

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:46:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237328.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_SRR6237328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:46:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,302,570
Mapped reads	2,037,251 / 88.48%
Unmapped reads	265,319 / 11.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,818 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	498,153 / 21.63%
Duplication rate	18.65%
Clipped reads	1,457,326 / 63.29%

2.2. ACGT Content

Number/percentage of A's	31,028,382 / 25.48%
Number/percentage of C's	20,837,825 / 17.11%
Number/percentage of T's	41,129,656 / 33.77%
Number/percentage of G's	28,773,268 / 23.63%
Number/percentage of N's	12,439 / 0.01%
GC Percentage	40.74%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.6217
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2.4. Mapping Quality

Mean Mapping Quality	42.34
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2.5. Mismatches and indels

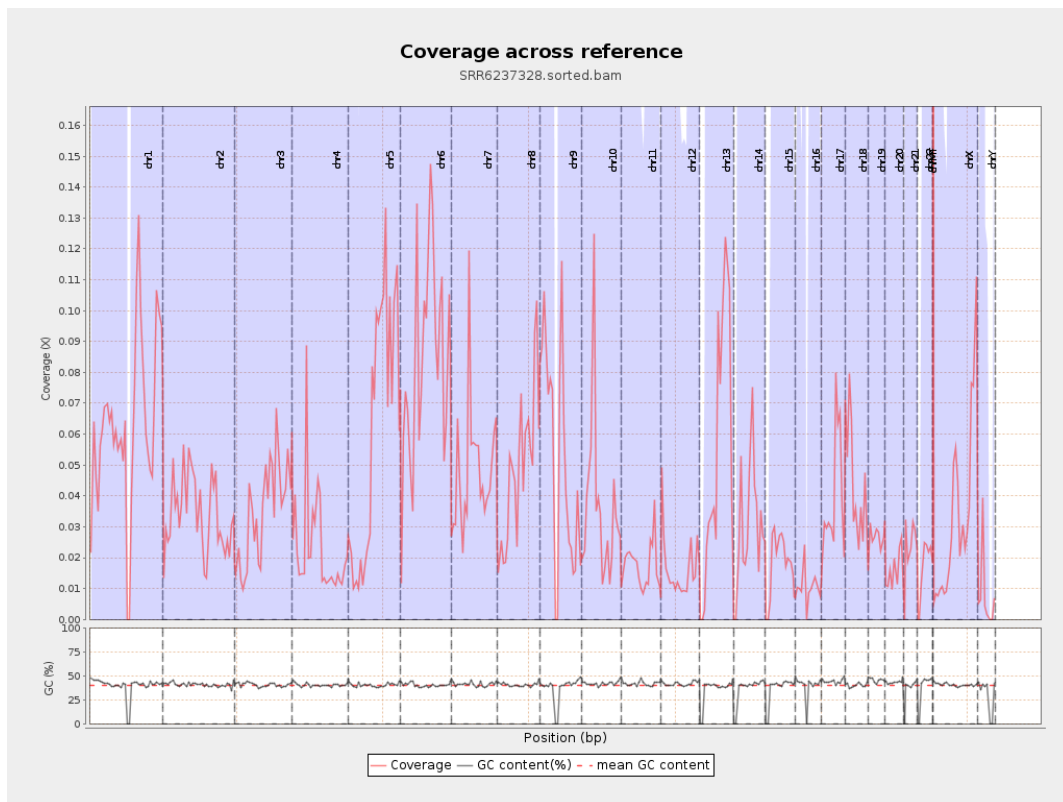
General error rate	0.71%
Mismatches	838,017
Insertions	9,492
Mapped reads with at least one insertion	0.46%
Deletions	45,560
Mapped reads with at least one deletion	2.2%
Homopolymer indels	40.43%

2.6. Chromosome stats

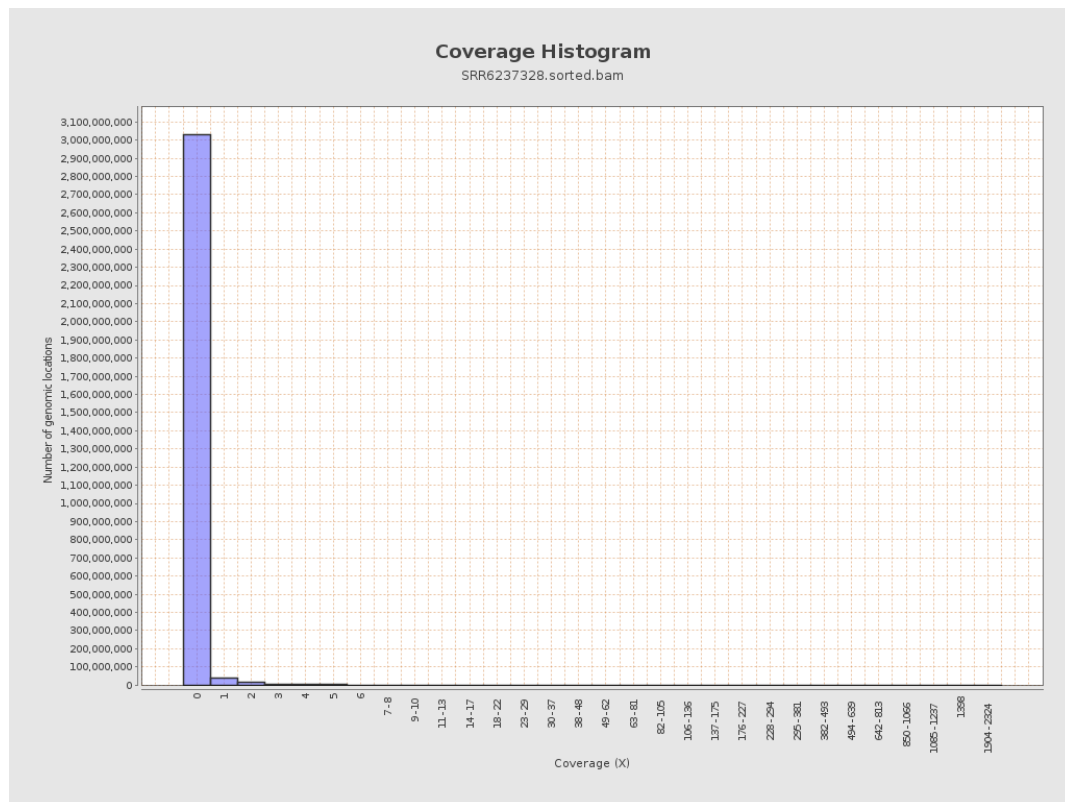
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15757229	0.0632	0.6357
chr2	243199373	8272929	0.034	1.2214
chr3	198022430	6797545	0.0343	0.3177
chr4	191154276	4406166	0.0231	0.4796
chr5	180915260	10909040	0.0603	0.4207
chr6	171115067	14524653	0.0849	0.7055
chr7	159138663	7745922	0.0487	0.8009

chr8	146364022	7167469	0.049	0.4853
chr9	141213431	7397463	0.0524	0.4704
chr10	135534747	4844345	0.0357	0.7656
chr11	135006516	2410765	0.0179	0.2579
chr12	133851895	2244799	0.0168	0.2244
chr13	115169878	6345181	0.0551	0.4722
chr14	107349540	3252042	0.0303	0.3092
chr15	102531392	1842297	0.018	0.268
chr16	90354753	928817	0.0103	0.2514
chr17	81195210	3273717	0.0403	0.37
chr18	78077248	3448705	0.0442	1.5057
chr19	59128983	1576371	0.0267	0.4017
chr20	63025520	1032021	0.0164	0.2512
chr21	48129895	1157200	0.024	0.3665
chr22	51304566	860146	0.0168	0.2108
chrMT	16571	16331	0.9855	1.4589
chrX	155270560	5167298	0.0333	0.3228
chrY	59373566	482273	0.0081	0.4518

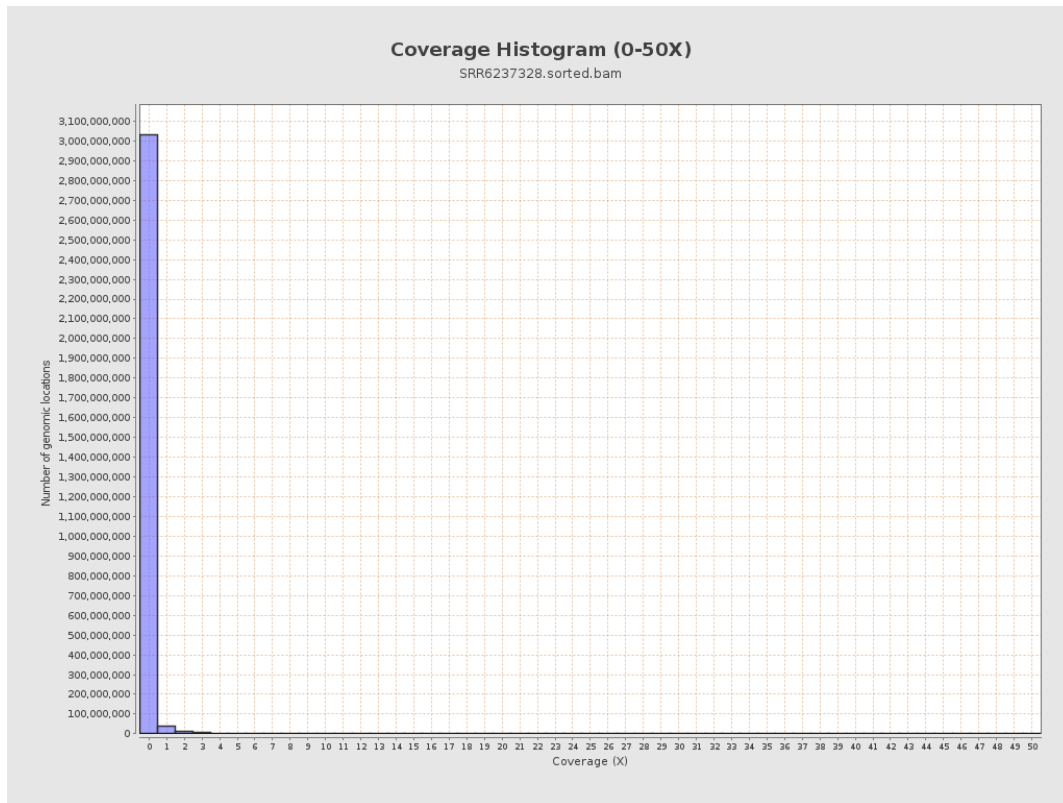
3. Results : Coverage across reference



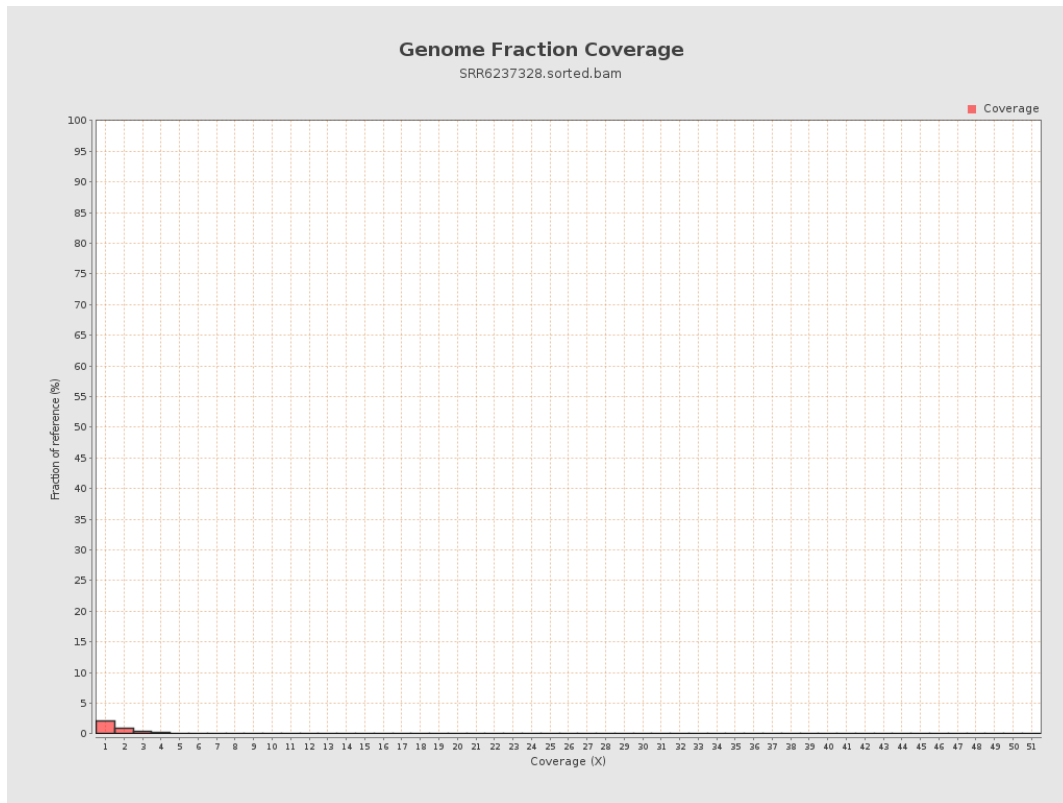
4. Results : Coverage Histogram



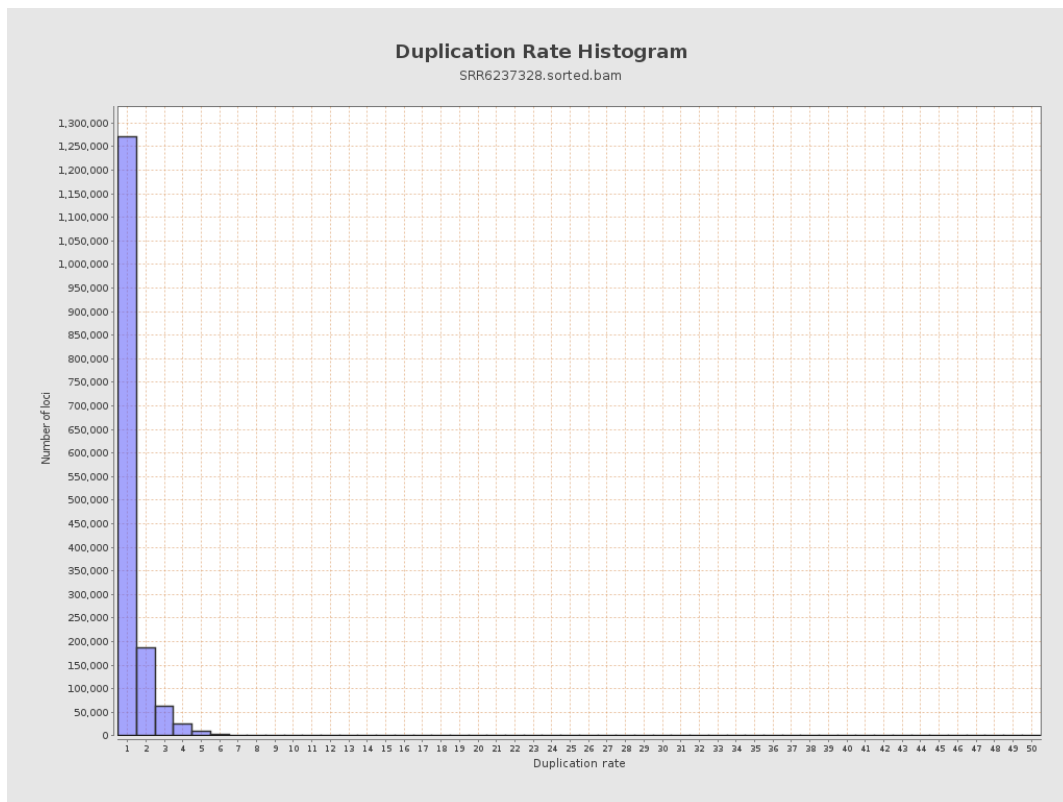
5. Results : Coverage Histogram (0-50X)



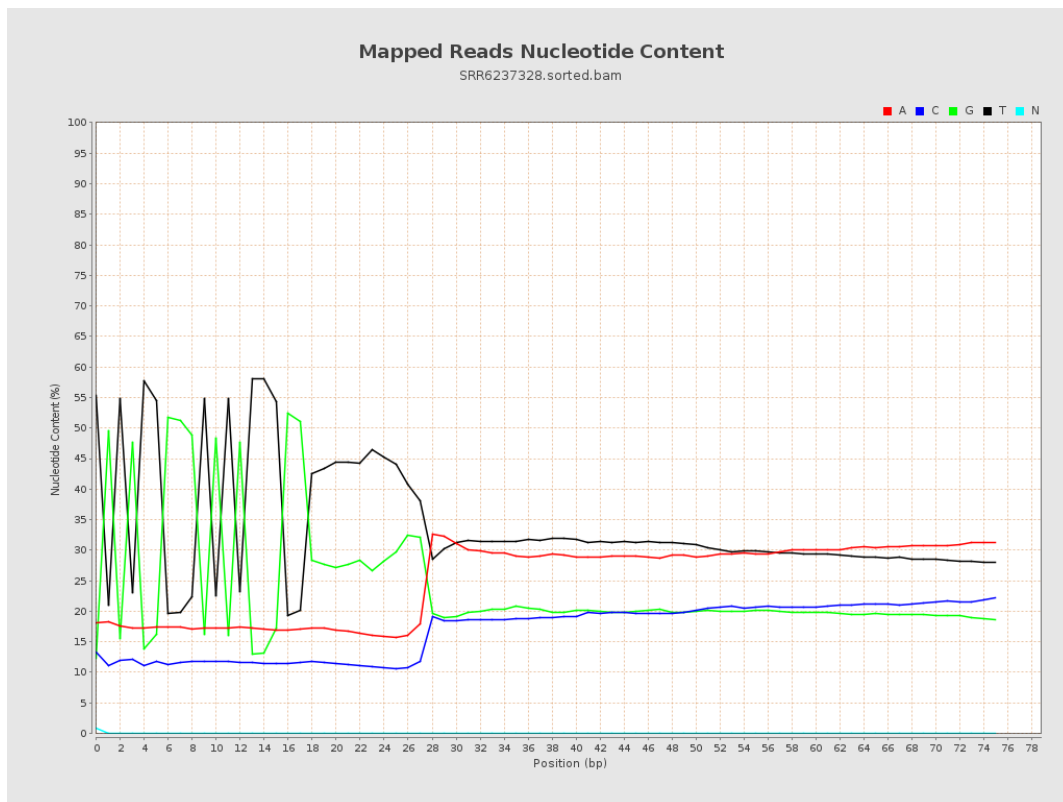
6. Results : Genome Fraction Coverage



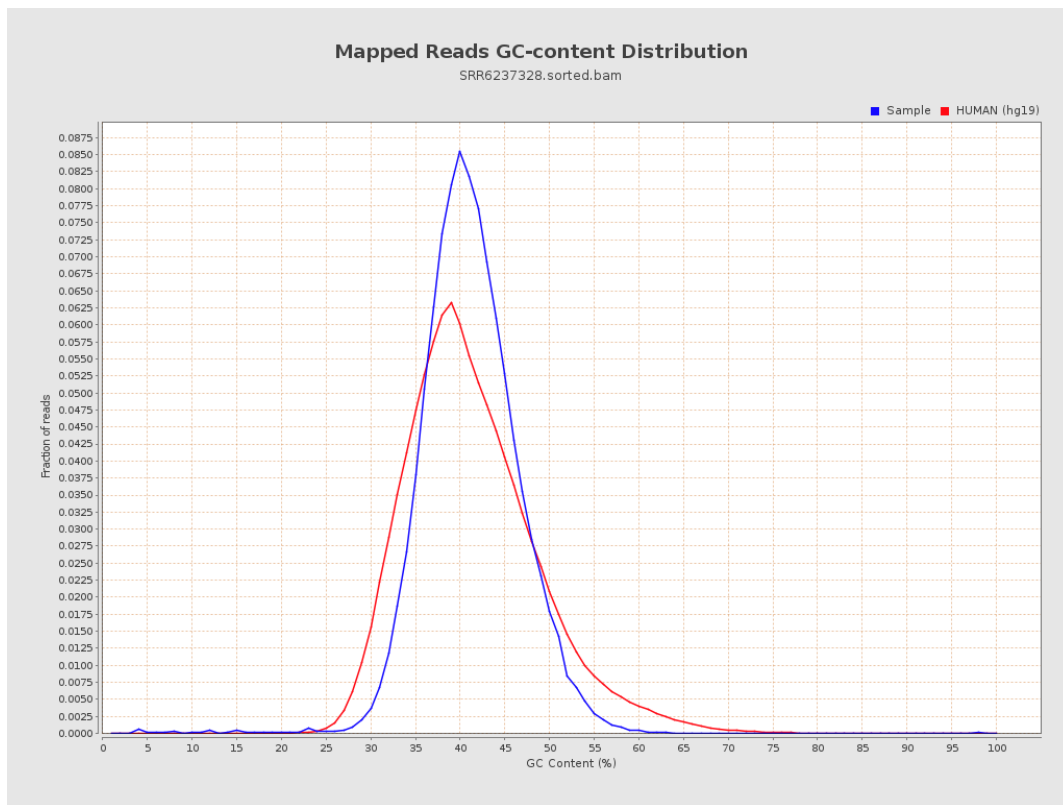
7. Results : Duplication Rate Histogram



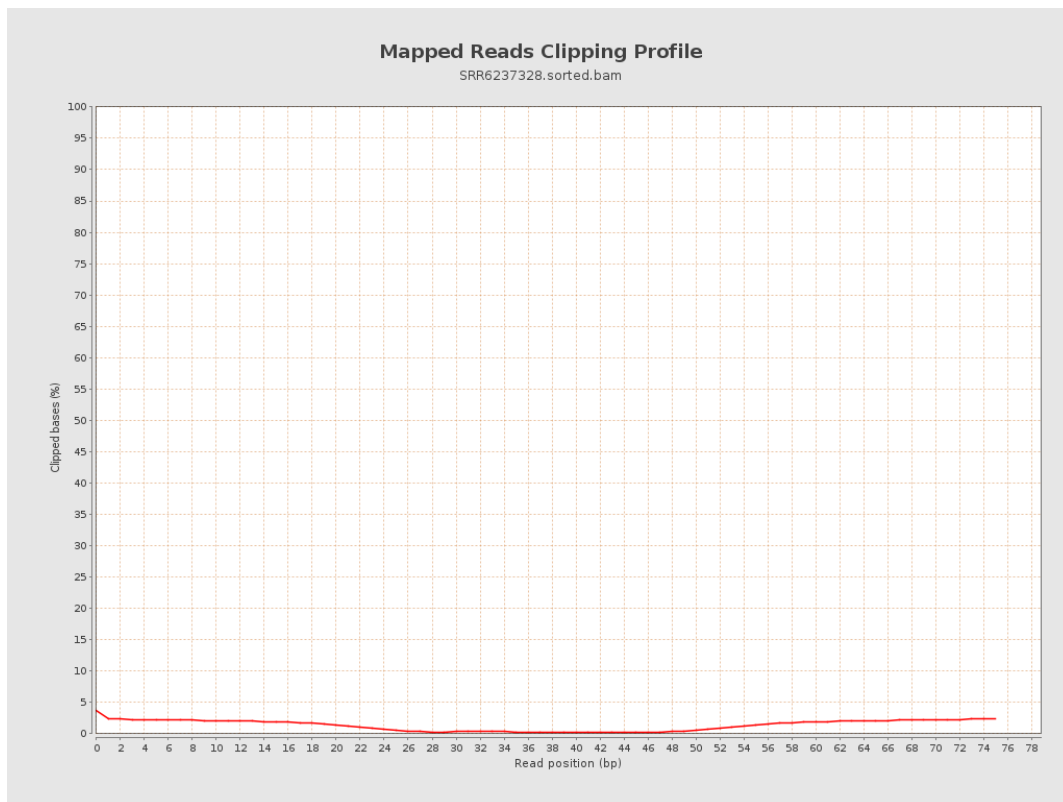
8. Results : Mapped Reads Nucleotide Content



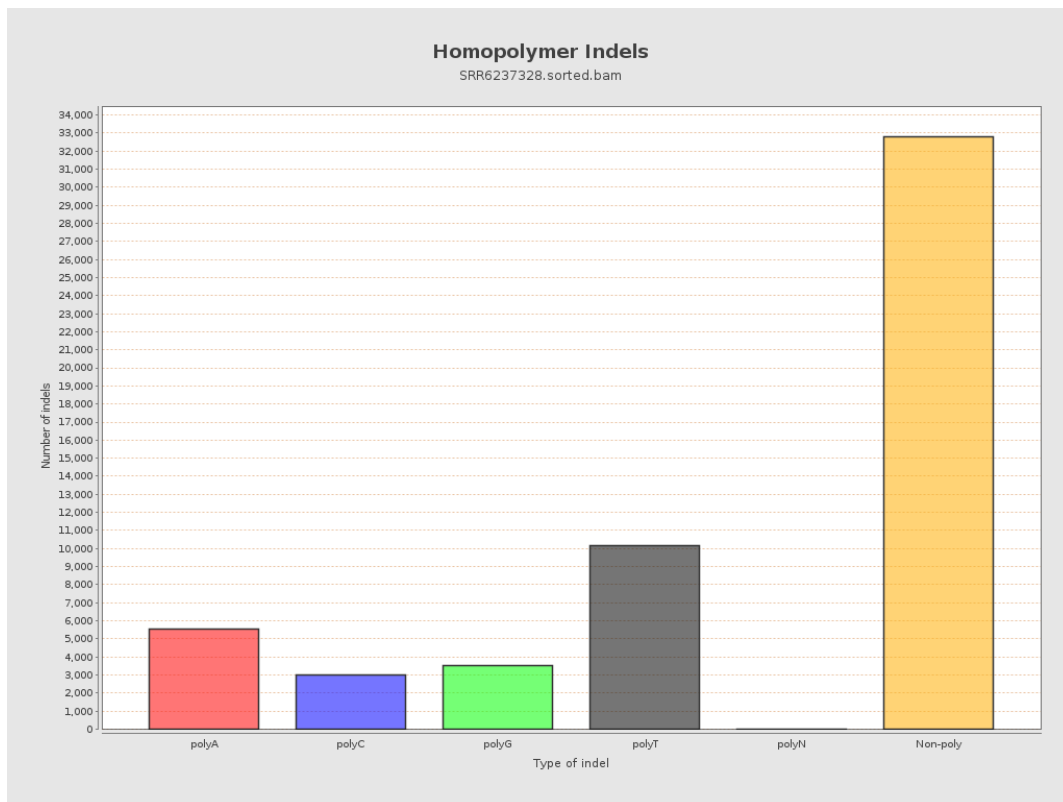
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

