

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:14:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013317.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_SRR6013317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:14:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,454,608
Mapped reads	1,138,690 / 78.28%
Unmapped reads	315,918 / 21.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,813 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	393,952 / 27.08%
Duplication rate	18.95%
Clipped reads	753,436 / 51.8%

2.2. ACGT Content

Number/percentage of A's	19,014,425 / 27.13%
Number/percentage of C's	12,234,579 / 17.46%
Number/percentage of T's	23,036,835 / 32.87%
Number/percentage of G's	15,789,670 / 22.53%
Number/percentage of N's	7,678 / 0.01%
GC Percentage	39.99%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.4966
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2.4. Mapping Quality

Mean Mapping Quality	38.79
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2.5. Mismatches and indels

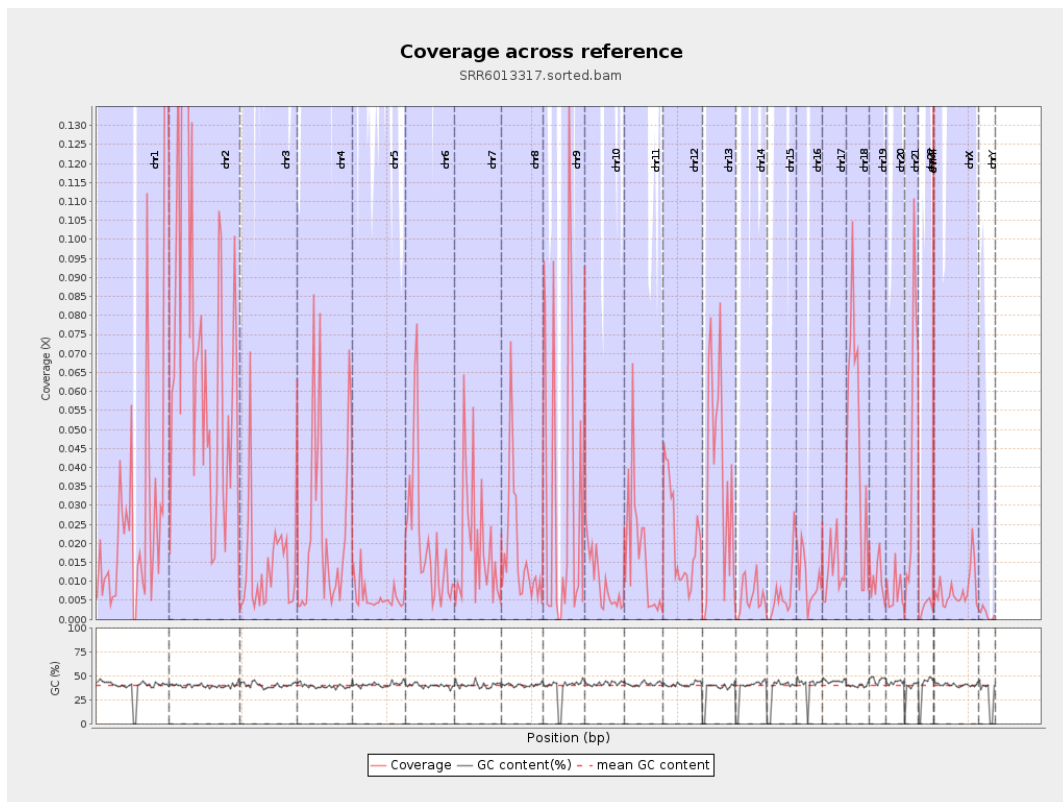
General error rate	0.87%
Mismatches	605,263
Insertions	4,642
Mapped reads with at least one insertion	0.4%
Deletions	28,081
Mapped reads with at least one deletion	2.43%
Homopolymer indels	43.63%

2.6. Chromosome stats

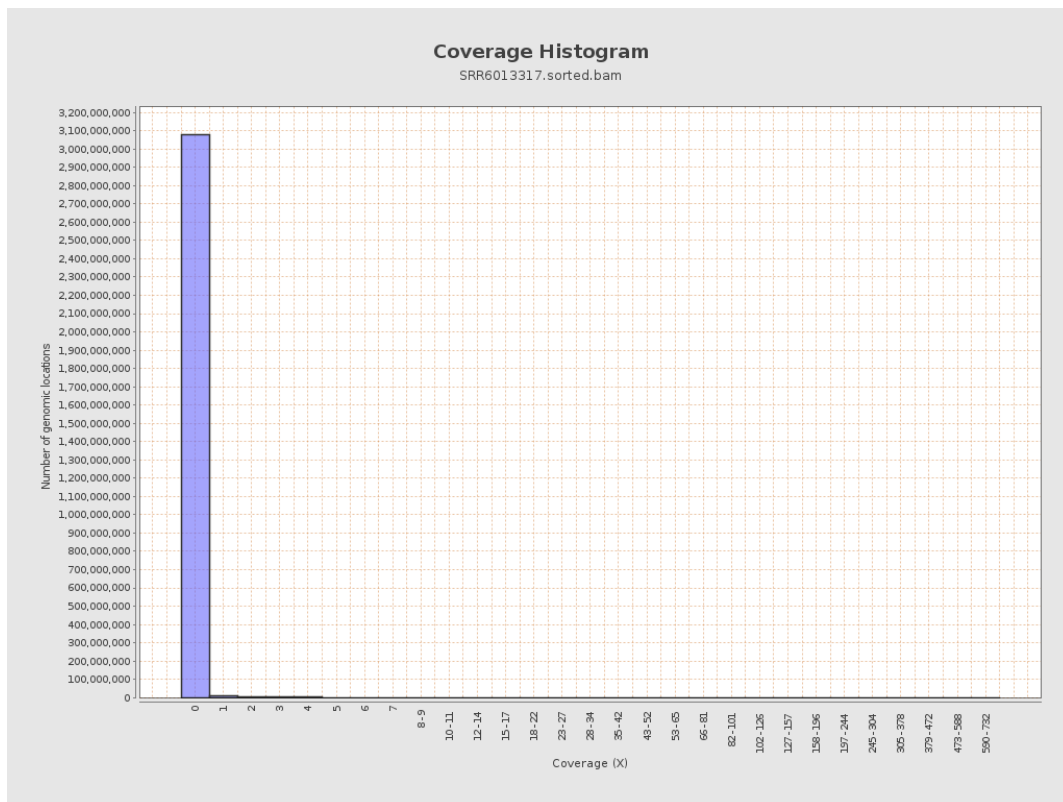
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7521643	0.0302	0.7642
chr2	243199373	18531473	0.0762	0.8668
chr3	198022430	2812522	0.0142	0.3231
chr4	191154276	4588301	0.024	0.4303
chr5	180915260	1080116	0.006	0.1721
chr6	171115067	3483269	0.0204	0.4164
chr7	159138663	3120397	0.0196	0.7502

chr8	146364022	2474759	0.0169	0.3955
chr9	141213431	4107252	0.0291	0.4945
chr10	135534747	1344989	0.0099	0.3004
chr11	135006516	2268018	0.0168	0.3559
chr12	133851895	2792240	0.0209	0.4026
chr13	115169878	4173691	0.0362	0.5643
chr14	107349540	623452	0.0058	0.1905
chr15	102531392	726149	0.0071	0.2303
chr16	90354753	952725	0.0105	0.2569
chr17	81195210	1097211	0.0135	0.314
chr18	78077248	3783366	0.0485	0.7295
chr19	59128983	630681	0.0107	0.4917
chr20	63025520	449652	0.0071	0.1972
chr21	48129895	2131242	0.0443	0.6104
chr22	51304566	165936	0.0032	0.1191
chrMT	16571	5182	0.3127	0.9803
chrX	155270560	1186462	0.0076	0.2233
chrY	59373566	79952	0.0013	0.0606

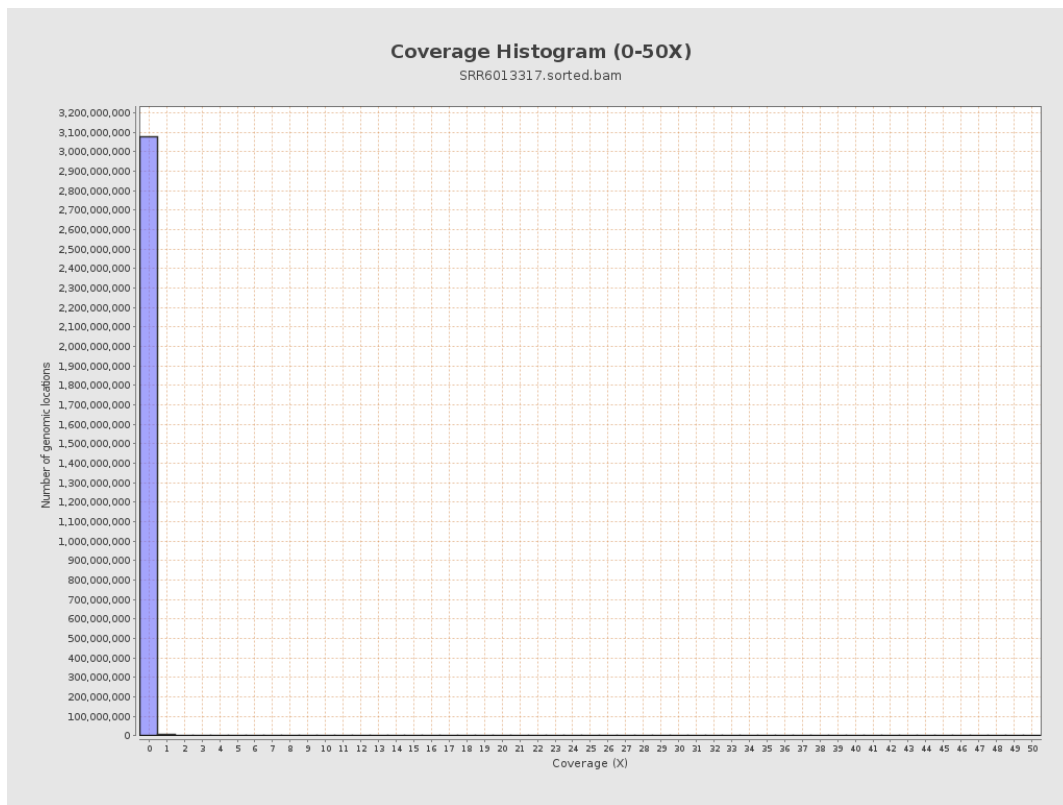
3. Results : Coverage across reference



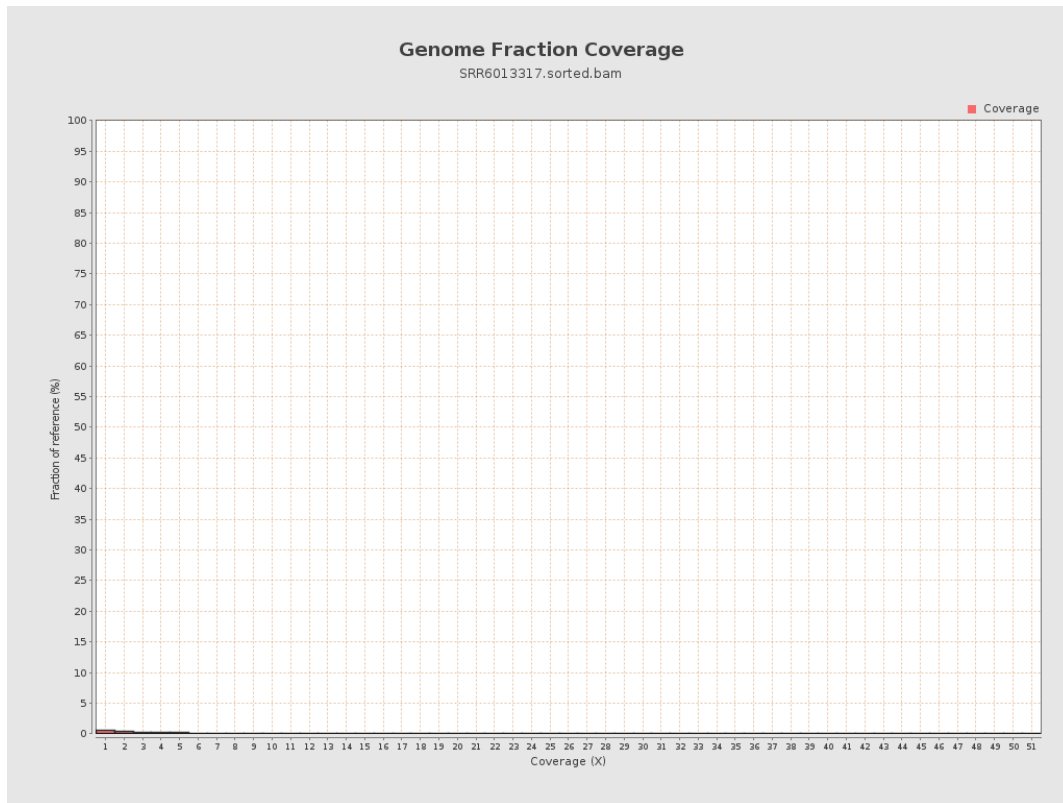
4. Results : Coverage Histogram



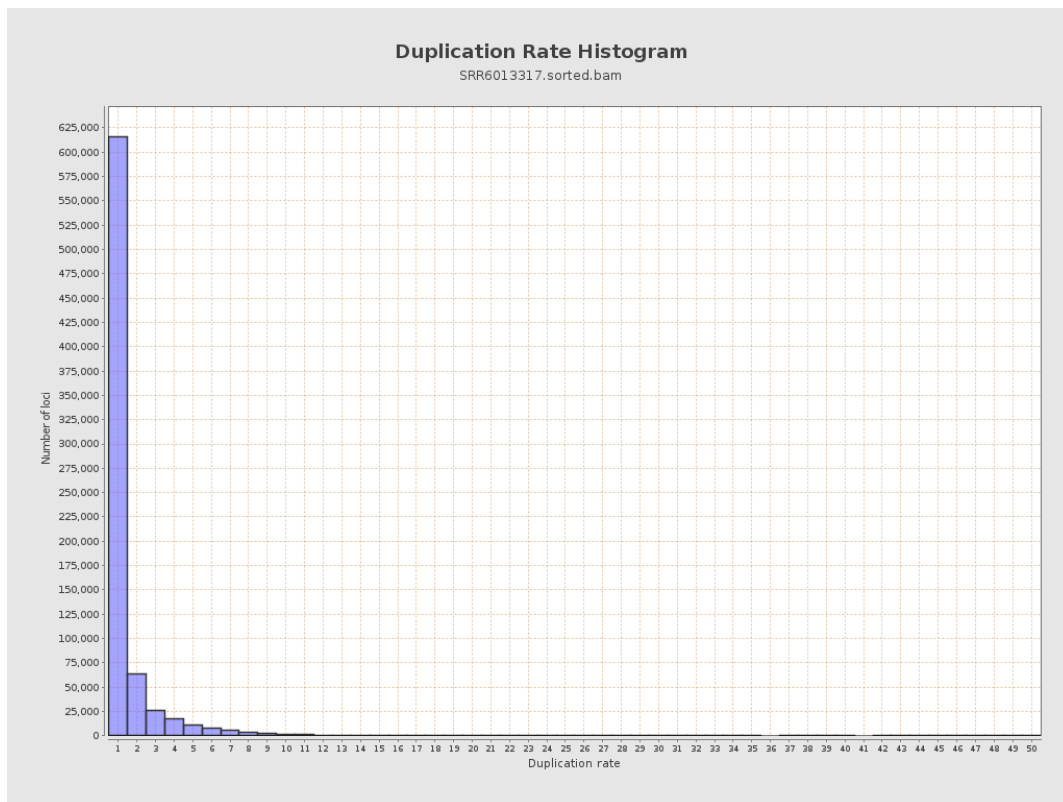
5. Results : Coverage Histogram (0-50X)



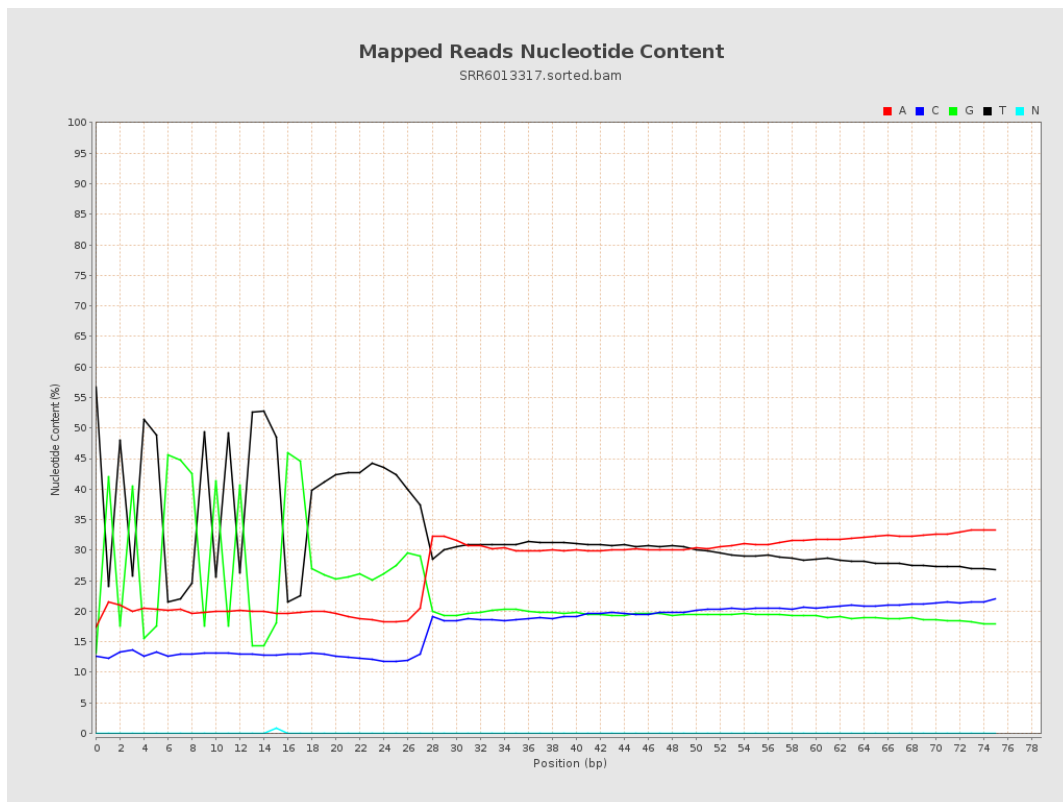
6. Results : Genome Fraction Coverage



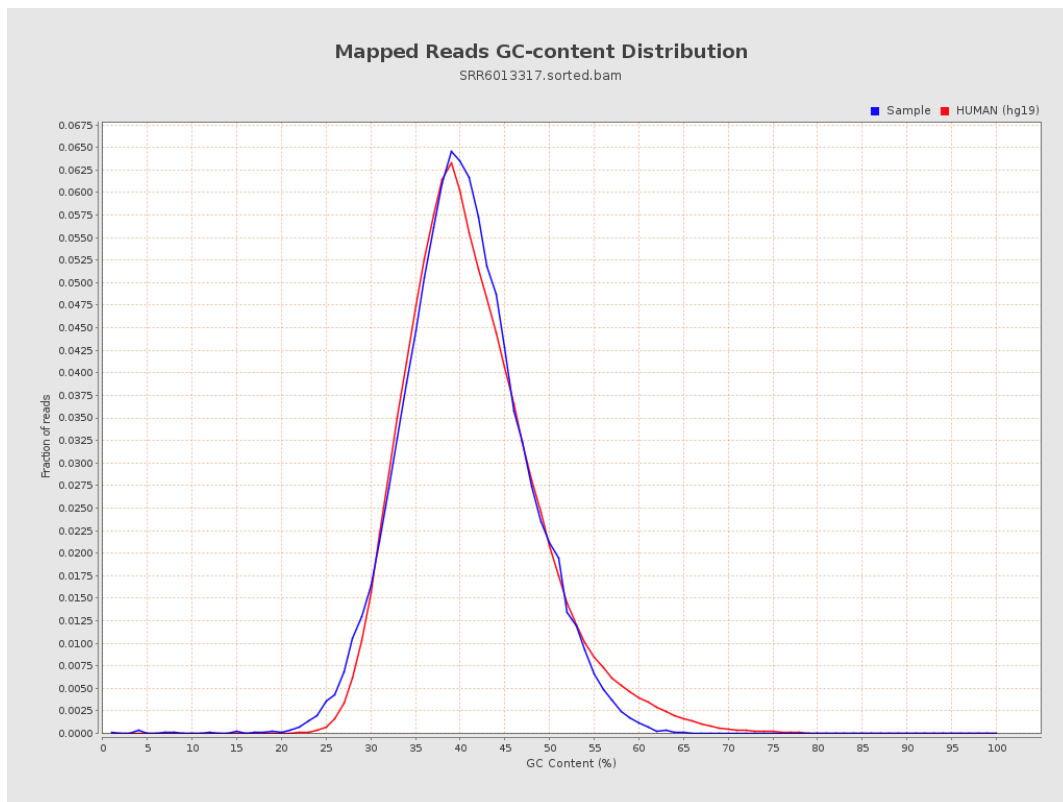
7. Results : Duplication Rate Histogram



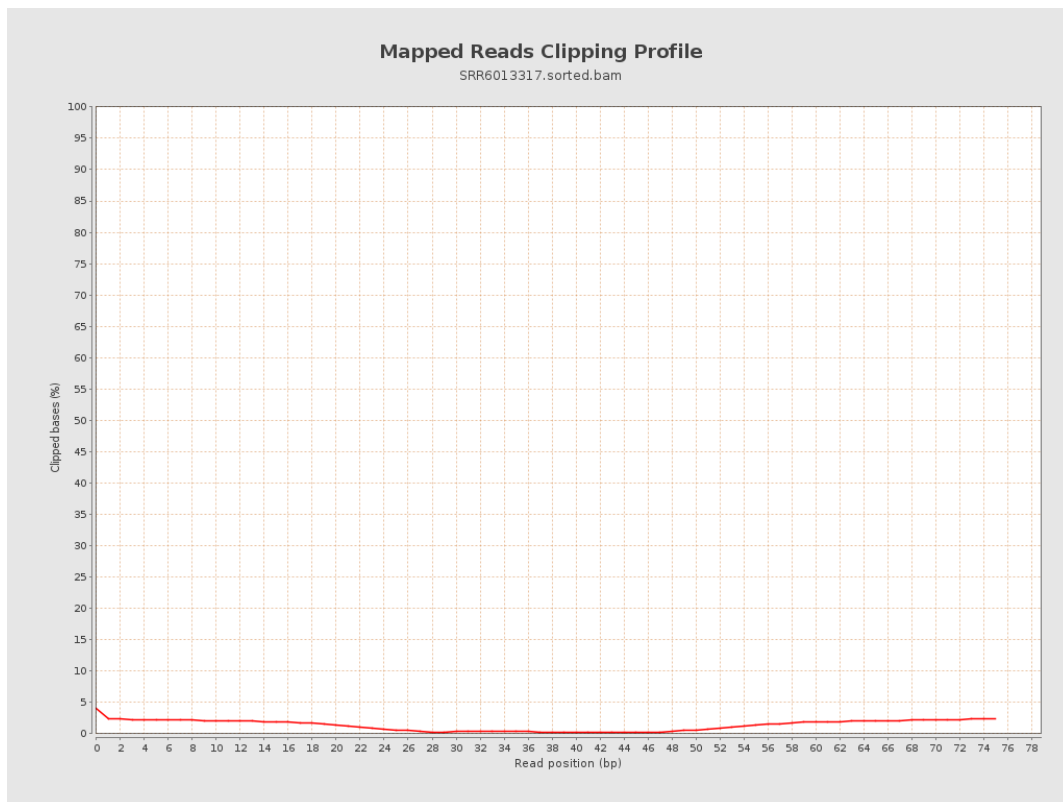
8. Results : Mapped Reads Nucleotide Content



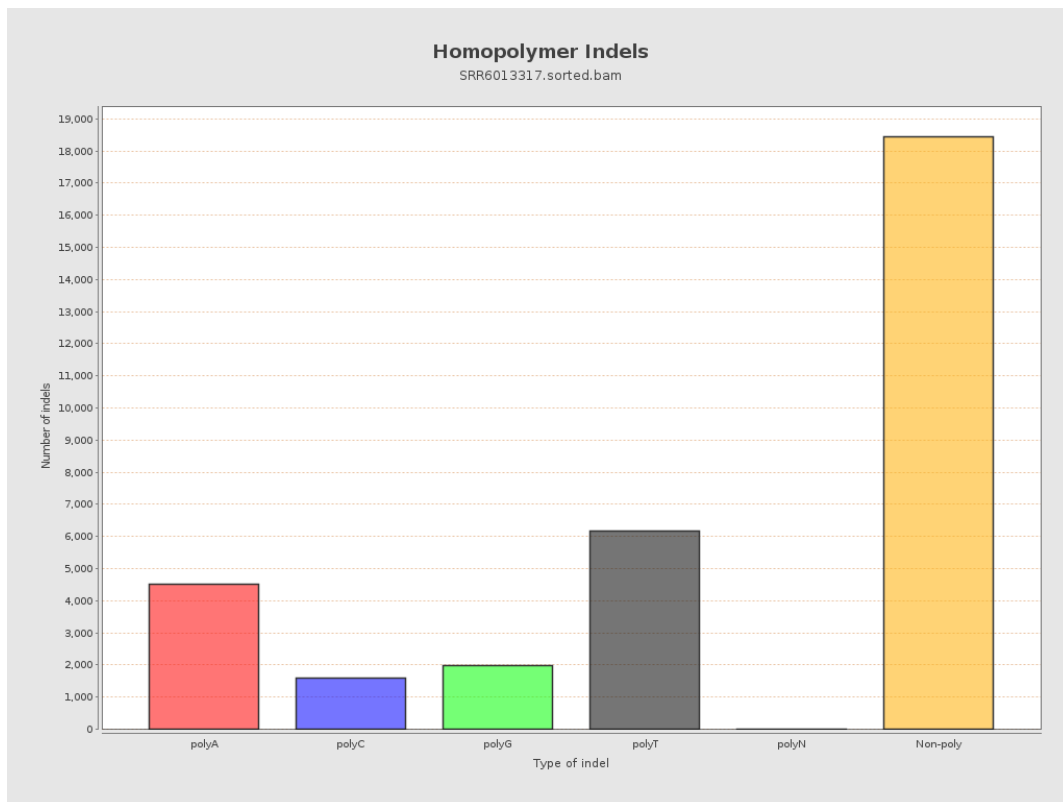
9. Results : Mapped Reads GC-content Distribution



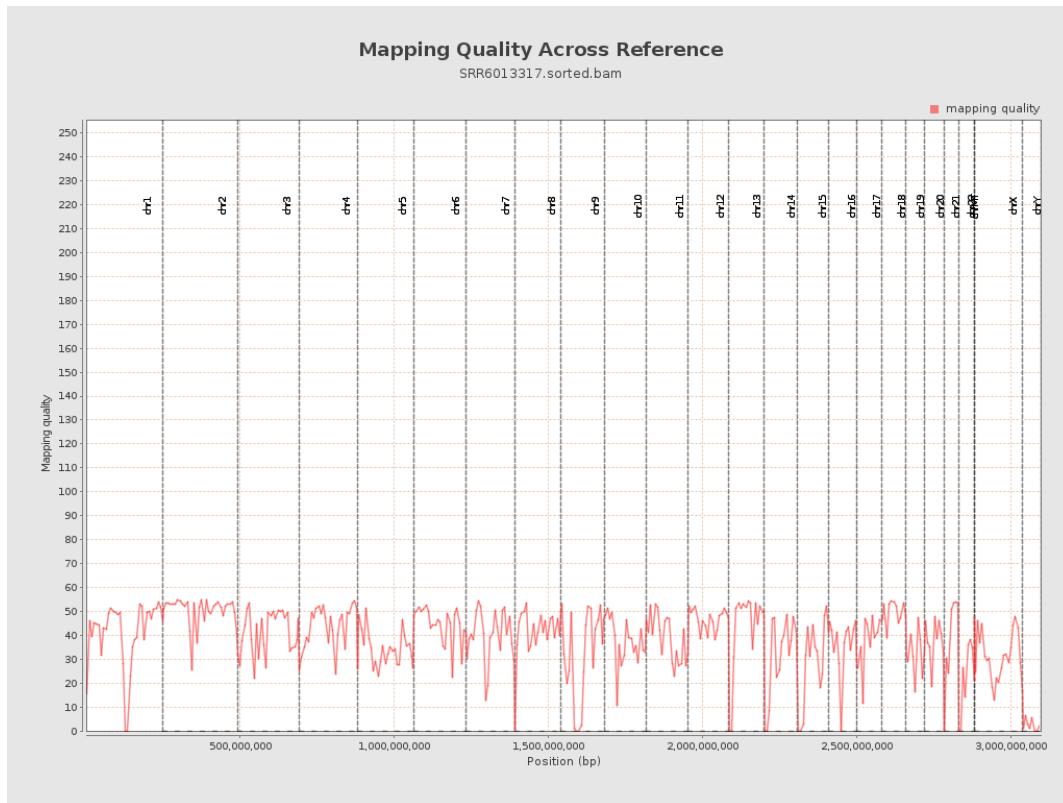
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

