

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:53:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083663.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_SRR3083663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:53:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,929,301
Mapped reads	1,548,722 / 80.27%
Unmapped reads	380,579 / 19.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,849 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	45,475 / 2.36%
Duplication rate	2.39%
Clipped reads	984,080 / 51.01%

2.2. ACGT Content

Number/percentage of A's	28,373,333 / 29.68%
Number/percentage of C's	18,245,431 / 19.08%
Number/percentage of T's	28,471,414 / 29.78%
Number/percentage of G's	20,512,118 / 21.45%
Number/percentage of N's	5,849 / 0.01%
GC Percentage	40.54%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2969
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2.4. Mapping Quality

Mean Mapping Quality	45.42
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2.5. Mismatches and indels

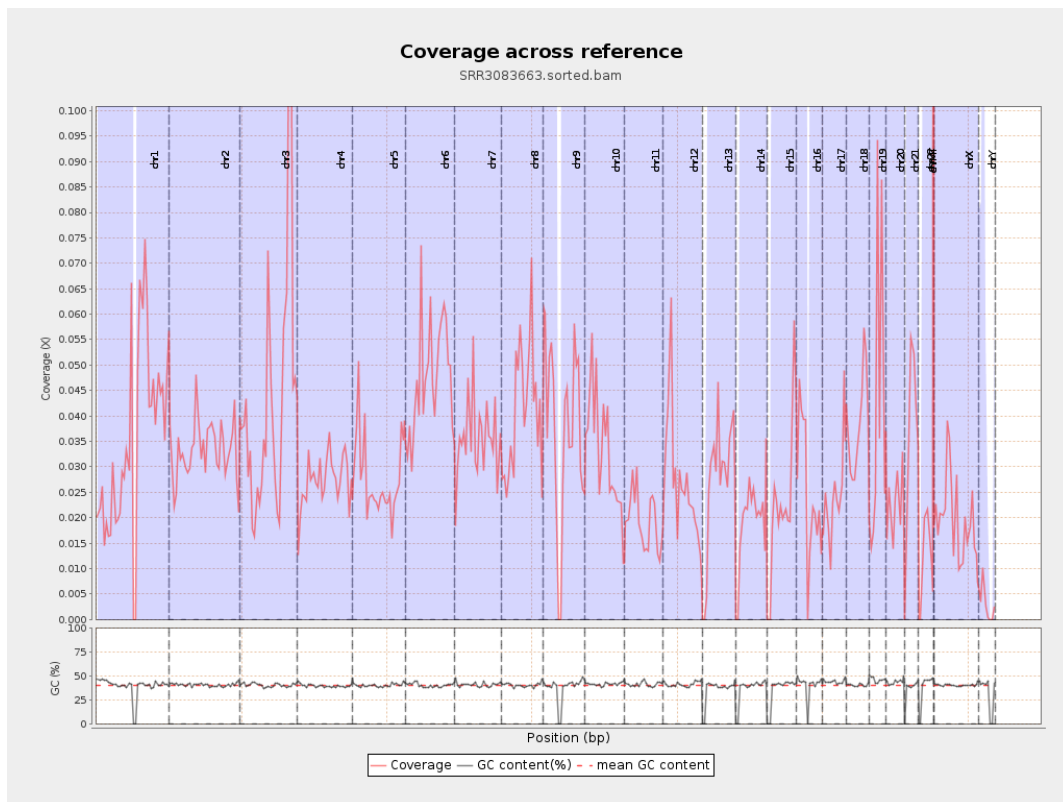
General error rate	0.86%
Mismatches	811,633
Insertions	7,042
Mapped reads with at least one insertion	0.45%
Deletions	19,921
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.41%

2.6. Chromosome stats

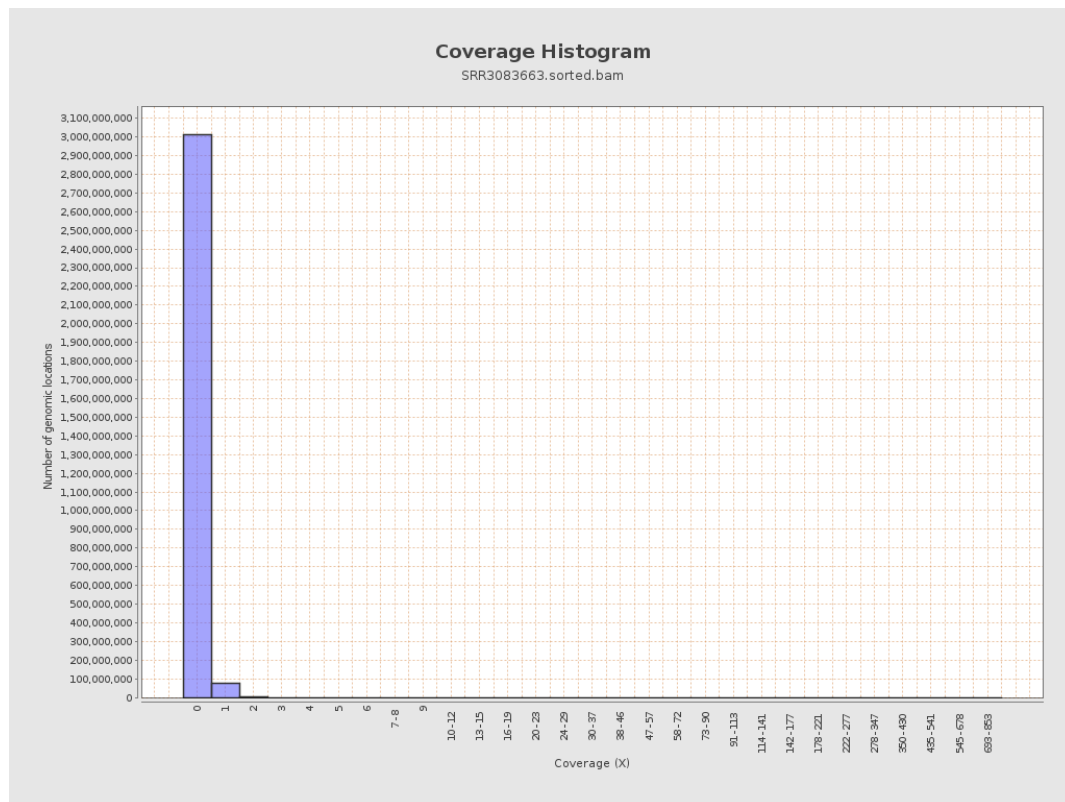
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8729155	0.035	0.6993
chr2	243199373	8107688	0.0333	0.2309
chr3	198022430	8552083	0.0432	0.2271
chr4	191154276	5209701	0.0273	0.1801
chr5	180915260	5010312	0.0277	0.1805
chr6	171115067	8110268	0.0474	0.2725
chr7	159138663	5694457	0.0358	0.3391

chr8	146364022	5996547	0.041	0.3387
chr9	141213431	5242227	0.0371	0.2279
chr10	135534747	4551475	0.0336	0.2804
chr11	135006516	2606263	0.0193	0.1655
chr12	133851895	3580421	0.0267	0.1765
chr13	115169878	3145769	0.0273	0.1781
chr14	107349540	2008487	0.0187	0.149
chr15	102531392	2343663	0.0229	0.1641
chr16	90354753	2261614	0.025	0.176
chr17	81195210	1992370	0.0245	0.1708
chr18	78077248	3020850	0.0387	0.3137
chr19	59128983	2431681	0.0411	0.4391
chr20	63025520	1437828	0.0228	0.1635
chr21	48129895	1728453	0.0359	0.207
chr22	51304566	617894	0.012	0.1172
chrMT	16571	11702	0.7062	0.9465
chrX	155270560	3076167	0.0198	0.1586
chrY	59373566	173184	0.0029	0.0724

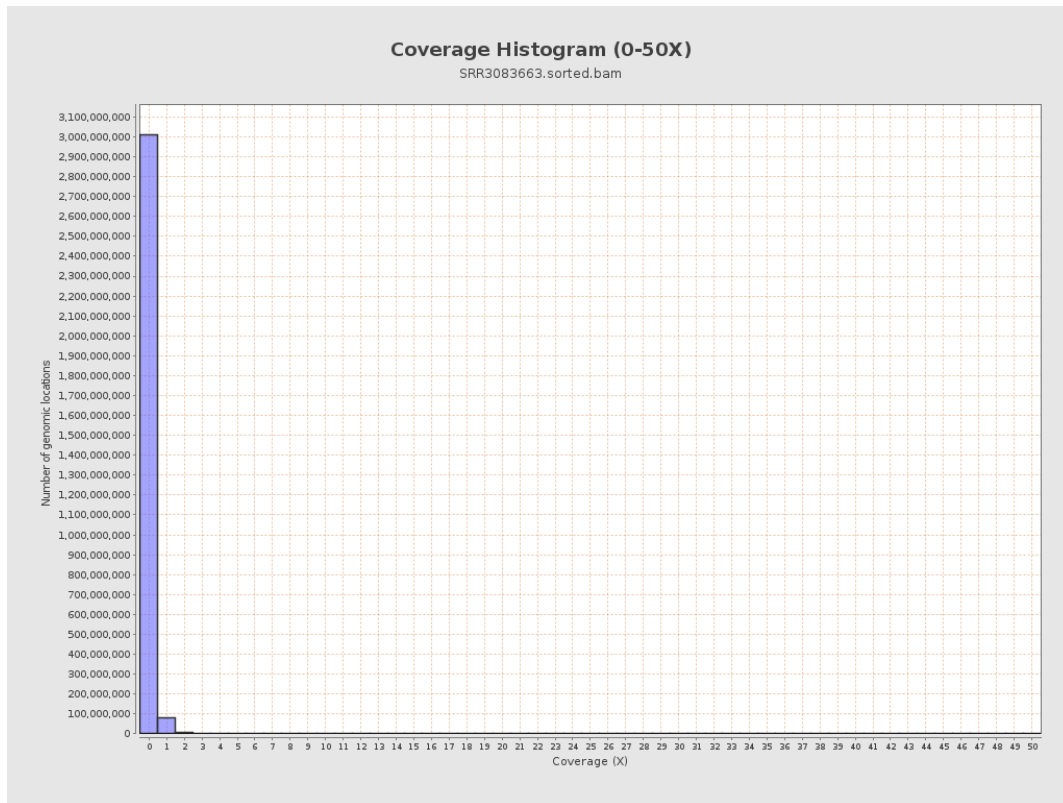
3. Results : Coverage across reference



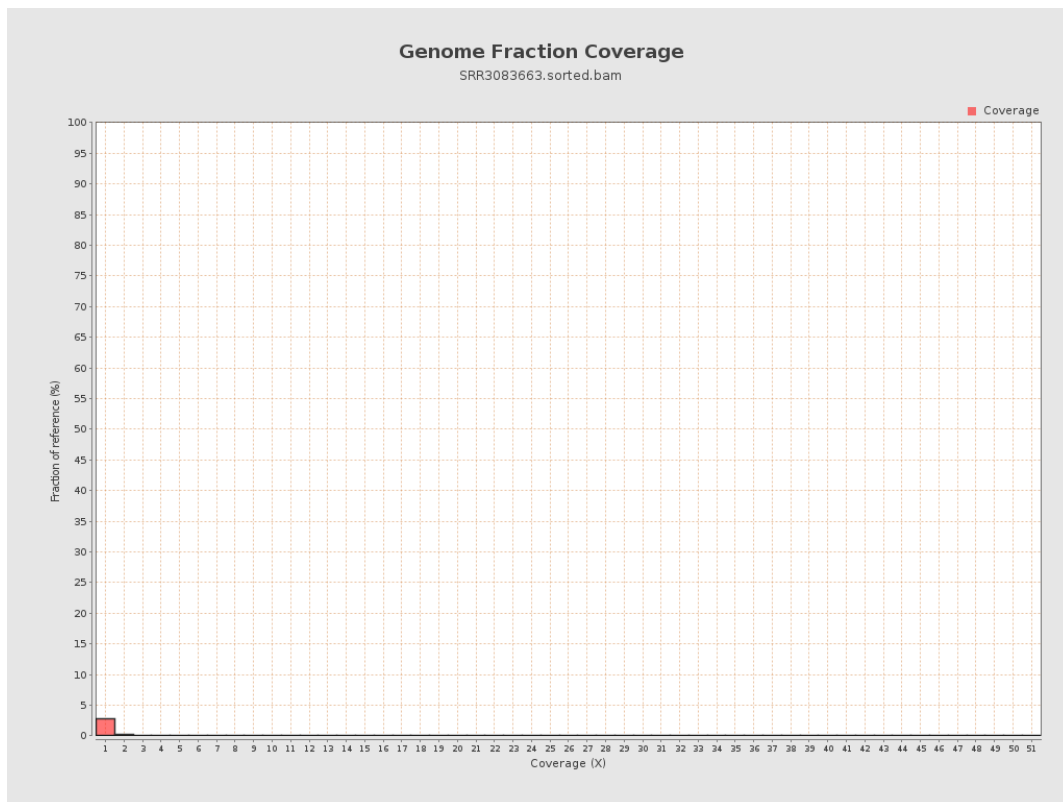
4. Results : Coverage Histogram



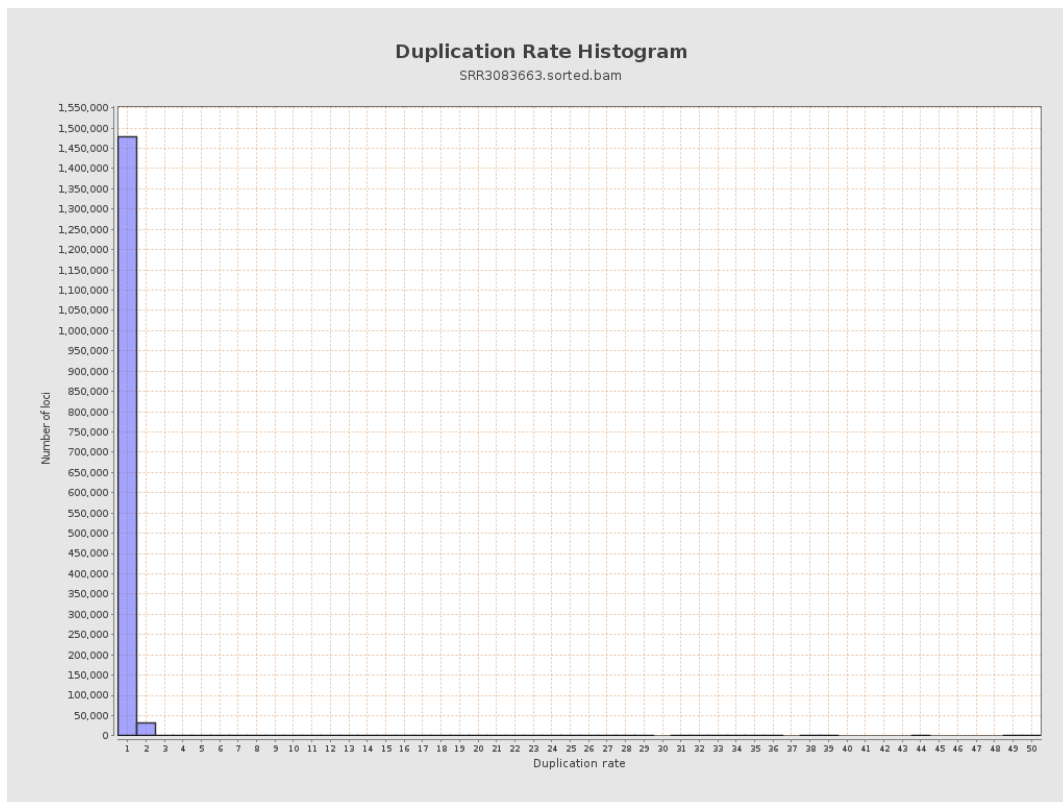
5. Results : Coverage Histogram (0-50X)



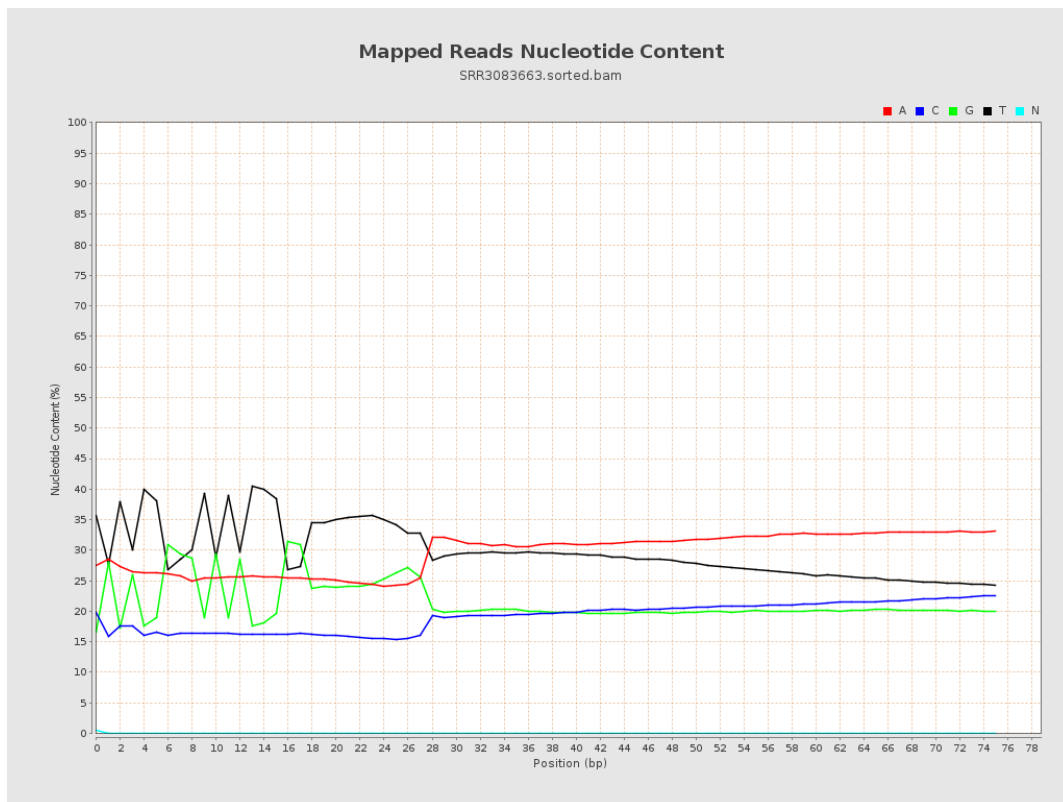
6. Results : Genome Fraction Coverage



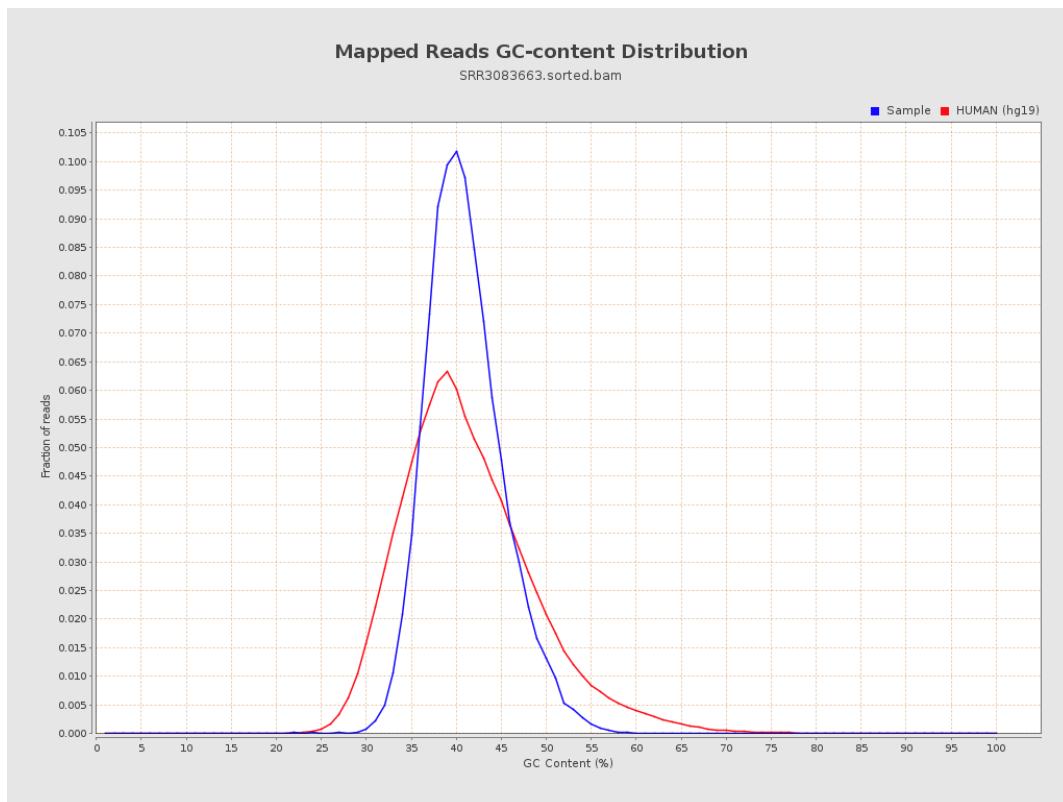
7. Results : Duplication Rate Histogram



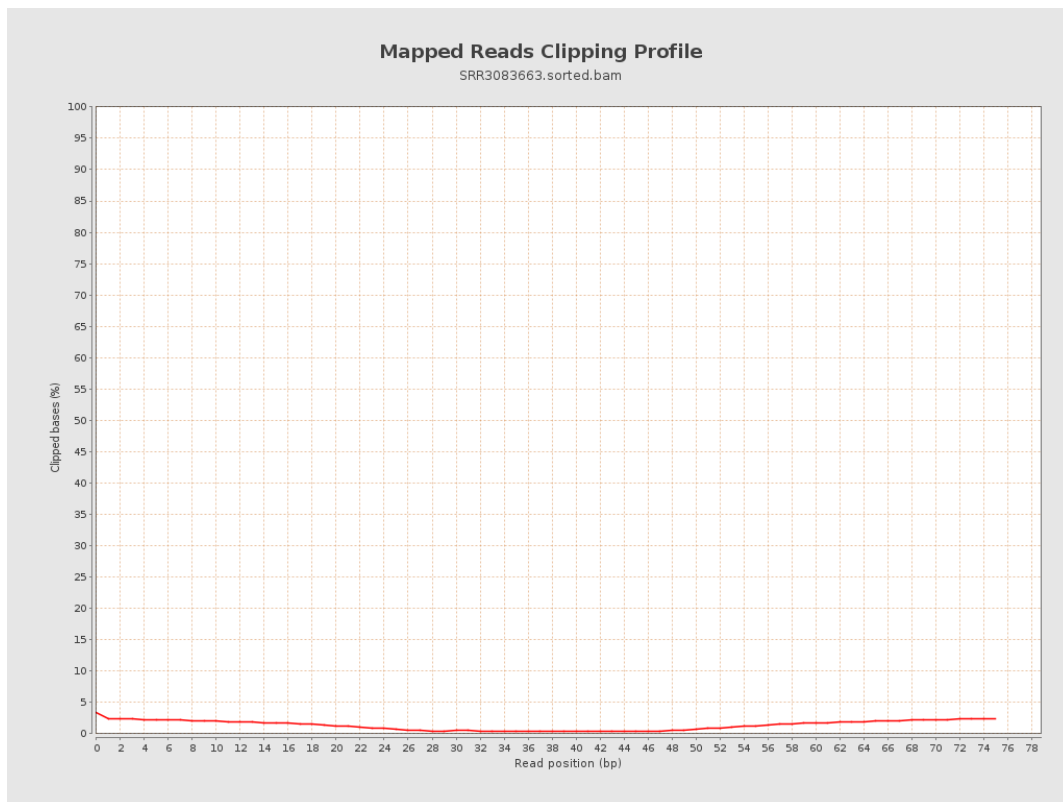
8. Results : Mapped Reads Nucleotide Content



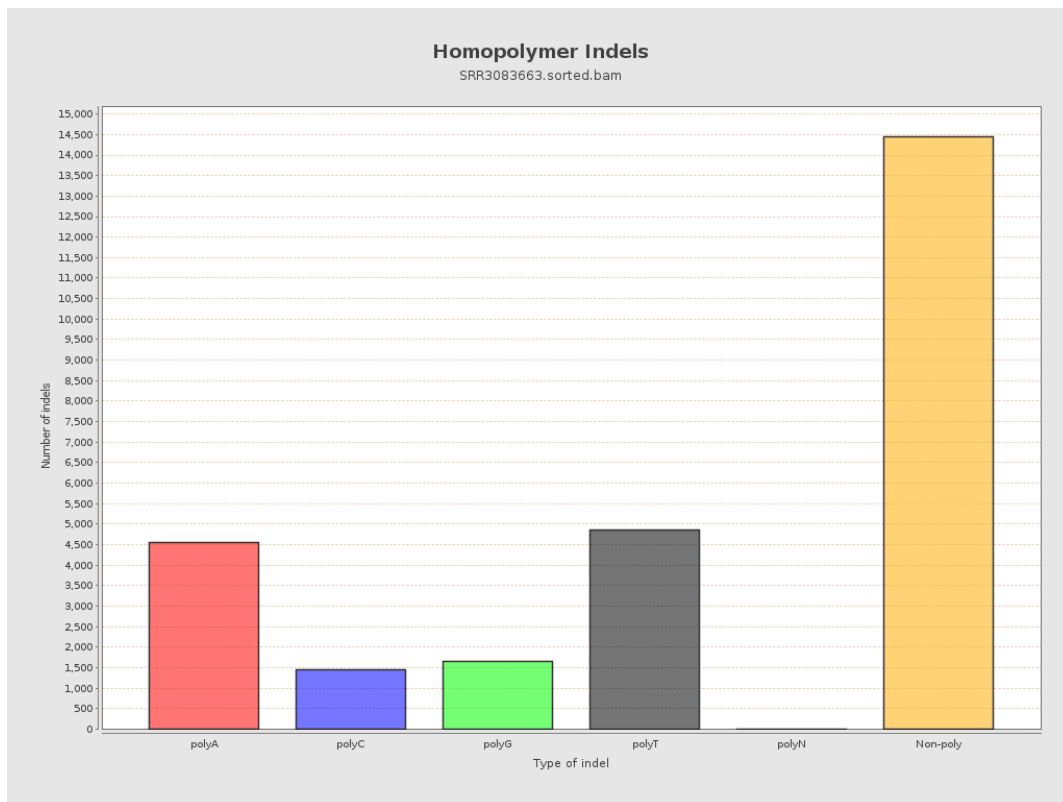
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

