

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013295.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_SRR6013295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013295.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,938,030
Mapped reads	1,707,475 / 88.1%
Unmapped reads	230,555 / 11.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,054 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	80,188 / 4.14%
Duplication rate	3.4%
Clipped reads	797,027 / 41.13%

2.2. ACGT Content

Number/percentage of A's	31,716,658 / 28.04%
Number/percentage of C's	20,510,214 / 18.13%
Number/percentage of T's	36,330,192 / 32.12%
Number/percentage of G's	24,517,864 / 21.68%
Number/percentage of N's	24,419 / 0.02%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0365

Standard Deviation	0.4345
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2.4. Mapping Quality

Mean Mapping Quality	45.69
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2.5. Mismatches and indels

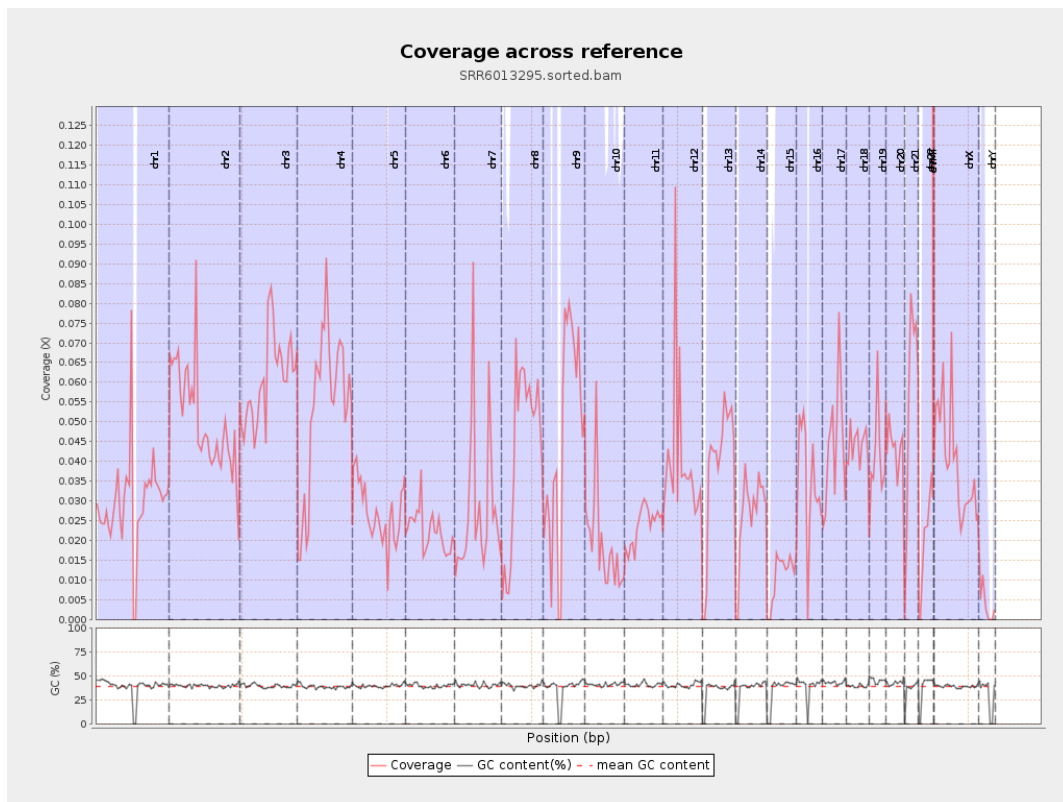
General error rate	0.87%
Mismatches	970,797
Insertions	8,677
Mapped reads with at least one insertion	0.5%
Deletions	28,548
Mapped reads with at least one deletion	1.65%
Homopolymer indels	46.56%

2.6. Chromosome stats

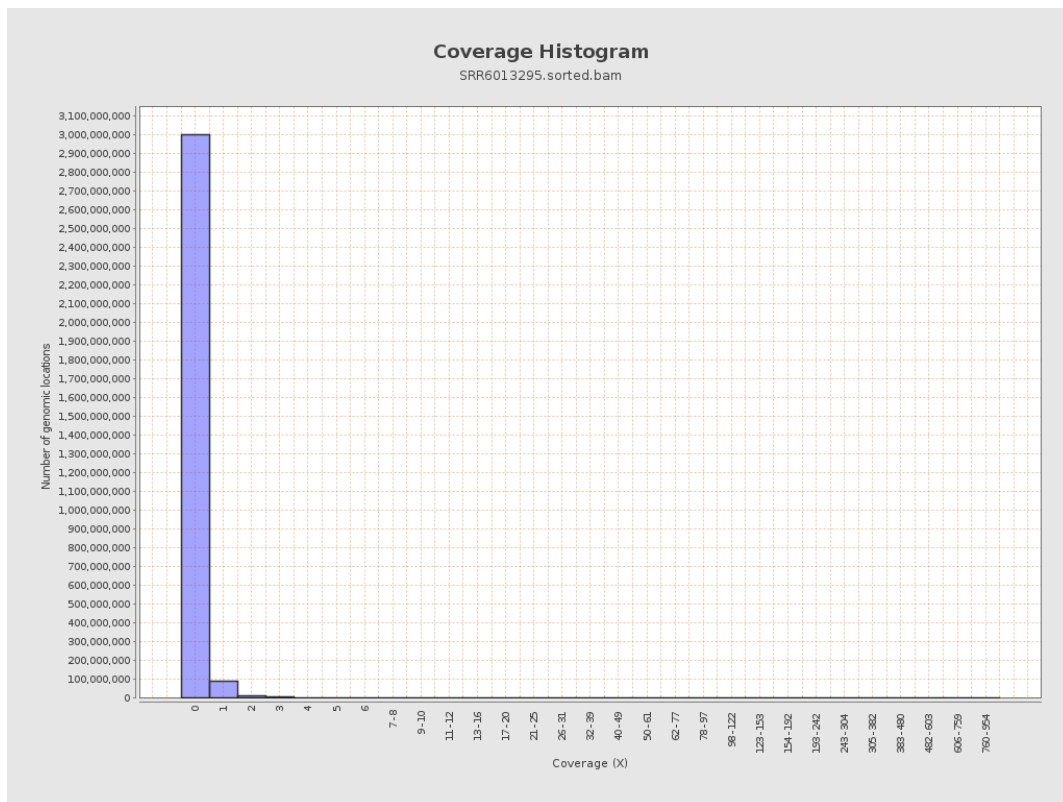
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7380229	0.0296	0.8141
chr2	243199373	12302297	0.0506	0.4867
chr3	198022430	12047963	0.0608	0.2776
chr4	191154276	10180316	0.0533	0.2789
chr5	180915260	4897399	0.0271	0.187
chr6	171115067	3848466	0.0225	0.2039
chr7	159138663	4508226	0.0283	0.8866

chr8	146364022	6316557	0.0432	0.534
chr9	141213431	6506736	0.0461	0.3901
chr10	135534747	2551482	0.0188	0.3811
chr11	135006516	3183218	0.0236	0.221
chr12	133851895	5359448	0.04	0.2385
chr13	115169878	4407277	0.0383	0.22
chr14	107349540	2872610	0.0268	0.2232
chr15	102531392	1135853	0.0111	0.1227
chr16	90354753	3163834	0.035	0.243
chr17	81195210	3567202	0.0439	0.2618
chr18	78077248	3445428	0.0441	0.6349
chr19	59128983	2490270	0.0421	0.5679
chr20	63025520	2720339	0.0432	0.2429
chr21	48129895	2687540	0.0558	0.2858
chr22	51304566	1042056	0.0203	0.1579
chrMT	16571	132480	7.9947	6.0602
chrX	155270560	6158038	0.0397	0.2556
chrY	59373566	242248	0.0041	0.1097

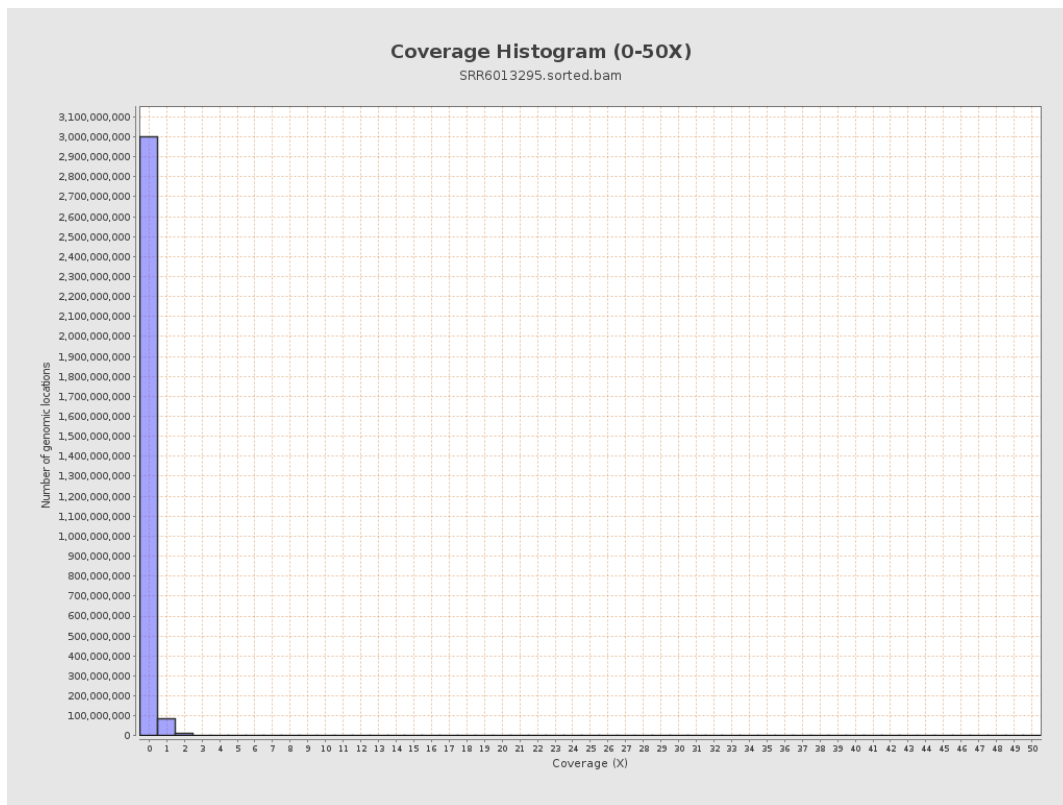
3. Results : Coverage across reference



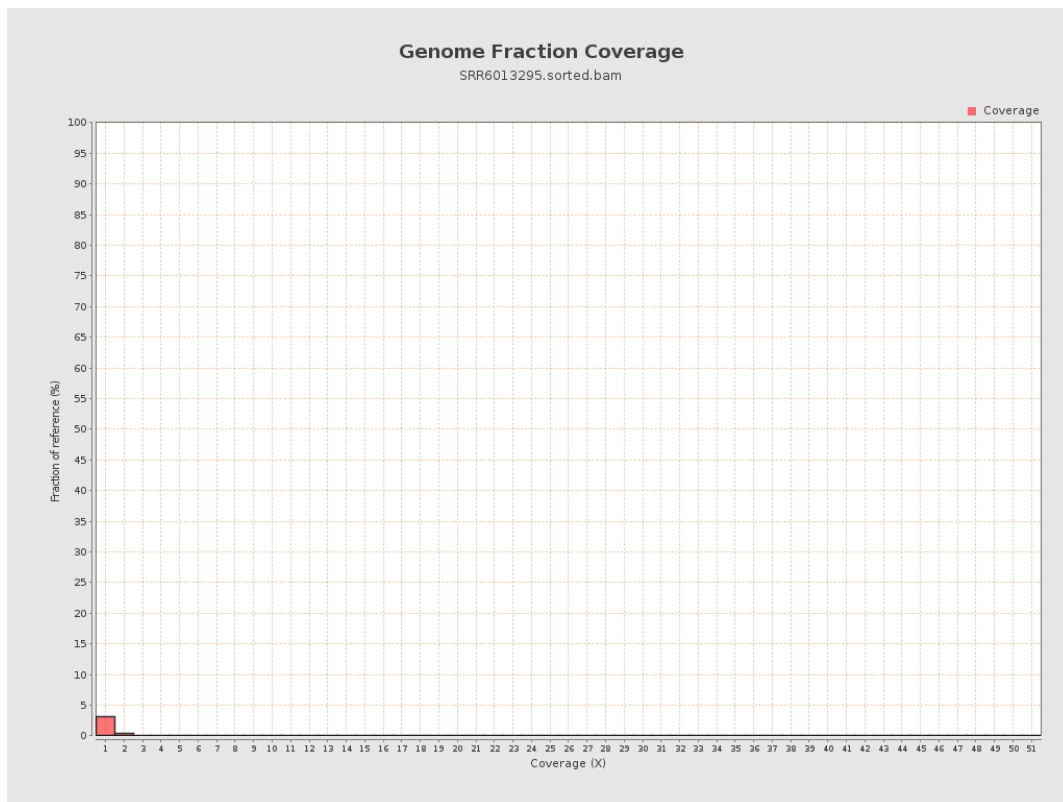
4. Results : Coverage Histogram



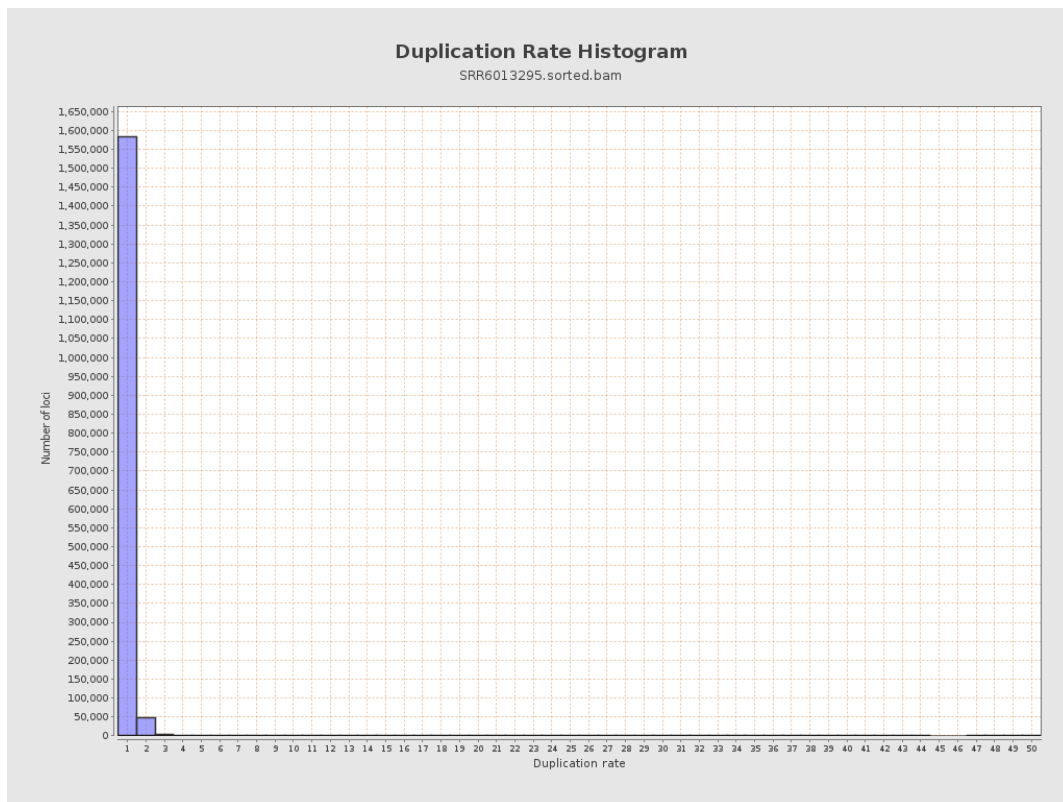
5. Results : Coverage Histogram (0-50X)



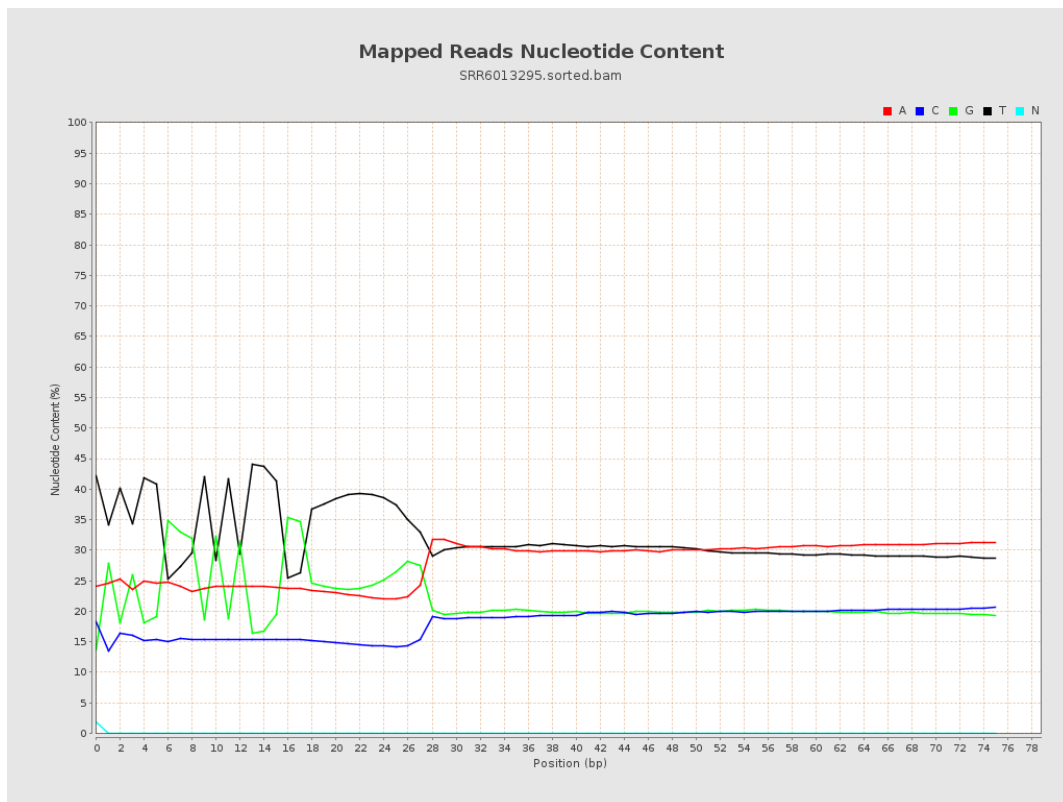
6. Results : Genome Fraction Coverage



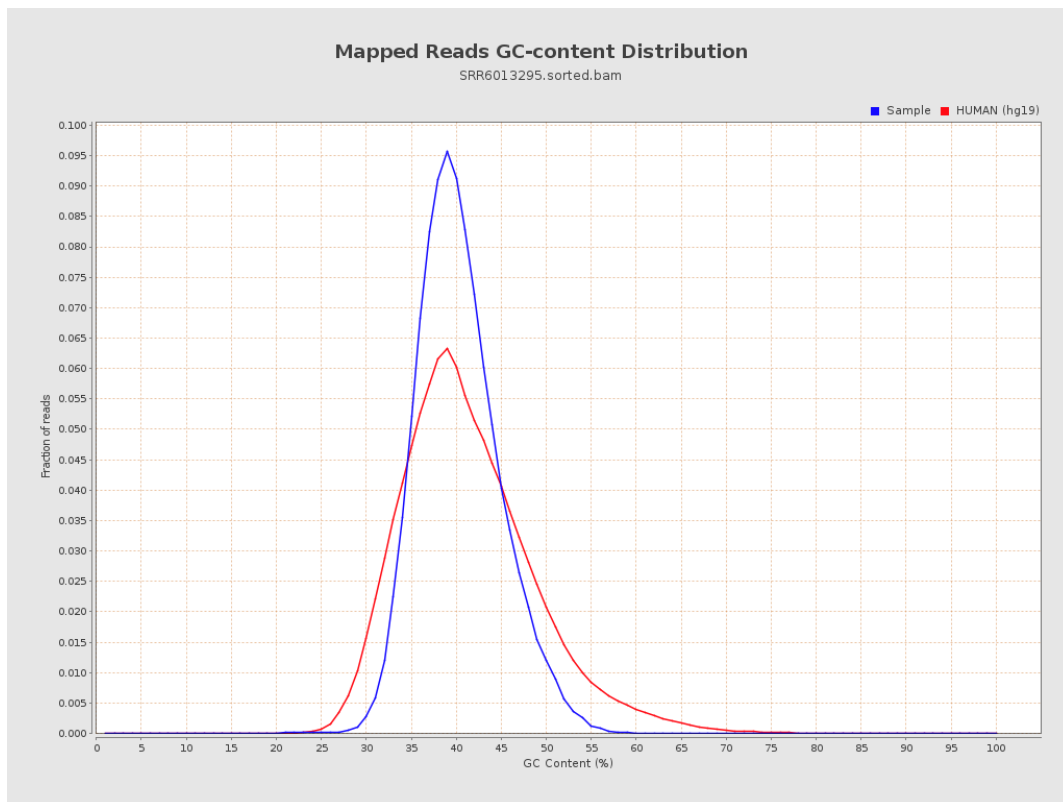
7. Results : Duplication Rate Histogram



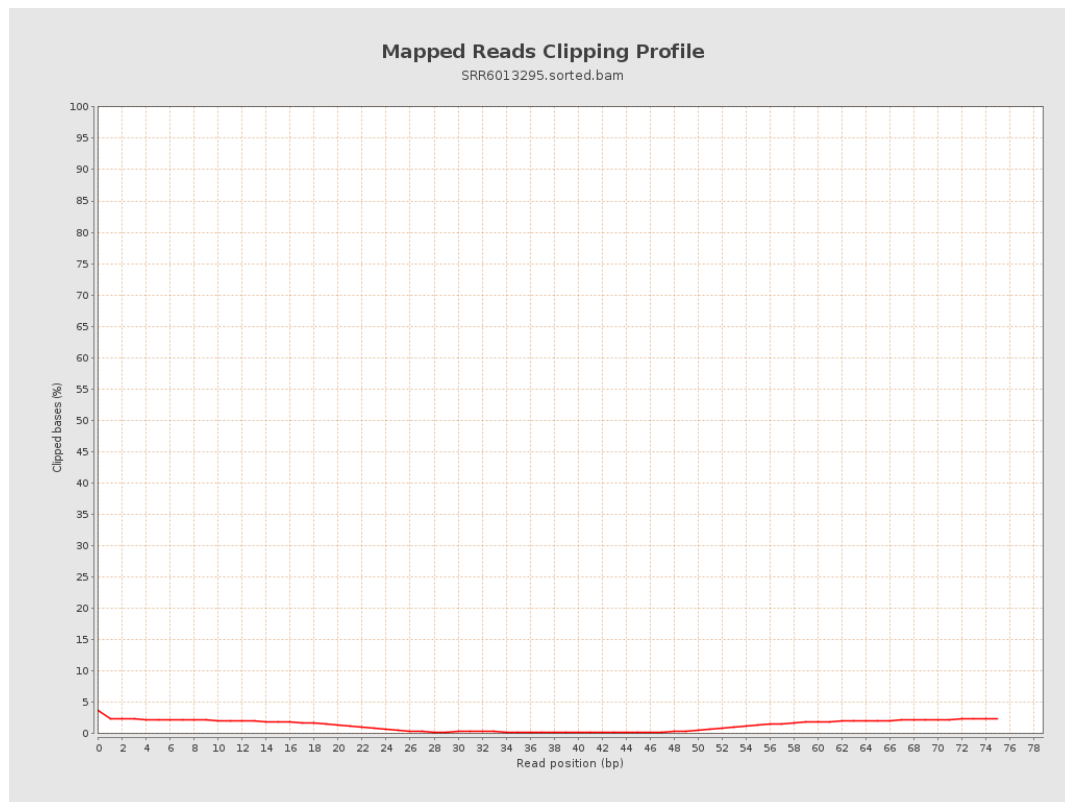
8. Results : Mapped Reads Nucleotide Content



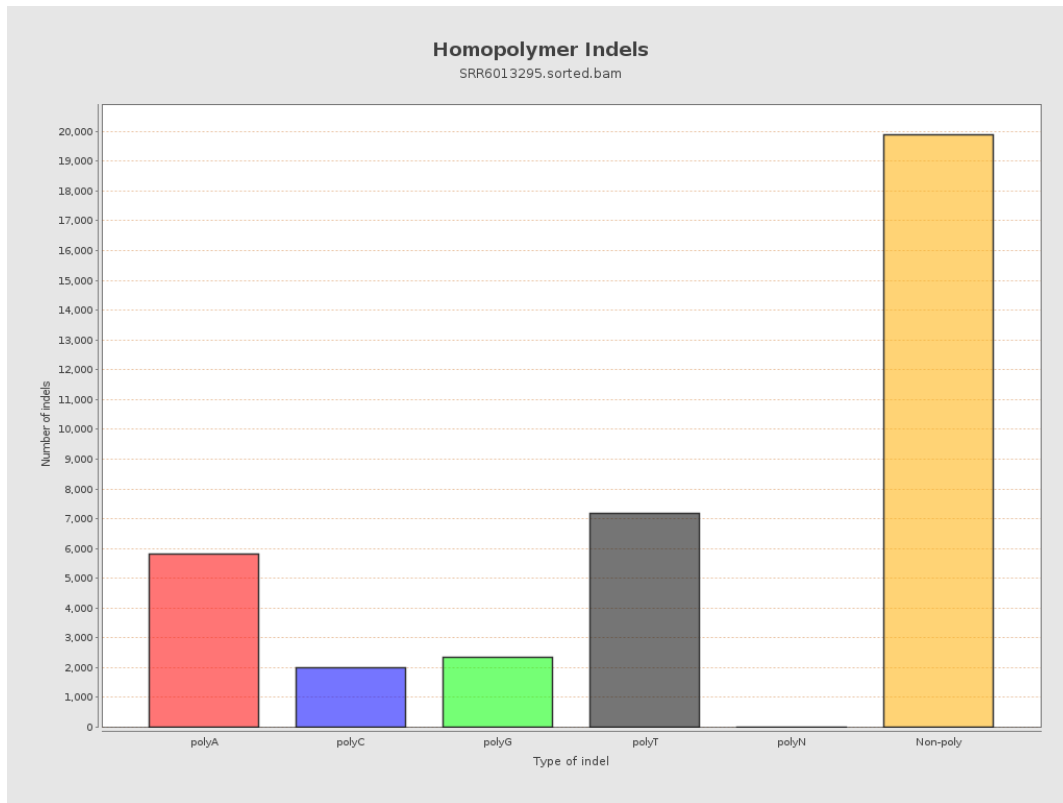
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

