

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:16:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080776.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_SRR3080776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080776.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:15:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,723,367
Mapped reads	2,399,270 / 88.1%
Unmapped reads	324,097 / 11.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,864 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	115,193 / 4.23%
Duplication rate	4.06%
Clipped reads	1,084,160 / 39.81%

2.2. ACGT Content

Number/percentage of A's	45,473,560 / 28.35%
Number/percentage of C's	30,960,043 / 19.3%
Number/percentage of T's	49,022,622 / 30.56%
Number/percentage of G's	34,941,097 / 21.78%
Number/percentage of N's	3,232 / 0%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.3552
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2.4. Mapping Quality

Mean Mapping Quality	46.34
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2.5. Mismatches and indels

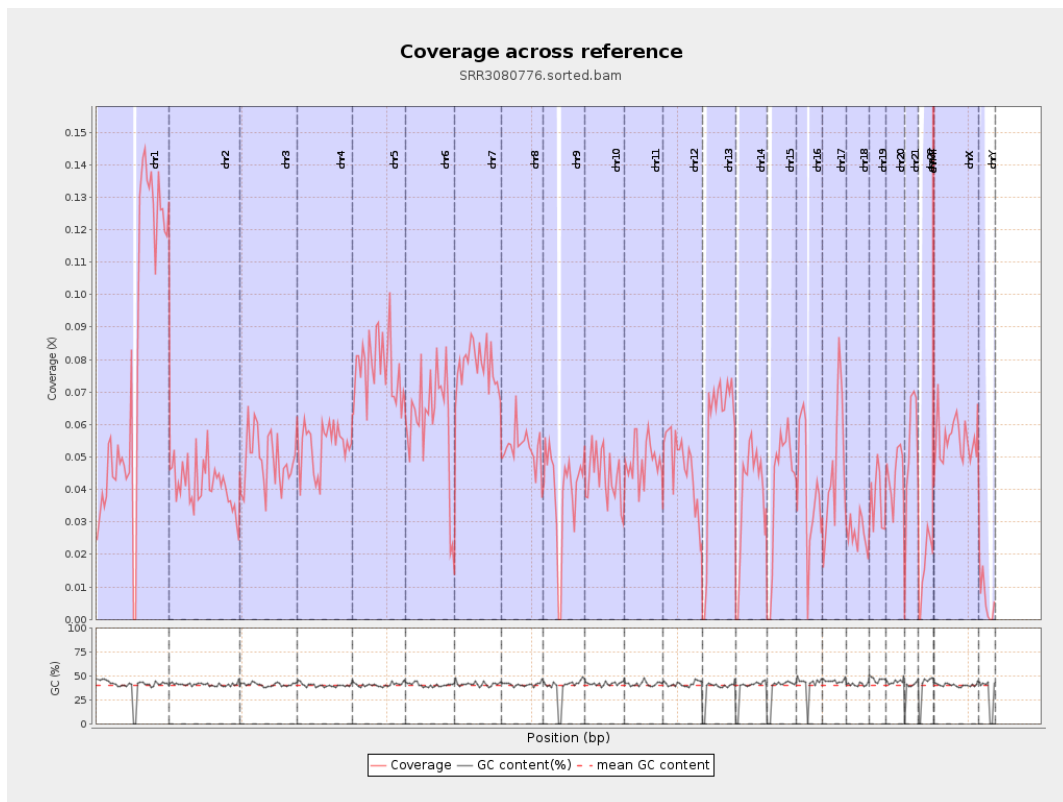
General error rate	0.76%
Mismatches	1,194,123
Insertions	11,994
Mapped reads with at least one insertion	0.5%
Deletions	34,896
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.89%

2.6. Chromosome stats

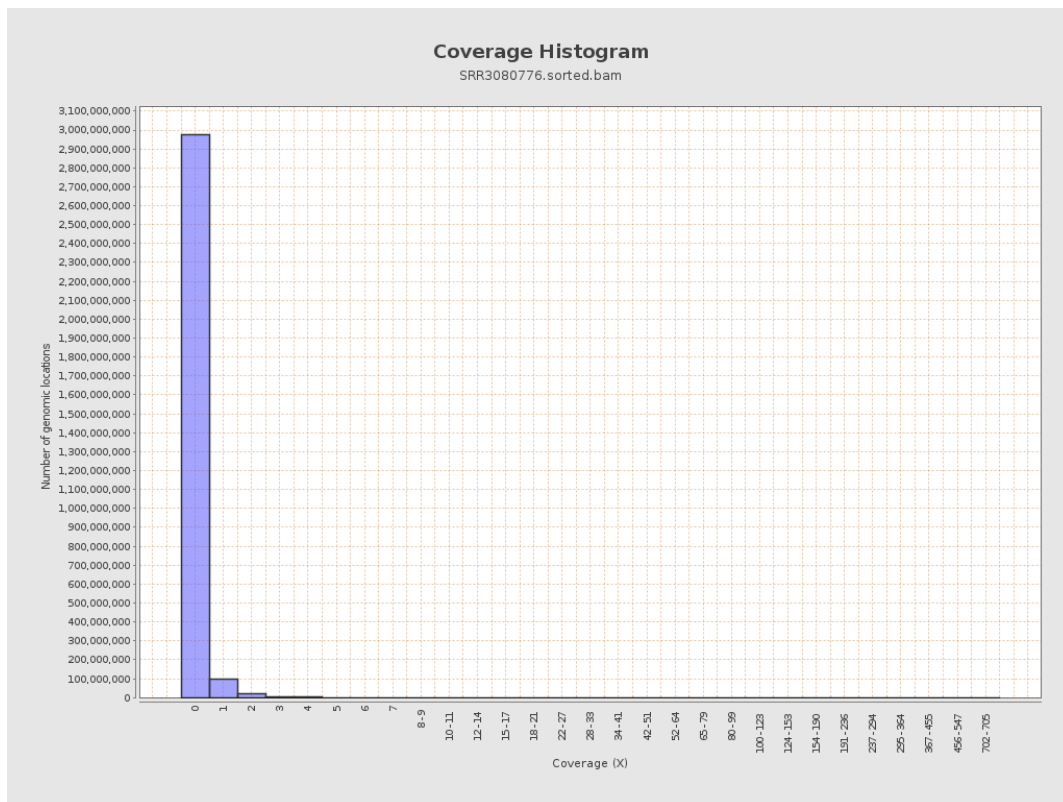
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19596248	0.0786	0.5759
chr2	243199373	10119022	0.0416	0.3966
chr3	198022430	9678991	0.0489	0.2765
chr4	191154276	10242509	0.0536	0.2991
chr5	180915260	13999218	0.0774	0.3507
chr6	171115067	10475380	0.0612	0.3599
chr7	159138663	12441153	0.0782	0.4644

chr8	146364022	7721305	0.0528	0.4387
chr9	141213431	5568319	0.0394	0.2829
chr10	135534747	5981870	0.0441	0.3013
chr11	135006516	6600287	0.0489	0.2979
chr12	133851895	6315451	0.0472	0.2736
chr13	115169878	6577329	0.0571	0.3026
chr14	107349540	4105588	0.0382	0.2509
chr15	102531392	4241980	0.0414	0.2627
chr16	90354753	3676020	0.0407	0.2591
chr17	81195210	3704602	0.0456	0.2761
chr18	78077248	2079704	0.0266	0.3906
chr19	59128983	2204170	0.0373	0.4102
chr20	63025520	2820377	0.0447	0.2691
chr21	48129895	2497019	0.0519	0.2939
chr22	51304566	846340	0.0165	0.1557
chrMT	16571	15782	0.9524	1.2872
chrX	155270560	8578640	0.0552	0.307
chrY	59373566	368818	0.0062	0.1312

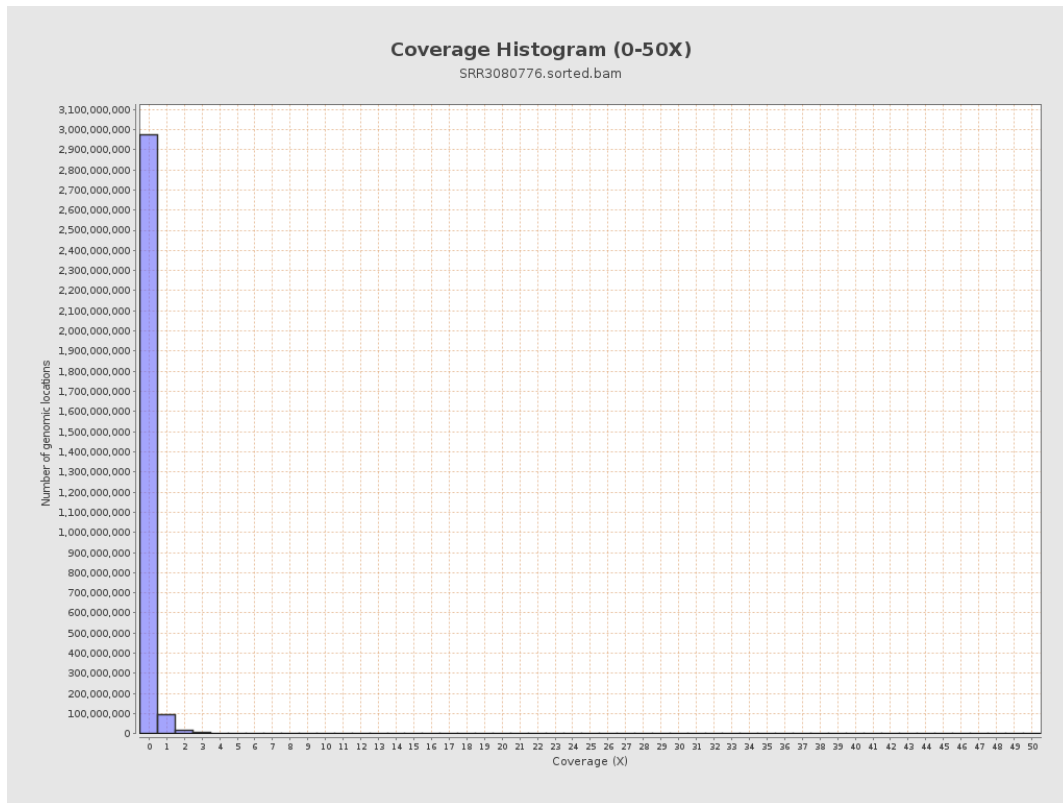
3. Results : Coverage across reference



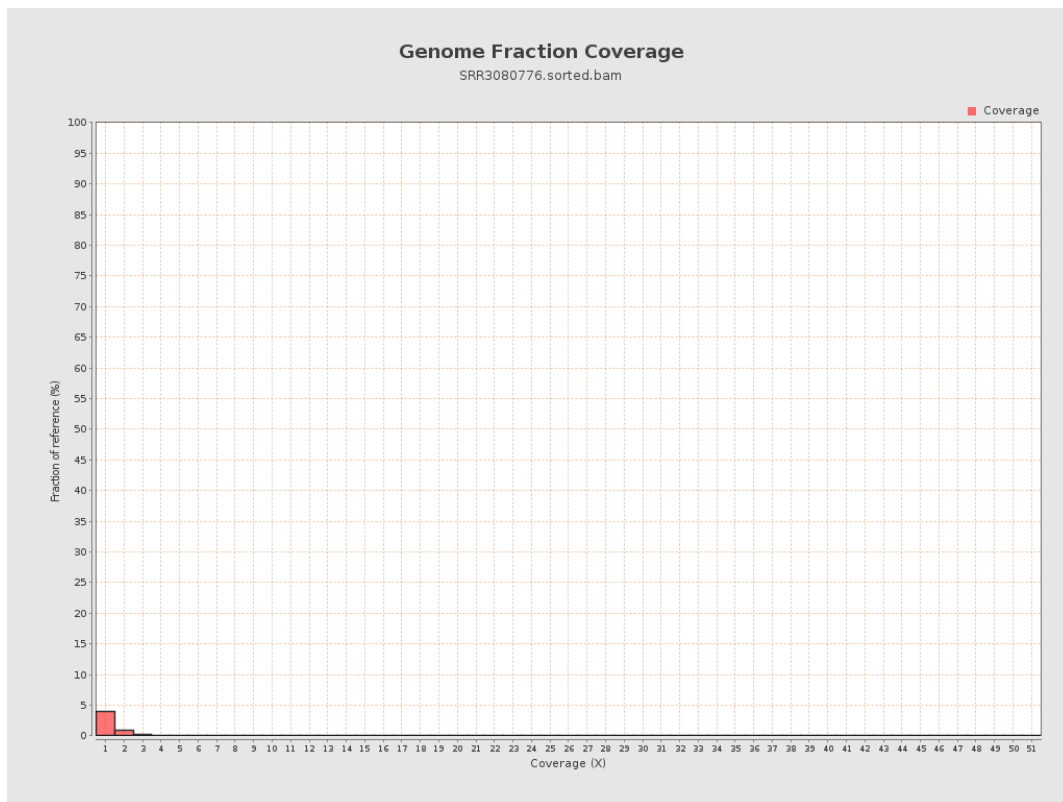
4. Results : Coverage Histogram



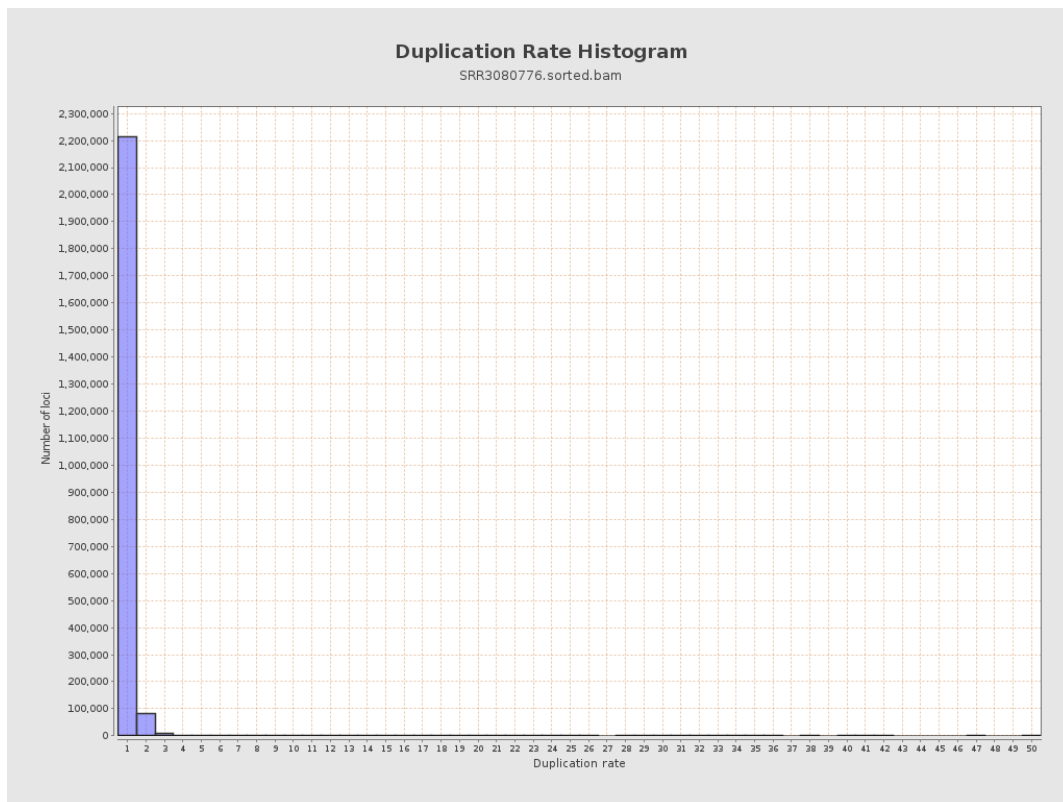
5. Results : Coverage Histogram (0-50X)



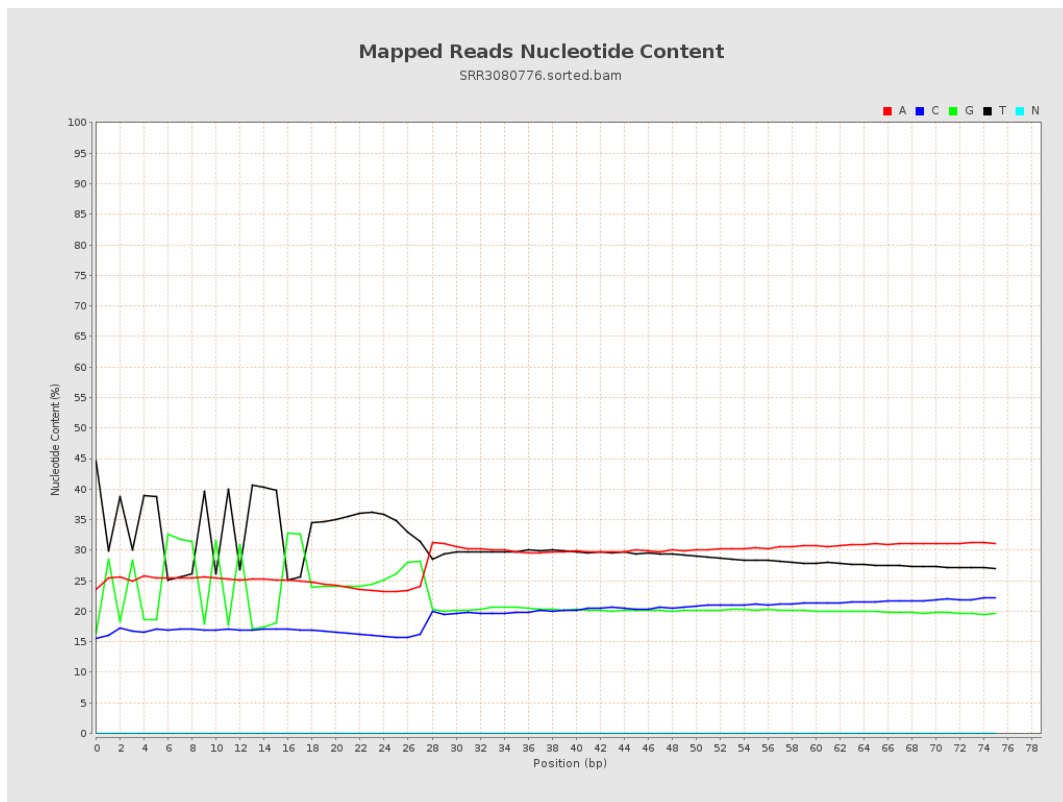
6. Results : Genome Fraction Coverage



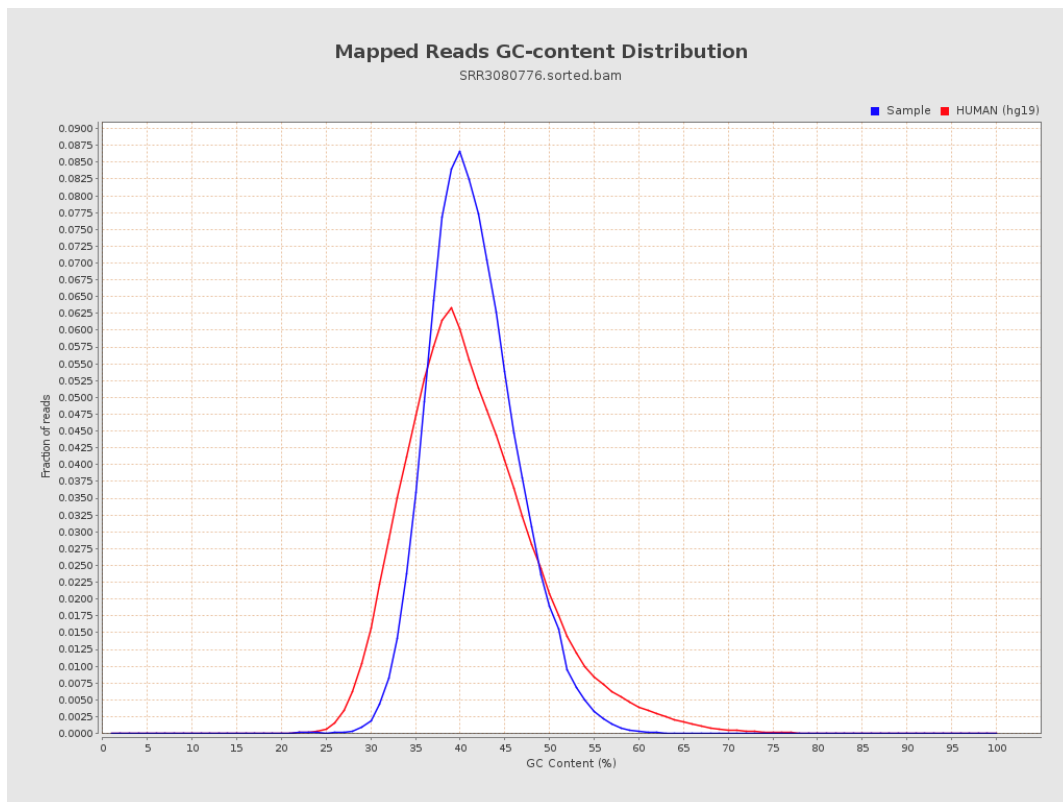
7. Results : Duplication Rate Histogram



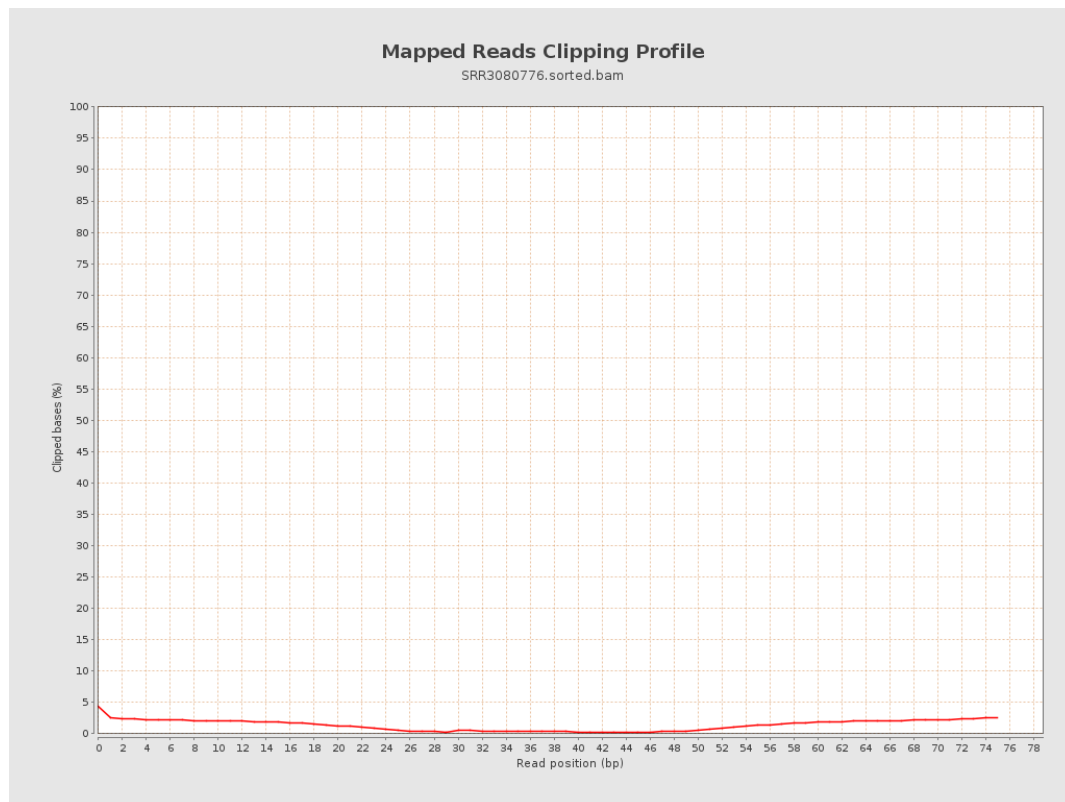
8. Results : Mapped Reads Nucleotide Content



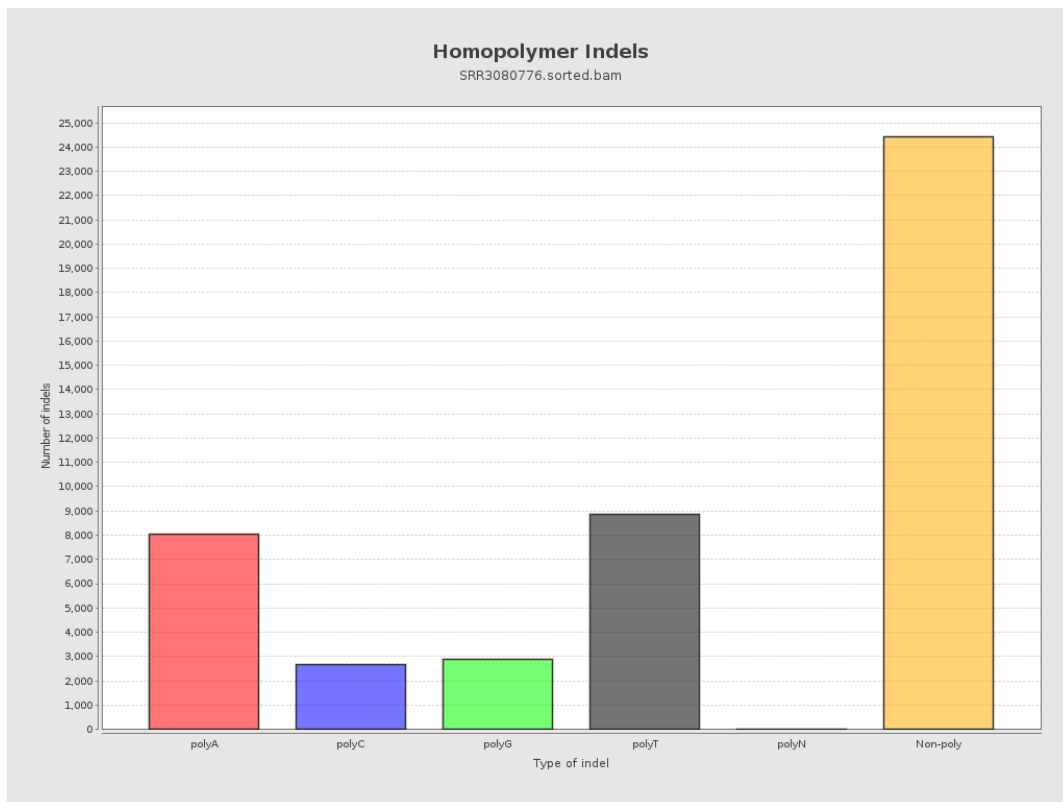
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

