

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:58:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068113.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_SRR6068113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:58:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,437,196
Mapped reads	1,795,456 / 73.67%
Unmapped reads	641,740 / 26.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,000 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	382,723 / 15.7%
Duplication rate	13.62%
Clipped reads	858,632 / 35.23%

2.2. ACGT Content

Number/percentage of A's	32,426,524 / 27.54%
Number/percentage of C's	20,805,270 / 17.67%
Number/percentage of T's	38,381,011 / 32.59%
Number/percentage of G's	26,004,734 / 22.08%
Number/percentage of N's	136,416 / 0.12%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.5479
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2.4. Mapping Quality

Mean Mapping Quality	46.61
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2.5. Mismatches and indels

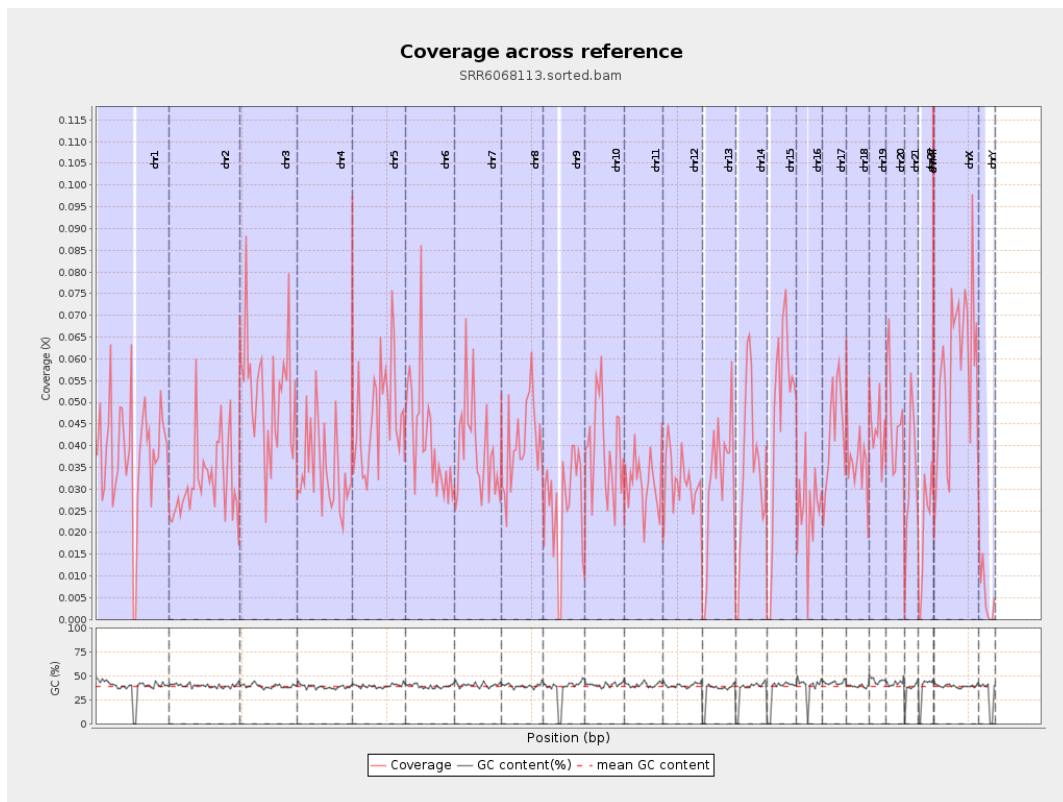
General error rate	0.88%
Mismatches	1,017,136
Insertions	8,738
Mapped reads with at least one insertion	0.48%
Deletions	27,825
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48%

2.6. Chromosome stats

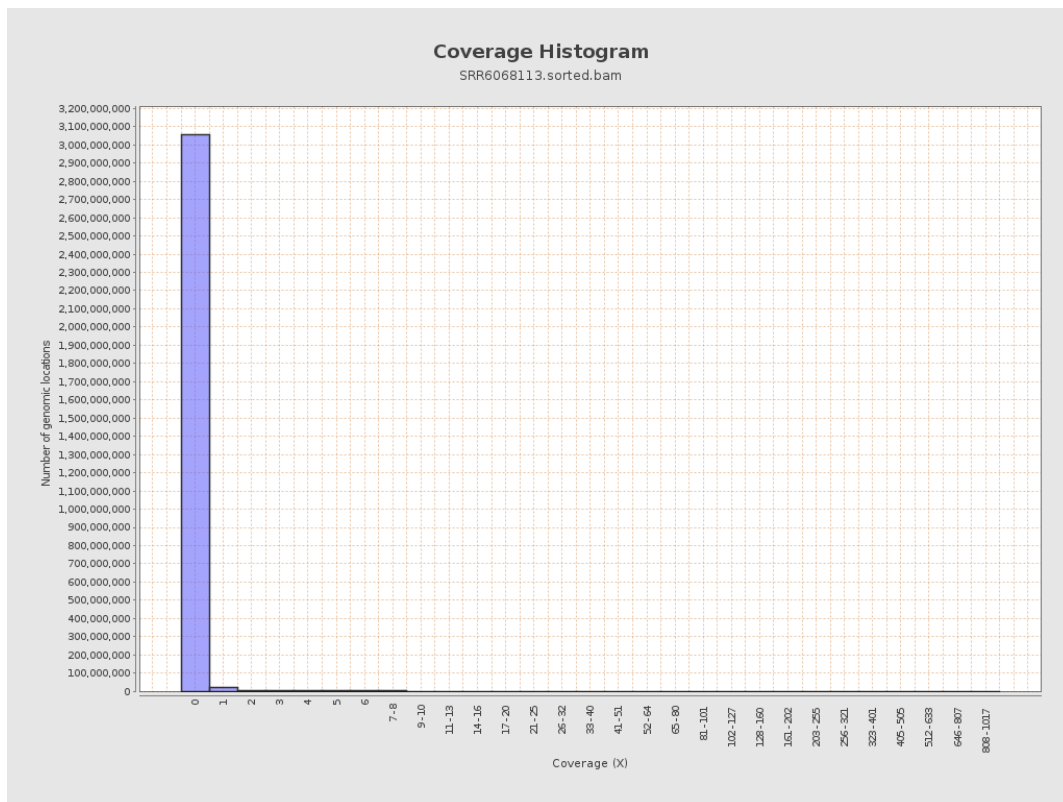
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9557179	0.0383	0.8795
chr2	243199373	7784891	0.032	0.5235
chr3	198022430	10301427	0.052	0.5585
chr4	191154276	6637658	0.0347	0.4542
chr5	180915260	8529269	0.0471	0.5227
chr6	171115067	7061577	0.0413	0.5137
chr7	159138663	6222961	0.0391	0.5991

chr8	146364022	5939280	0.0406	0.6584
chr9	141213431	3793238	0.0269	0.4166
chr10	135534747	5330161	0.0393	0.5218
chr11	135006516	4278587	0.0317	0.4401
chr12	133851895	4215125	0.0315	0.4295
chr13	115169878	3606276	0.0313	0.4308
chr14	107349540	3722767	0.0347	0.4421
chr15	102531392	4788810	0.0467	0.5226
chr16	90354753	2307559	0.0255	0.3786
chr17	81195210	3485095	0.0429	0.4803
chr18	78077248	2853001	0.0365	0.5987
chr19	59128983	2579870	0.0436	0.6301
chr20	63025520	2914095	0.0462	0.5135
chr21	48129895	1539325	0.032	0.4246
chr22	51304566	1074926	0.021	0.3176
chrMT	16571	7001	0.4225	1.1937
chrX	155270560	8945487	0.0576	0.5982
chrY	59373566	323800	0.0055	0.1624

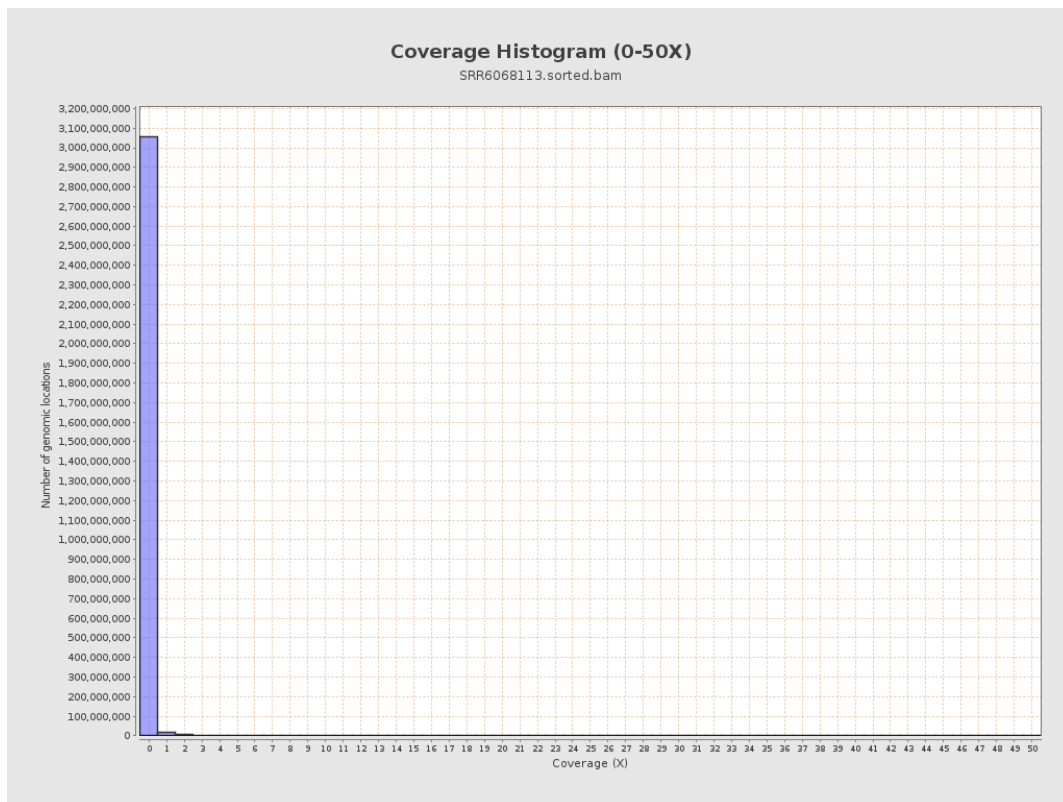
3. Results : Coverage across reference



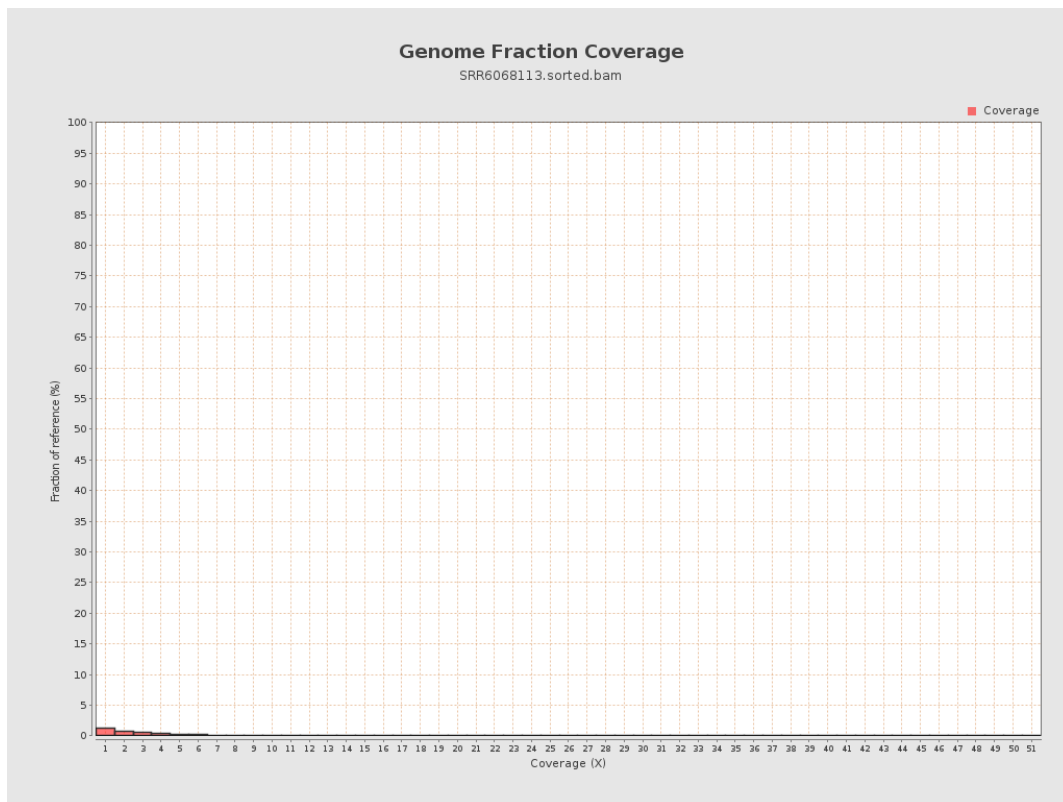
4. Results : Coverage Histogram



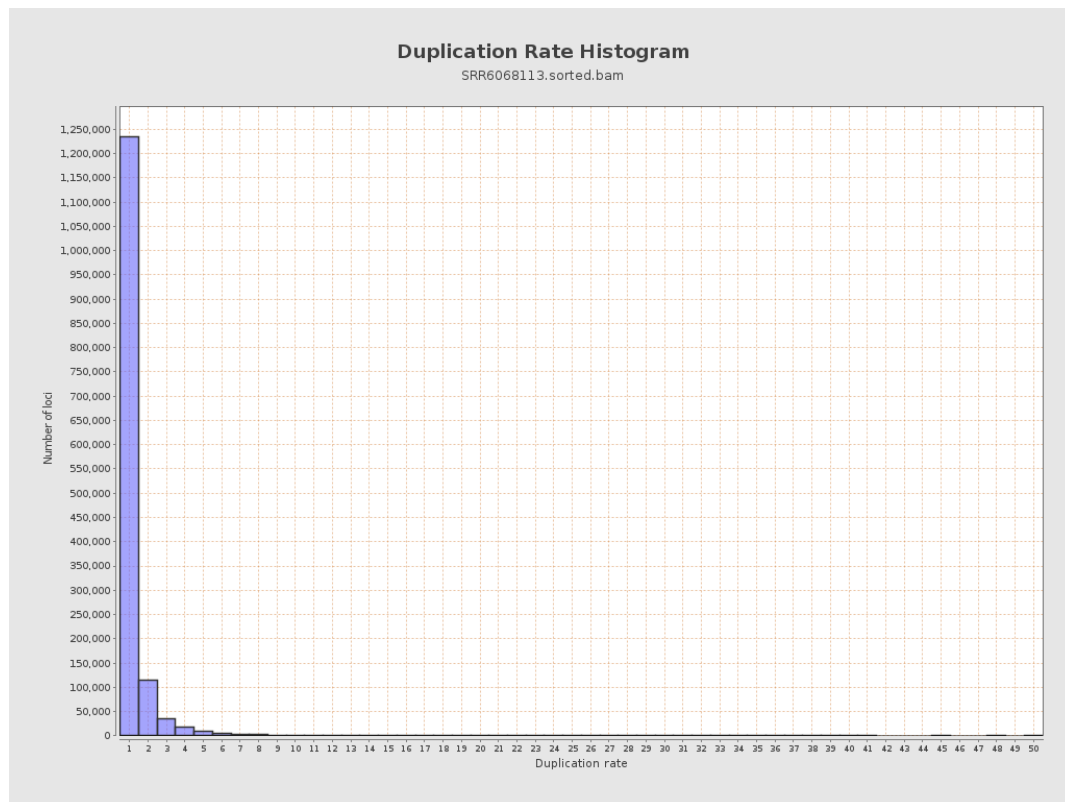
5. Results : Coverage Histogram (0-50X)



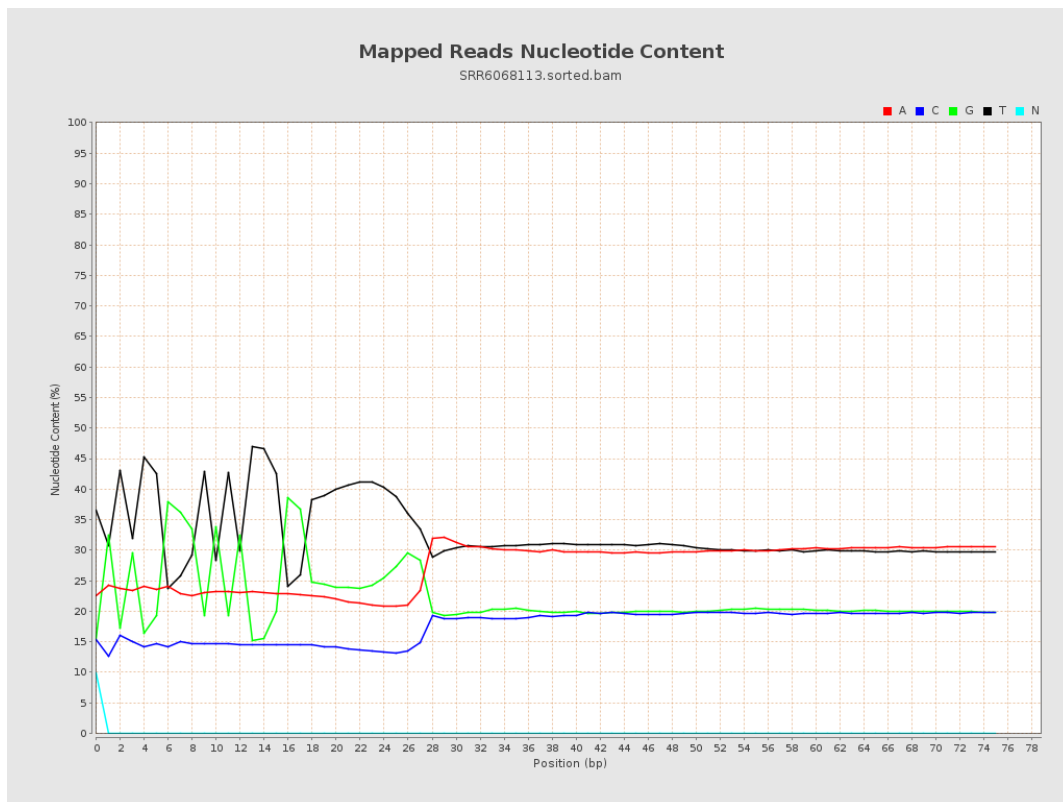
6. Results : Genome Fraction Coverage



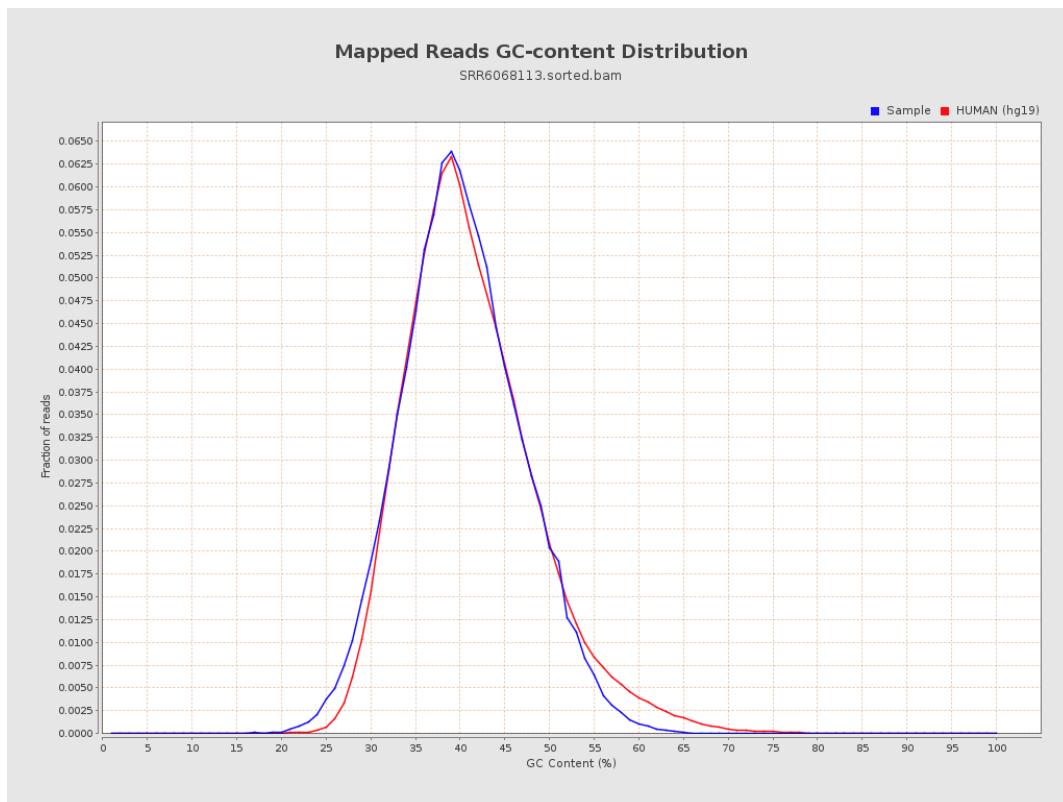
7. Results : Duplication Rate Histogram



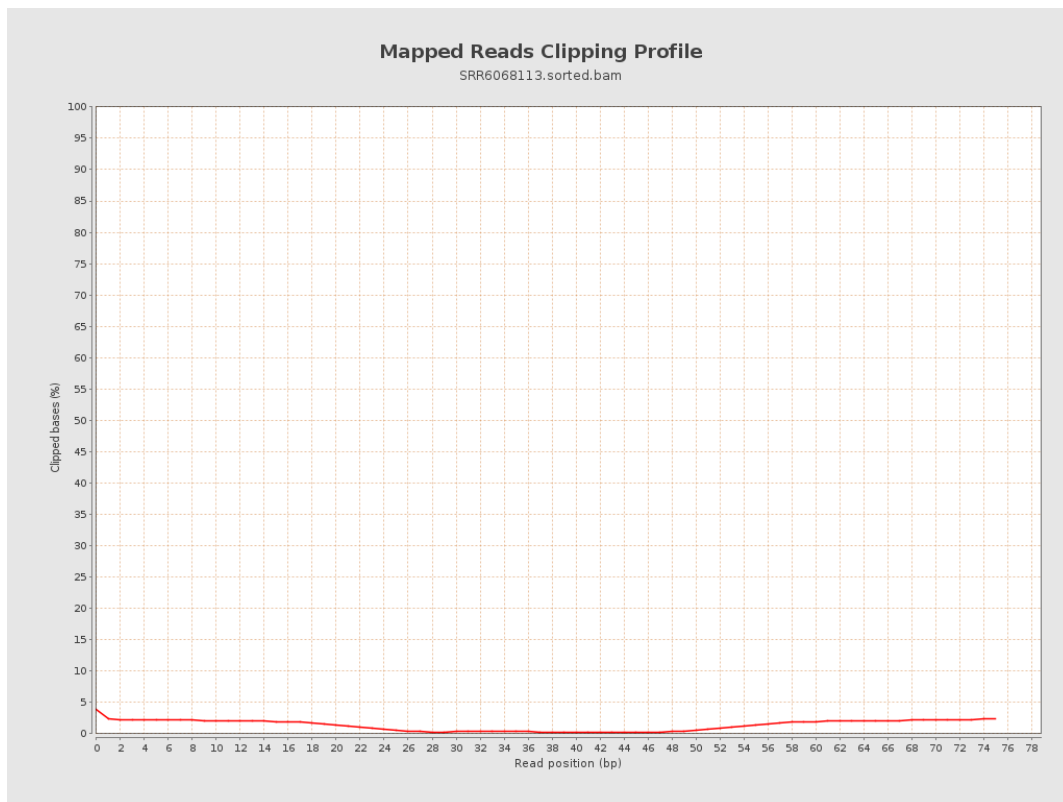
8. Results : Mapped Reads Nucleotide Content



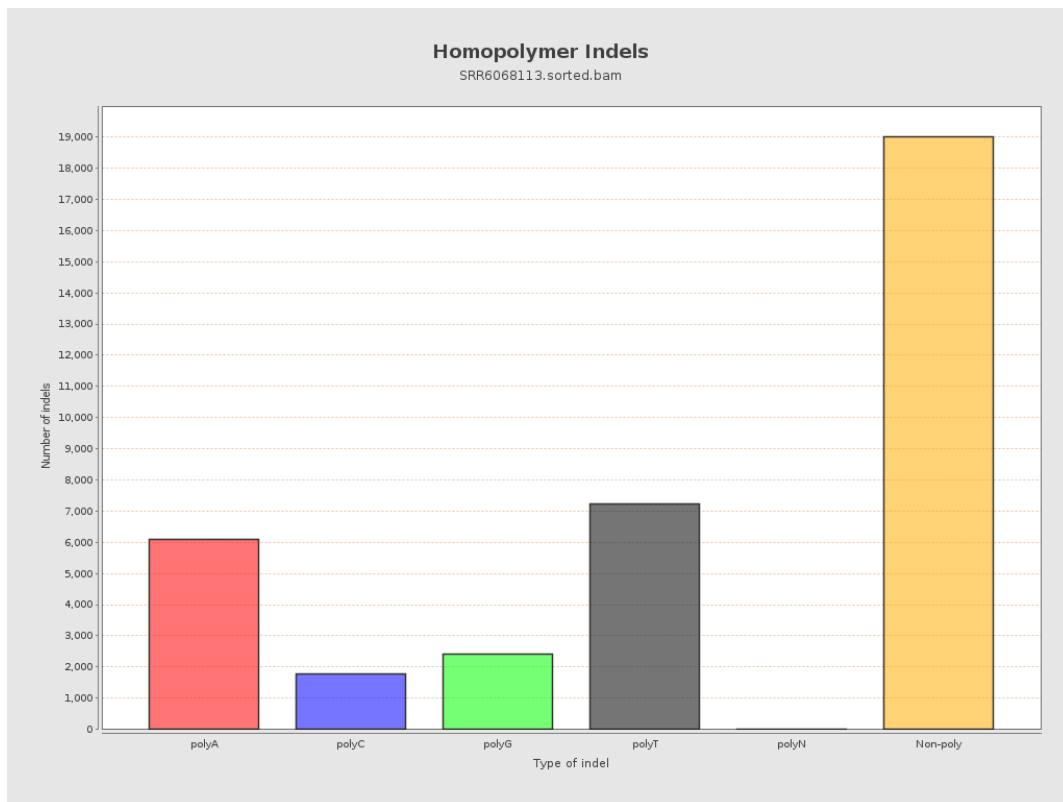
9. Results : Mapped Reads GC-content Distribution



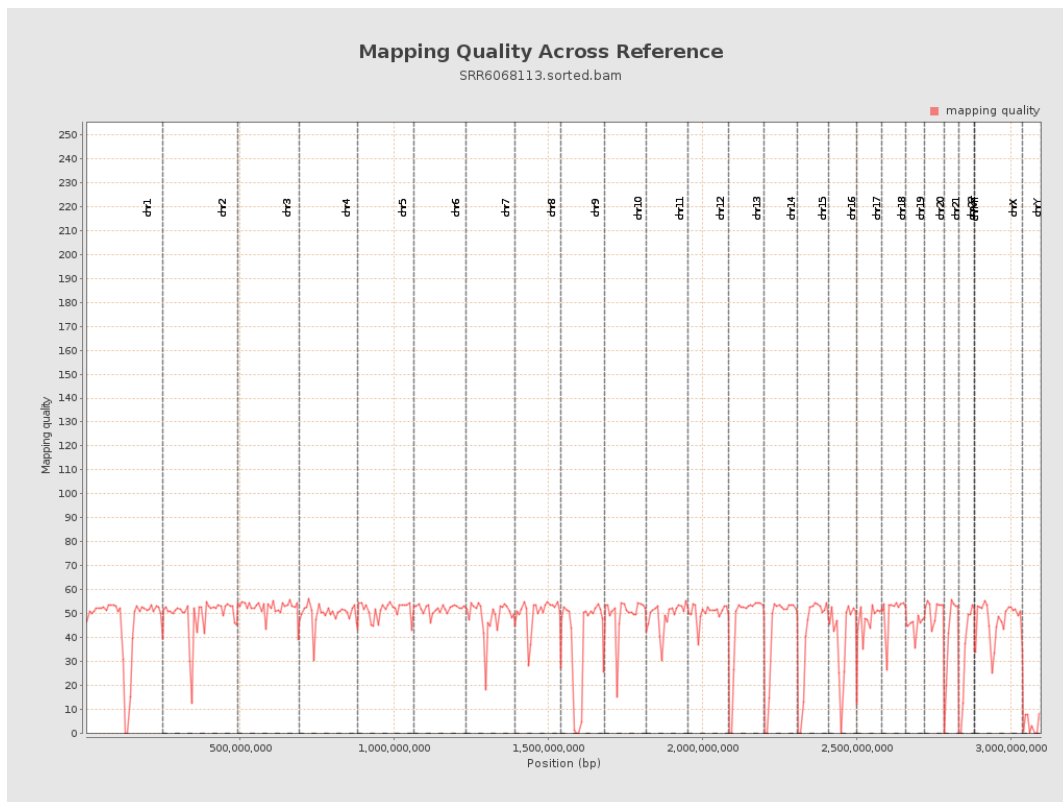
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

