

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 10:34:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695912.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695912 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695912.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 10:34:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,134,411
Mapped reads	13,983,678 / 92.4%
Unmapped reads	1,150,733 / 7.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	224,334 / 1.48%
Read min/max/mean length	8 / 357 / 143.31
Duplicated reads (estimated)	3,022,315 / 19.97%
Duplication rate	18.4%
Clipped reads	3,676,011 / 24.29%

2.2. ACGT Content

Number/percentage of A's	583,714,828 / 28.51%
Number/percentage of C's	436,011,654 / 21.29%
Number/percentage of T's	580,830,664 / 28.36%
Number/percentage of G's	447,160,655 / 21.84%
Number/percentage of N's	0 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.6657

Standard Deviation	1.5555
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2.4. Mapping Quality

Mean Mapping Quality	52.21
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2.5. Mismatches and indels

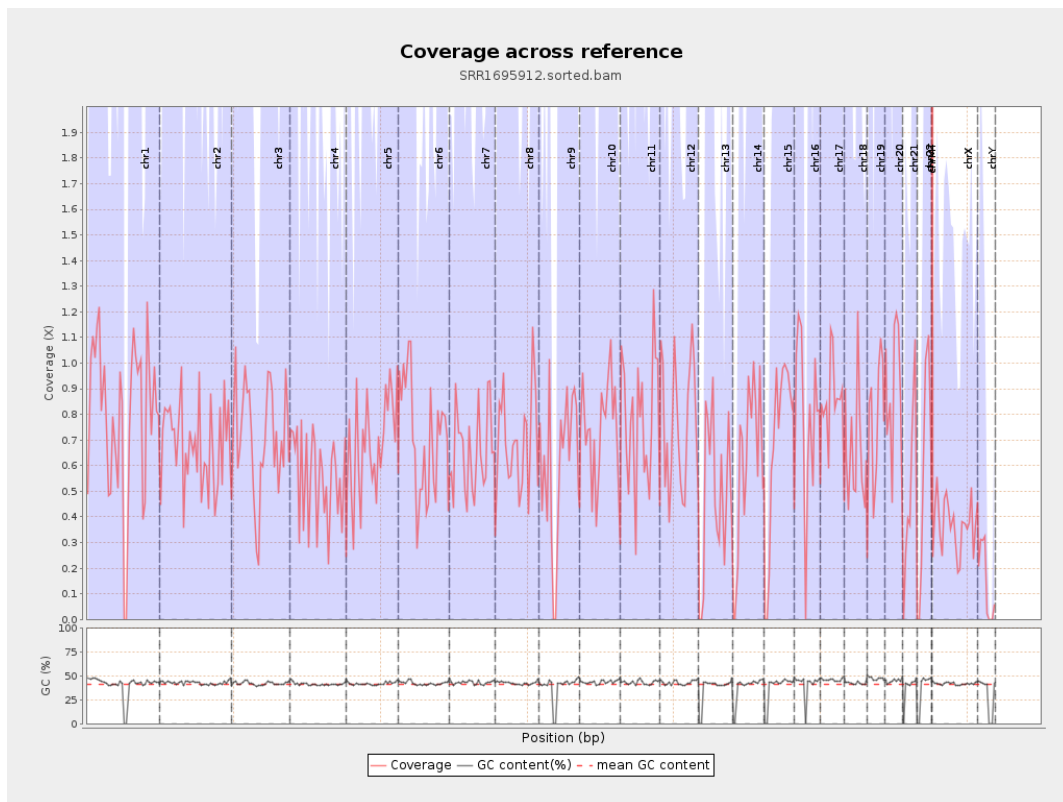
General error rate	1.72%
Mismatches	20,736,193
Insertions	13,333,008
Mapped reads with at least one insertion	51.85%
Deletions	11,859,381
Mapped reads with at least one deletion	49.81%
Homopolymer indels	37.1%

2.6. Chromosome stats

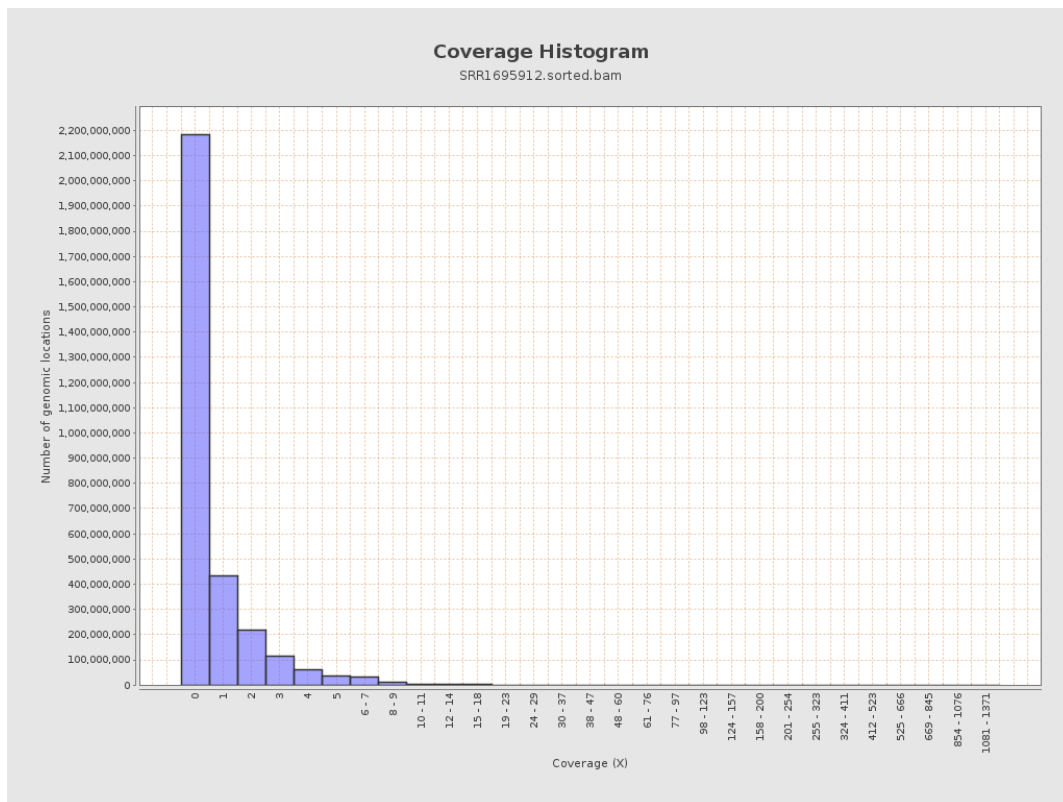
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	198560961	0.7966	2.1279
chr2	243199373	165687986	0.6813	1.4965
chr3	198022430	142056372	0.7174	1.4685
chr4	191154276	106274192	0.556	1.3195
chr5	180915260	123595517	0.6832	1.457
chr6	171115067	121524912	0.7102	1.5053
chr7	159138663	103992806	0.6535	1.4443

chr8	146364022	102453433	0.7	1.4742
chr9	141213431	84138858	0.5958	1.4609
chr10	135534747	101000382	0.7452	1.7596
chr11	135006516	105538995	0.7817	1.6227
chr12	133851895	102313092	0.7644	1.5534
chr13	115169878	55394191	0.481	1.217
chr14	107349540	64992839	0.6054	1.3921
chr15	102531392	69693125	0.6797	1.4704
chr16	90354753	69611470	0.7704	1.6041
chr17	81195210	69263594	0.8531	1.8563
chr18	78077248	51100273	0.6545	1.7562
chr19	59128983	47451630	0.8025	1.9155
chr20	63025520	56317065	0.8936	1.7267
chr21	48129895	24772419	0.5147	1.4026
chr22	51304566	29114823	0.5675	1.3927
chrMT	16571	378398	22.835	14.2848
chrX	155270560	56692046	0.3651	1.0206
chrY	59373566	8980929	0.1513	0.9597

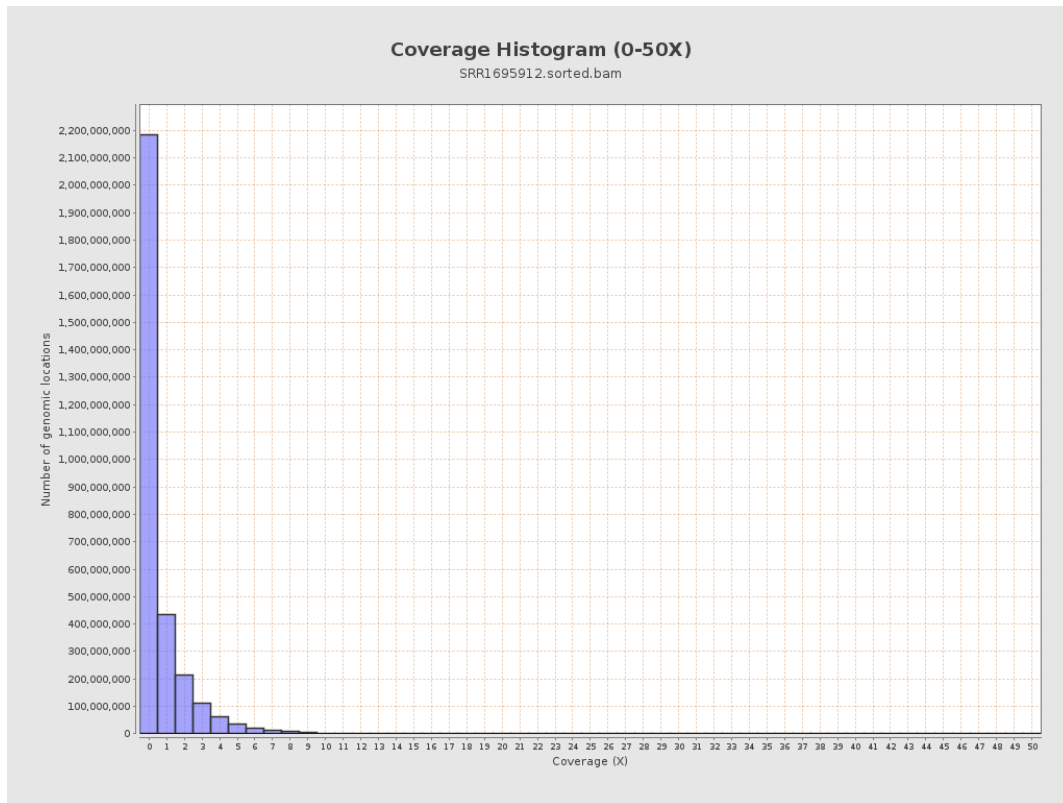
3. Results : Coverage across reference



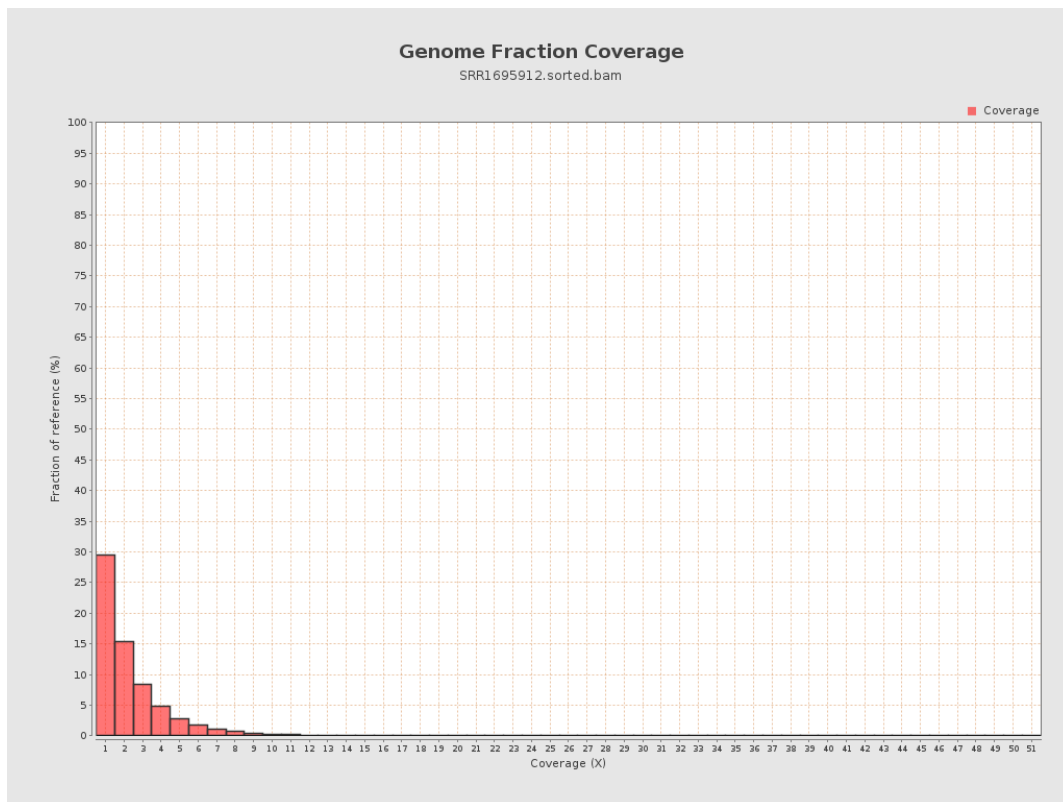
4. Results : Coverage Histogram



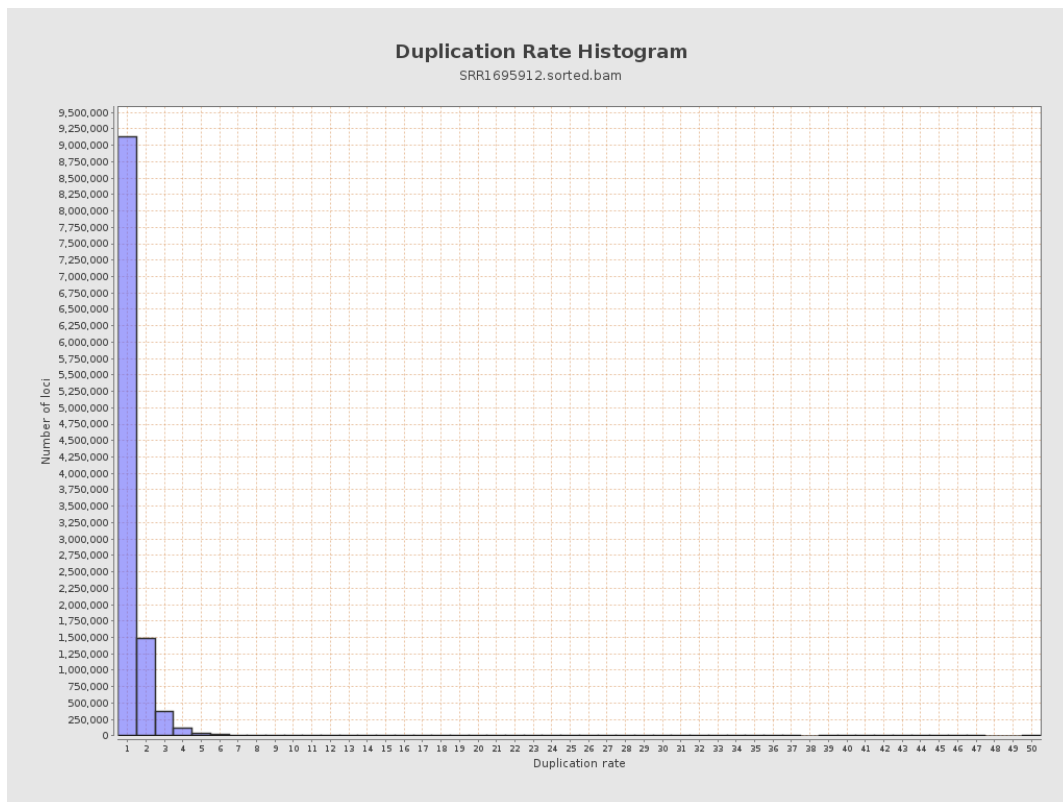
5. Results : Coverage Histogram (0-50X)



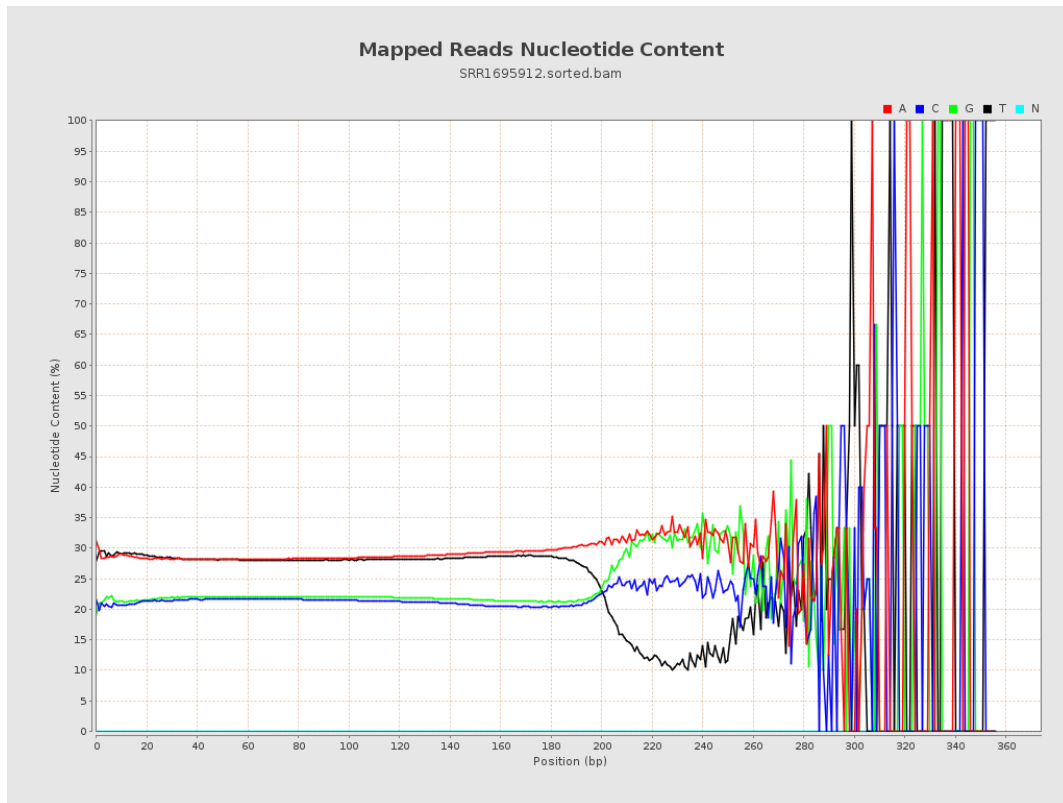
6. Results : Genome Fraction Coverage



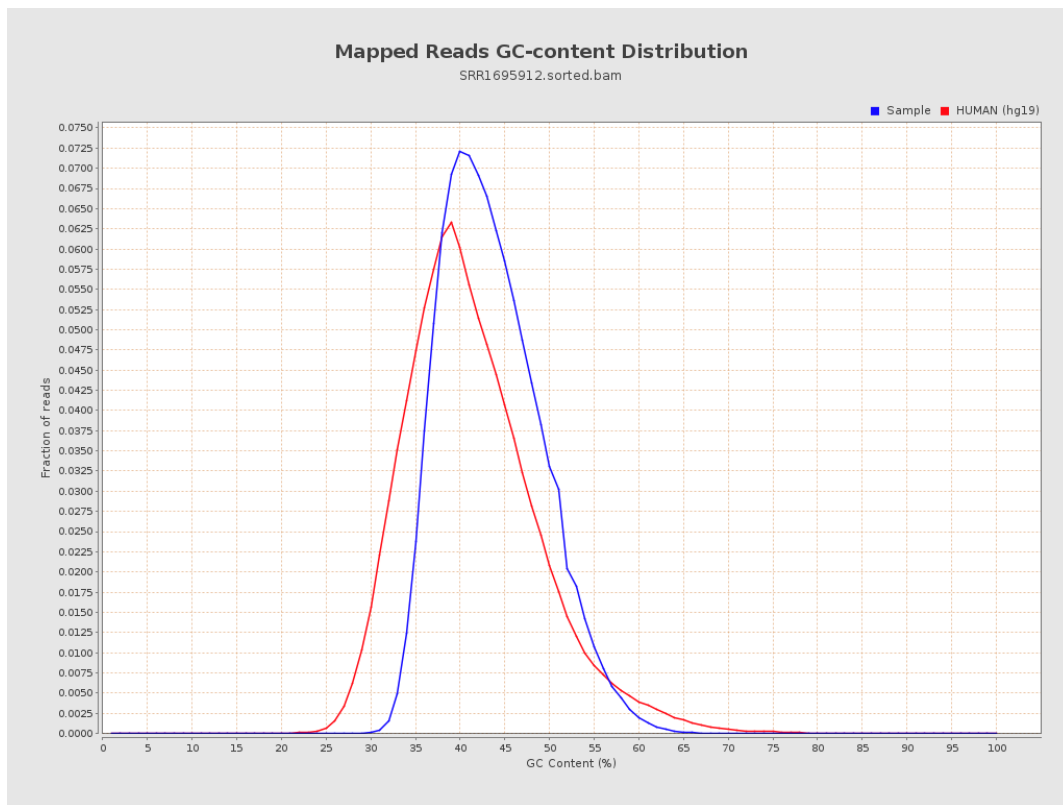
7. Results : Duplication Rate Histogram



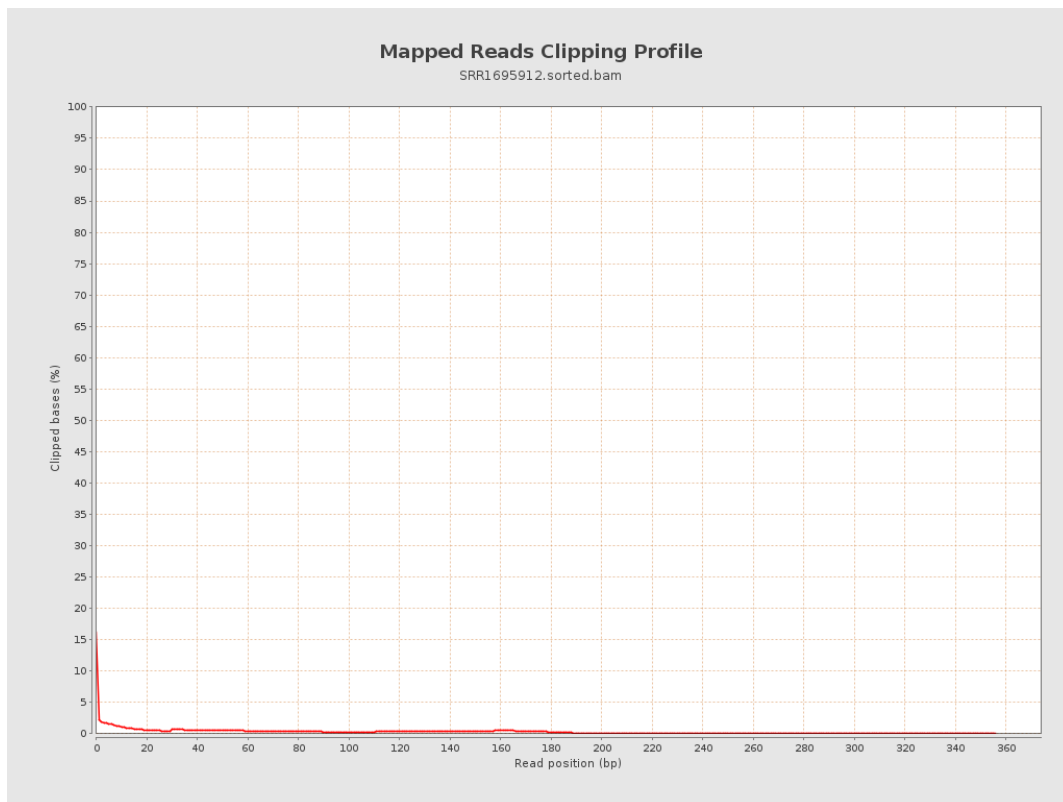
8. Results : Mapped Reads Nucleotide Content



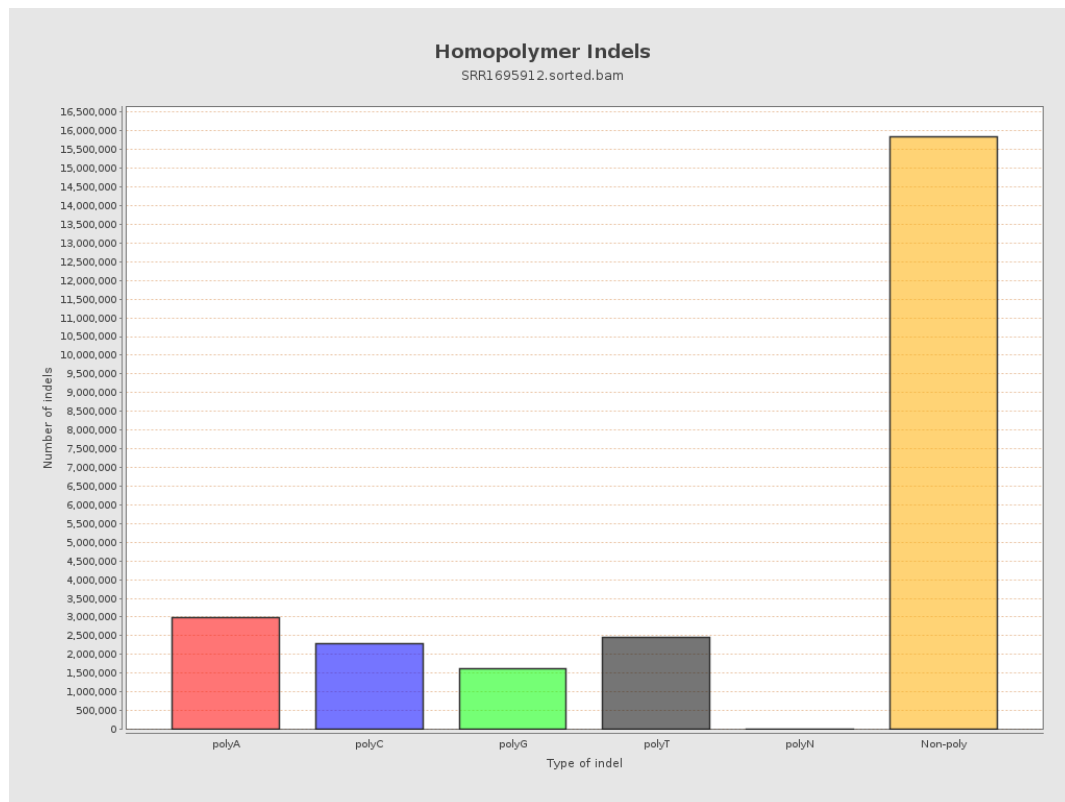
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

