

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:51:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548999.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_SRR1548999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548999.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:51:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,603,071
Mapped reads	7,422,075 / 86.27%
Unmapped reads	1,180,996 / 13.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	717,939 / 8.35%
Duplication rate	8.93%
Clipped reads	359,944 / 4.18%

2.2. ACGT Content

Number/percentage of A's	89,140,615 / 30.25%
Number/percentage of C's	57,929,102 / 19.66%
Number/percentage of T's	89,226,982 / 30.28%
Number/percentage of G's	58,401,149 / 19.82%
Number/percentage of N's	2,899 / 0%
GC Percentage	39.47%

2.3. Coverage

Mean	0.0952
Standard Deviation	0.8514

2.4. Mapping Quality

Mean Mapping Quality	44.88
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2.5. Mismatches and indels

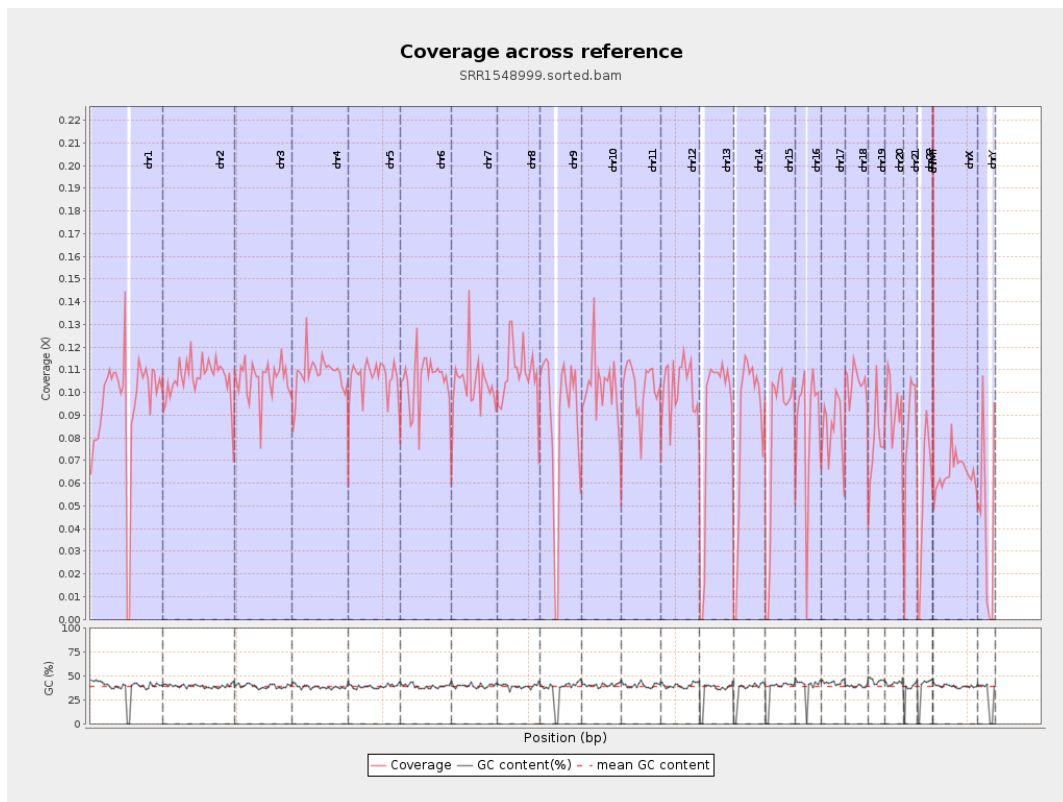
General error rate	0.29%
Mismatches	831,833
Insertions	8,509
Mapped reads with at least one insertion	0.11%
Deletions	24,797
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.2%

2.6. Chromosome stats

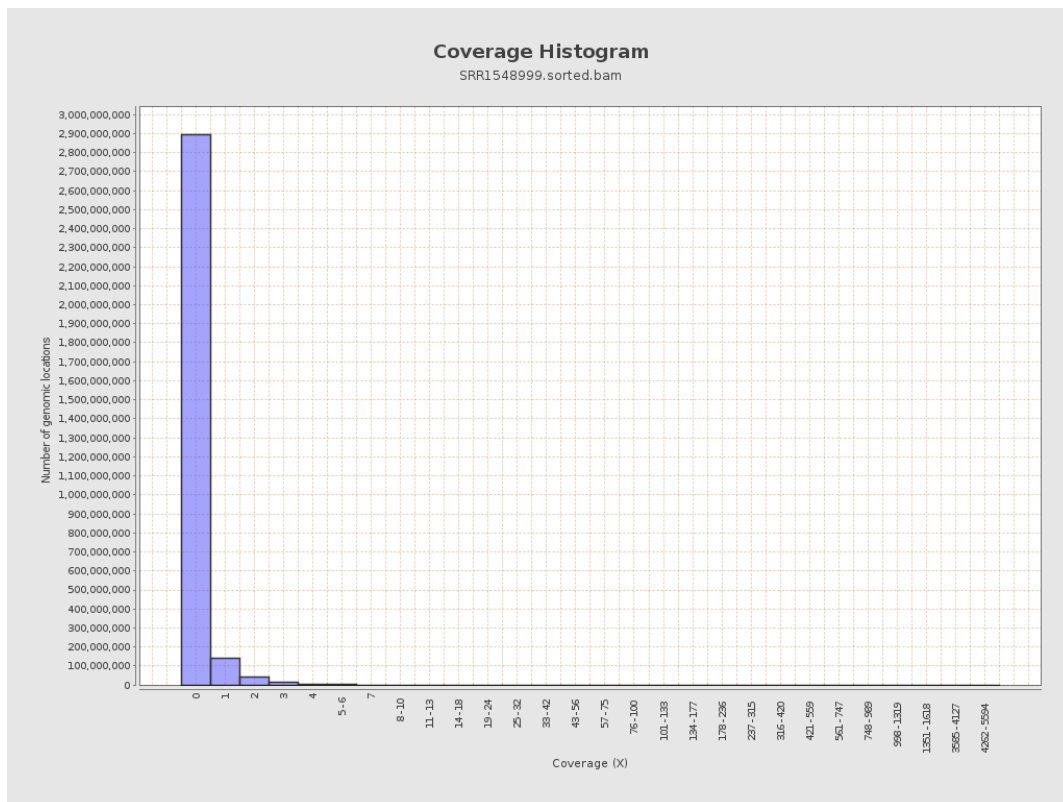
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23559639	0.0945	1.1754
chr2	243199373	25852298	0.1063	0.5625
chr3	198022430	20977473	0.1059	0.4471
chr4	191154276	20728620	0.1084	0.4907
chr5	180915260	19148410	0.1058	0.4499
chr6	171115067	18042477	0.1054	0.4956
chr7	159138663	16485873	0.1036	0.82
chr8	146364022	15792113	0.1079	2.7627

chr9	141213431	12542022	0.0888	0.51
chr10	135534747	13857209	0.1022	0.606
chr11	135006516	13726513	0.1017	0.5401
chr12	133851895	13665171	0.1021	0.4528
chr13	115169878	10141608	0.0881	0.4051
chr14	107349540	9239725	0.0861	0.4547
chr15	102531392	8352473	0.0815	0.3846
chr16	90354753	7592693	0.084	0.4243
chr17	81195210	6926967	0.0853	0.4163
chr18	78077248	8171254	0.1047	0.9906
chr19	59128983	4643881	0.0785	0.8722
chr20	63025520	5840467	0.0927	0.4367
chr21	48129895	3911327	0.0813	0.4558
chr22	51304566	2813150	0.0548	0.3414
chrMT	16571	6448	0.3891	0.7902
chrX	155270560	9977426	0.0643	0.4176
chrY	59373566	2737341	0.0461	0.5343

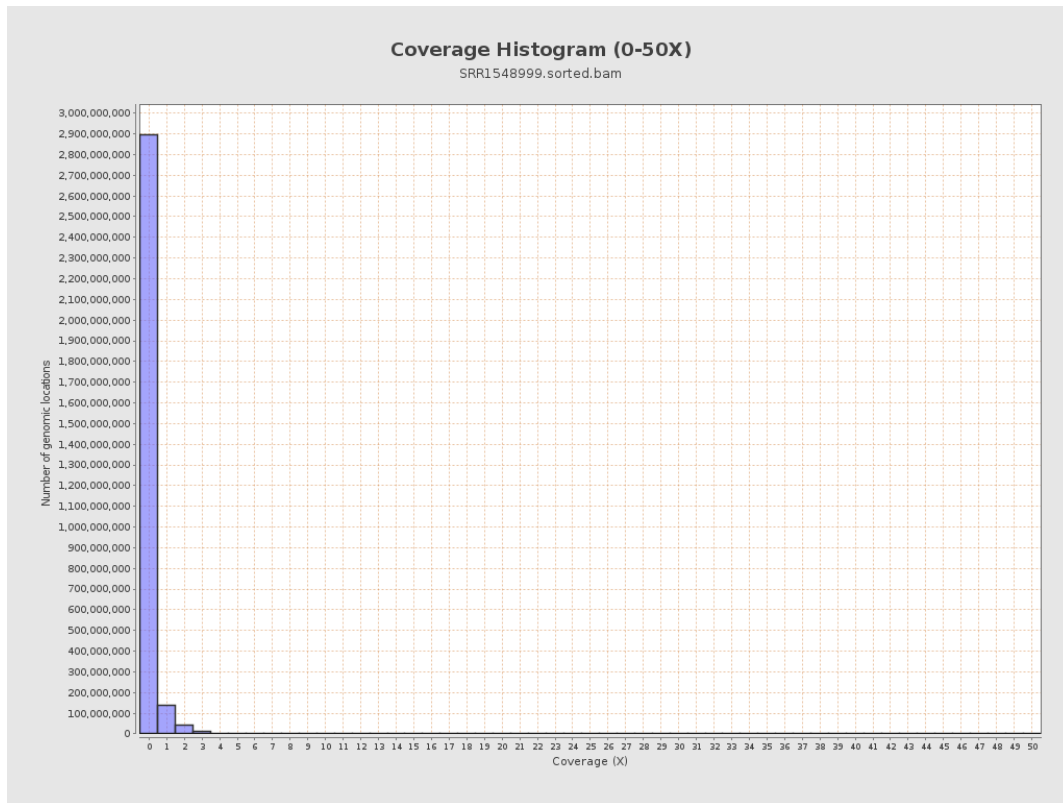
3. Results : Coverage across reference



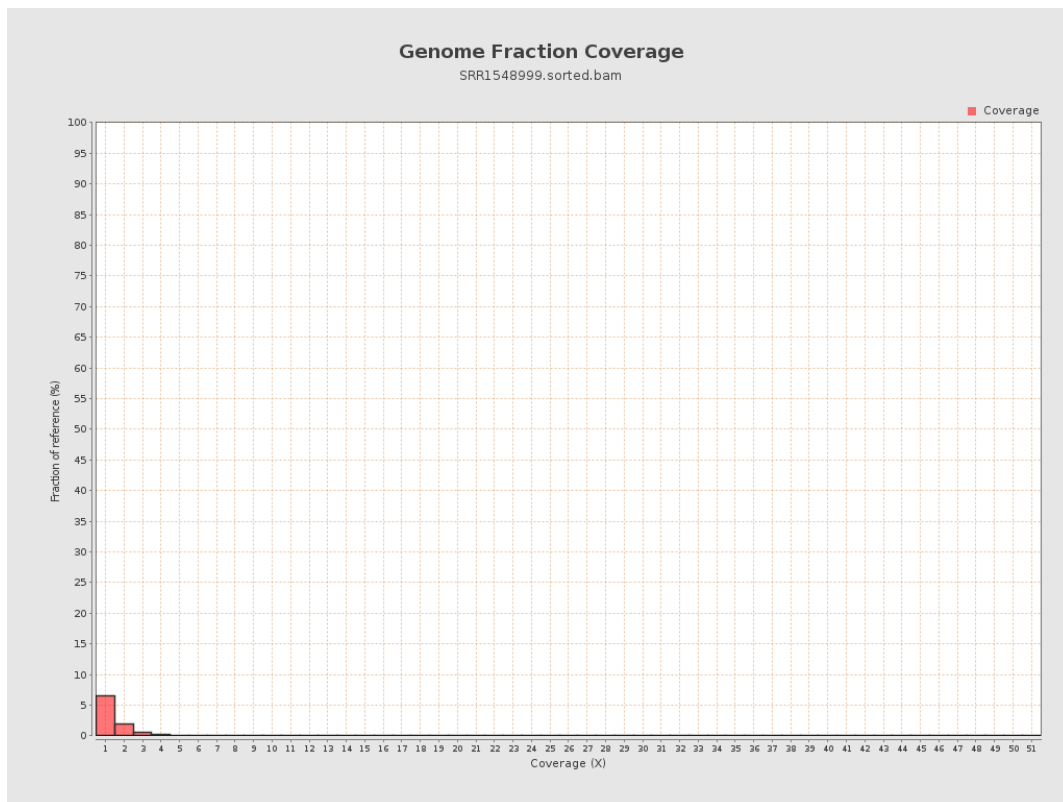
4. Results : Coverage Histogram



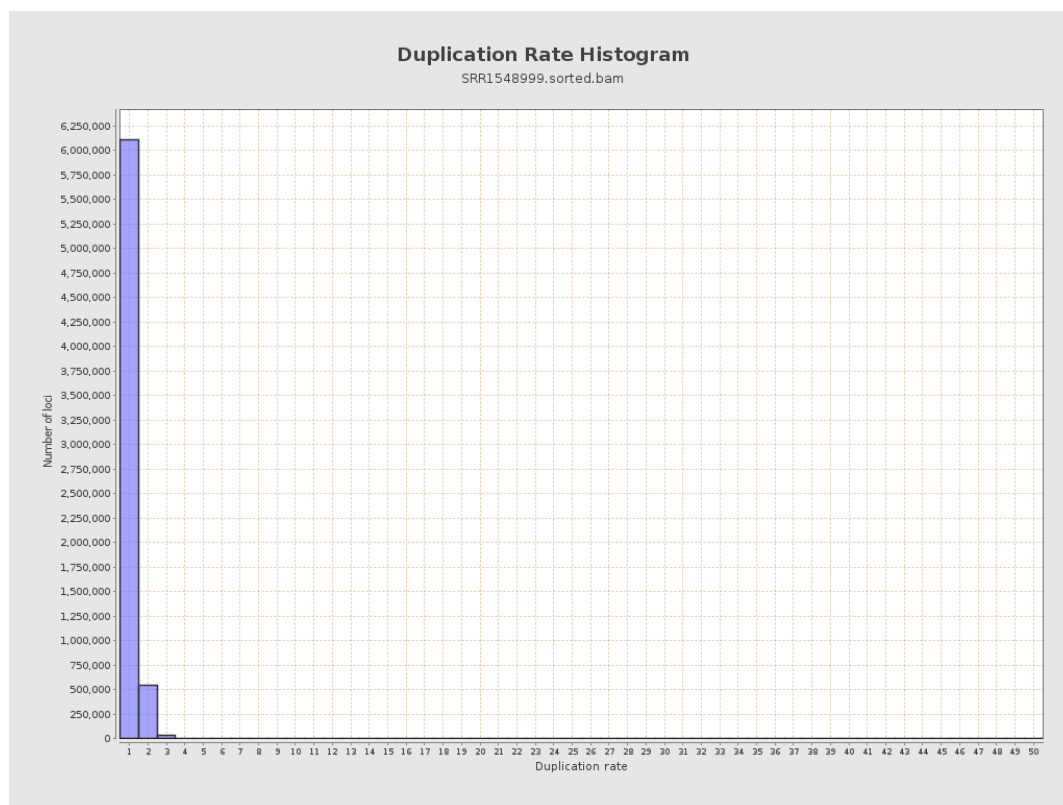
5. Results : Coverage Histogram (0-50X)



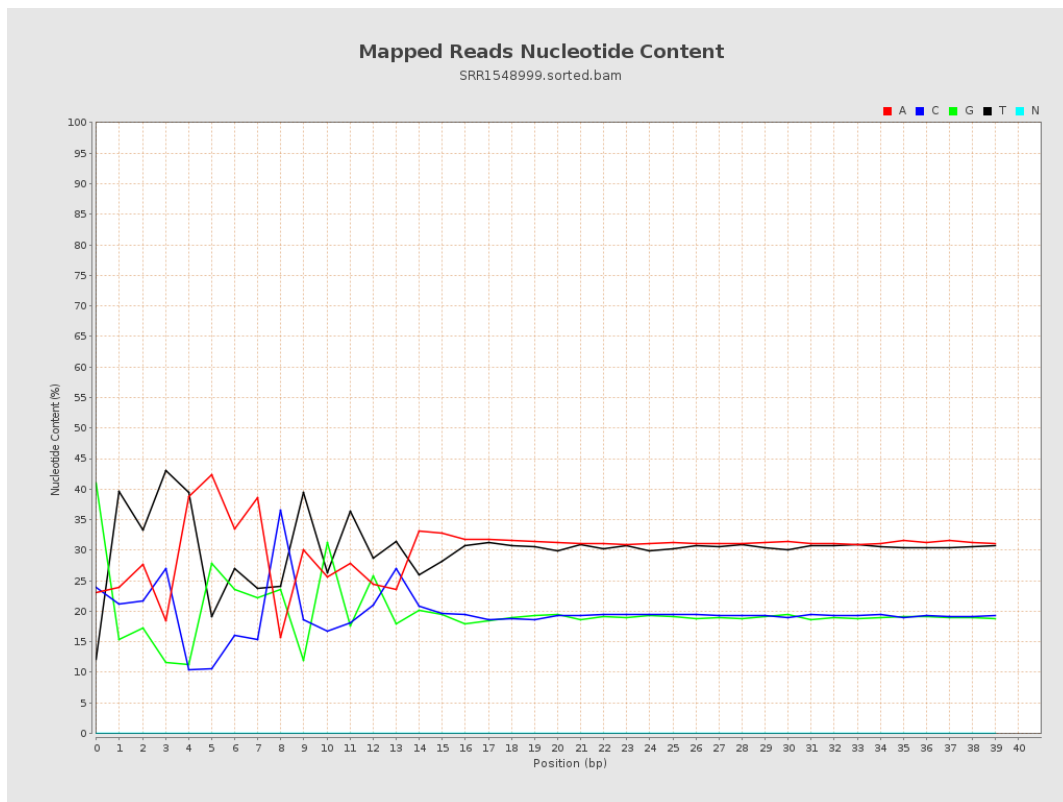
6. Results : Genome Fraction Coverage



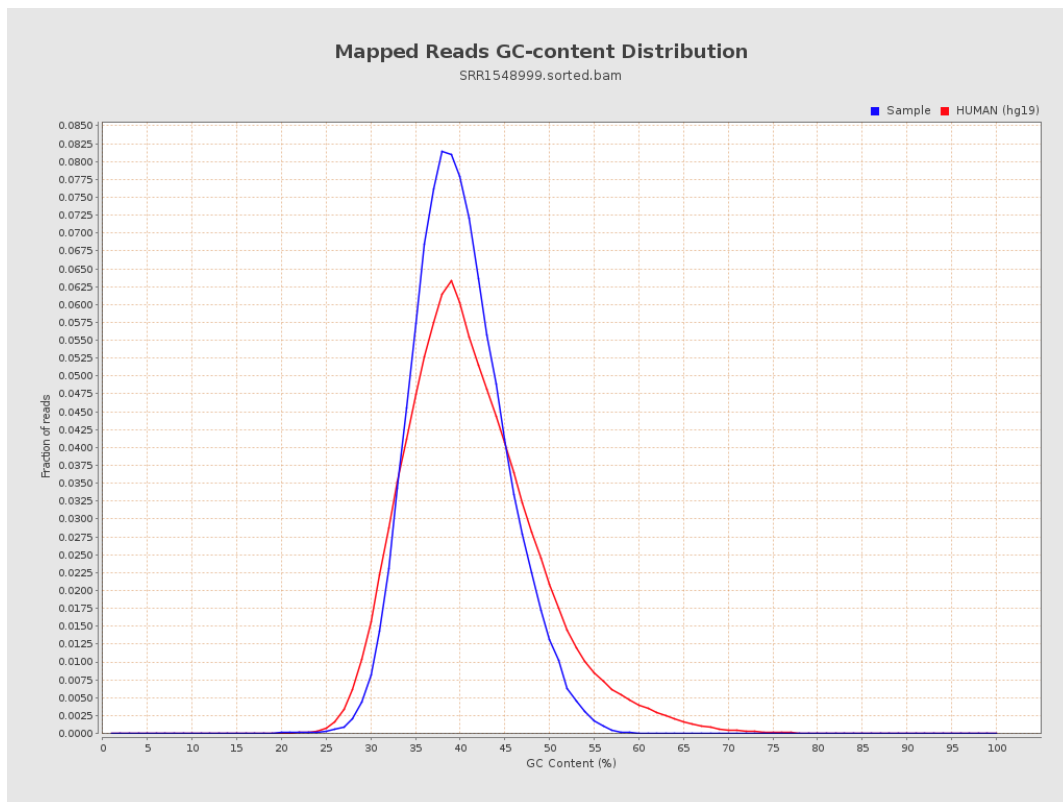
7. Results : Duplication Rate Histogram



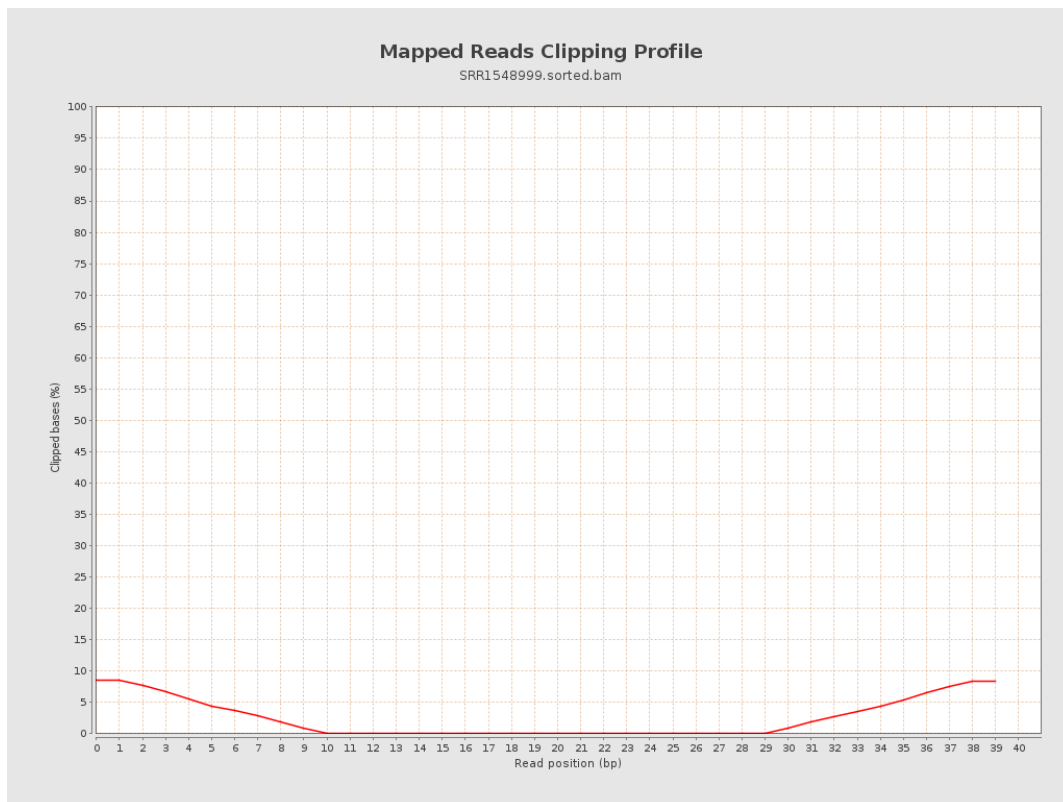
8. Results : Mapped Reads Nucleotide Content



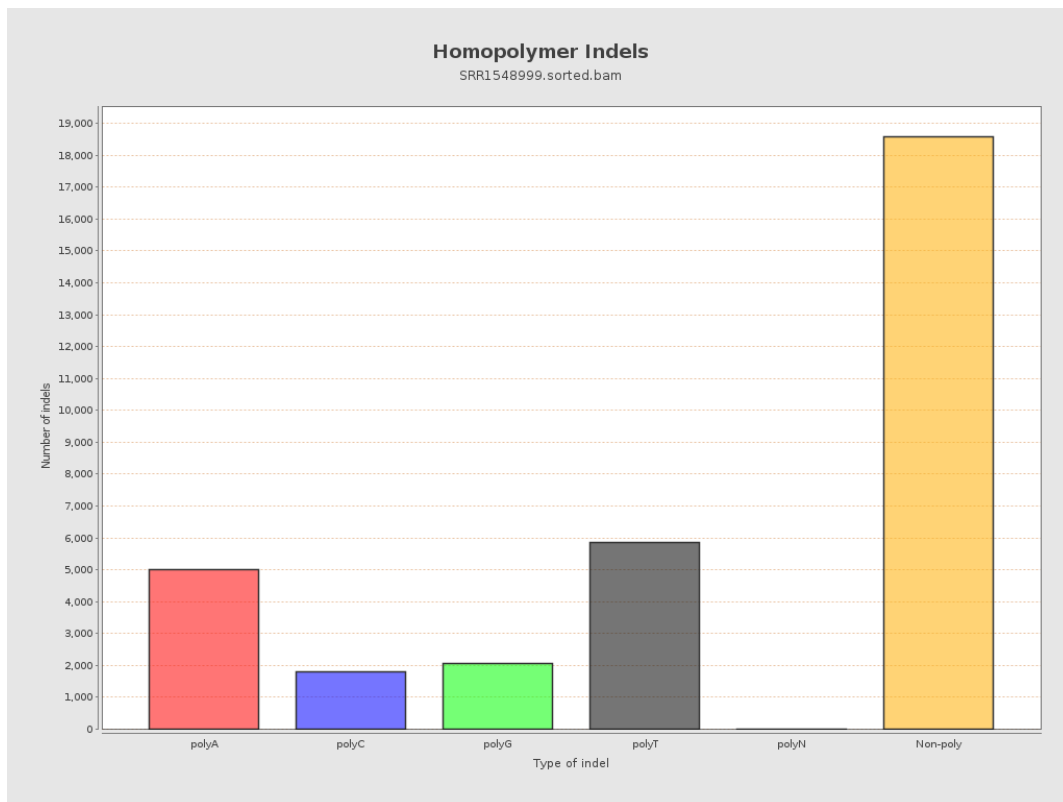
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

