

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:58:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068130.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_SRR6068130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:58:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,051,642
Mapped reads	3,781,282 / 93.33%
Unmapped reads	270,360 / 6.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,570 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	834,228 / 20.59%
Duplication rate	17.32%
Clipped reads	2,233,947 / 55.14%

2.2. ACGT Content

Number/percentage of A's	60,683,503 / 25.54%
Number/percentage of C's	41,170,788 / 17.33%
Number/percentage of T's	79,387,179 / 33.41%
Number/percentage of G's	56,367,281 / 23.72%
Number/percentage of N's	25,209 / 0.01%
GC Percentage	41.05%

2.3. Coverage

Mean	0.0768

Standard Deviation	0.7571
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2.4. Mapping Quality

Mean Mapping Quality	45.75
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2.5. Mismatches and indels

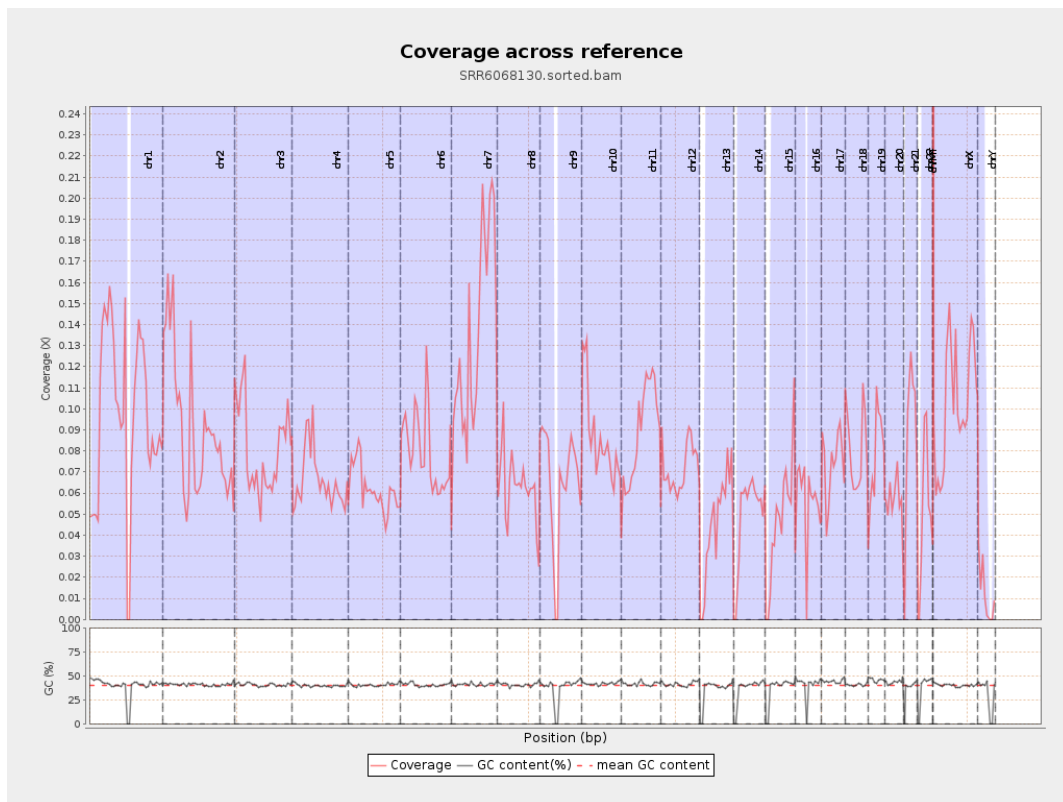
General error rate	0.63%
Mismatches	1,462,703
Insertions	15,156
Mapped reads with at least one insertion	0.4%
Deletions	69,275
Mapped reads with at least one deletion	1.81%
Homopolymer indels	47.45%

2.6. Chromosome stats

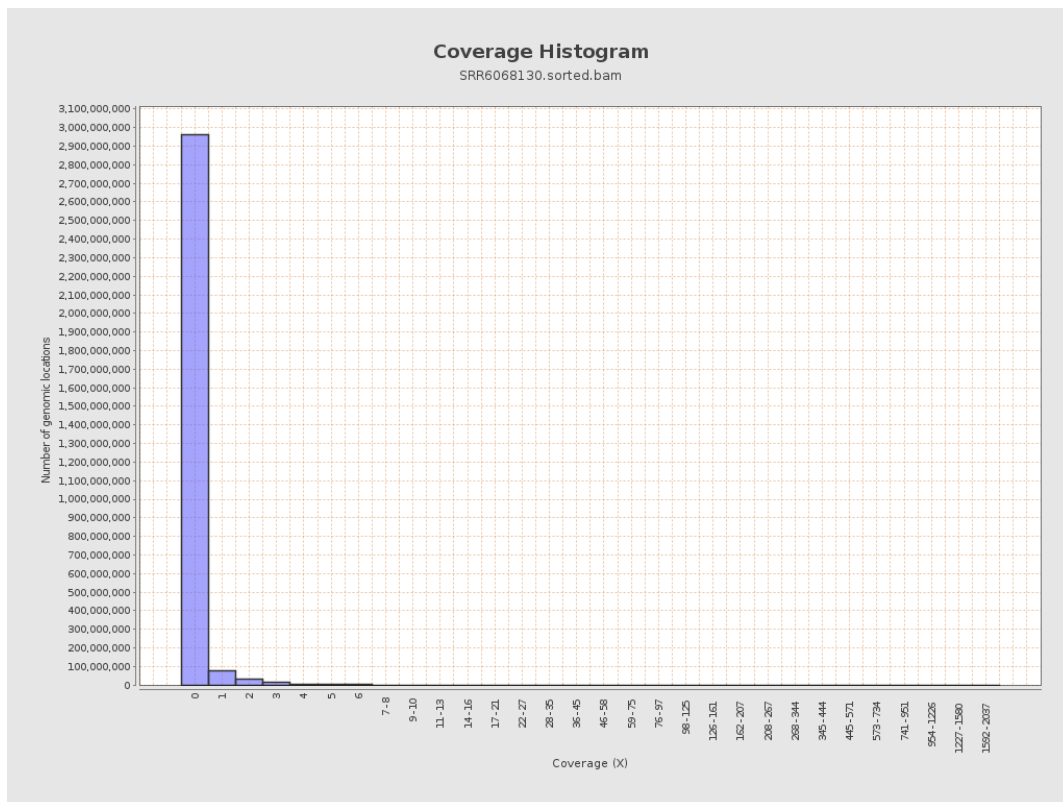
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24243812	0.0973	1.536
chr2	243199373	22141970	0.091	1.0842
chr3	198022430	15986669	0.0807	0.4579
chr4	191154276	12705276	0.0665	0.435
chr5	180915260	11208759	0.062	0.4044
chr6	171115067	13759031	0.0804	0.5375
chr7	159138663	21622189	0.1359	1.14

chr8	146364022	9100585	0.0622	0.8013
chr9	141213431	9199615	0.0651	0.5716
chr10	135534747	11704304	0.0864	0.5712
chr11	135006516	12049814	0.0893	0.6007
chr12	133851895	9654640	0.0721	0.4496
chr13	115169878	5243339	0.0455	0.3608
chr14	107349540	5316579	0.0495	0.3853
chr15	102531392	4791332	0.0467	0.3863
chr16	90354753	4997372	0.0553	0.4046
chr17	81195210	6061152	0.0746	0.471
chr18	78077248	6310032	0.0808	0.8804
chr19	59128983	4614465	0.078	0.8954
chr20	63025520	3602249	0.0572	0.4062
chr21	48129895	4110950	0.0854	0.4812
chr22	51304566	2600774	0.0507	0.3575
chrMT	16571	176387	10.6443	8.105
chrX	155270560	15855736	0.1021	0.5881
chrY	59373566	699250	0.0118	0.2397

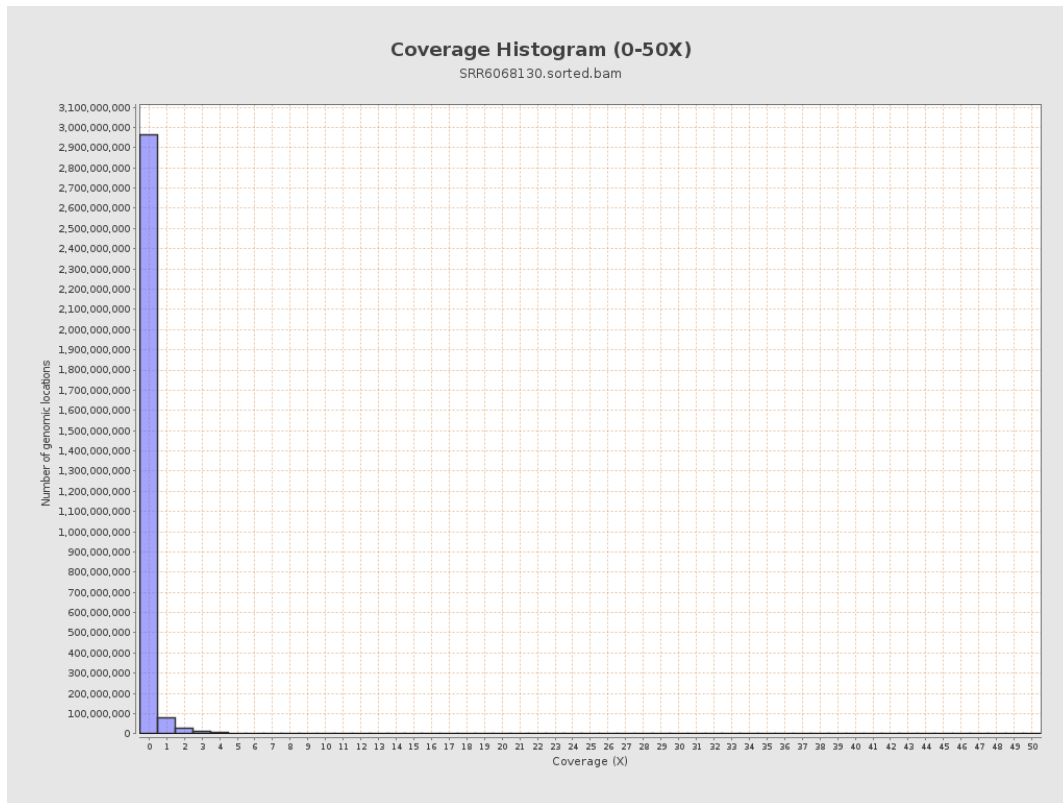
3. Results : Coverage across reference



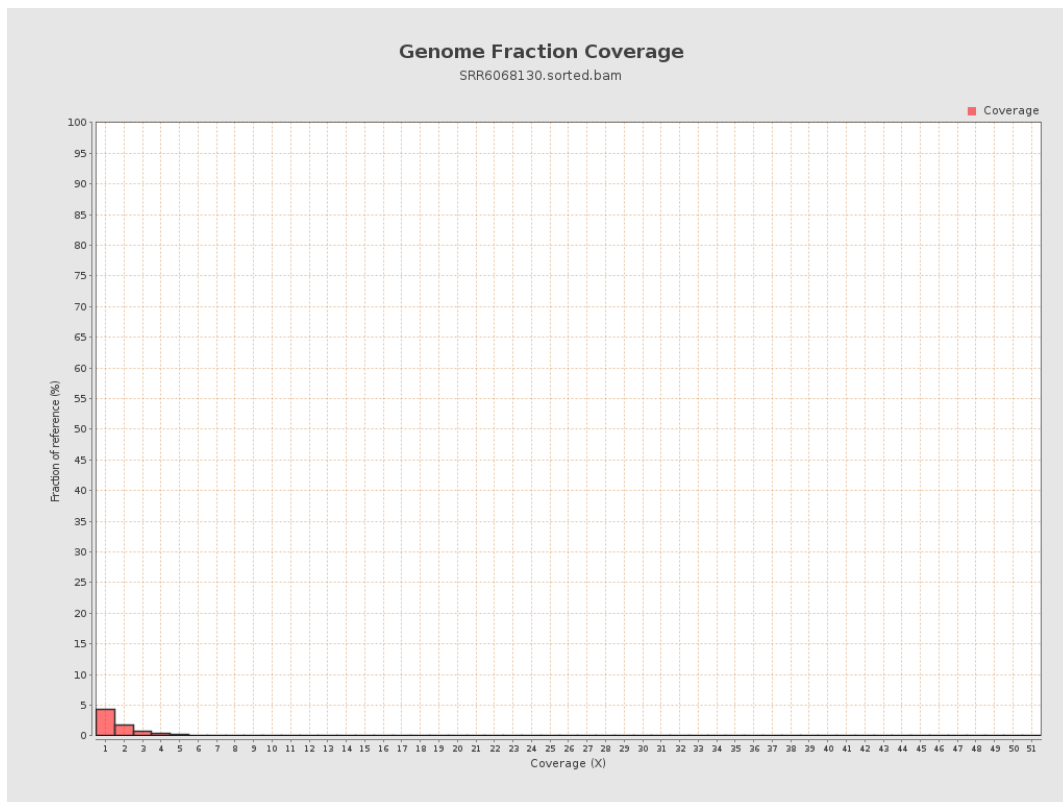
4. Results : Coverage Histogram



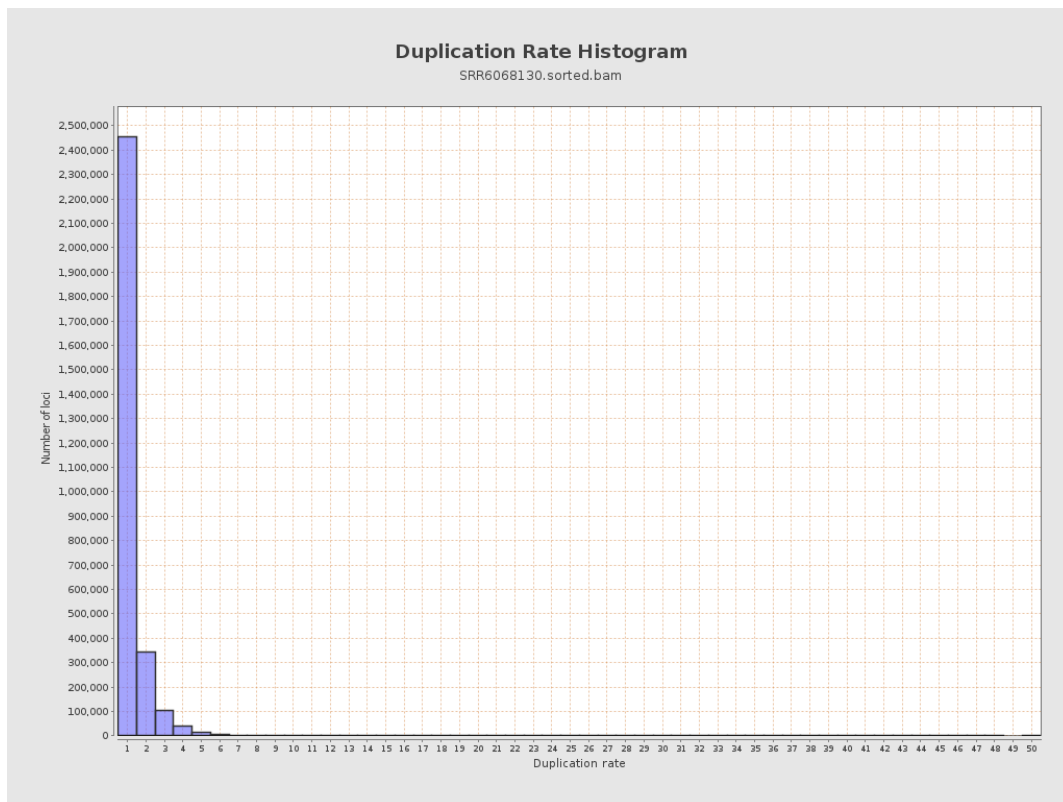
5. Results : Coverage Histogram (0-50X)



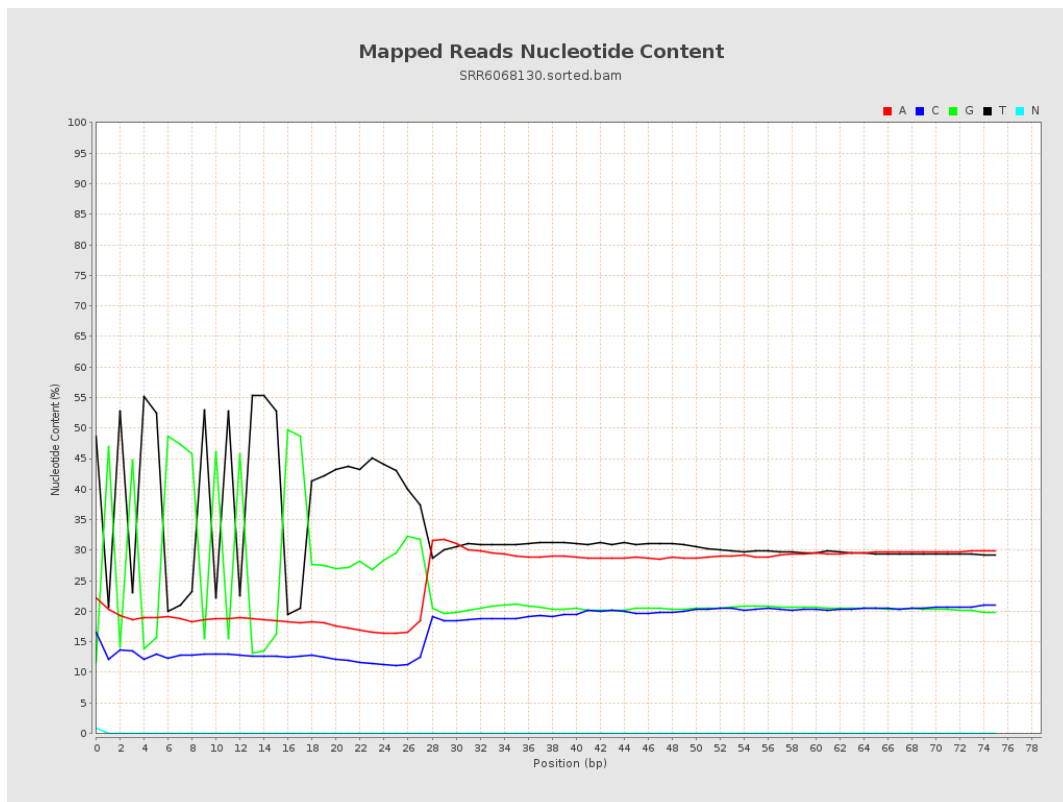
6. Results : Genome Fraction Coverage



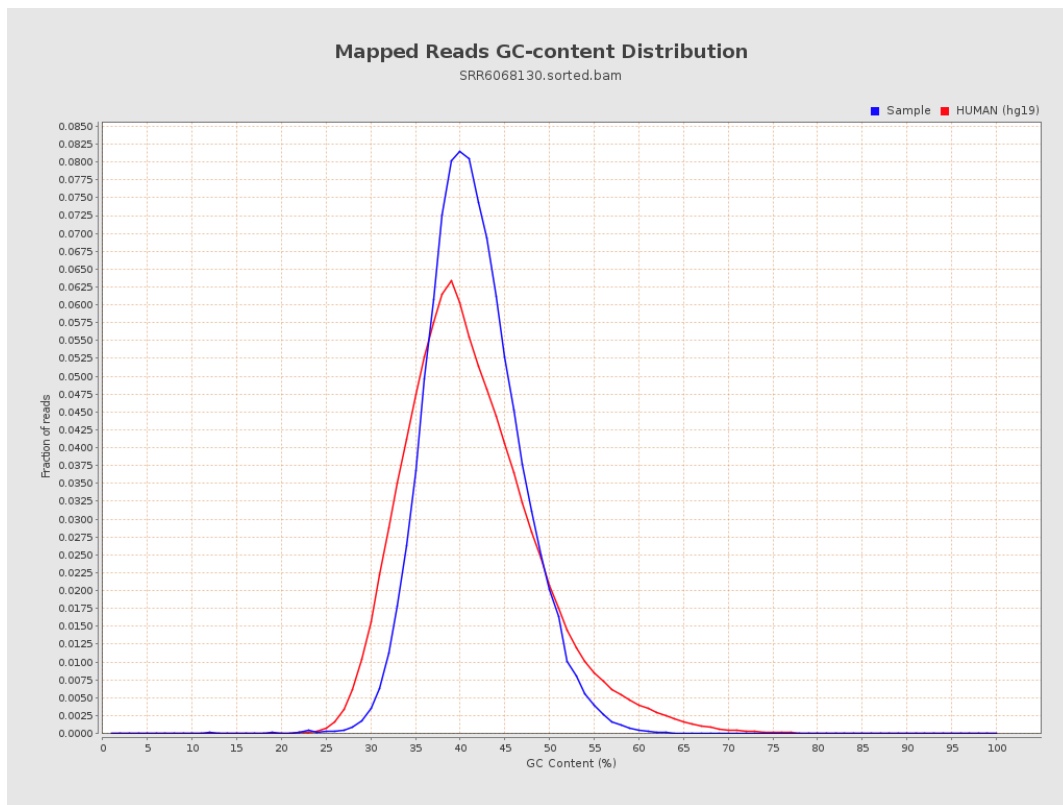
7. Results : Duplication Rate Histogram



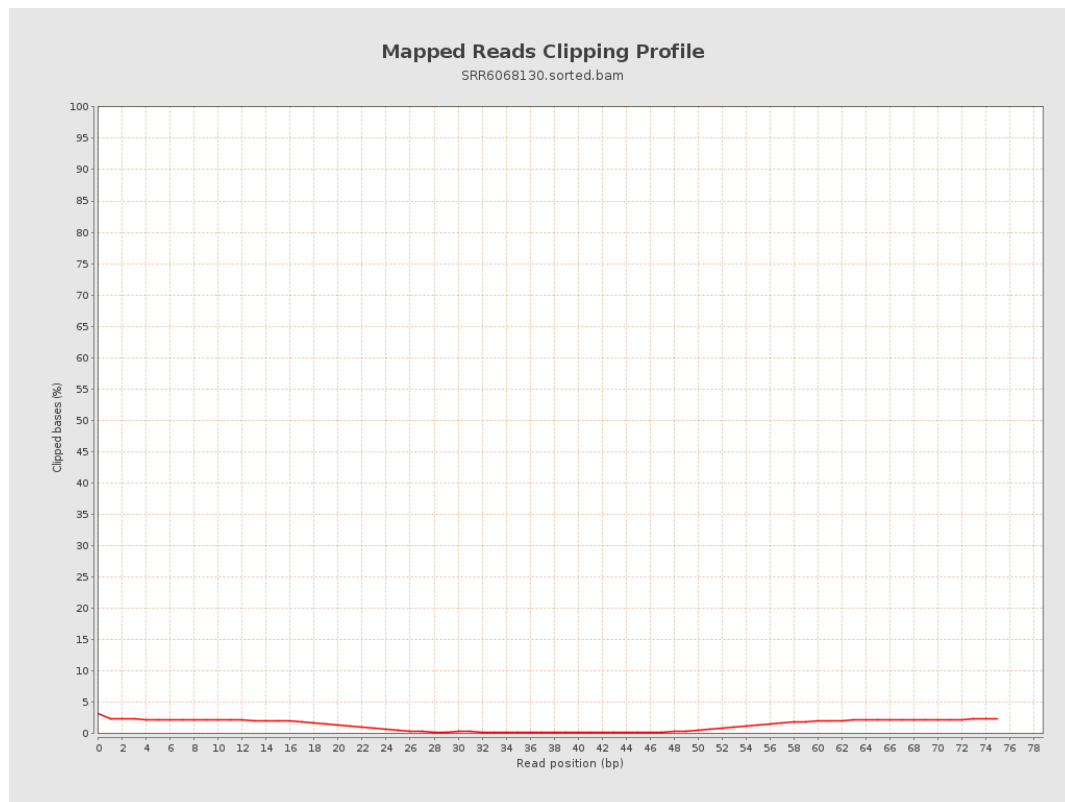
8. Results : Mapped Reads Nucleotide Content



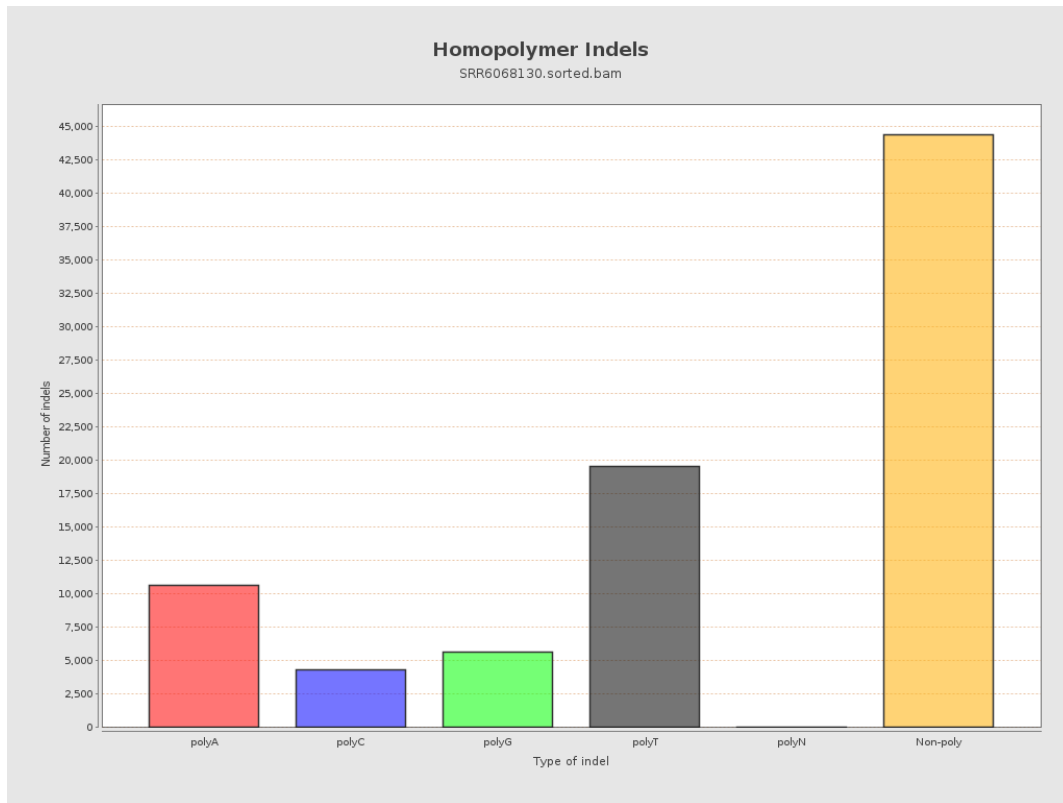
9. Results : Mapped Reads GC-content Distribution



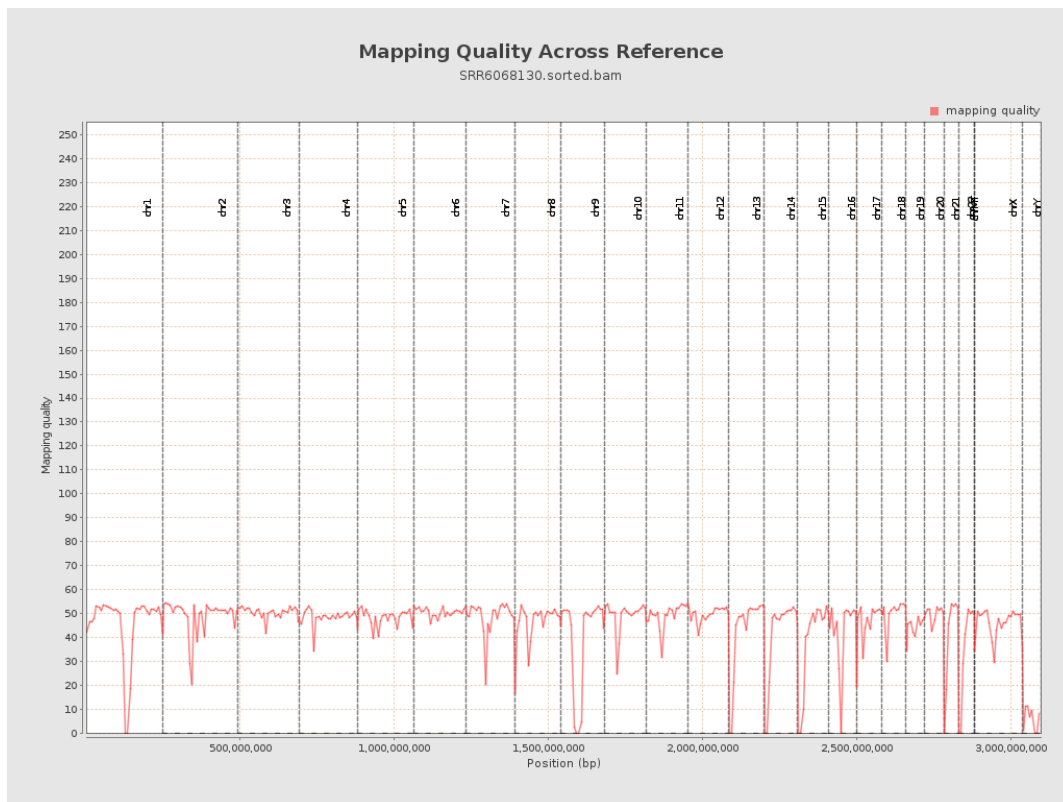
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

