

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:59:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549085.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_SRR1549085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:59:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,981,392
Mapped reads	6,973,326 / 87.37%
Unmapped reads	1,008,066 / 12.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	217,820 / 2.73%
Duplication rate	2.12%
Clipped reads	340,154 / 4.26%

2.2. ACGT Content

Number/percentage of A's	83,025,429 / 29.98%
Number/percentage of C's	55,806,418 / 20.15%
Number/percentage of T's	83,916,815 / 30.31%
Number/percentage of G's	54,090,219 / 19.53%
Number/percentage of N's	66,689 / 0.02%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0895
Standard Deviation	0.6577

2.4. Mapping Quality

Mean Mapping Quality	44.79
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2.5. Mismatches and indels

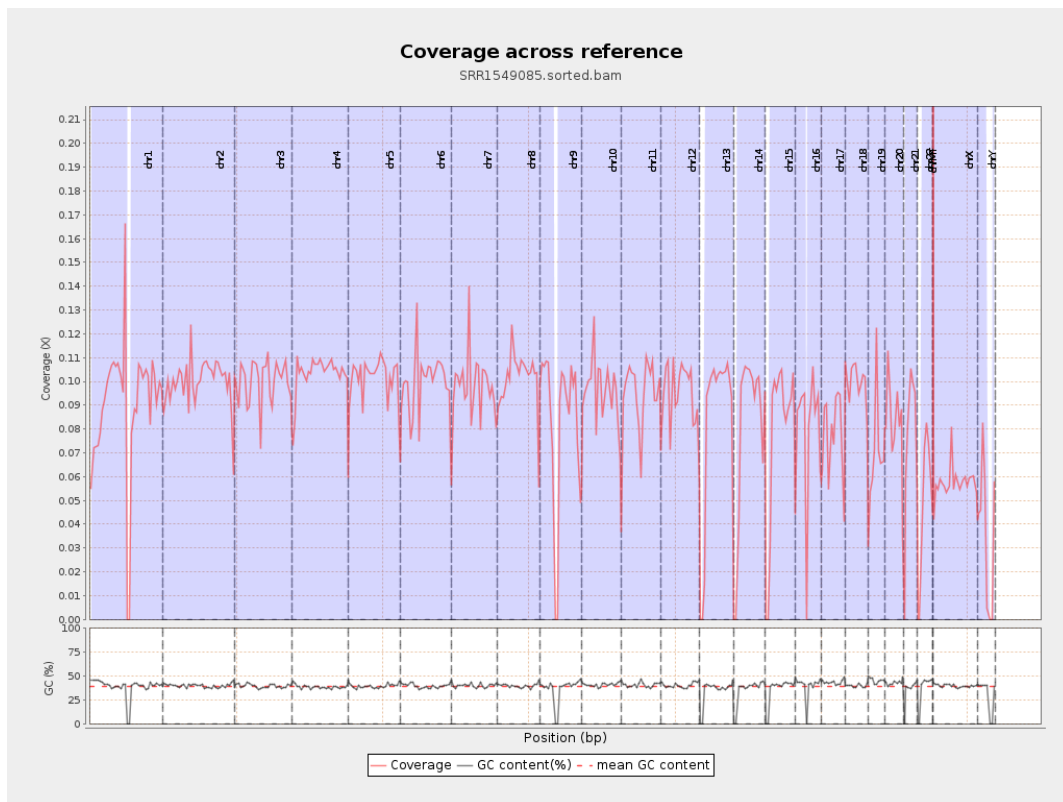
General error rate	0.4%
Mismatches	1,089,731
Insertions	6,455
Mapped reads with at least one insertion	0.09%
Deletions	20,874
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.75%

2.6. Chromosome stats

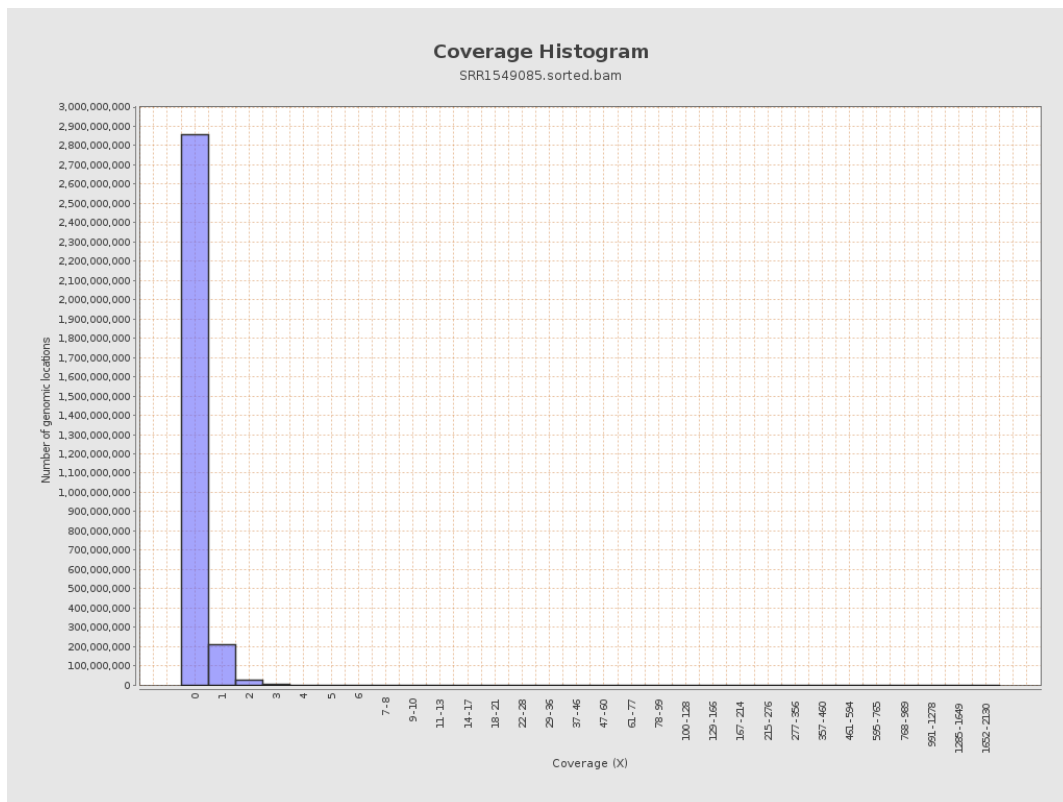
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22463006	0.0901	1.5134
chr2	243199373	24352755	0.1001	0.5132
chr3	198022430	19833015	0.1002	0.3609
chr4	191154276	19784482	0.1035	0.3667
chr5	180915260	18234392	0.1008	0.3699
chr6	171115067	17143742	0.1002	0.4829
chr7	159138663	15503743	0.0974	0.6975
chr8	146364022	14839616	0.1014	0.9513

chr9	141213431	11776632	0.0834	0.4906
chr10	135534747	13025264	0.0961	0.5346
chr11	135006516	12858385	0.0952	0.5282
chr12	133851895	12754318	0.0953	0.3607
chr13	115169878	9624678	0.0836	0.3175
chr14	107349540	8688056	0.0809	0.3648
chr15	102531392	7891834	0.077	0.3066
chr16	90354753	7111439	0.0787	0.3817
chr17	81195210	6370014	0.0785	0.357
chr18	78077248	7812993	0.1001	0.9352
chr19	59128983	4195115	0.0709	1.163
chr20	63025520	5362778	0.0851	0.3362
chr21	48129895	3677085	0.0764	0.3586
chr22	51304566	2526862	0.0493	0.2806
chrMT	16571	10836	0.6539	1.0965
chrX	155270560	8931188	0.0575	0.3495
chrY	59373566	2159510	0.0364	0.3234

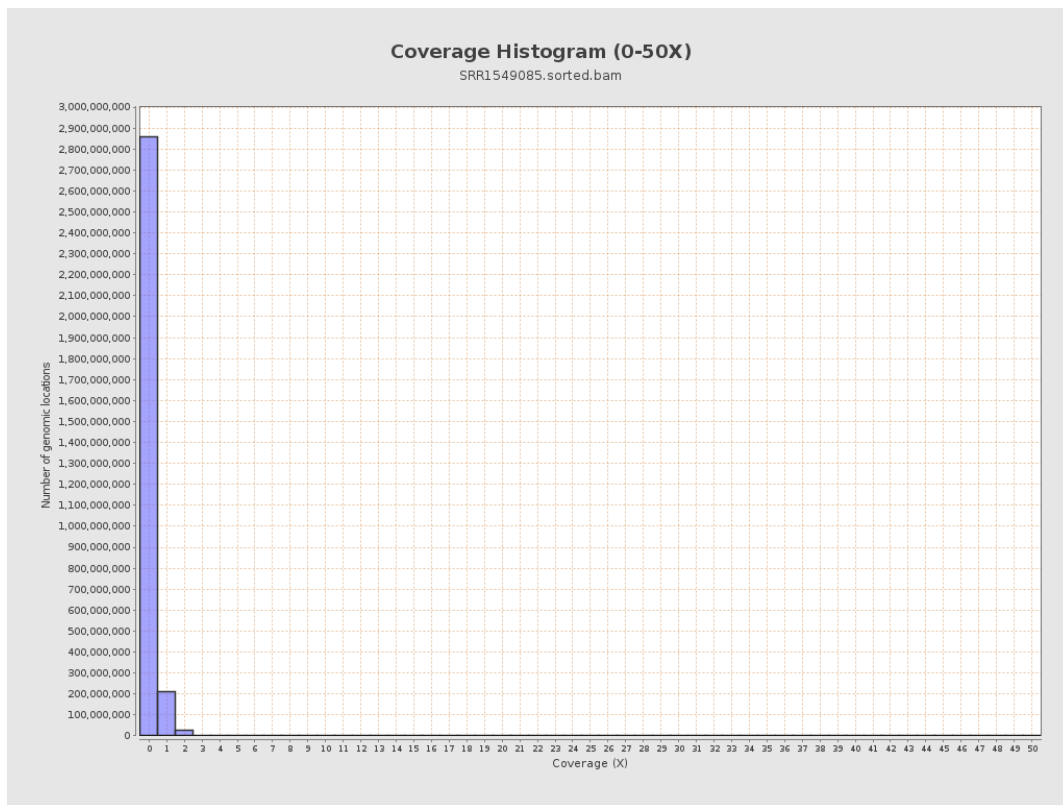
3. Results : Coverage across reference



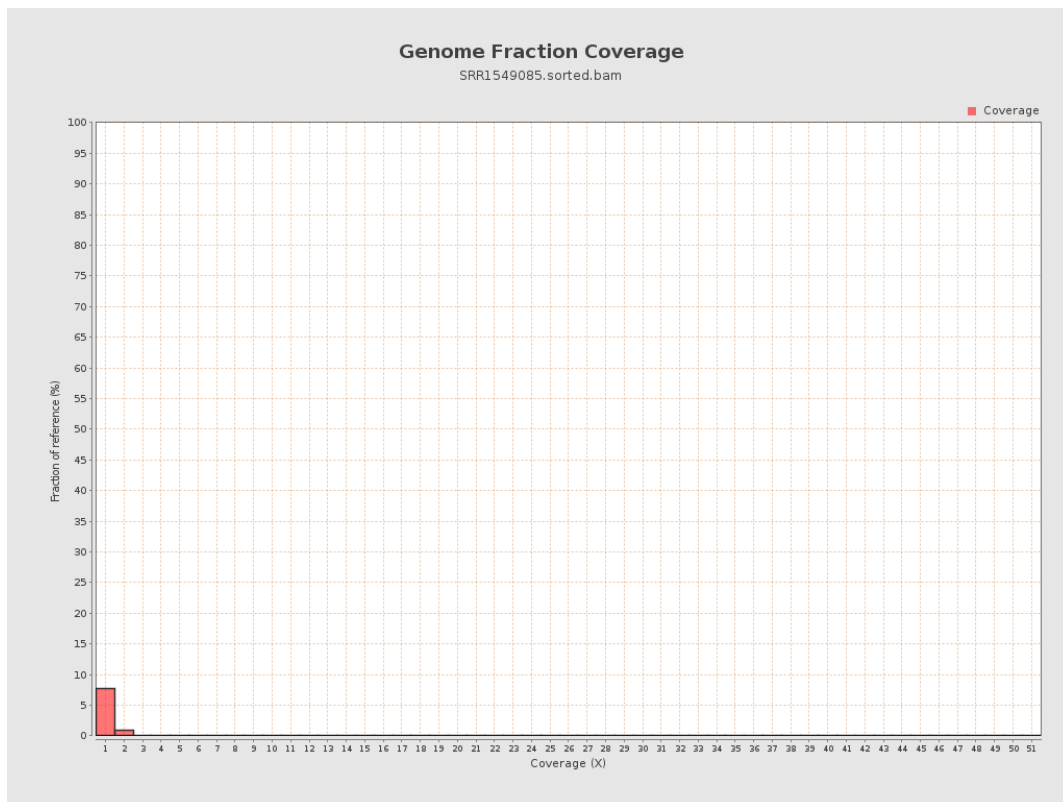
4. Results : Coverage Histogram



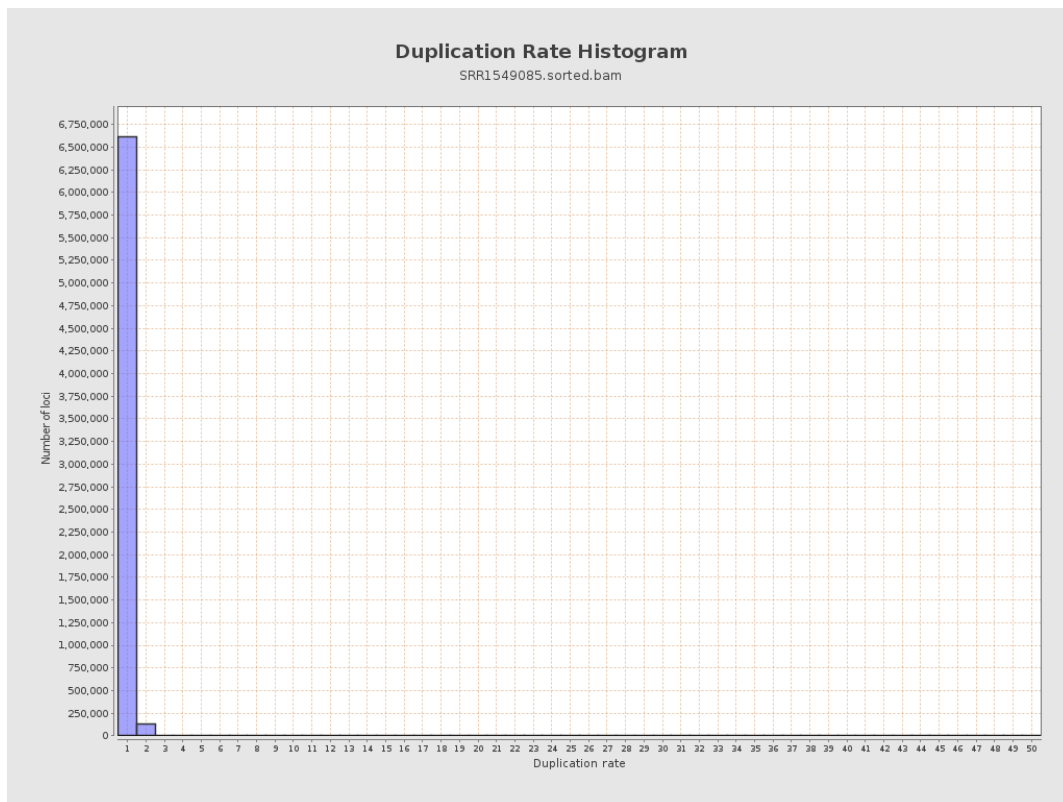
5. Results : Coverage Histogram (0-50X)



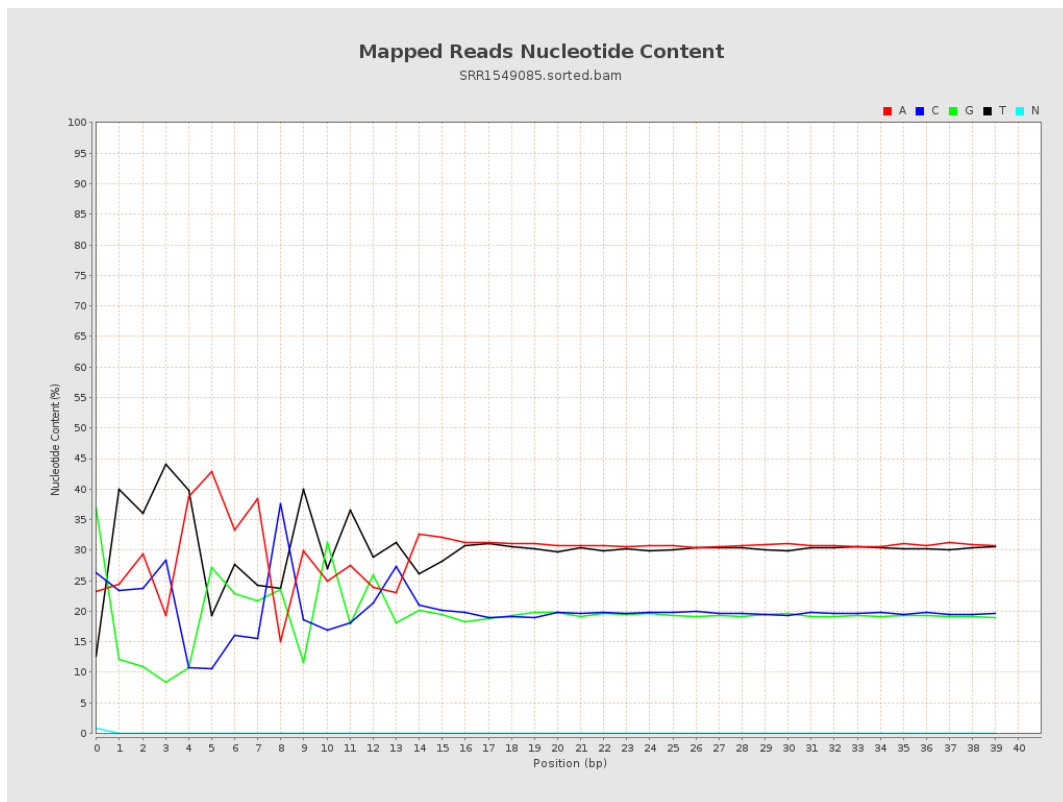
6. Results : Genome Fraction Coverage



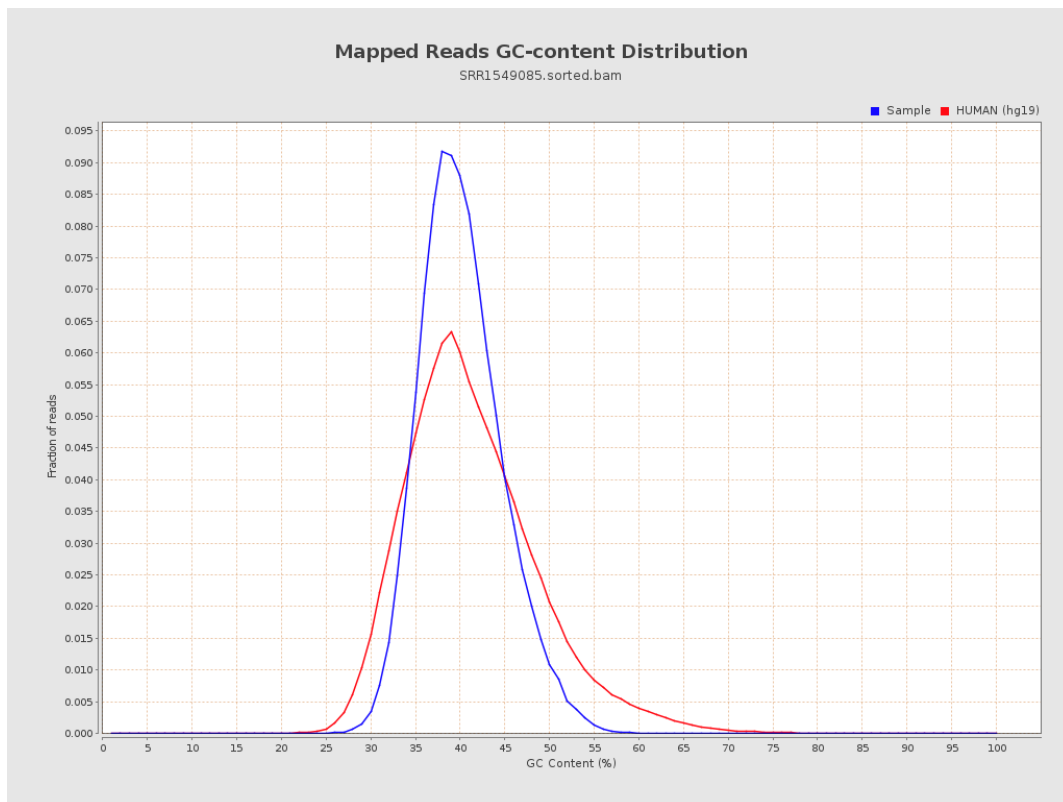
7. Results : Duplication Rate Histogram



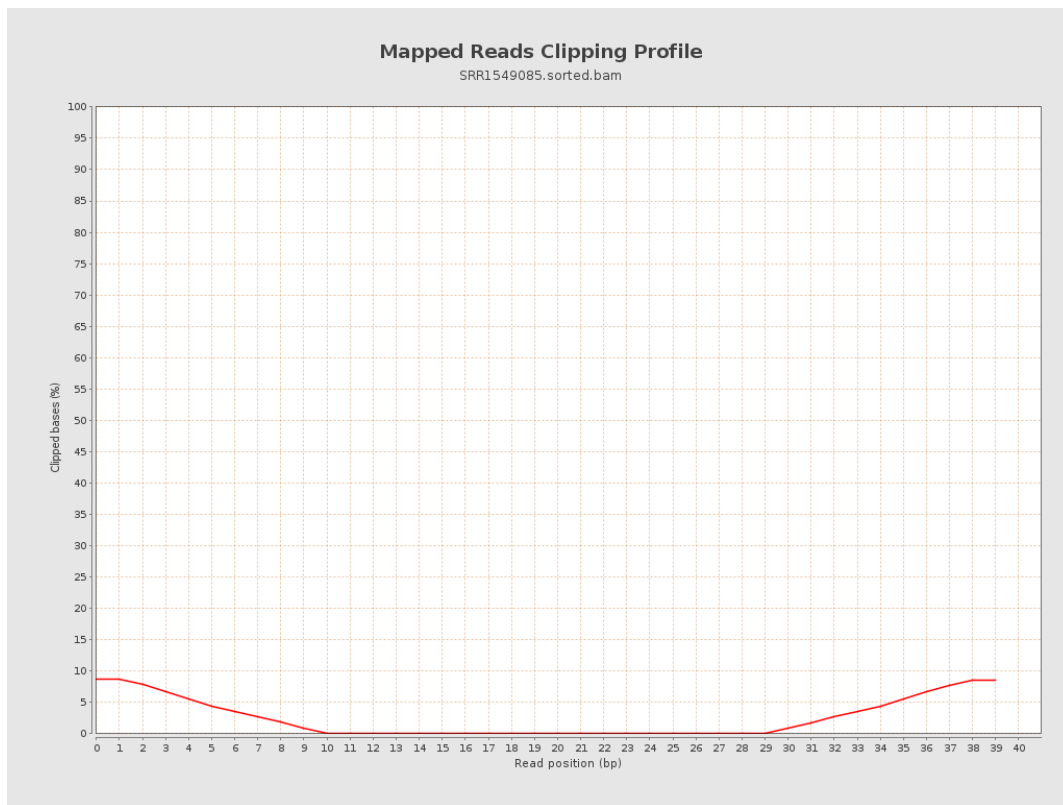
8. Results : Mapped Reads Nucleotide Content



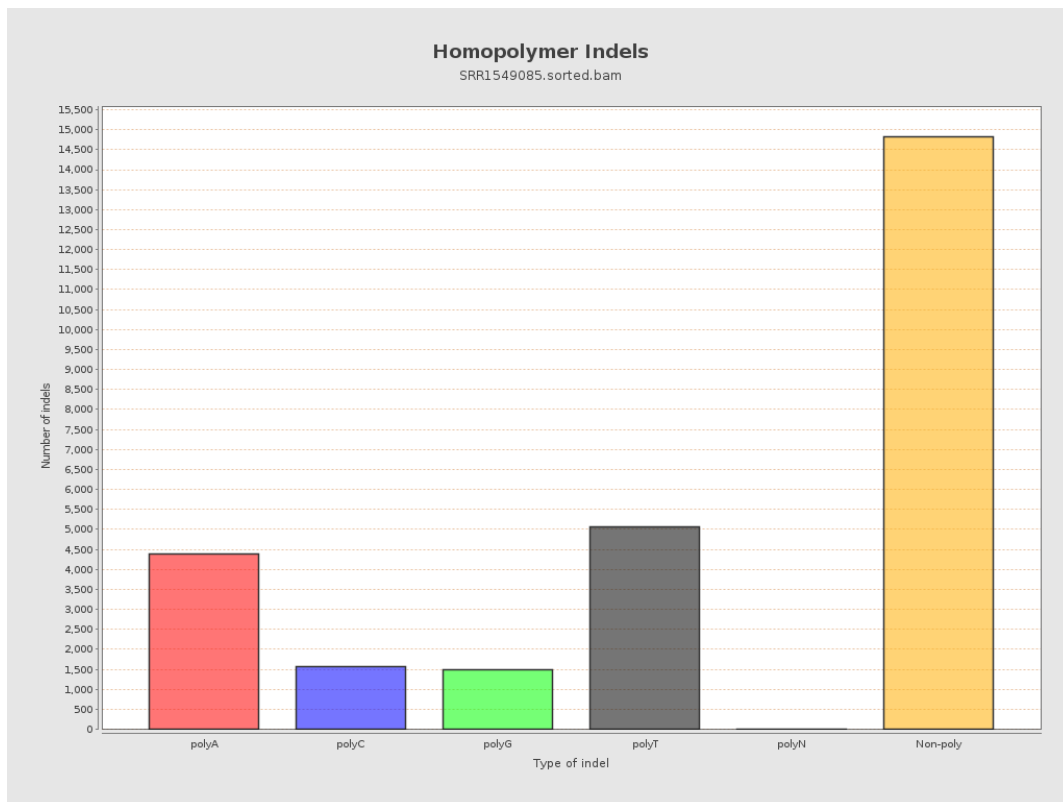
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

