

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:14:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237606.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_SRR6237606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:14:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,302,131
Mapped reads	1,154,375 / 88.65%
Unmapped reads	147,756 / 11.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,358 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	39,088 / 3%
Duplication rate	2.65%
Clipped reads	624,208 / 47.94%

2.2. ACGT Content

Number/percentage of A's	19,616,823 / 26.56%
Number/percentage of C's	12,836,471 / 17.38%
Number/percentage of T's	24,006,471 / 32.5%
Number/percentage of G's	17,271,780 / 23.38%
Number/percentage of N's	128,343 / 0.17%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2277
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2.4. Mapping Quality

Mean Mapping Quality	44.57
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2.5. Mismatches and indels

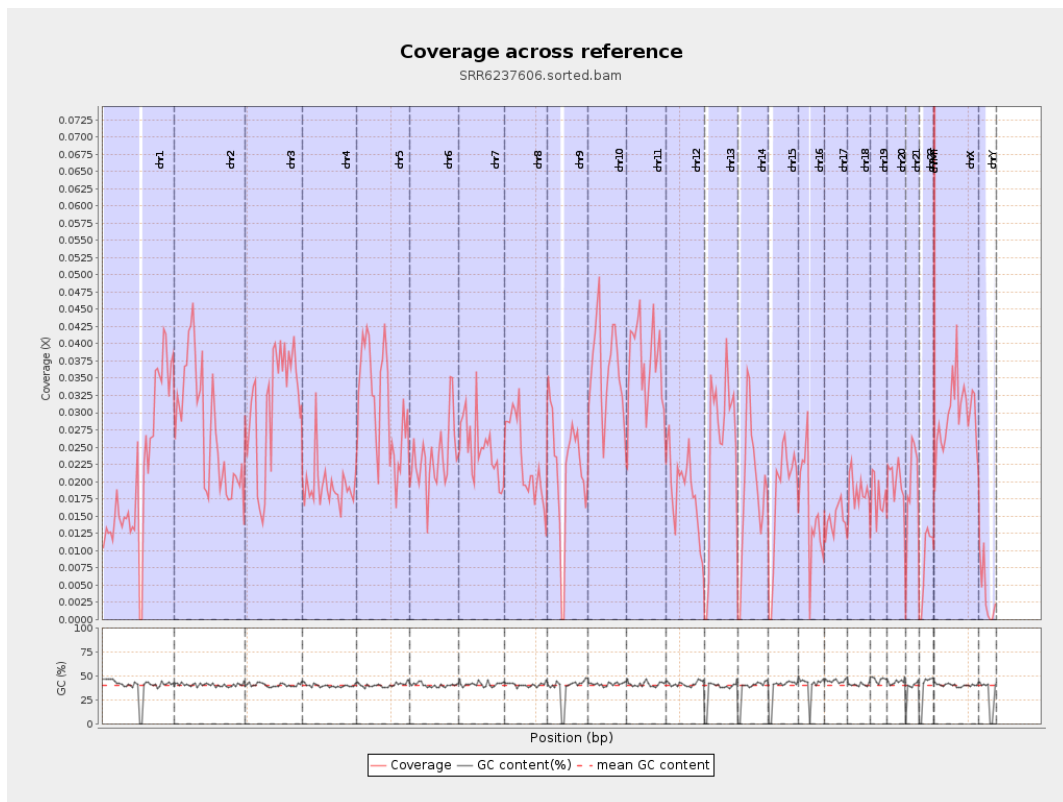
General error rate	0.88%
Mismatches	641,743
Insertions	6,279
Mapped reads with at least one insertion	0.54%
Deletions	24,426
Mapped reads with at least one deletion	2.09%
Homopolymer indels	45.46%

2.6. Chromosome stats

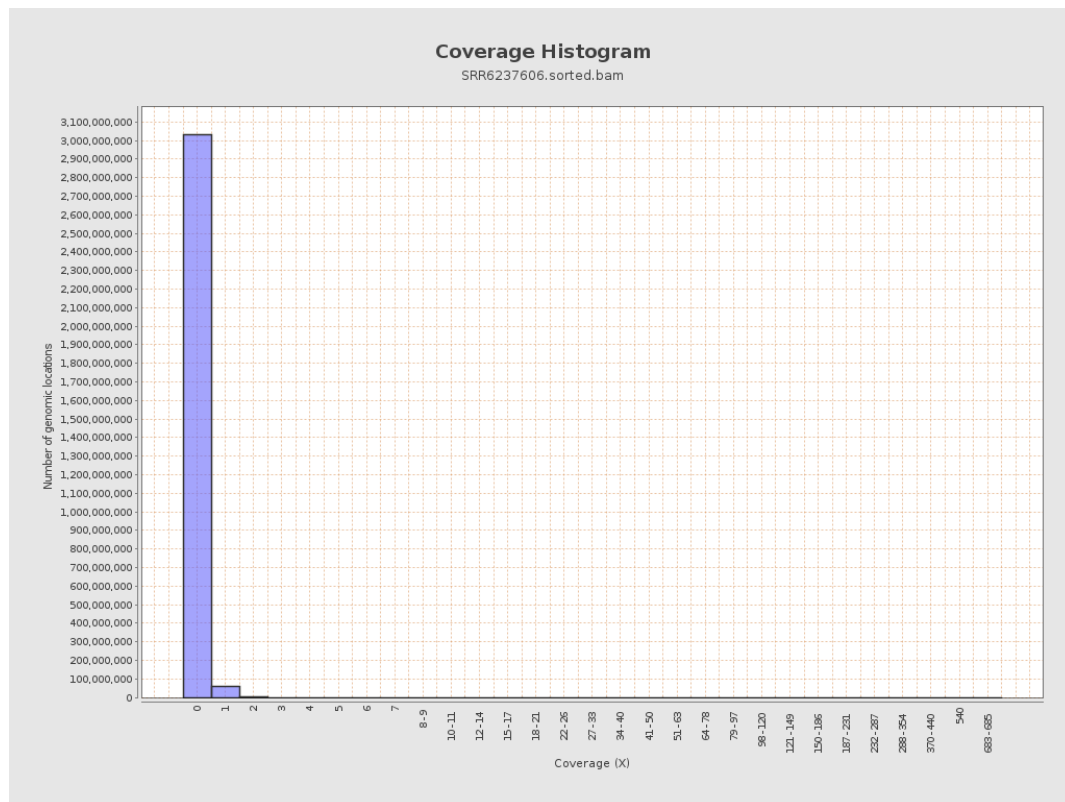
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5388625	0.0216	0.2913
chr2	243199373	6637314	0.0273	0.3537
chr3	198022430	6210028	0.0314	0.1929
chr4	191154276	3702340	0.0194	0.1646
chr5	180915260	5633956	0.0311	0.1927
chr6	171115067	4016810	0.0235	0.1951
chr7	159138663	3925315	0.0247	0.2729

chr8	146364022	3395145	0.0232	0.2951
chr9	141213431	3103195	0.022	0.1965
chr10	135534747	4924496	0.0363	0.2569
chr11	135006516	5040003	0.0373	0.2474
chr12	133851895	2481522	0.0185	0.1508
chr13	115169878	2932317	0.0255	0.1766
chr14	107349540	2053783	0.0191	0.1552
chr15	102531392	1863430	0.0182	0.1487
chr16	90354753	1419742	0.0157	0.1742
chr17	81195210	1165450	0.0144	0.1428
chr18	78077248	1460073	0.0187	0.2842
chr19	59128983	1046495	0.0177	0.2375
chr20	63025520	1262804	0.02	0.158
chr21	48129895	933575	0.0194	0.1598
chr22	51304566	439866	0.0086	0.0995
chrMT	16571	12869	0.7766	1.0814
chrX	155270560	4636715	0.0299	0.2006
chrY	59373566	214080	0.0036	0.0985

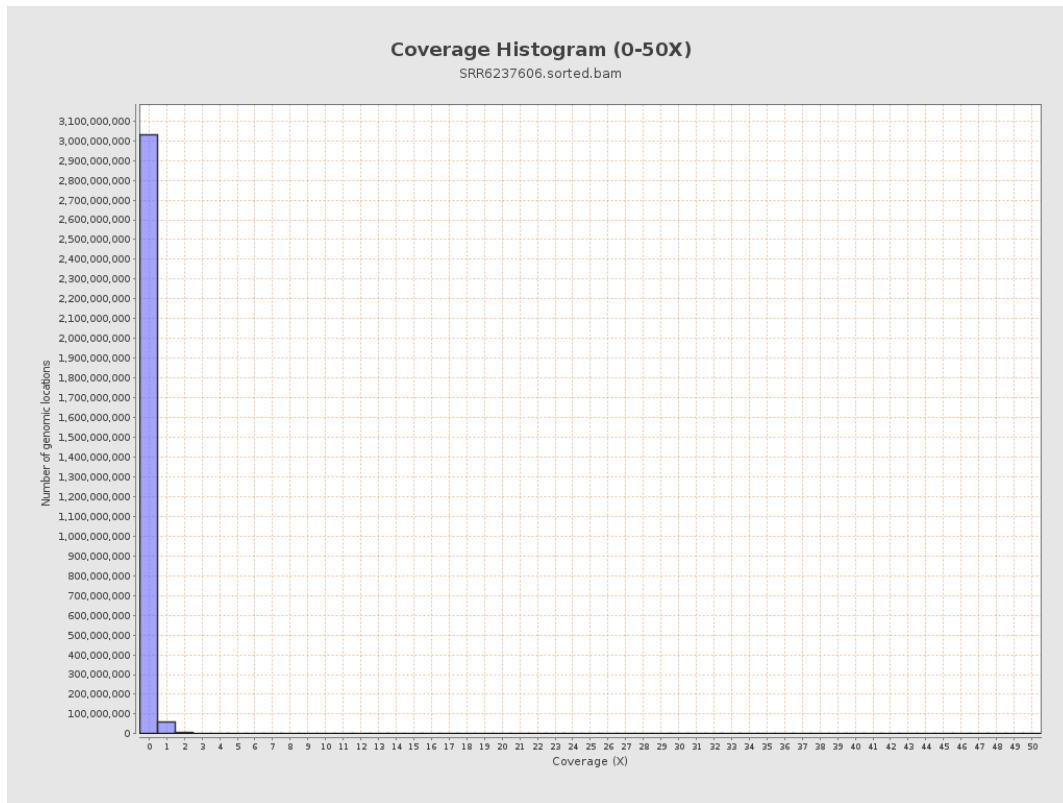
3. Results : Coverage across reference



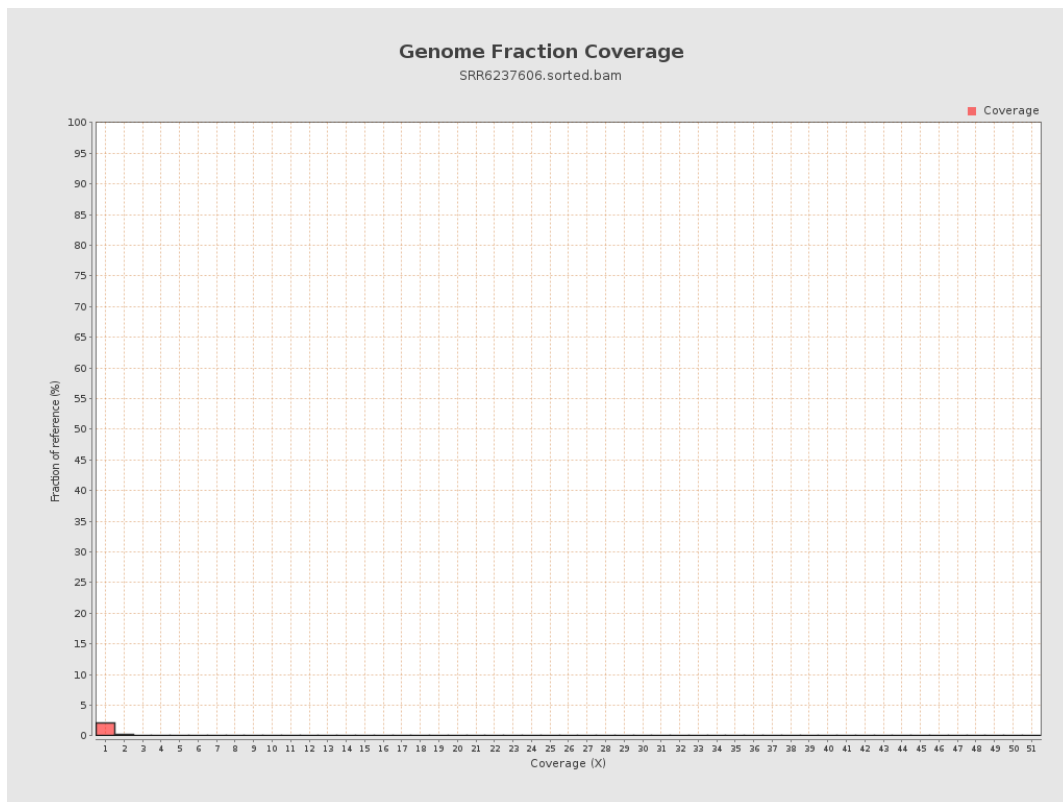
4. Results : Coverage Histogram



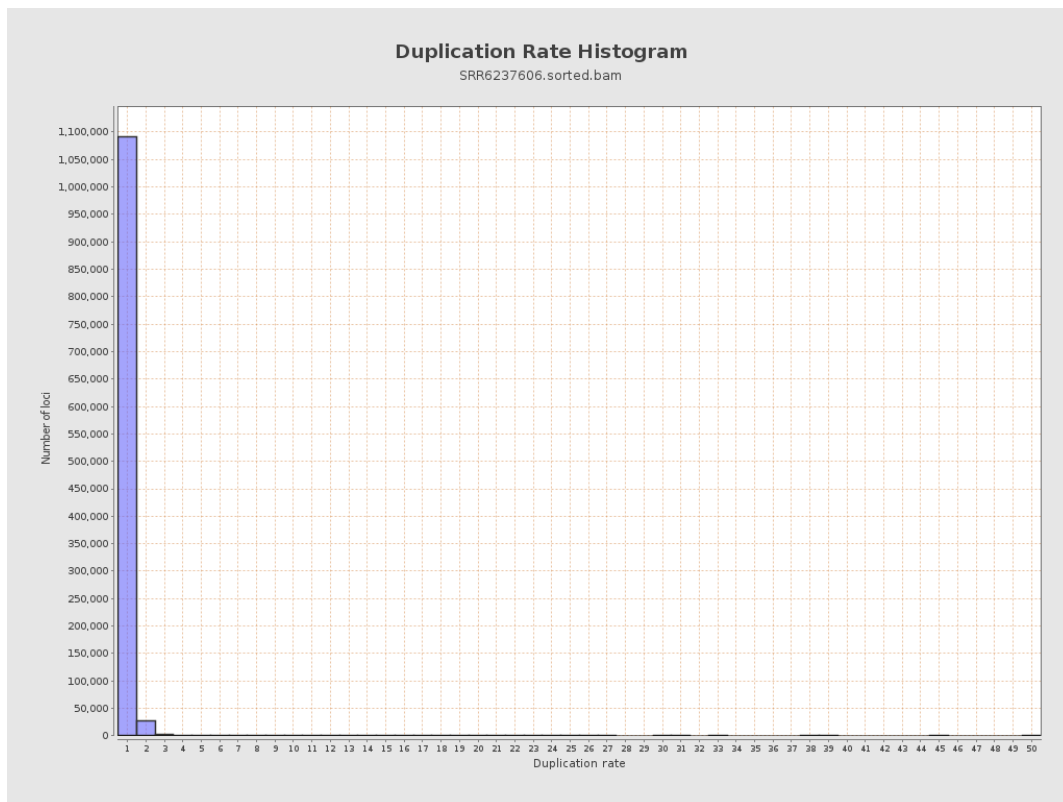
5. Results : Coverage Histogram (0-50X)



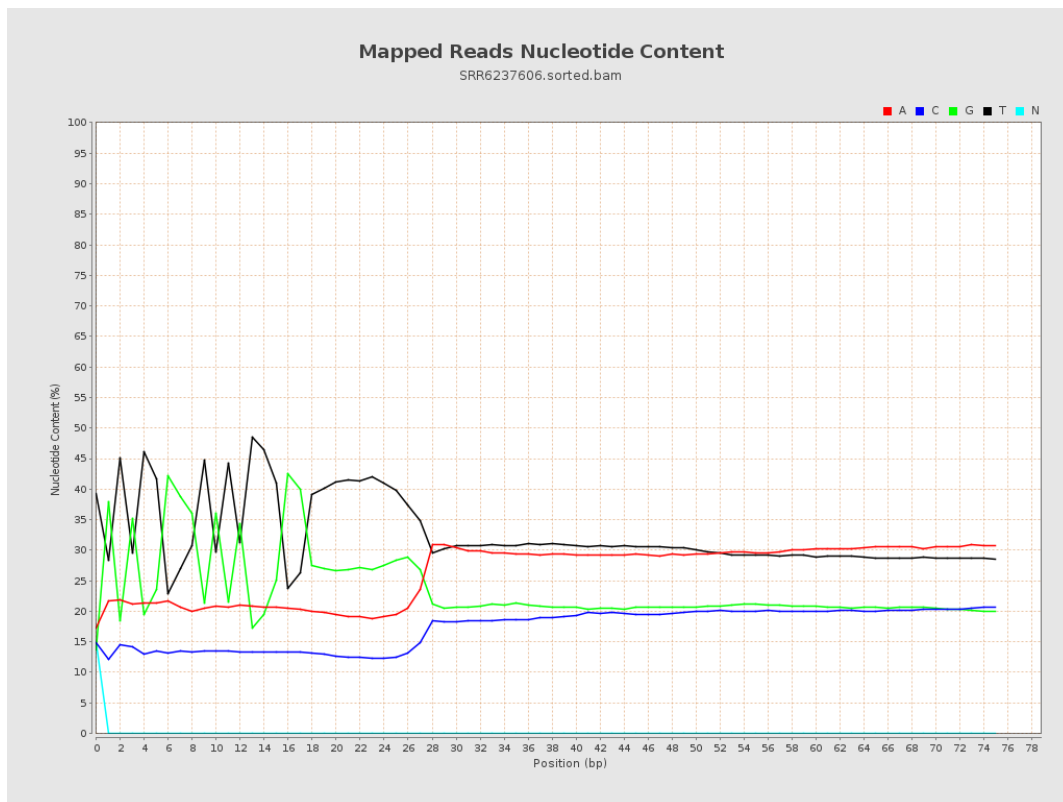
6. Results : Genome Fraction Coverage



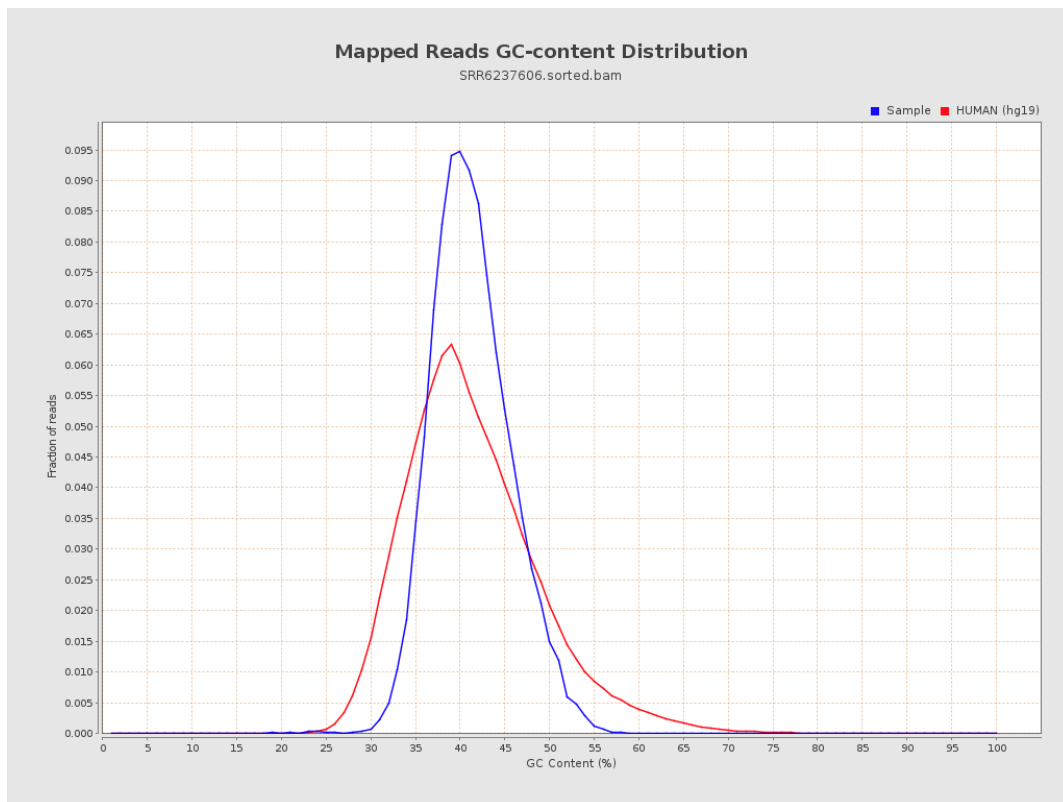
7. Results : Duplication Rate Histogram



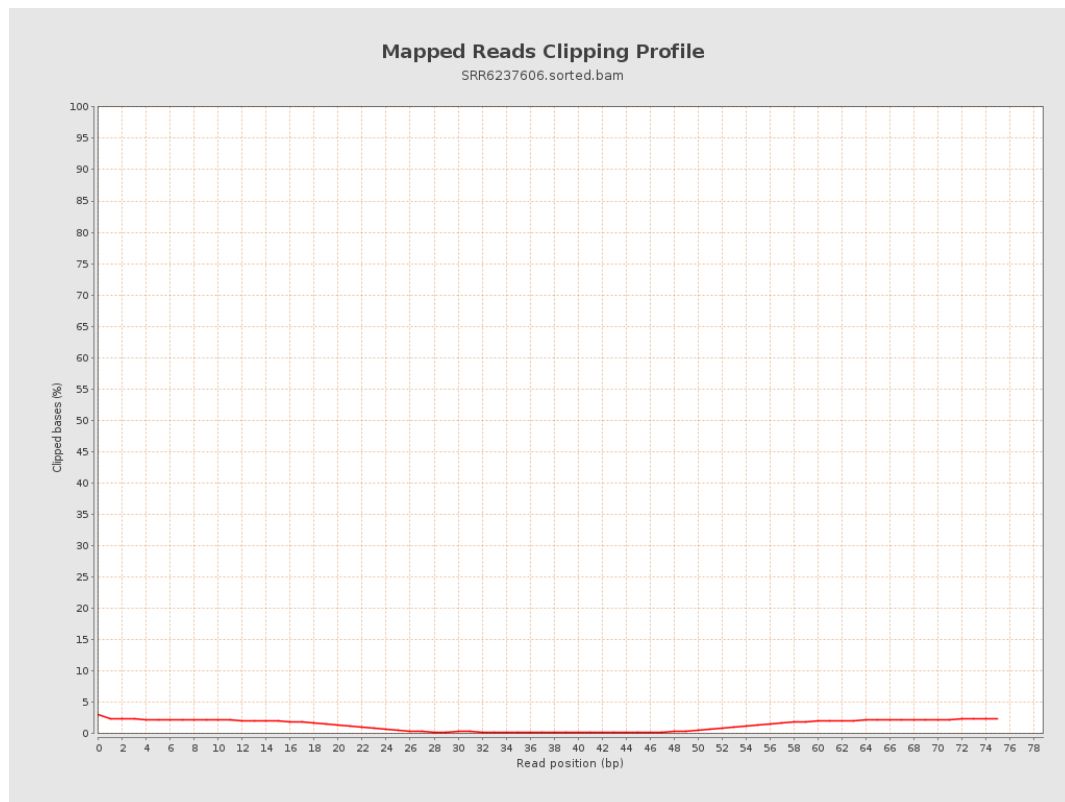
8. Results : Mapped Reads Nucleotide Content



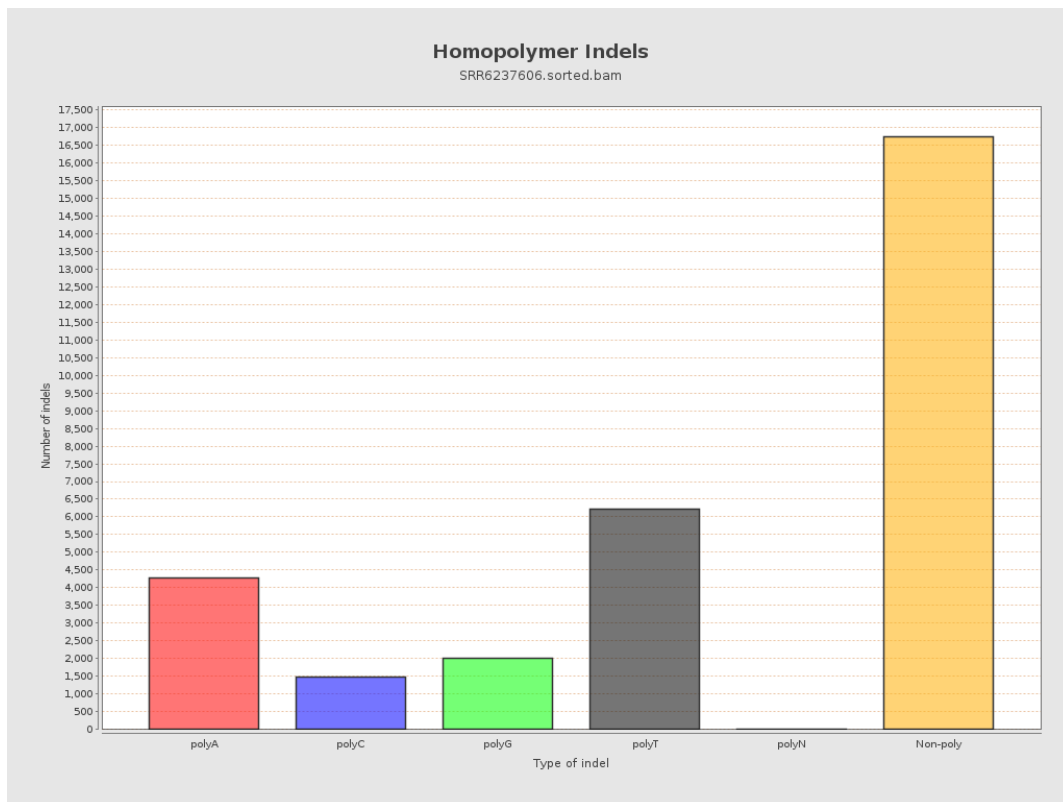
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

