

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:50:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013269.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_SRR6013269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013269.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:50:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,002,099
Mapped reads	1,767,215 / 88.27%
Unmapped reads	234,884 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,716 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	84,744 / 4.23%
Duplication rate	3.67%
Clipped reads	765,888 / 38.25%

2.2. ACGT Content

Number/percentage of A's	33,411,978 / 28.17%
Number/percentage of C's	21,810,470 / 18.39%
Number/percentage of T's	37,822,516 / 31.89%
Number/percentage of G's	25,521,567 / 21.52%
Number/percentage of N's	25,364 / 0.02%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3849
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2.4. Mapping Quality

Mean Mapping Quality	45.91
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2.5. Mismatches and indels

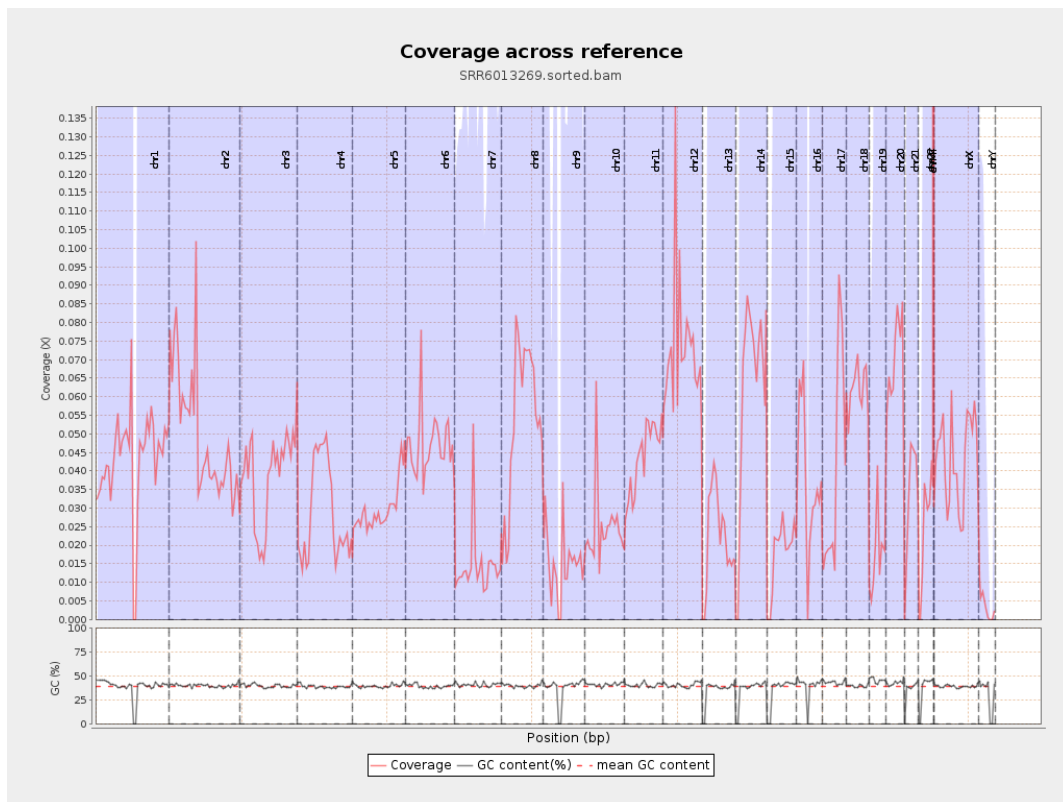
General error rate	0.84%
Mismatches	982,853
Insertions	8,403
Mapped reads with at least one insertion	0.47%
Deletions	29,942
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.31%

2.6. Chromosome stats

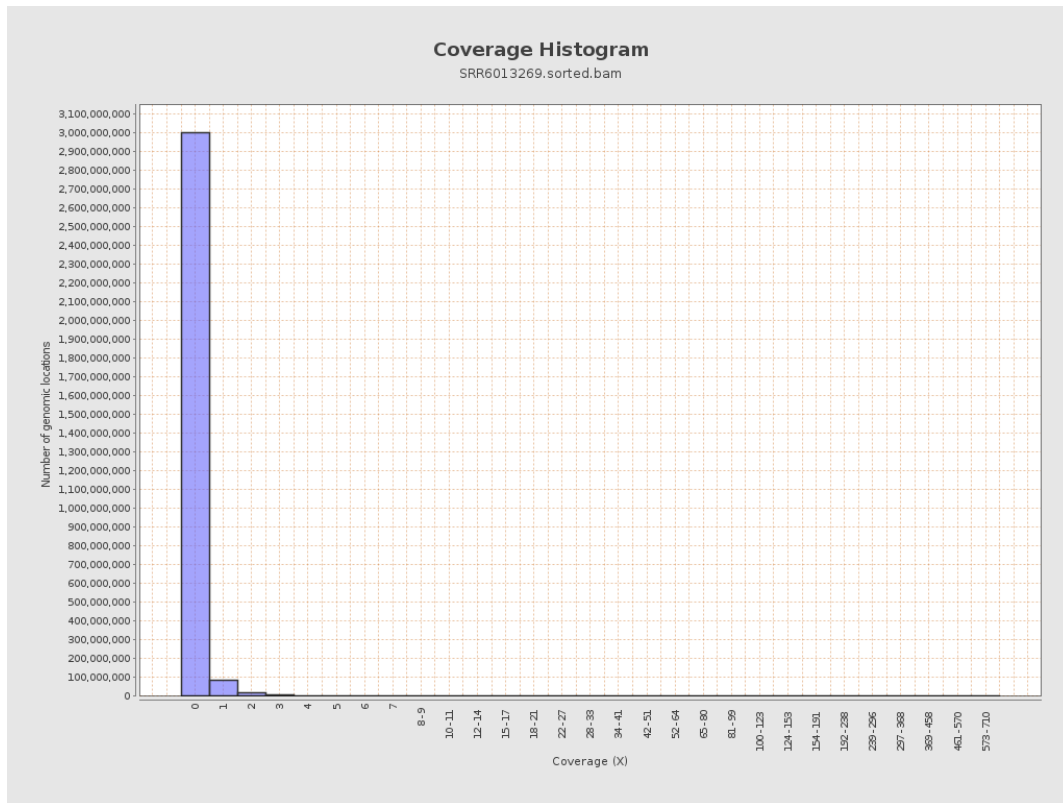
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10769507	0.0432	0.6621
chr2	243199373	12175044	0.0501	0.5578
chr3	198022430	7594416	0.0384	0.2304
chr4	191154276	5487501	0.0287	0.2047
chr5	180915260	5385316	0.0298	0.2012
chr6	171115067	8067801	0.0471	0.3768
chr7	159138663	2329524	0.0146	0.43

chr8	146364022	7923070	0.0541	0.483
chr9	141213431	2111389	0.015	0.3286
chr10	135534747	3325228	0.0245	0.4272
chr11	135006516	5870134	0.0435	0.3088
chr12	133851895	9850711	0.0736	0.3225
chr13	115169878	2537731	0.022	0.1714
chr14	107349540	6651973	0.062	0.299
chr15	102531392	1836851	0.0179	0.1555
chr16	90354753	3425166	0.0379	0.2498
chr17	81195210	3197691	0.0394	0.2408
chr18	78077248	4838262	0.062	0.6398
chr19	59128983	1100183	0.0186	0.462
chr20	63025520	4410684	0.07	0.3166
chr21	48129895	1597225	0.0332	0.2159
chr22	51304566	1252637	0.0244	0.1785
chrMT	16571	34454	2.0792	2.2334
chrX	155270560	6668210	0.0429	0.2696
chrY	59373566	201837	0.0034	0.0745

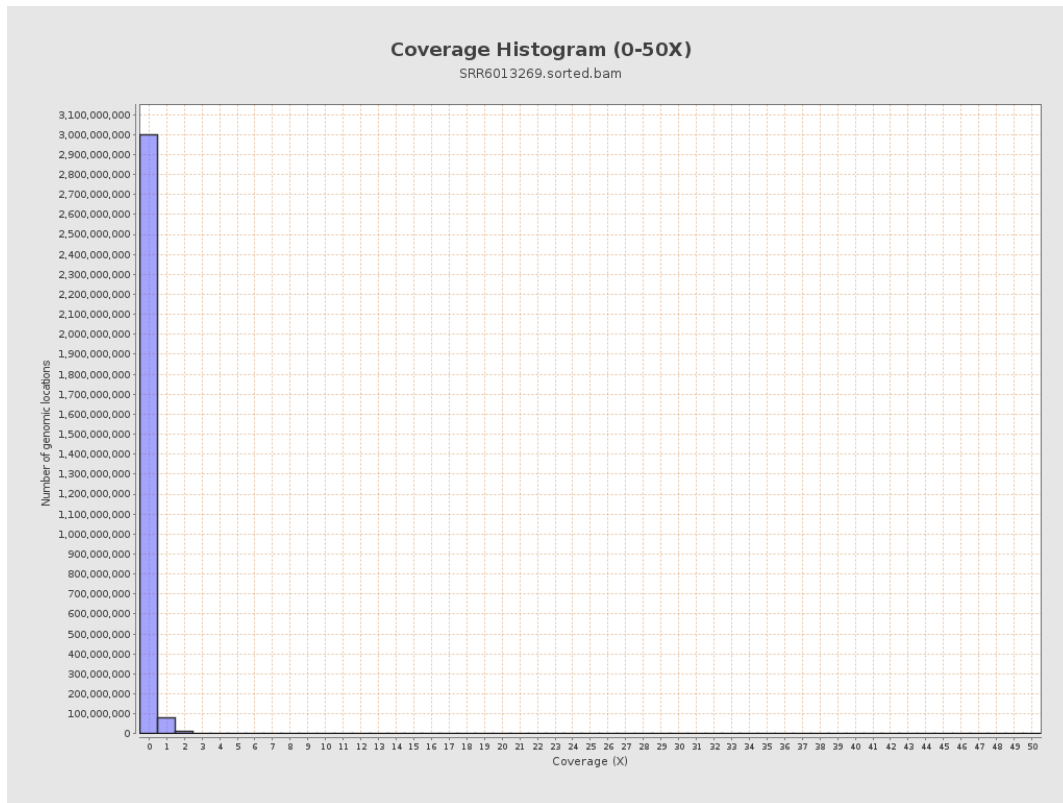
3. Results : Coverage across reference



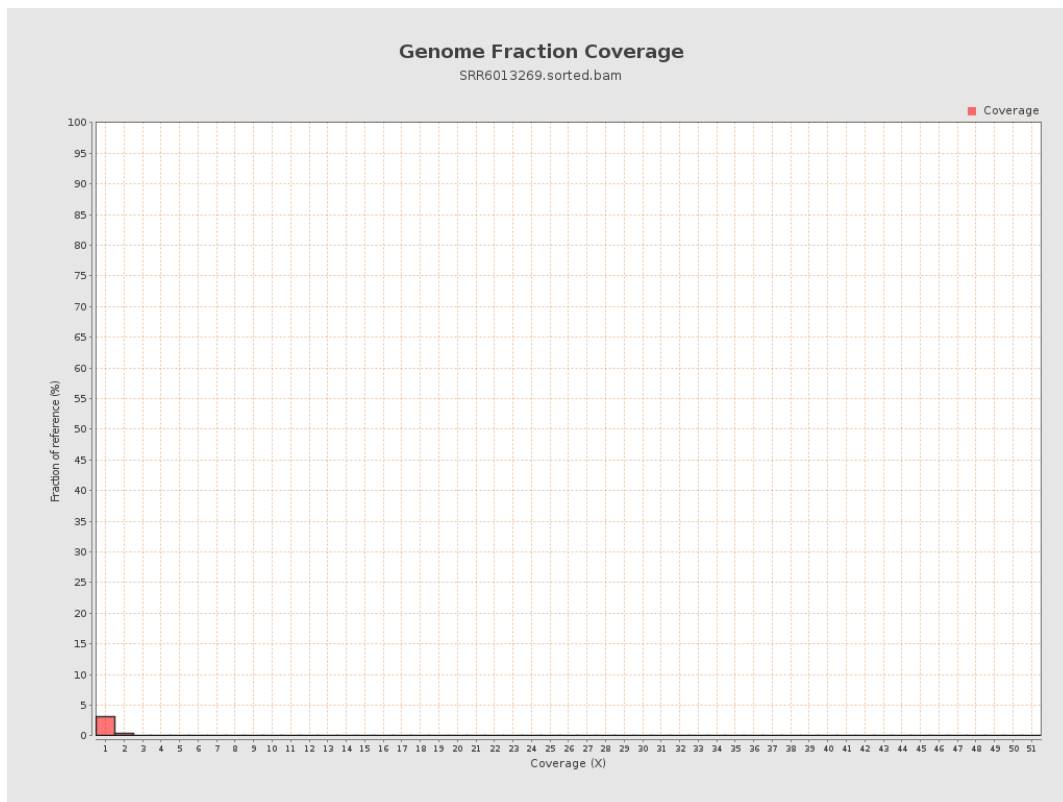
4. Results : Coverage Histogram



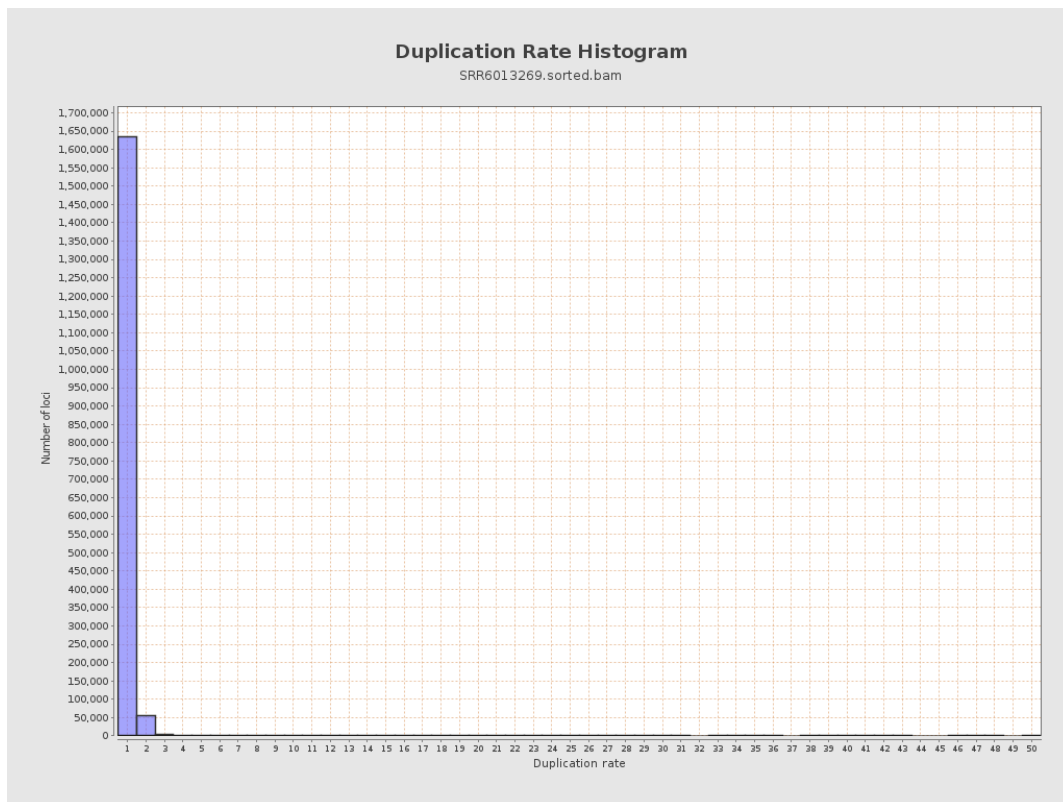
5. Results : Coverage Histogram (0-50X)



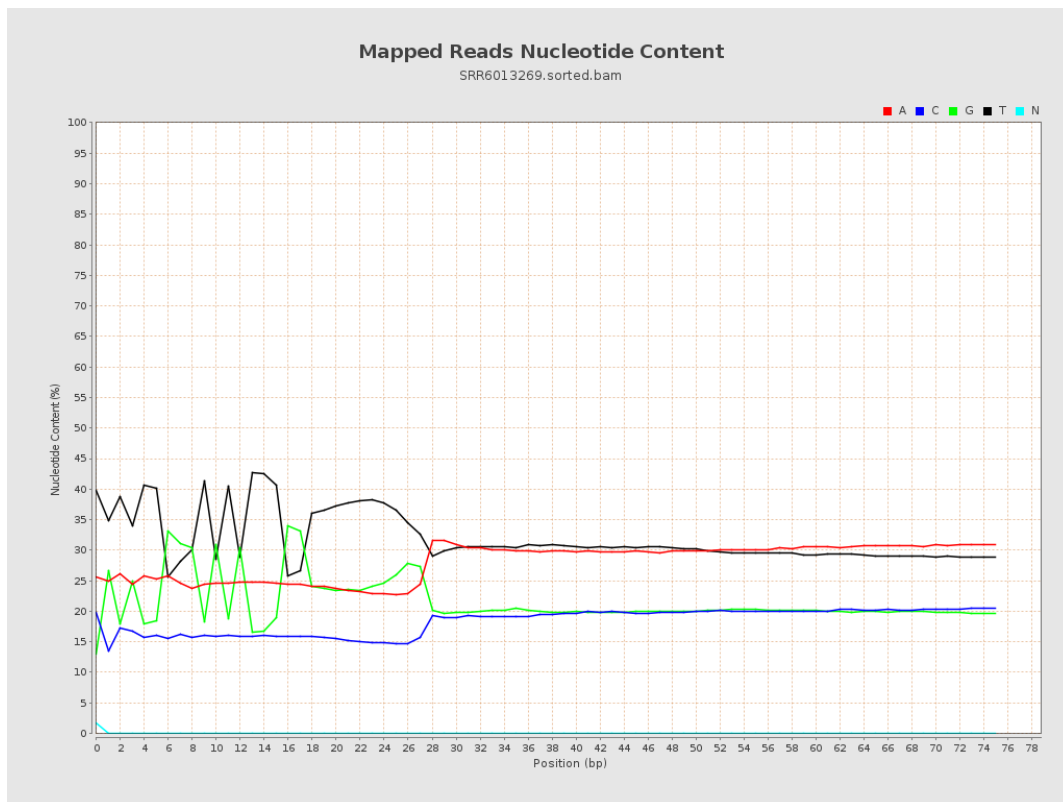
6. Results : Genome Fraction Coverage



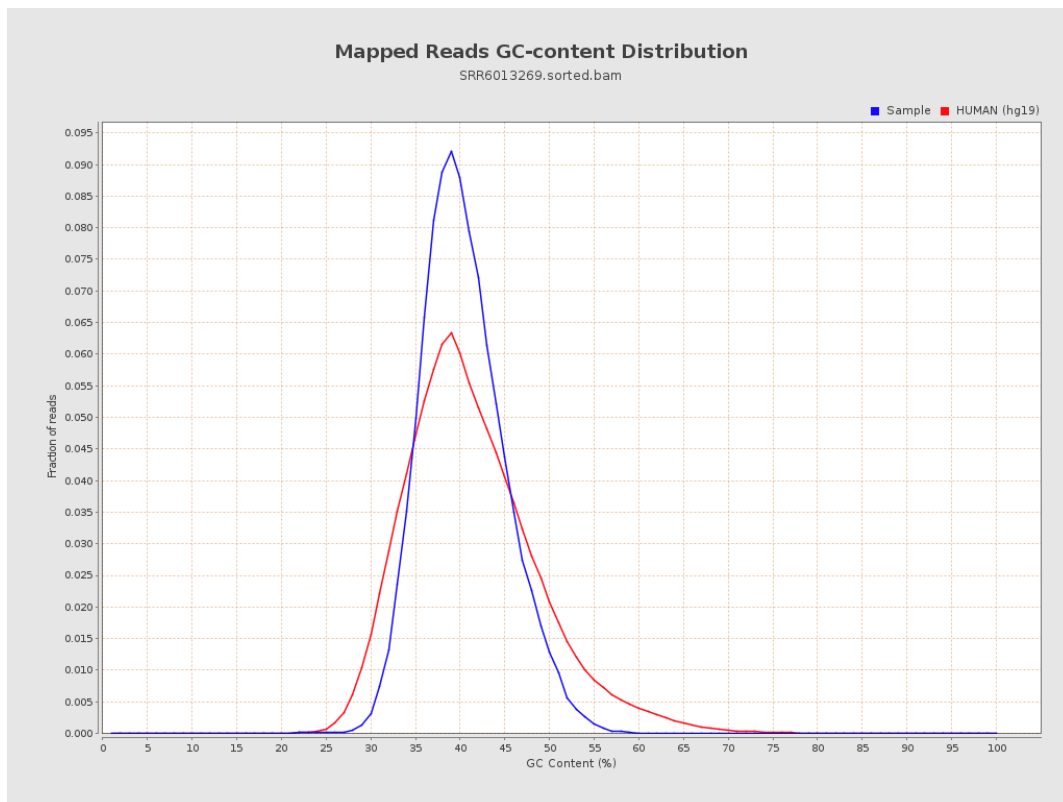
7. Results : Duplication Rate Histogram



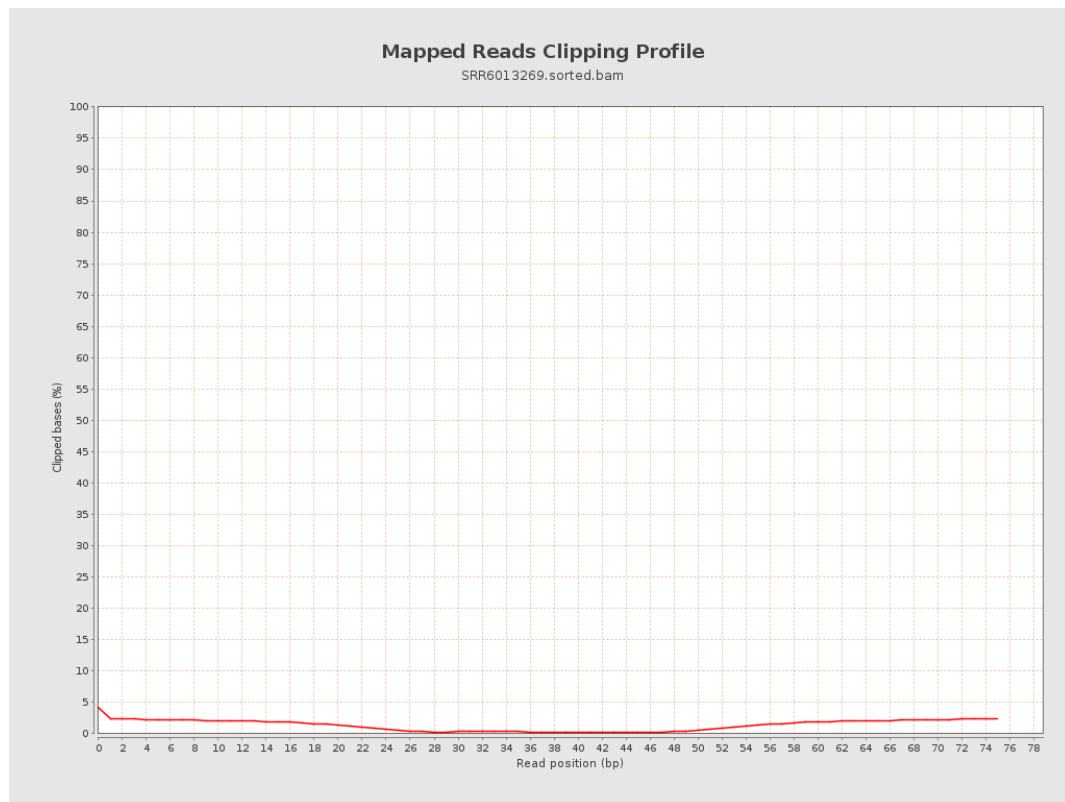
8. Results : Mapped Reads Nucleotide Content



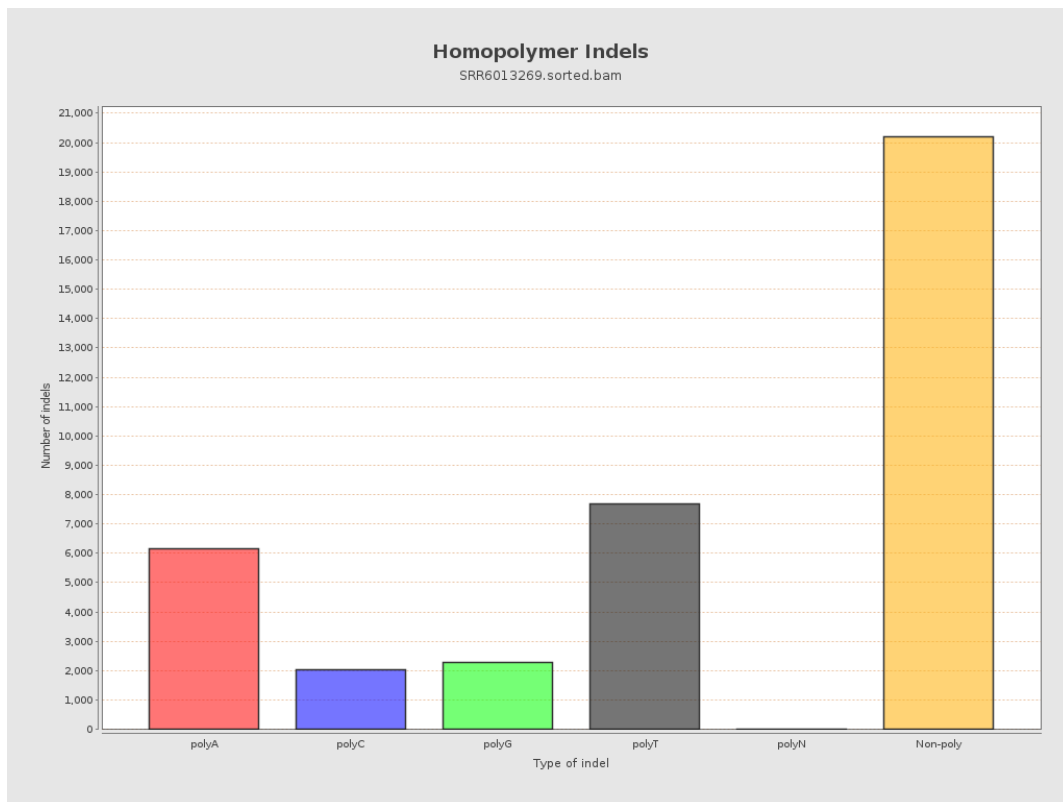
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

