

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:42:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716145.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_SRR9716145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:42:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,659,740
Mapped reads	1,537,486 / 92.63%
Unmapped reads	122,254 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,469 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	95,769 / 5.77%
Duplication rate	4.99%
Clipped reads	1,543,863 / 93.02%

2.2. ACGT Content

Number/percentage of A's	23,227,001 / 25.55%
Number/percentage of C's	19,142,711 / 21.05%
Number/percentage of T's	26,932,945 / 29.62%
Number/percentage of G's	21,619,200 / 23.78%
Number/percentage of N's	676 / 0%
GC Percentage	44.83%

2.3. Coverage

Mean	0.0294

Standard Deviation	0.2667
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2.4. Mapping Quality

Mean Mapping Quality	45.22
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2.5. Mismatches and indels

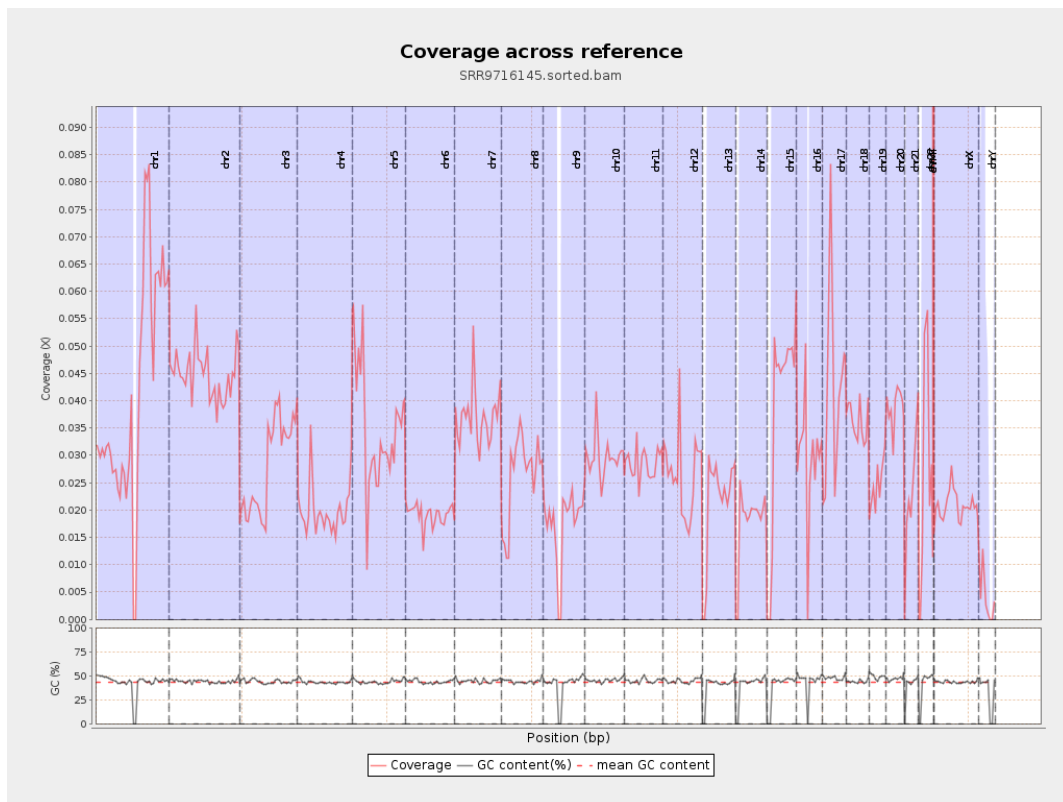
General error rate	0.49%
Mismatches	436,108
Insertions	5,746
Mapped reads with at least one insertion	0.37%
Deletions	15,844
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.4%

2.6. Chromosome stats

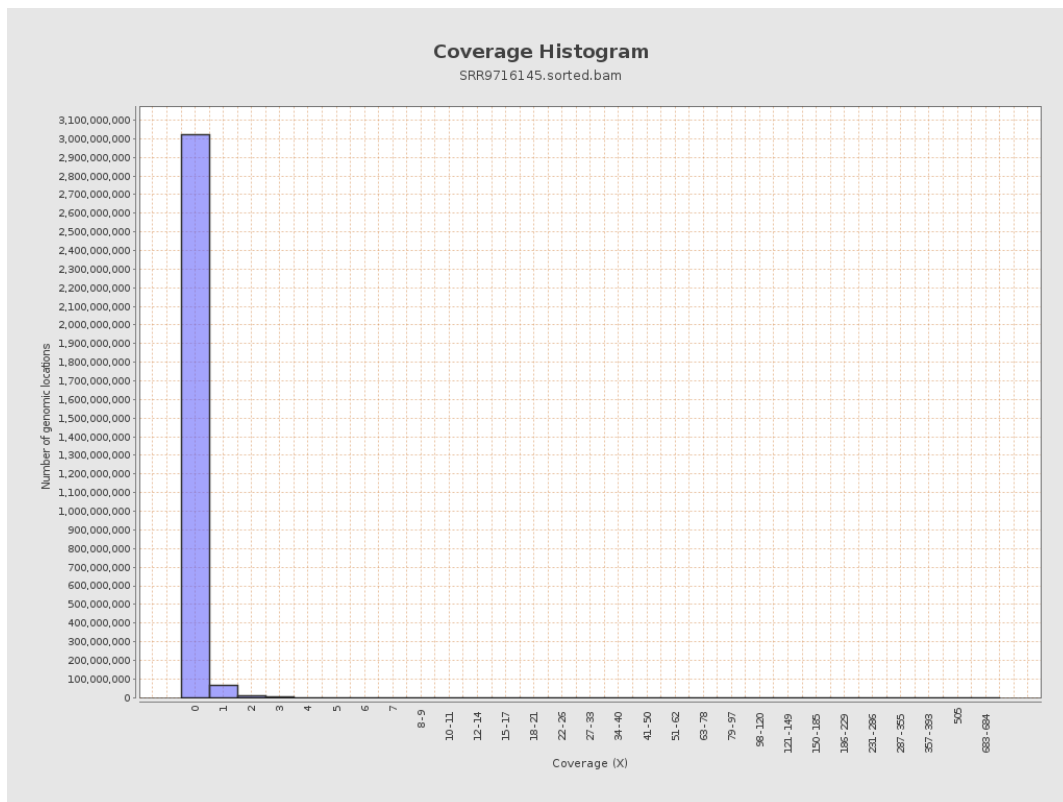
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10347825	0.0415	0.3933
chr2	243199373	10901820	0.0448	0.393
chr3	198022430	5516290	0.0279	0.1924
chr4	191154276	3782364	0.0198	0.1914
chr5	180915260	6259013	0.0346	0.216
chr6	171115067	3281158	0.0192	0.1743
chr7	159138663	5890948	0.037	0.3816

chr8	146364022	3868276	0.0264	0.2452
chr9	141213431	2434872	0.0172	0.2
chr10	135534747	4007583	0.0296	0.2464
chr11	135006516	3843465	0.0285	0.2524
chr12	133851895	3510278	0.0262	0.1902
chr13	115169878	2455042	0.0213	0.1715
chr14	107349540	1898371	0.0177	0.161
chr15	102531392	3961466	0.0386	0.2285
chr16	90354753	2686583	0.0297	0.2103
chr17	81195210	3485955	0.0429	0.2578
chr18	78077248	2825282	0.0362	0.457
chr19	59128983	1476951	0.025	0.2909
chr20	63025520	2439747	0.0387	0.2313
chr21	48129895	1142029	0.0237	0.1936
chr22	51304566	1346314	0.0262	0.1899
chrMT	16571	128814	7.7735	5.6605
chrX	155270560	3229830	0.0208	0.1814
chrY	59373566	227963	0.0038	0.1062

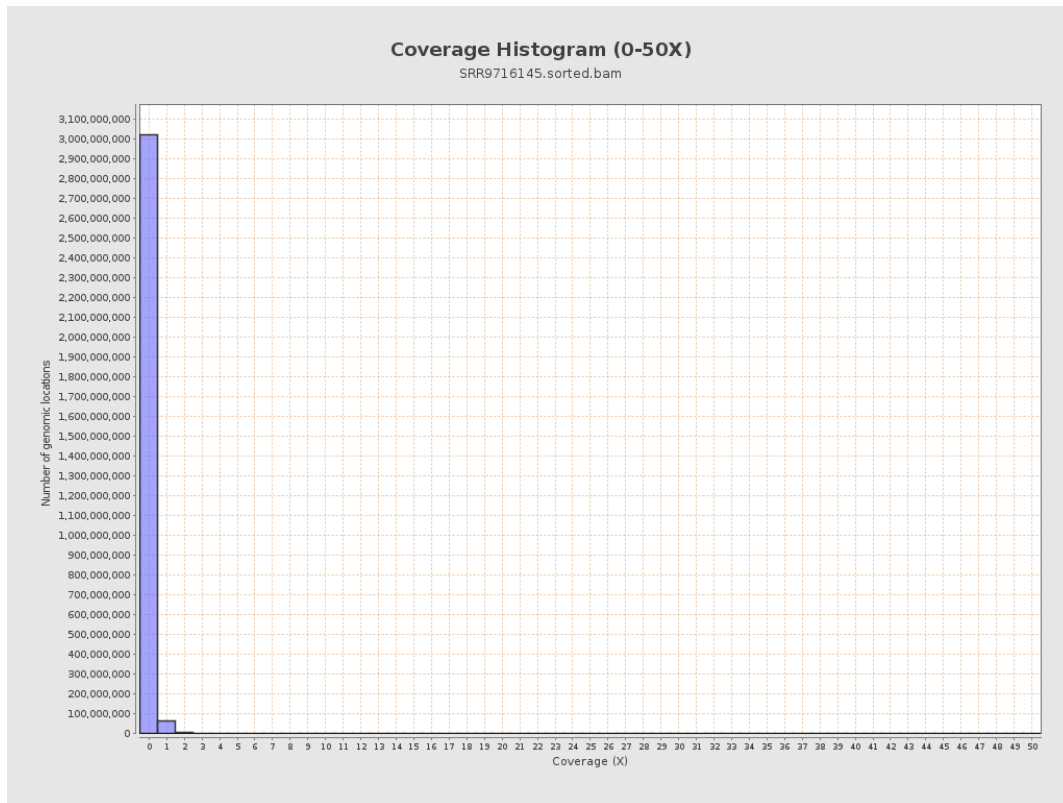
3. Results : Coverage across reference



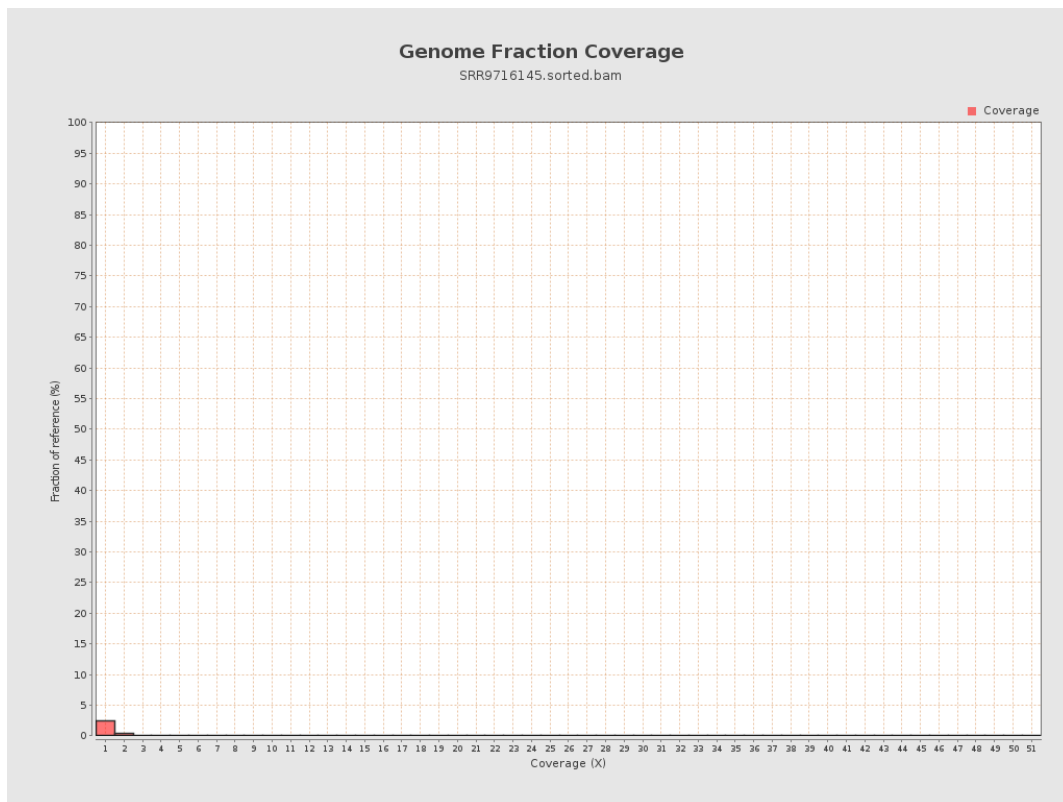
4. Results : Coverage Histogram



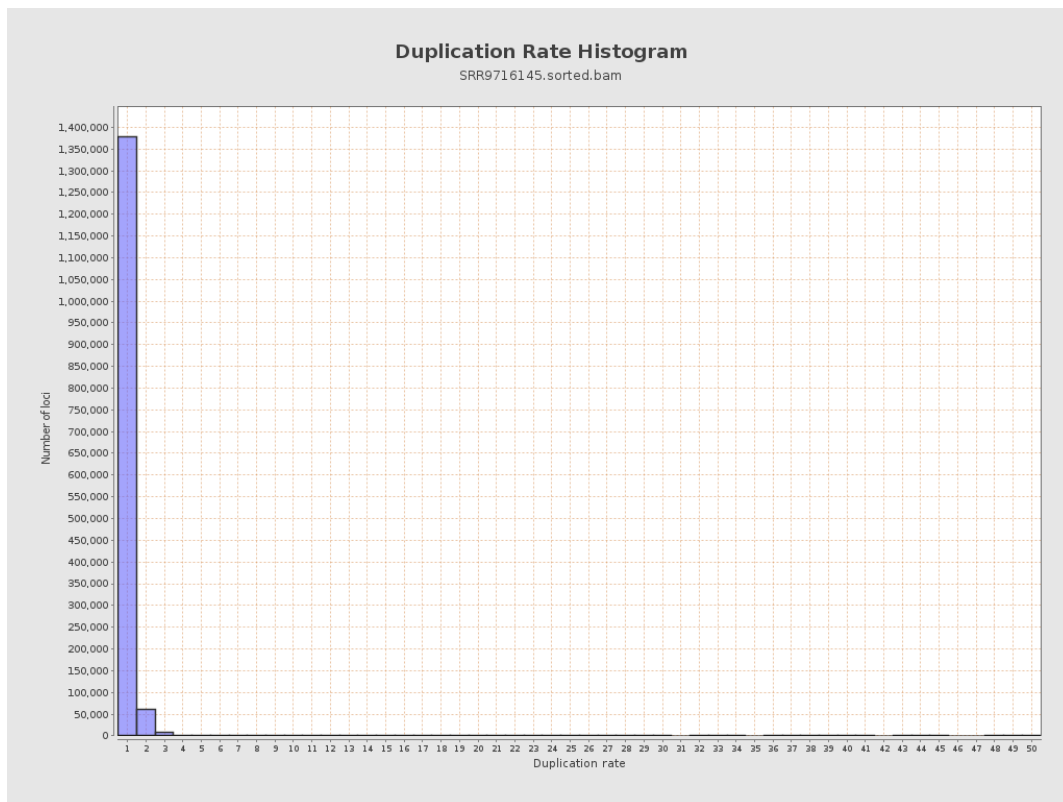
5. Results : Coverage Histogram (0-50X)



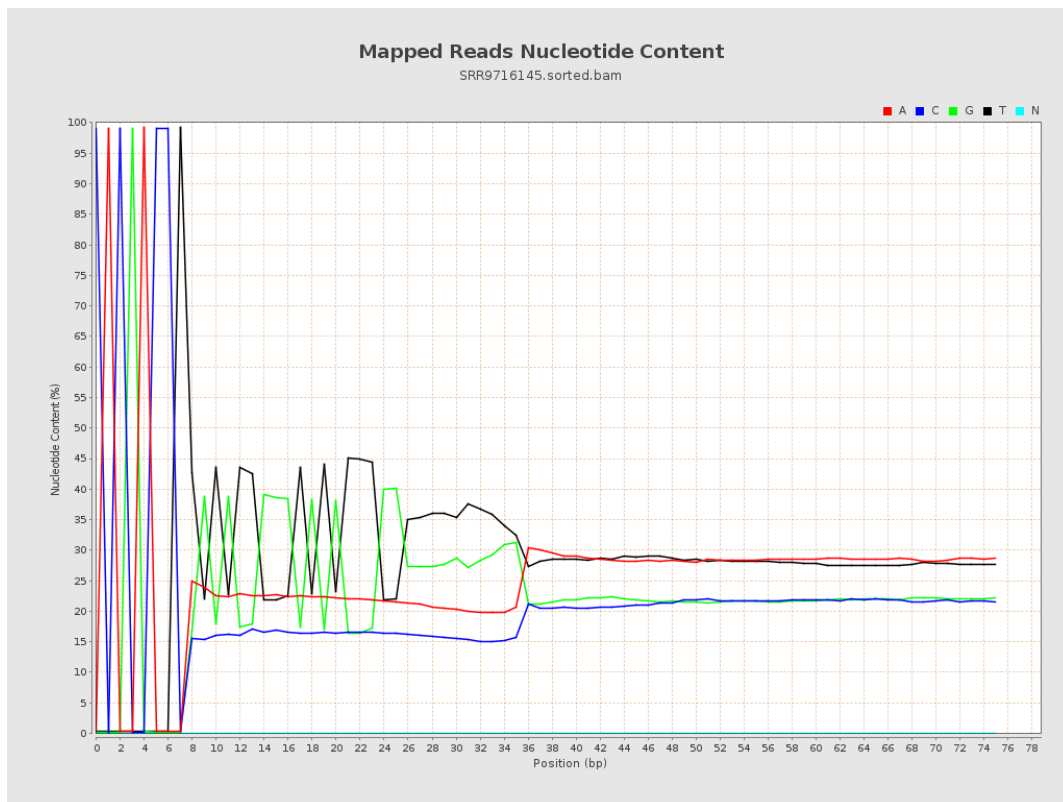
6. Results : Genome Fraction Coverage



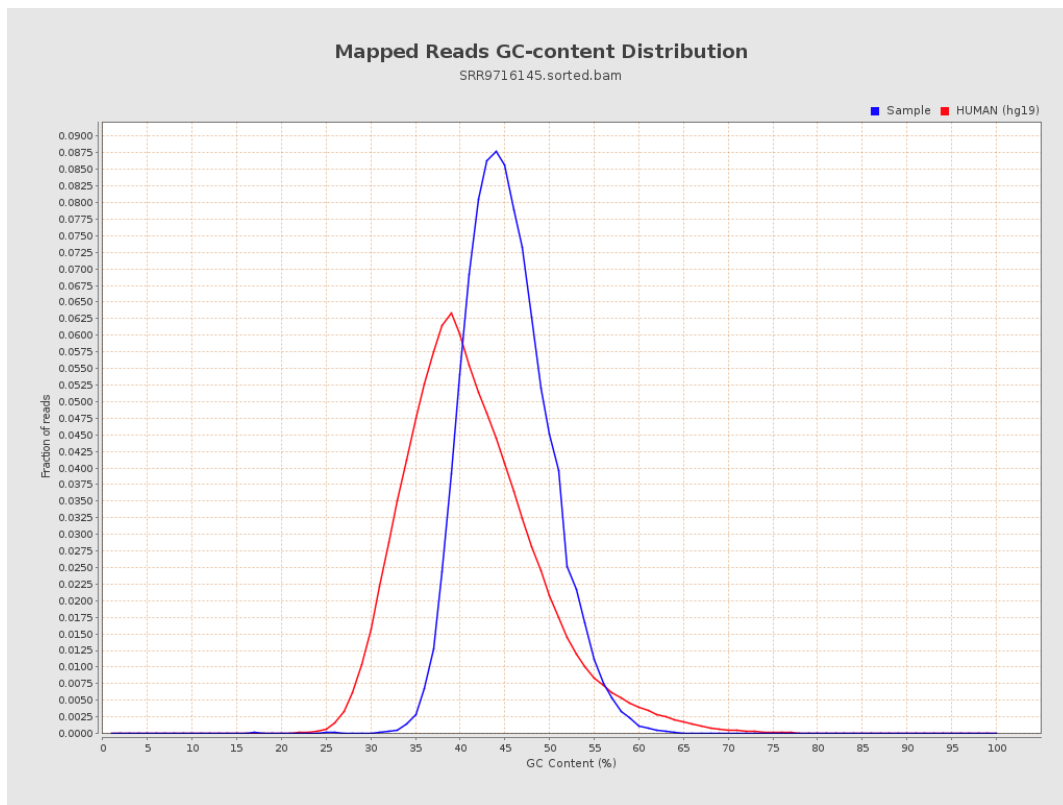
7. Results : Duplication Rate Histogram



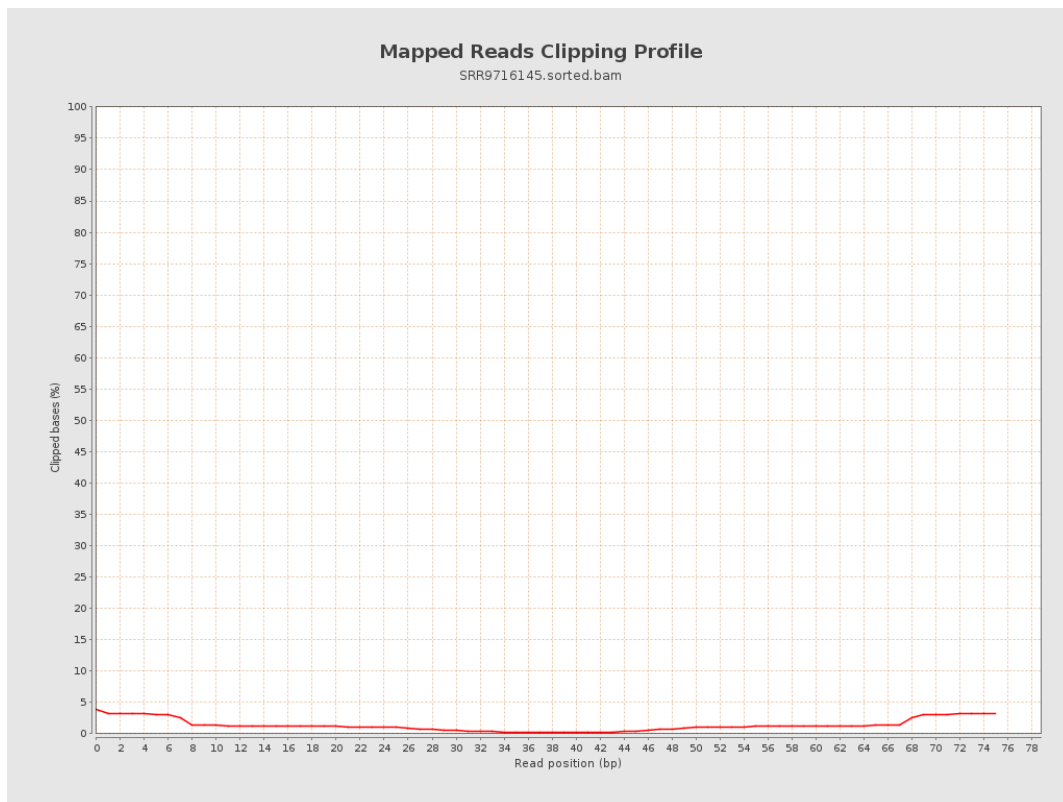
8. Results : Mapped Reads Nucleotide Content



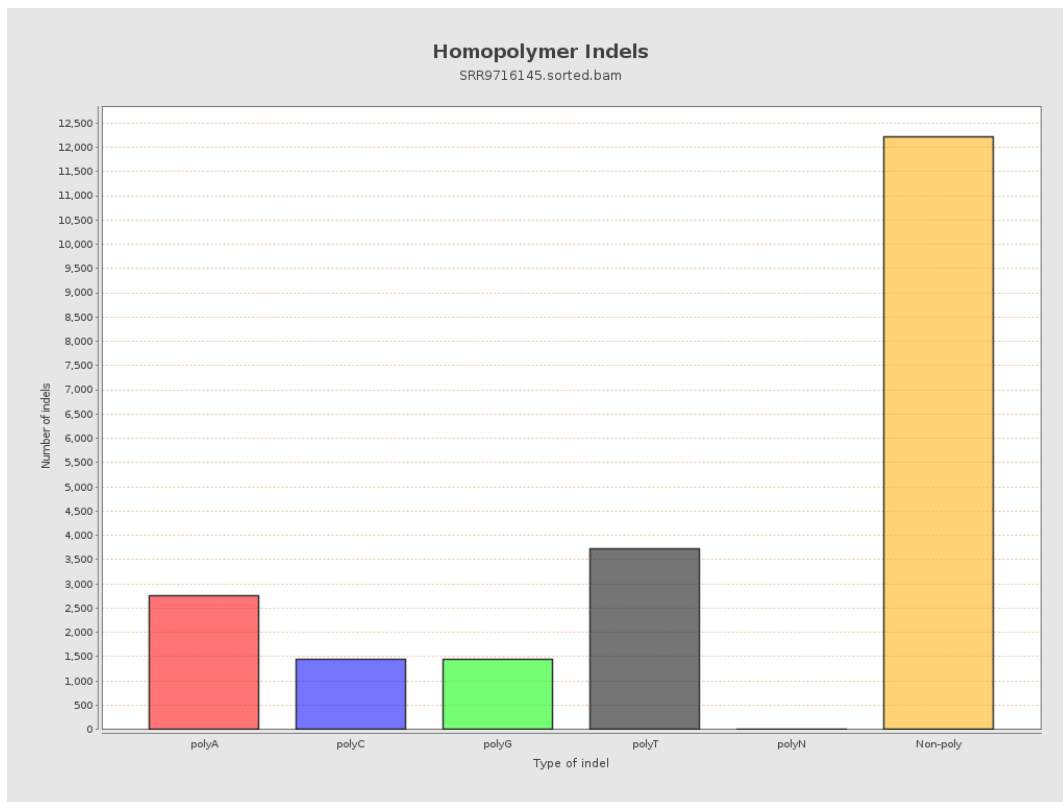
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

