

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:10:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524287.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_SRR10524287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524287.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:10:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,916,732
Mapped reads	1,770,755 / 92.38%
Unmapped reads	145,977 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,394 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	84,110 / 4.39%
Duplication rate	3.53%
Clipped reads	1,775,305 / 92.62%

2.2. ACGT Content

Number/percentage of A's	25,983,912 / 25.08%
Number/percentage of C's	18,350,742 / 17.71%
Number/percentage of T's	32,522,752 / 31.39%
Number/percentage of G's	26,745,393 / 25.81%
Number/percentage of N's	13,339 / 0.01%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.3399
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2.4. Mapping Quality

Mean Mapping Quality	46.3
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2.5. Mismatches and indels

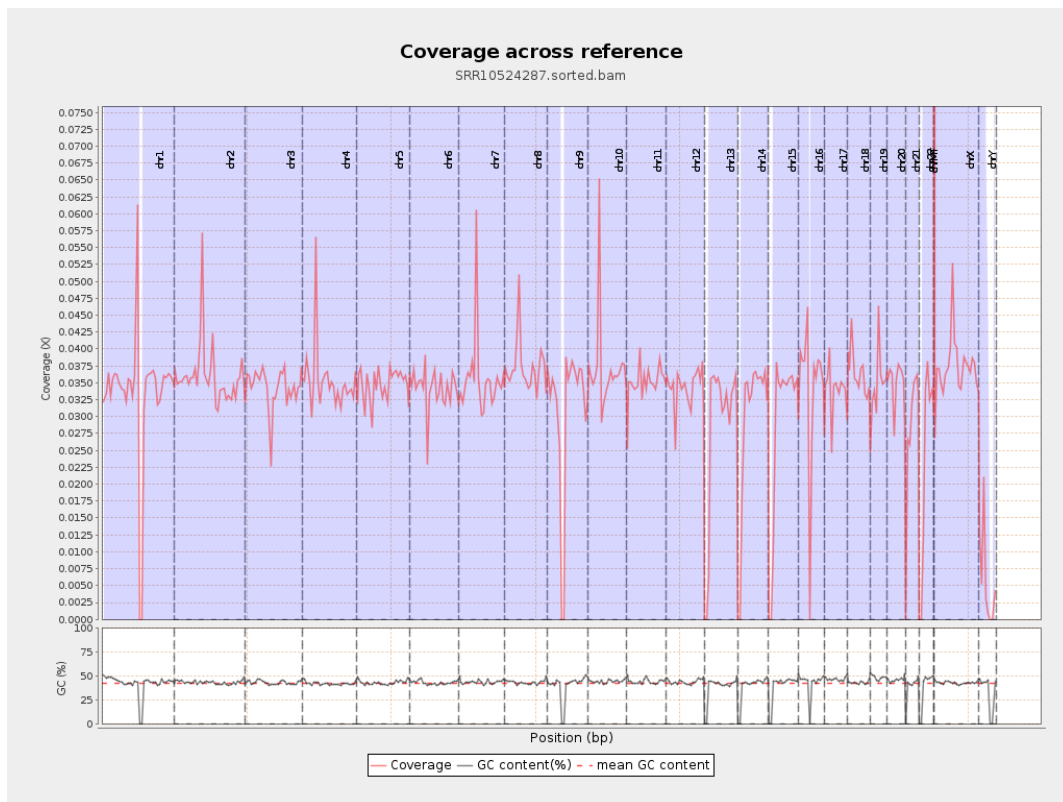
General error rate	0.5%
Mismatches	510,874
Insertions	6,072
Mapped reads with at least one insertion	0.34%
Deletions	19,450
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.9%

2.6. Chromosome stats

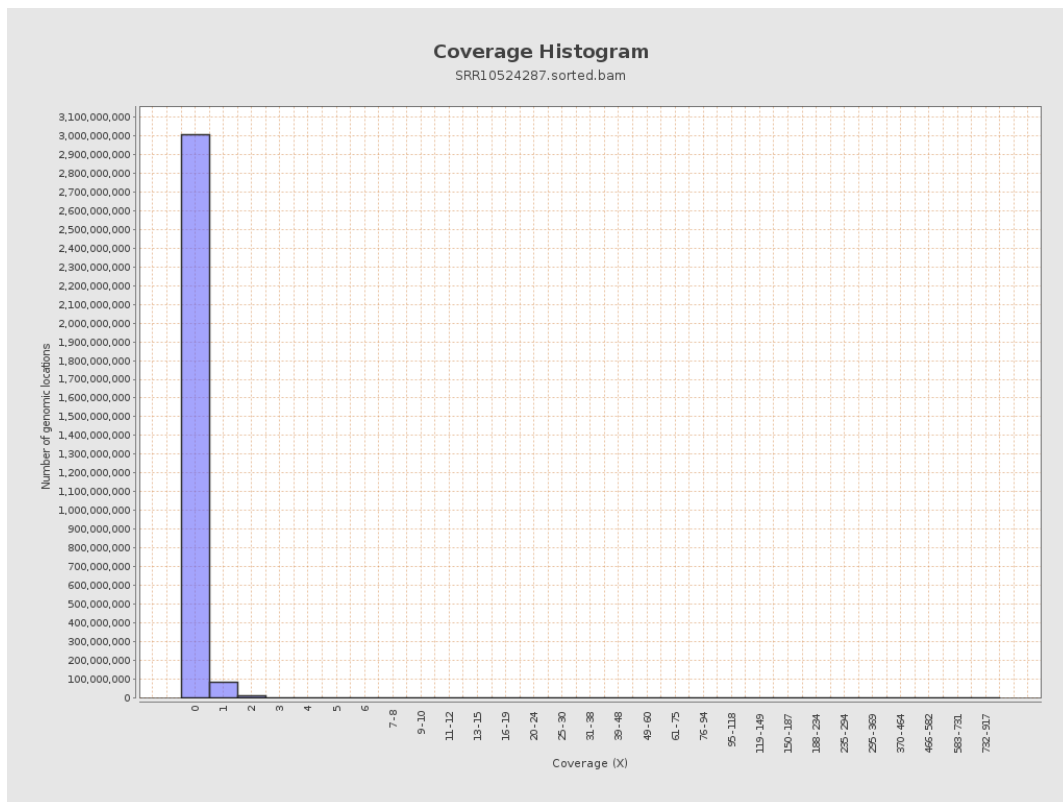
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8327488	0.0334	0.7058
chr2	243199373	8748264	0.036	0.3506
chr3	198022430	6777405	0.0342	0.2033
chr4	191154276	6739587	0.0353	0.2375
chr5	180915260	6310028	0.0349	0.2077
chr6	171115067	5850731	0.0342	0.2232
chr7	159138663	5675934	0.0357	0.4507

chr8	146364022	5463971	0.0373	0.343
chr9	141213431	4360291	0.0309	0.2898
chr10	135534747	5031183	0.0371	0.316
chr11	135006516	4767879	0.0353	0.2899
chr12	133851895	4592299	0.0343	0.2114
chr13	115169878	3247377	0.0282	0.1845
chr14	107349540	3151961	0.0294	0.2018
chr15	102531392	2922905	0.0285	0.185
chr16	90354753	3042014	0.0337	0.2191
chr17	81195210	2757830	0.034	0.2229
chr18	78077248	2840974	0.0364	0.5812
chr19	59128983	2078334	0.0351	0.4487
chr20	63025520	2198826	0.0349	0.2102
chr21	48129895	1370868	0.0285	0.2149
chr22	51304566	1230760	0.024	0.17
chrMT	16571	6943	0.419	0.7196
chrX	155270560	5818164	0.0375	0.2466
chrY	59373566	335447	0.0056	0.1626

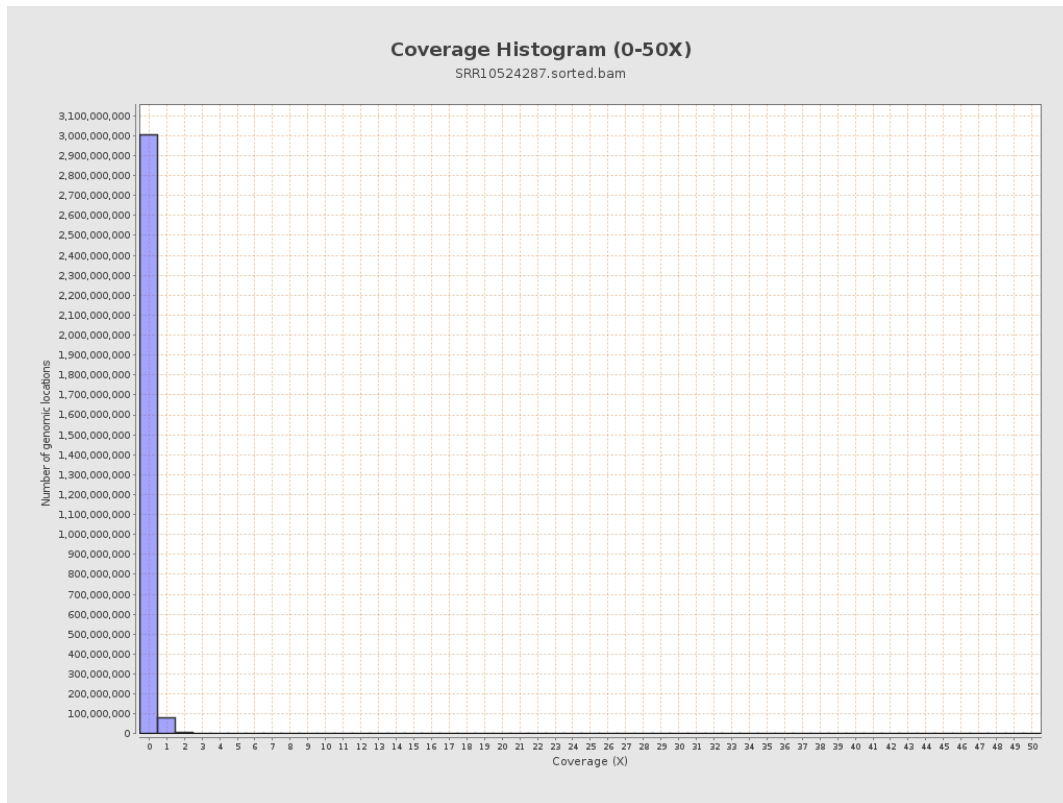
3. Results : Coverage across reference



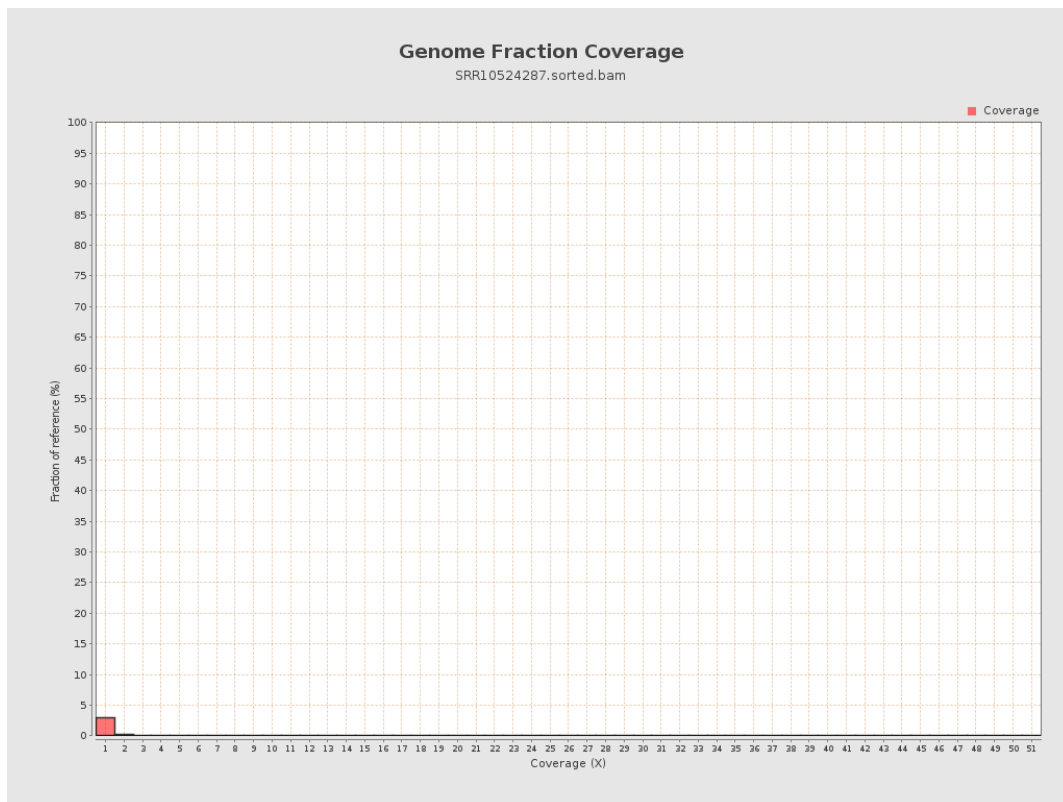
4. Results : Coverage Histogram



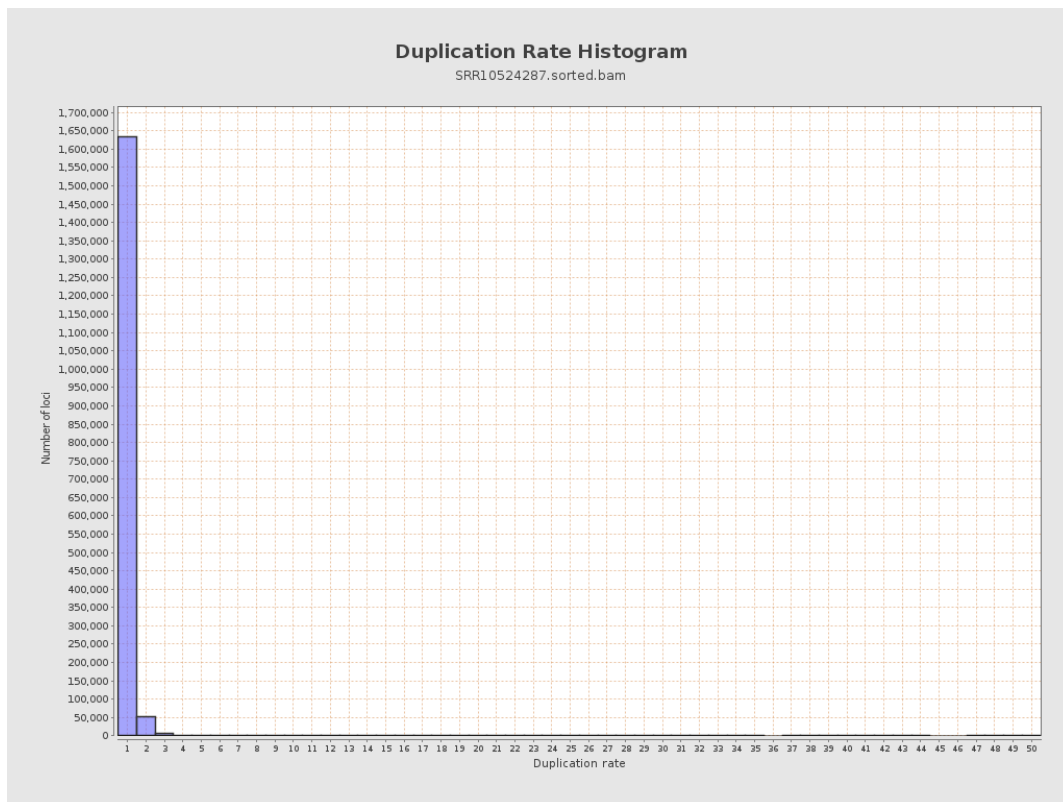
5. Results : Coverage Histogram (0-50X)



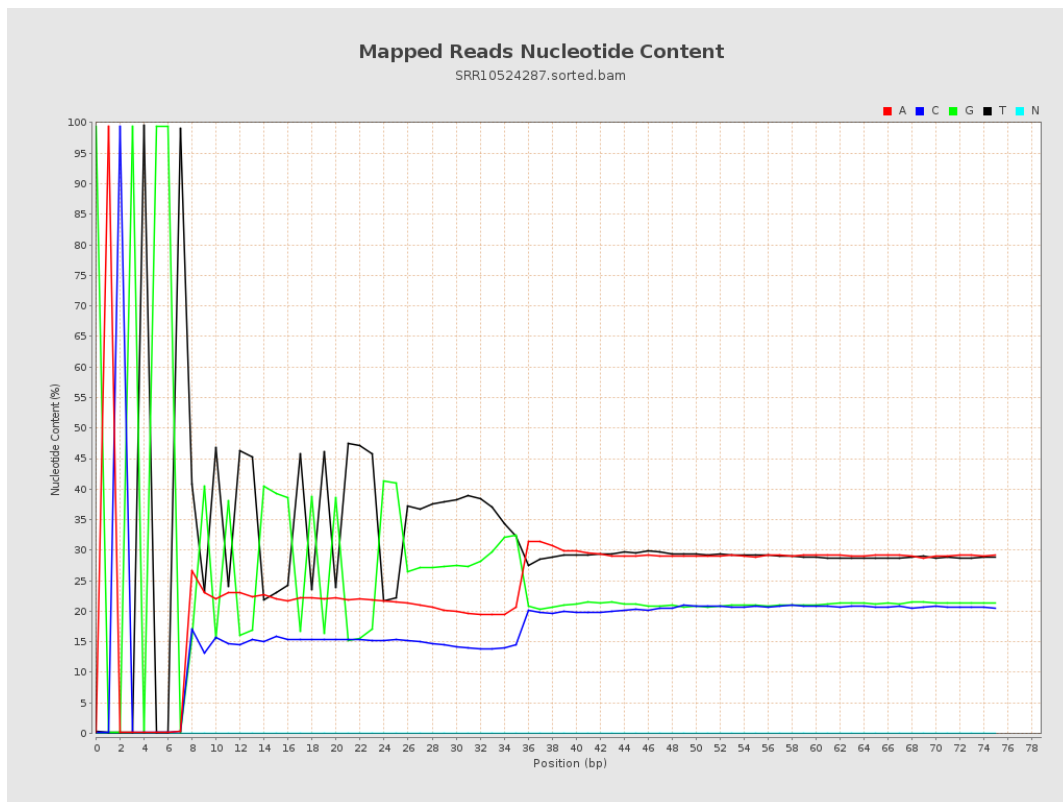
6. Results : Genome Fraction Coverage



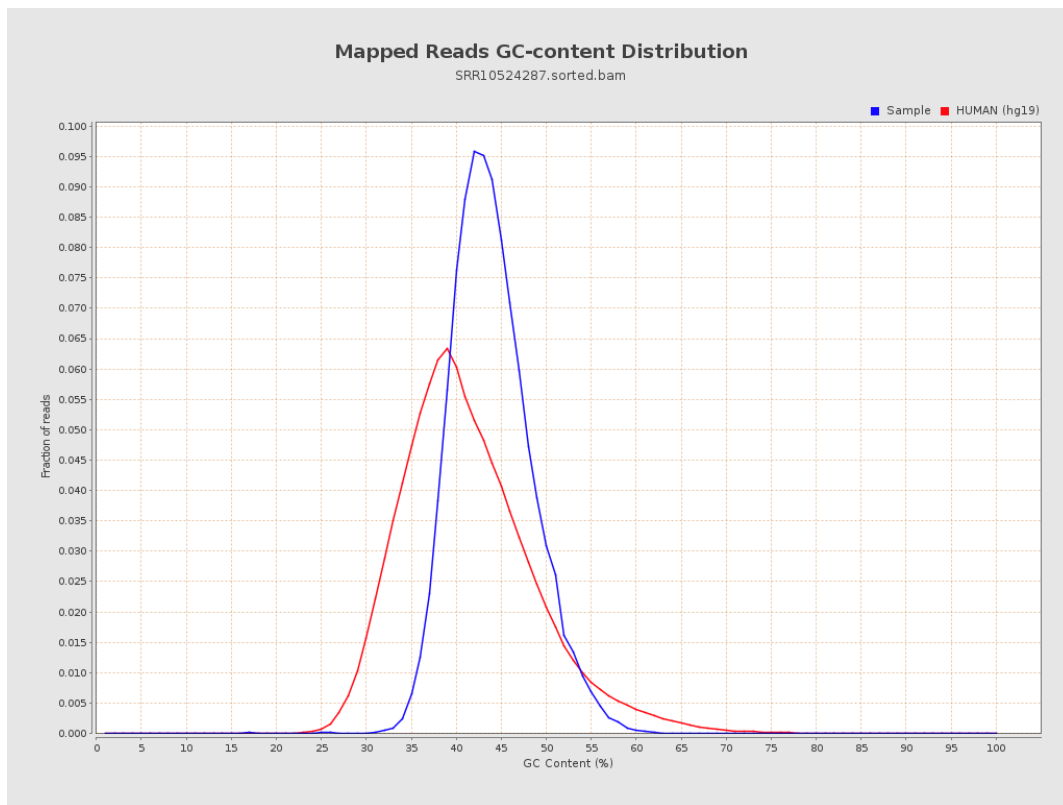
7. Results : Duplication Rate Histogram



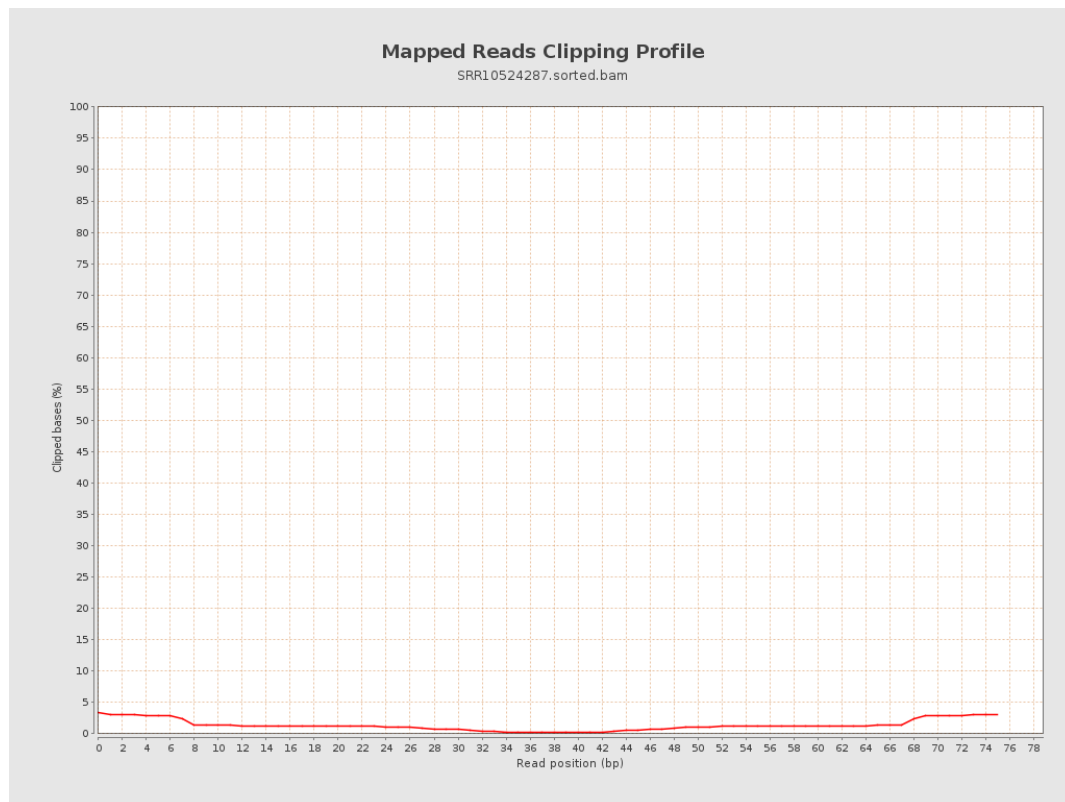
8. Results : Mapped Reads Nucleotide Content



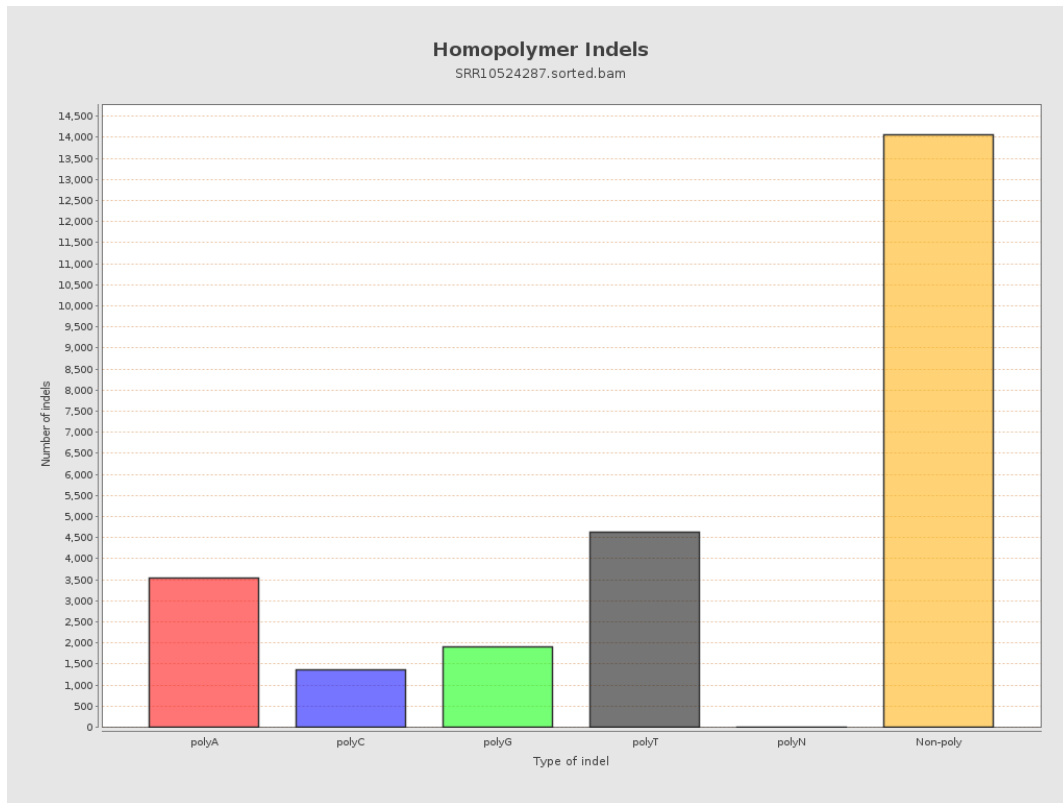
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

