

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:35:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068125.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_SRR6068125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:35:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,910,470
Mapped reads	3,714,614 / 94.99%
Unmapped reads	195,856 / 5.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,158 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	284,903 / 7.29%
Duplication rate	5.37%
Clipped reads	1,644,624 / 42.06%

2.2. ACGT Content

Number/percentage of A's	68,072,657 / 27.46%
Number/percentage of C's	46,248,911 / 18.66%
Number/percentage of T's	77,990,553 / 31.46%
Number/percentage of G's	55,559,190 / 22.41%
Number/percentage of N's	28,185 / 0.01%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0801

Standard Deviation	1.2349
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2.4. Mapping Quality

Mean Mapping Quality	43.99
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2.5. Mismatches and indels

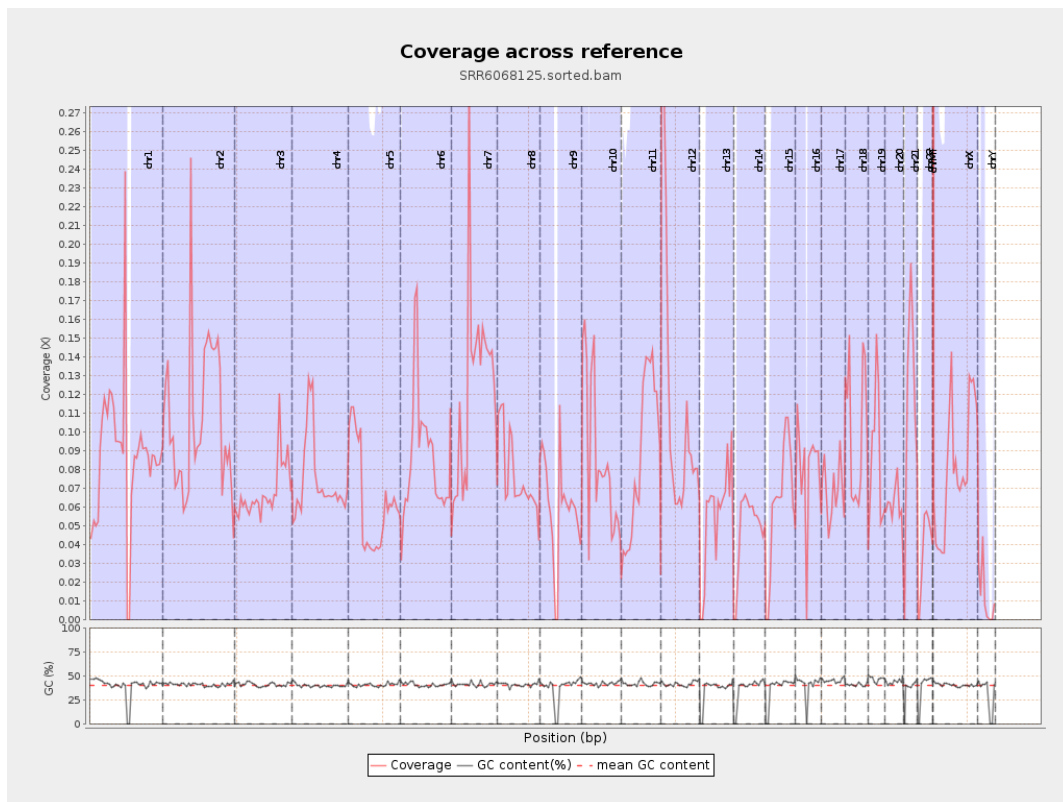
General error rate	0.65%
Mismatches	1,587,007
Insertions	17,793
Mapped reads with at least one insertion	0.47%
Deletions	62,190
Mapped reads with at least one deletion	1.66%
Homopolymer indels	44.27%

2.6. Chromosome stats

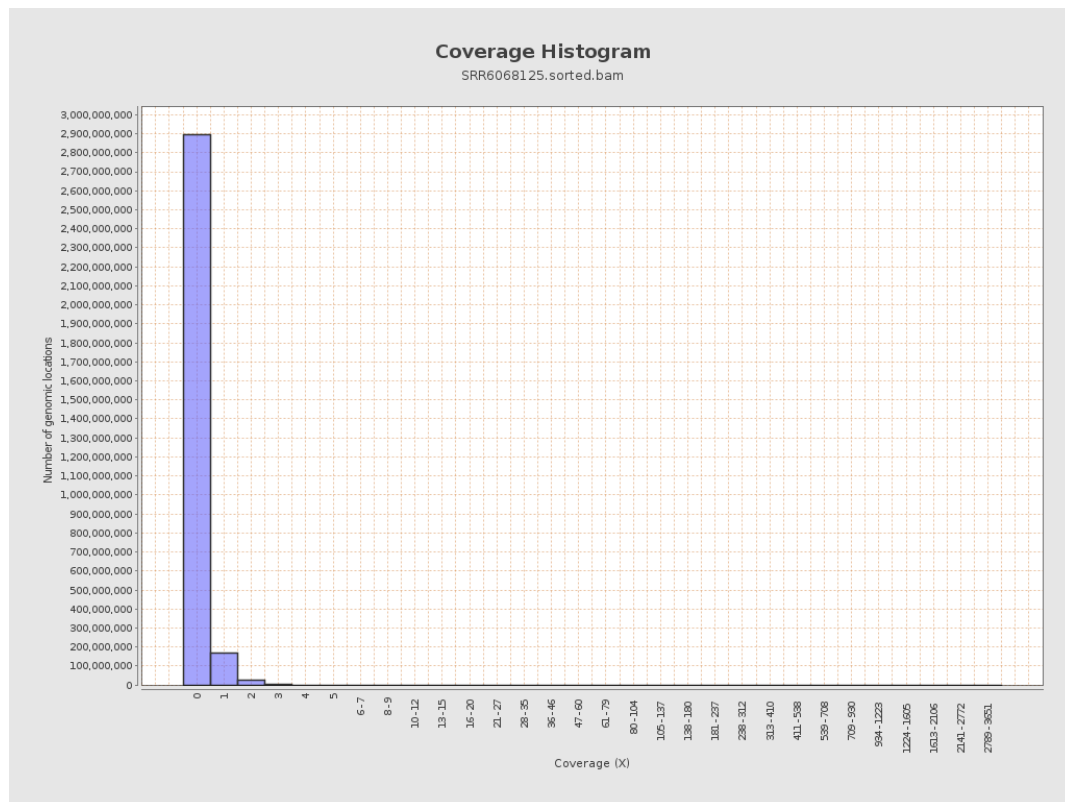
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21789751	0.0874	3.0087
chr2	243199373	26010839	0.107	1.1321
chr3	198022430	13419052	0.0678	0.3108
chr4	191154276	14273828	0.0747	0.3607
chr5	180915260	11422398	0.0631	0.3137
chr6	171115067	14873339	0.0869	0.5025
chr7	159138663	19507118	0.1226	2.3778

chr8	146364022	11086891	0.0757	1.4271
chr9	141213431	8403302	0.0595	0.9166
chr10	135534747	11612827	0.0857	0.7421
chr11	135006516	11736263	0.0869	0.5359
chr12	133851895	15547417	0.1162	0.4628
chr13	115169878	6429328	0.0558	0.2826
chr14	107349540	5231270	0.0487	0.4322
chr15	102531392	6319986	0.0616	0.3203
chr16	90354753	7077290	0.0783	0.4453
chr17	81195210	5644846	0.0695	0.3508
chr18	78077248	7815177	0.1001	1.7532
chr19	59128983	5289996	0.0895	1.8846
chr20	63025520	3850893	0.0611	0.3687
chr21	48129895	5385984	0.1119	0.4425
chr22	51304566	1892464	0.0369	0.2194
chrMT	16571	175124	10.5681	5.9955
chrX	155270560	12483812	0.0804	0.4726
chrY	59373566	731400	0.0123	0.4651

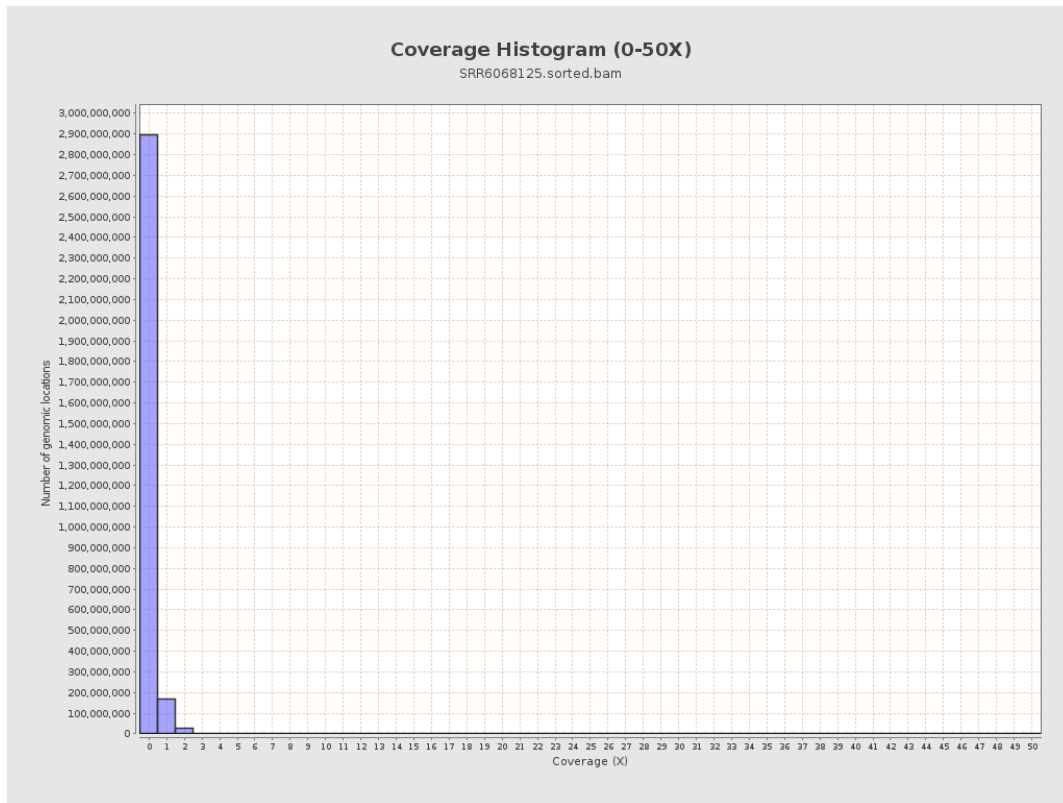
3. Results : Coverage across reference



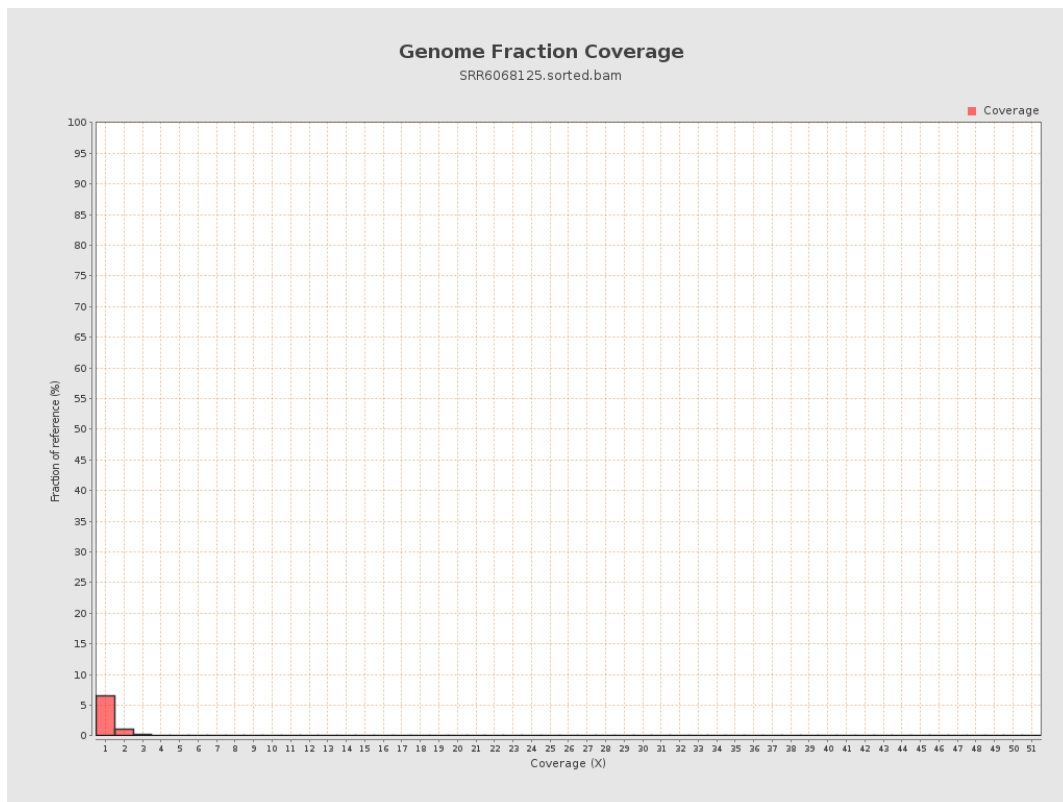
4. Results : Coverage Histogram



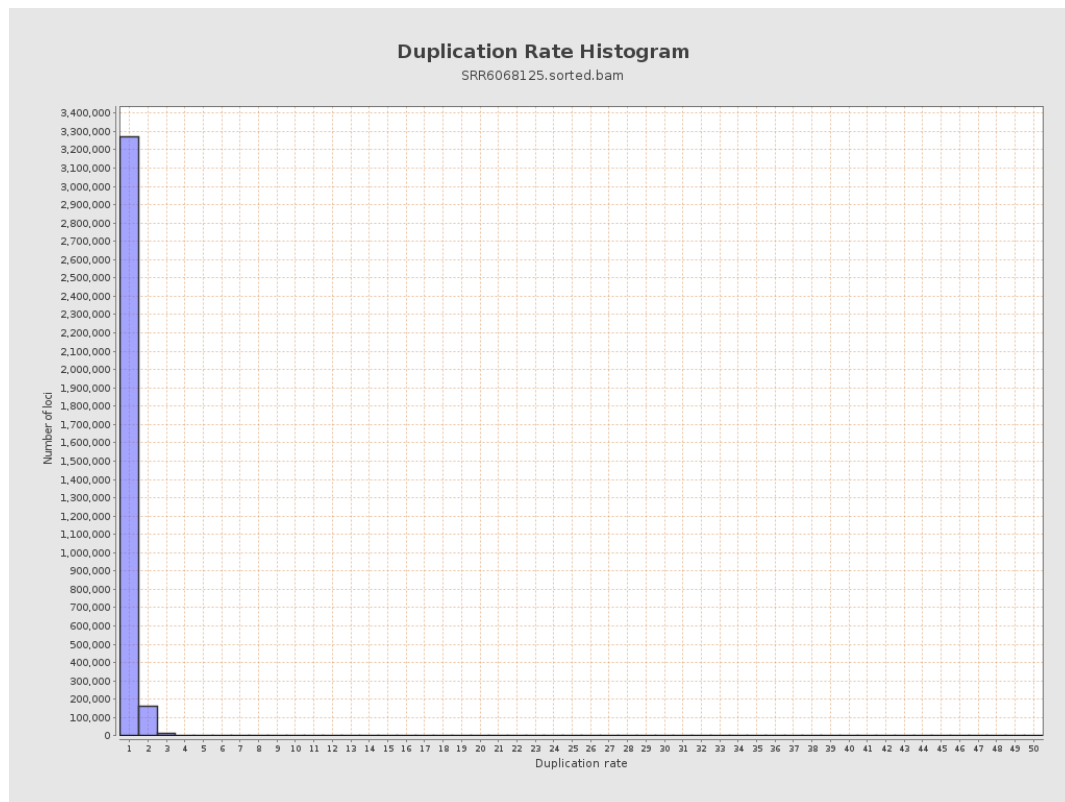
5. Results : Coverage Histogram (0-50X)



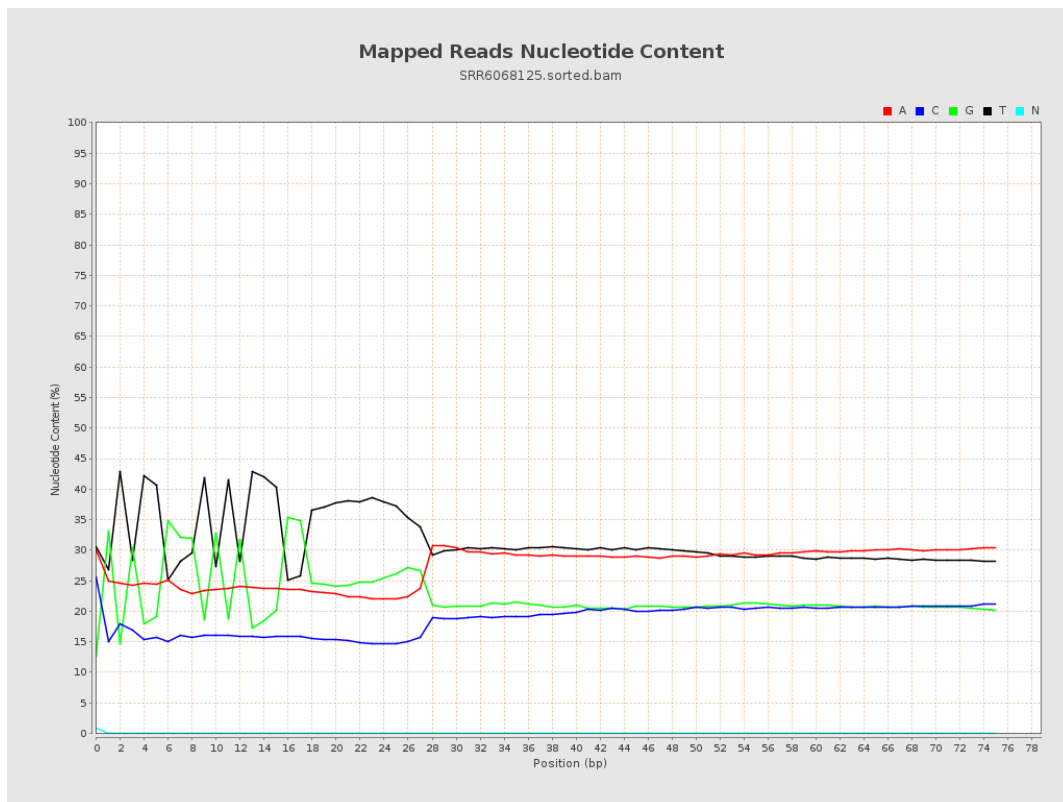
6. Results : Genome Fraction Coverage



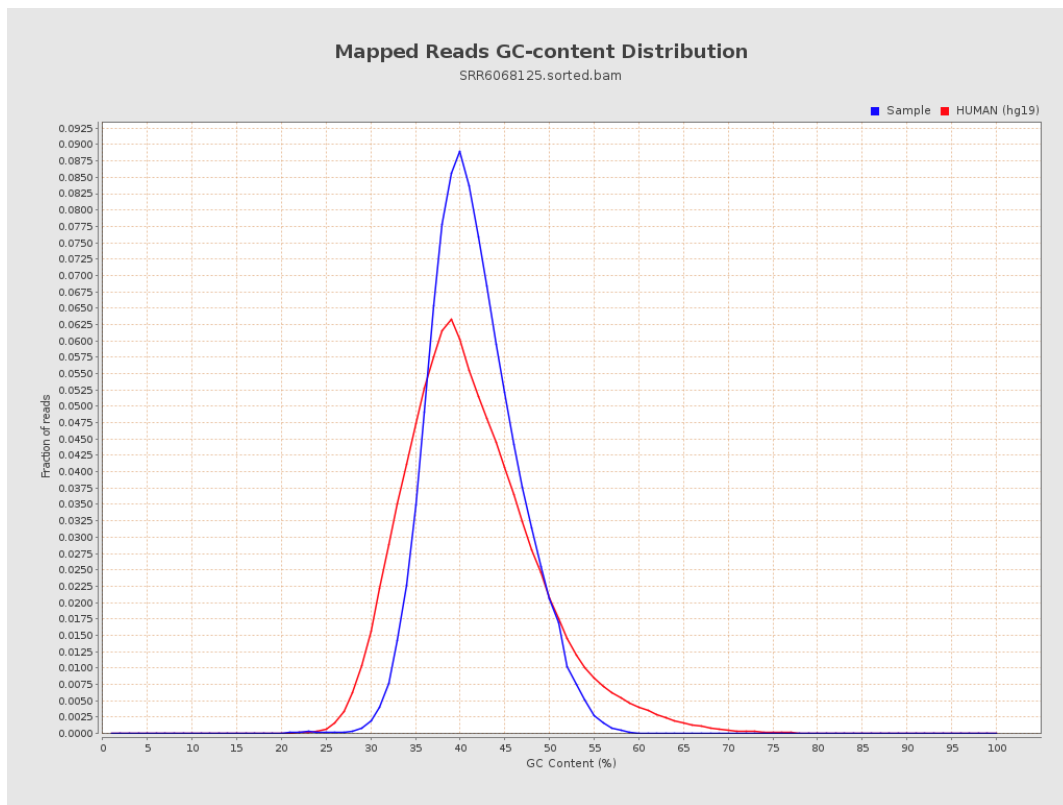
7. Results : Duplication Rate Histogram



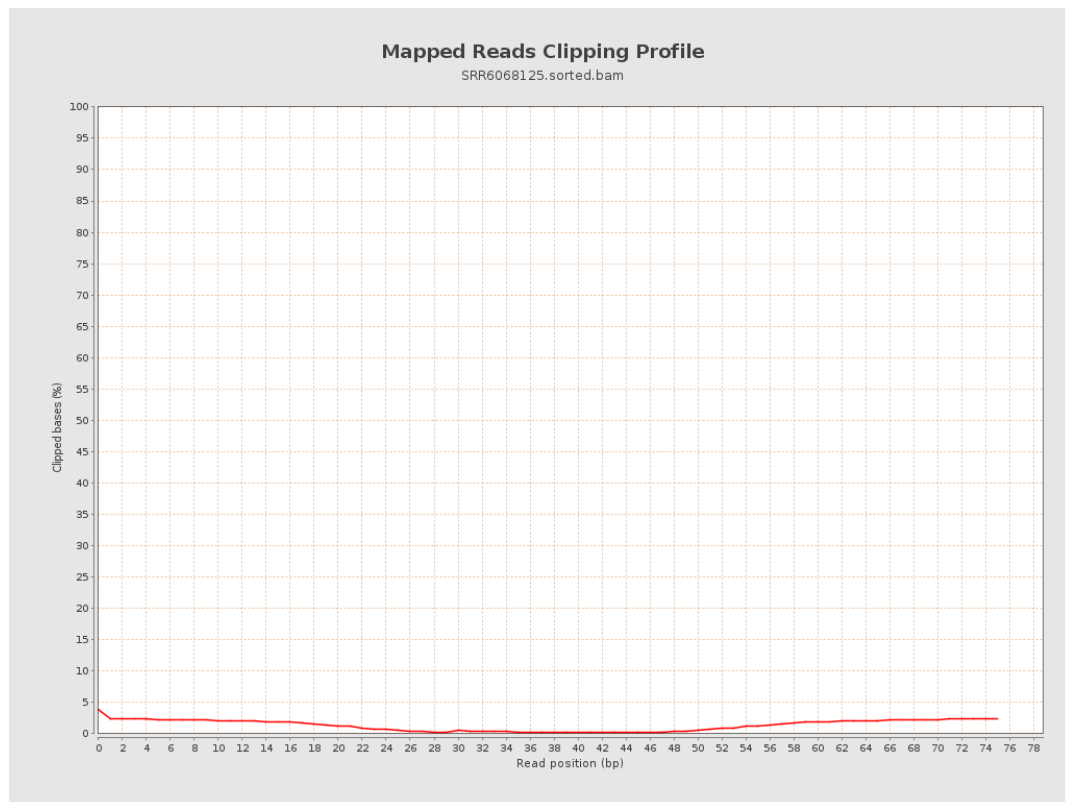
8. Results : Mapped Reads Nucleotide Content



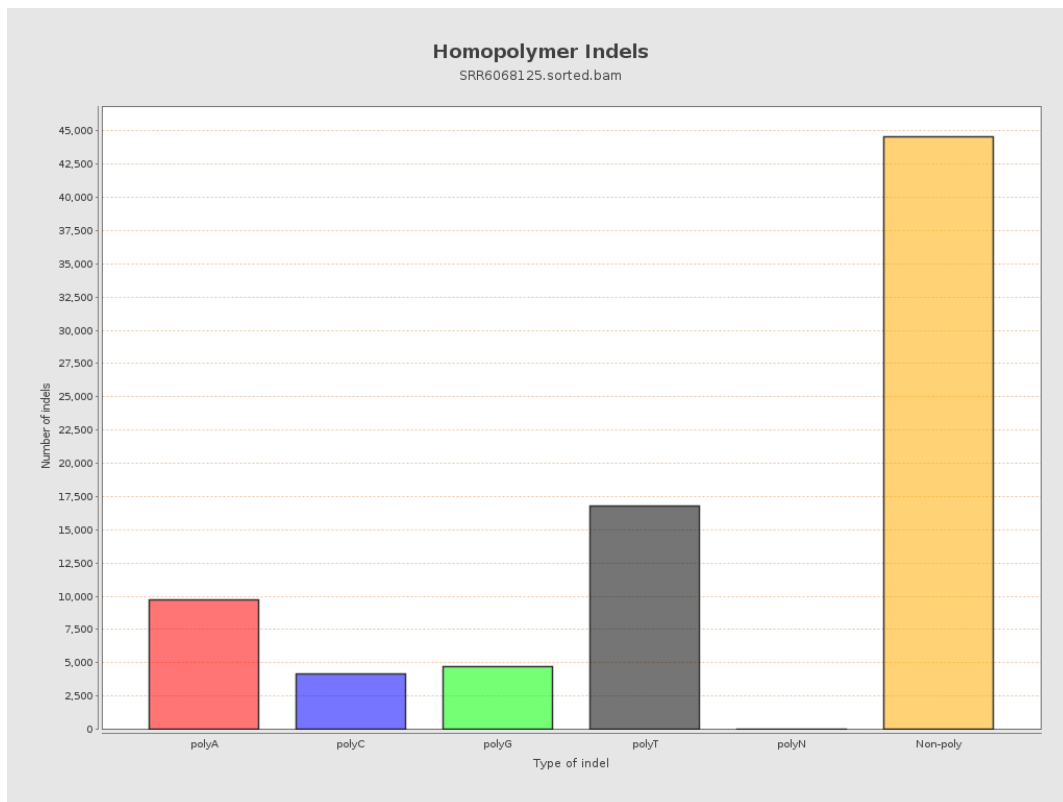
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

