

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:17:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013298.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_SRR6013298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013298.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:17:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,096,355
Mapped reads	1,851,594 / 88.32%
Unmapped reads	244,761 / 11.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,374 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	74,725 / 3.56%
Duplication rate	3.2%
Clipped reads	863,659 / 41.2%

2.2. ACGT Content

Number/percentage of A's	34,283,671 / 27.96%
Number/percentage of C's	22,416,177 / 18.28%
Number/percentage of T's	38,971,003 / 31.78%
Number/percentage of G's	26,936,192 / 21.96%
Number/percentage of N's	26,640 / 0.02%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.3653
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2.4. Mapping Quality

Mean Mapping Quality	45.57
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2.5. Mismatches and indels

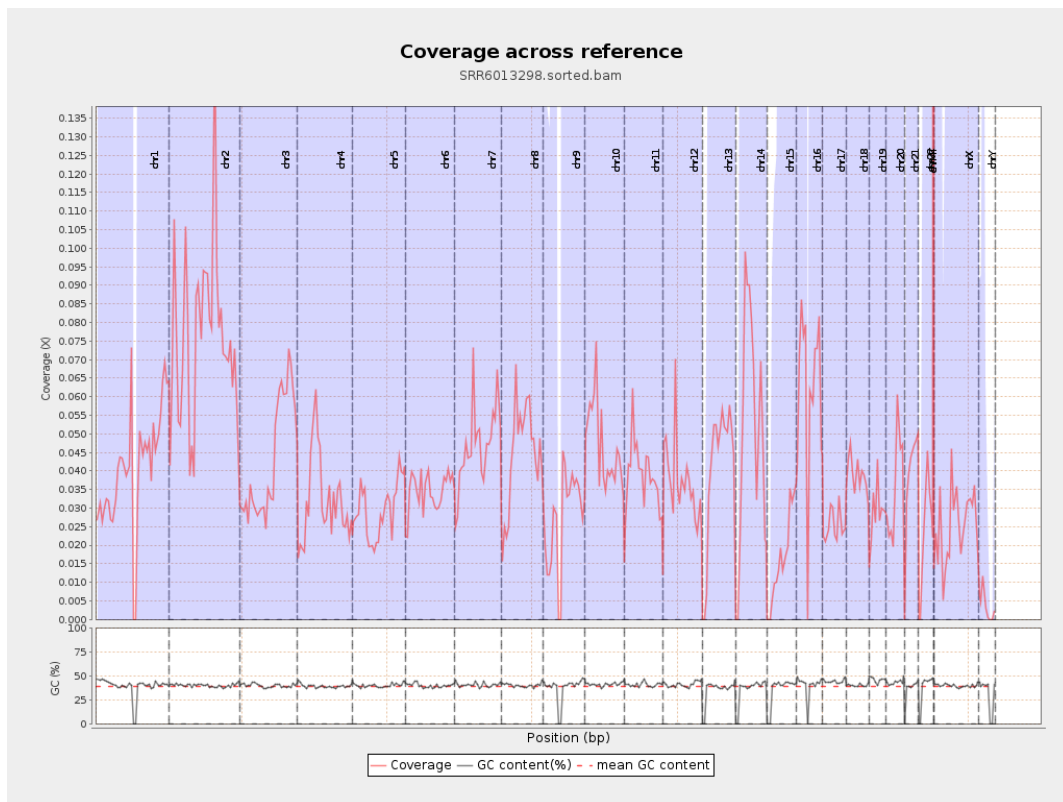
General error rate	0.83%
Mismatches	997,623
Insertions	8,960
Mapped reads with at least one insertion	0.48%
Deletions	31,077
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.62%

2.6. Chromosome stats

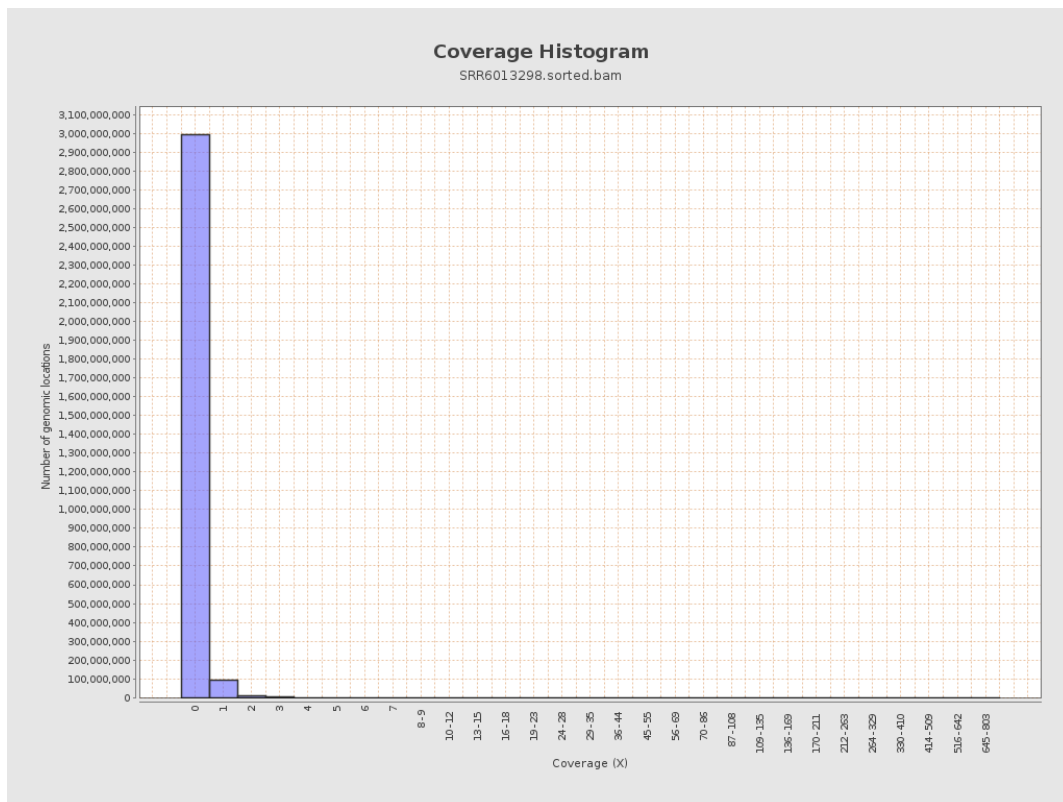
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10117678	0.0406	0.733
chr2	243199373	18441816	0.0758	0.46
chr3	198022430	8500460	0.0429	0.236
chr4	191154276	6098854	0.0319	0.2098
chr5	180915260	5326293	0.0294	0.1949
chr6	171115067	5863942	0.0343	0.2518
chr7	159138663	7505376	0.0472	0.5221

chr8	146364022	6481647	0.0443	0.3752
chr9	141213431	3781223	0.0268	0.271
chr10	135534747	6355270	0.0469	0.3844
chr11	135006516	5190346	0.0384	0.2769
chr12	133851895	5001223	0.0374	0.2237
chr13	115169878	4655991	0.0404	0.2281
chr14	107349540	5683566	0.0529	0.2769
chr15	102531392	1727815	0.0169	0.1515
chr16	90354753	5684873	0.0629	0.3082
chr17	81195210	2052225	0.0253	0.188
chr18	78077248	3060704	0.0392	0.4701
chr19	59128983	1727383	0.0292	0.5744
chr20	63025520	2222124	0.0353	0.2174
chr21	48129895	1876444	0.039	0.2357
chr22	51304566	1208363	0.0236	0.171
chrMT	16571	17428	1.0517	1.3602
chrX	155270560	3901306	0.0251	0.1957
chrY	59373566	204612	0.0034	0.0957

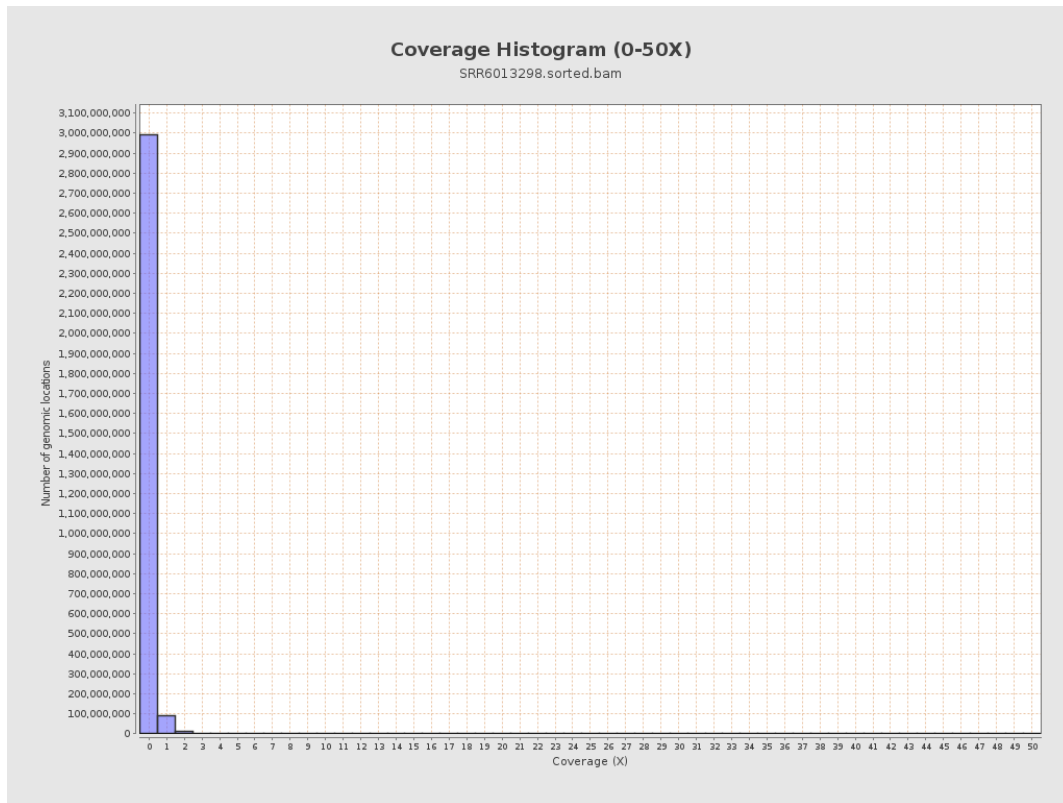
3. Results : Coverage across reference



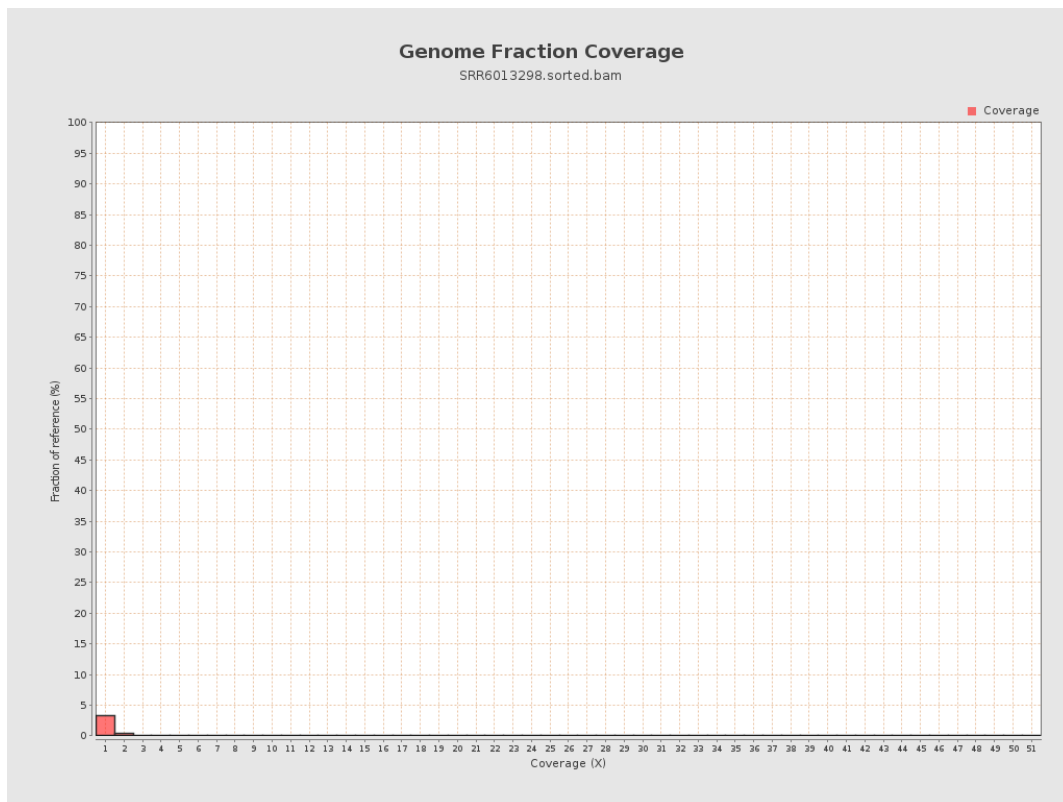
4. Results : Coverage Histogram



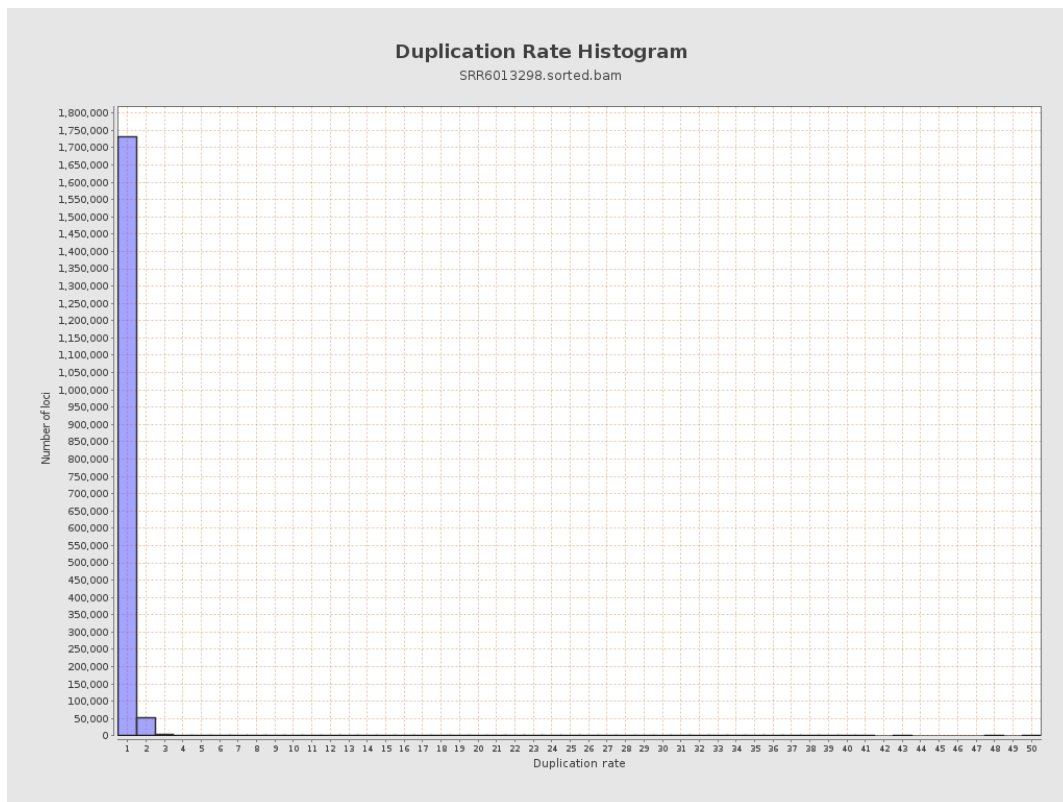
5. Results : Coverage Histogram (0-50X)



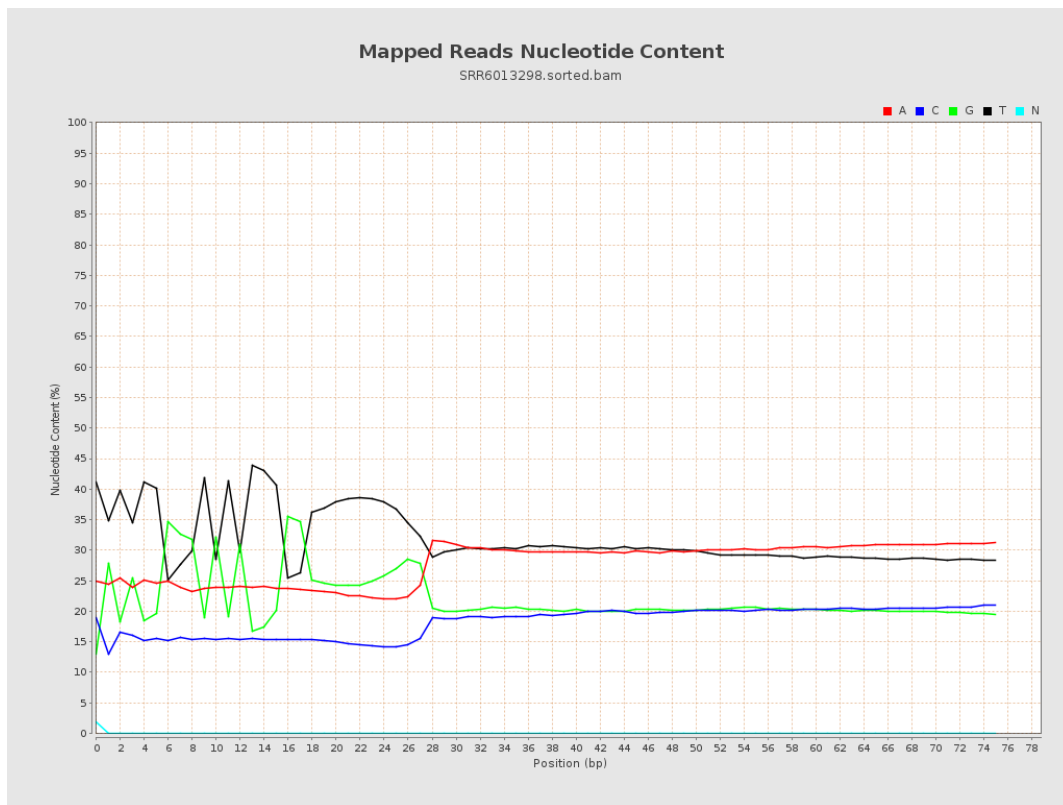
6. Results : Genome Fraction Coverage



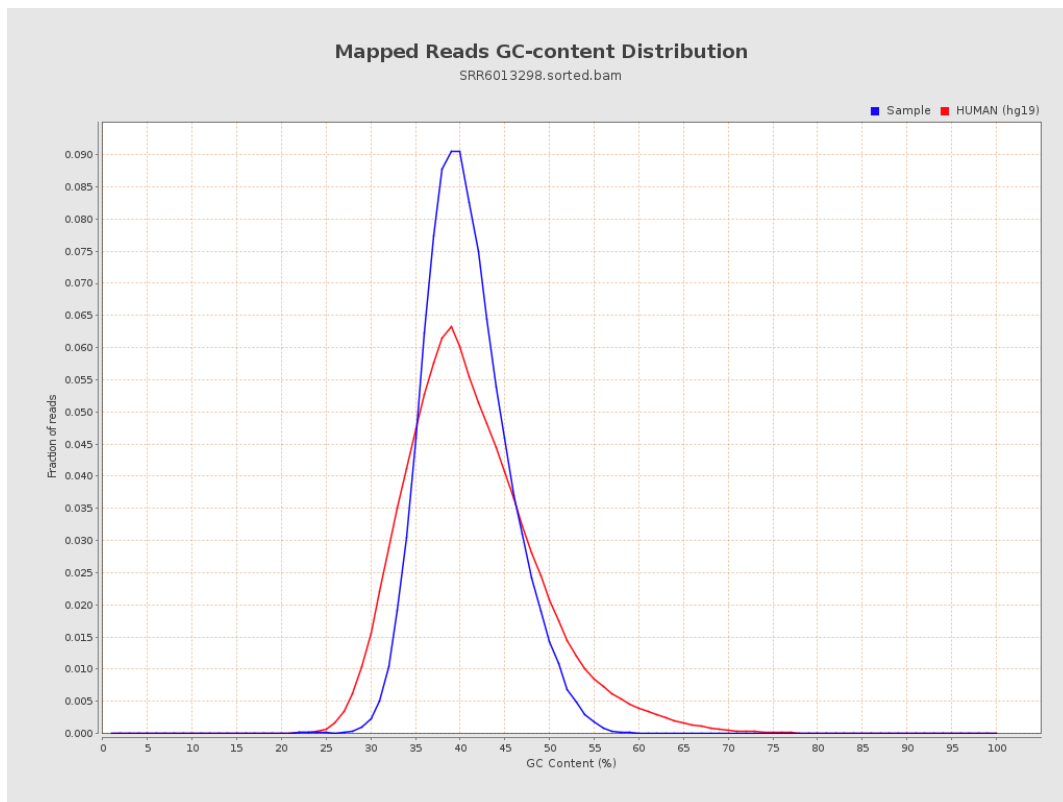
7. Results : Duplication Rate Histogram



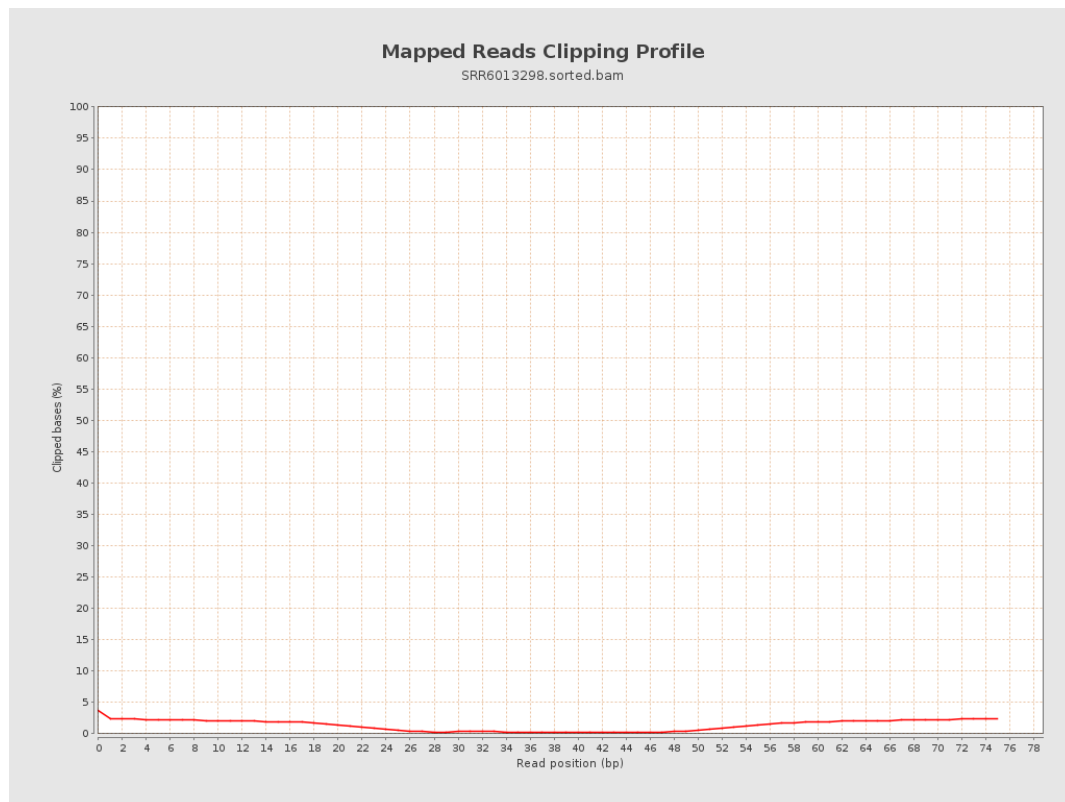
8. Results : Mapped Reads Nucleotide Content



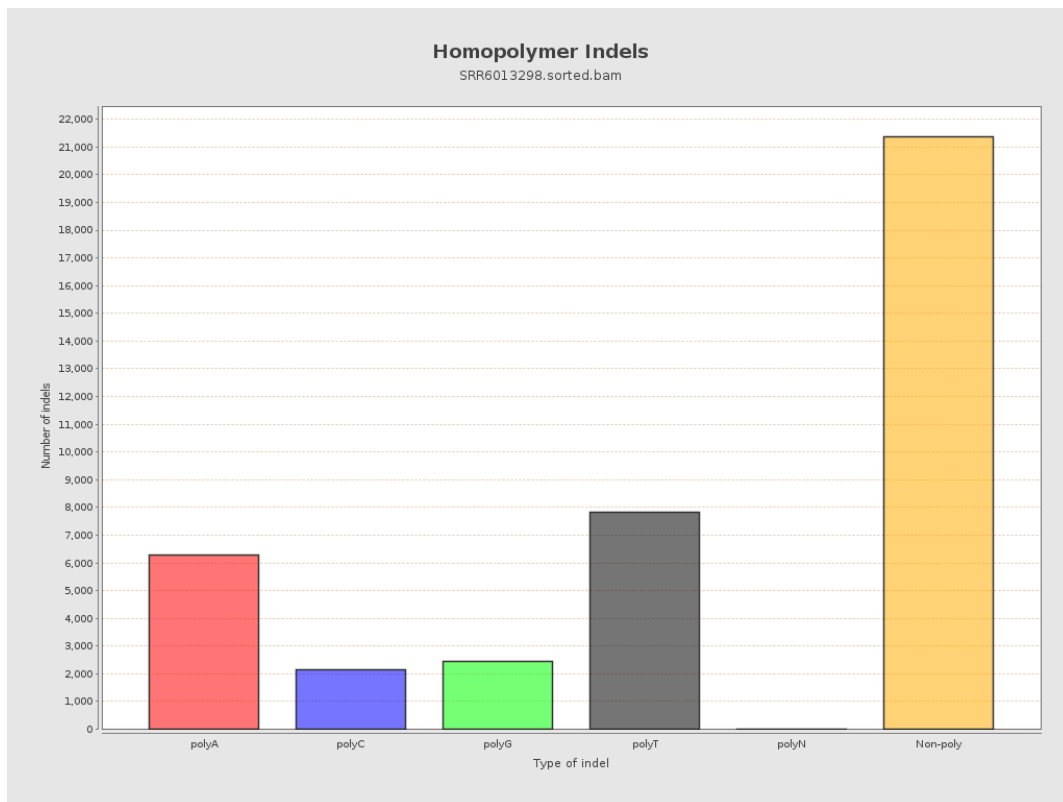
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

