

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:07:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237603.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_SRR6237603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:07:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	918,258
Mapped reads	697,704 / 75.98%
Unmapped reads	220,554 / 24.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,484 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	13,628 / 1.48%
Duplication rate	1.65%
Clipped reads	369,363 / 40.22%

2.2. ACGT Content

Number/percentage of A's	13,322,299 / 29.52%
Number/percentage of C's	7,996,739 / 17.72%
Number/percentage of T's	13,467,190 / 29.84%
Number/percentage of G's	10,261,362 / 22.74%
Number/percentage of N's	76,338 / 0.17%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0146

Standard Deviation	0.1404
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2.4. Mapping Quality

Mean Mapping Quality	46.95
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2.5. Mismatches and indels

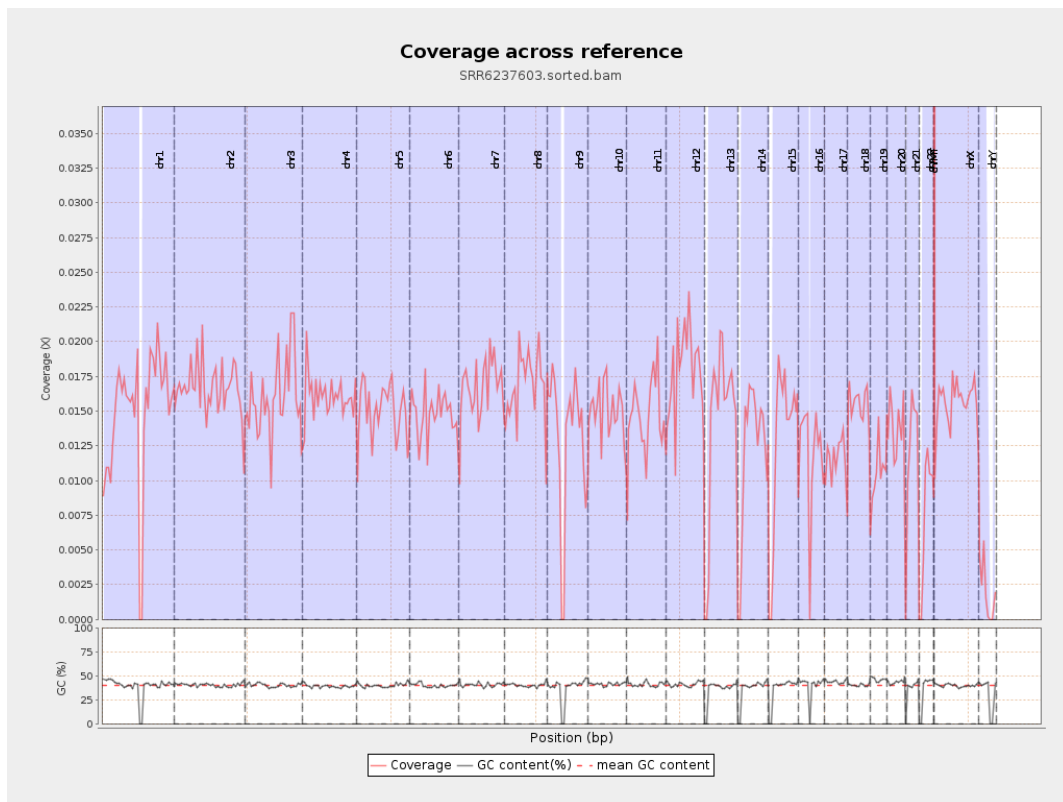
General error rate	1%
Mismatches	444,963
Insertions	3,490
Mapped reads with at least one insertion	0.5%
Deletions	14,053
Mapped reads with at least one deletion	1.99%
Homopolymer indels	47.61%

2.6. Chromosome stats

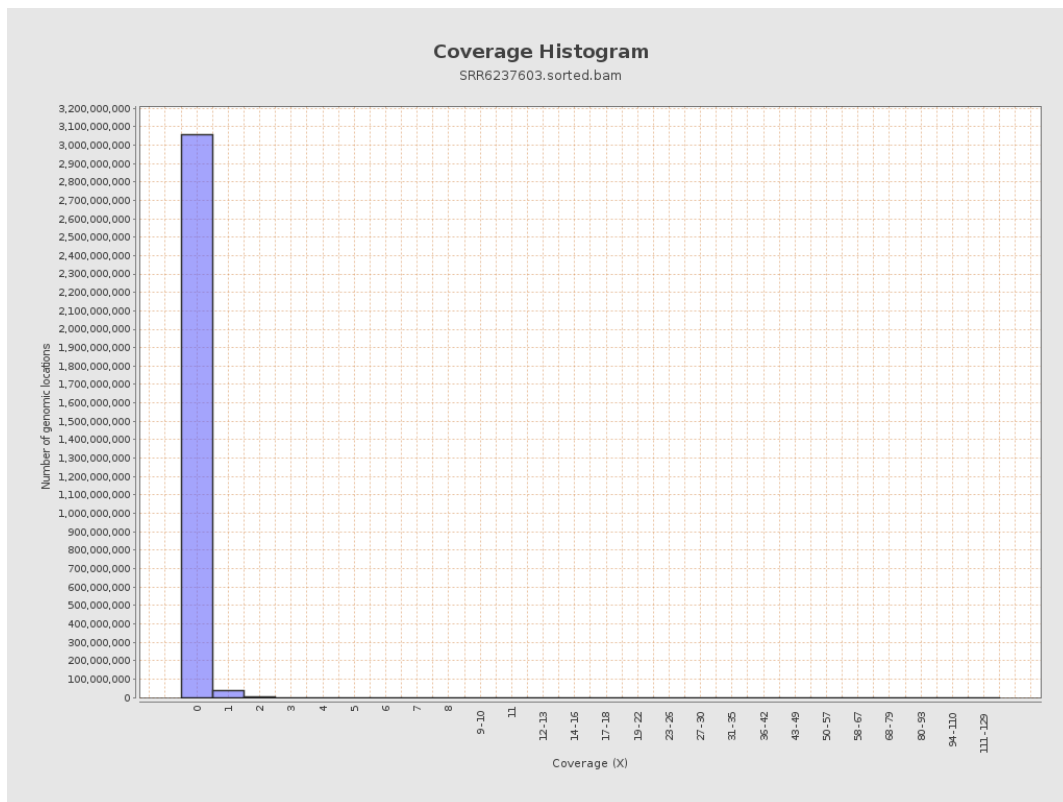
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3714991	0.0149	0.1657
chr2	243199373	4053325	0.0167	0.154
chr3	198022430	3165648	0.016	0.1369
chr4	191154276	3047759	0.0159	0.1356
chr5	180915260	2737462	0.0151	0.1305
chr6	171115067	2528422	0.0148	0.1354
chr7	159138663	2663143	0.0167	0.1668

chr8	146364022	2461818	0.0168	0.1541
chr9	141213431	1846058	0.0131	0.1342
chr10	135534747	2021870	0.0149	0.1403
chr11	135006516	1992270	0.0148	0.1407
chr12	133851895	2406036	0.018	0.1469
chr13	115169878	1618877	0.0141	0.1285
chr14	107349540	1295658	0.0121	0.1186
chr15	102531392	1326101	0.0129	0.1232
chr16	90354753	1058461	0.0117	0.1185
chr17	81195210	934092	0.0115	0.1168
chr18	78077248	1224330	0.0157	0.1844
chr19	59128983	631477	0.0107	0.1255
chr20	63025520	864539	0.0137	0.1264
chr21	48129895	580528	0.0121	0.1223
chr22	51304566	394223	0.0077	0.094
chrMT	16571	30928	1.8664	1.6042
chrX	155270560	2432276	0.0157	0.1361
chrY	59373566	115719	0.0019	0.0519

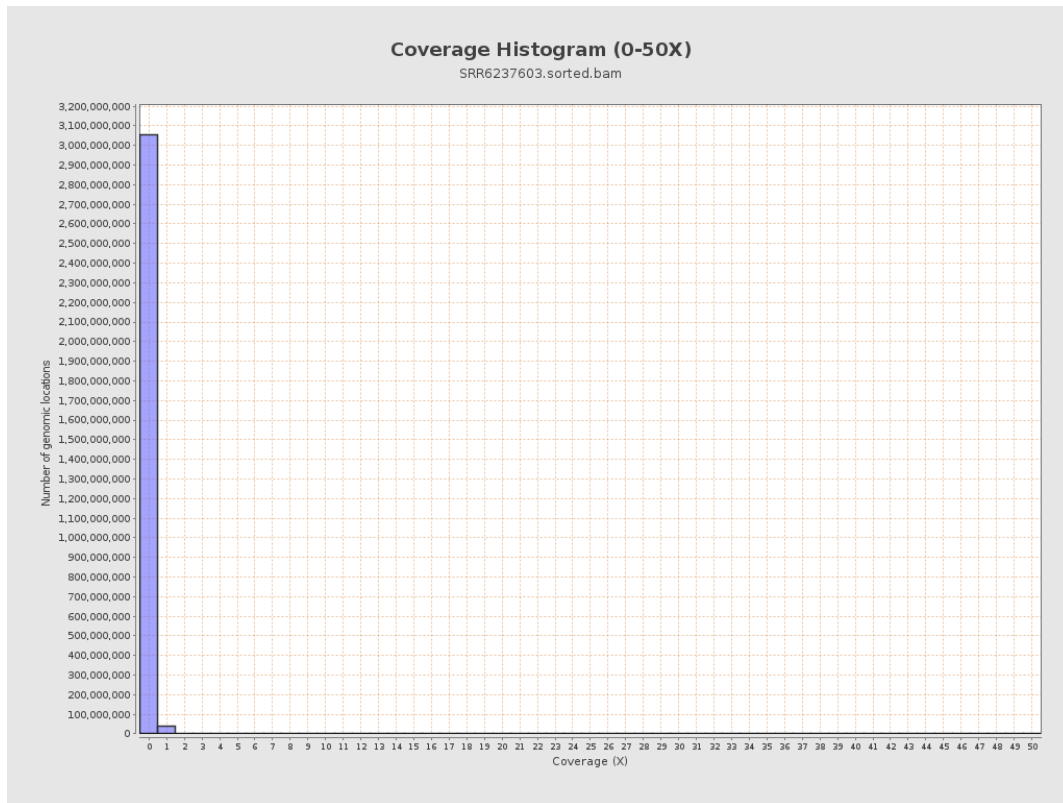
3. Results : Coverage across reference



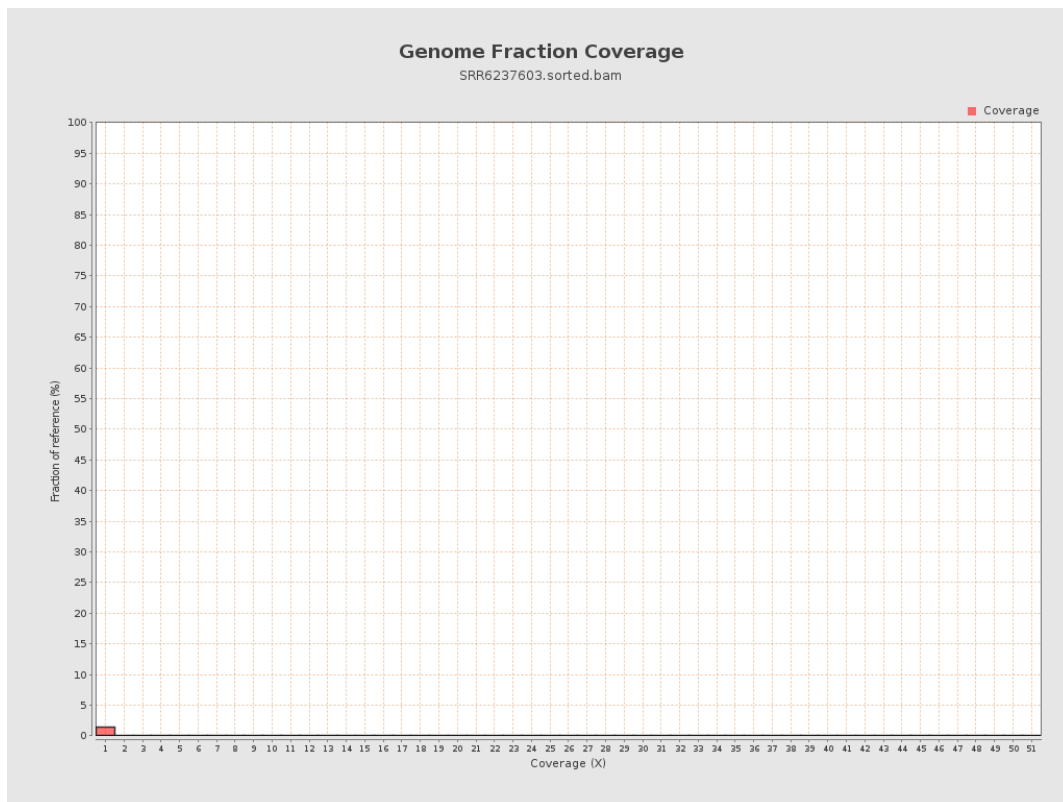
4. Results : Coverage Histogram



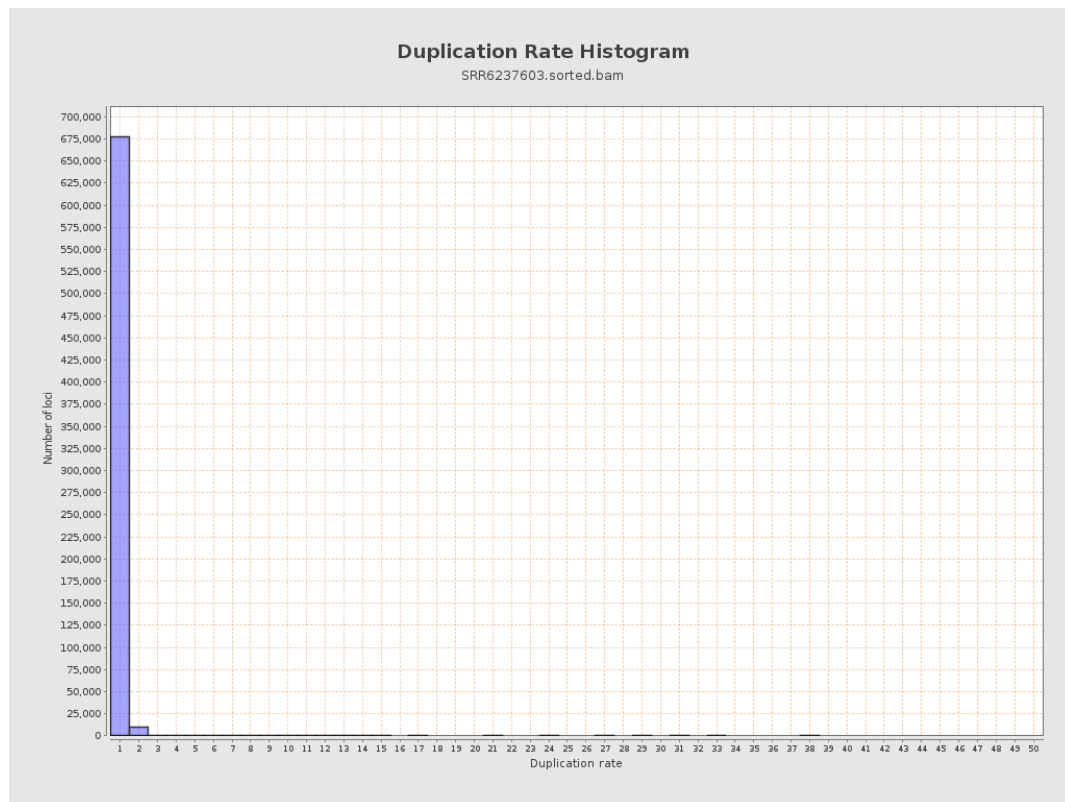
5. Results : Coverage Histogram (0-50X)



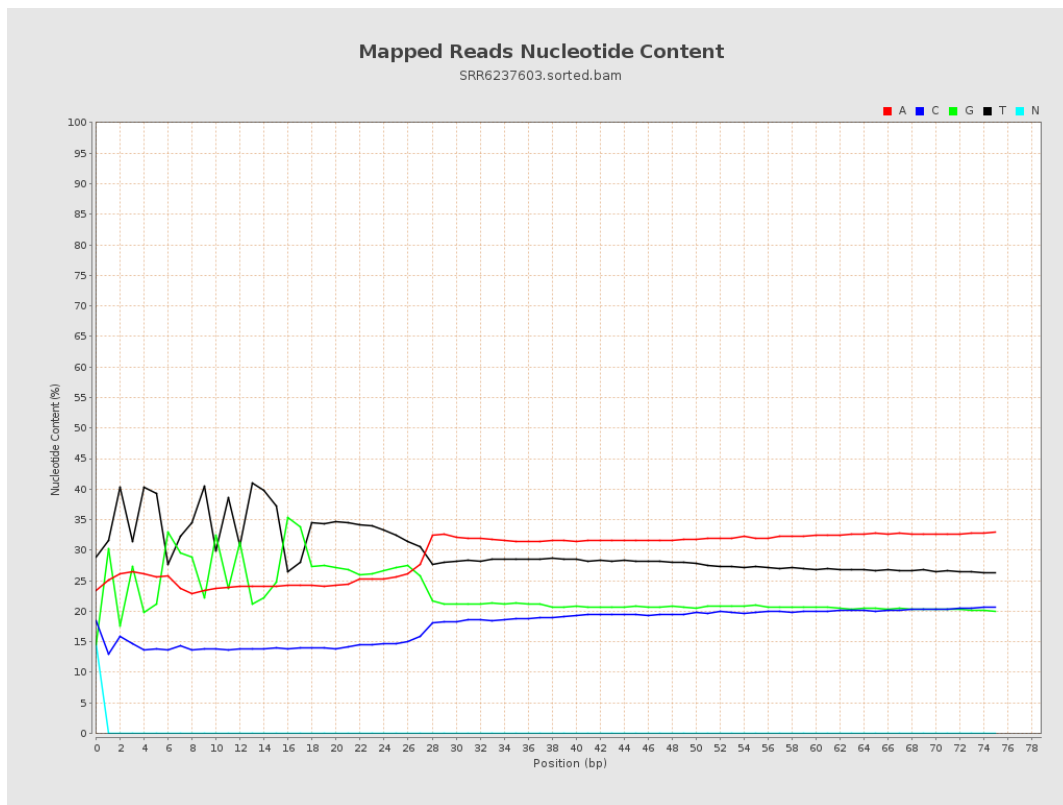
6. Results : Genome Fraction Coverage



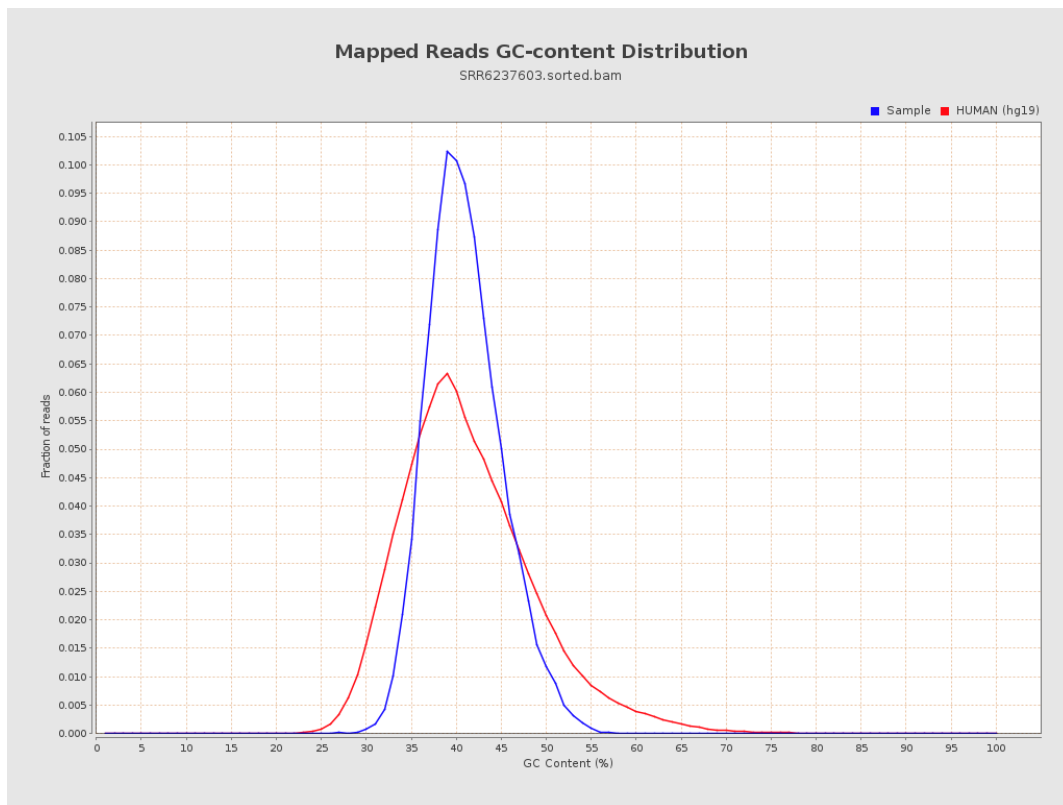
7. Results : Duplication Rate Histogram



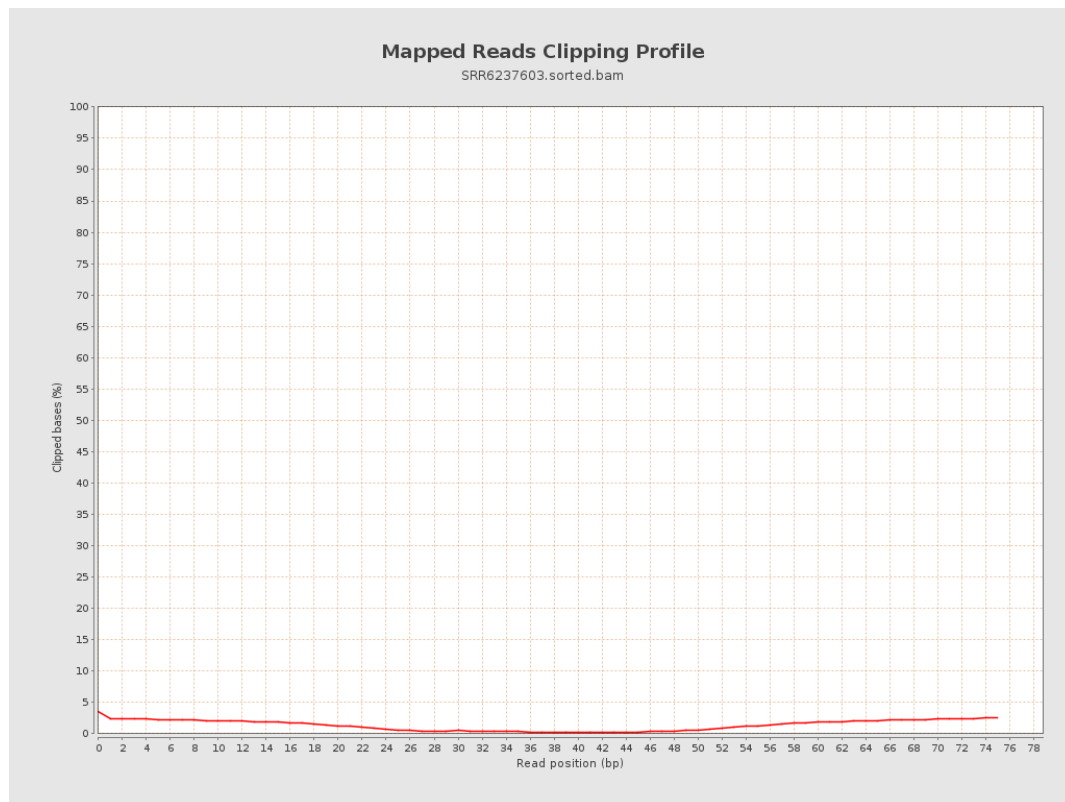
8. Results : Mapped Reads Nucleotide Content



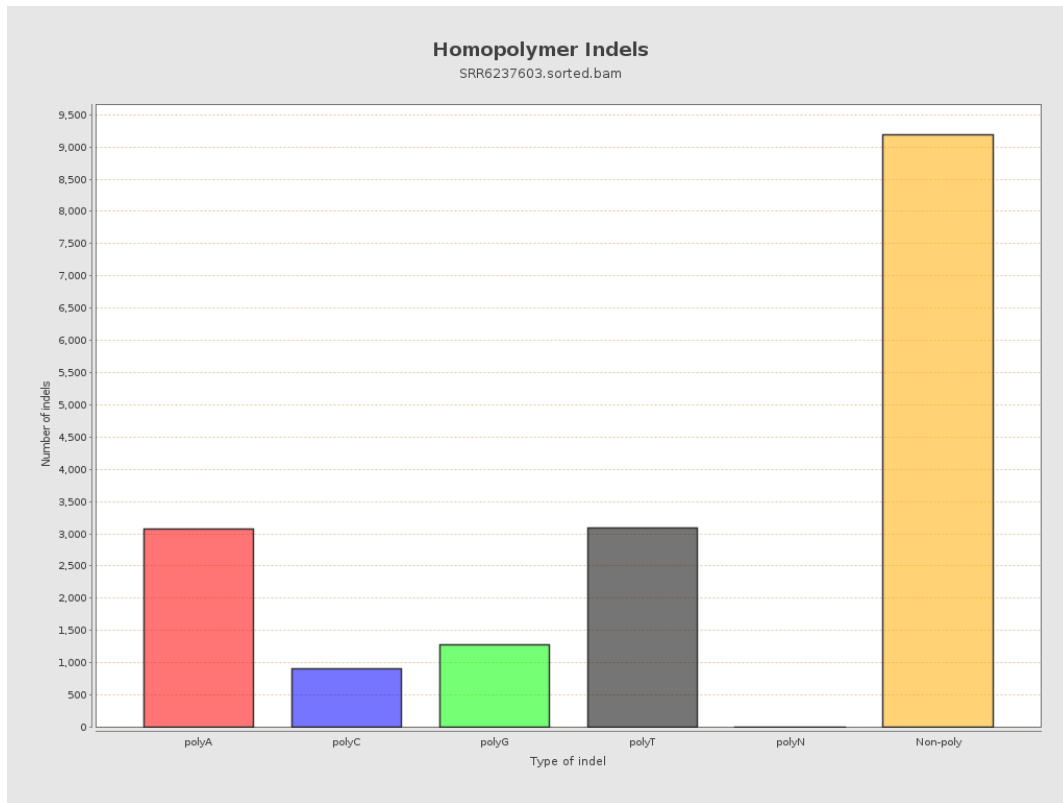
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

