

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:20:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013299.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_SRR6013299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:20:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,117,951
Mapped reads	1,901,970 / 89.8%
Unmapped reads	215,981 / 10.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,222 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	70,123 / 3.31%
Duplication rate	2.81%
Clipped reads	853,606 / 40.3%

2.2. ACGT Content

Number/percentage of A's	35,661,860 / 28.13%
Number/percentage of C's	23,305,303 / 18.38%
Number/percentage of T's	39,947,096 / 31.51%
Number/percentage of G's	27,850,573 / 21.97%
Number/percentage of N's	26,660 / 0.02%
GC Percentage	40.35%

2.3. Coverage

Mean	0.041

Standard Deviation	0.3841
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2.4. Mapping Quality

Mean Mapping Quality	46.13
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2.5. Mismatches and indels

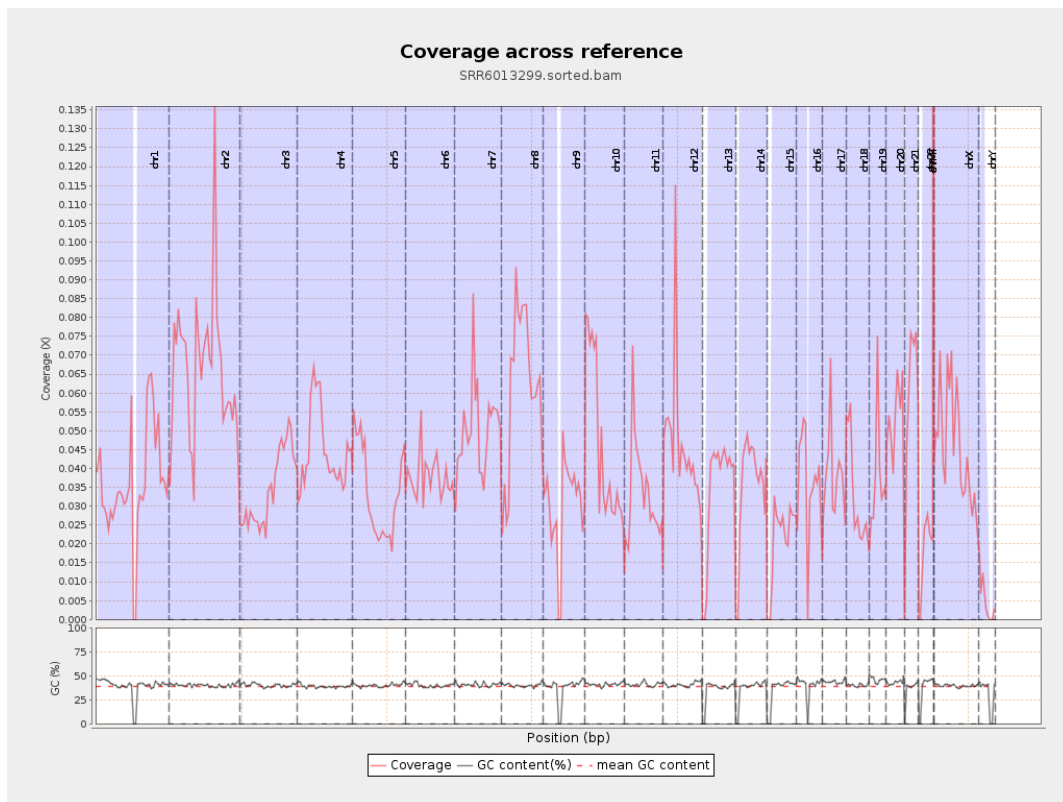
General error rate	0.78%
Mismatches	976,498
Insertions	8,732
Mapped reads with at least one insertion	0.46%
Deletions	26,842
Mapped reads with at least one deletion	1.4%
Homopolymer indels	45.92%

2.6. Chromosome stats

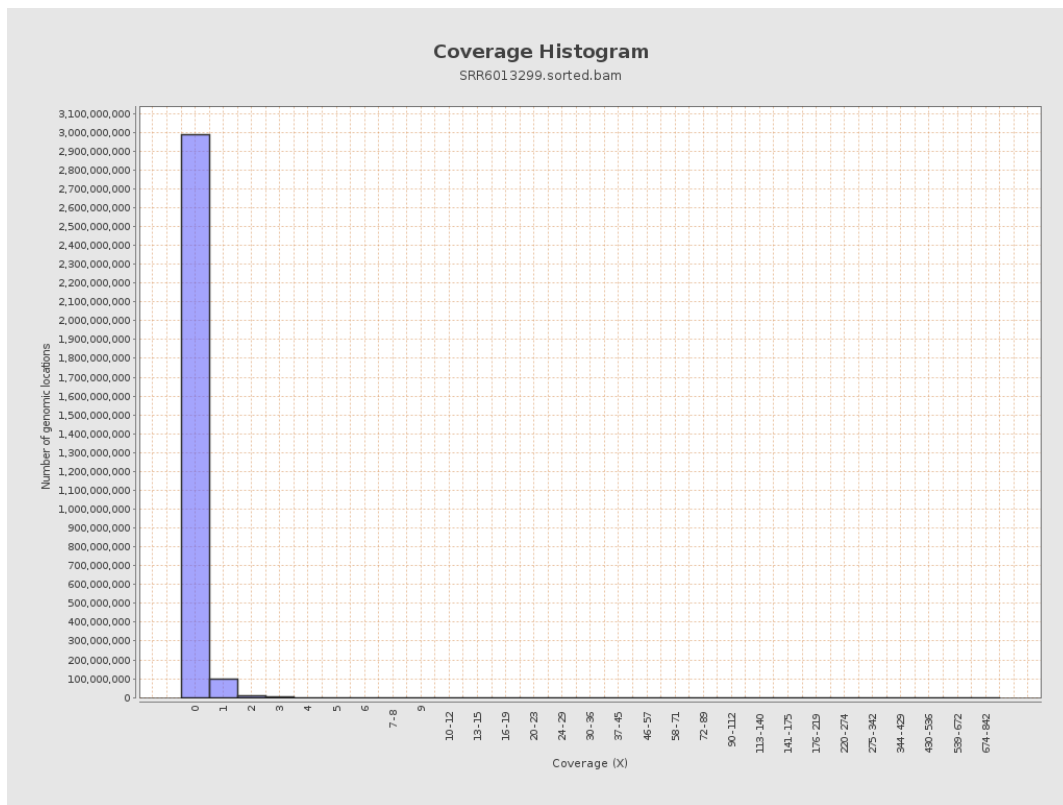
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9034202	0.0362	0.7192
chr2	243199373	16091236	0.0662	0.4425
chr3	198022430	6835397	0.0345	0.2042
chr4	191154276	8562004	0.0448	0.244
chr5	180915260	6042785	0.0334	0.204
chr6	171115067	6468702	0.0378	0.2824
chr7	159138663	8074847	0.0507	0.6598

chr8	146364022	8997816	0.0615	0.4739
chr9	141213431	4246465	0.0301	0.3214
chr10	135534747	6348817	0.0468	0.3664
chr11	135006516	4509250	0.0334	0.2872
chr12	133851895	6239799	0.0466	0.2435
chr13	115169878	3905701	0.0339	0.2012
chr14	107349540	3742965	0.0349	0.2208
chr15	102531392	2201845	0.0215	0.1665
chr16	90354753	3258130	0.0361	0.2228
chr17	81195210	3072229	0.0378	0.2634
chr18	78077248	2535349	0.0325	0.5821
chr19	59128983	2236132	0.0378	0.4738
chr20	63025520	3336666	0.0529	0.2666
chr21	48129895	2838222	0.059	0.2871
chr22	51304566	885320	0.0173	0.1423
chrMT	16571	17875	1.0787	1.1585
chrX	155270560	7068392	0.0455	0.2784
chrY	59373566	288621	0.0049	0.1033

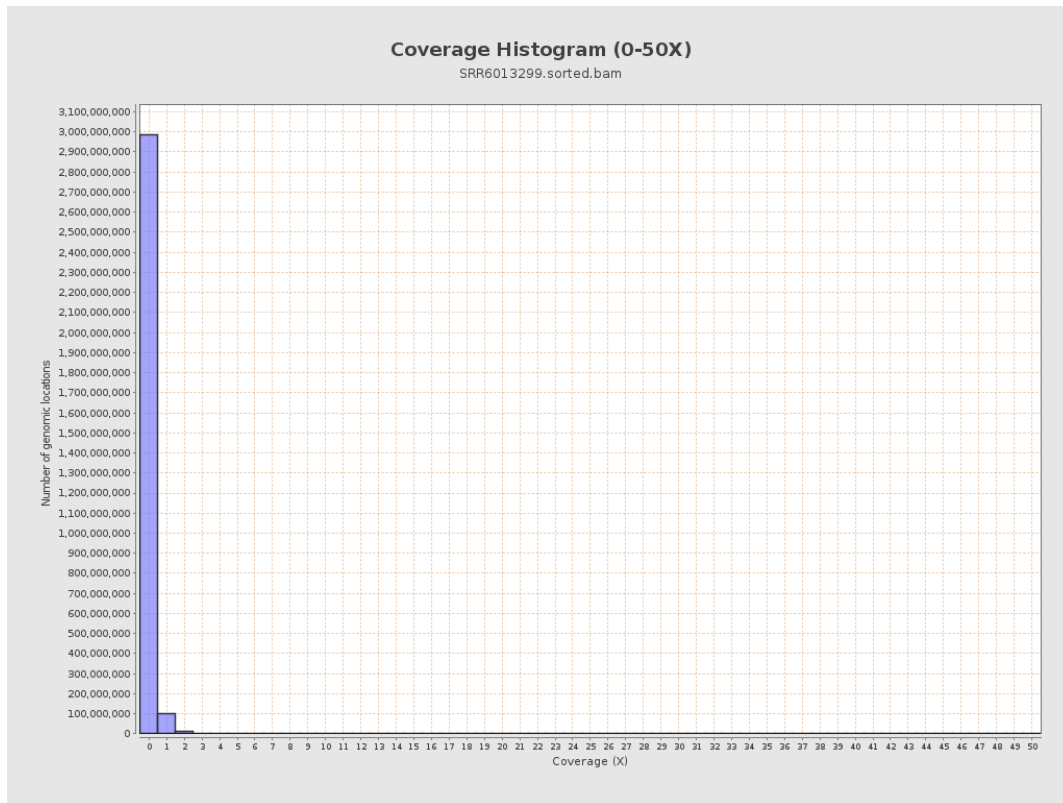
3. Results : Coverage across reference



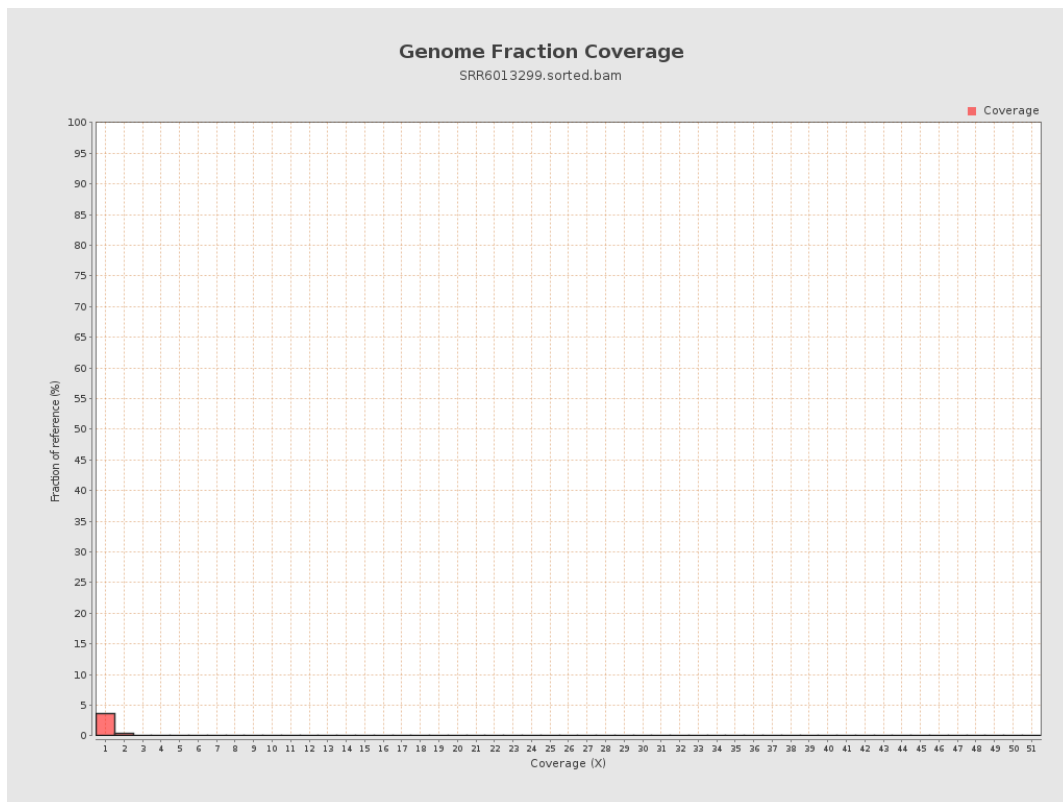
4. Results : Coverage Histogram



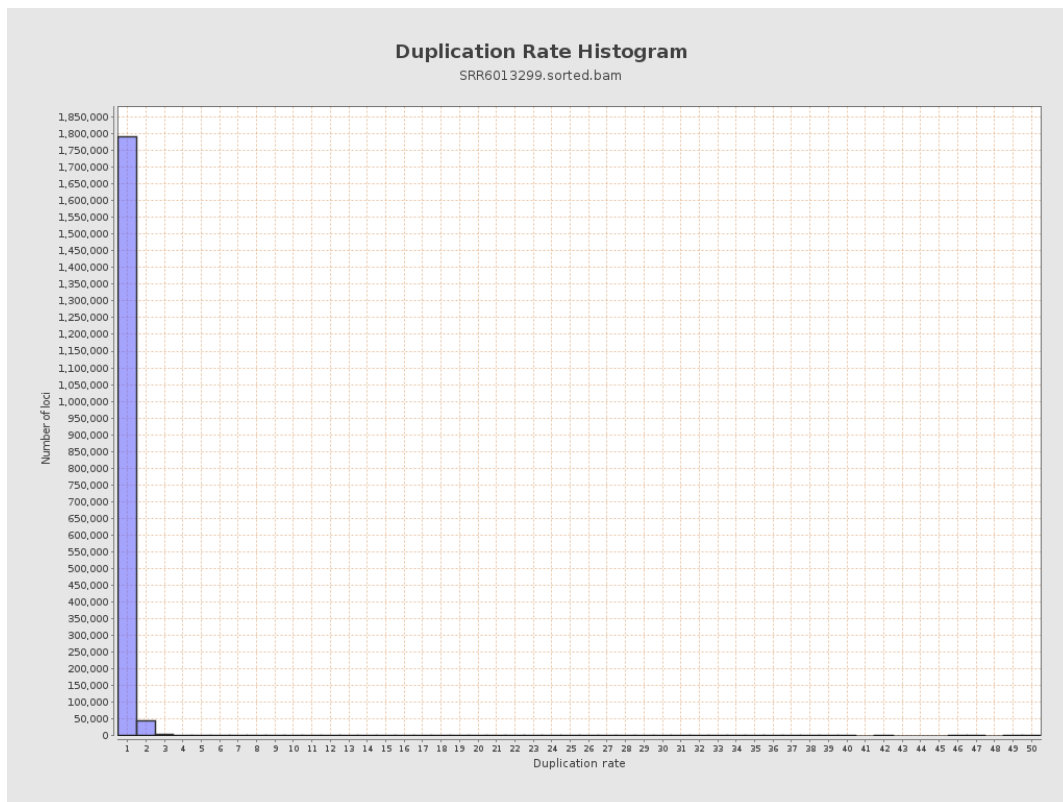
5. Results : Coverage Histogram (0-50X)



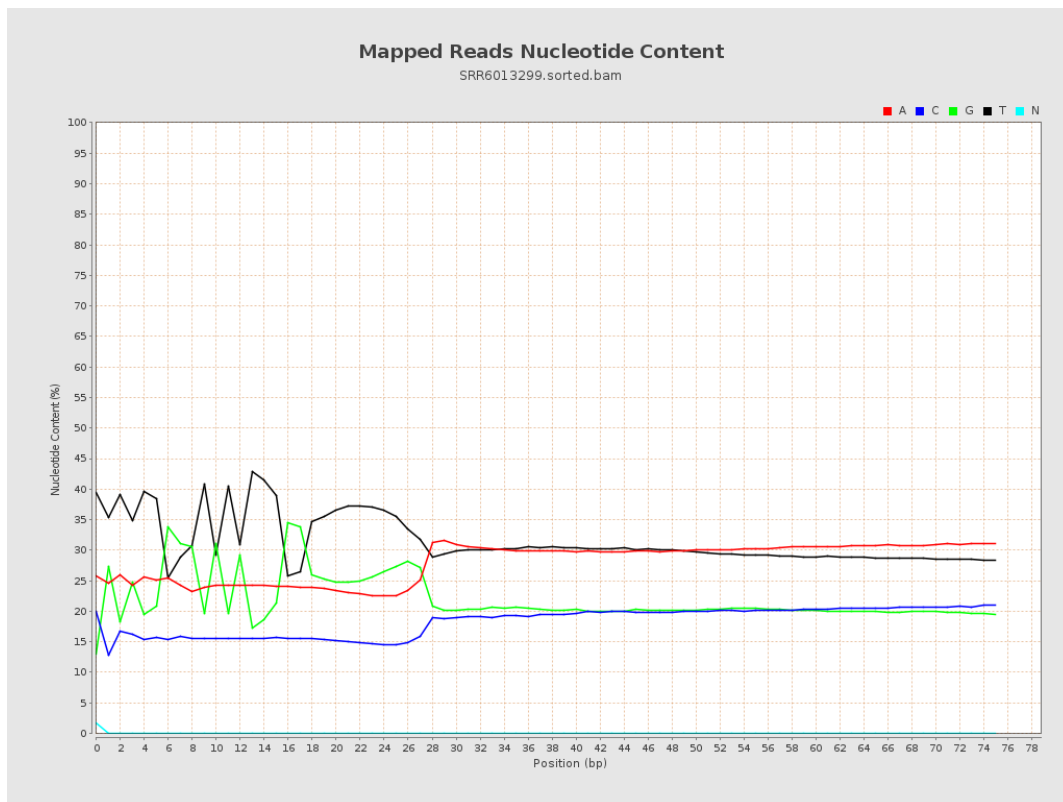
6. Results : Genome Fraction Coverage



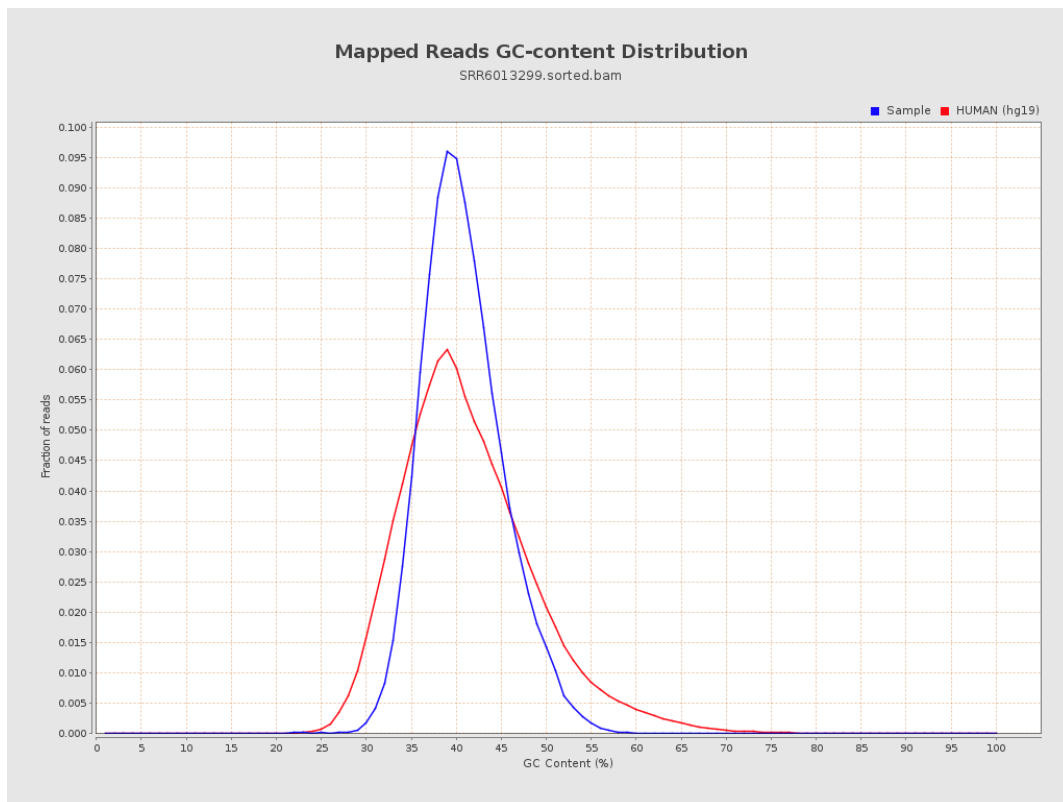
7. Results : Duplication Rate Histogram



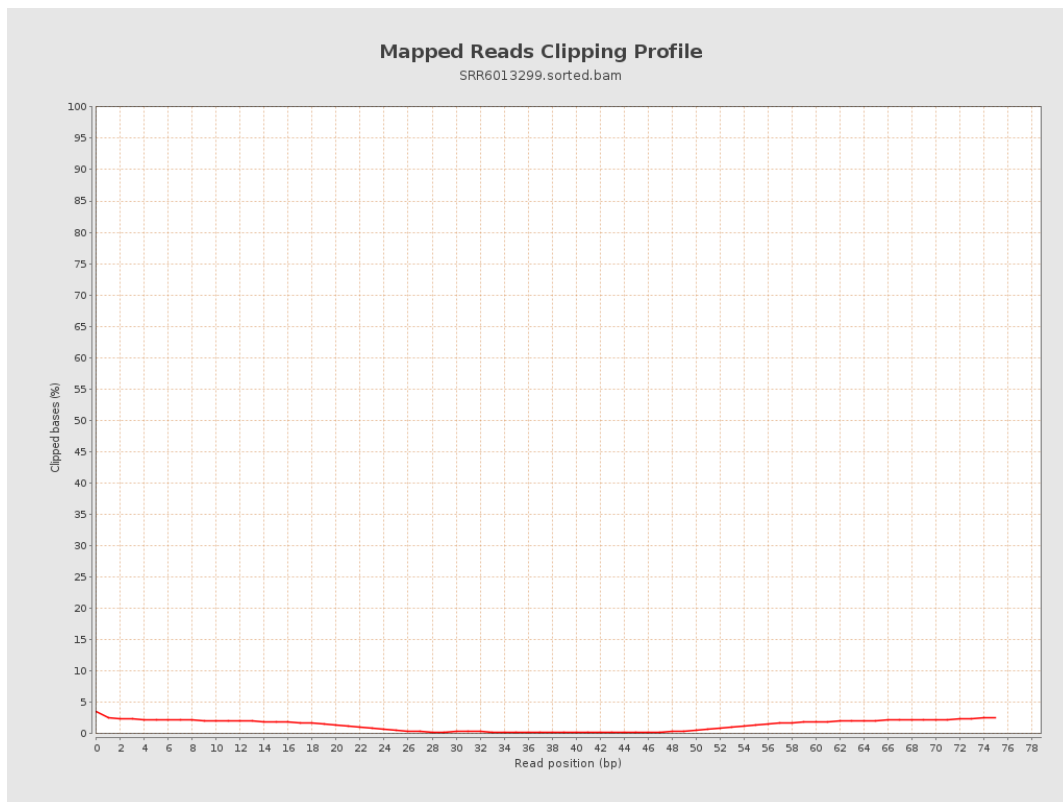
8. Results : Mapped Reads Nucleotide Content



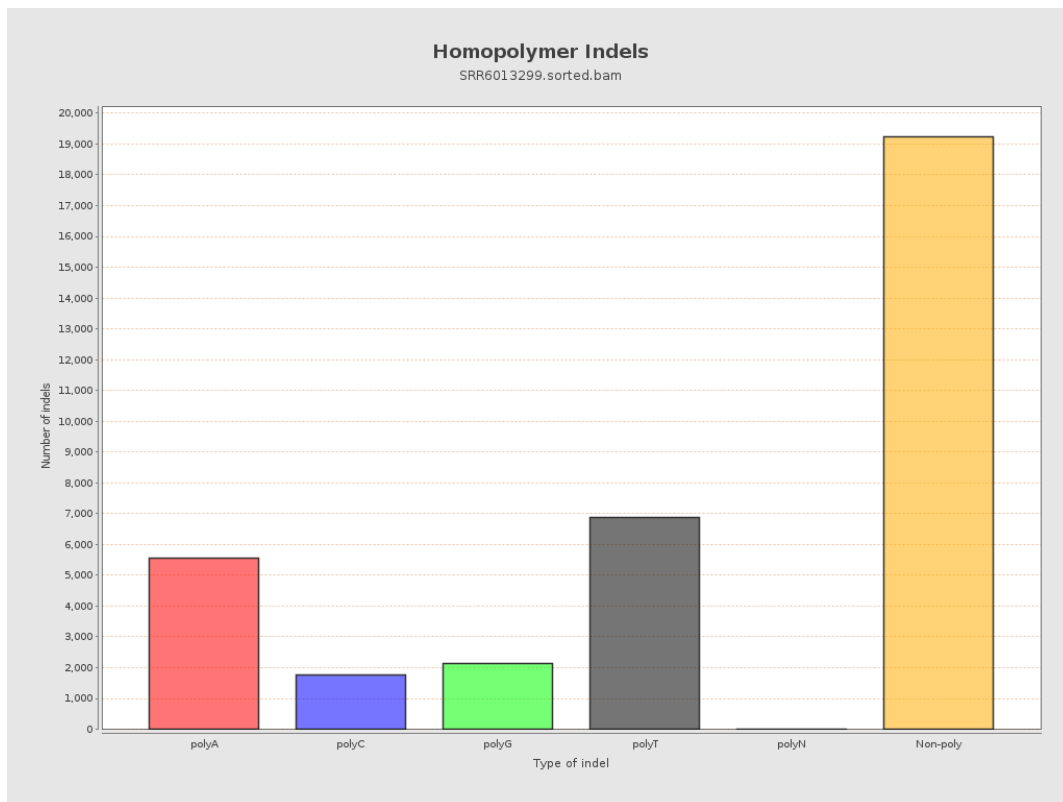
9. Results : Mapped Reads GC-content Distribution



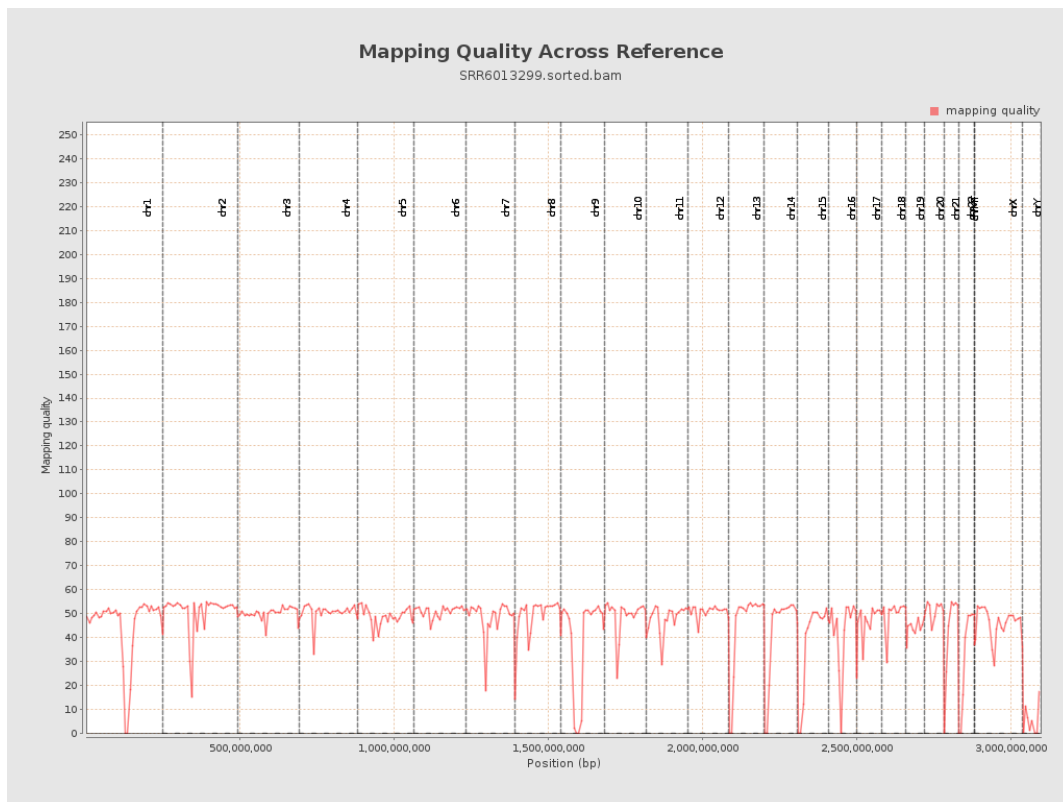
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

