

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237272.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_SRR6237272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237272.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:35:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,979,902
Mapped reads	1,808,955 / 91.37%
Unmapped reads	170,947 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,354 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	62,269 / 3.15%
Duplication rate	2.14%
Clipped reads	554,346 / 28%

2.2. ACGT Content

Number/percentage of A's	38,401,548 / 30.14%
Number/percentage of C's	24,208,752 / 19%
Number/percentage of T's	39,190,592 / 30.76%
Number/percentage of G's	25,620,100 / 20.11%
Number/percentage of N's	2,373 / 0%
GC Percentage	39.1%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.5159
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2.4. Mapping Quality

Mean Mapping Quality	45.6
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2.5. Mismatches and indels

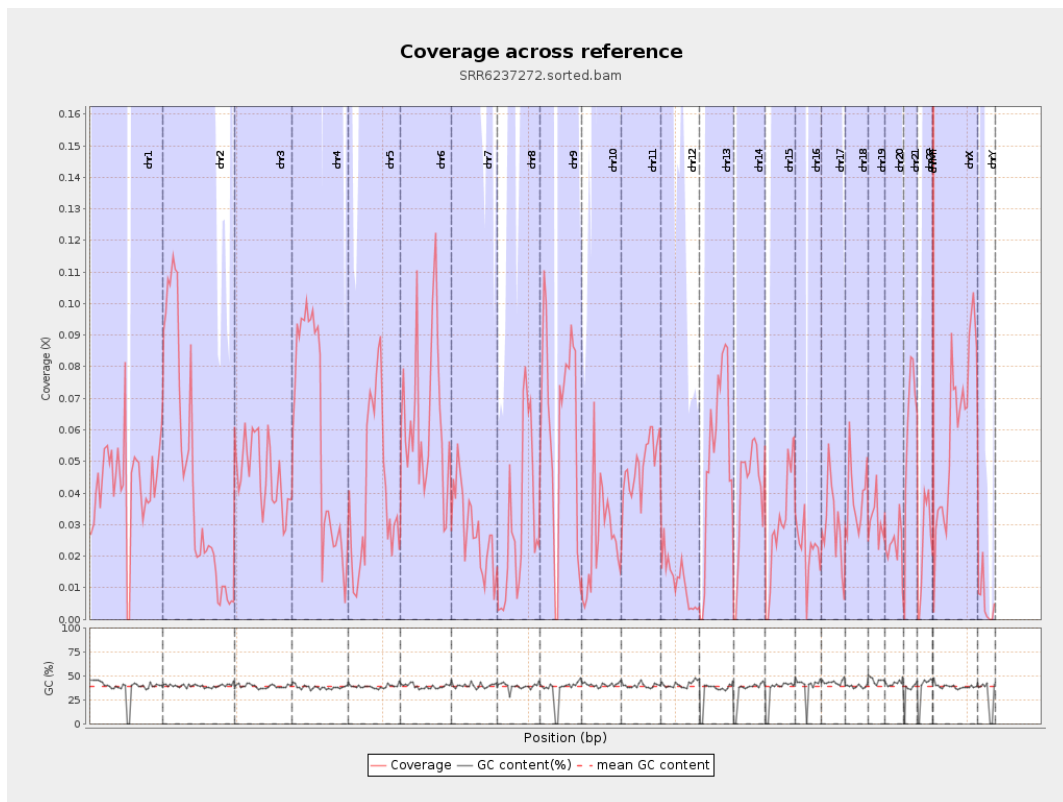
General error rate	0.82%
Mismatches	1,027,993
Insertions	10,747
Mapped reads with at least one insertion	0.59%
Deletions	37,414
Mapped reads with at least one deletion	2.04%
Homopolymer indels	45.97%

2.6. Chromosome stats

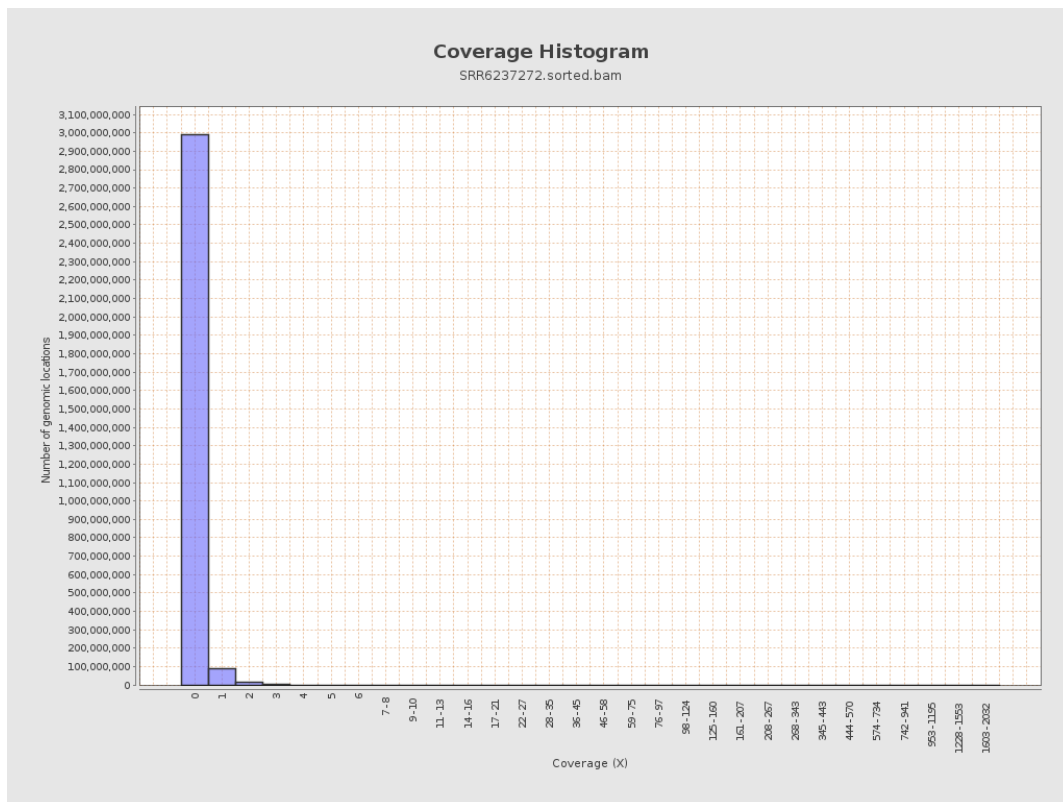
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10740251	0.0431	0.8969
chr2	243199373	10779832	0.0443	0.4455
chr3	198022430	9172535	0.0463	0.2531
chr4	191154276	11107670	0.0581	0.3373
chr5	180915260	7259736	0.0401	0.2465
chr6	171115067	10863483	0.0635	0.6181
chr7	159138663	4467199	0.0281	0.2601

chr8	146364022	4450683	0.0304	1.2626
chr9	141213431	8830419	0.0625	0.5031
chr10	135534747	3438894	0.0254	0.4396
chr11	135006516	6581617	0.0488	0.3732
chr12	133851895	1584399	0.0118	0.1586
chr13	115169878	6070997	0.0527	0.266
chr14	107349540	4317297	0.0402	0.2948
chr15	102531392	3015138	0.0294	0.1958
chr16	90354753	2003148	0.0222	0.2477
chr17	81195210	2452510	0.0302	0.2344
chr18	78077248	3024255	0.0387	0.8683
chr19	59128983	1881641	0.0318	0.514
chr20	63025520	1524505	0.0242	0.2073
chr21	48129895	2958660	0.0615	0.353
chr22	51304566	1241374	0.0242	0.1756
chrMT	16571	32199	1.9431	1.8491
chrX	155270560	9359998	0.0603	0.3263
chrY	59373566	331291	0.0056	0.2115

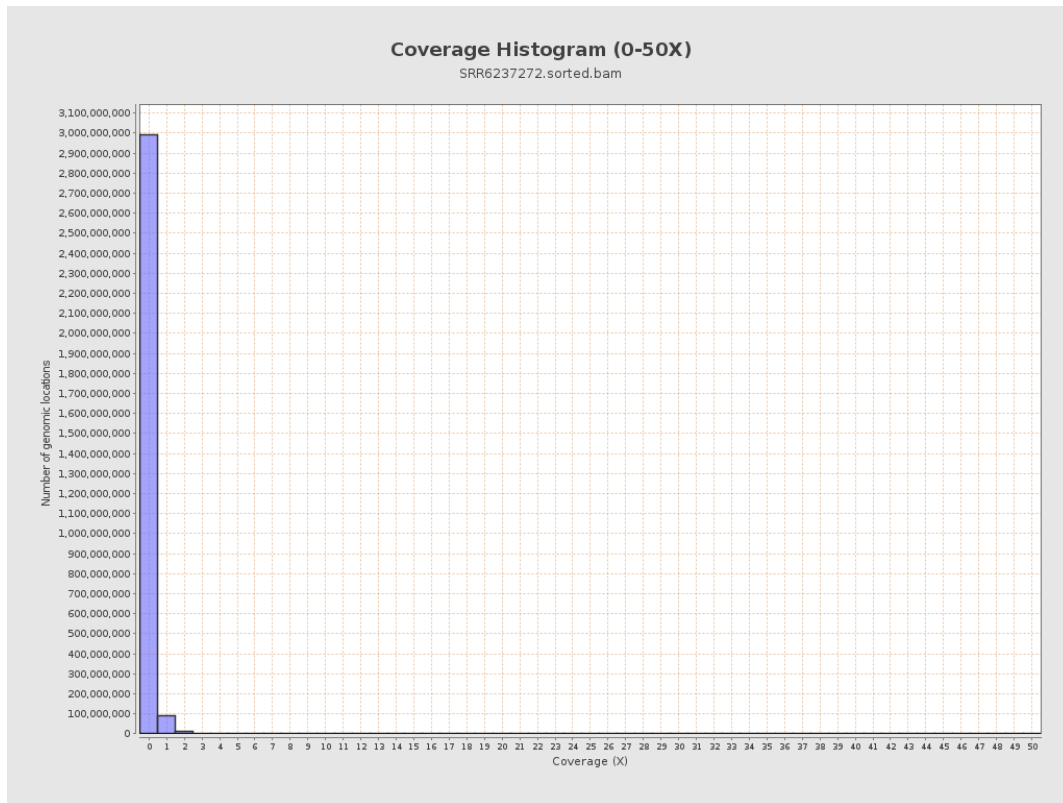
3. Results : Coverage across reference



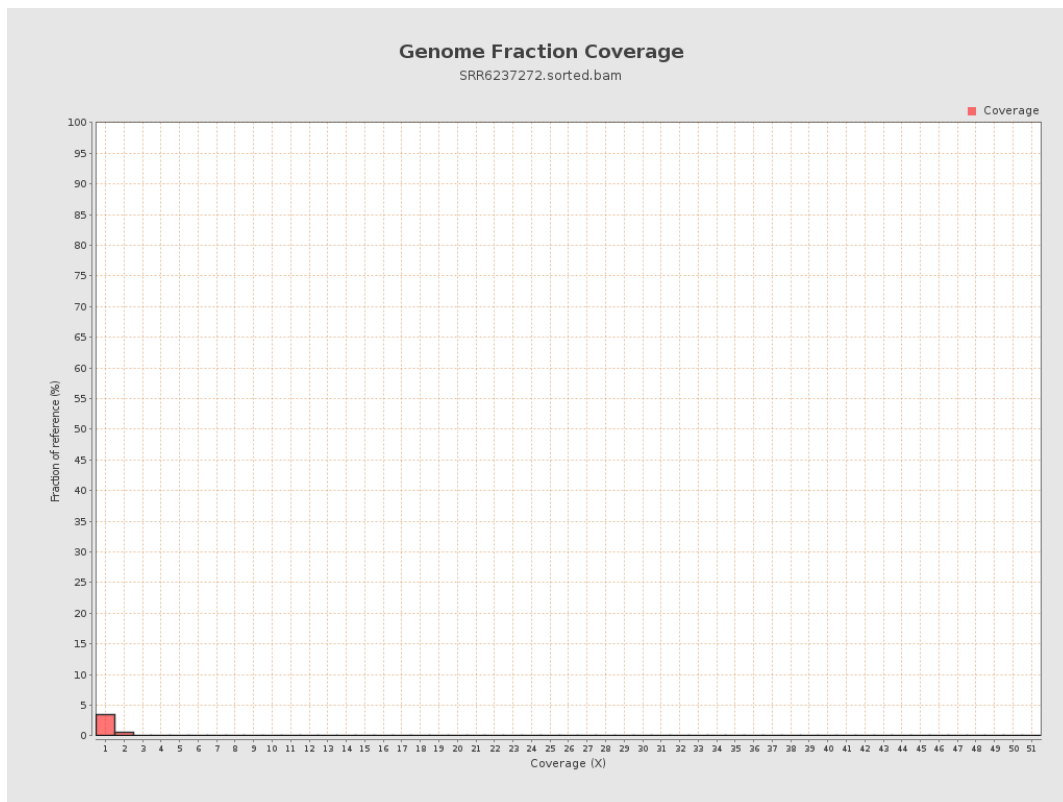
4. Results : Coverage Histogram



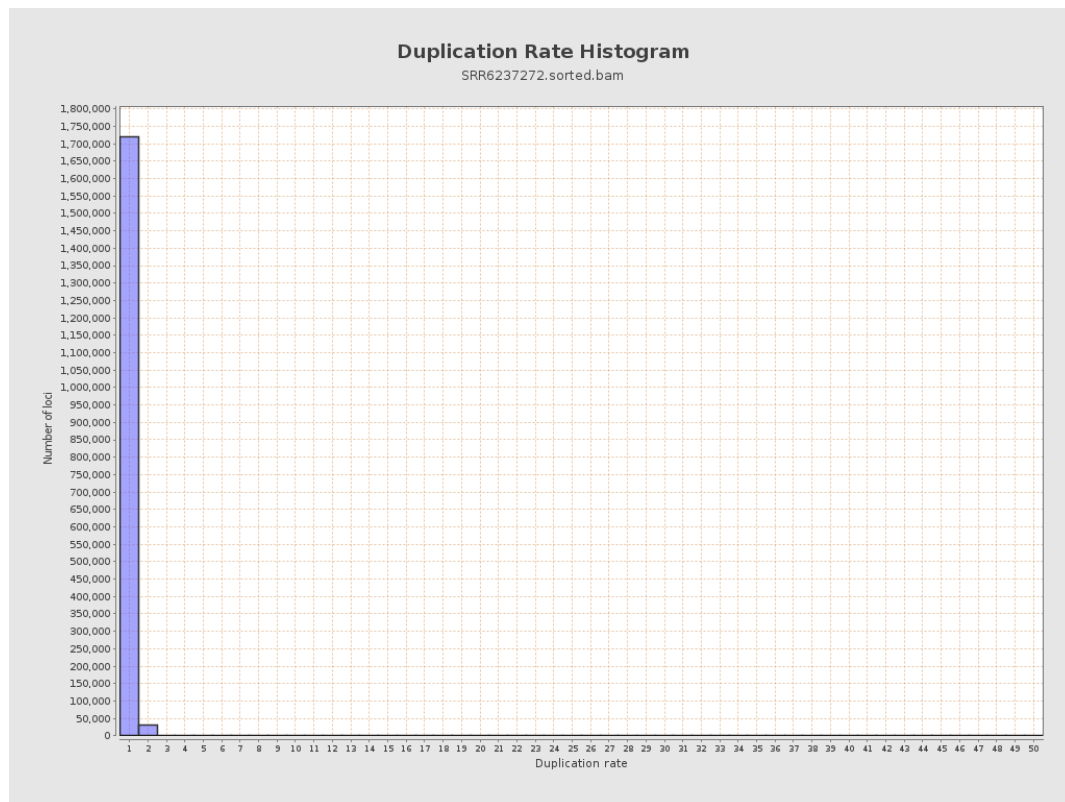
5. Results : Coverage Histogram (0-50X)



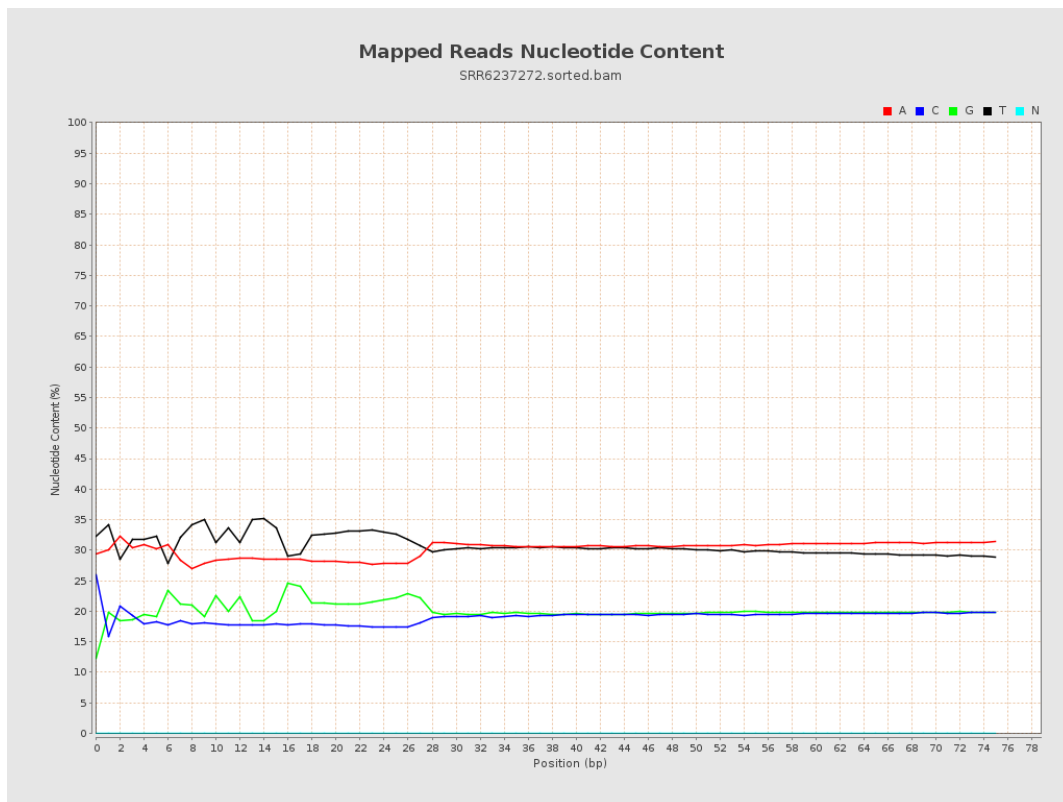
6. Results : Genome Fraction Coverage



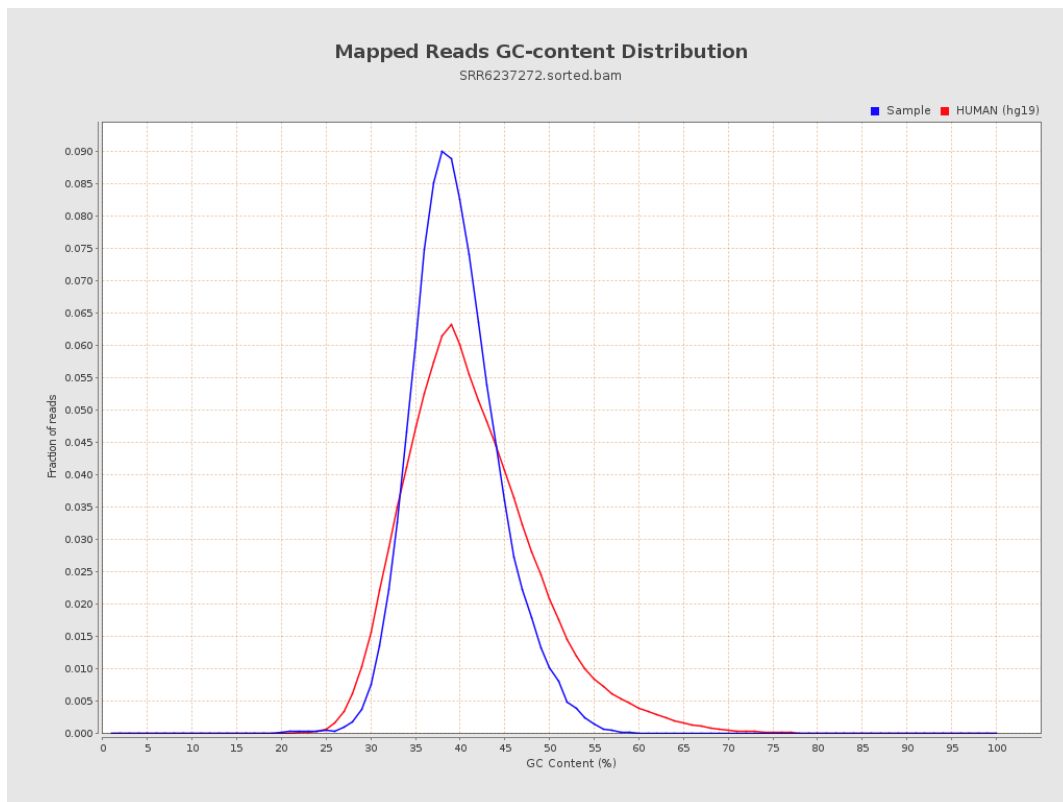
7. Results : Duplication Rate Histogram



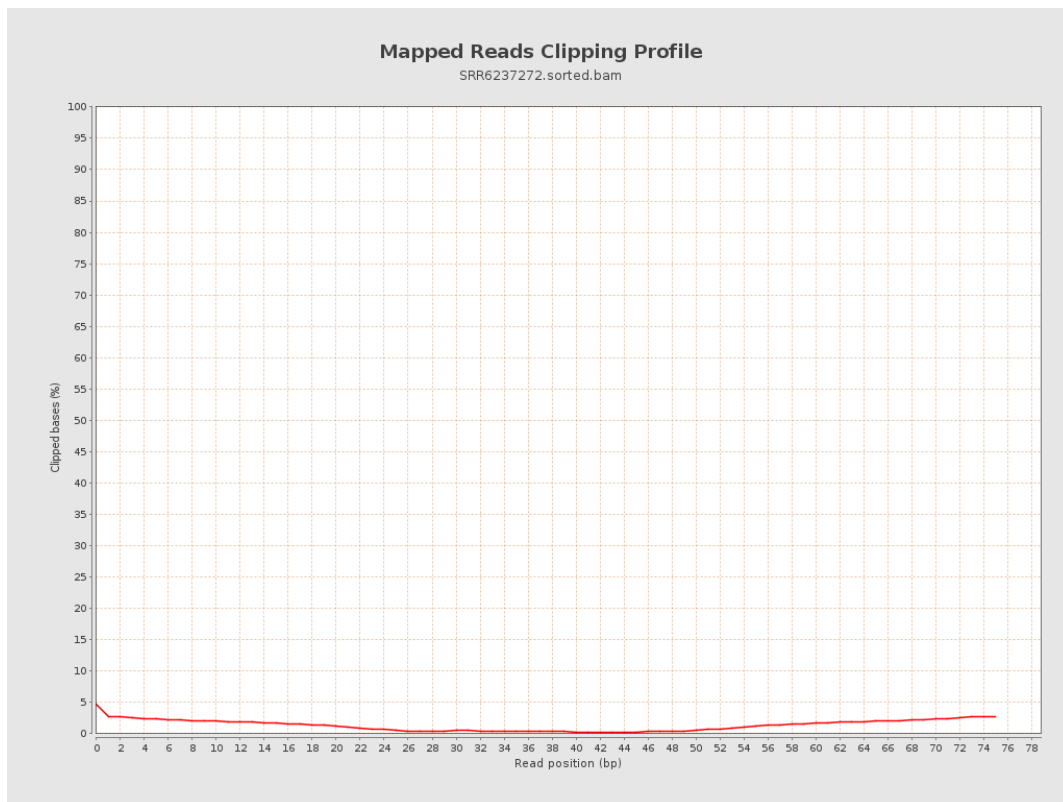
8. Results : Mapped Reads Nucleotide Content



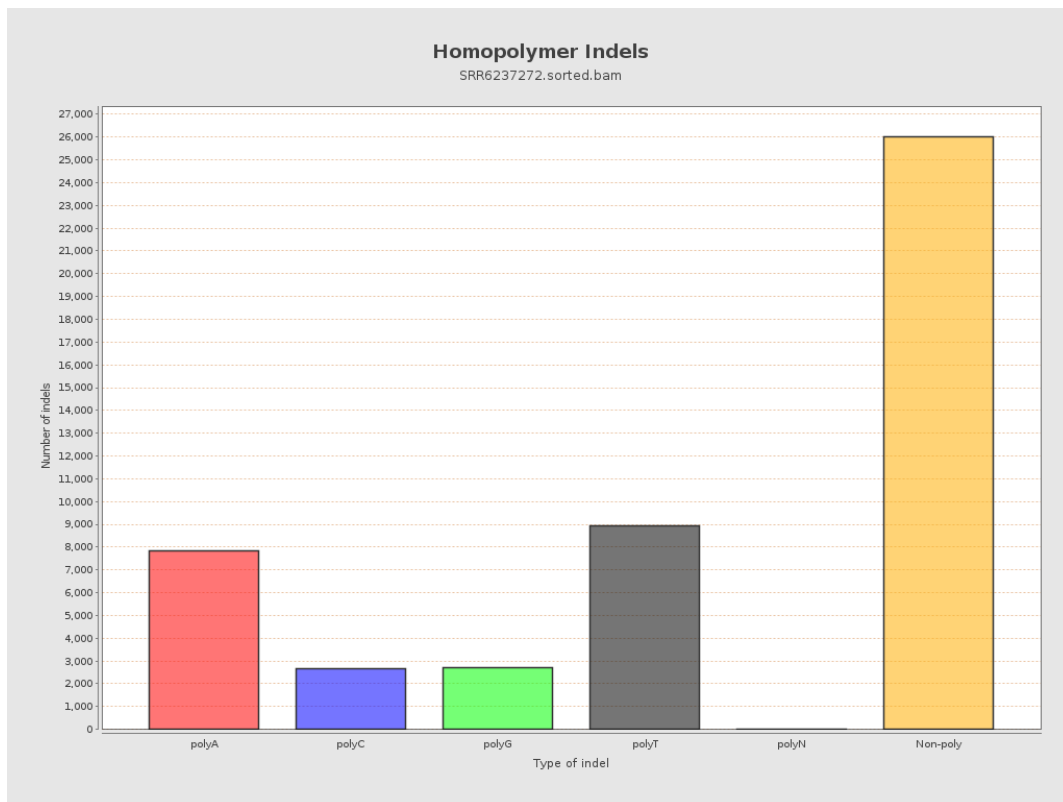
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

