

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:04:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695987.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695987 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 09:04:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,302,520
Mapped reads	13,911,670 / 90.91%
Unmapped reads	1,390,850 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,079 / 0.13%
Read min/max/mean length	8 / 359 / 143.94
Duplicated reads (estimated)	3,059,826 / 20%
Duplication rate	19.04%
Clipped reads	3,746,530 / 24.48%

2.2. ACGT Content

Number/percentage of A's	588,574,565 / 28.56%
Number/percentage of C's	442,374,513 / 21.46%
Number/percentage of T's	580,813,798 / 28.18%
Number/percentage of G's	449,251,286 / 21.8%
Number/percentage of N's	0 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.6706

Standard Deviation	2.1281
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2.4. Mapping Quality

Mean Mapping Quality	52.68
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2.5. Mismatches and indels

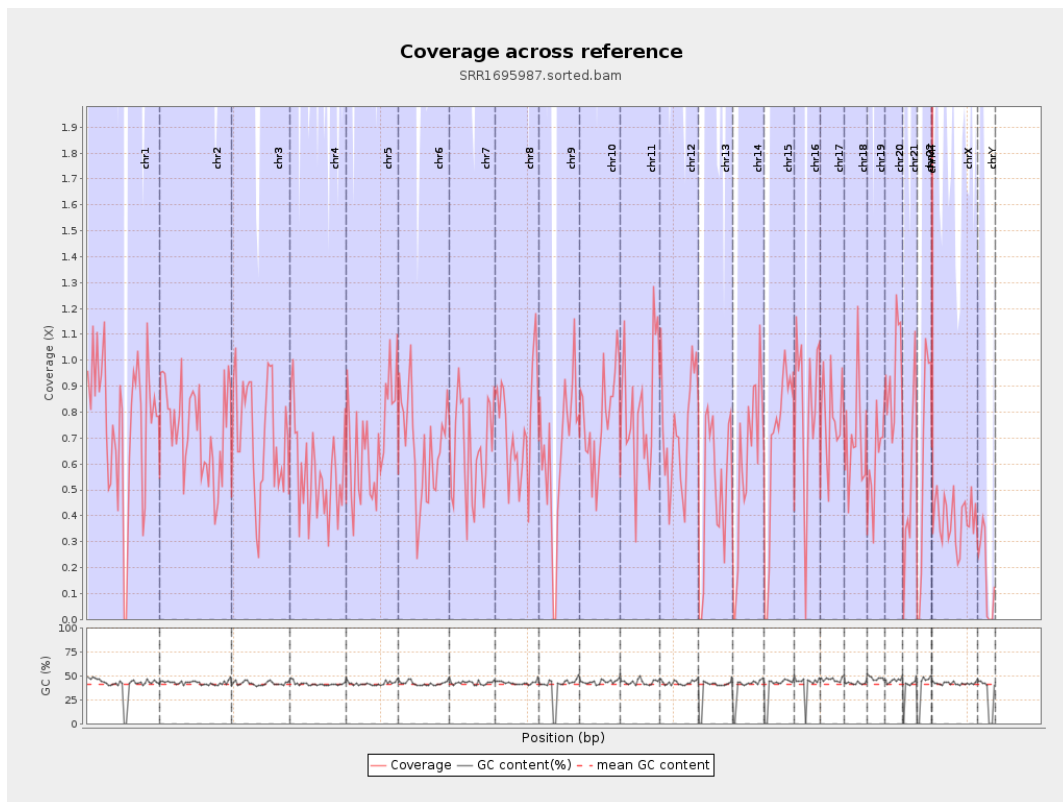
General error rate	2.06%
Mismatches	29,422,157
Insertions	12,162,636
Mapped reads with at least one insertion	48.72%
Deletions	13,339,961
Mapped reads with at least one deletion	54.07%
Homopolymer indels	37.87%

2.6. Chromosome stats

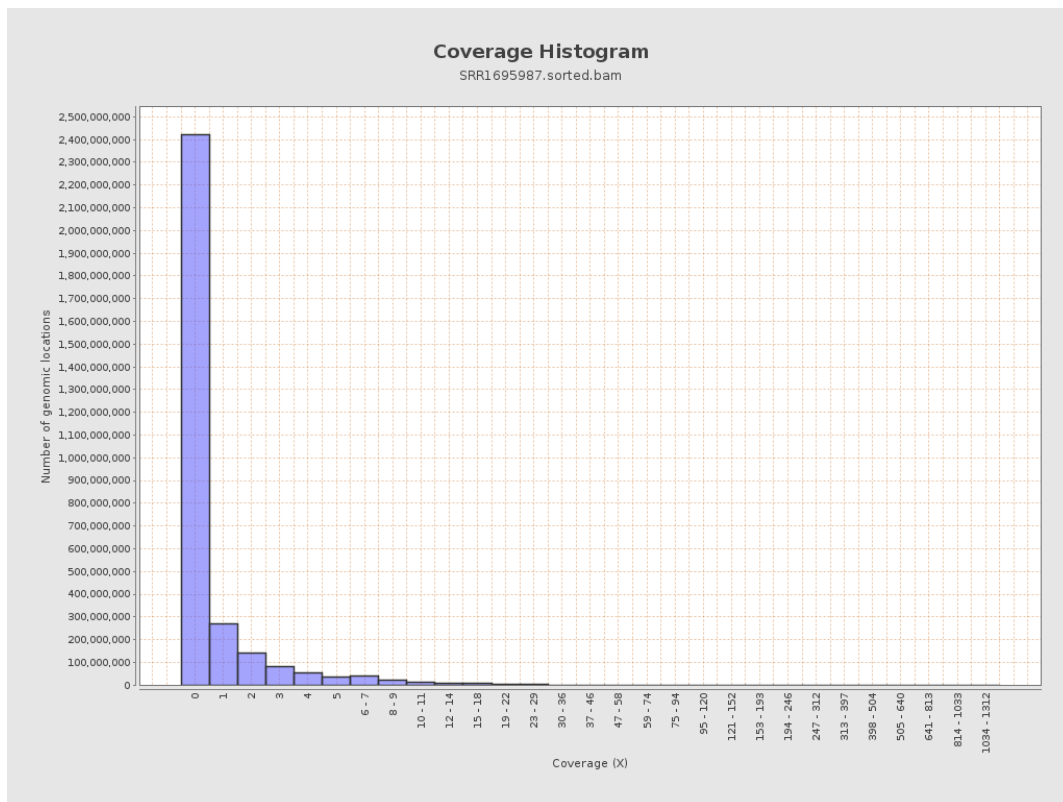
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	188916496	0.7579	2.6052
chr2	243199373	178748495	0.735	2.3695
chr3	198022430	141265348	0.7134	2.0234
chr4	191154276	107918920	0.5646	1.897
chr5	180915260	124734033	0.6895	1.9852
chr6	171115067	114250544	0.6677	1.9404
chr7	159138663	103969283	0.6533	1.9374

chr8	146364022	107837760	0.7368	2.1118
chr9	141213431	90700456	0.6423	2.2242
chr10	135534747	105178413	0.776	2.2053
chr11	135006516	109286995	0.8095	2.3192
chr12	133851895	96512373	0.721	2.0558
chr13	115169878	58226460	0.5056	1.6948
chr14	107349540	64516677	0.601	1.8743
chr15	102531392	69388755	0.6768	2.0732
chr16	90354753	72224200	0.7993	2.6005
chr17	81195210	63286622	0.7794	2.2894
chr18	78077248	55432599	0.71	2.3597
chr19	59128983	35741322	0.6045	2.0554
chr20	63025520	59591398	0.9455	2.516
chr21	48129895	26099741	0.5423	2.5993
chr22	51304566	32104006	0.6258	2.0407
chrMT	16571	176763	10.667	13.8456
chrX	155270560	59306944	0.382	1.3063
chrY	59373566	10502209	0.1769	1.1591

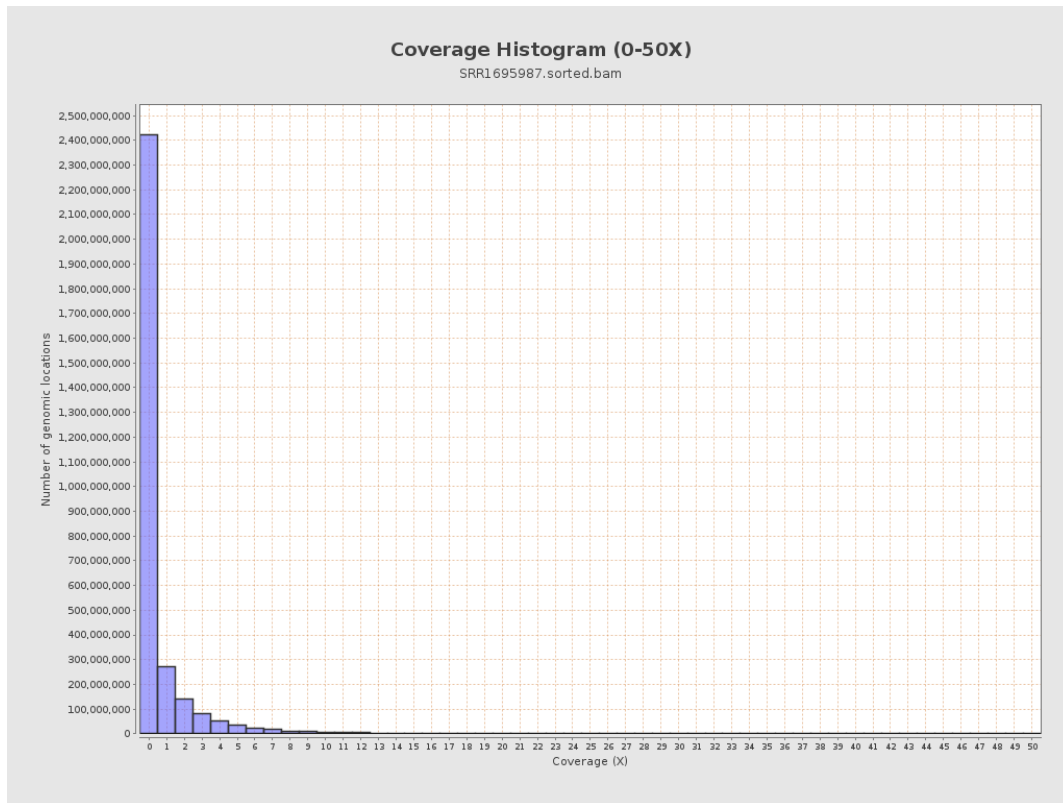
3. Results : Coverage across reference



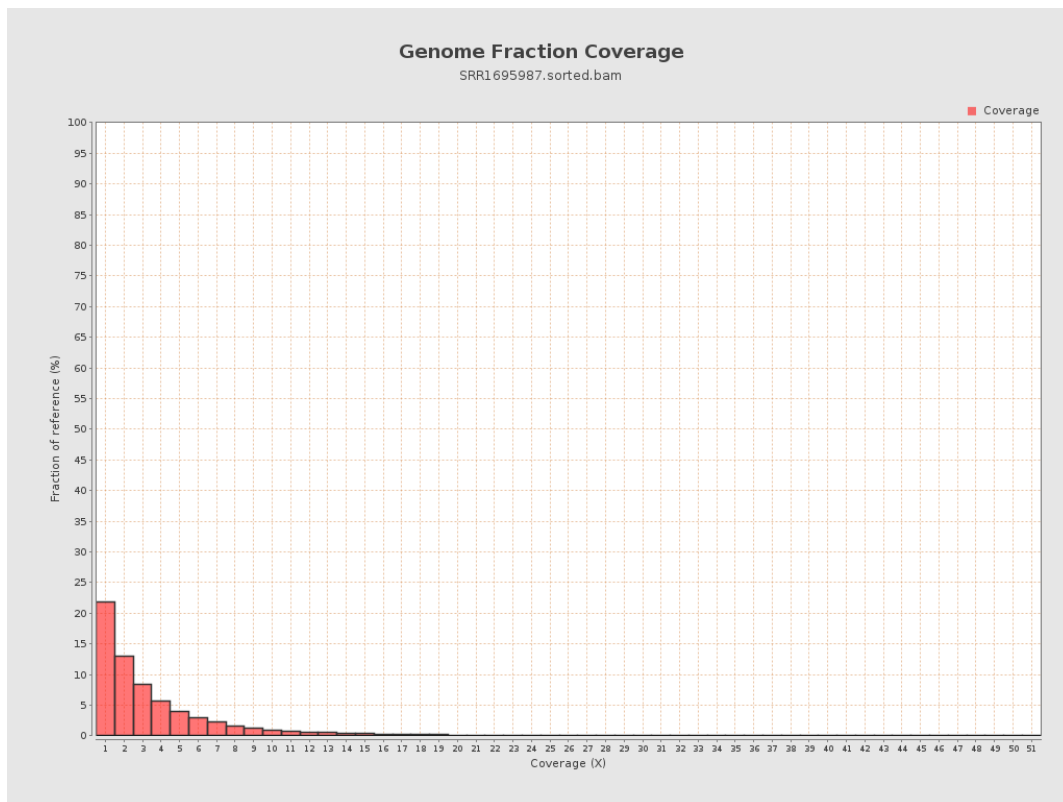
4. Results : Coverage Histogram



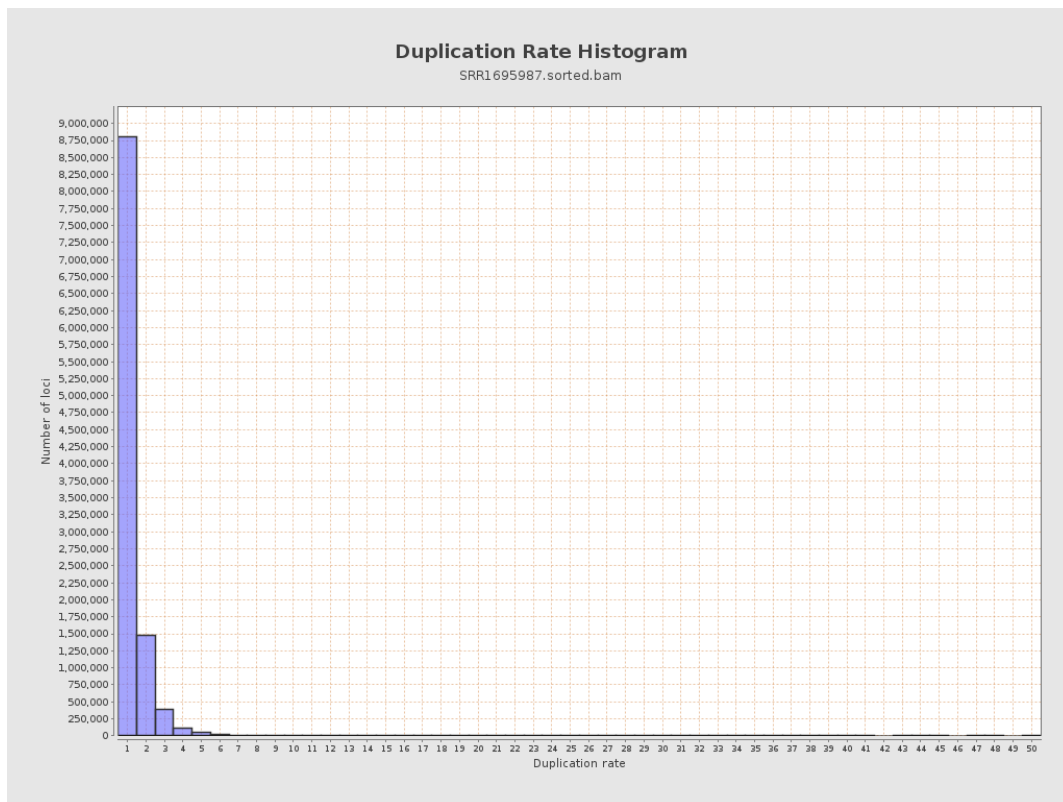
5. Results : Coverage Histogram (0-50X)



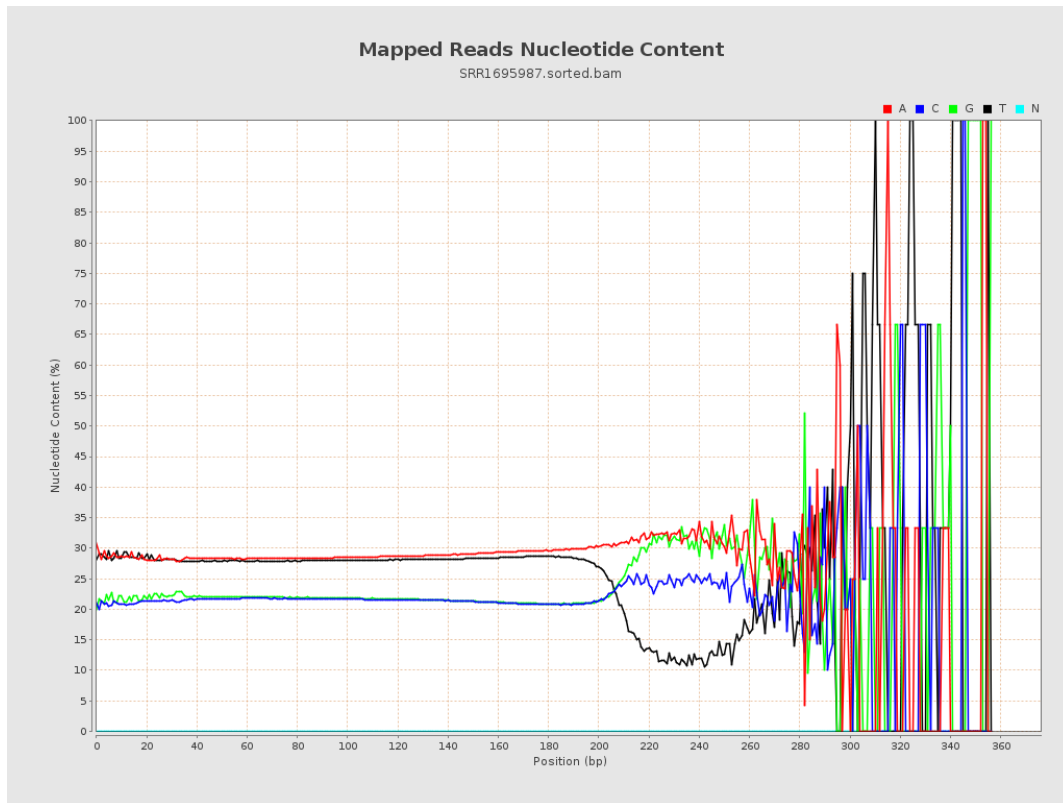
6. Results : Genome Fraction Coverage



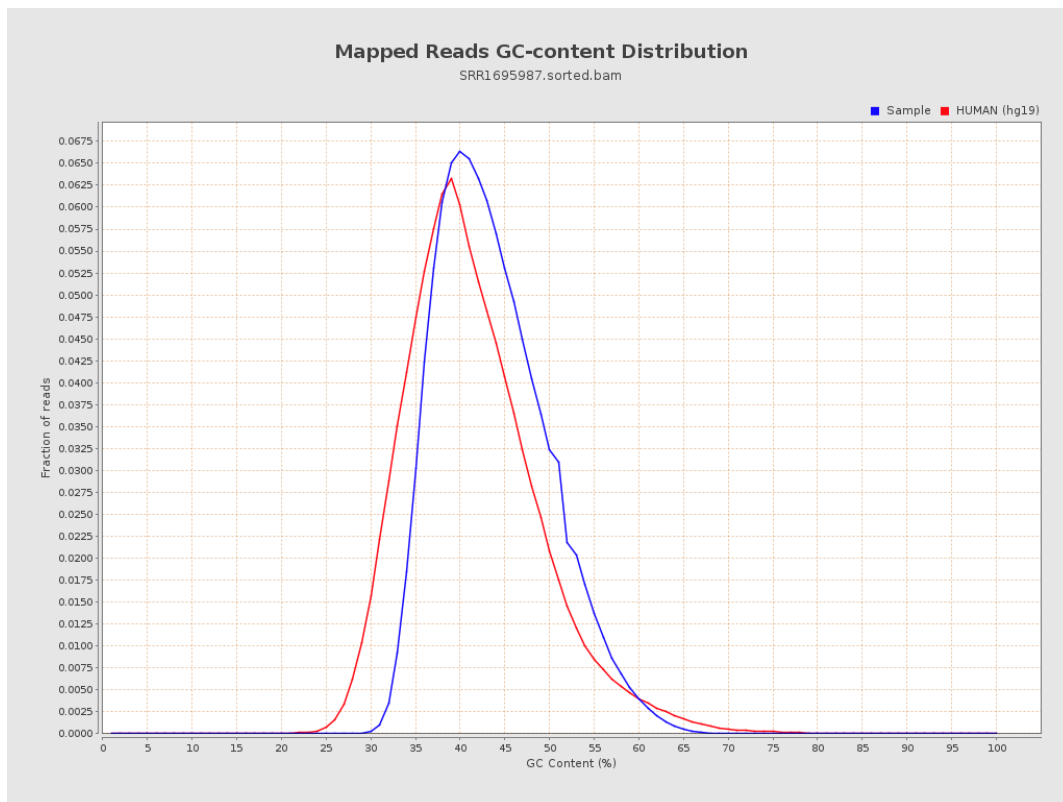
7. Results : Duplication Rate Histogram



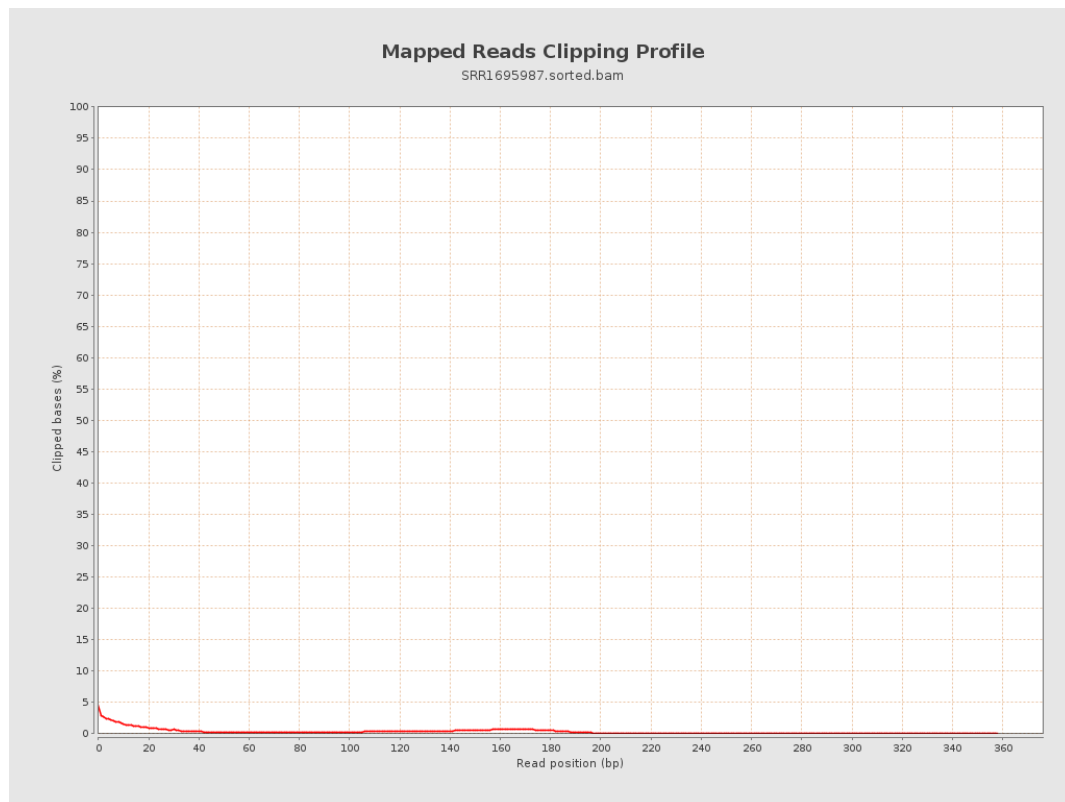
8. Results : Mapped Reads Nucleotide Content



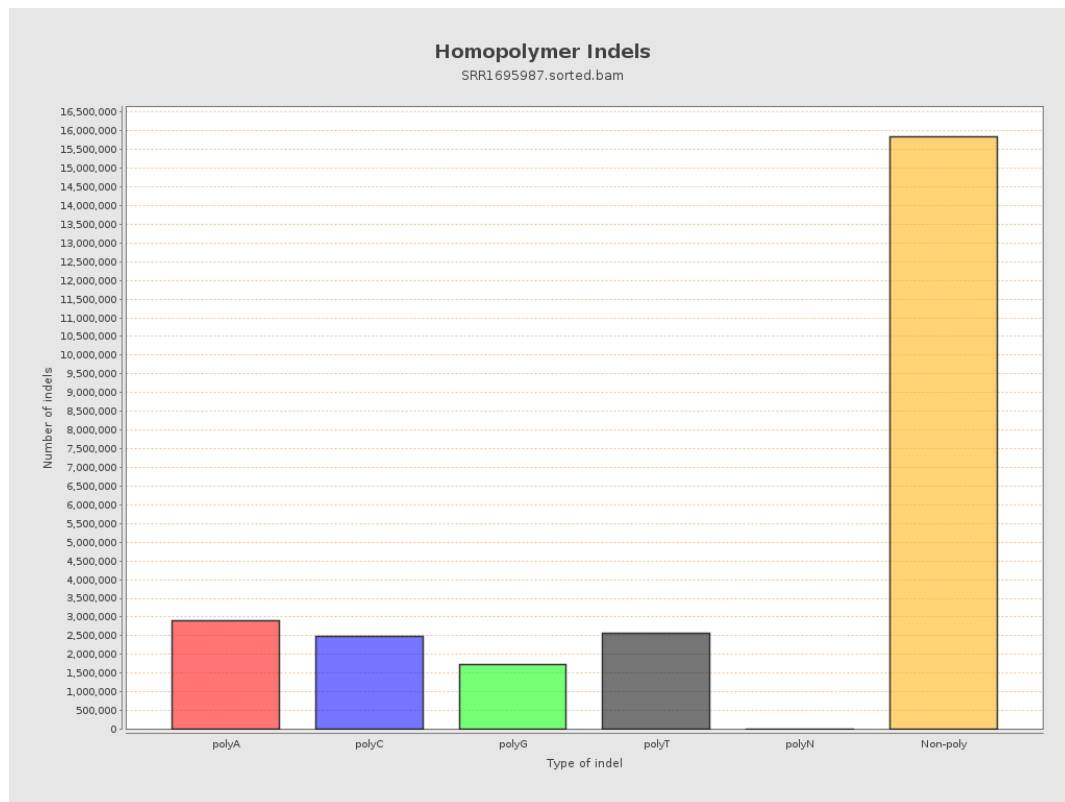
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

