

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:19:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238485.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_SRR6238485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238485.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:19:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,501,836
Mapped reads	2,875,739 / 82.12%
Unmapped reads	626,097 / 17.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,052 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	1,217,199 / 34.76%
Duplication rate	22.18%
Clipped reads	1,887,414 / 53.9%

2.2. ACGT Content

Number/percentage of A's	43,619,919 / 24.85%
Number/percentage of C's	29,836,289 / 16.99%
Number/percentage of T's	60,571,021 / 34.5%
Number/percentage of G's	41,534,130 / 23.66%
Number/percentage of N's	3,911 / 0%
GC Percentage	40.65%

2.3. Coverage

Mean	0.0567

Standard Deviation	1.1522
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2.4. Mapping Quality

Mean Mapping Quality	35.96
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2.5. Mismatches and indels

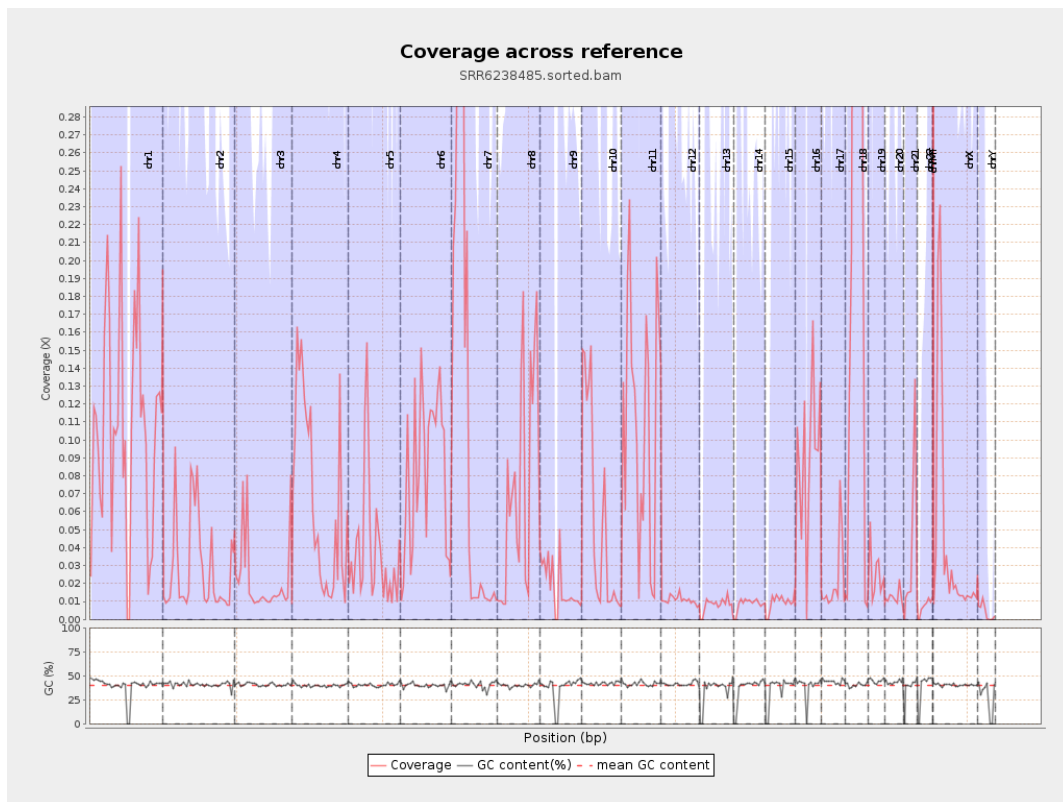
General error rate	0.58%
Mismatches	994,466
Insertions	10,617
Mapped reads with at least one insertion	0.37%
Deletions	47,395
Mapped reads with at least one deletion	1.64%
Homopolymer indels	41.36%

2.6. Chromosome stats

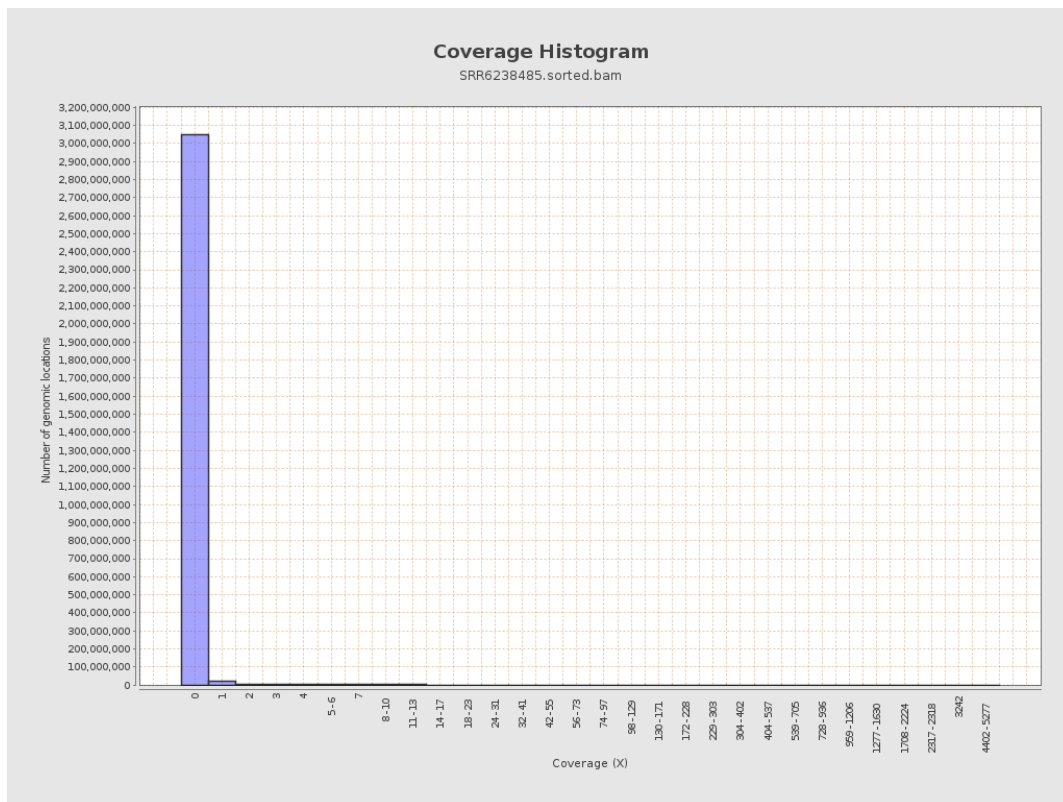
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26159386	0.105	1.3197
chr2	243199373	6913926	0.0284	2.3646
chr3	198022430	4453807	0.0225	0.4399
chr4	191154276	12768173	0.0668	0.746
chr5	180915260	6833185	0.0378	0.5519
chr6	171115067	14272391	0.0834	1.114
chr7	159138663	17777682	0.1117	1.1122

chr8	146364022	11245617	0.0768	1.3112
chr9	141213431	2543995	0.018	0.5212
chr10	135534747	7523391	0.0555	0.6932
chr11	135006516	14333142	0.1062	1.0968
chr12	133851895	1450329	0.0108	0.3271
chr13	115169878	946398	0.0082	0.624
chr14	107349540	919644	0.0086	0.3633
chr15	102531392	937872	0.0091	0.5261
chr16	90354753	8009199	0.0886	0.9177
chr17	81195210	1827308	0.0225	0.4496
chr18	78077248	25094815	0.3214	3.3213
chr19	59128983	1491383	0.0252	0.6827
chr20	63025520	804897	0.0128	0.2865
chr21	48129895	1975729	0.041	0.5905
chr22	51304566	370474	0.0072	0.2292
chrMT	16571	29571	1.7845	3.8423
chrX	155270560	6710748	0.0432	0.6385
chrY	59373566	250817	0.0042	0.3807

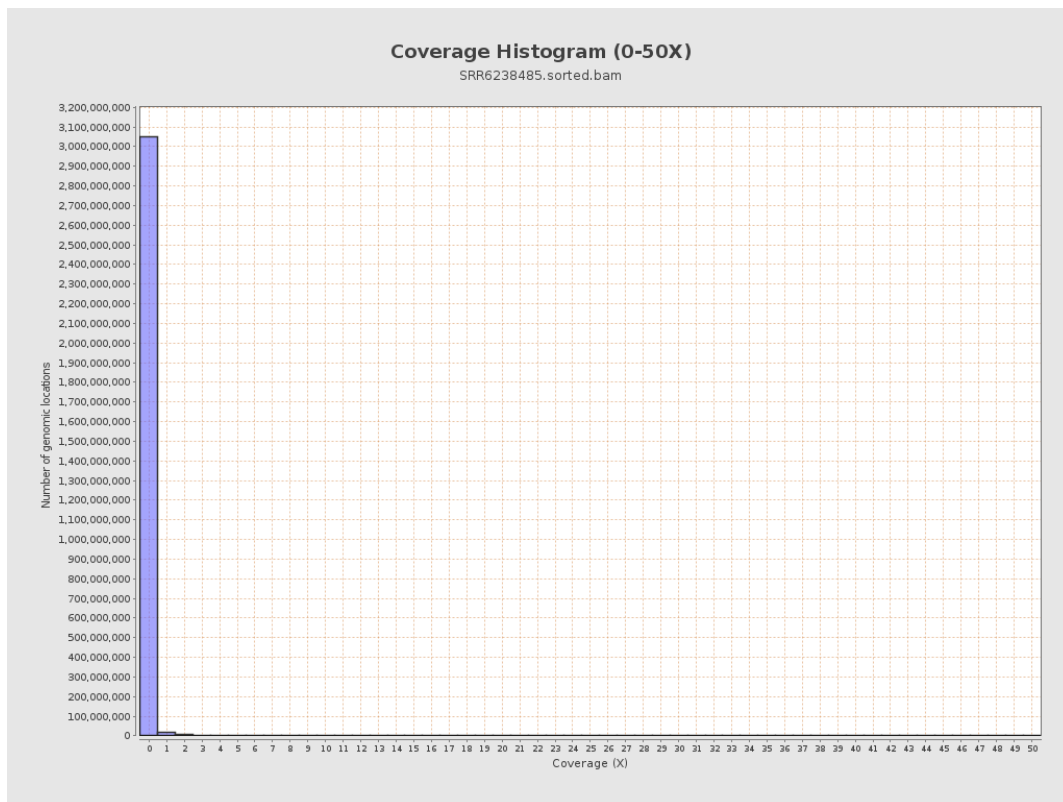
3. Results : Coverage across reference



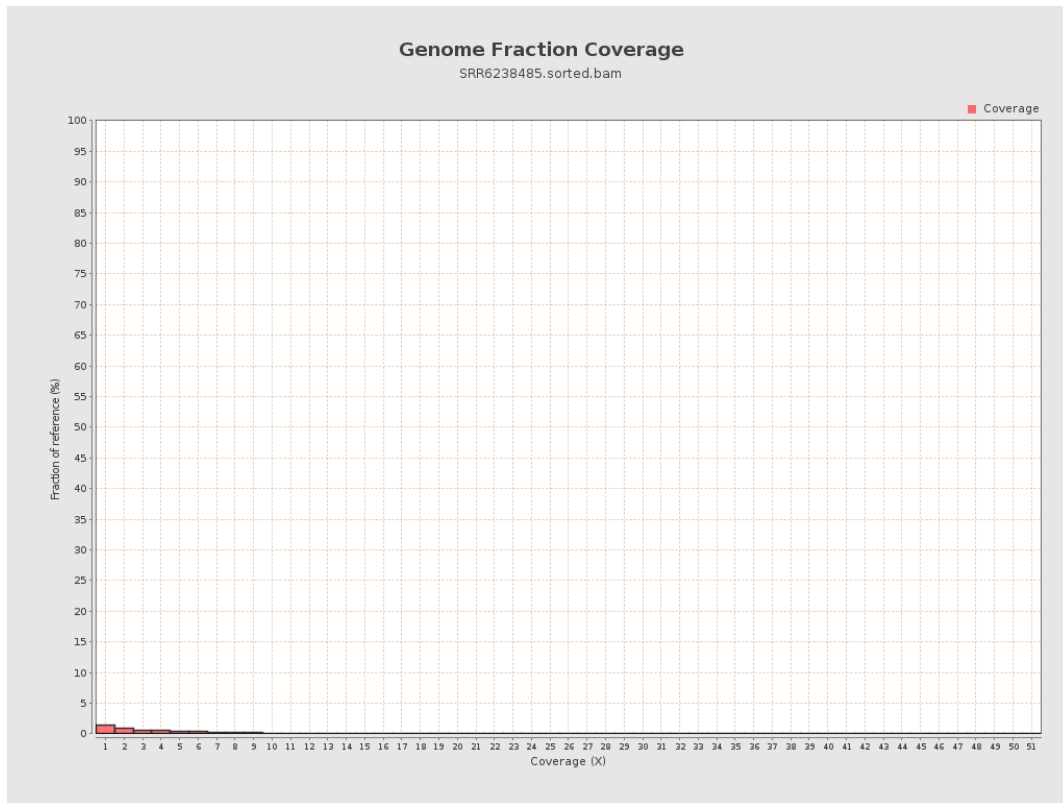
4. Results : Coverage Histogram



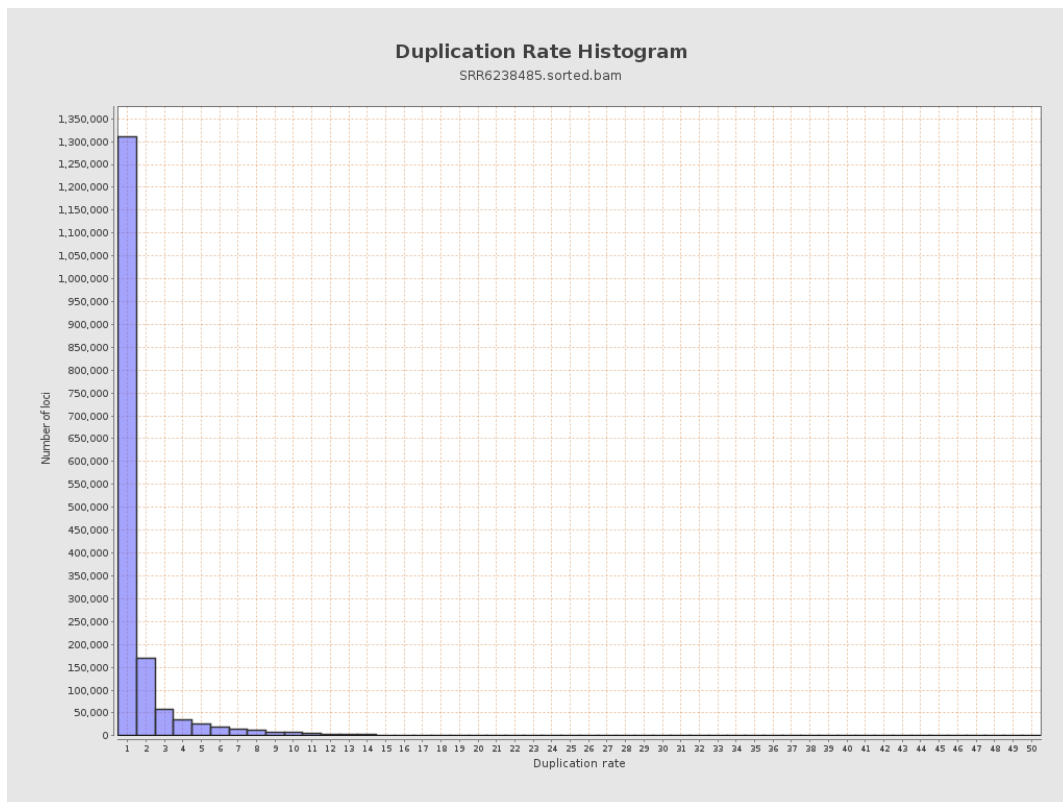
5. Results : Coverage Histogram (0-50X)



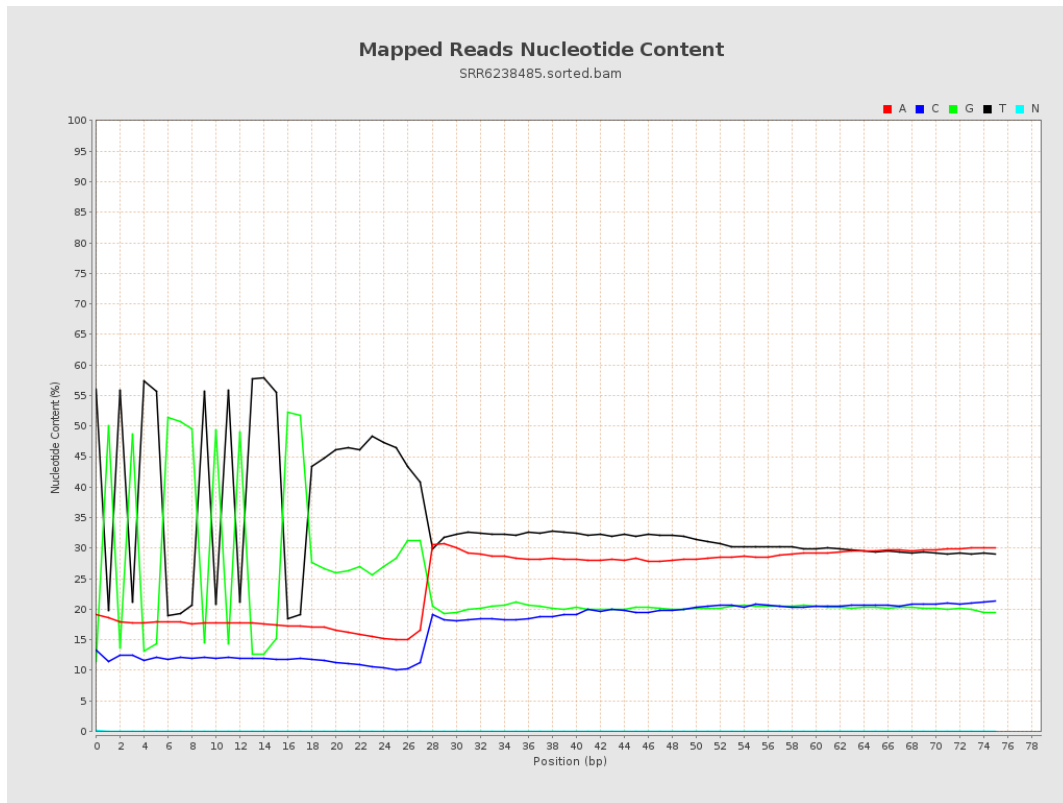
6. Results : Genome Fraction Coverage



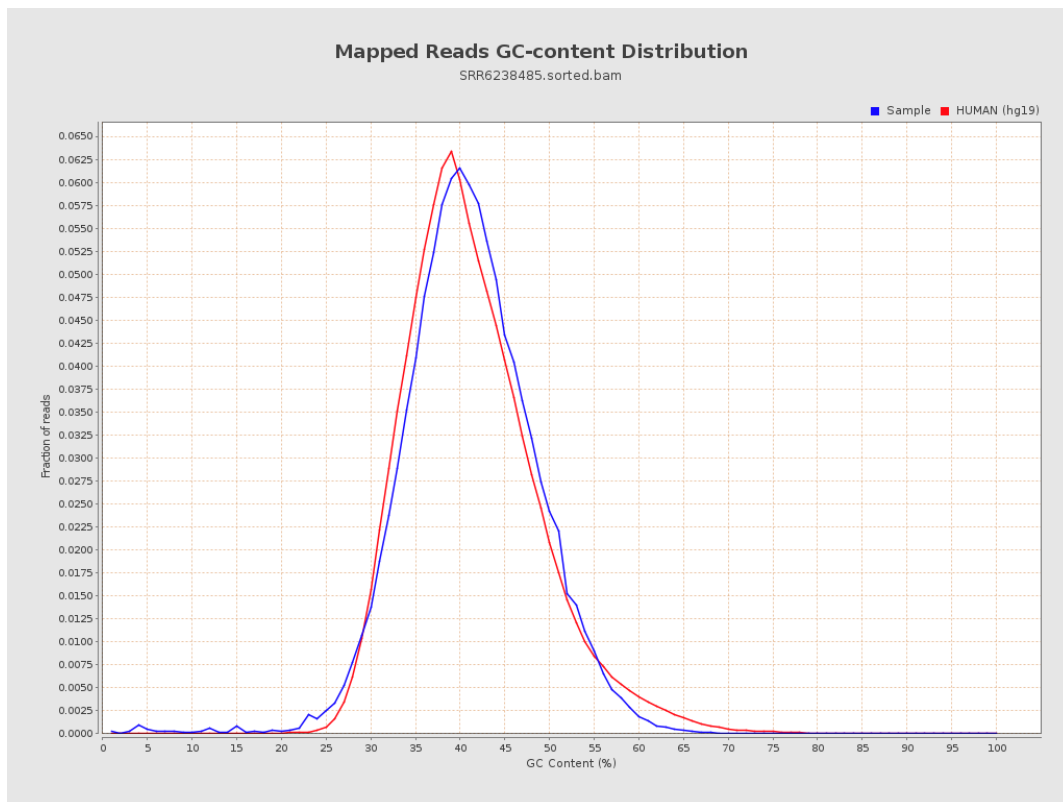
7. Results : Duplication Rate Histogram



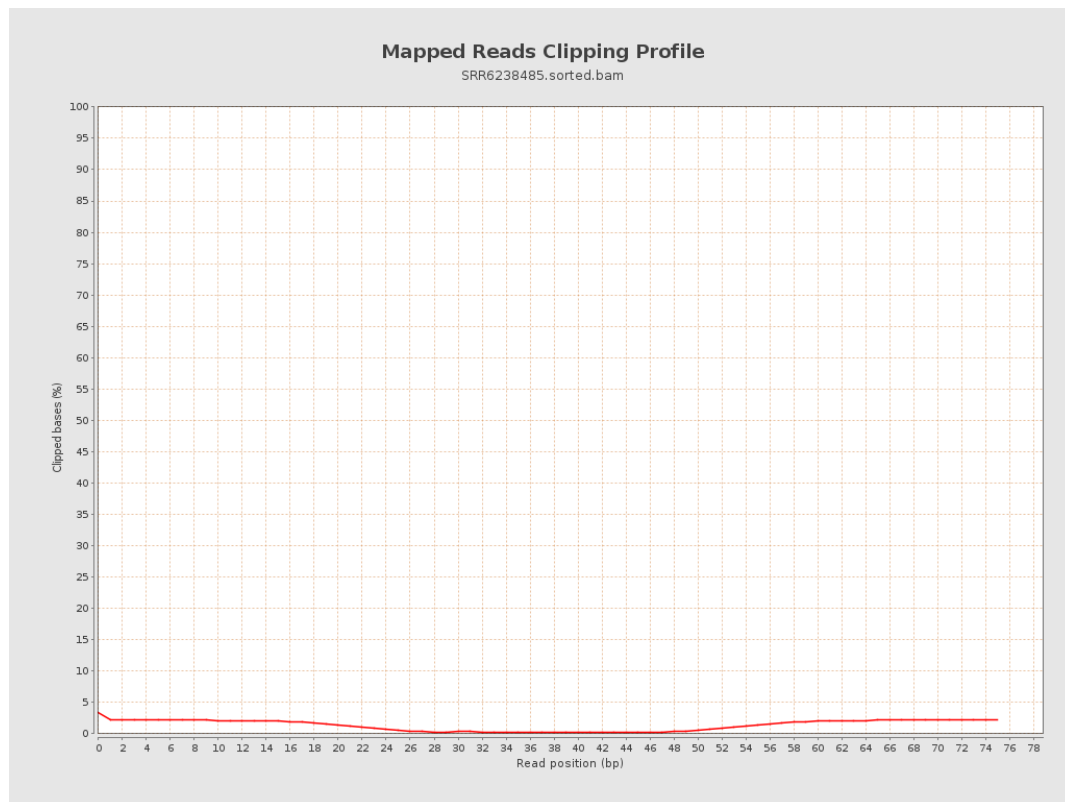
8. Results : Mapped Reads Nucleotide Content



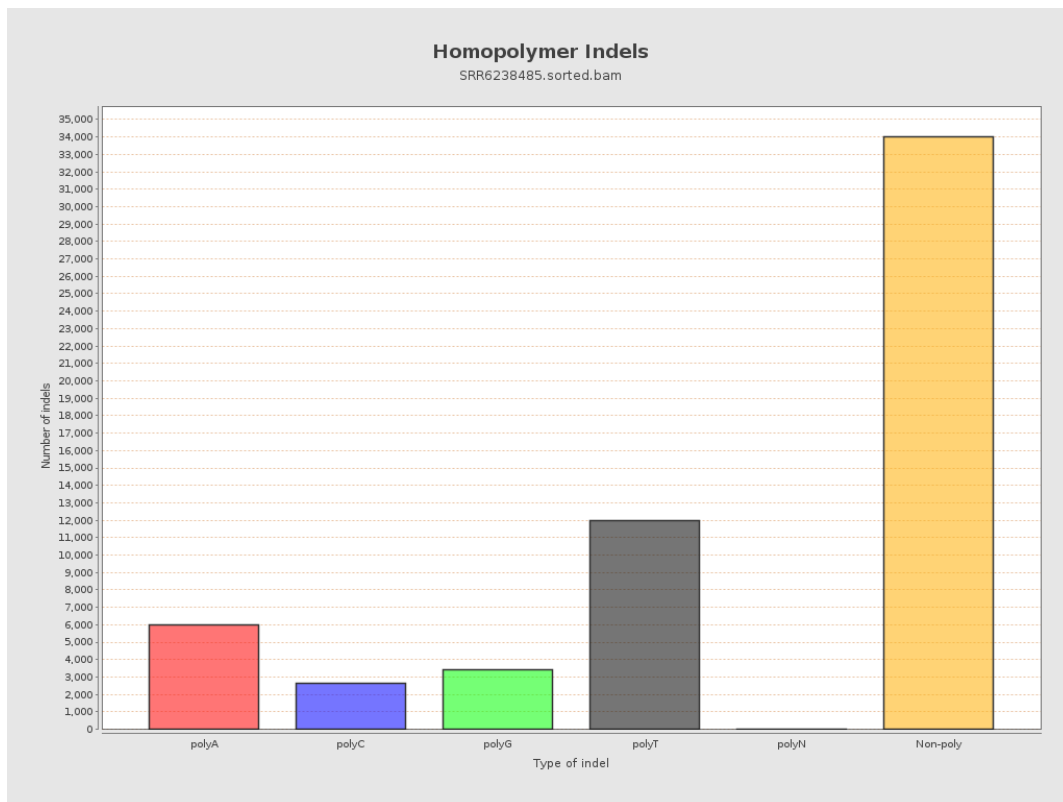
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

