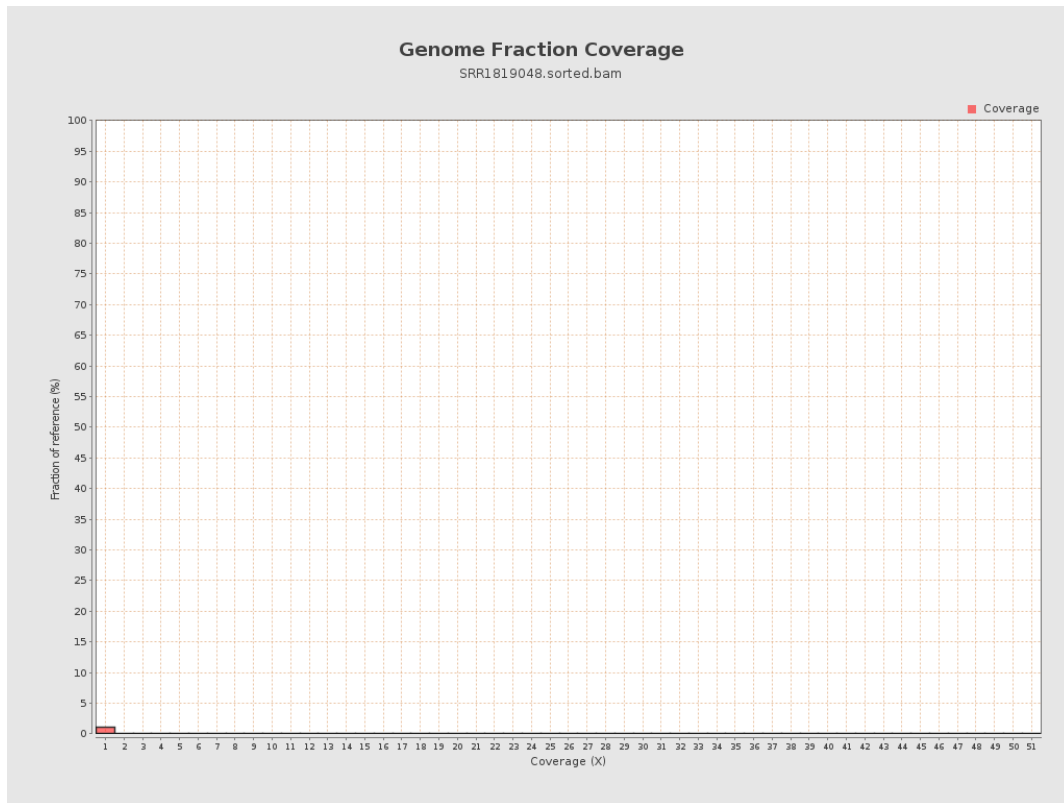
4. Results : Coverage Histogram



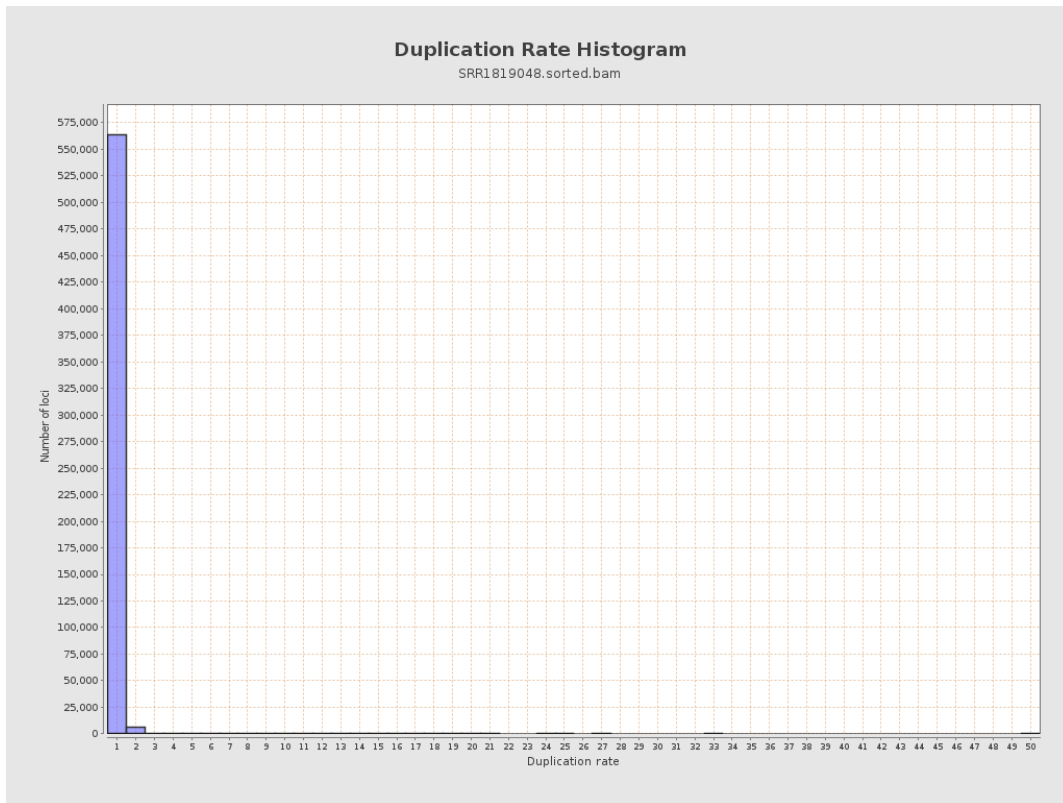
5. Results : Coverage Histogram (0-50X)



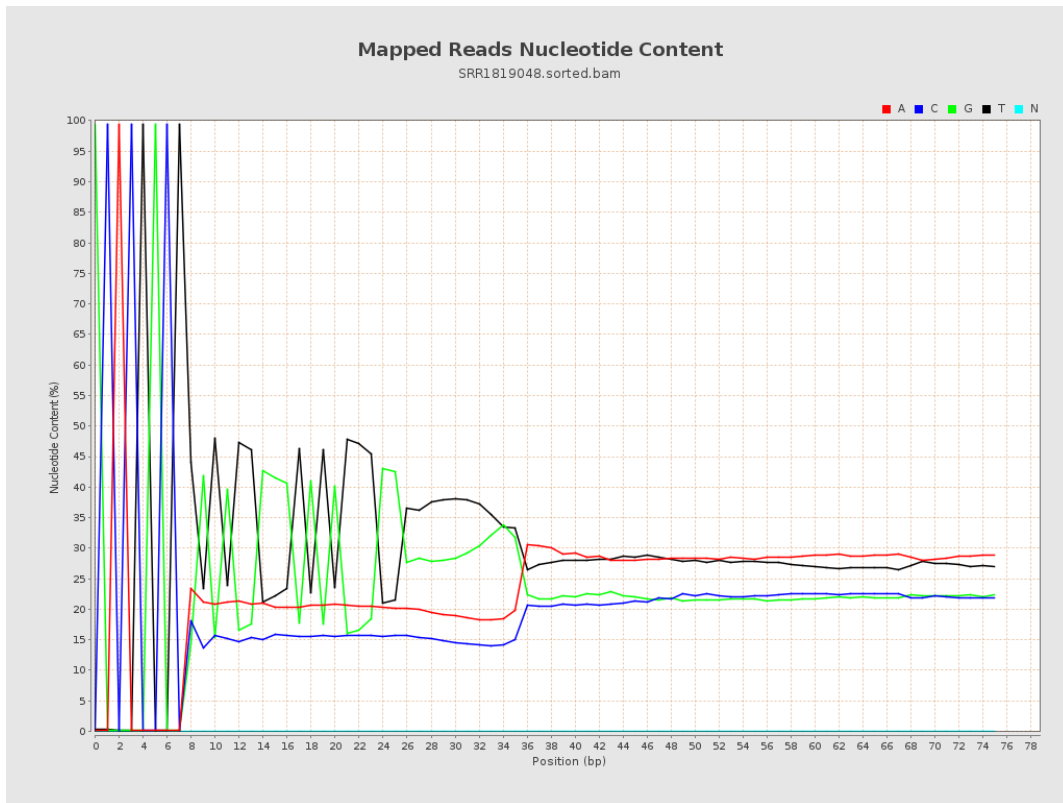
6. Results : Genome Fraction Coverage



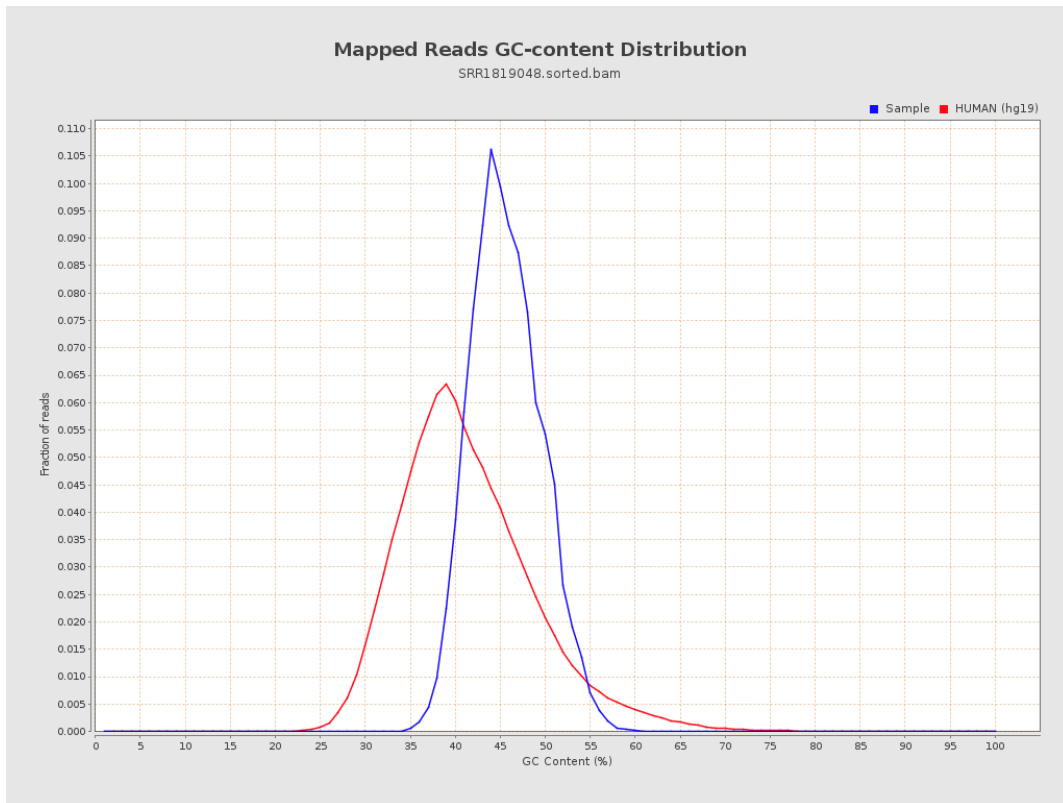
7. Results : Duplication Rate Histogram



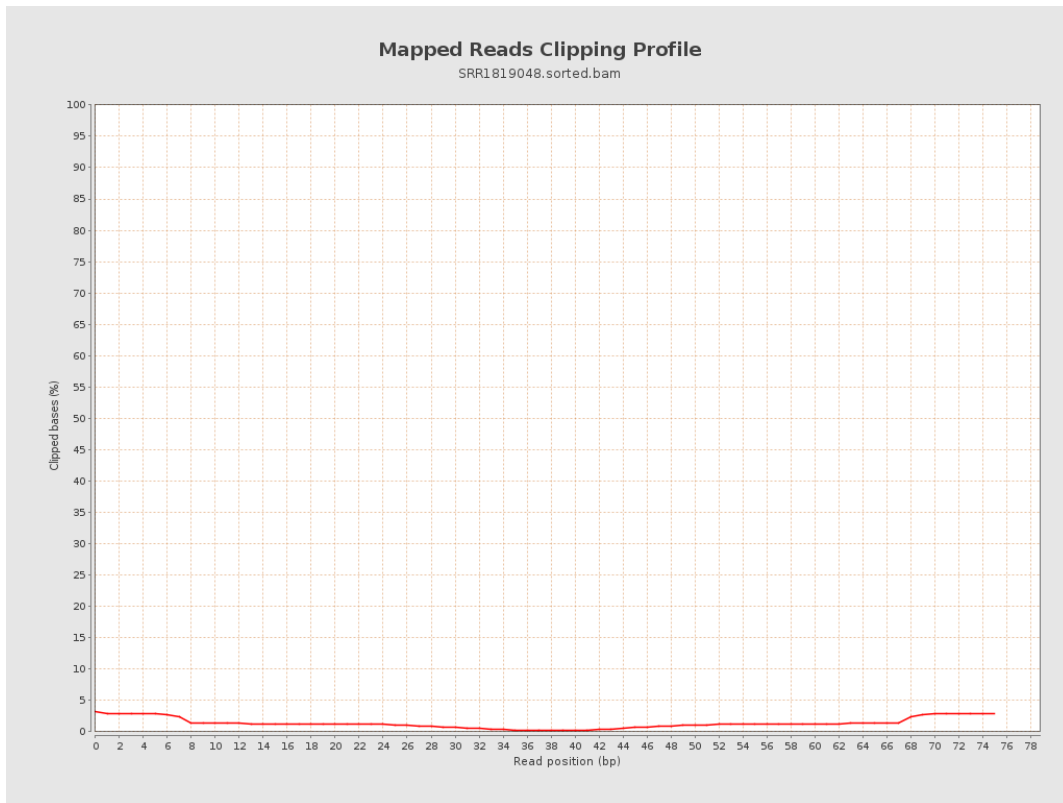
8. Results : Mapped Reads Nucleotide Content



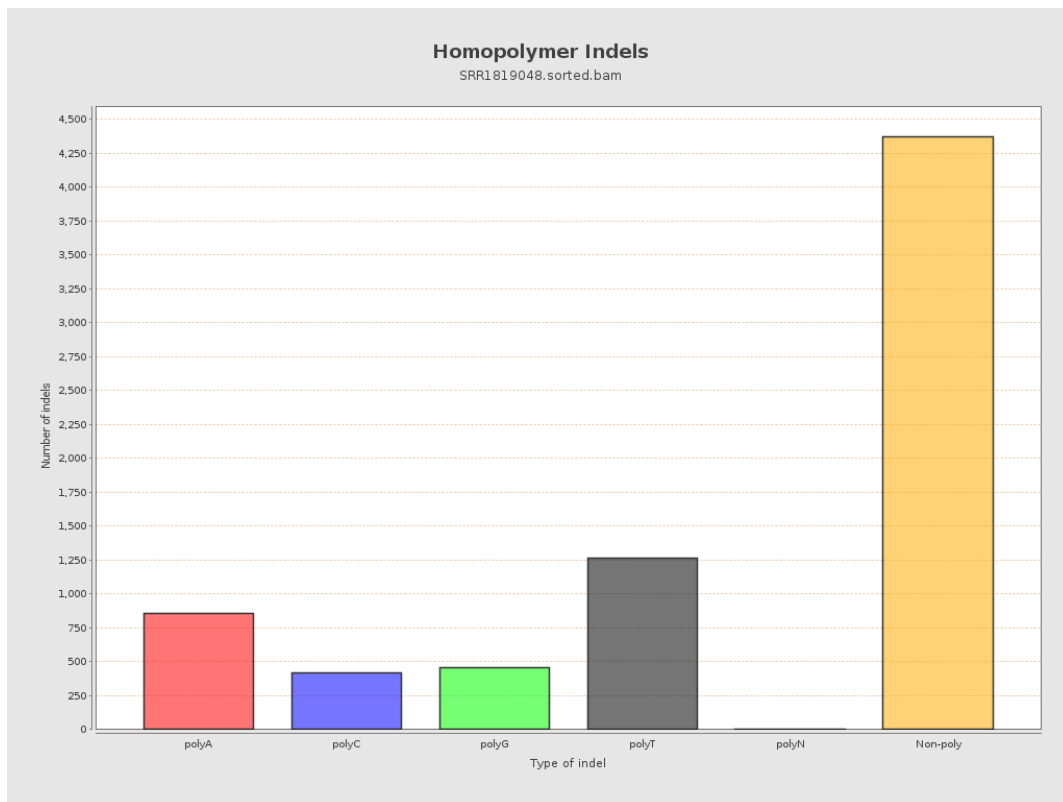
9. Results : Mapped Reads GC-content Distribution



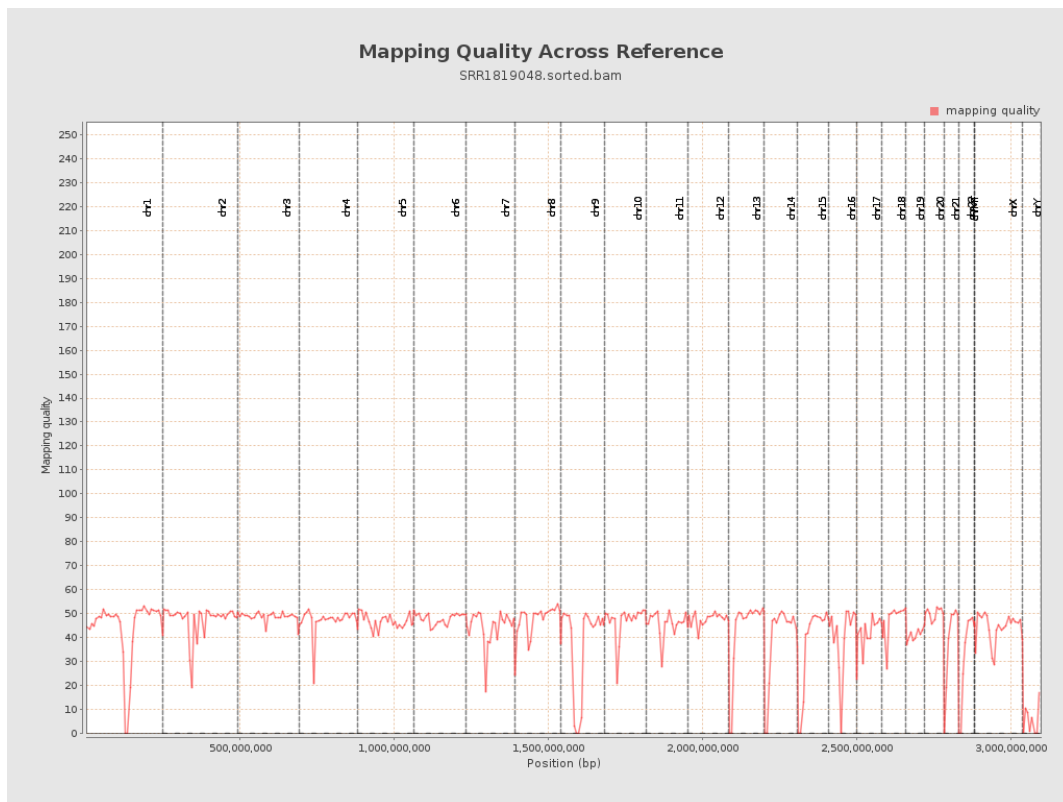
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

