

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:20:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013361.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_SRR6013361 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013361.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:20:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013361.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,231,860
Mapped reads	1,898,417 / 85.06%
Unmapped reads	333,443 / 14.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,709 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	124,412 / 5.57%
Duplication rate	5.19%
Clipped reads	935,719 / 41.93%

2.2. ACGT Content

Number/percentage of A's	34,236,558 / 27.58%
Number/percentage of C's	22,291,441 / 17.96%
Number/percentage of T's	39,984,415 / 32.21%
Number/percentage of G's	27,613,494 / 22.25%
Number/percentage of N's	1,771 / 0%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.4043
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2.4. Mapping Quality

Mean Mapping Quality	45.91
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2.5. Mismatches and indels

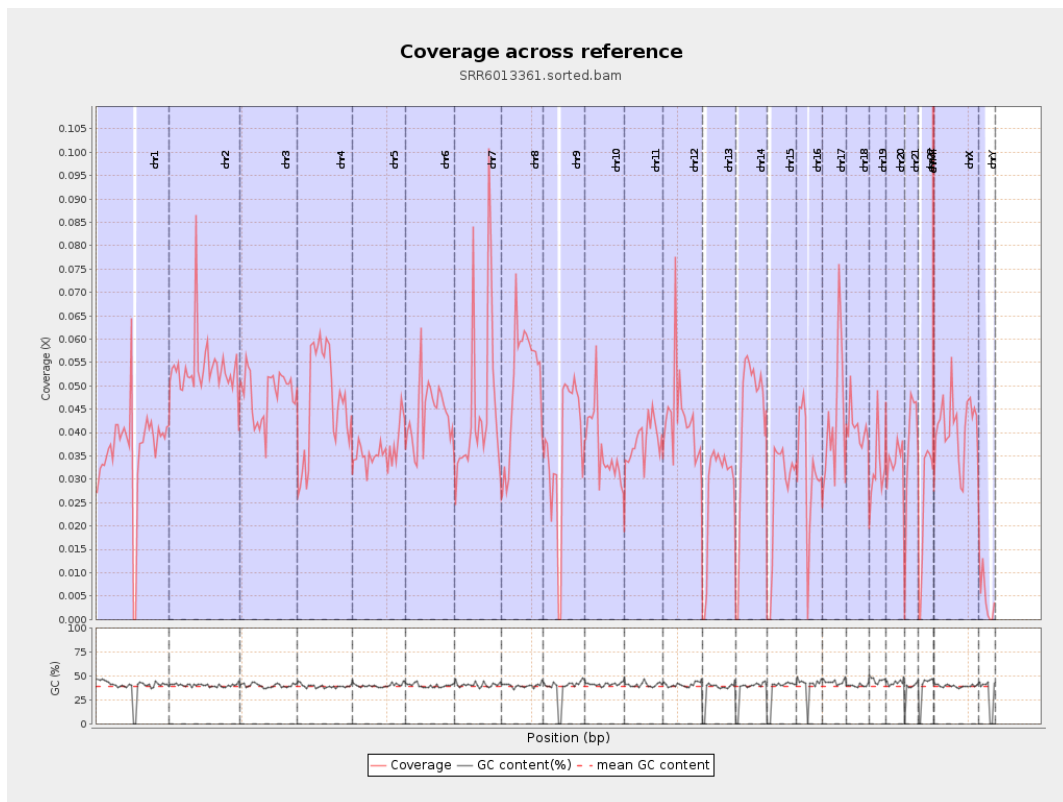
General error rate	0.81%
Mismatches	987,087
Insertions	9,258
Mapped reads with at least one insertion	0.48%
Deletions	37,714
Mapped reads with at least one deletion	1.96%
Homopolymer indels	48.84%

2.6. Chromosome stats

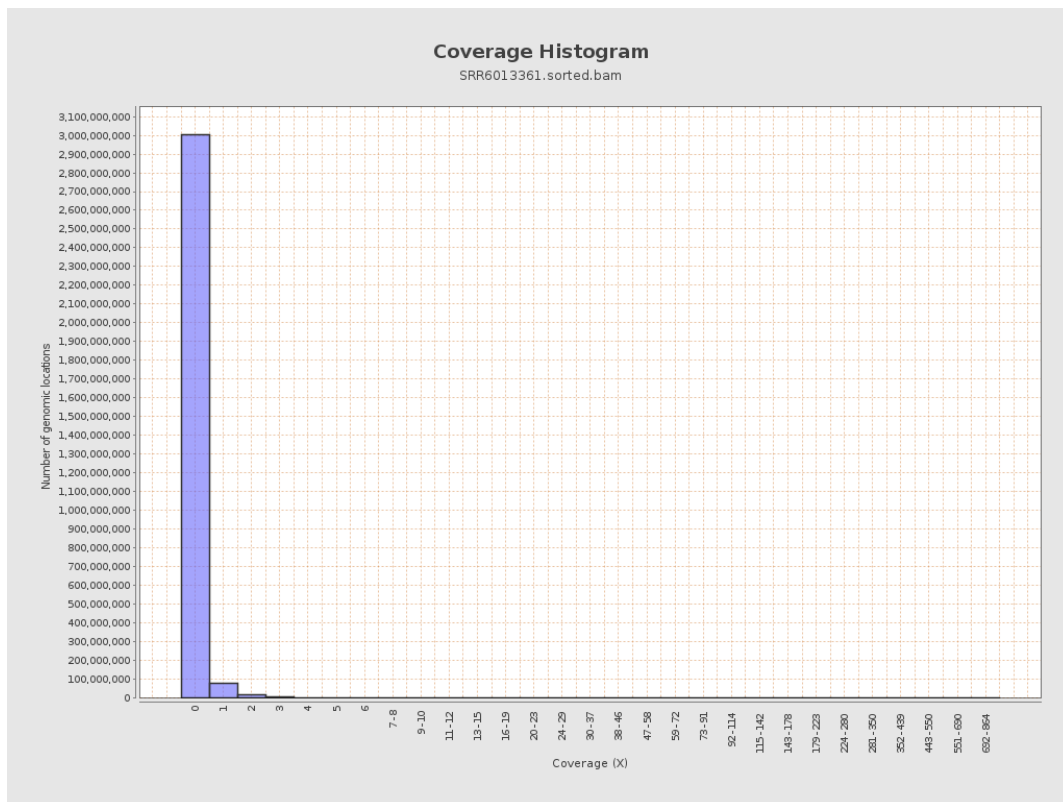
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9042946	0.0363	0.6275
chr2	243199373	13080015	0.0538	0.4993
chr3	198022430	9552639	0.0482	0.2766
chr4	191154276	8832751	0.0462	0.286
chr5	180915260	6565882	0.0363	0.24
chr6	171115067	7507288	0.0439	0.312
chr7	159138663	7266498	0.0457	0.7076

chr8	146364022	7428528	0.0508	0.5909
chr9	141213431	5169924	0.0366	0.3597
chr10	135534747	4949143	0.0365	0.3551
chr11	135006516	5131821	0.038	0.3353
chr12	133851895	5776674	0.0432	0.2659
chr13	115169878	3176432	0.0276	0.2083
chr14	107349540	4590570	0.0428	0.2747
chr15	102531392	2770054	0.027	0.2108
chr16	90354753	2922935	0.0323	0.2408
chr17	81195210	3434877	0.0423	0.279
chr18	78077248	3206817	0.0411	0.6789
chr19	59128983	1948921	0.033	0.4426
chr20	63025520	2139013	0.0339	0.2418
chr21	48129895	1787422	0.0371	0.2549
chr22	51304566	1255599	0.0245	0.1915
chrMT	16571	50506	3.0479	2.8449
chrX	155270560	6339597	0.0408	0.2771
chrY	59373566	266863	0.0045	0.1121

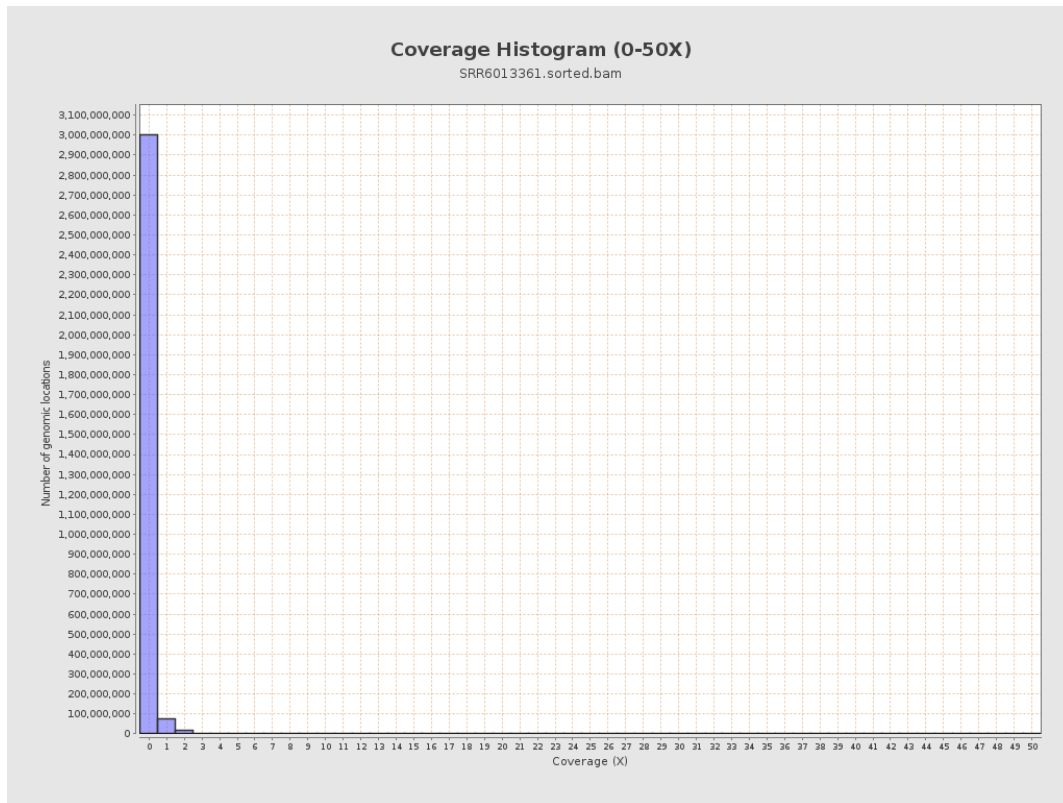
3. Results : Coverage across reference



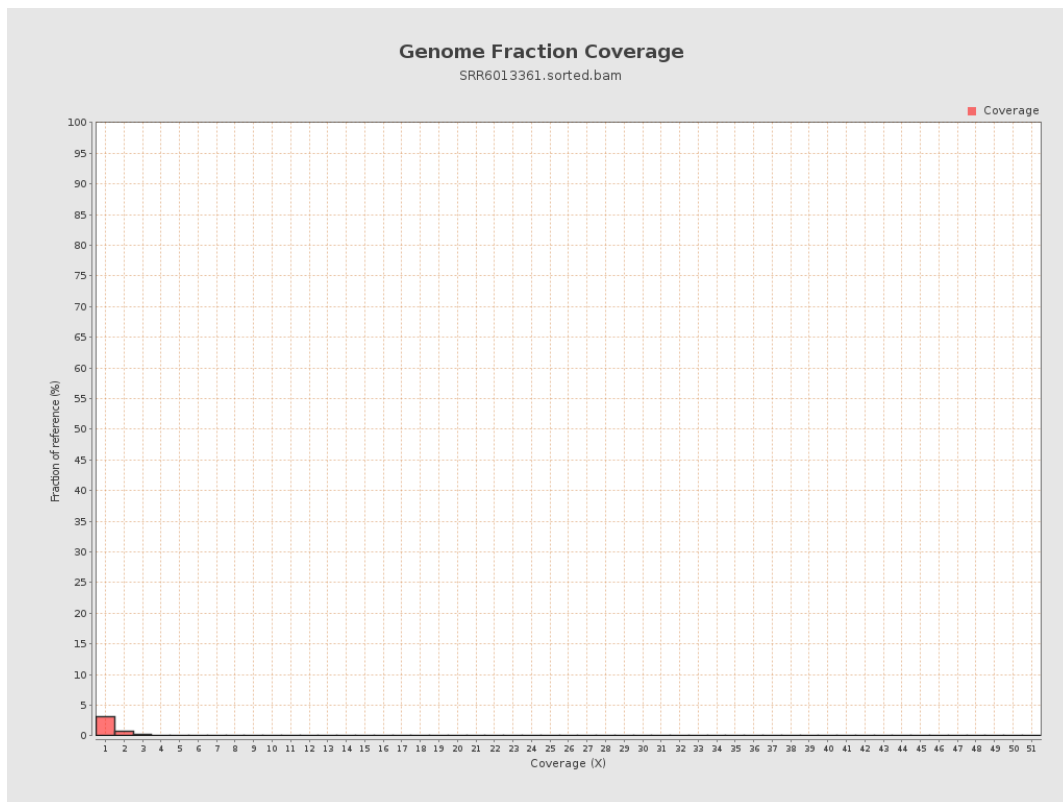
4. Results : Coverage Histogram



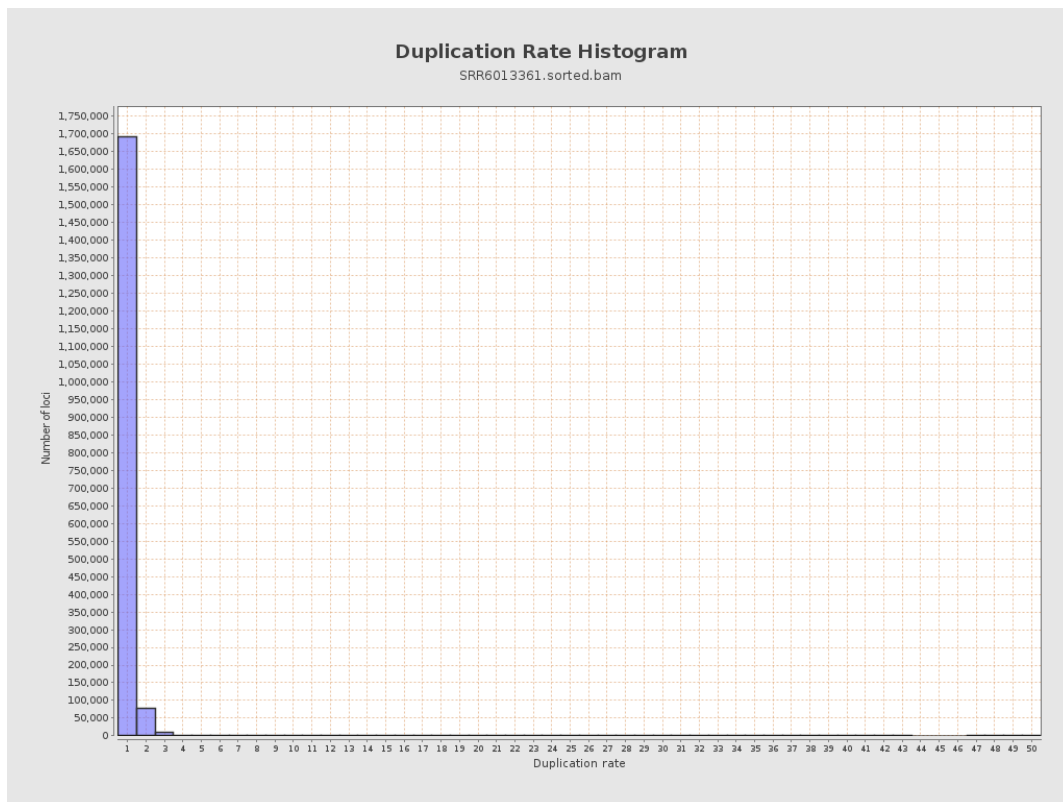
5. Results : Coverage Histogram (0-50X)



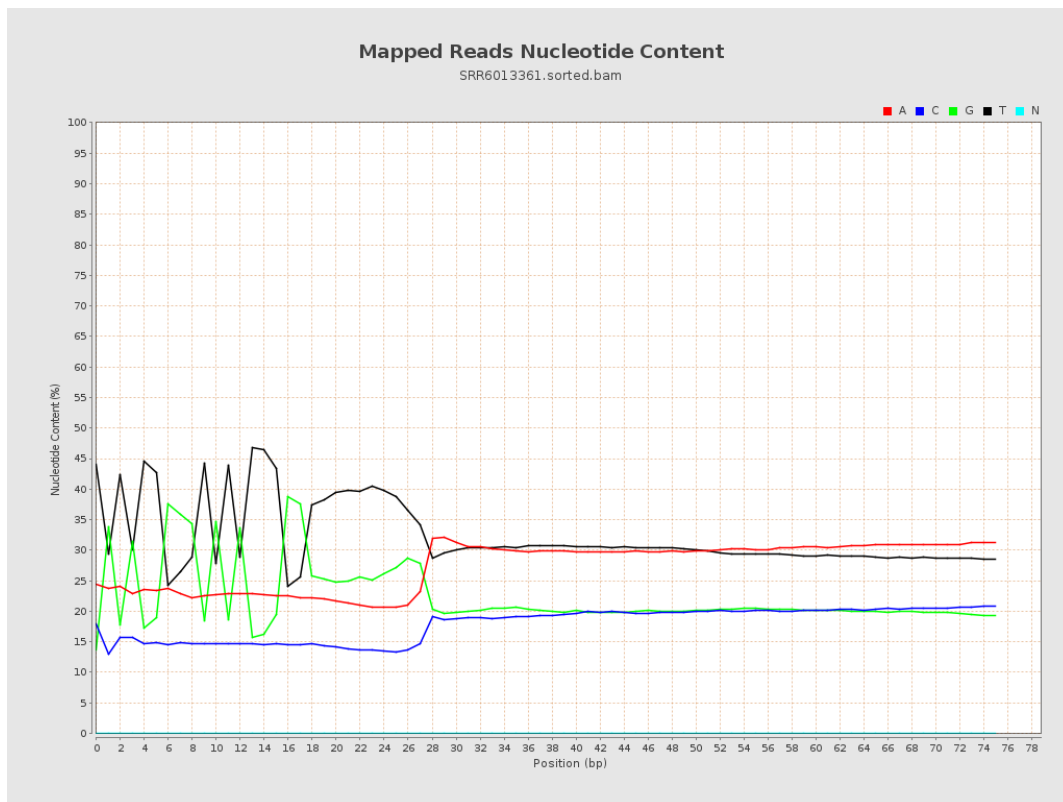
6. Results : Genome Fraction Coverage



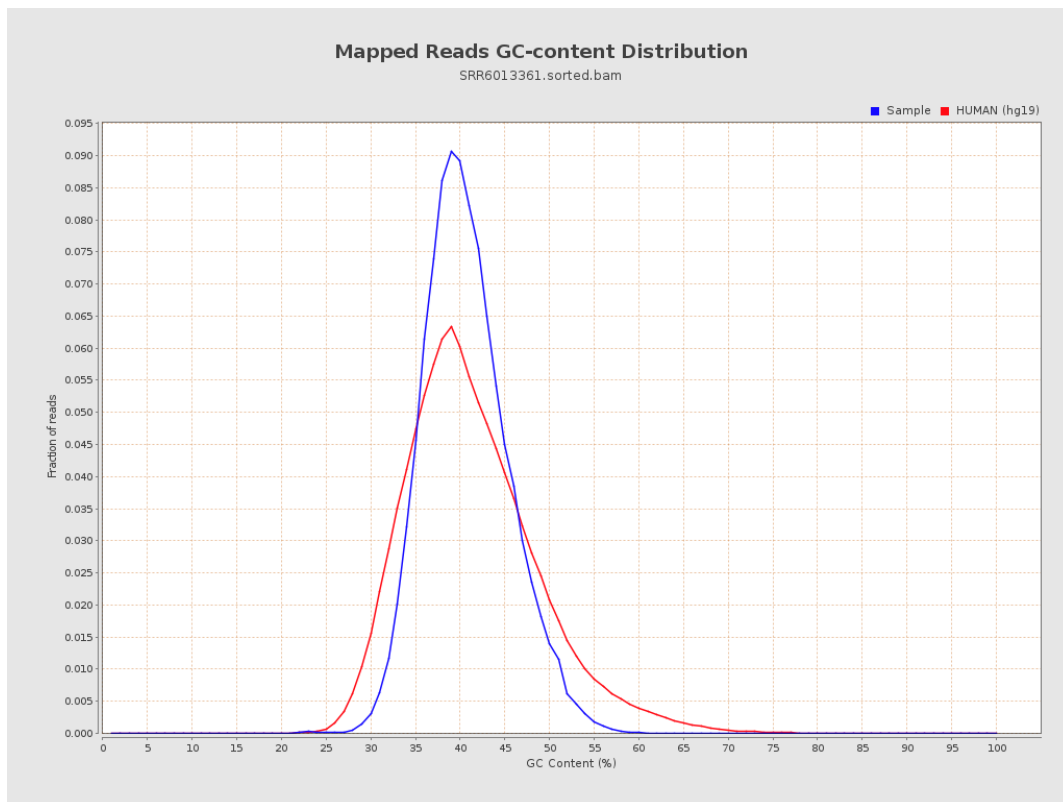
7. Results : Duplication Rate Histogram



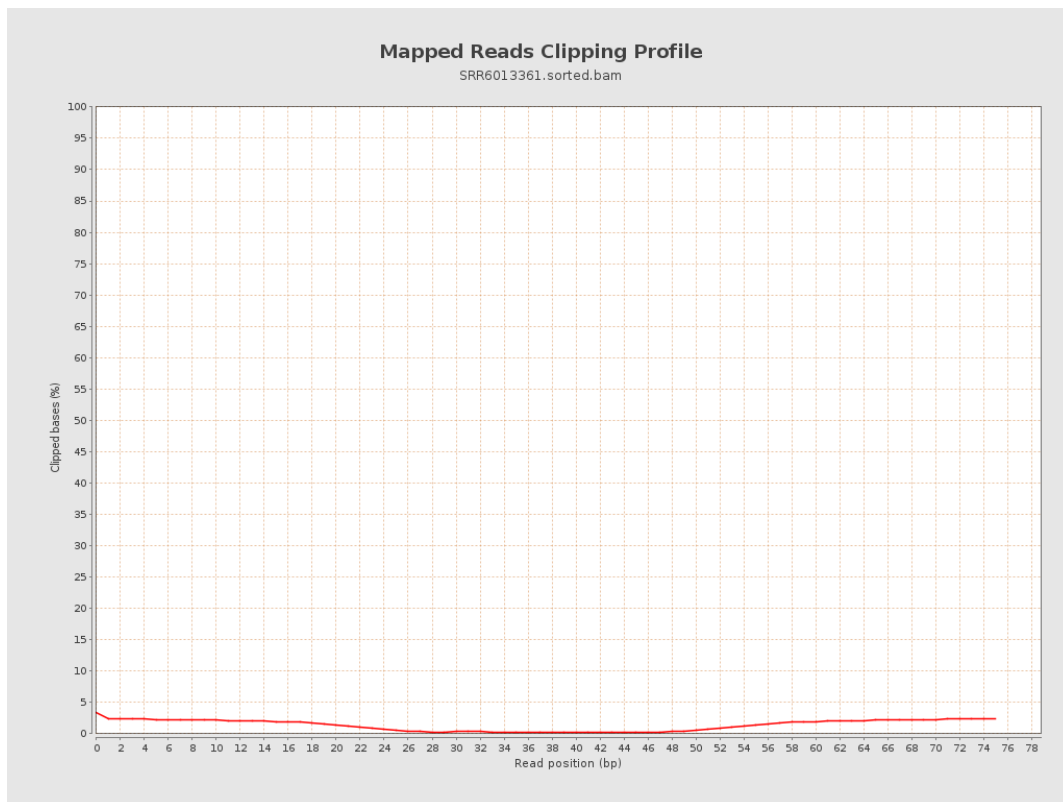
8. Results : Mapped Reads Nucleotide Content



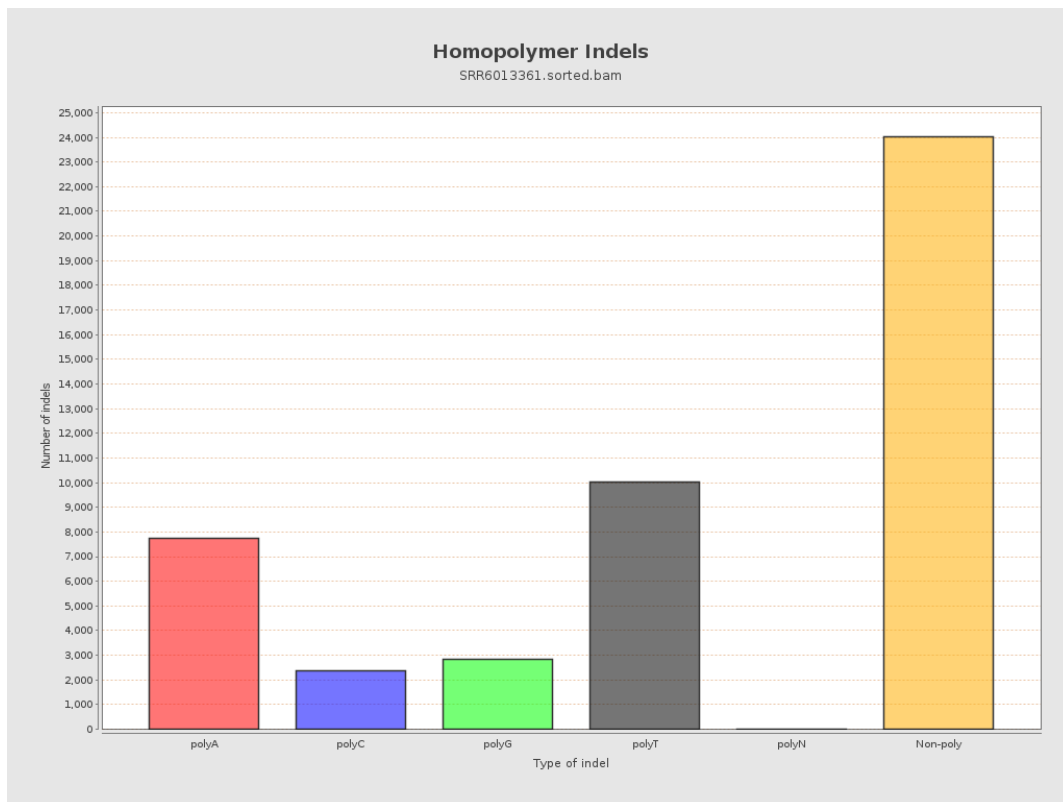
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

