

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:49:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068080.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_SRR6068080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:49:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,520,027
Mapped reads	2,280,656 / 90.5%
Unmapped reads	239,371 / 9.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,926 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	107,060 / 4.25%
Duplication rate	3.49%
Clipped reads	1,038,624 / 41.21%

2.2. ACGT Content

Number/percentage of A's	42,707,133 / 28.12%
Number/percentage of C's	27,707,678 / 18.24%
Number/percentage of T's	48,468,498 / 31.91%
Number/percentage of G's	33,001,025 / 21.73%
Number/percentage of N's	3,203 / 0%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.5131
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2.4. Mapping Quality

Mean Mapping Quality	45.75
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2.5. Mismatches and indels

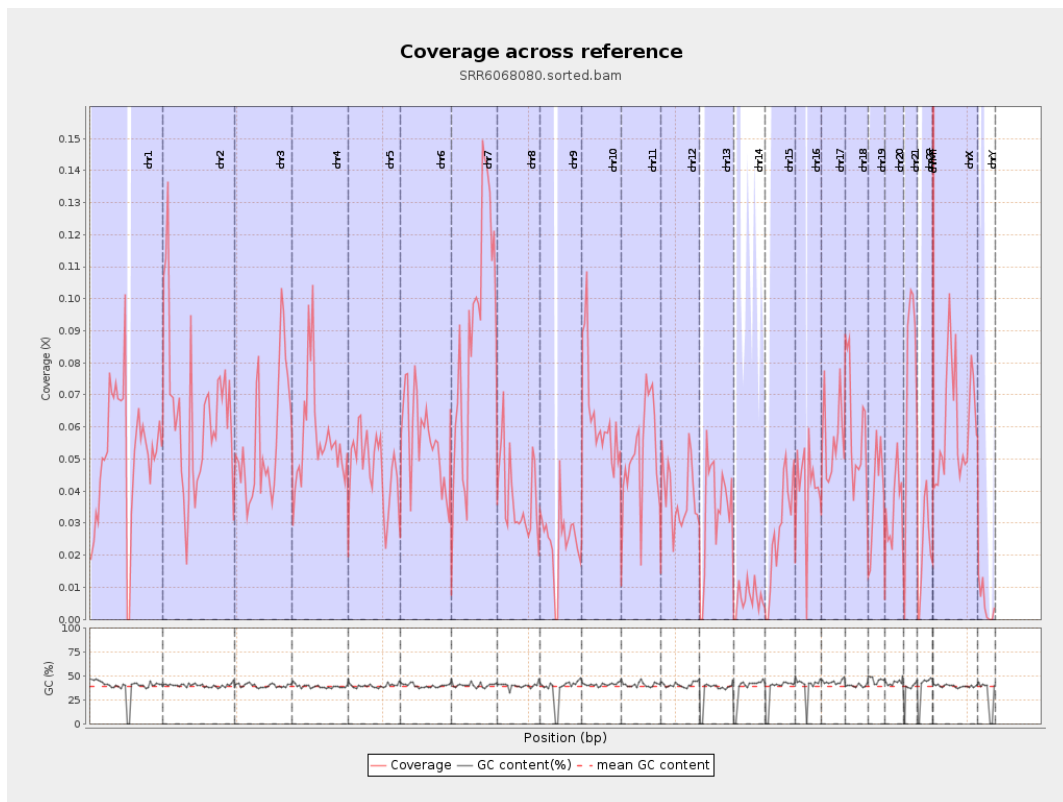
General error rate	0.79%
Mismatches	1,185,102
Insertions	11,752
Mapped reads with at least one insertion	0.51%
Deletions	41,607
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.94%

2.6. Chromosome stats

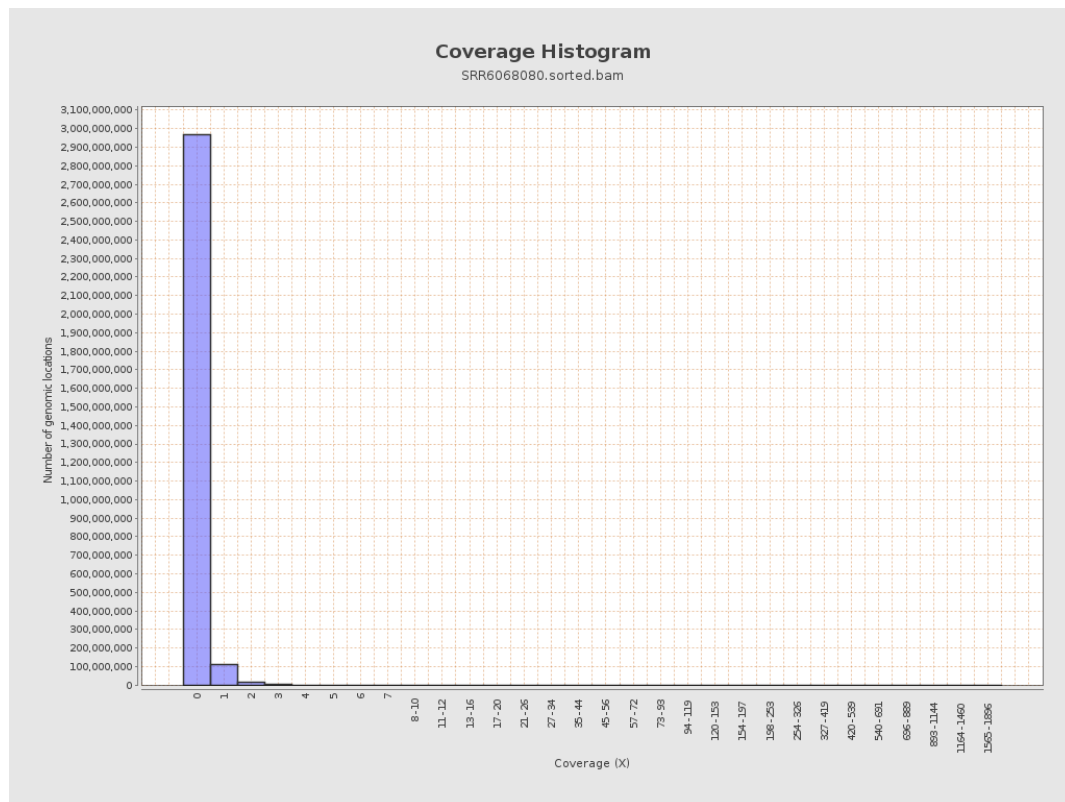
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12851952	0.0516	0.9402
chr2	243199373	15511970	0.0638	0.555
chr3	198022430	11095390	0.056	0.2717
chr4	191154276	10869086	0.0569	0.2863
chr5	180915260	8463833	0.0468	0.251
chr6	171115067	9661657	0.0565	0.3096
chr7	159138663	14201414	0.0892	0.7422

chr8	146364022	5578735	0.0381	1.0995
chr9	141213431	3464166	0.0245	0.4
chr10	135534747	8609773	0.0635	0.3587
chr11	135006516	7046966	0.0522	0.391
chr12	133851895	5188782	0.0388	0.2528
chr13	115169878	3943819	0.0342	0.2129
chr14	107349540	720513	0.0067	0.1754
chr15	102531392	2869116	0.028	0.2
chr16	90354753	3672072	0.0406	0.2586
chr17	81195210	4615634	0.0568	0.3012
chr18	78077248	4622927	0.0592	0.7603
chr19	59128983	2285138	0.0386	0.6687
chr20	63025520	2212239	0.0351	0.2536
chr21	48129895	3534019	0.0734	0.3201
chr22	51304566	1147059	0.0224	0.1672
chrMT	16571	30874	1.8631	1.8629
chrX	155270560	9469790	0.061	0.3395
chrY	59373566	287779	0.0048	0.111

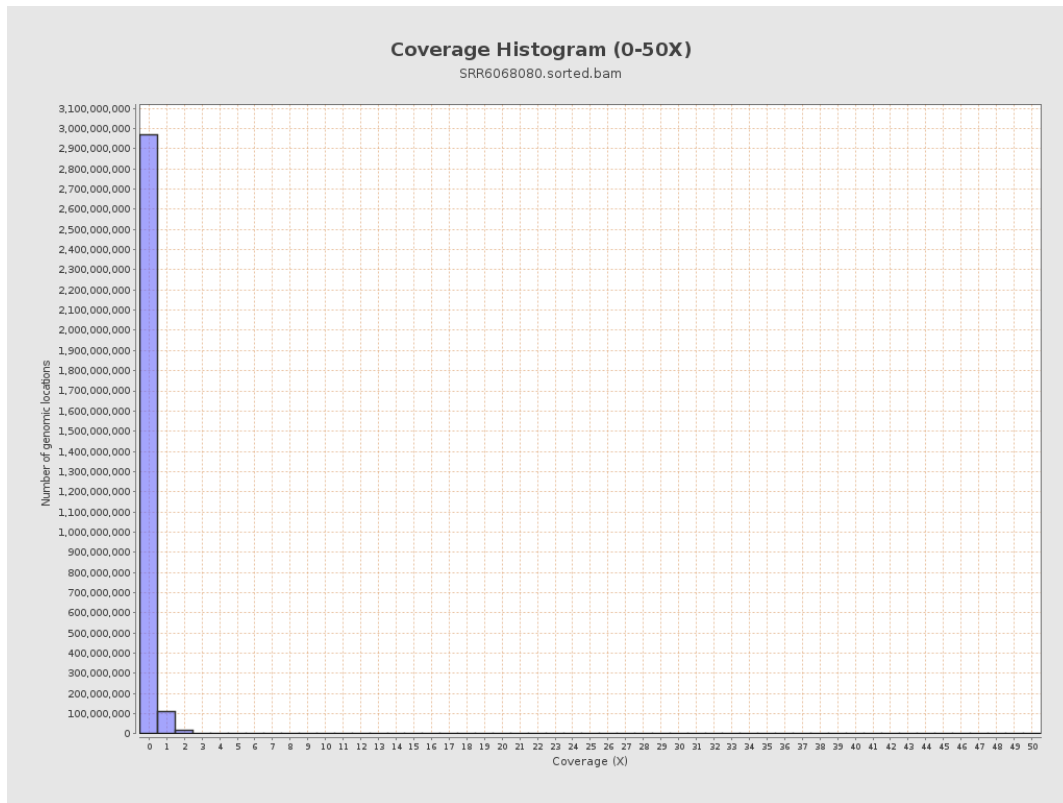
3. Results : Coverage across reference



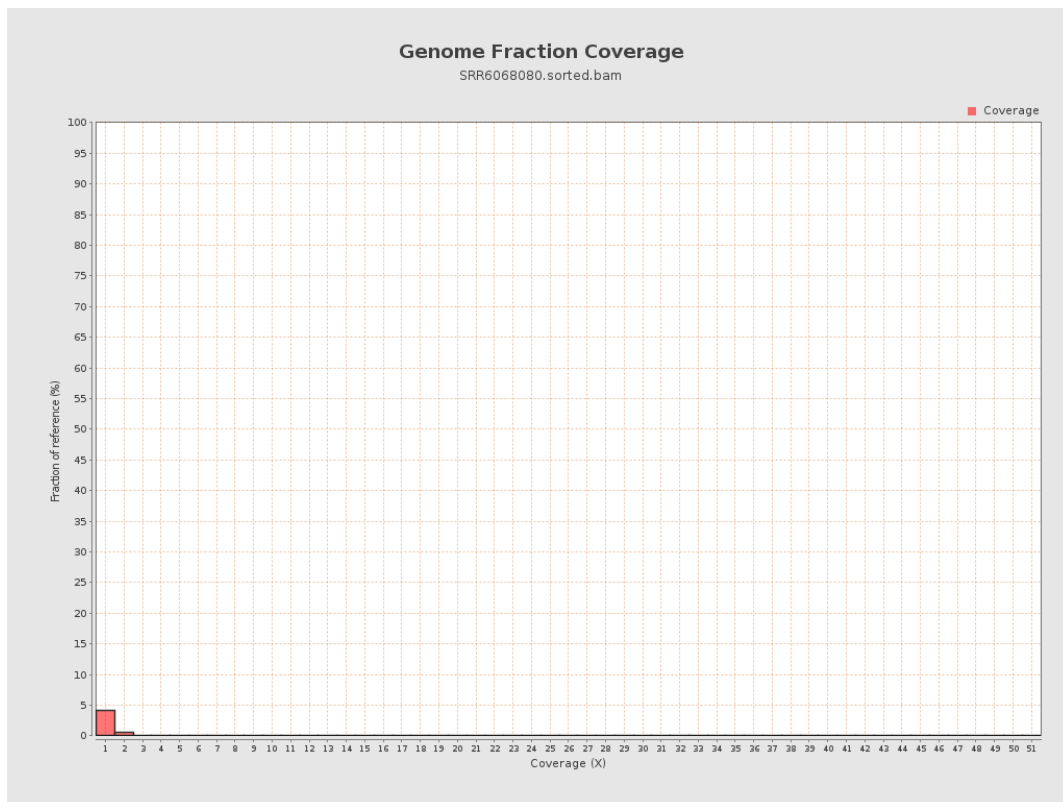
4. Results : Coverage Histogram



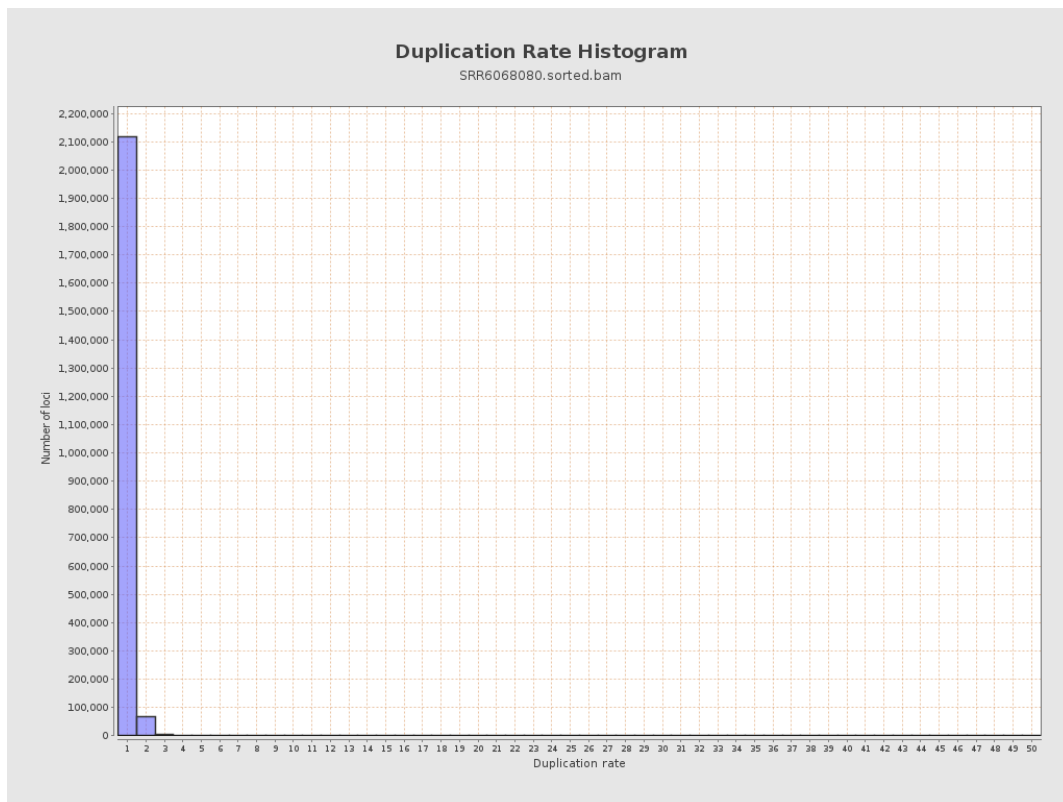
5. Results : Coverage Histogram (0-50X)



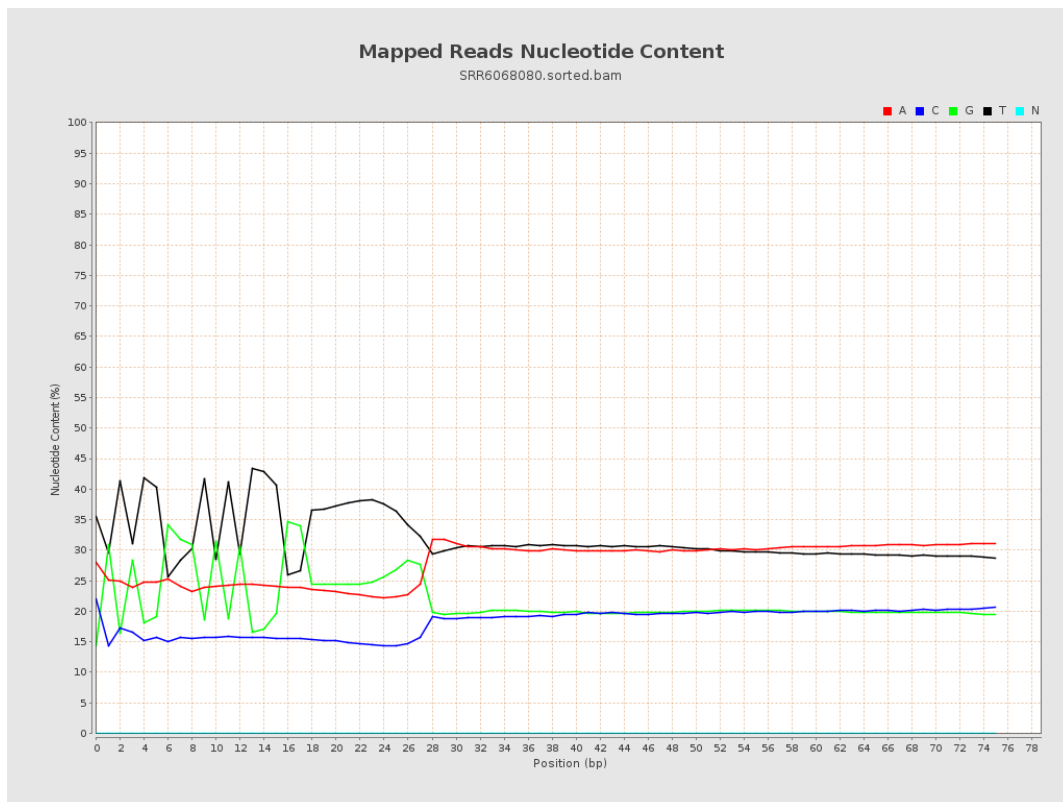
6. Results : Genome Fraction Coverage



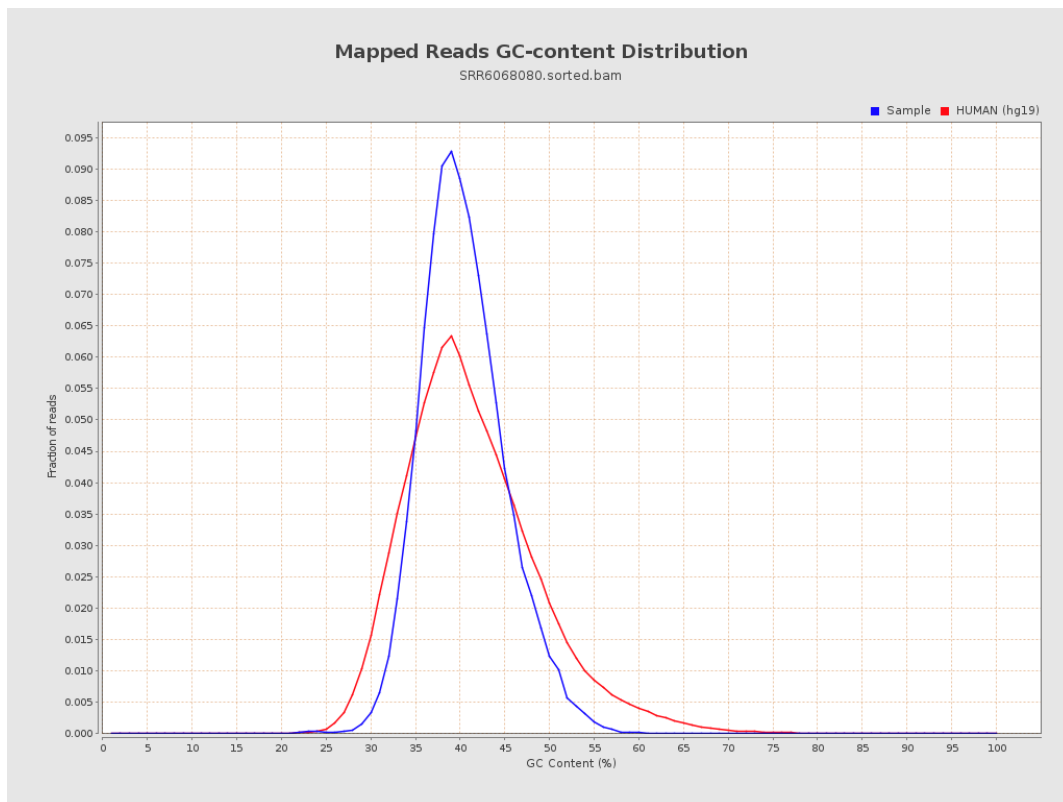
7. Results : Duplication Rate Histogram



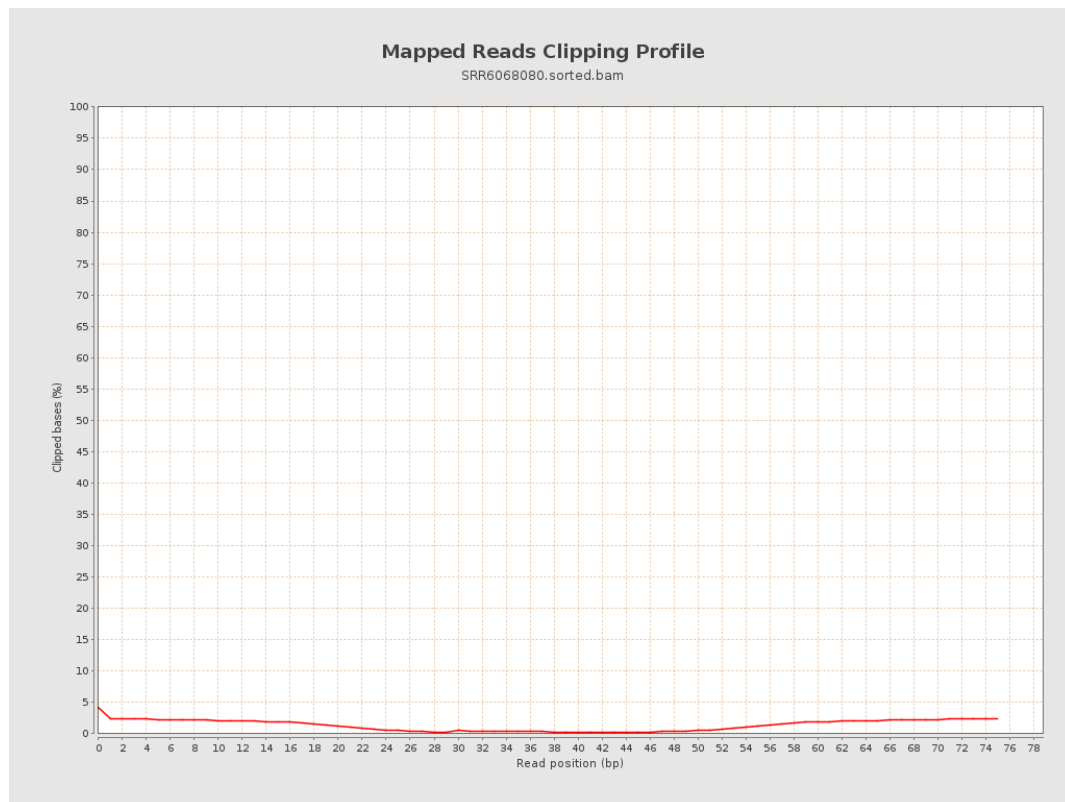
8. Results : Mapped Reads Nucleotide Content



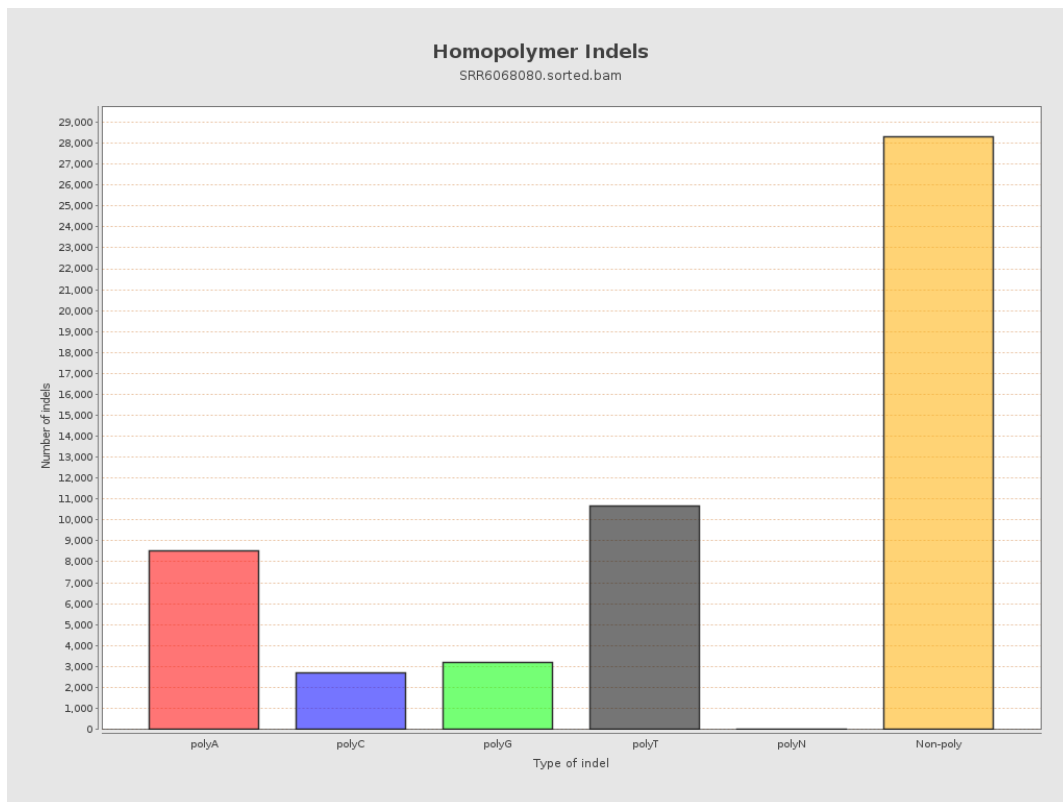
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

