

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:06:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013209.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_SRR6013209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:06:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,466,736
Mapped reads	7,538,257 / 89.03%
Unmapped reads	928,479 / 10.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,251 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	598,961 / 7.07%
Duplication rate	5.63%
Clipped reads	2,941,686 / 34.74%

2.2. ACGT Content

Number/percentage of A's	145,592,034 / 28.41%
Number/percentage of C's	93,797,470 / 18.3%
Number/percentage of T's	163,208,798 / 31.85%
Number/percentage of G's	109,740,589 / 21.41%
Number/percentage of N's	113,748 / 0.02%
GC Percentage	39.72%

2.3. Coverage

Mean	0.1656

Standard Deviation	1.5386
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2.4. Mapping Quality

Mean Mapping Quality	46.7
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2.5. Mismatches and indels

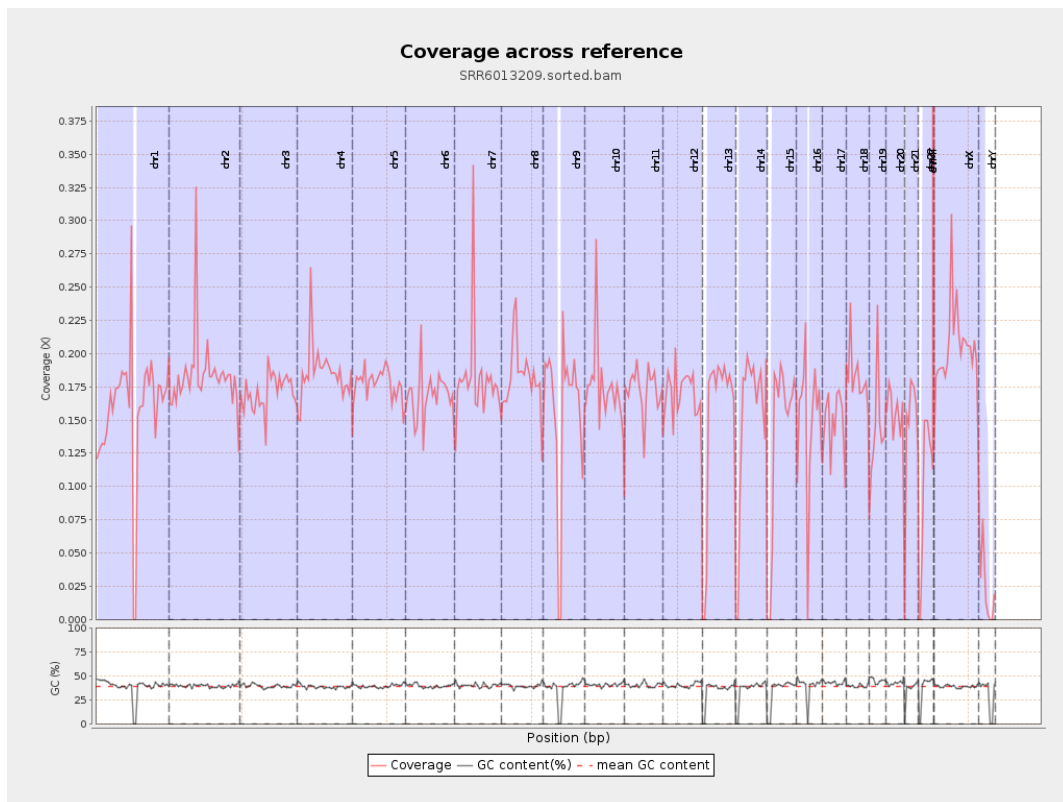
General error rate	0.81%
Mismatches	4,077,920
Insertions	40,174
Mapped reads with at least one insertion	0.53%
Deletions	120,766
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.3%

2.6. Chromosome stats

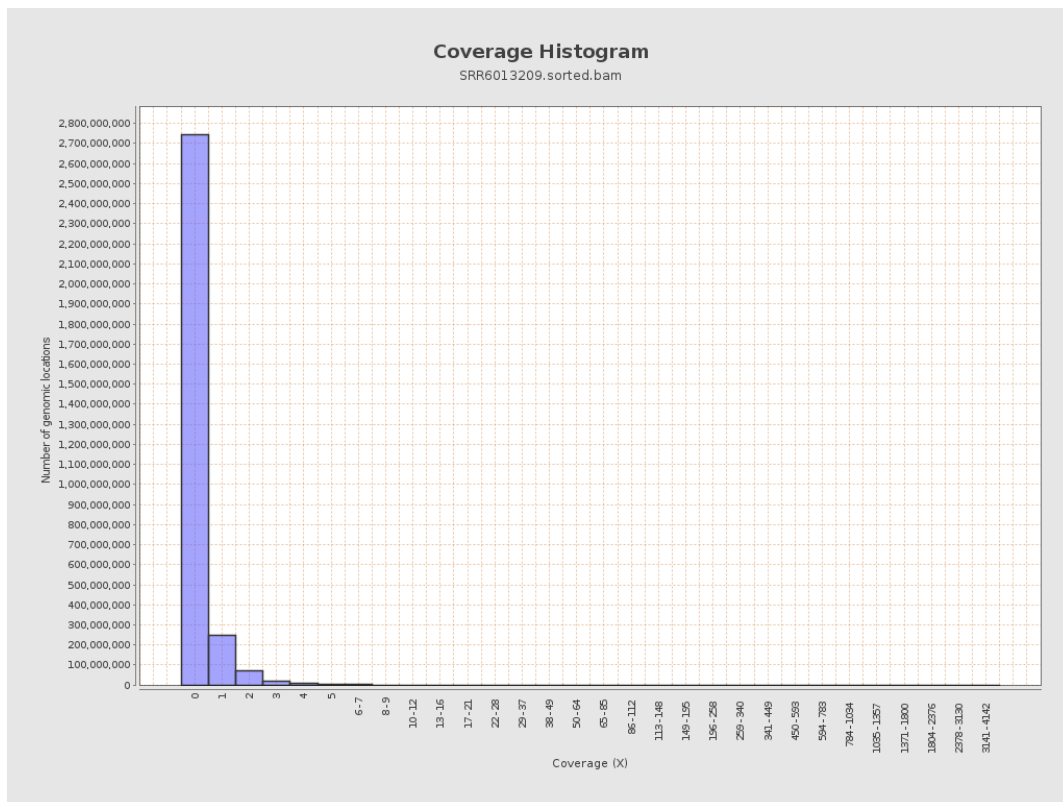
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	39526313	0.1586	2.998
chr2	243199373	44648494	0.1836	1.7418
chr3	198022430	33812932	0.1708	0.5622
chr4	191154276	35421873	0.1853	0.7527
chr5	180915260	32073485	0.1773	0.588
chr6	171115067	28826982	0.1685	0.8137
chr7	159138663	28970856	0.182	2.4514

chr8	146364022	26612833	0.1818	2.595
chr9	141213431	22073765	0.1563	1.3939
chr10	135534747	23738795	0.1751	1.2908
chr11	135006516	23145657	0.1714	1.0196
chr12	133851895	22695356	0.1696	0.6095
chr13	115169878	17303405	0.1502	0.5285
chr14	107349540	15987856	0.1489	0.6408
chr15	102531392	14292956	0.1394	0.5194
chr16	90354753	13432897	0.1487	0.7354
chr17	81195210	11876700	0.1463	0.681
chr18	78077248	14258949	0.1826	3.0056
chr19	59128983	8603351	0.1455	2.097
chr20	63025520	9708539	0.154	0.5981
chr21	48129895	6930194	0.144	0.6712
chr22	51304566	5006956	0.0976	0.4066
chrMT	16571	601287	36.2855	21.7295
chrX	155270560	31699877	0.2042	0.8514
chrY	59373566	1412165	0.0238	0.5562

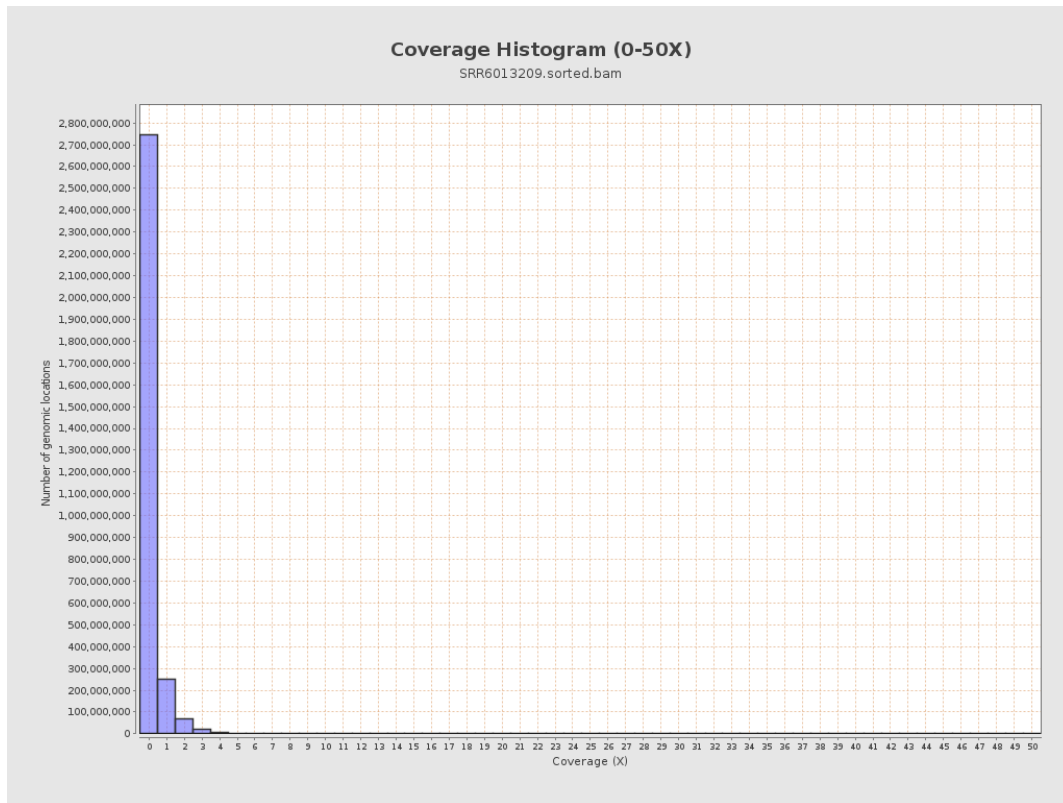
3. Results : Coverage across reference



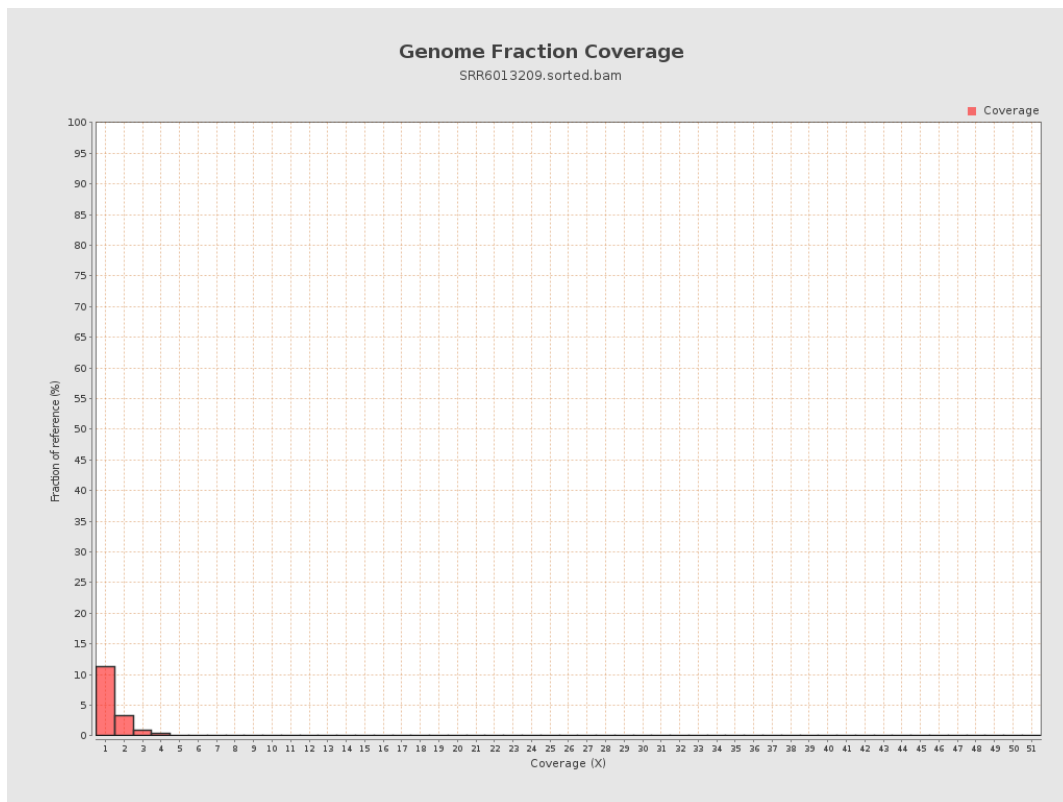
4. Results : Coverage Histogram



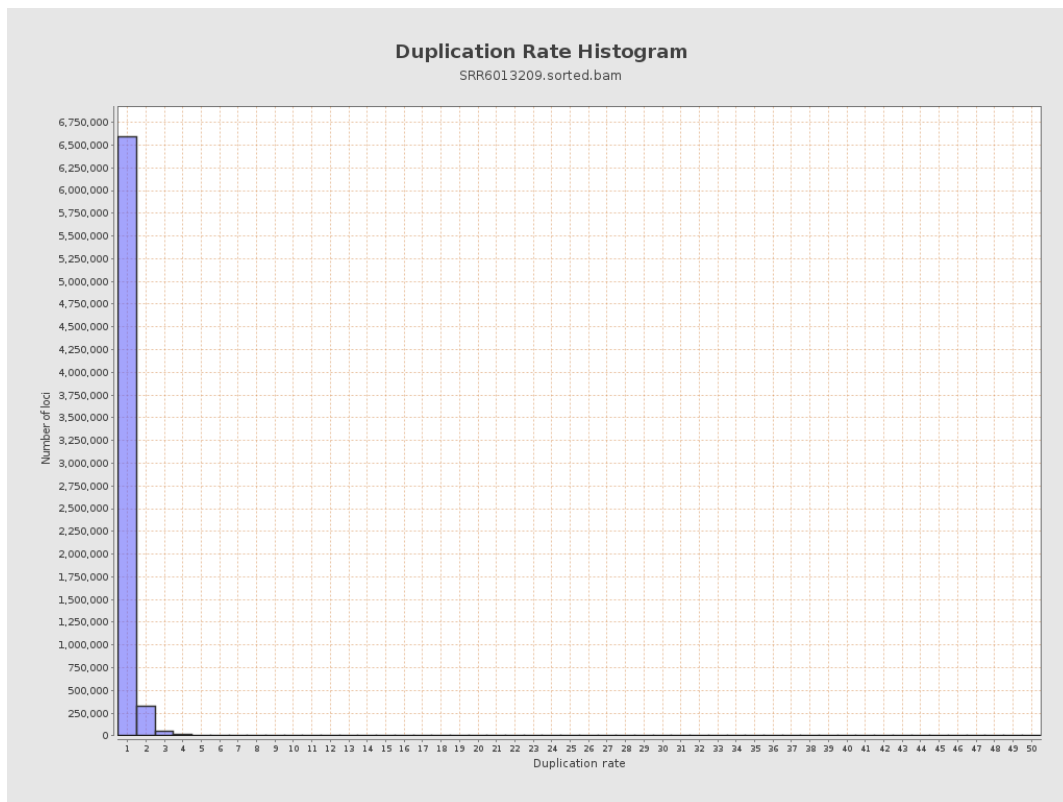
5. Results : Coverage Histogram (0-50X)



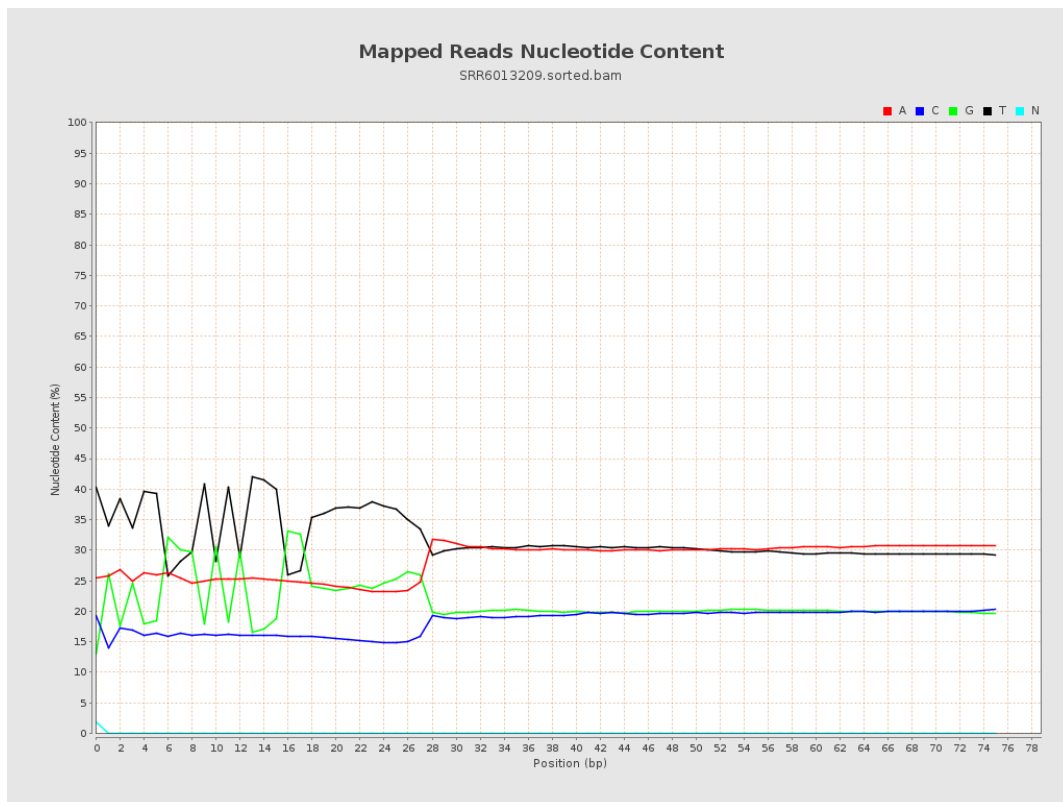
6. Results : Genome Fraction Coverage



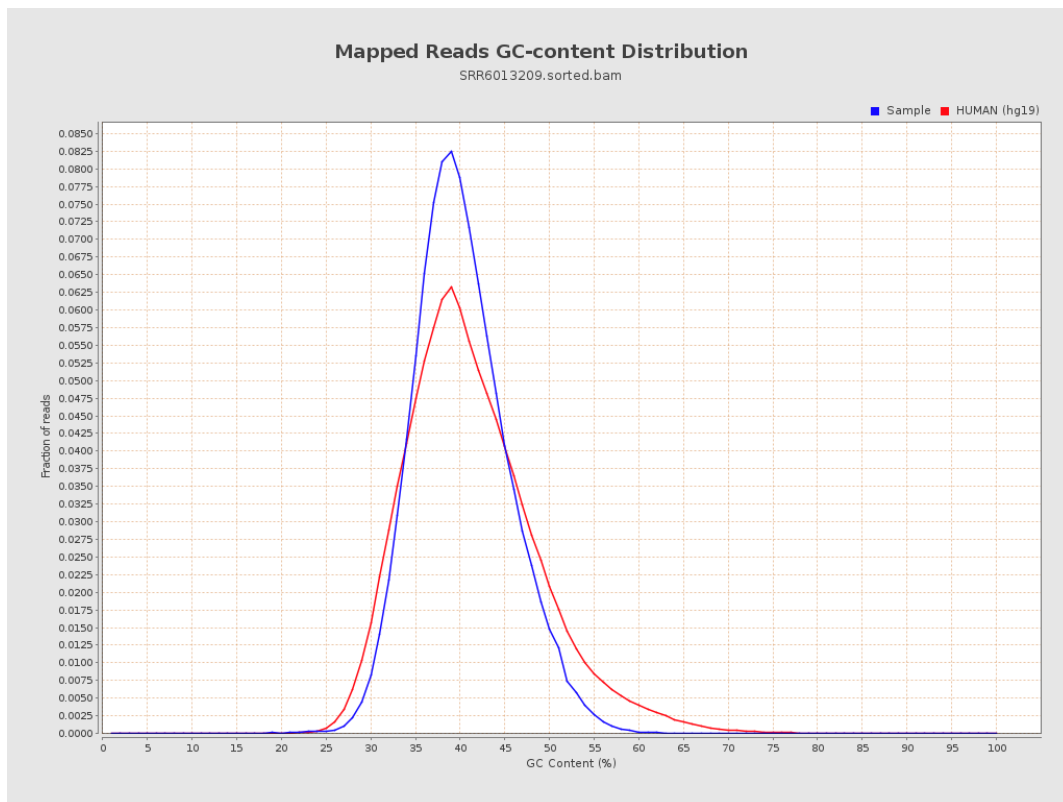
7. Results : Duplication Rate Histogram



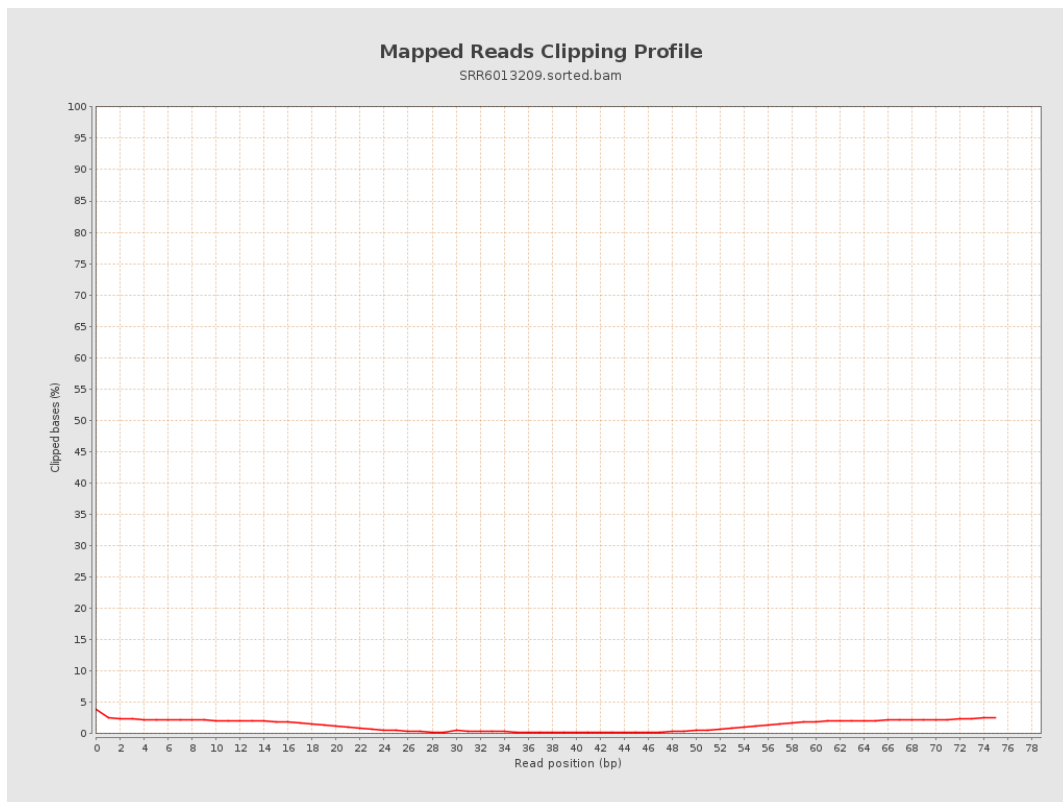
8. Results : Mapped Reads Nucleotide Content



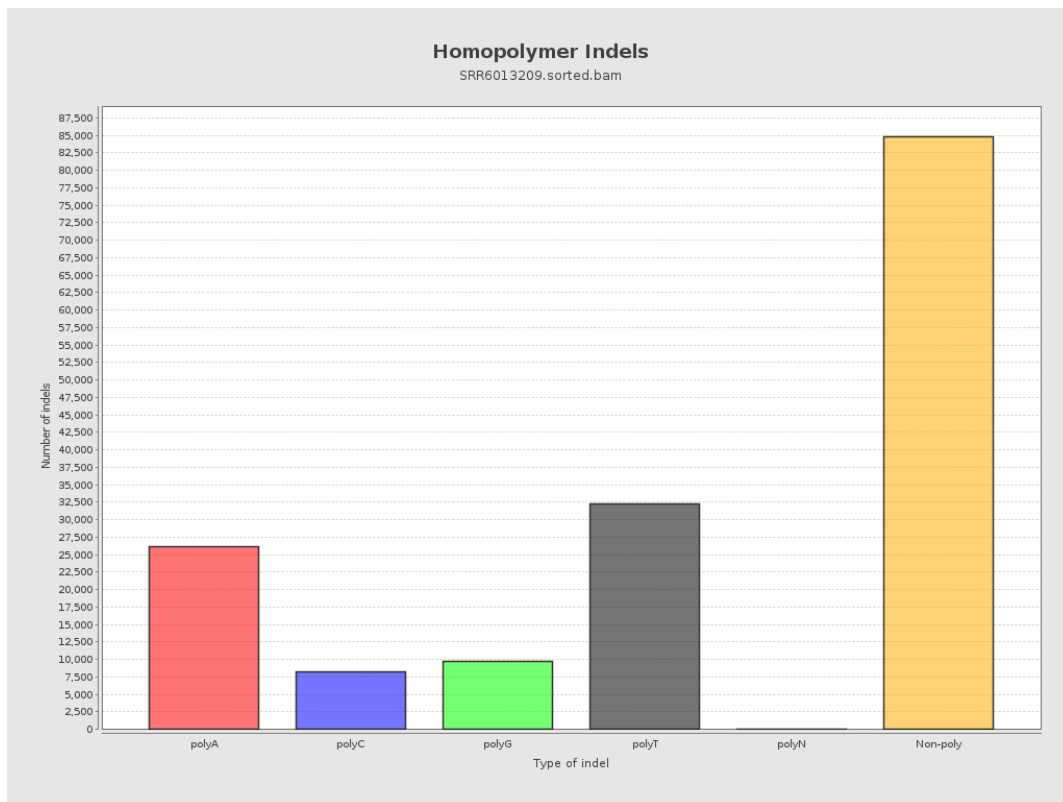
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

