

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:56:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237314.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_SRR6237314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:56:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,828,738
Mapped reads	2,304,239 / 81.46%
Unmapped reads	524,499 / 18.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,534 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	286,660 / 10.13%
Duplication rate	9.35%
Clipped reads	1,153,261 / 40.77%

2.2. ACGT Content

Number/percentage of A's	40,931,648 / 27.09%
Number/percentage of C's	27,750,457 / 18.37%
Number/percentage of T's	48,088,418 / 31.83%
Number/percentage of G's	34,310,197 / 22.71%
Number/percentage of N's	2,328 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.5385
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2.4. Mapping Quality

Mean Mapping Quality	40.98
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2.5. Mismatches and indels

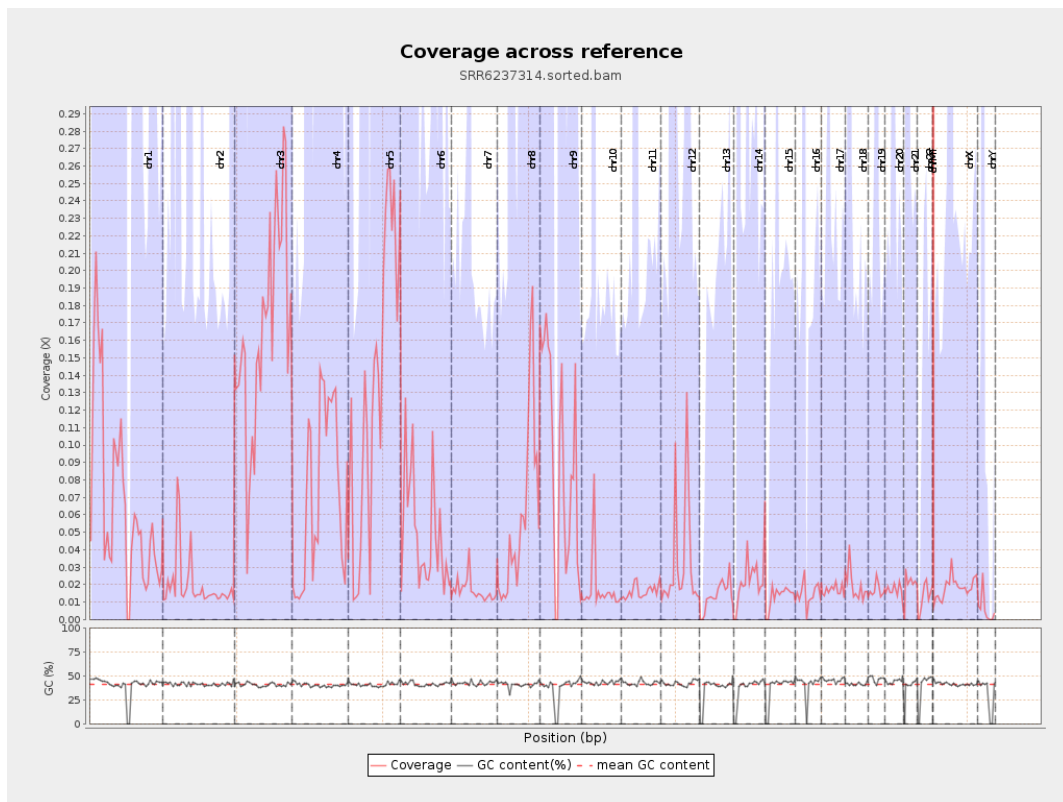
General error rate	0.82%
Mismatches	1,209,554
Insertions	11,544
Mapped reads with at least one insertion	0.5%
Deletions	33,526
Mapped reads with at least one deletion	1.44%
Homopolymer indels	46.66%

2.6. Chromosome stats

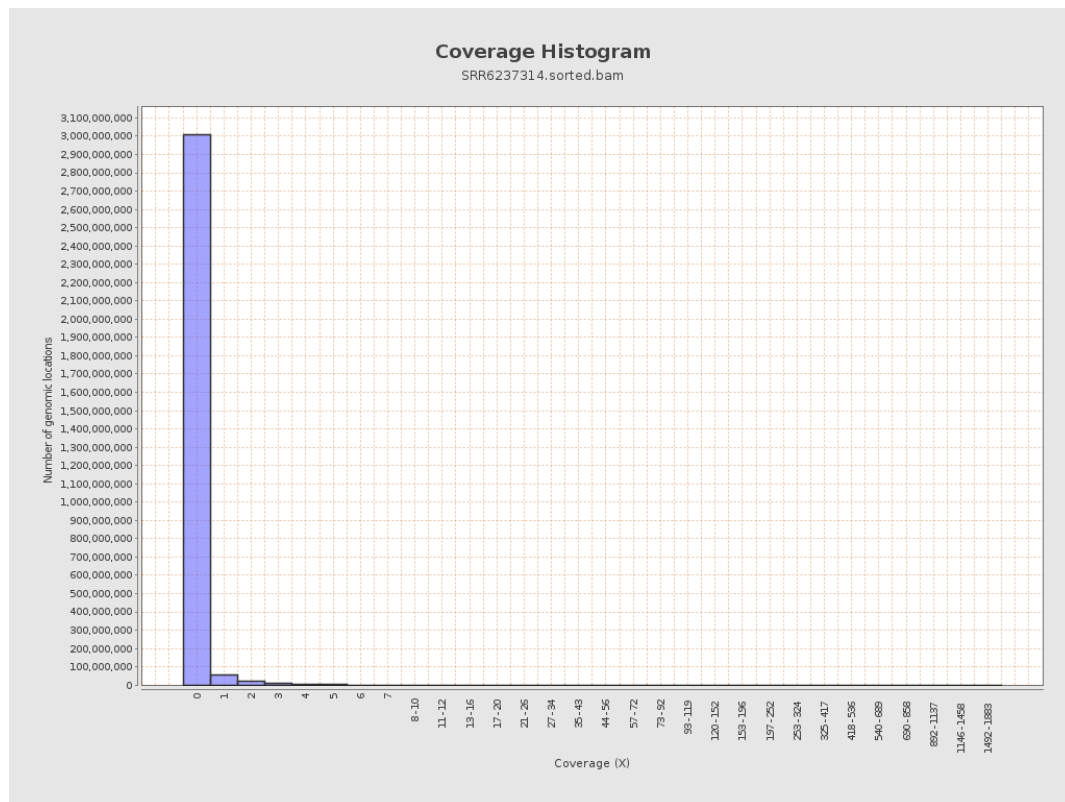
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16662025	0.0668	0.4911
chr2	243199373	4889706	0.0201	0.5801
chr3	198022430	32770405	0.1655	0.6592
chr4	191154276	14100085	0.0738	0.5119
chr5	180915260	24692526	0.1365	0.6051
chr6	171115067	8318362	0.0486	0.3727
chr7	159138663	2647371	0.0166	0.3382

chr8	146364022	8713731	0.0595	1.1721
chr9	141213431	12953577	0.0917	0.7213
chr10	135534747	2275355	0.0168	0.6064
chr11	135006516	2186342	0.0162	0.2686
chr12	133851895	4346732	0.0325	0.3628
chr13	115169878	1614680	0.014	0.1757
chr14	107349540	2278178	0.0212	0.4374
chr15	102531392	1338982	0.0131	0.1932
chr16	90354753	1287833	0.0143	0.2774
chr17	81195210	1365220	0.0168	0.2131
chr18	78077248	1521749	0.0195	0.9497
chr19	59128983	1011666	0.0171	0.3599
chr20	63025520	1068811	0.017	0.2374
chr21	48129895	992787	0.0206	0.3614
chr22	51304566	639029	0.0125	0.1632
chrMT	16571	284106	17.1448	13.7799
chrX	155270560	2821467	0.0182	0.2821
chrY	59373566	360345	0.0061	0.294

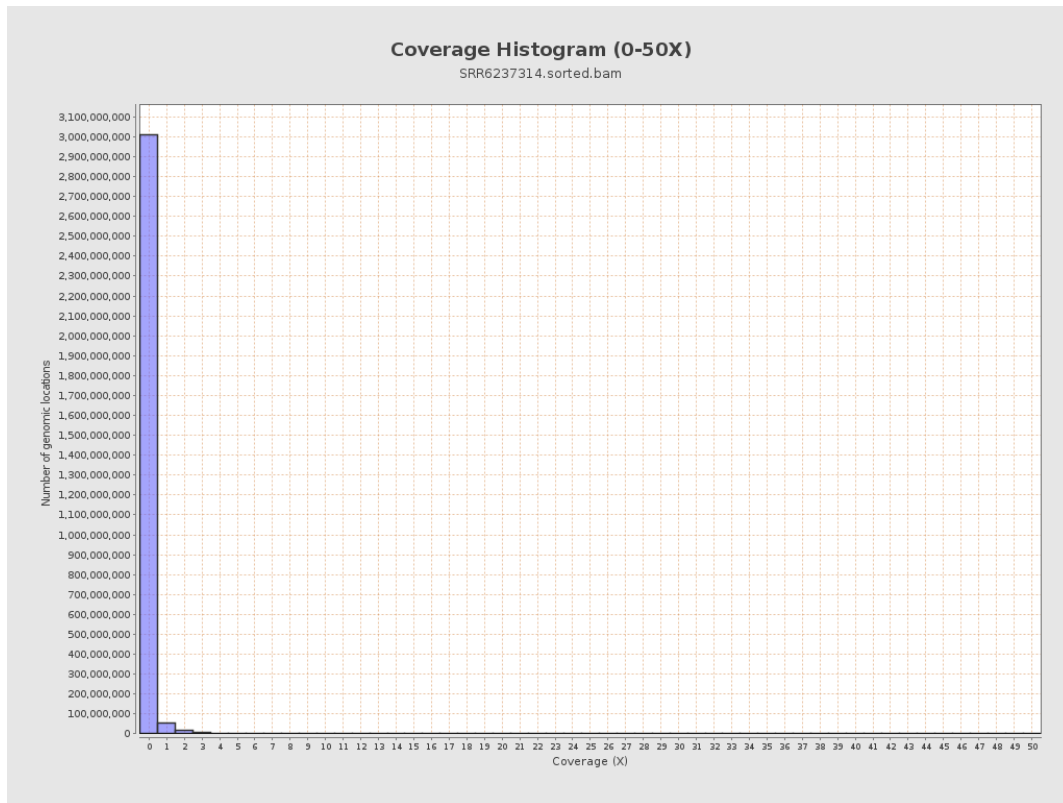
3. Results : Coverage across reference



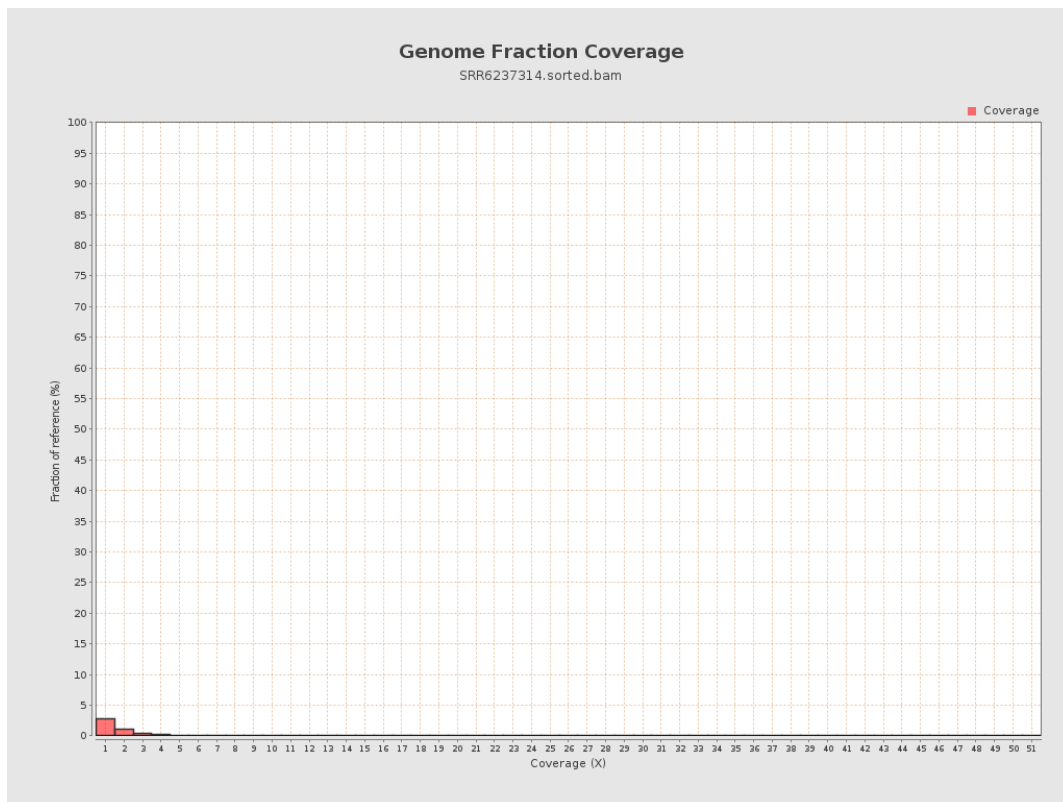
4. Results : Coverage Histogram



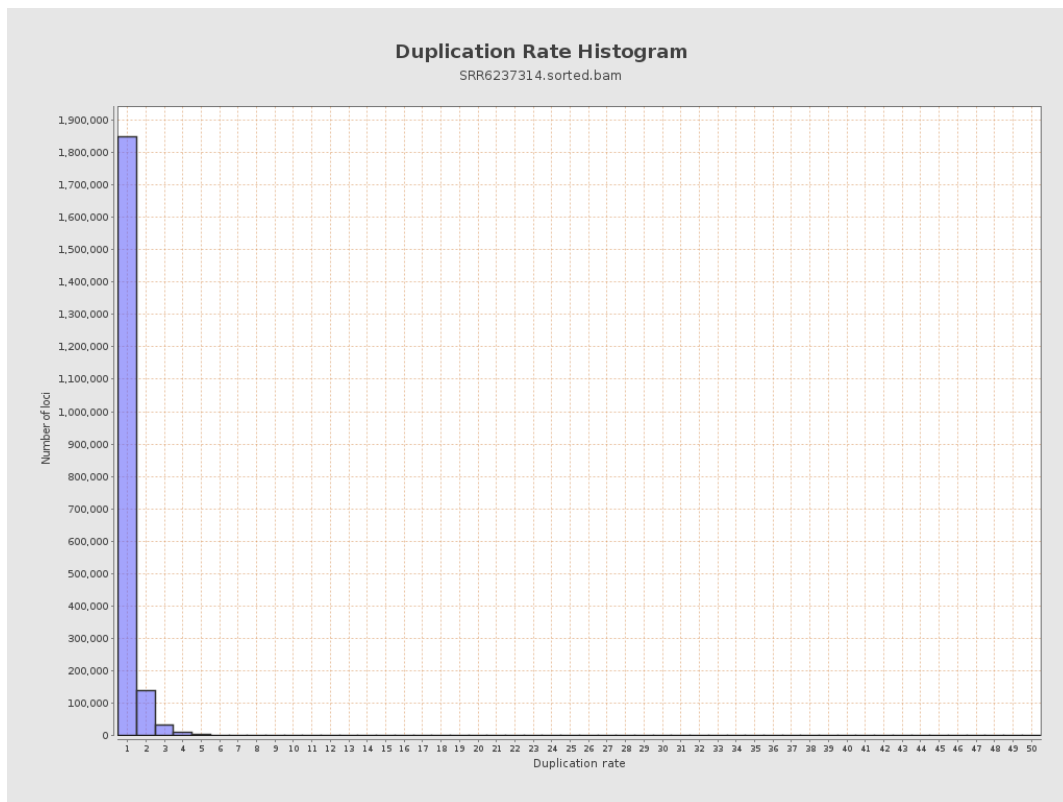
5. Results : Coverage Histogram (0-50X)



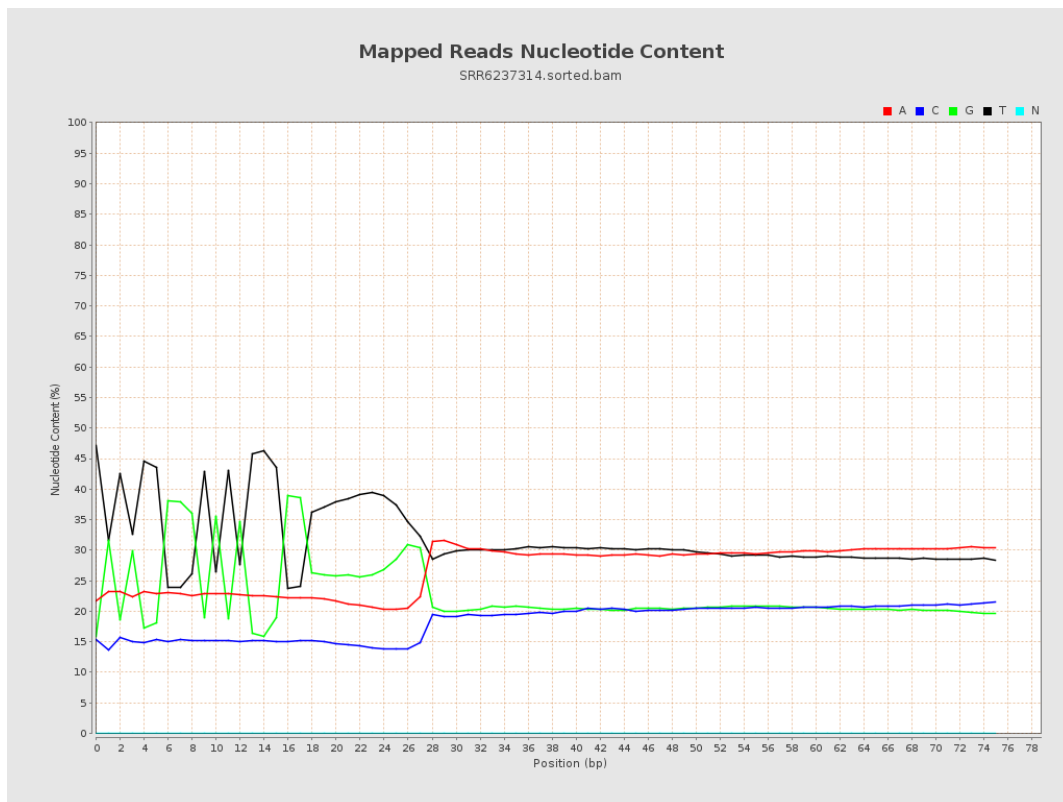
6. Results : Genome Fraction Coverage



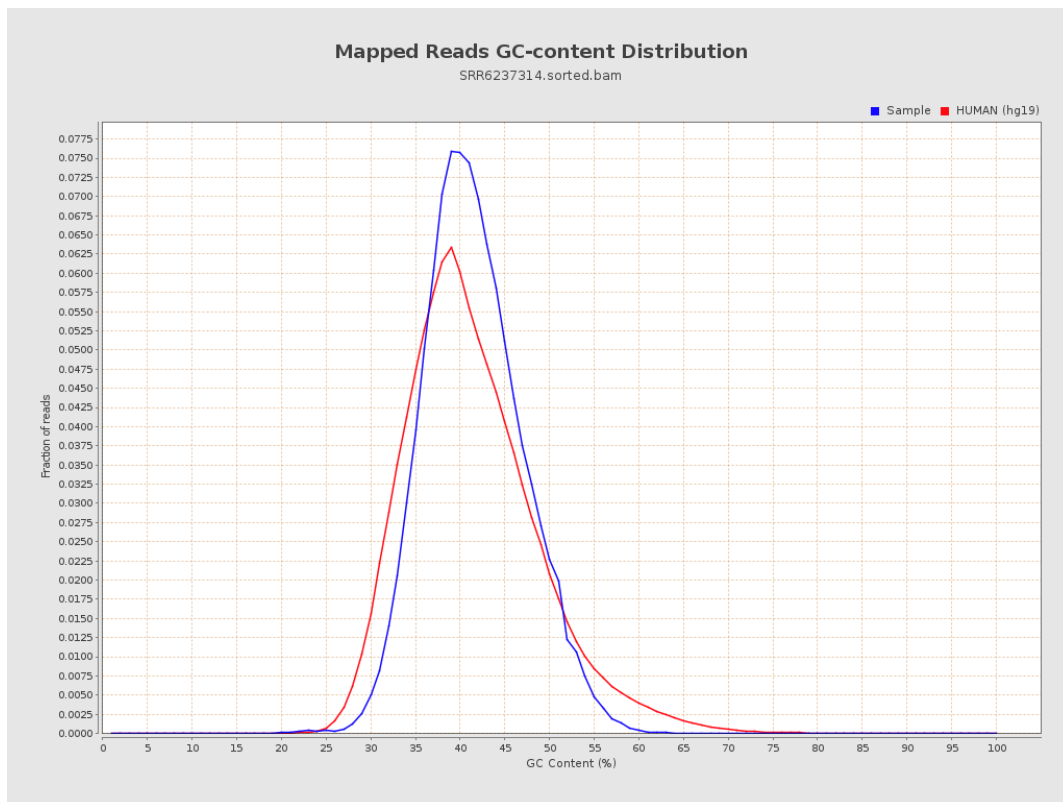
7. Results : Duplication Rate Histogram



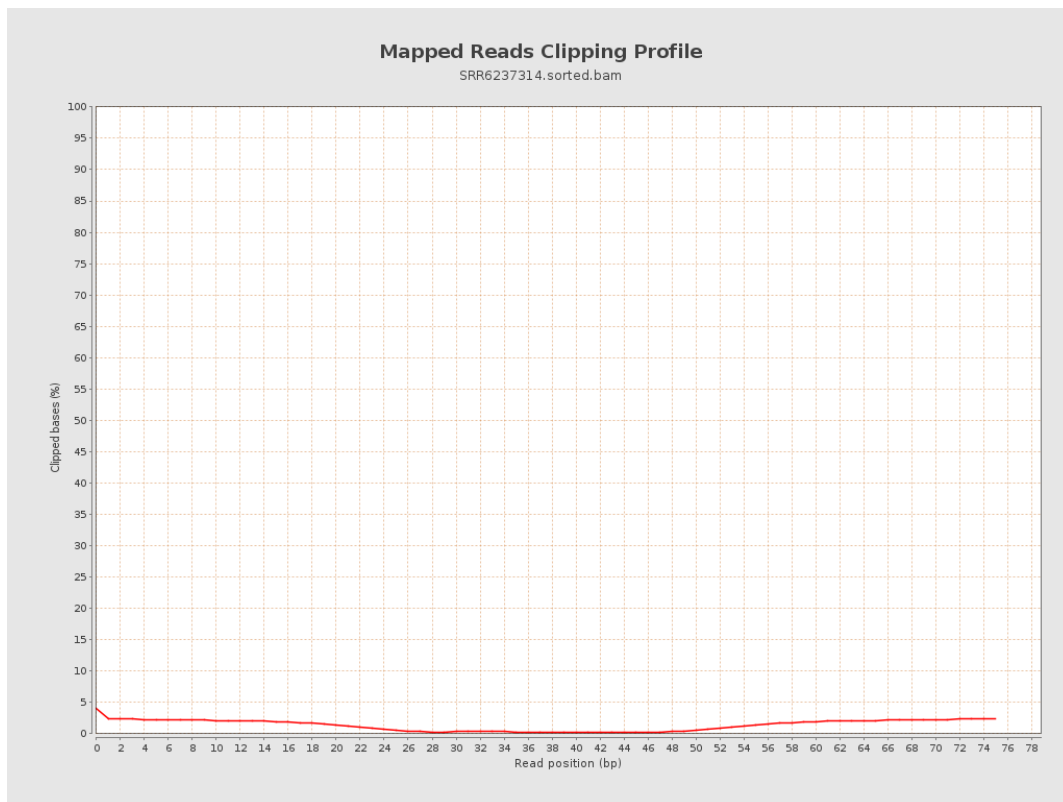
8. Results : Mapped Reads Nucleotide Content



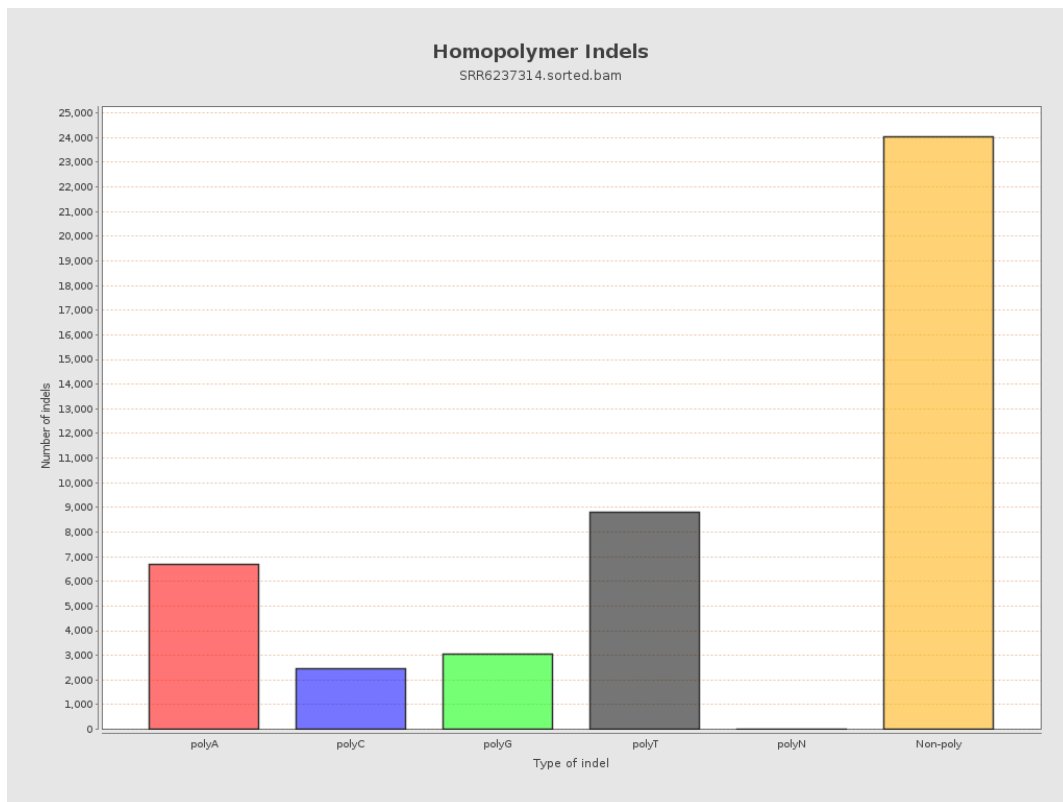
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

