

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:32:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716792.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_SRR9716792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:32:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,613,702
Mapped reads	1,412,524 / 87.53%
Unmapped reads	201,178 / 12.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,640 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	34,604 / 2.14%
Duplication rate	1.72%
Clipped reads	1,414,643 / 87.66%

2.2. ACGT Content

Number/percentage of A's	20,036,510 / 25.08%
Number/percentage of C's	15,296,930 / 19.15%
Number/percentage of T's	25,473,436 / 31.89%
Number/percentage of G's	19,079,373 / 23.88%
Number/percentage of N's	499 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0258

Standard Deviation	0.2245
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2.4. Mapping Quality

Mean Mapping Quality	42.3
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2.5. Mismatches and indels

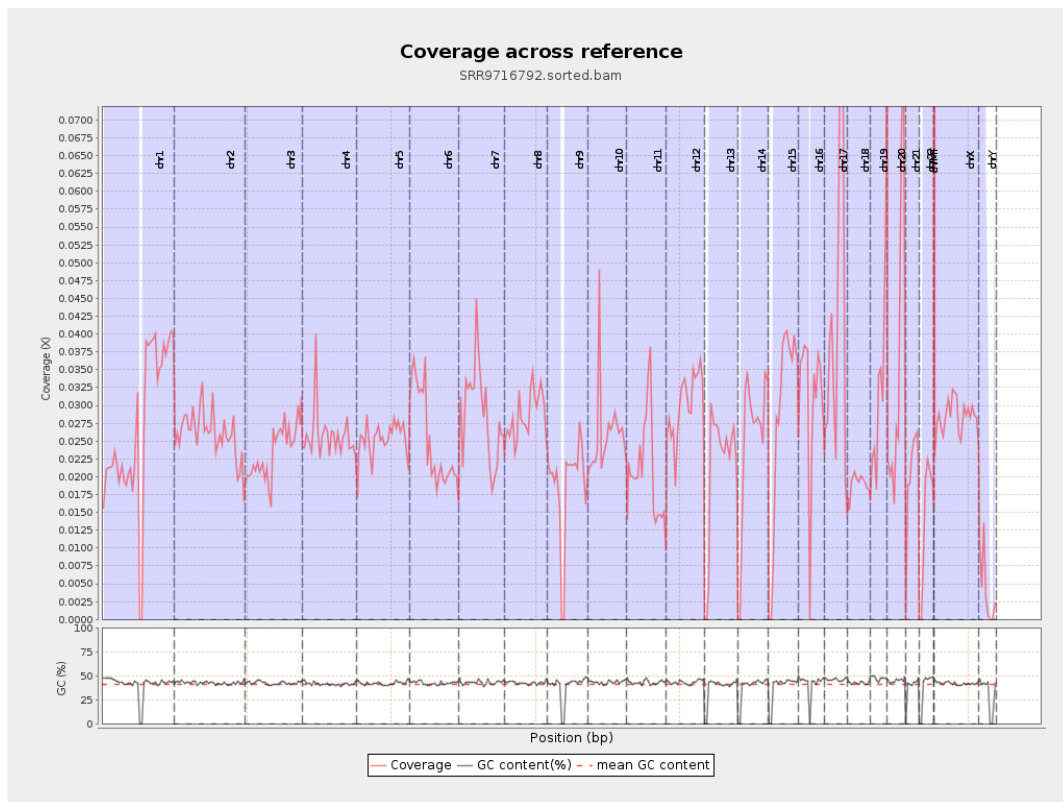
General error rate	0.53%
Mismatches	414,827
Insertions	5,840
Mapped reads with at least one insertion	0.41%
Deletions	14,992
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.46%

2.6. Chromosome stats

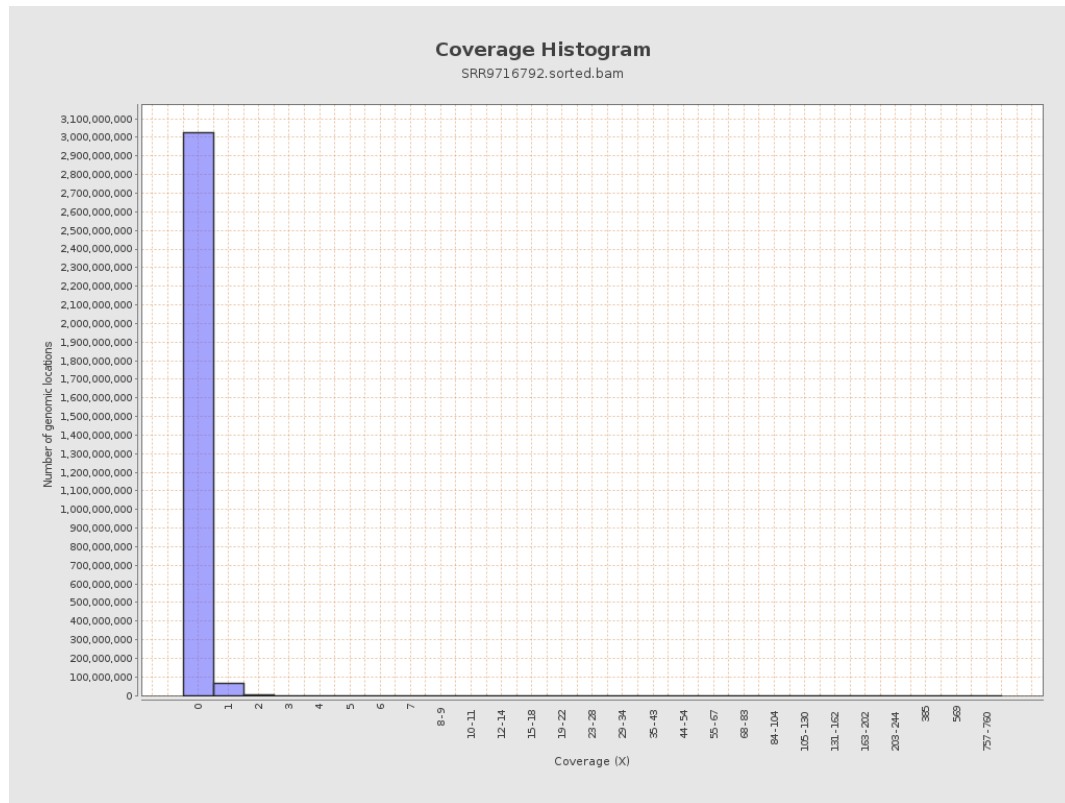
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6709175	0.0269	0.2576
chr2	243199373	6327267	0.026	0.3515
chr3	198022430	4648911	0.0235	0.1672
chr4	191154276	4925624	0.0258	0.1853
chr5	180915260	4613744	0.0255	0.1715
chr6	171115067	4307137	0.0252	0.2037
chr7	159138663	4593700	0.0289	0.3126

chr8	146364022	4189073	0.0286	0.2148
chr9	141213431	2663539	0.0189	0.1688
chr10	135534747	3525856	0.026	0.2669
chr11	135006516	2847922	0.0211	0.1912
chr12	133851895	4014873	0.03	0.1875
chr13	115169878	2454351	0.0213	0.1573
chr14	107349540	2702234	0.0252	0.1787
chr15	102531392	2943256	0.0287	0.1889
chr16	90354753	2762826	0.0306	0.1993
chr17	81195210	3542686	0.0436	0.2372
chr18	78077248	1479088	0.0189	0.2603
chr19	59128983	1955349	0.0331	0.2582
chr20	63025520	2280109	0.0362	0.2137
chr21	48129895	985621	0.0205	0.1652
chr22	51304566	730351	0.0142	0.1294
chrMT	16571	45734	2.7599	2.5661
chrX	155270560	4419426	0.0285	0.1932
chrY	59373566	242647	0.0041	0.1122

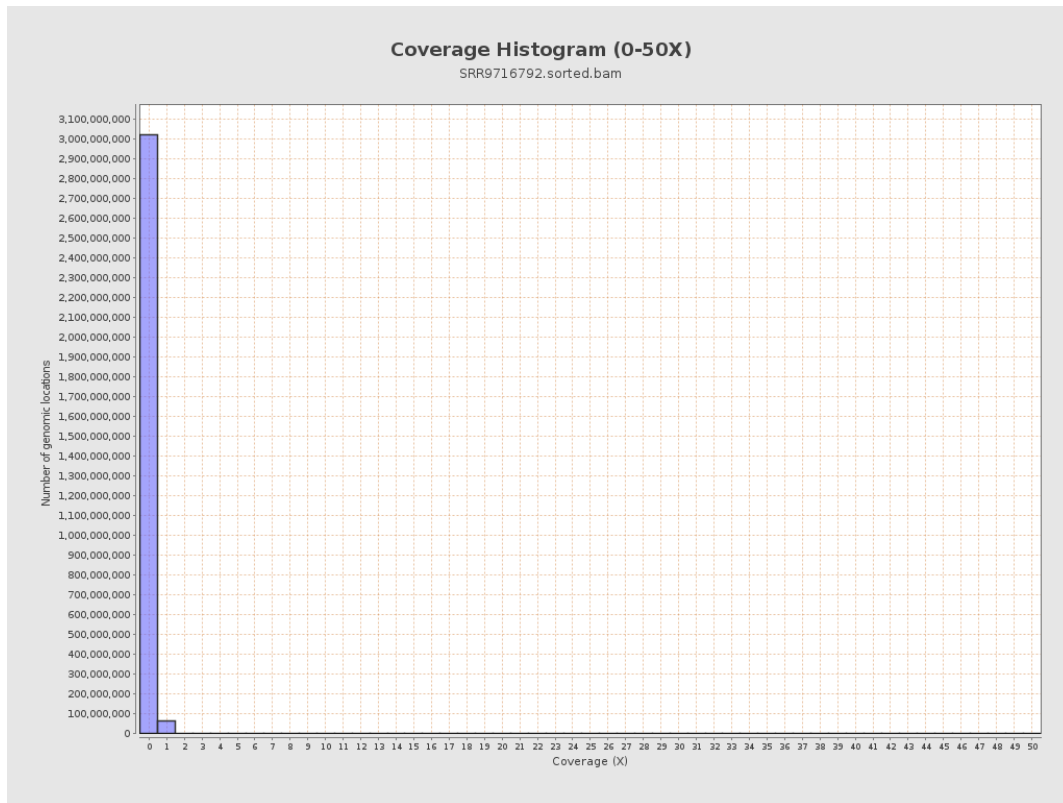
3. Results : Coverage across reference



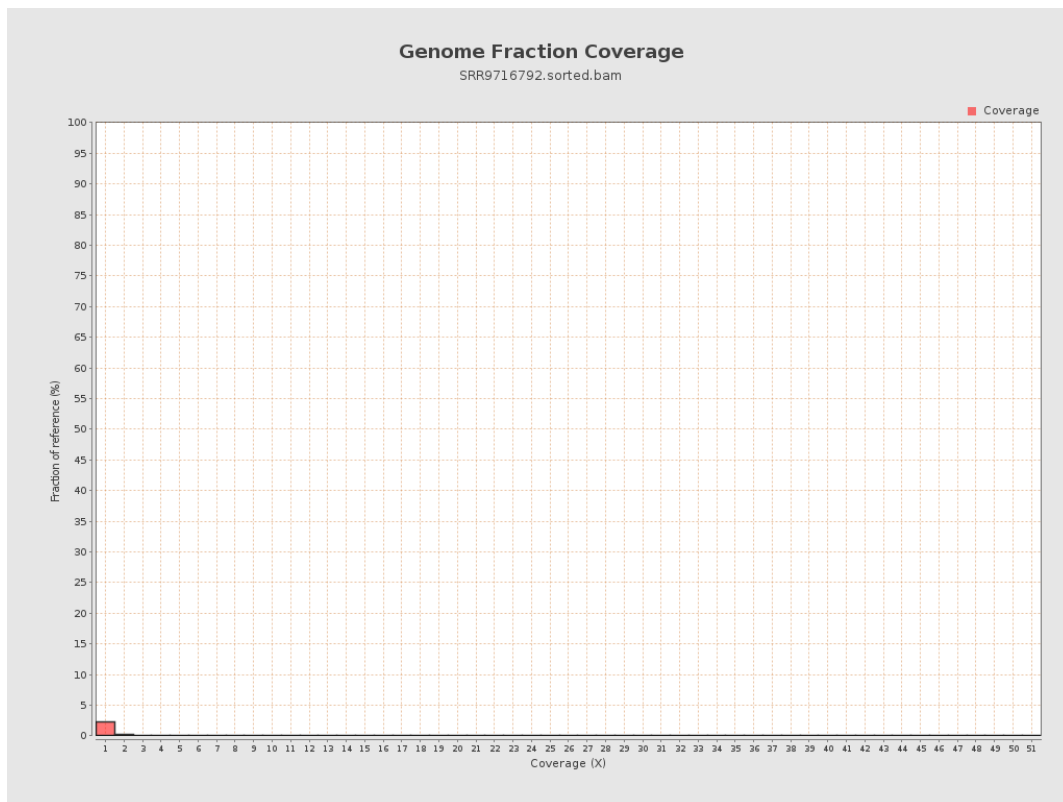
4. Results : Coverage Histogram



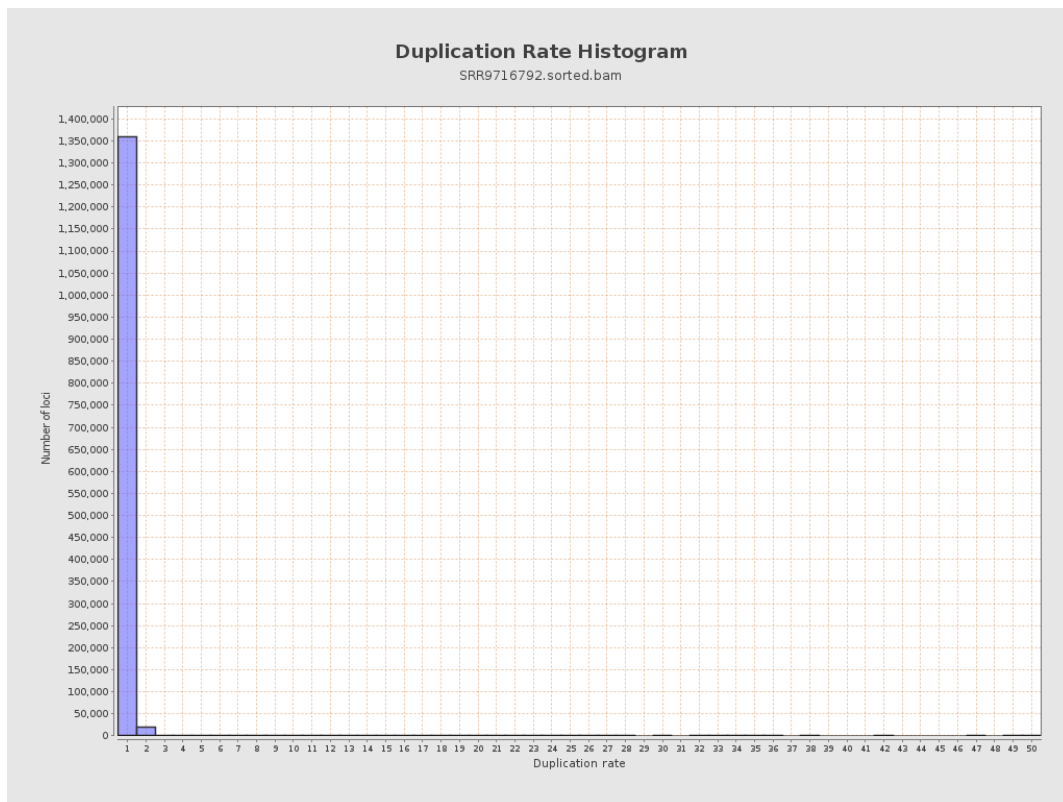
5. Results : Coverage Histogram (0-50X)



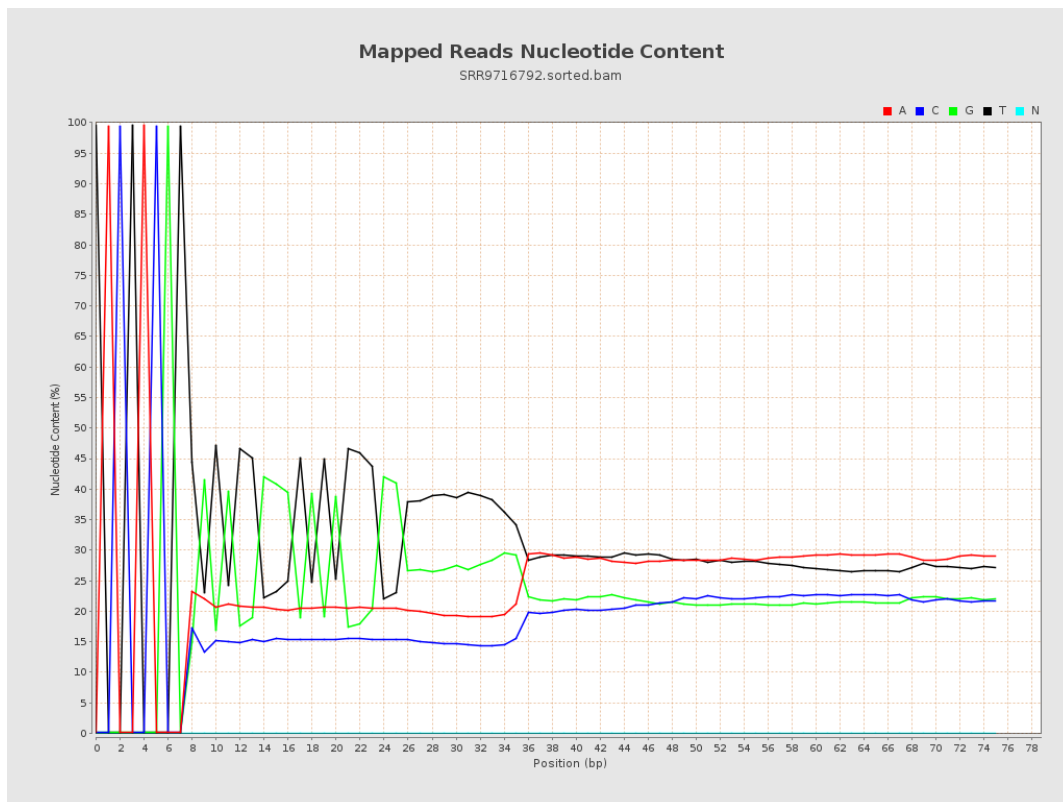
6. Results : Genome Fraction Coverage



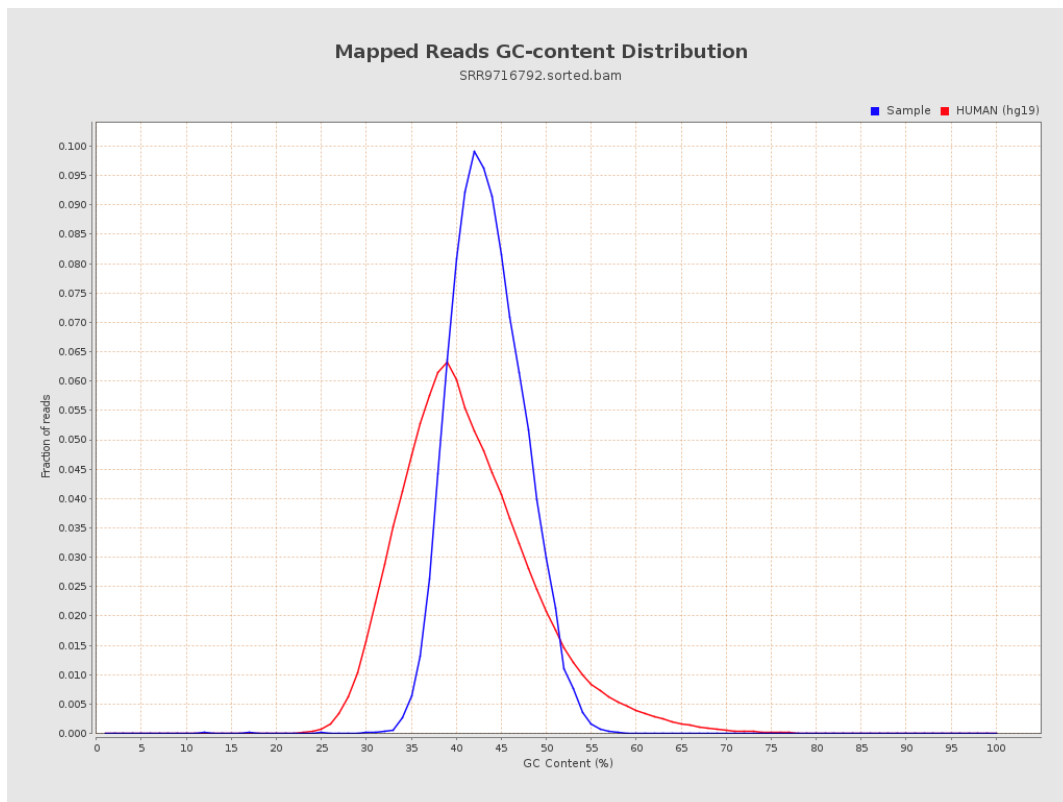
7. Results : Duplication Rate Histogram



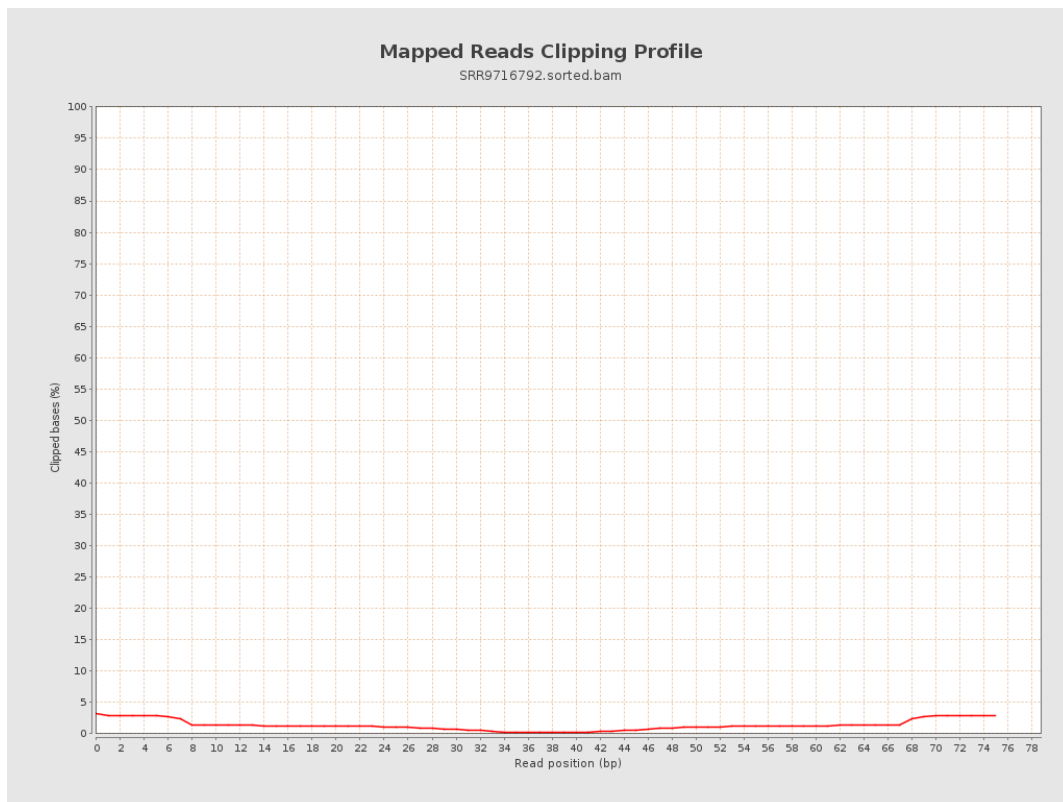
8. Results : Mapped Reads Nucleotide Content



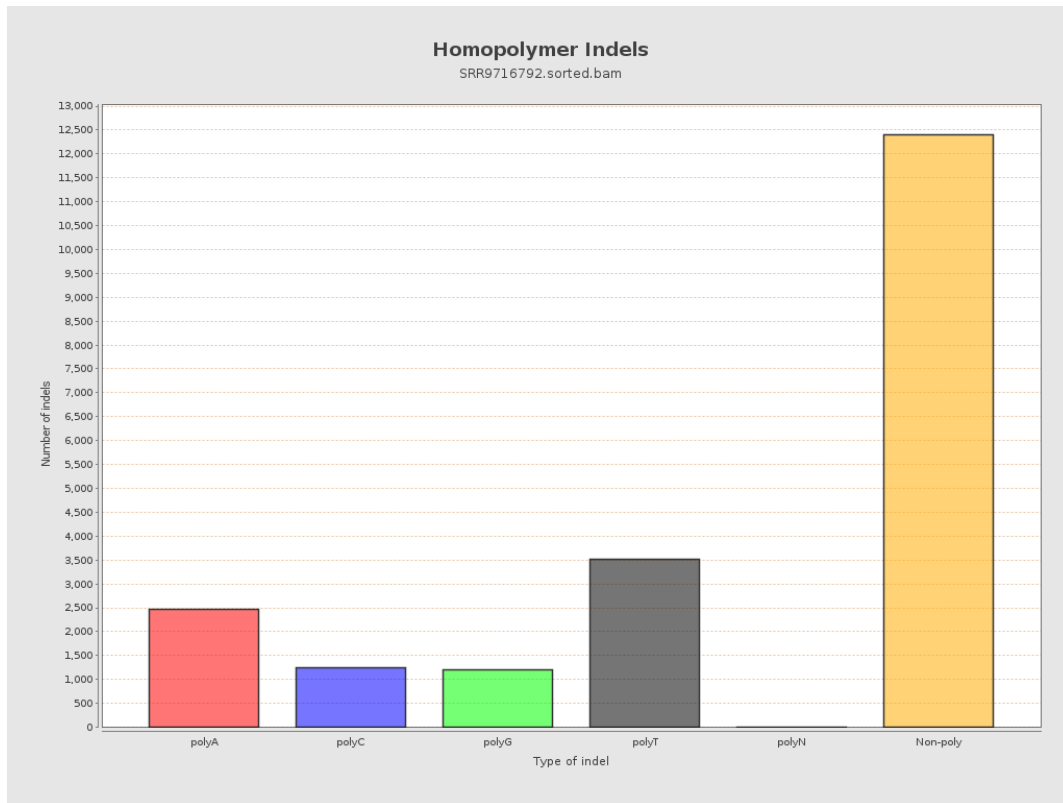
9. Results : Mapped Reads GC-content Distribution



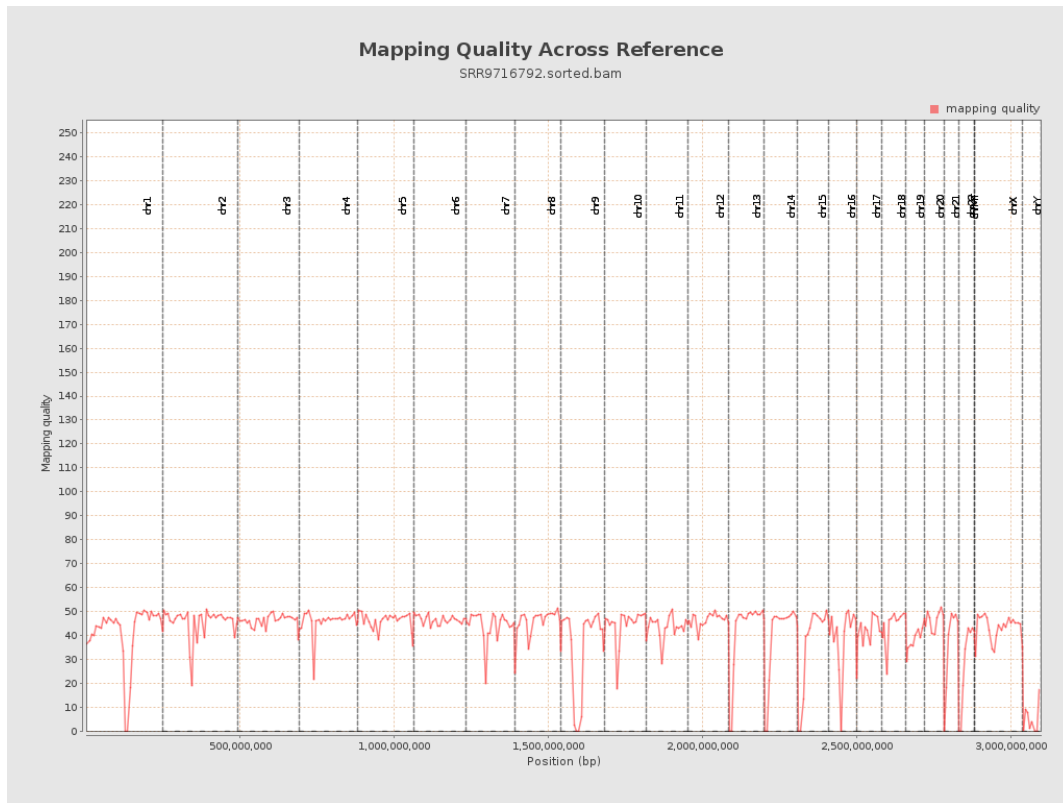
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

