

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 14:38:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751168.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_SRR8751168 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751168.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 14:38:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,666,128
Mapped reads	5,058,061 / 89.27%
Unmapped reads	608,067 / 10.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	294,521 / 5.2%
Read min/max/mean length	30 / 101 / 103.14
Duplicated reads (estimated)	213,314 / 3.76%
Duplication rate	2.18%
Clipped reads	1,302,711 / 22.99%

2.2. ACGT Content

Number/percentage of A's	145,631,319 / 29.4%
Number/percentage of C's	101,752,177 / 20.54%
Number/percentage of T's	146,507,588 / 29.58%
Number/percentage of G's	101,400,519 / 20.47%
Number/percentage of N's	2,745 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.1601

Standard Deviation	1.7612
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2.4. Mapping Quality

Mean Mapping Quality	50.89
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2.5. Mismatches and indels

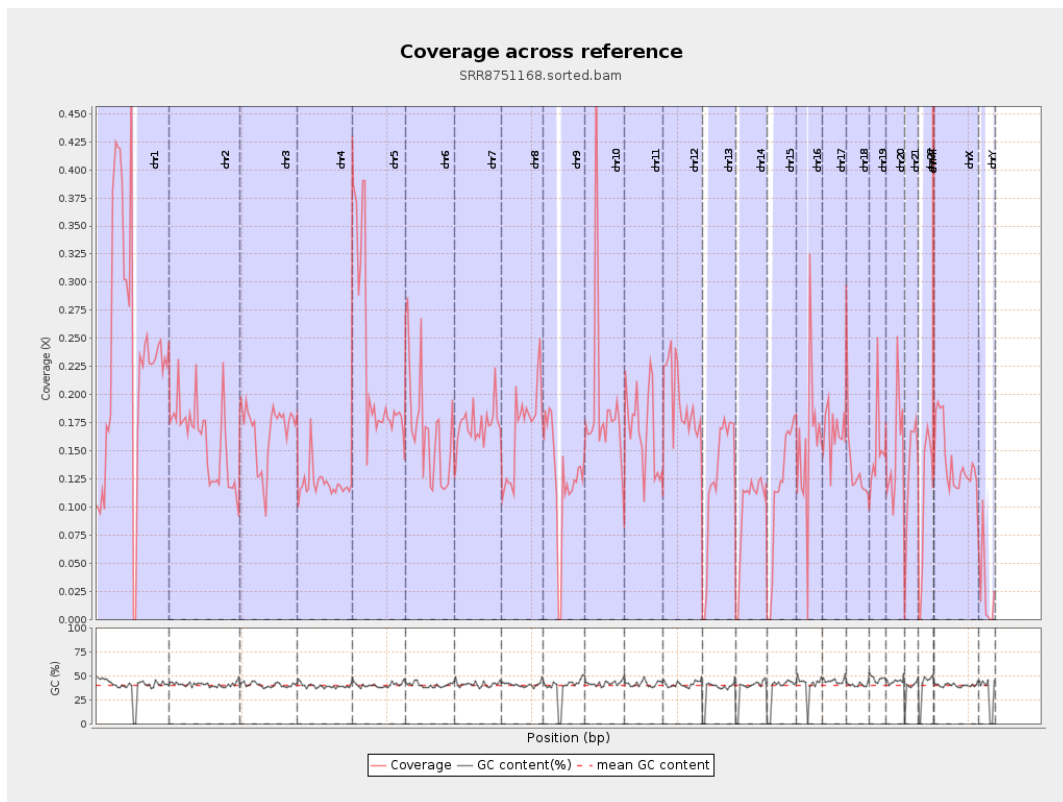
General error rate	0.54%
Mismatches	2,086,108
Insertions	439,175
Mapped reads with at least one insertion	8.26%
Deletions	78,970
Mapped reads with at least one deletion	1.53%
Homopolymer indels	53.73%

2.6. Chromosome stats

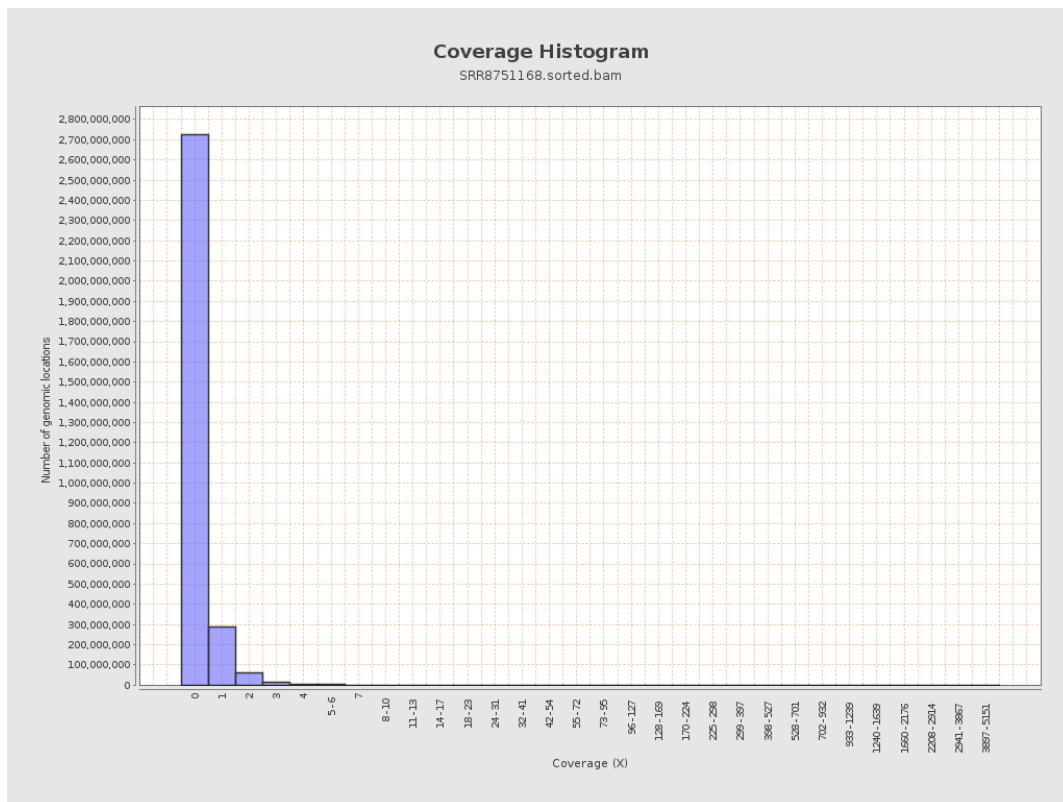
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	58986558	0.2367	4.8196
chr2	243199373	38669453	0.159	0.7471
chr3	198022430	33036874	0.1668	0.6373
chr4	191154276	23002915	0.1203	0.5815
chr5	180915260	40518389	0.224	0.5857
chr6	171115067	28812006	0.1684	1.0859
chr7	159138663	27671269	0.1739	1.059

chr8	146364022	24615271	0.1682	0.6538
chr9	141213431	17694536	0.1253	0.7818
chr10	135534747	25602521	0.1889	2.959
chr11	135006516	22568516	0.1672	0.8767
chr12	133851895	26052410	0.1946	0.5486
chr13	115169878	14490204	0.1258	0.4317
chr14	107349540	10410443	0.097	0.4144
chr15	102531392	11872442	0.1158	0.4141
chr16	90354753	13955759	0.1545	1.2917
chr17	81195210	13533257	0.1667	0.7715
chr18	78077248	10503059	0.1345	1.816
chr19	59128983	9023184	0.1526	3.2337
chr20	63025520	9295615	0.1475	2.3267
chr21	48129895	6302765	0.131	0.529
chr22	51304566	5437939	0.106	0.4062
chrMT	16571	310630	18.7454	8.6865
chrX	155270560	21693745	0.1397	0.5538
chrY	59373566	1407764	0.0237	0.9547

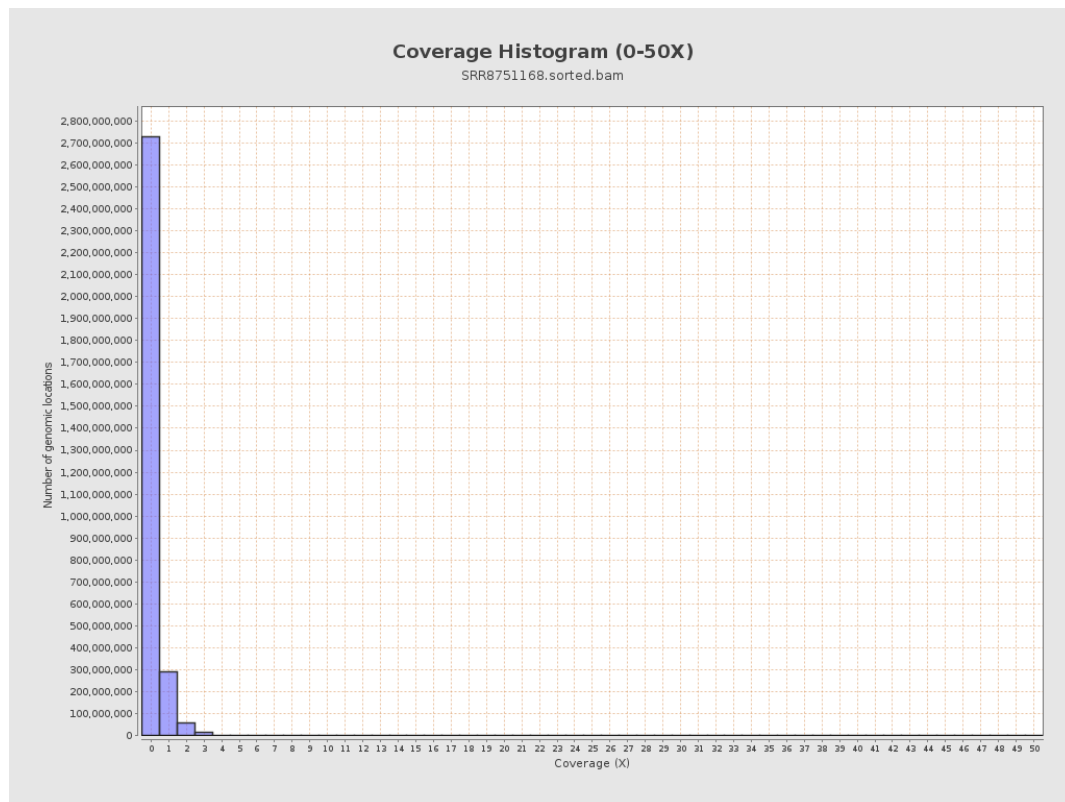
3. Results : Coverage across reference



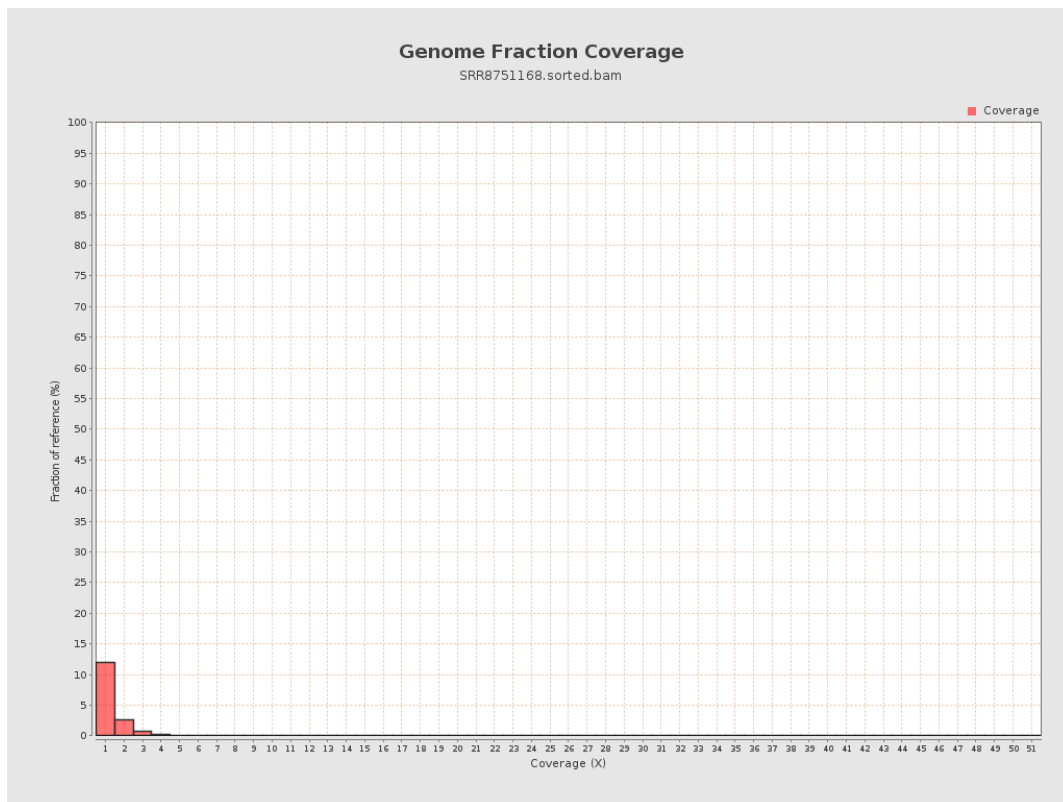
4. Results : Coverage Histogram



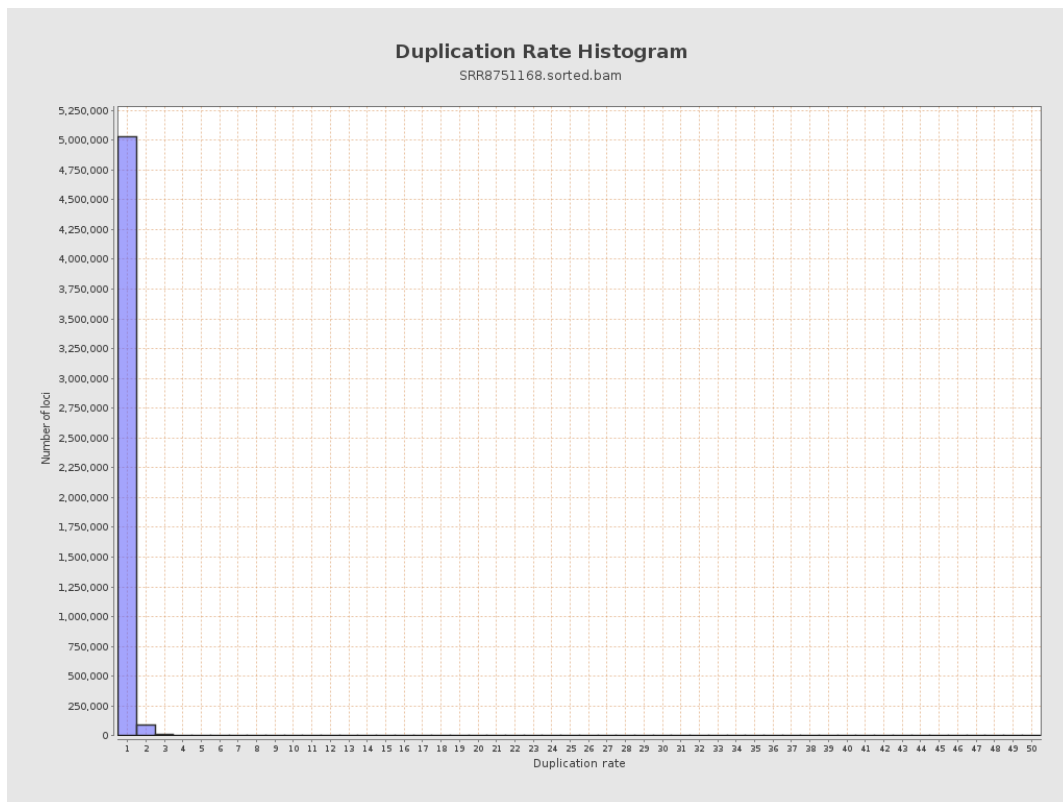
5. Results : Coverage Histogram (0-50X)



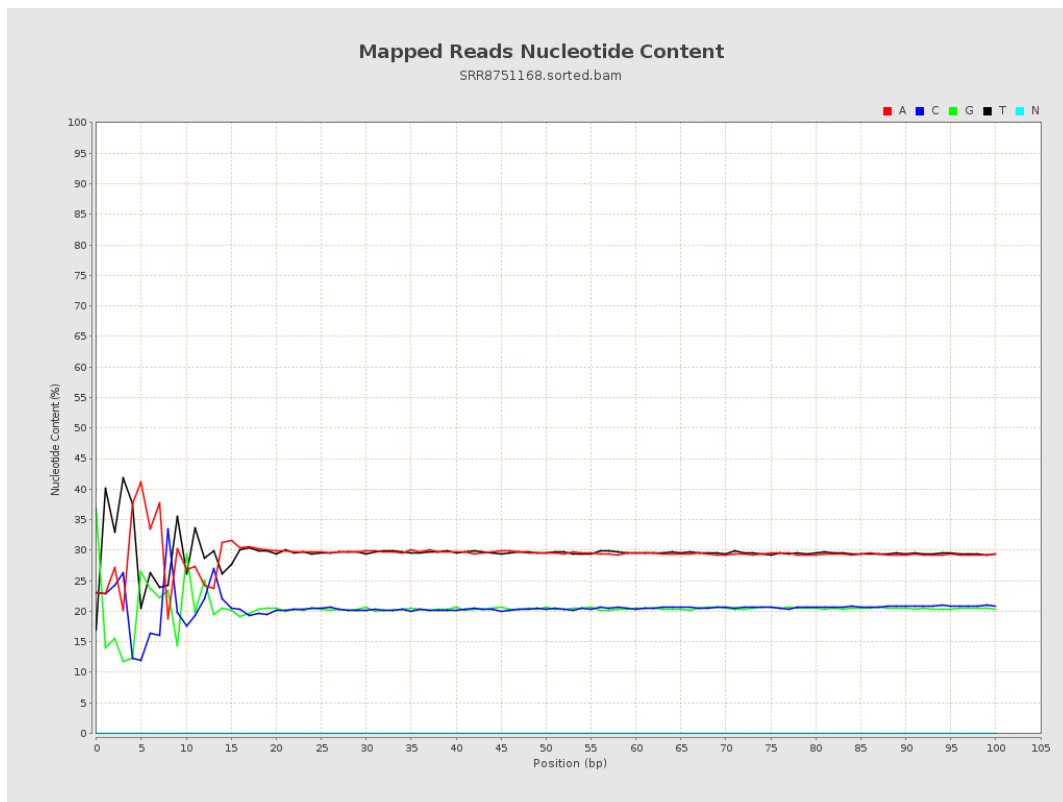
6. Results : Genome Fraction Coverage



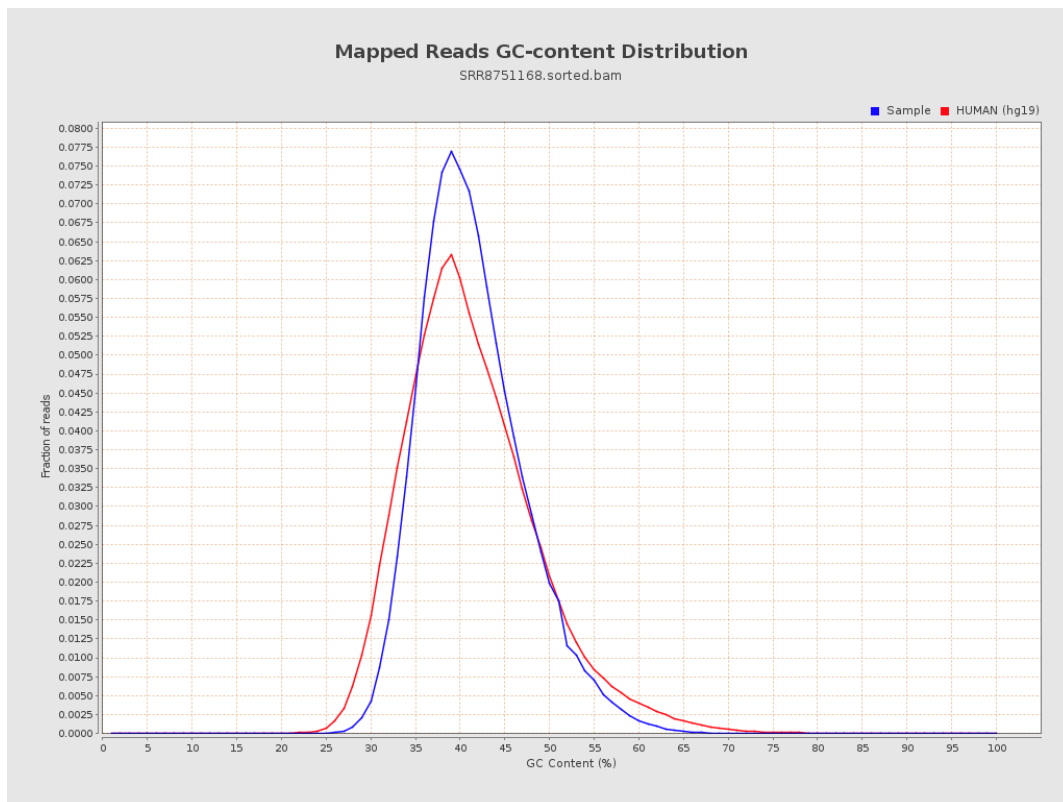
7. Results : Duplication Rate Histogram



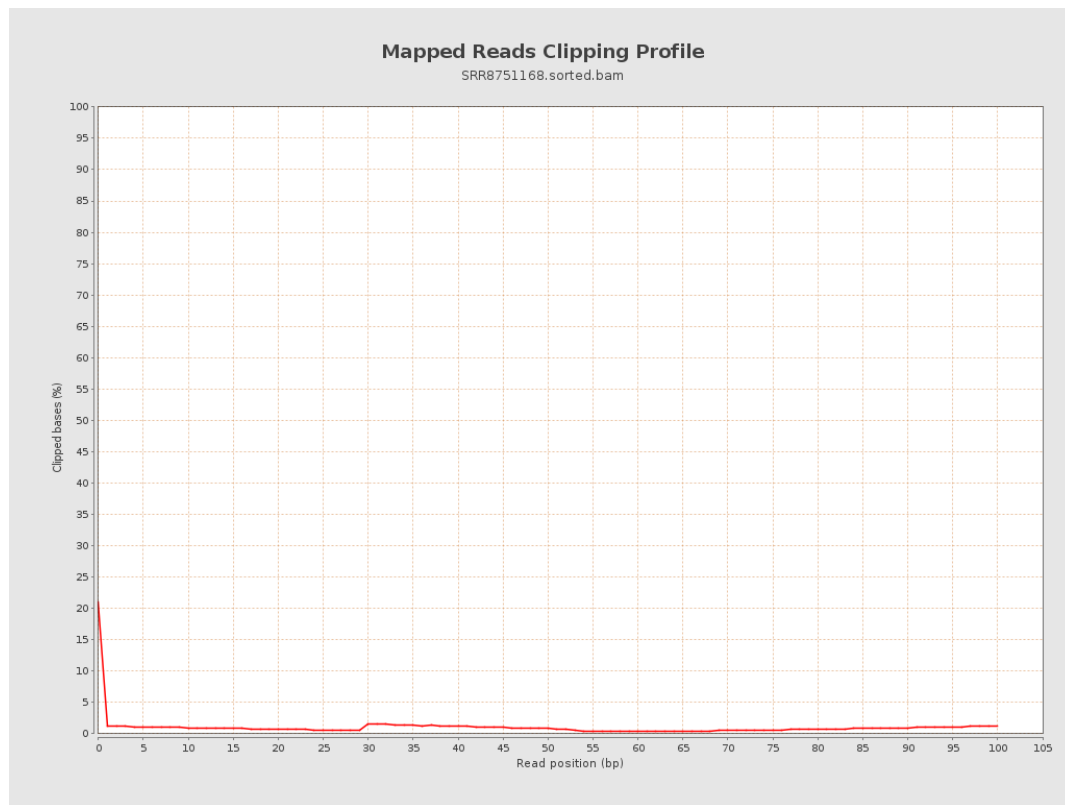
8. Results : Mapped Reads Nucleotide Content



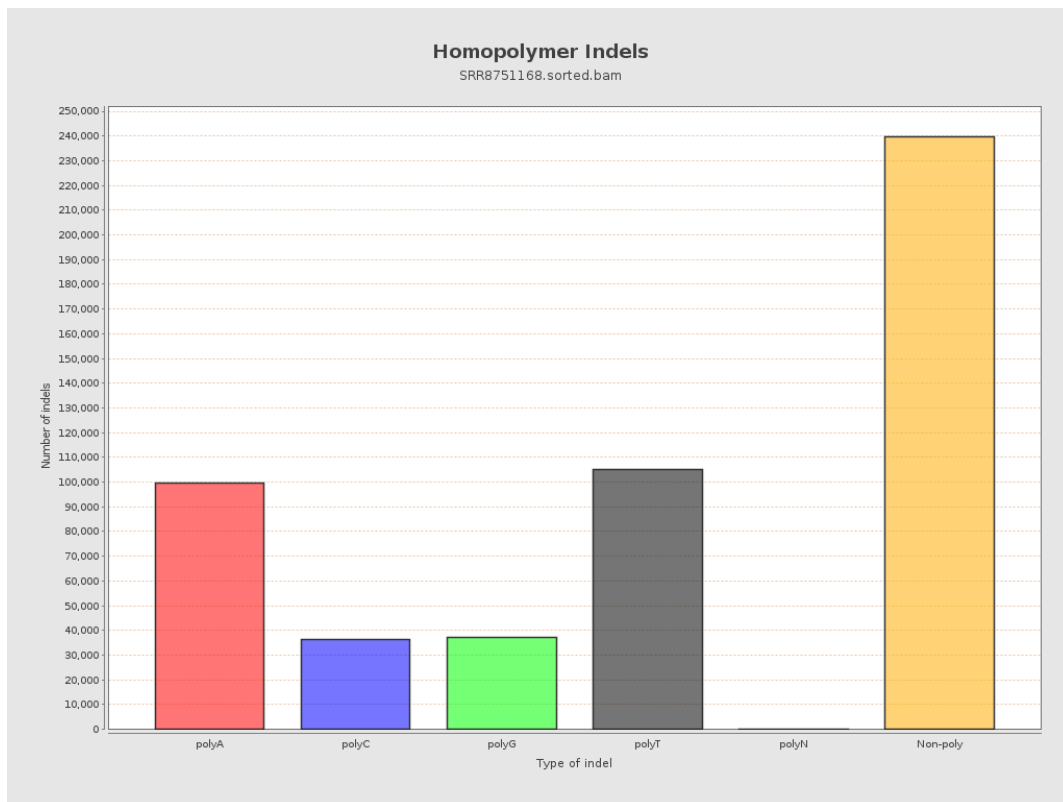
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

