

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:57:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238605.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_SRR6238605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:57:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,656,271
Mapped reads	2,690,461 / 73.58%
Unmapped reads	965,810 / 26.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,341 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,394,998 / 38.15%
Duplication rate	23.27%
Clipped reads	1,891,418 / 51.73%

2.2. ACGT Content

Number/percentage of A's	40,840,891 / 25.3%
Number/percentage of C's	27,517,834 / 17.04%
Number/percentage of T's	55,003,994 / 34.07%
Number/percentage of G's	38,076,072 / 23.58%
Number/percentage of N's	3,708 / 0%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0522

Standard Deviation	1.5239
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2.4. Mapping Quality

Mean Mapping Quality	40.43
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2.5. Mismatches and indels

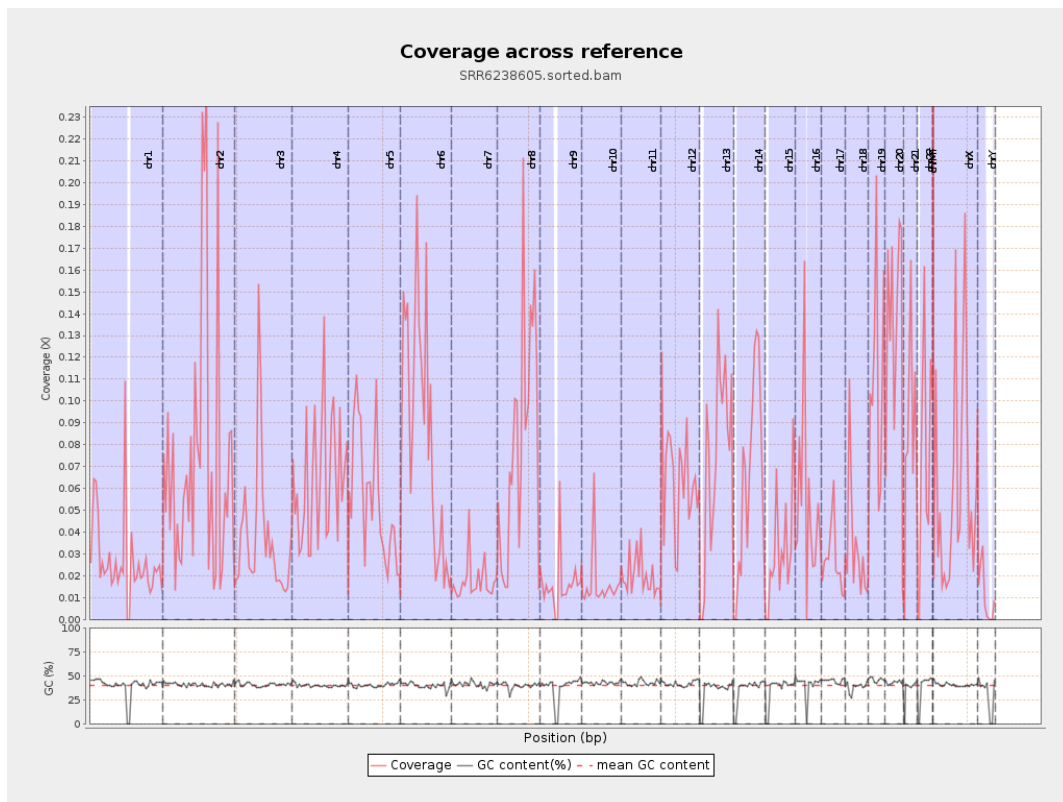
General error rate	0.65%
Mismatches	1,030,863
Insertions	11,568
Mapped reads with at least one insertion	0.43%
Deletions	43,817
Mapped reads with at least one deletion	1.61%
Homopolymer indels	40.94%

2.6. Chromosome stats

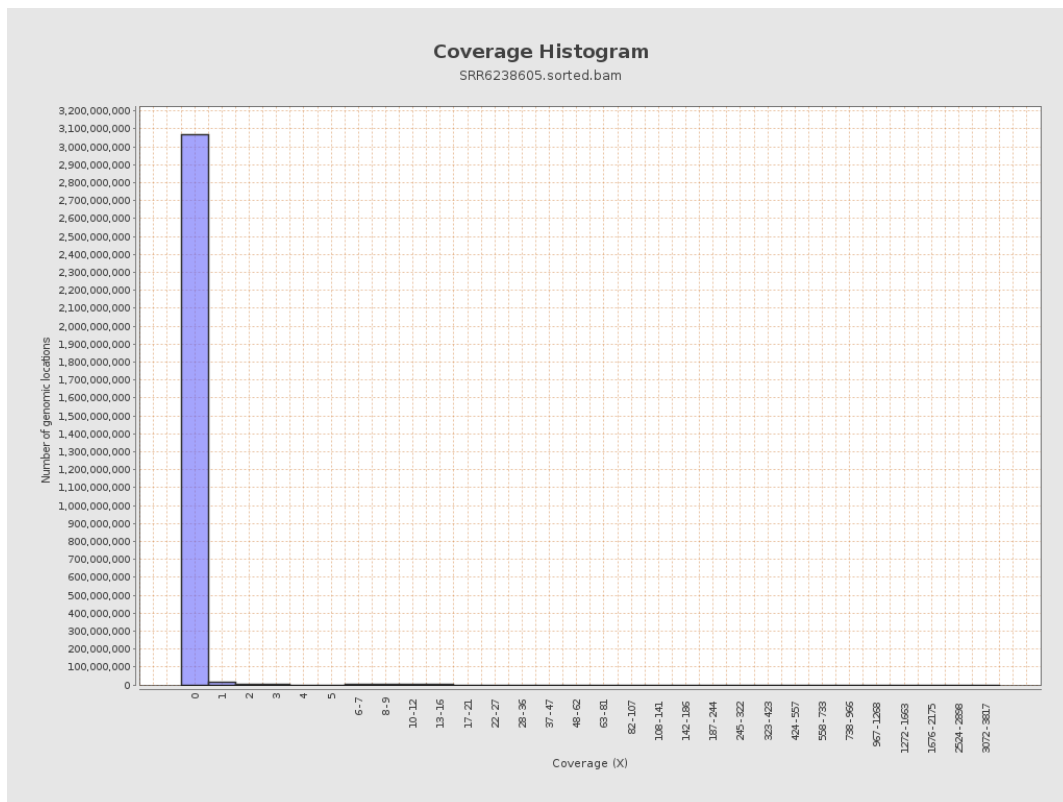
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6637050	0.0266	1.6721
chr2	243199373	18252364	0.0751	1.9532
chr3	198022430	7569821	0.0382	0.8695
chr4	191154276	12428519	0.065	1.1148
chr5	180915260	9886999	0.0546	1.0167
chr6	171115067	14741764	0.0862	1.5614
chr7	159138663	2795329	0.0176	0.8152

chr8	146364022	11784841	0.0805	2.1392
chr9	141213431	2244598	0.0159	0.6603
chr10	135534747	2106997	0.0155	0.734
chr11	135006516	2735577	0.0203	0.7306
chr12	133851895	8547993	0.0639	1.1241
chr13	115169878	8561278	0.0743	1.4204
chr14	107349540	7169558	0.0668	1.3495
chr15	102531392	3323991	0.0324	0.9827
chr16	90354753	4649996	0.0515	1.011
chr17	81195210	2266772	0.0279	0.6893
chr18	78077248	2684049	0.0344	5.0475
chr19	59128983	6451123	0.1091	1.872
chr20	63025520	8662354	0.1374	1.7062
chr21	48129895	4091565	0.085	1.2783
chr22	51304566	3702126	0.0722	1.1221
chrMT	16571	14971	0.9034	3.6472
chrX	155270560	9534625	0.0614	1.1394
chrY	59373566	672863	0.0113	0.7849

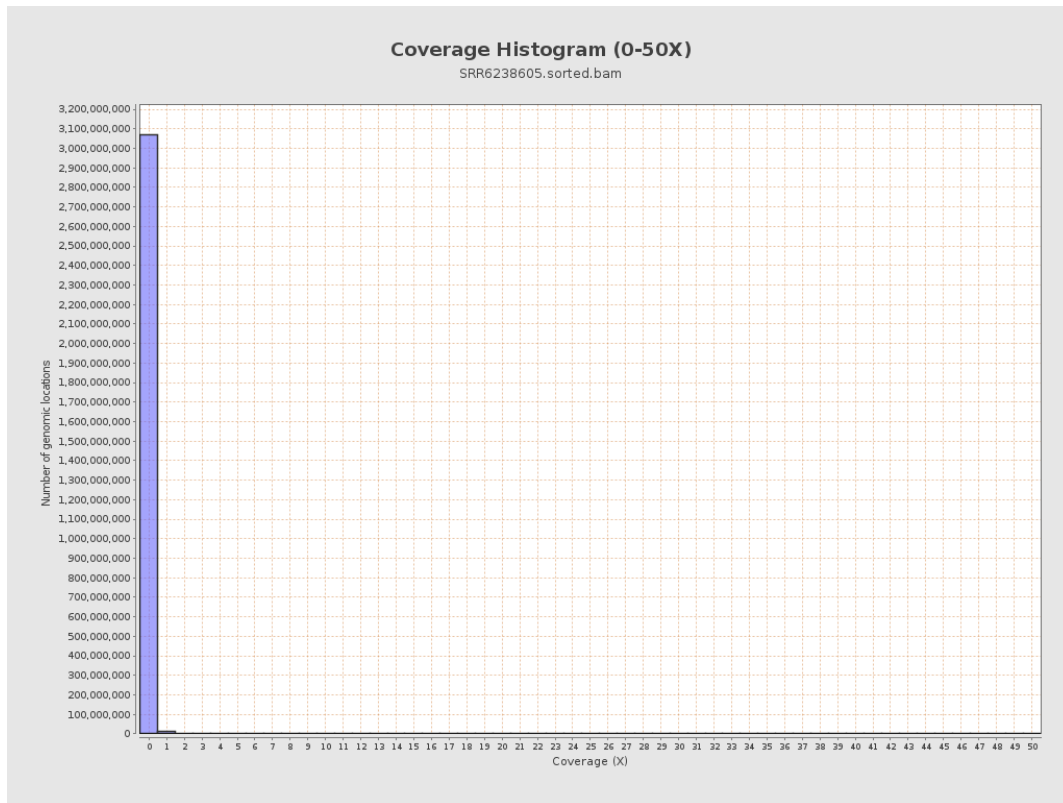
3. Results : Coverage across reference



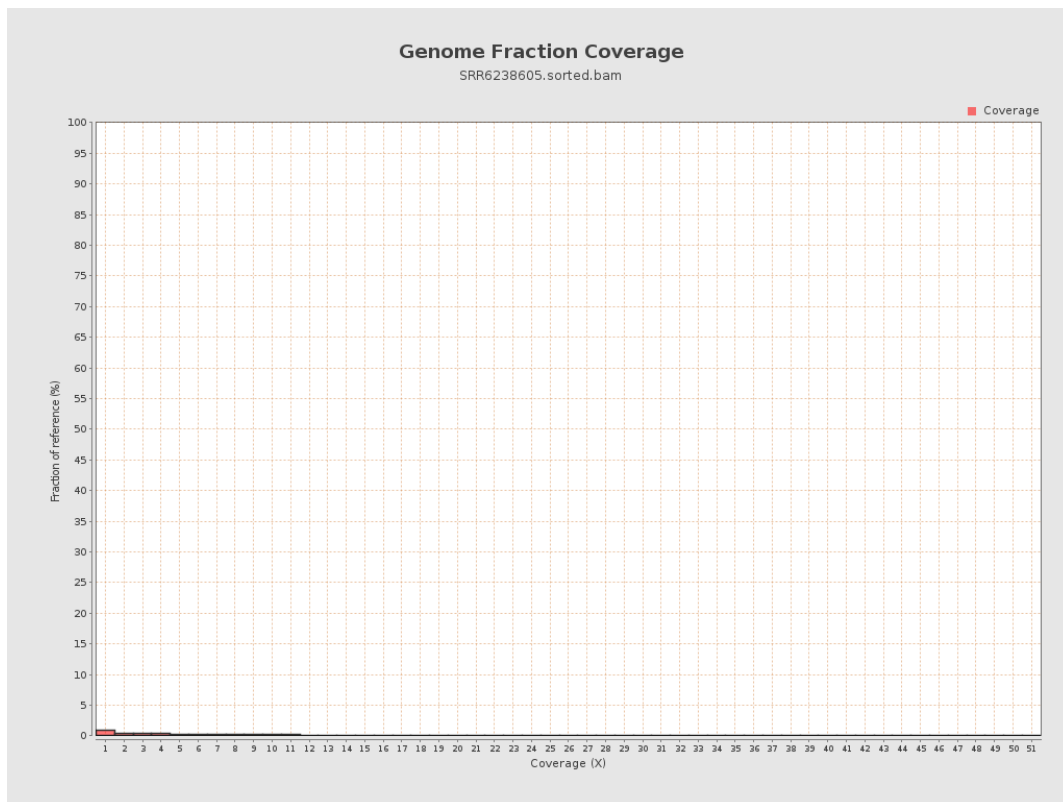
4. Results : Coverage Histogram



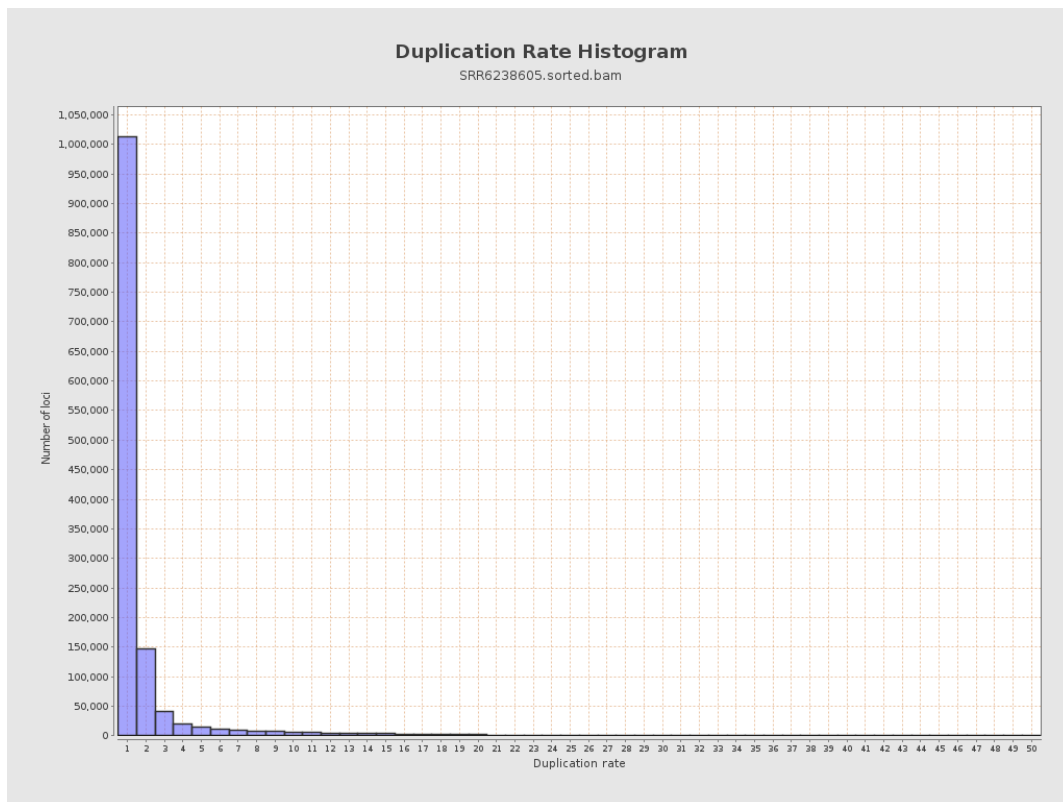
5. Results : Coverage Histogram (0-50X)



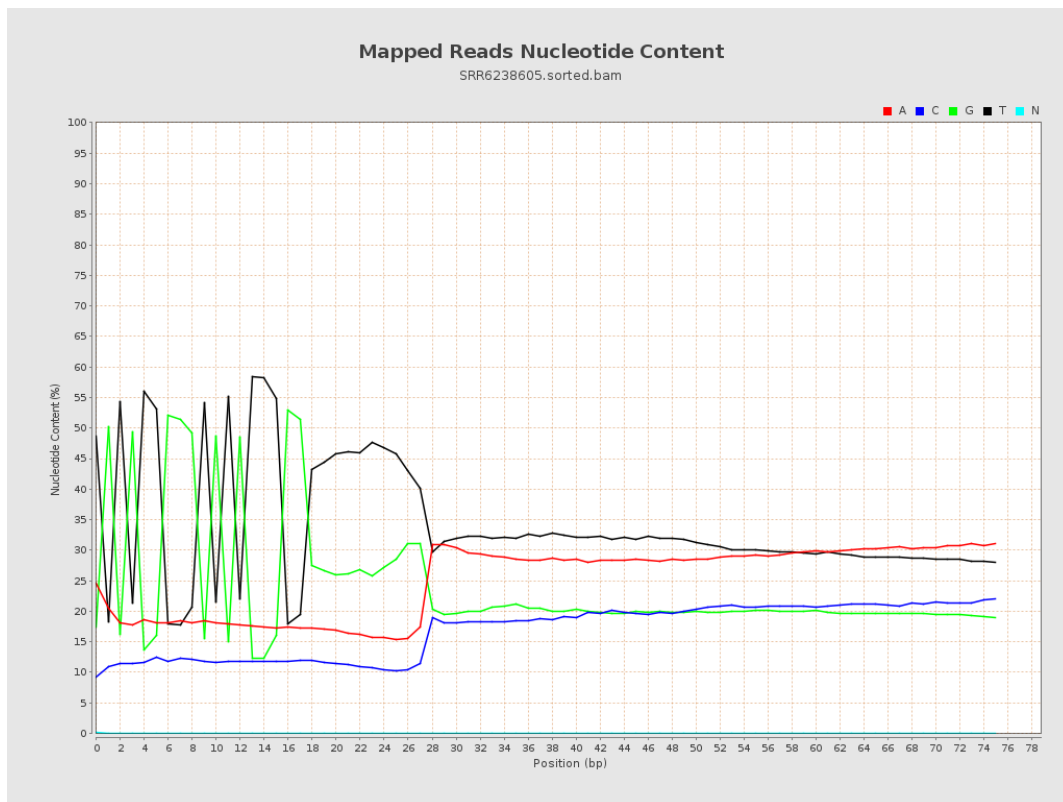
6. Results : Genome Fraction Coverage



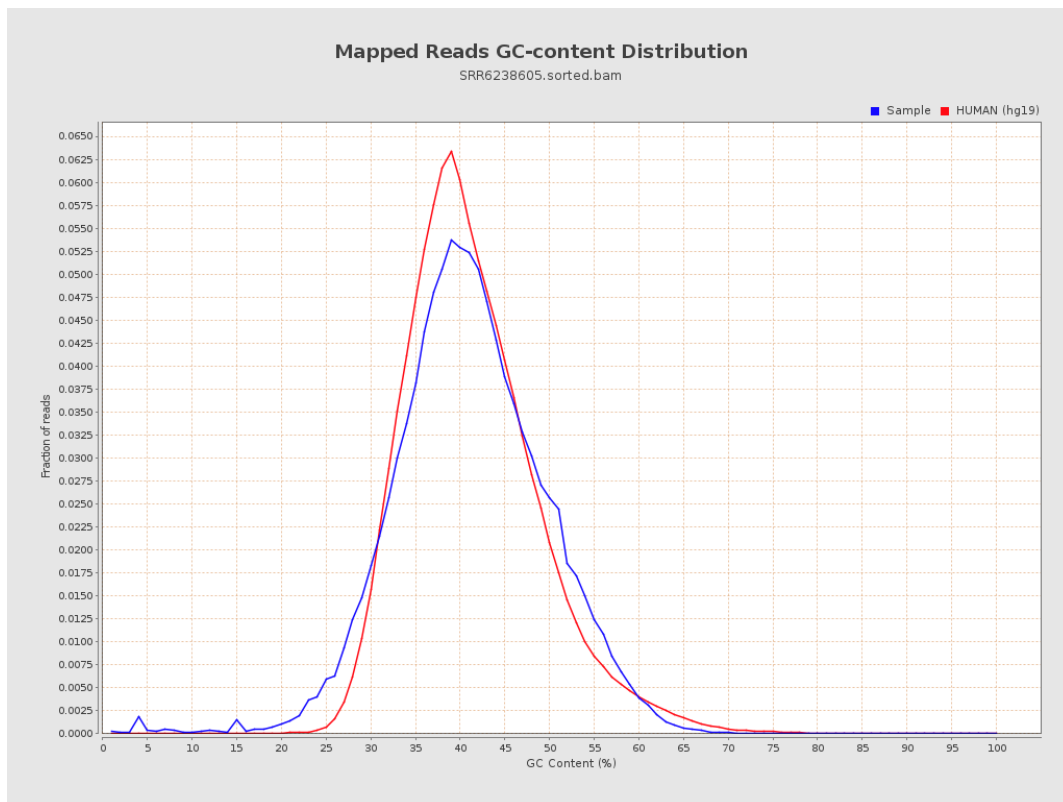
7. Results : Duplication Rate Histogram



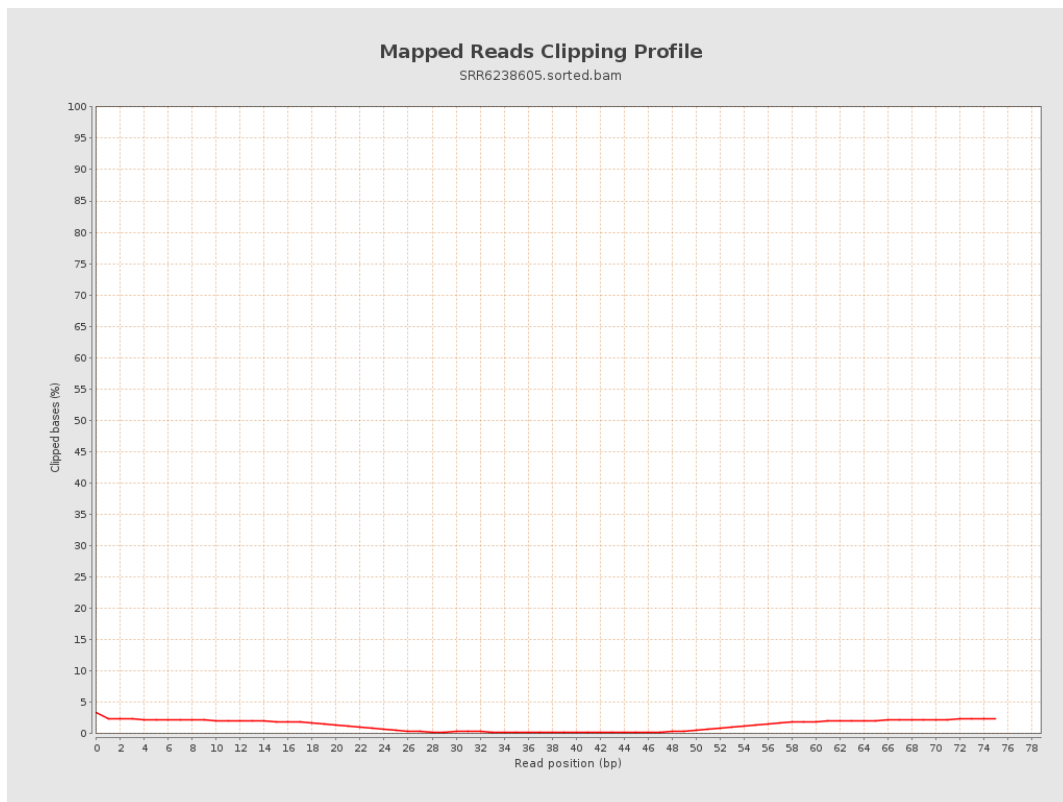
8. Results : Mapped Reads Nucleotide Content



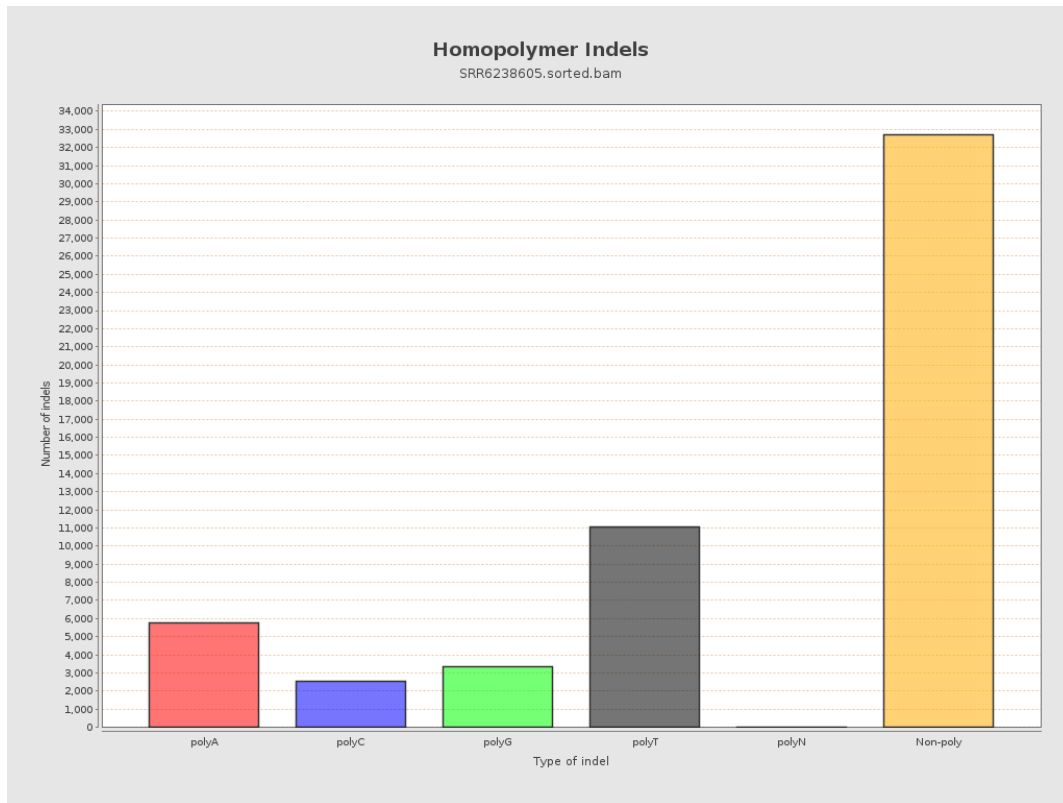
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

