

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:16:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237285.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_SRR6237285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237285.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:16:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,348,509
Mapped reads	407,174 / 12.16%
Unmapped reads	2,941,335 / 87.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,313 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	41,588 / 1.24%
Duplication rate	8.62%
Clipped reads	248,793 / 7.43%

2.2. ACGT Content

Number/percentage of A's	6,694,368 / 26.32%
Number/percentage of C's	4,428,579 / 17.41%
Number/percentage of T's	8,414,532 / 33.08%
Number/percentage of G's	5,899,216 / 23.19%
Number/percentage of N's	2,619 / 0.01%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0082

Standard Deviation	0.154
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	45.6
----------------------	------

2.5. Mismatches and indels

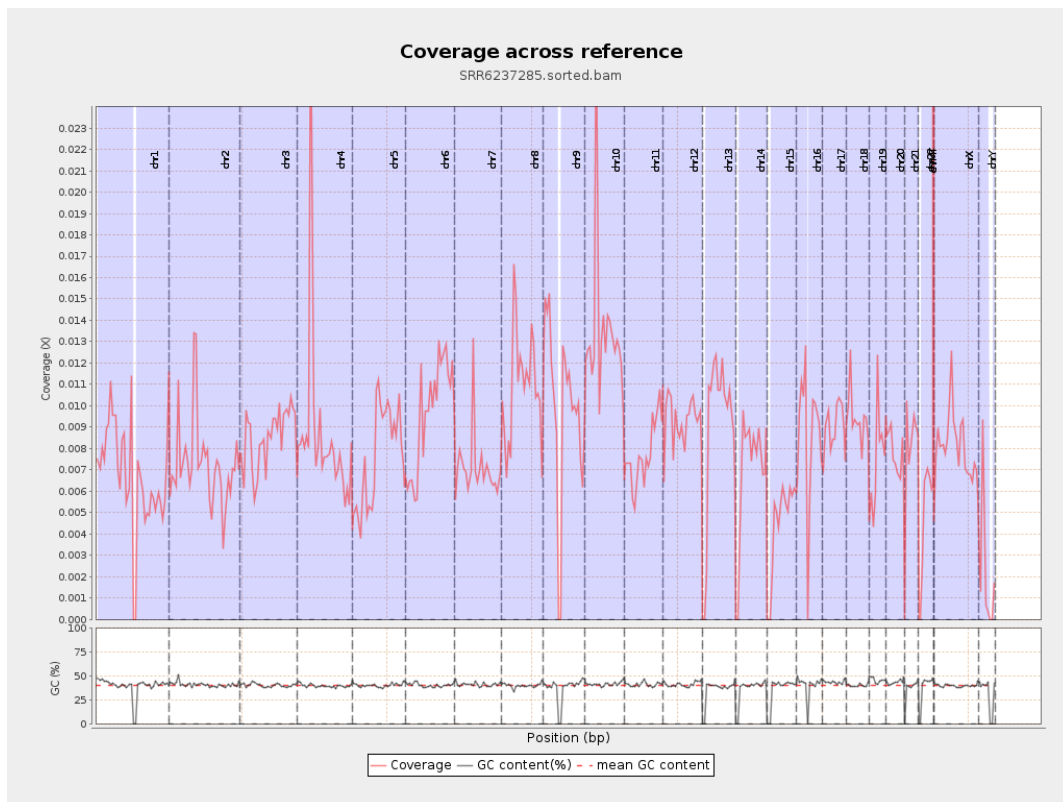
General error rate	0.73%
Mismatches	178,151
Insertions	2,355
Mapped reads with at least one insertion	0.57%
Deletions	8,343
Mapped reads with at least one deletion	2.02%
Homopolymer indels	42.7%

2.6. Chromosome stats

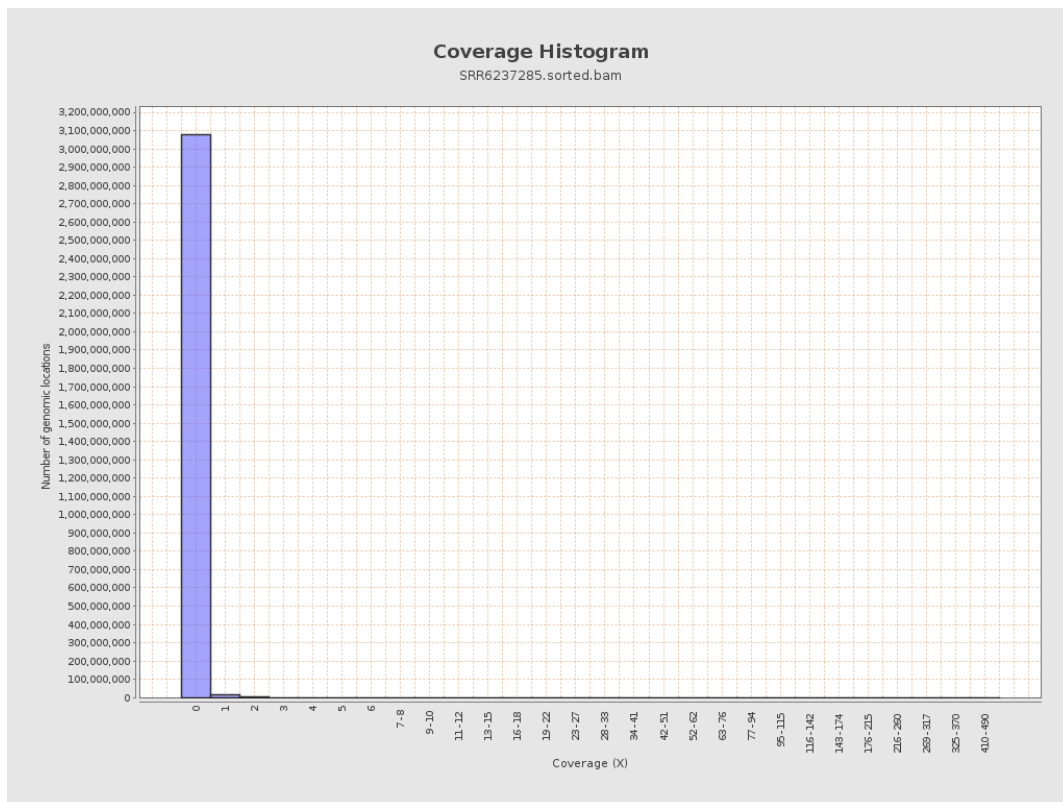
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1662387	0.0067	0.1611
chr2	243199373	1770531	0.0073	0.2304
chr3	198022430	1693658	0.0086	0.1111
chr4	191154276	1630012	0.0085	0.1501
chr5	180915260	1388577	0.0077	0.1051
chr6	171115067	1654961	0.0097	0.1267
chr7	159138663	1134165	0.0071	0.1229

chr8	146364022	1596177	0.0109	0.3045
chr9	141213431	1392849	0.0099	0.1346
chr10	135534747	1823911	0.0135	0.2097
chr11	135006516	1040240	0.0077	0.1147
chr12	133851895	1240797	0.0093	0.1169
chr13	115169878	1031810	0.009	0.1181
chr14	107349540	739050	0.0069	0.1001
chr15	102531392	461150	0.0045	0.0797
chr16	90354753	782913	0.0087	0.1193
chr17	81195210	724511	0.0089	0.1206
chr18	78077248	737849	0.0095	0.195
chr19	59128983	445544	0.0075	0.1375
chr20	63025520	493481	0.0078	0.113
chr21	48129895	384593	0.008	0.1228
chr22	51304566	236148	0.0046	0.0803
chrMT	16571	17967	1.0842	1.3603
chrX	155270560	1255009	0.0081	0.1119
chrY	59373566	116190	0.002	0.1109

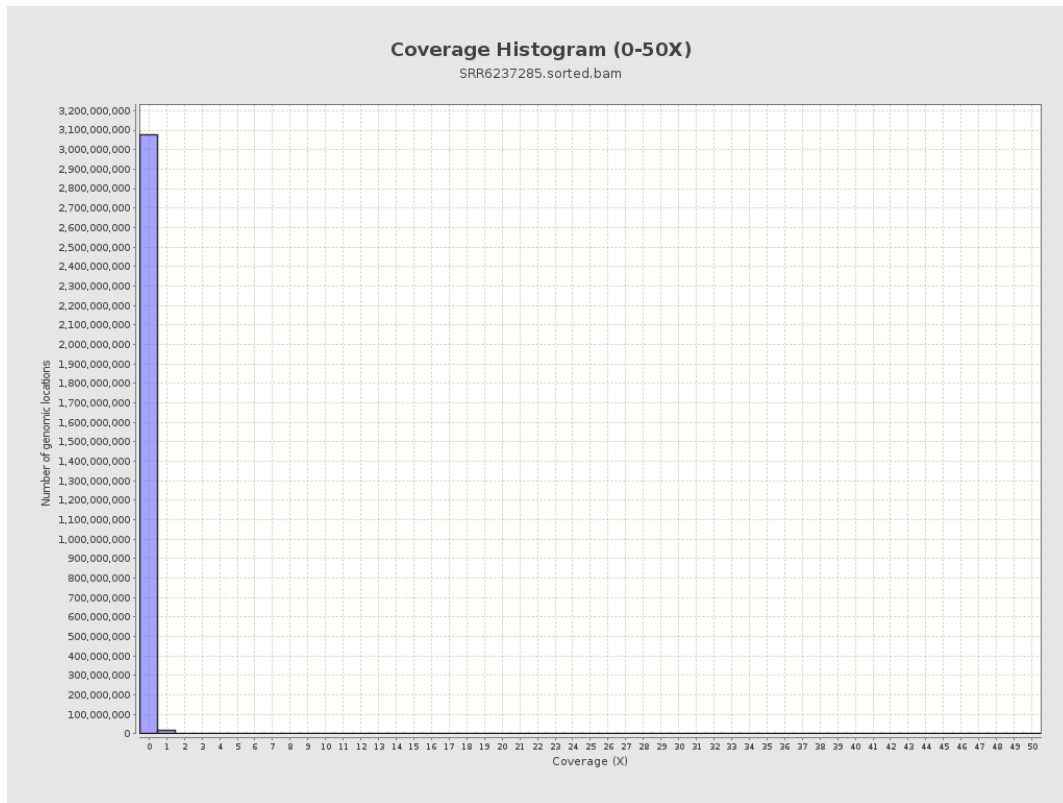
3. Results : Coverage across reference



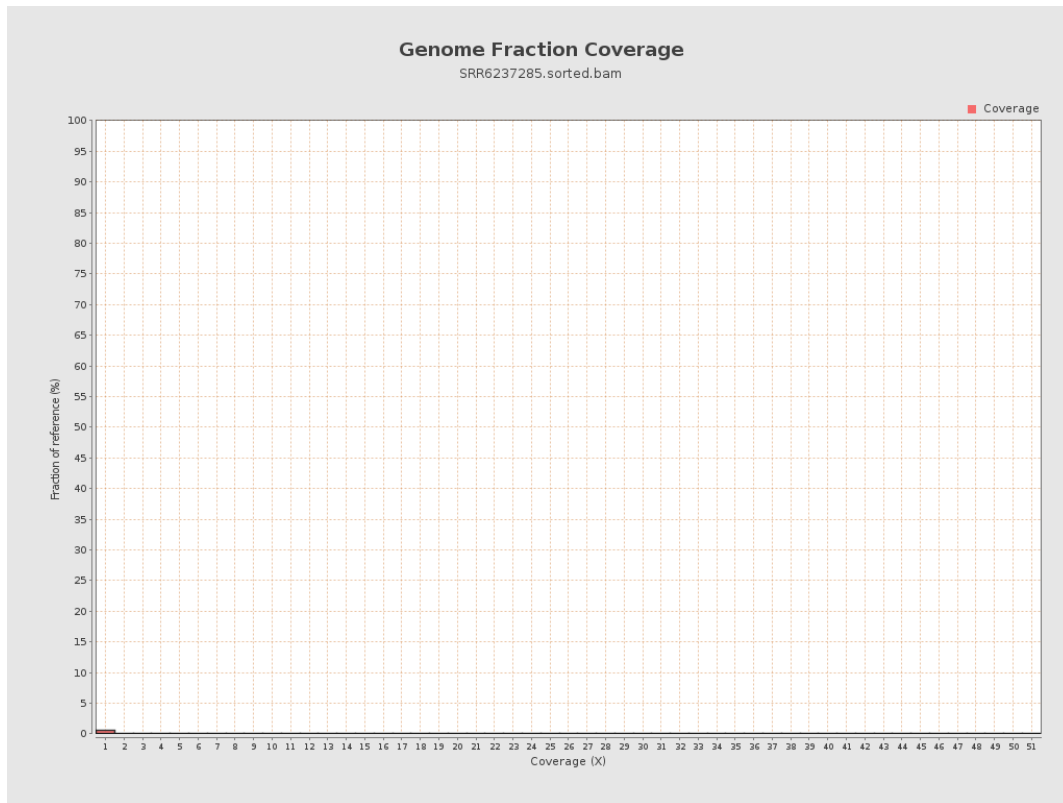
4. Results : Coverage Histogram



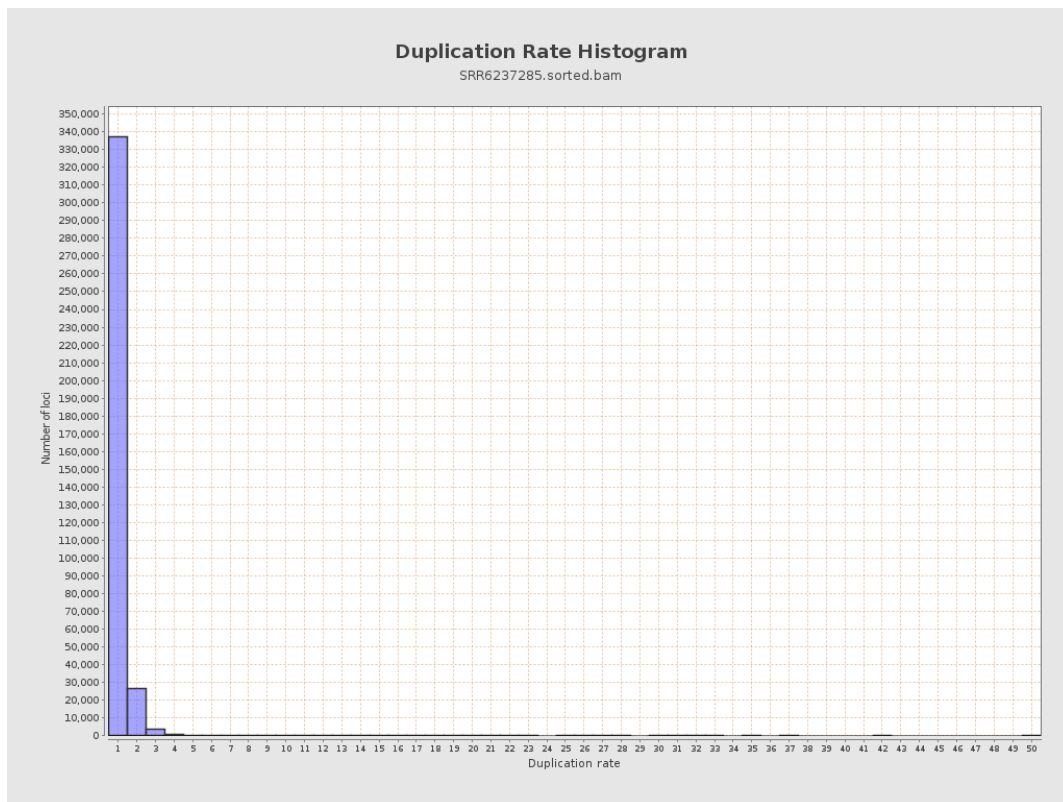
5. Results : Coverage Histogram (0-50X)



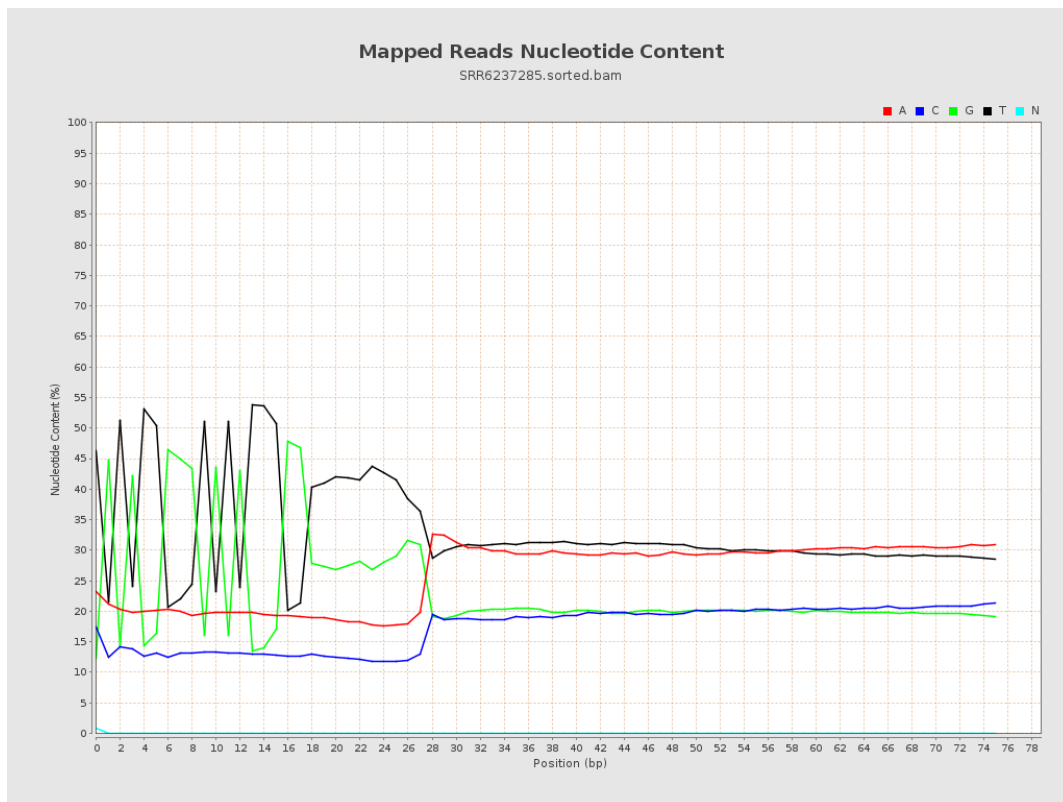
6. Results : Genome Fraction Coverage



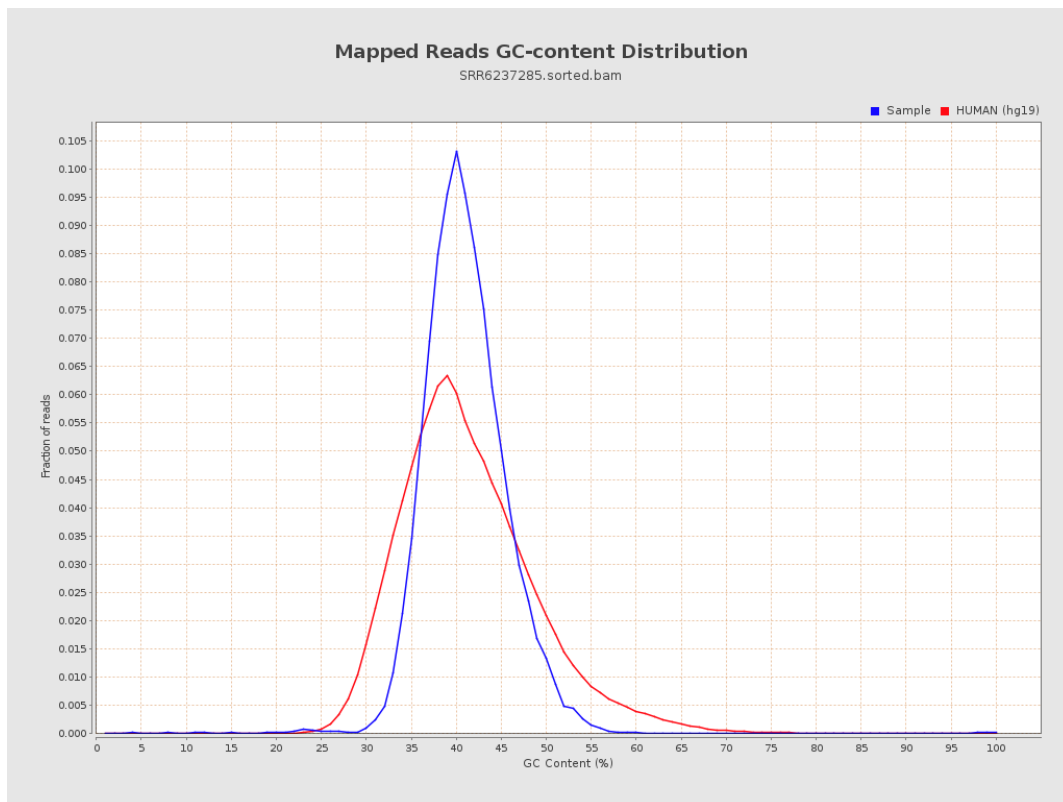
7. Results : Duplication Rate Histogram



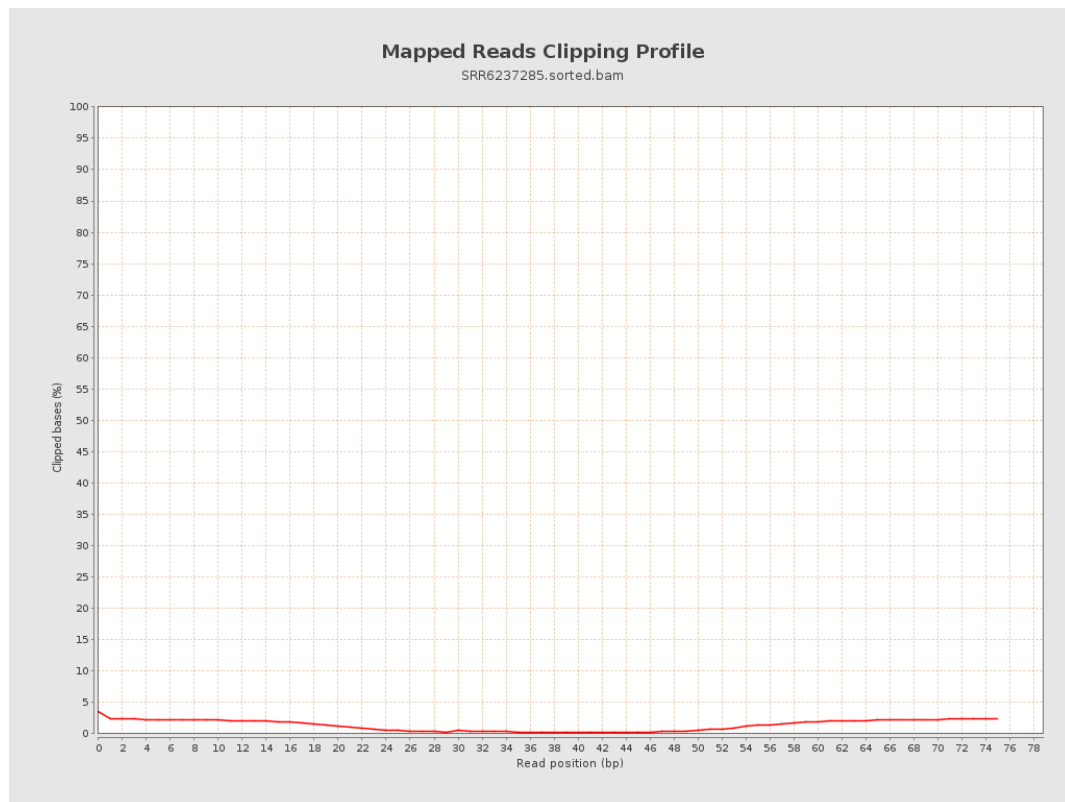
8. Results : Mapped Reads Nucleotide Content



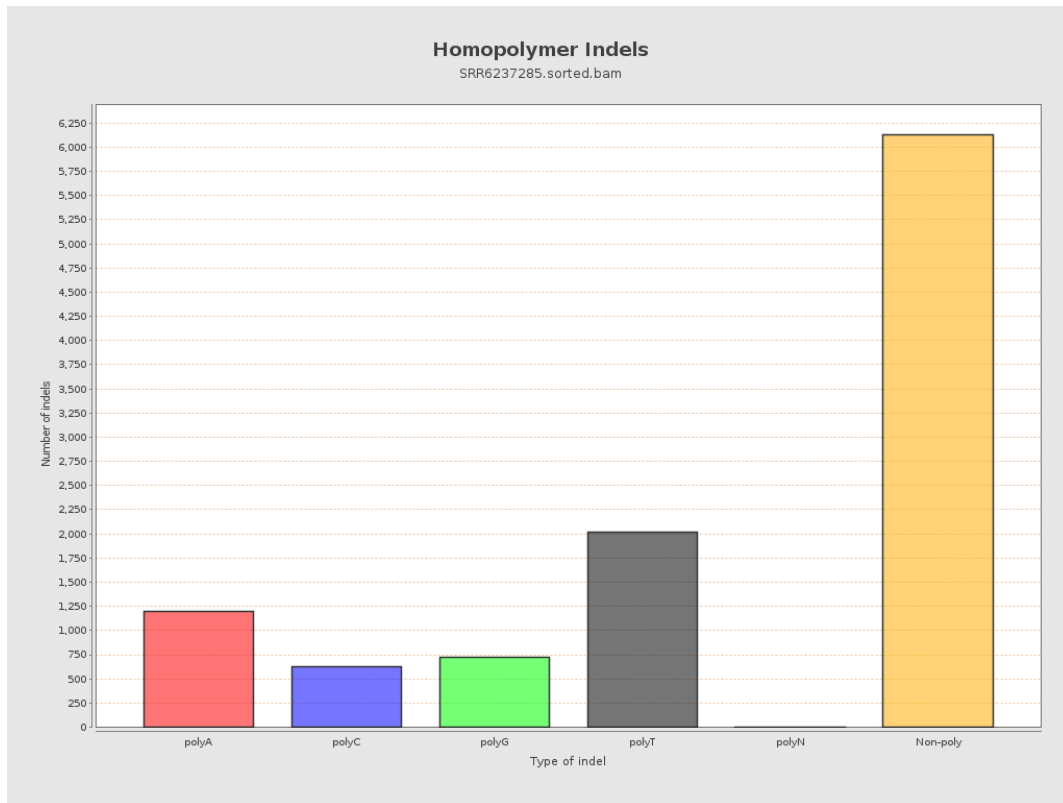
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

