

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:58:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068177.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_SRR6068177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:58:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,399,613
Mapped reads	3,193,525 / 93.94%
Unmapped reads	206,088 / 6.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,913 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	331,115 / 9.74%
Duplication rate	8.63%
Clipped reads	1,686,091 / 49.6%

2.2. ACGT Content

Number/percentage of A's	54,282,509 / 26.45%
Number/percentage of C's	36,257,591 / 17.67%
Number/percentage of T's	67,466,765 / 32.88%
Number/percentage of G's	47,190,020 / 22.99%
Number/percentage of N's	23,144 / 0.01%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0663

Standard Deviation	0.7441
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2.4. Mapping Quality

Mean Mapping Quality	45.96
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2.5. Mismatches and indels

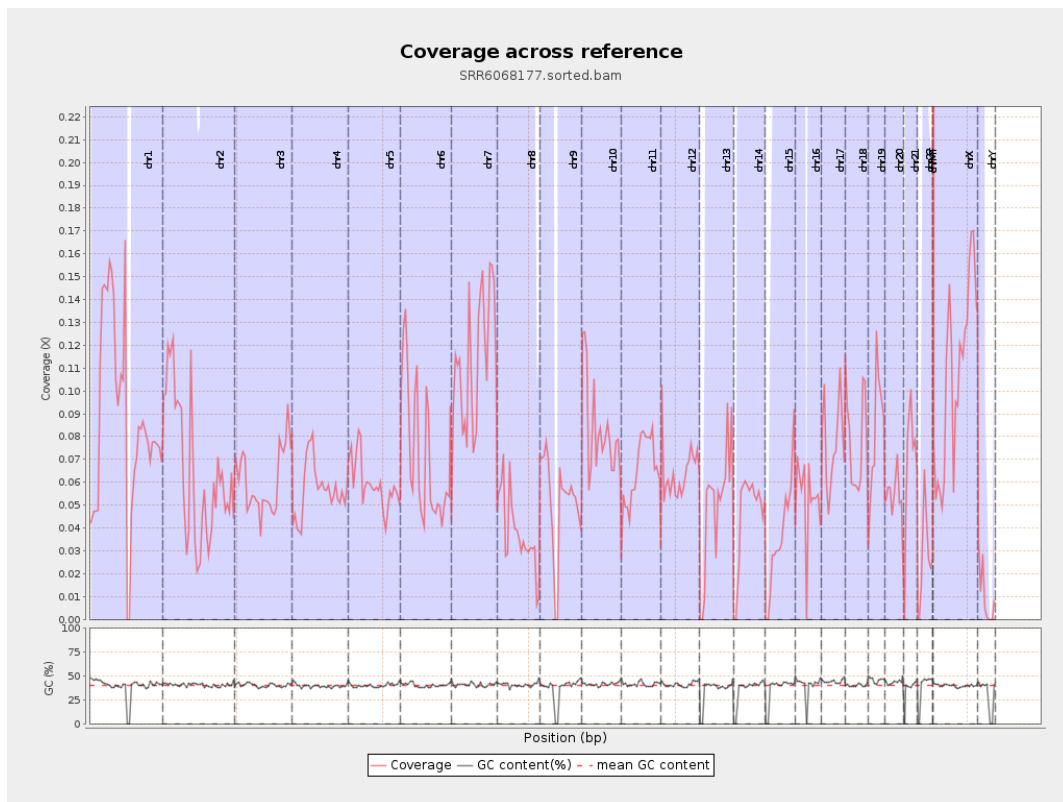
General error rate	0.59%
Mismatches	1,178,424
Insertions	13,053
Mapped reads with at least one insertion	0.4%
Deletions	51,150
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.16%

2.6. Chromosome stats

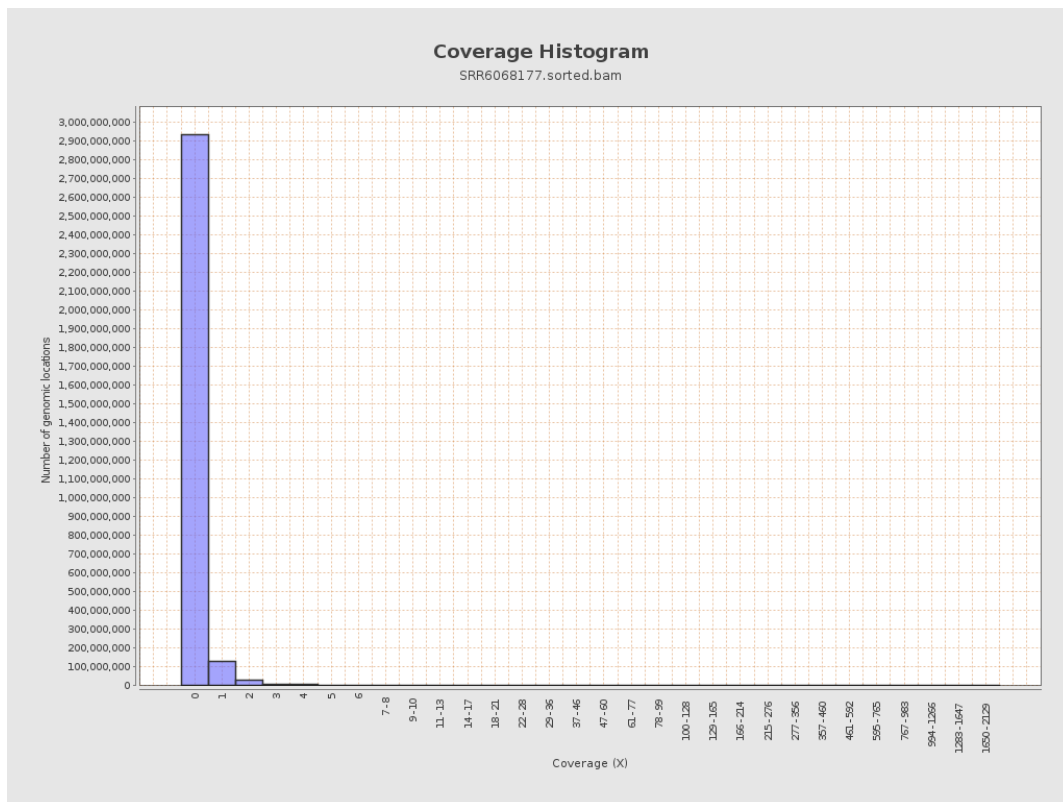
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21811621	0.0875	1.7762
chr2	243199373	15888681	0.0653	0.9293
chr3	198022430	12020412	0.0607	0.3034
chr4	191154276	10908369	0.0571	0.312
chr5	180915260	10736280	0.0593	0.304
chr6	171115067	12353610	0.0722	0.4437
chr7	159138663	18081512	0.1136	1.0075

chr8	146364022	5498259	0.0376	0.843
chr9	141213431	7291624	0.0516	0.4852
chr10	135534747	11259647	0.0831	0.5112
chr11	135006516	8828462	0.0654	0.411
chr12	133851895	8625051	0.0644	0.3477
chr13	115169878	5842019	0.0507	0.3054
chr14	107349540	4937537	0.046	0.3188
chr15	102531392	3726742	0.0363	0.2677
chr16	90354753	4720756	0.0522	0.3114
chr17	81195210	6364229	0.0784	0.375
chr18	78077248	6034308	0.0773	0.9209
chr19	59128983	4878717	0.0825	1.1433
chr20	63025520	3415259	0.0542	0.3116
chr21	48129895	3231010	0.0671	0.3334
chr22	51304566	1397617	0.0272	0.1978
chrMT	16571	380106	22.938	12.4246
chrX	155270560	16478947	0.1061	0.4677
chrY	59373566	598504	0.0101	0.2723

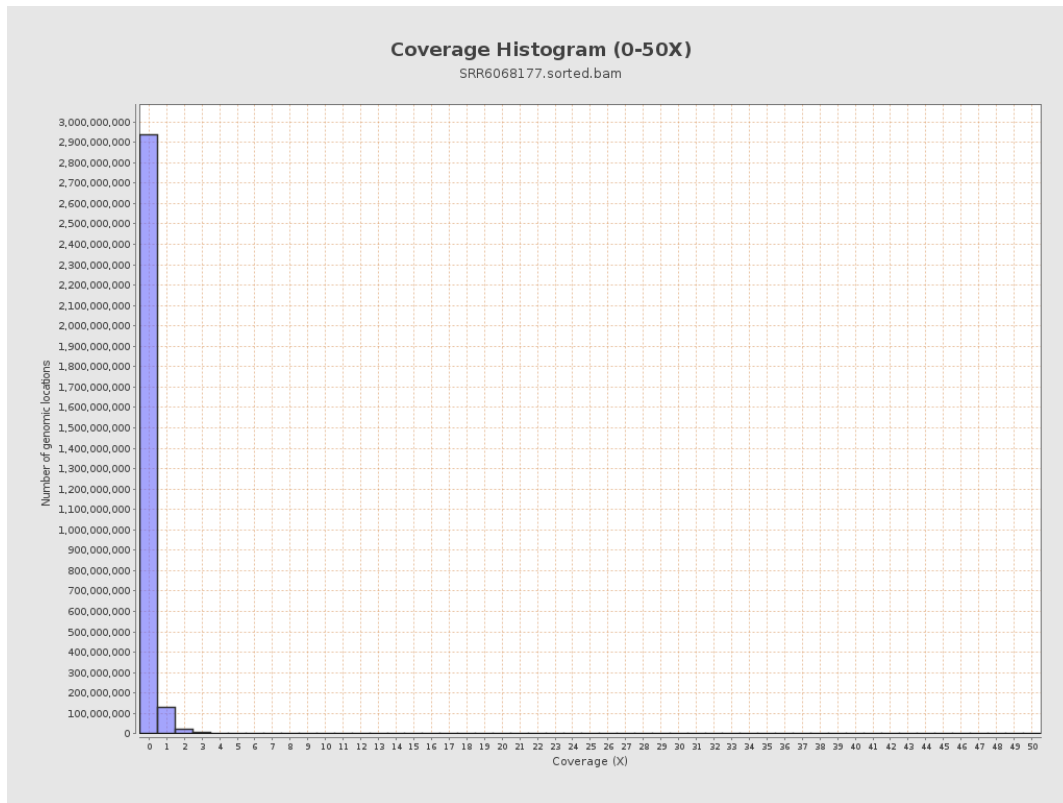
3. Results : Coverage across reference



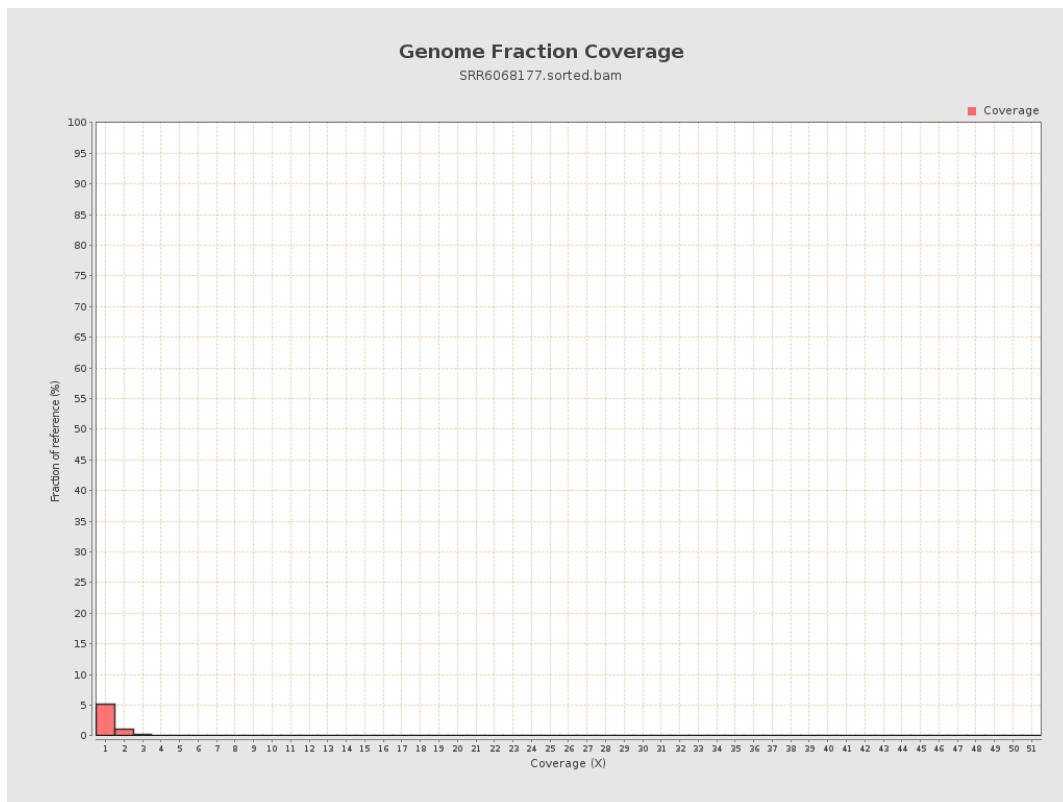
4. Results : Coverage Histogram



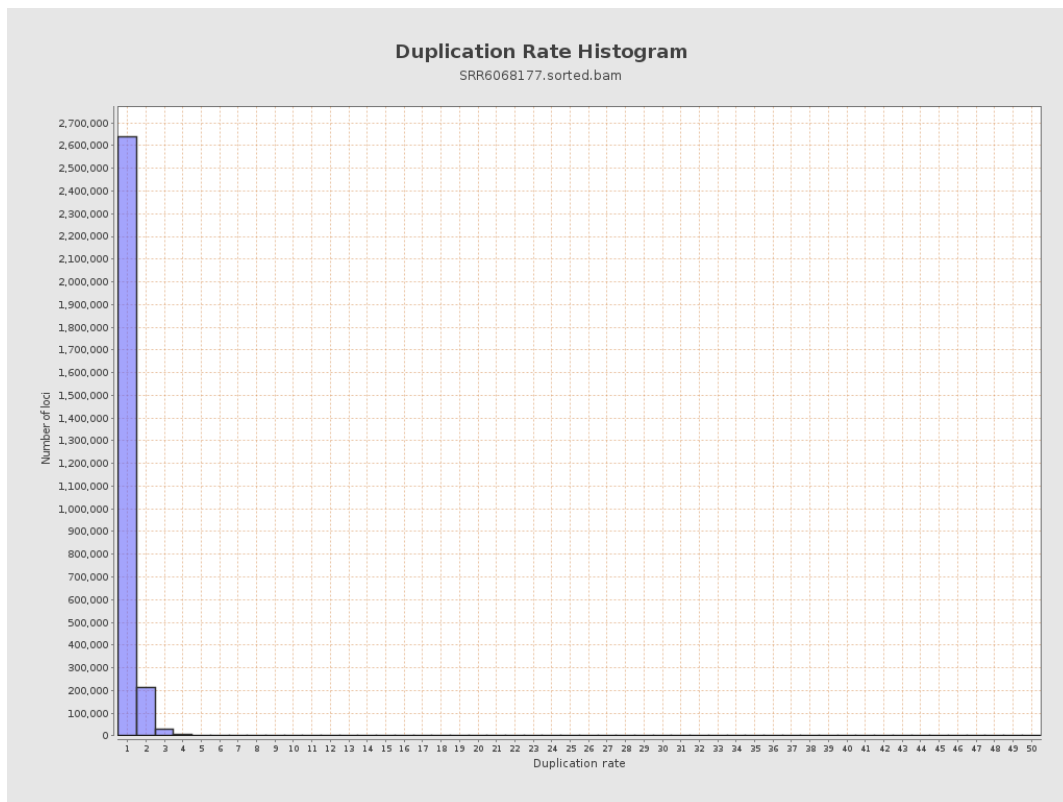
5. Results : Coverage Histogram (0-50X)



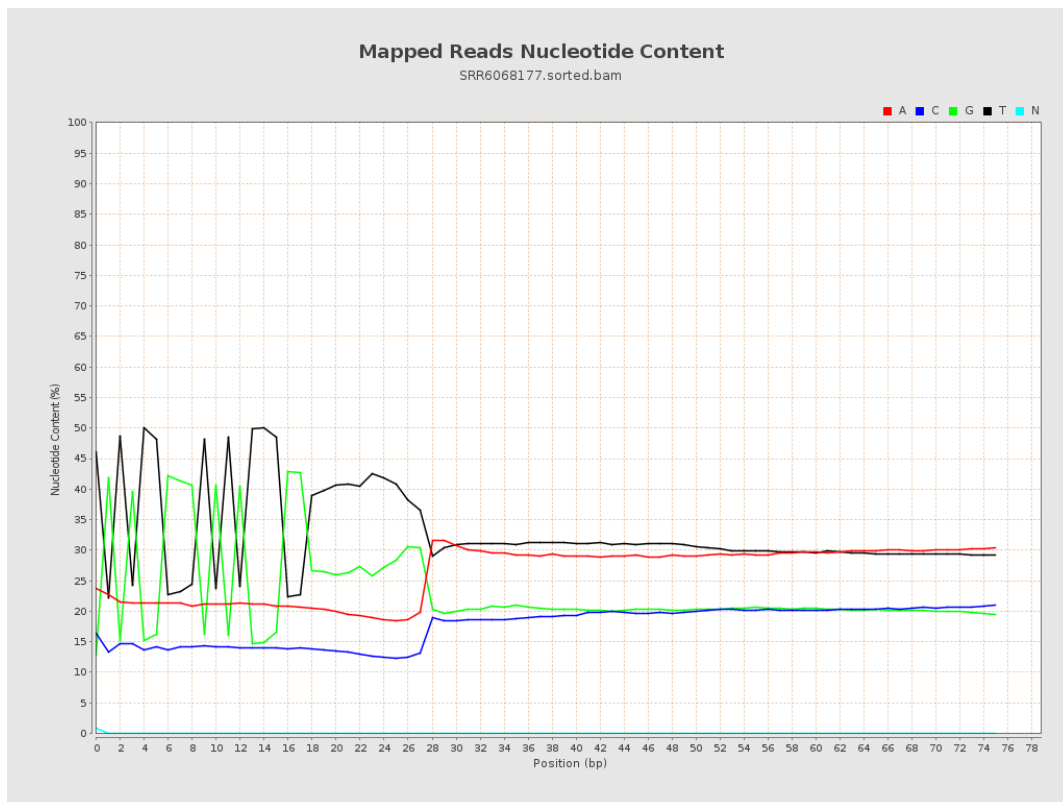
6. Results : Genome Fraction Coverage



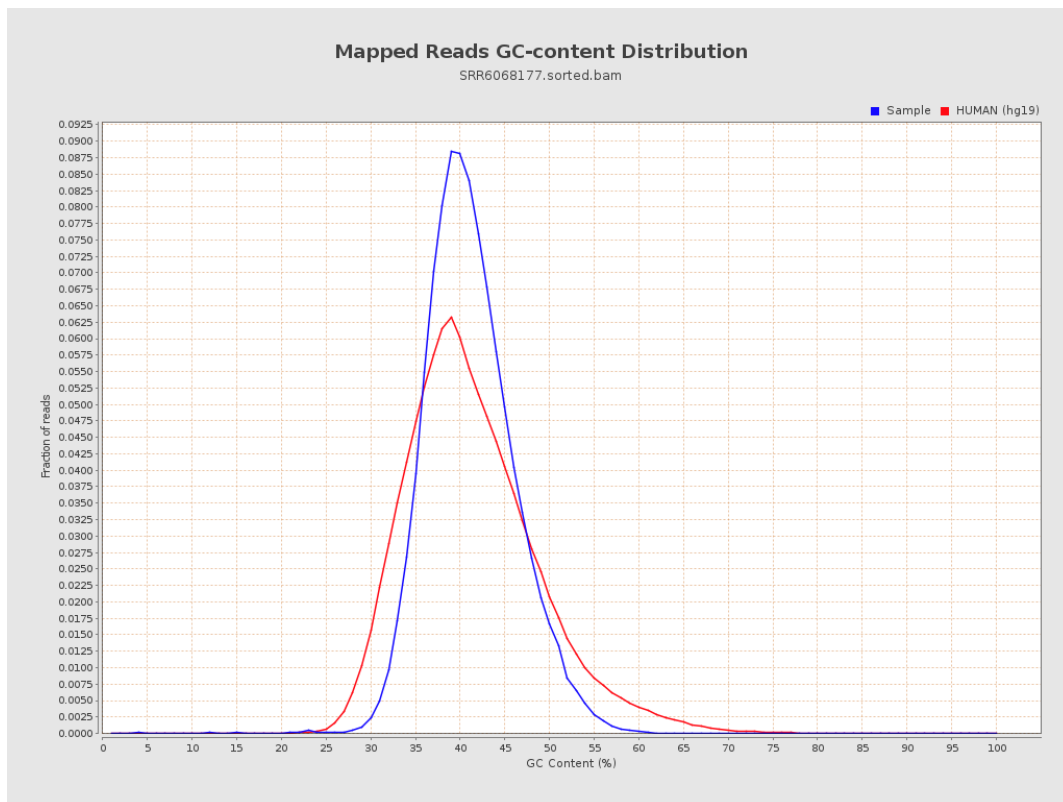
7. Results : Duplication Rate Histogram



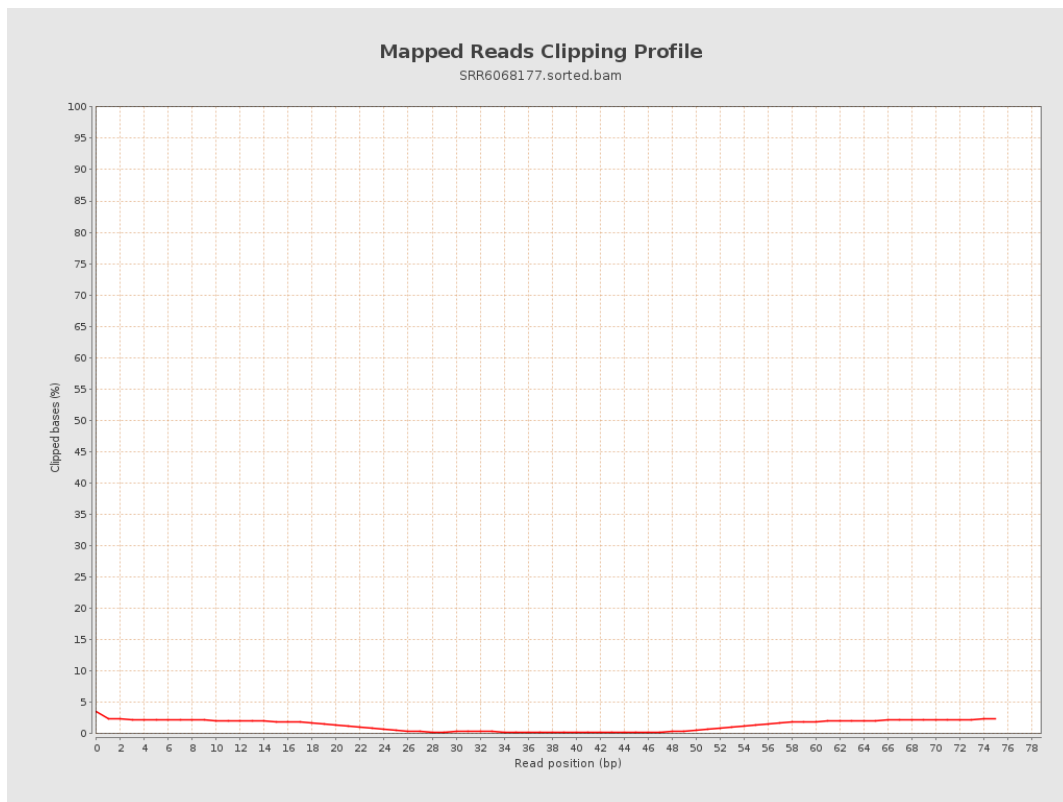
8. Results : Mapped Reads Nucleotide Content



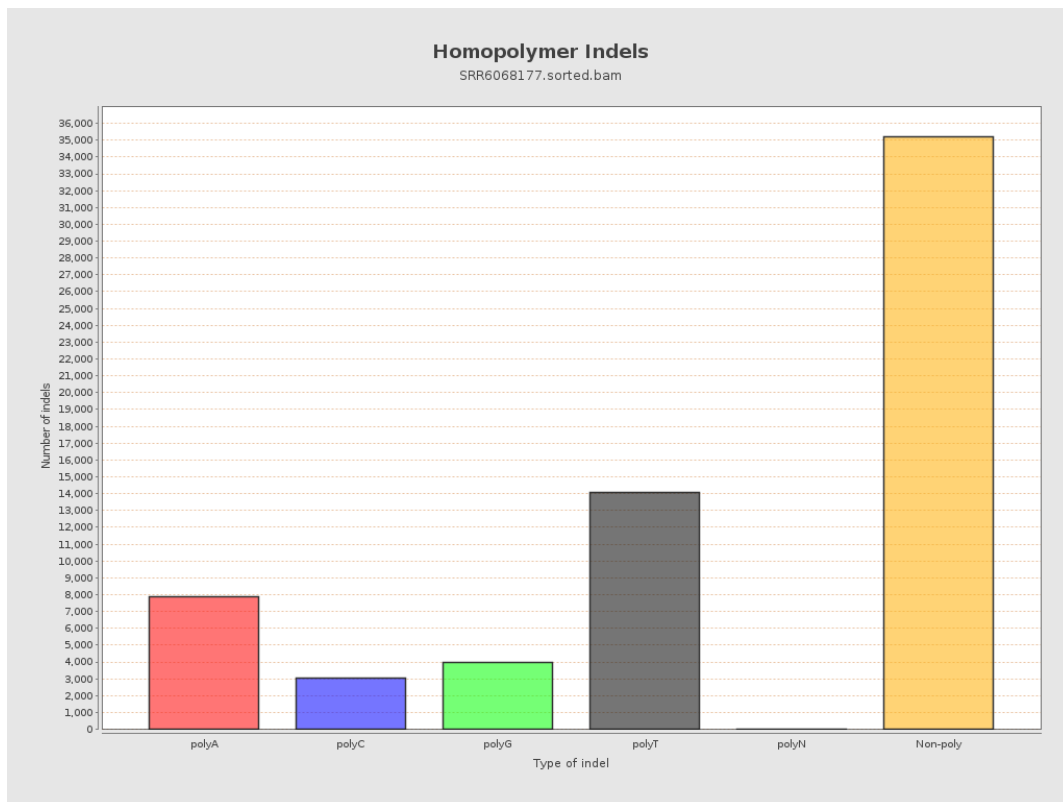
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

