

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:08:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818748.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_SRR1818748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:08:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	379,262
Mapped reads	368,407 / 97.14%
Unmapped reads	10,855 / 2.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,746 / 0.72%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	82,097 / 21.65%
Duplication rate	20.15%
Clipped reads	370,780 / 97.76%

2.2. ACGT Content

Number/percentage of A's	6,866,718 / 27.49%
Number/percentage of C's	5,474,590 / 21.92%
Number/percentage of T's	7,041,588 / 28.19%
Number/percentage of G's	5,595,932 / 22.4%
Number/percentage of N's	1,465 / 0.01%
GC Percentage	44.32%

2.3. Coverage

Mean	0.0081

Standard Deviation	0.1445
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2.4. Mapping Quality

Mean Mapping Quality	47.29
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2.5. Mismatches and indels

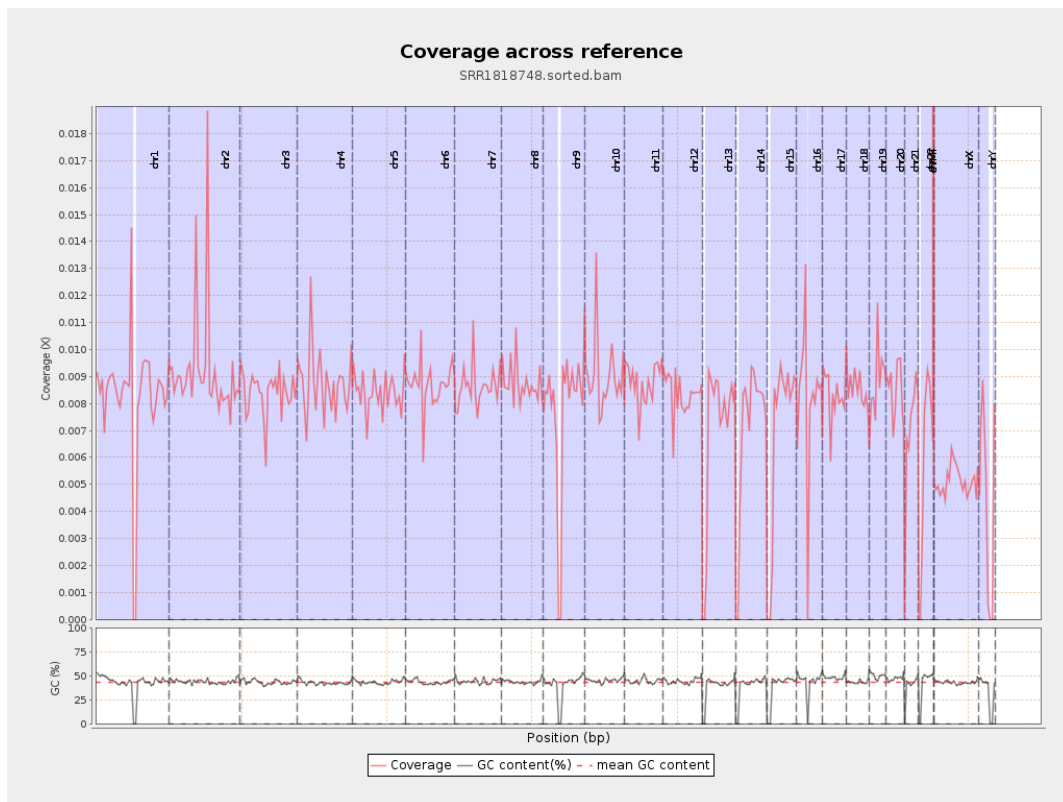
General error rate	0.52%
Mismatches	125,729
Insertions	2,457
Mapped reads with at least one insertion	0.66%
Deletions	6,481
Mapped reads with at least one deletion	1.74%
Homopolymer indels	42.48%

2.6. Chromosome stats

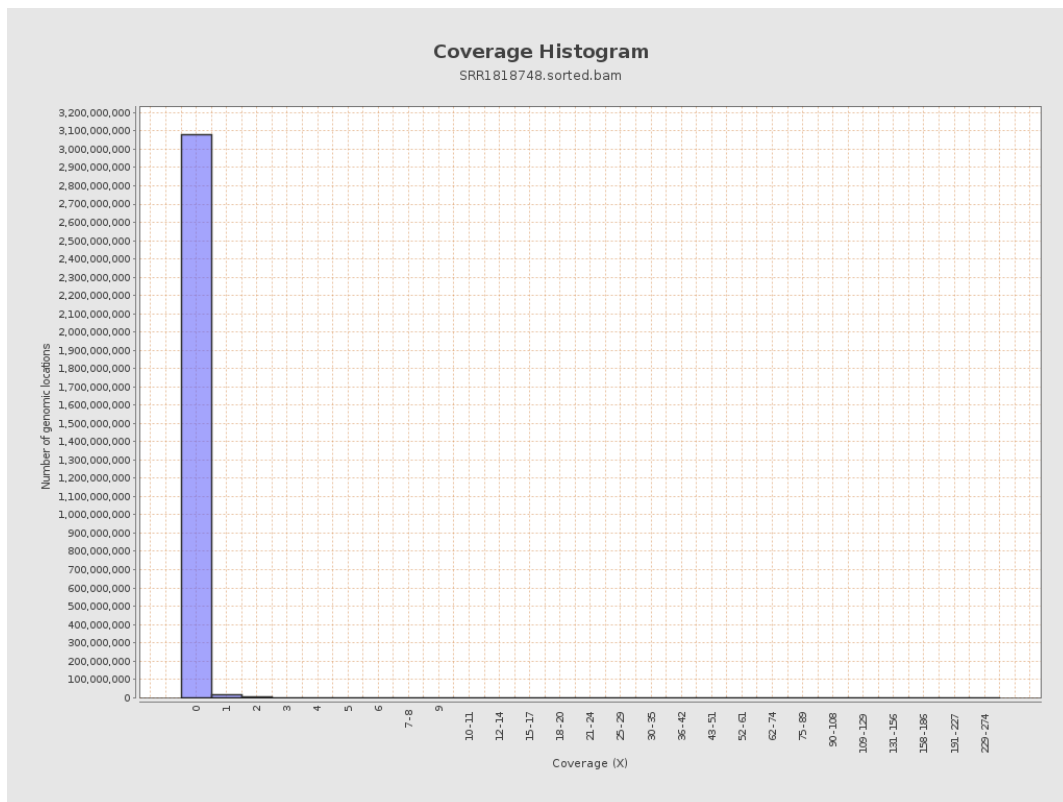
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2046770	0.0082	0.1816
chr2	243199373	2240600	0.0092	0.2203
chr3	198022430	1662153	0.0084	0.1188
chr4	191154276	1664652	0.0087	0.1339
chr5	180915260	1518584	0.0084	0.1223
chr6	171115067	1487784	0.0087	0.1294
chr7	159138663	1374386	0.0086	0.1328

chr8	146364022	1281255	0.0088	0.129
chr9	141213431	1078379	0.0076	0.1254
chr10	135534747	1214038	0.009	0.1512
chr11	135006516	1184279	0.0088	0.1289
chr12	133851895	1115692	0.0083	0.1203
chr13	115169878	797782	0.0069	0.1086
chr14	107349540	752131	0.007	0.1125
chr15	102531392	710733	0.0069	0.1104
chr16	90354753	742700	0.0082	0.1709
chr17	81195210	669747	0.0082	0.1226
chr18	78077248	666930	0.0085	0.1531
chr19	59128983	523972	0.0089	0.1659
chr20	63025520	531928	0.0084	0.1235
chr21	48129895	335157	0.007	0.1117
chr22	51304566	296852	0.0058	0.1044
chrMT	16571	44230	2.6691	3.1373
chrX	155270560	794092	0.0051	0.0978
chrY	59373566	256001	0.0043	0.2203

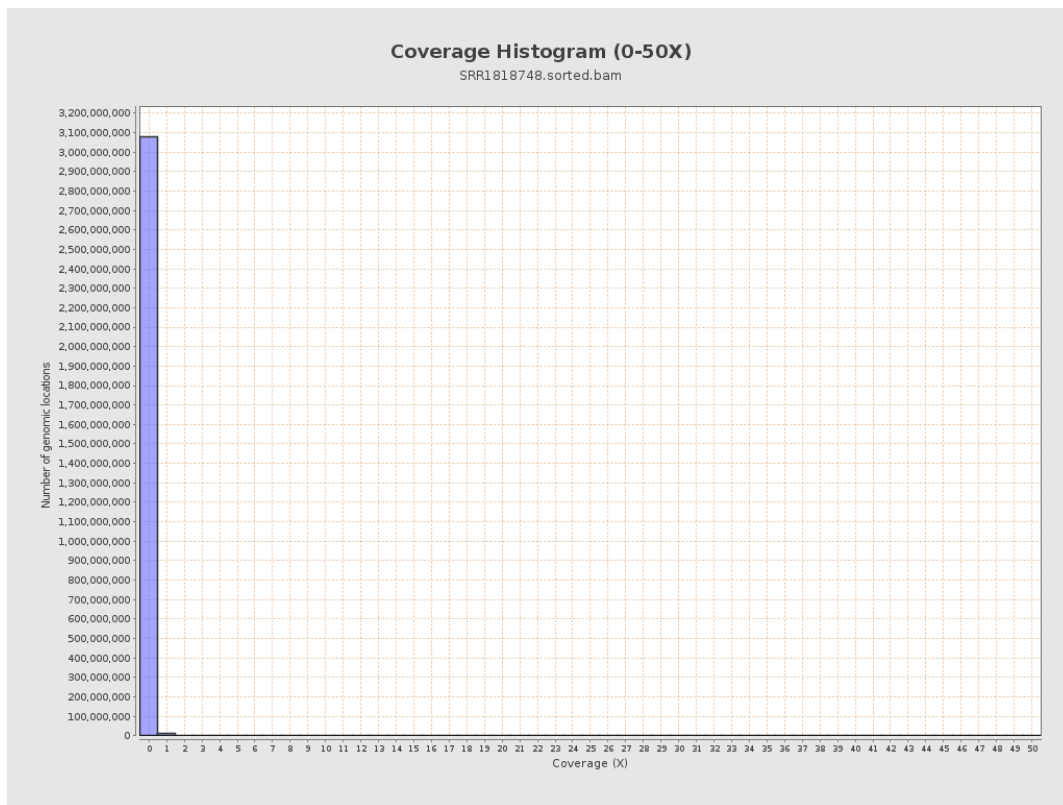
3. Results : Coverage across reference



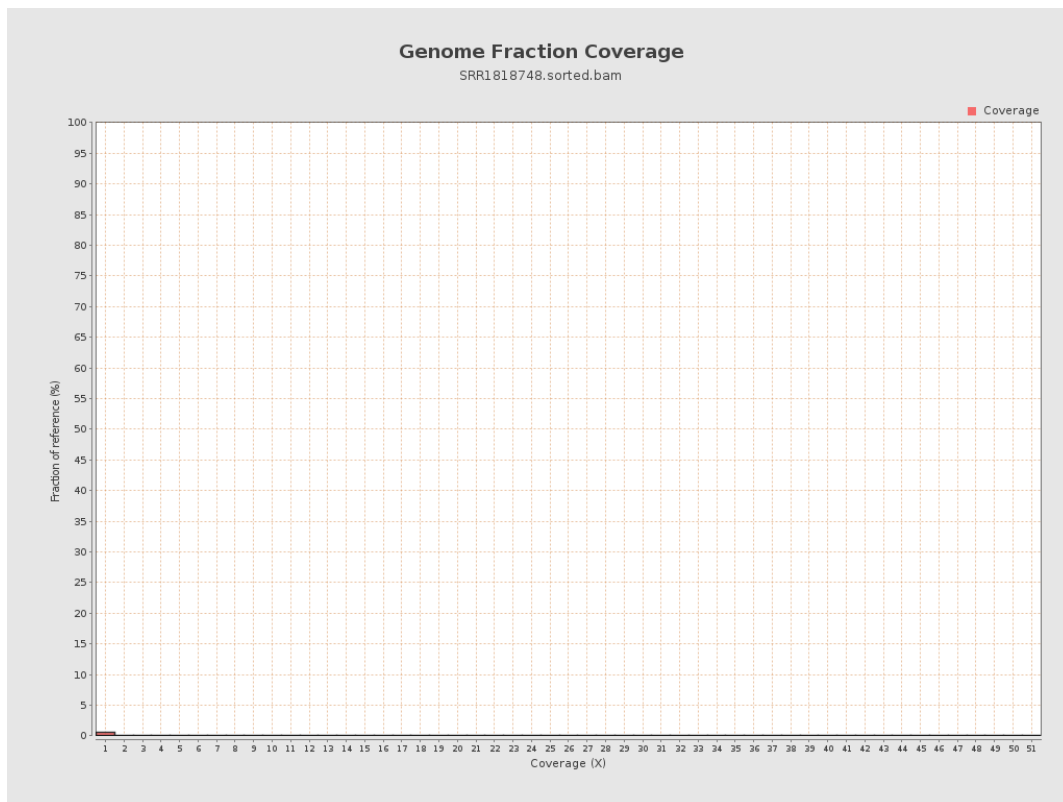
4. Results : Coverage Histogram



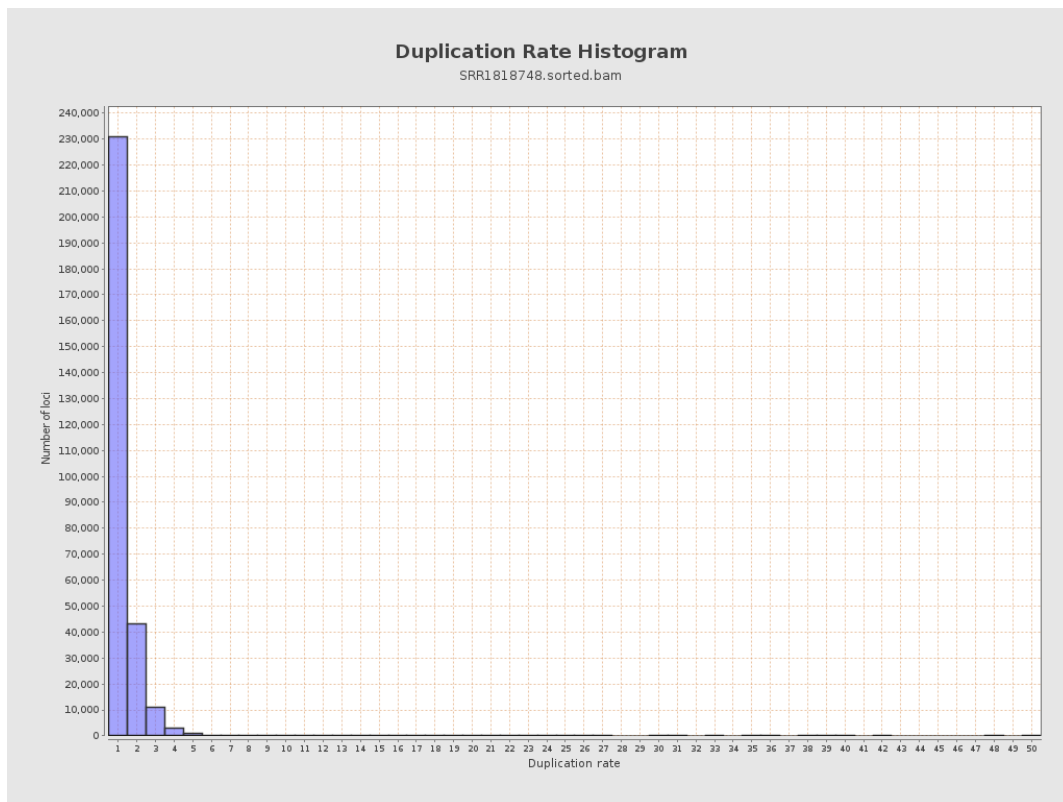
5. Results : Coverage Histogram (0-50X)



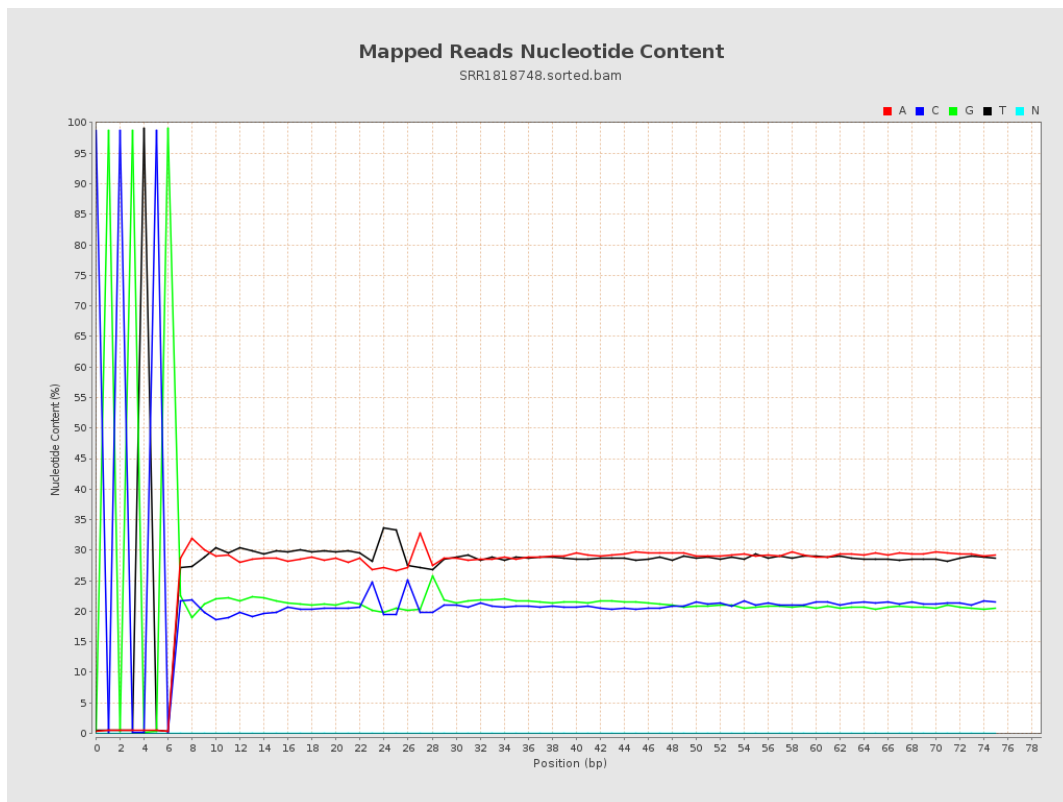
6. Results : Genome Fraction Coverage



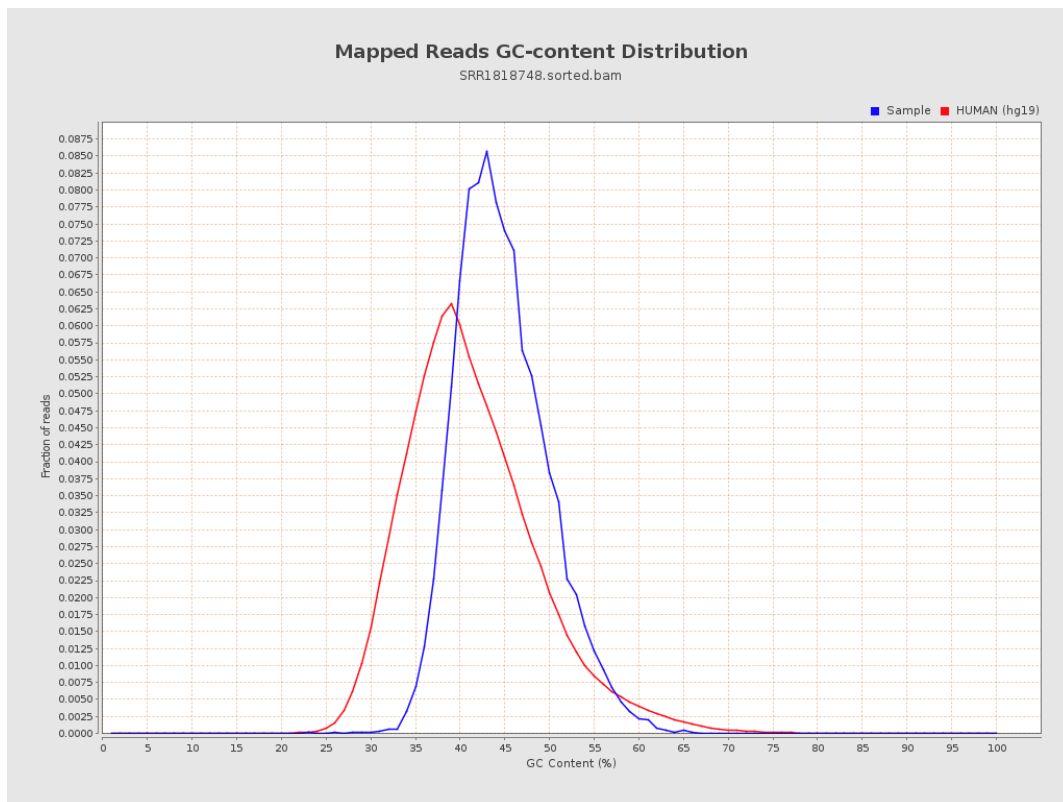
7. Results : Duplication Rate Histogram



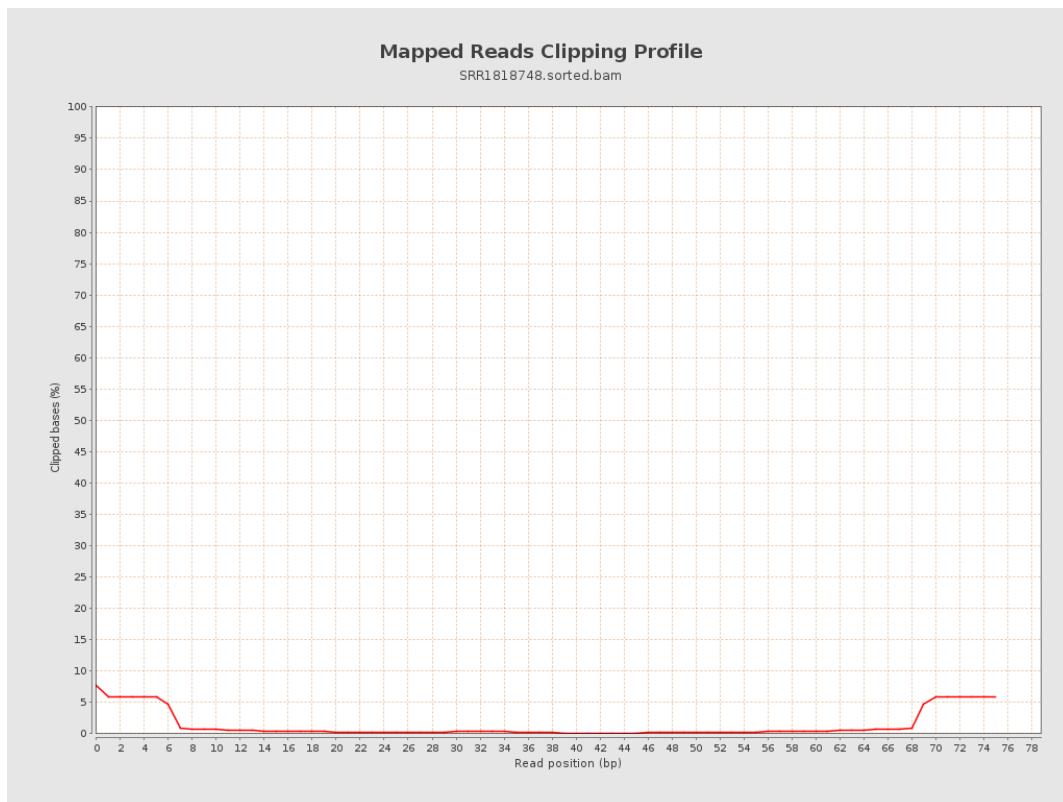
8. Results : Mapped Reads Nucleotide Content



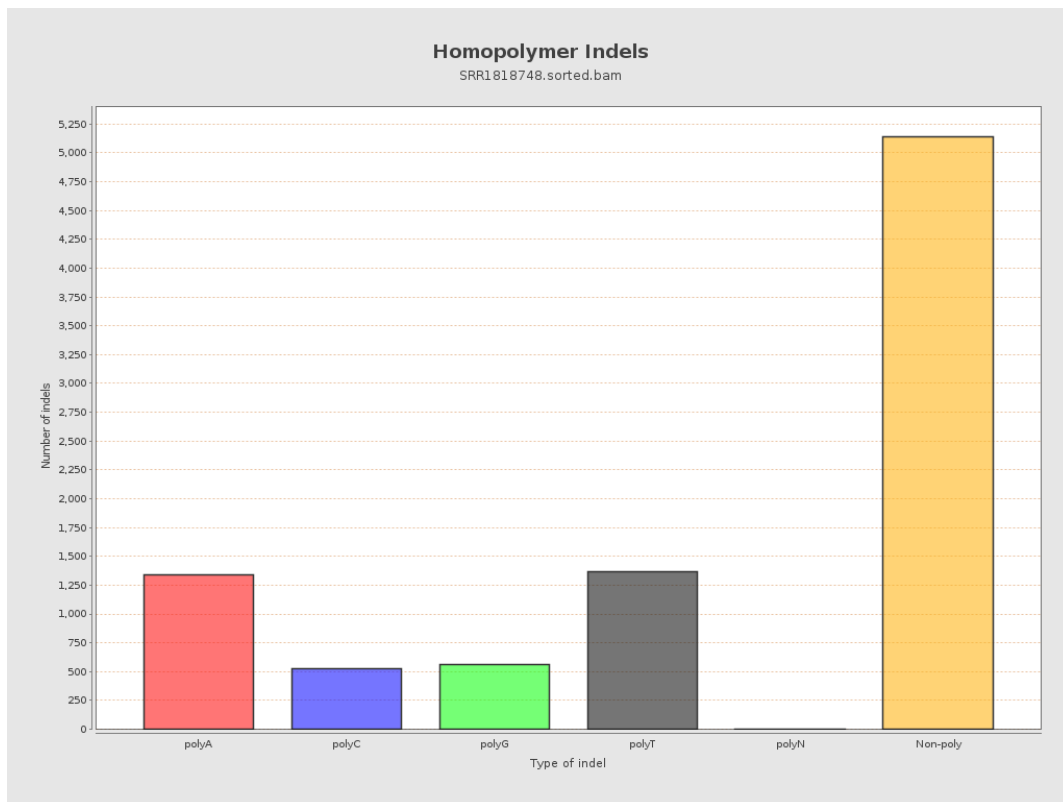
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

