

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:03:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013229.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_SRR6013229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:03:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,141,346
Mapped reads	1,878,238 / 87.71%
Unmapped reads	263,108 / 12.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,381 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	113,461 / 5.3%
Duplication rate	4.51%
Clipped reads	805,539 / 37.62%

2.2. ACGT Content

Number/percentage of A's	35,052,030 / 27.83%
Number/percentage of C's	23,180,831 / 18.41%
Number/percentage of T's	40,239,304 / 31.95%
Number/percentage of G's	27,442,054 / 21.79%
Number/percentage of N's	27,012 / 0.02%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0407

Standard Deviation	0.4197
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2.4. Mapping Quality

Mean Mapping Quality	44.6
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2.5. Mismatches and indels

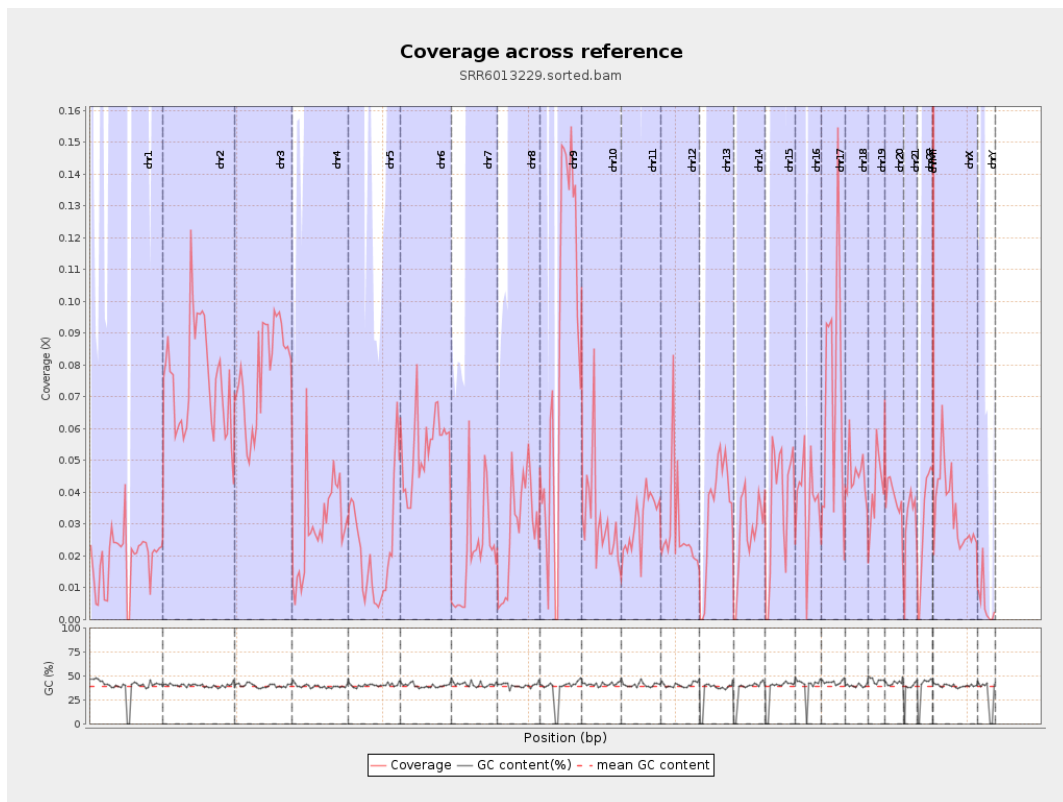
General error rate	0.85%
Mismatches	1,041,964
Insertions	10,426
Mapped reads with at least one insertion	0.55%
Deletions	30,503
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.09%

2.6. Chromosome stats

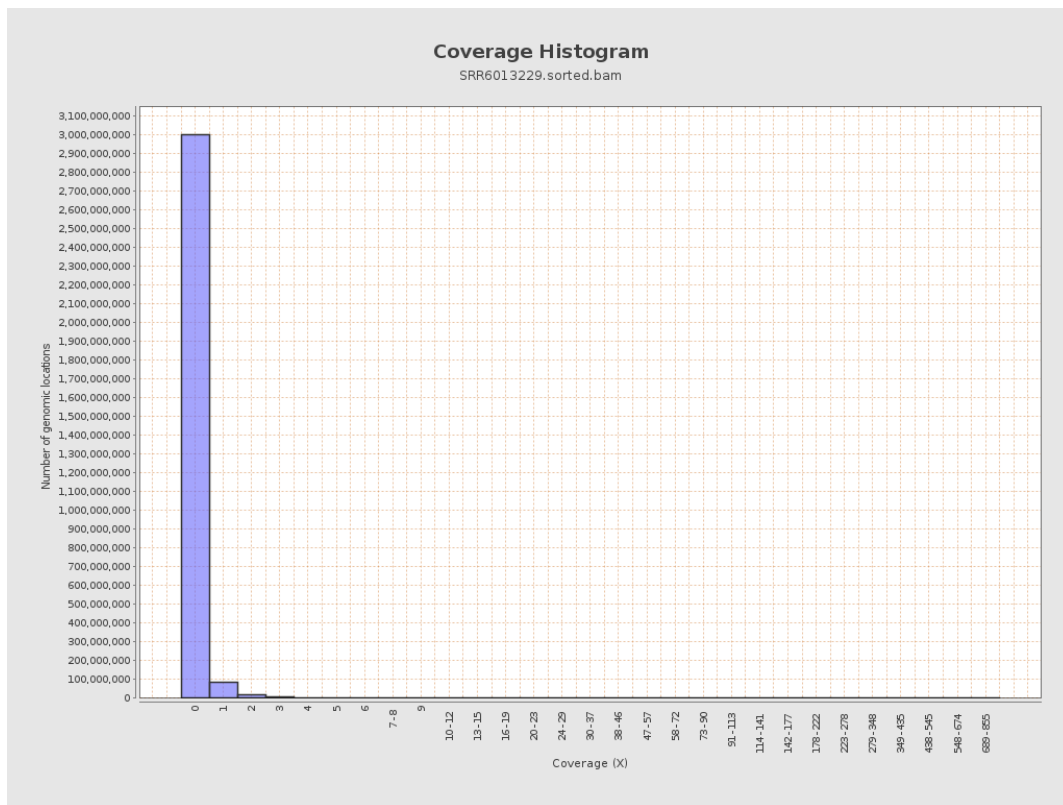
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4733146	0.019	0.5149
chr2	243199373	18340580	0.0754	0.6298
chr3	198022430	15397006	0.0778	0.3342
chr4	191154276	5659368	0.0296	0.3216
chr5	180915260	4079252	0.0225	0.1888
chr6	171115067	9220430	0.0539	0.352
chr7	159138663	3283827	0.0206	0.5044

chr8	146364022	4120446	0.0282	0.3762
chr9	141213431	11794302	0.0835	0.5484
chr10	135534747	4167618	0.0307	0.5413
chr11	135006516	4152181	0.0308	0.2862
chr12	133851895	3650455	0.0273	0.2248
chr13	115169878	3970954	0.0345	0.2201
chr14	107349540	2952639	0.0275	0.2406
chr15	102531392	3716189	0.0362	0.2272
chr16	90354753	3302574	0.0366	0.2832
chr17	81195210	5990294	0.0738	0.3962
chr18	78077248	3555944	0.0455	0.9042
chr19	59128983	2495027	0.0422	0.453
chr20	63025520	2400436	0.0381	0.2496
chr21	48129895	1455048	0.0302	0.3108
chr22	51304566	1569448	0.0306	0.2067
chrMT	16571	395068	23.8409	13.7869
chrX	155270560	5278879	0.034	0.2536
chrY	59373566	314965	0.0053	0.2664

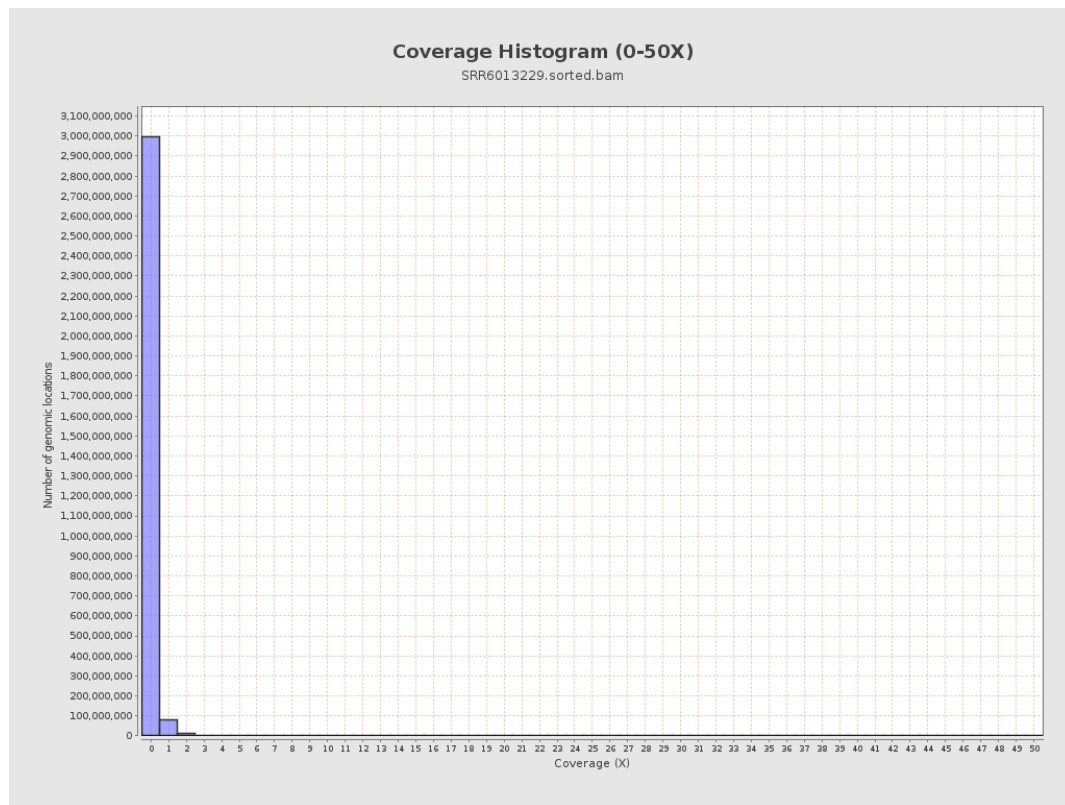
3. Results : Coverage across reference



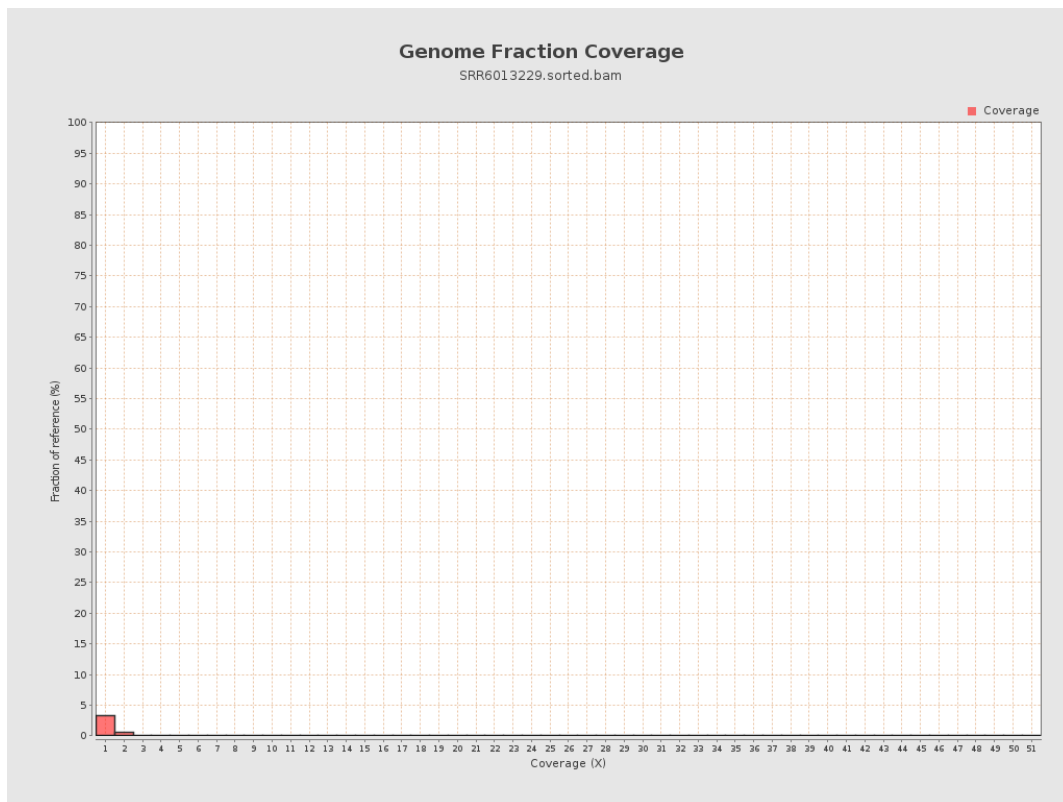
4. Results : Coverage Histogram



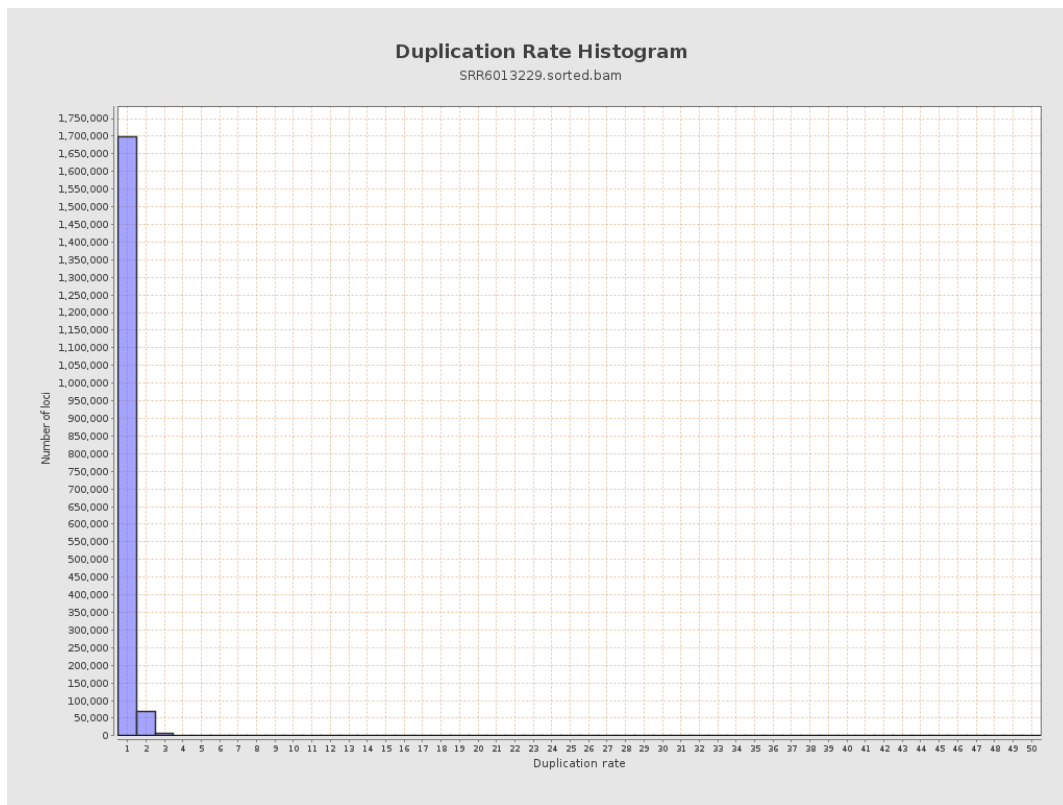
5. Results : Coverage Histogram (0-50X)



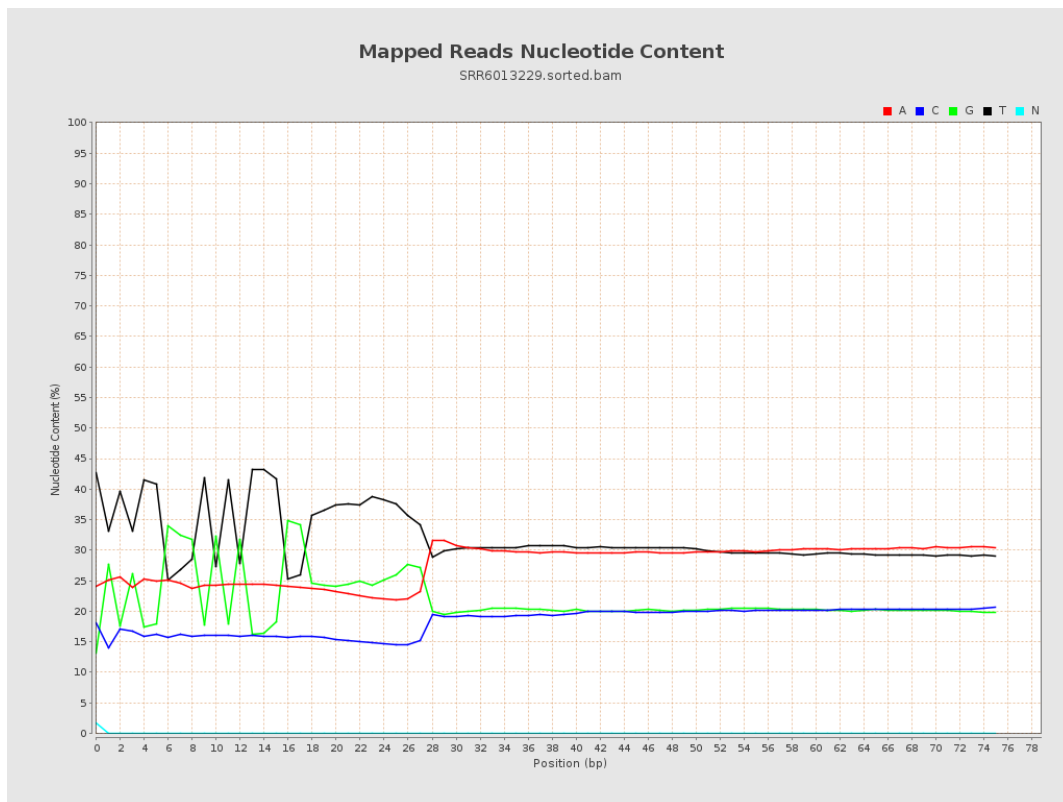
6. Results : Genome Fraction Coverage



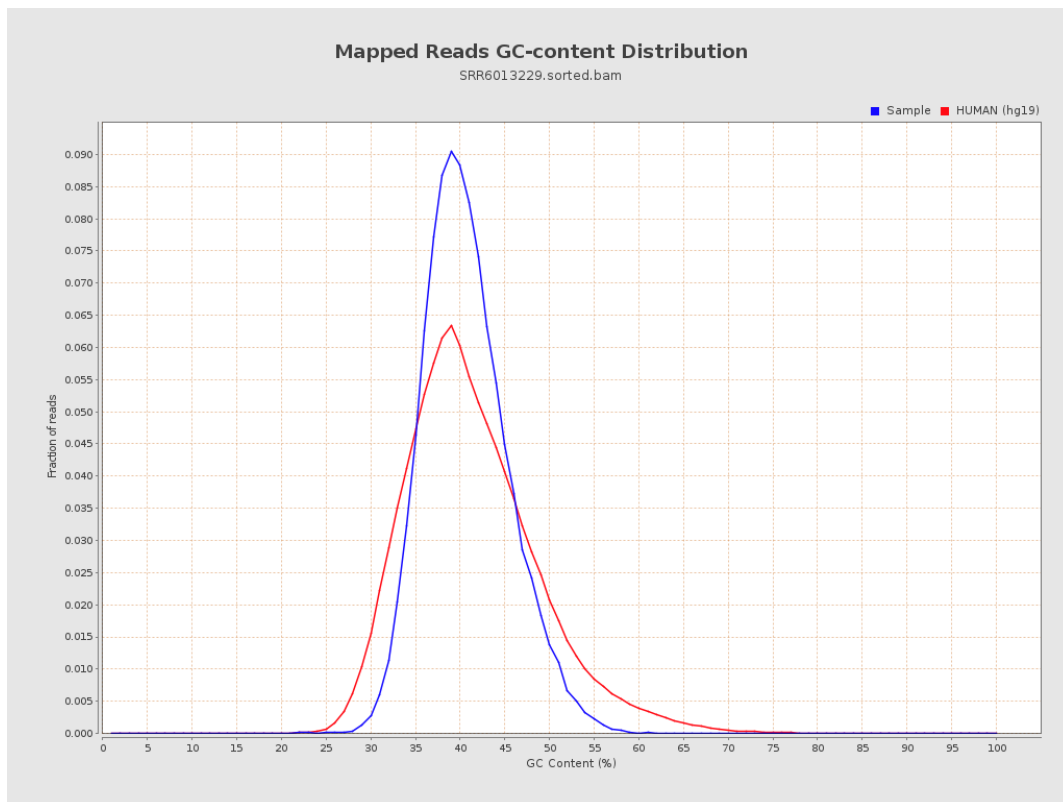
7. Results : Duplication Rate Histogram



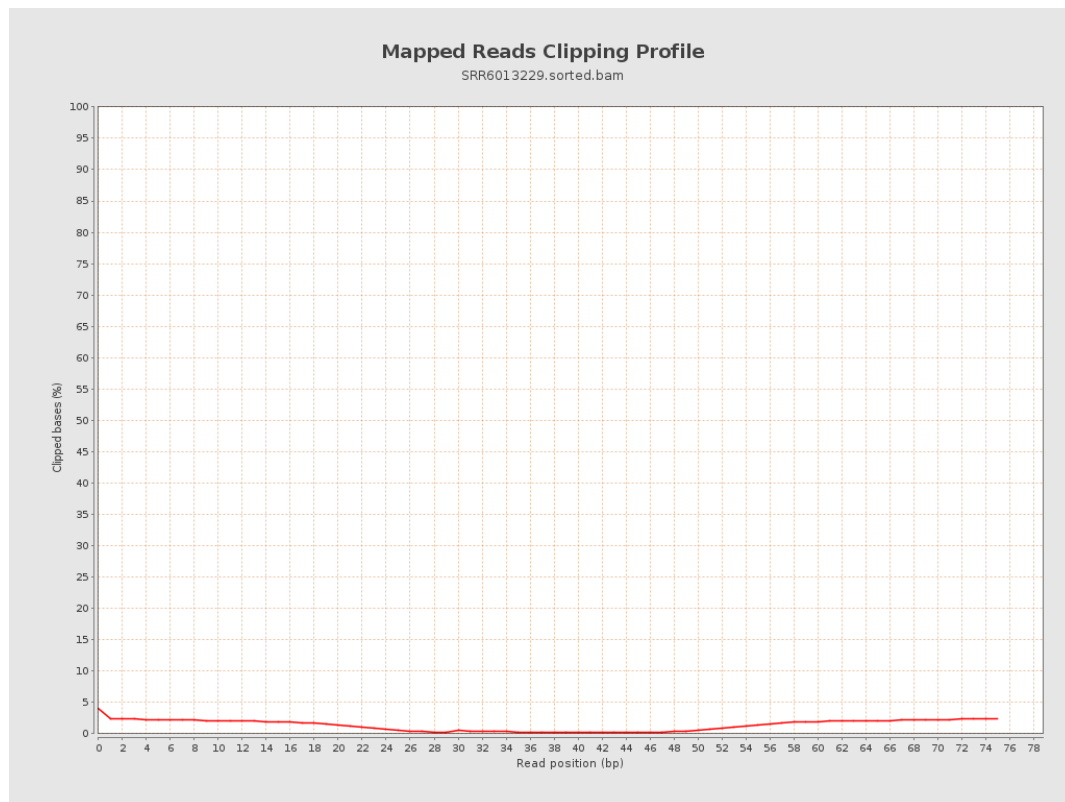
8. Results : Mapped Reads Nucleotide Content



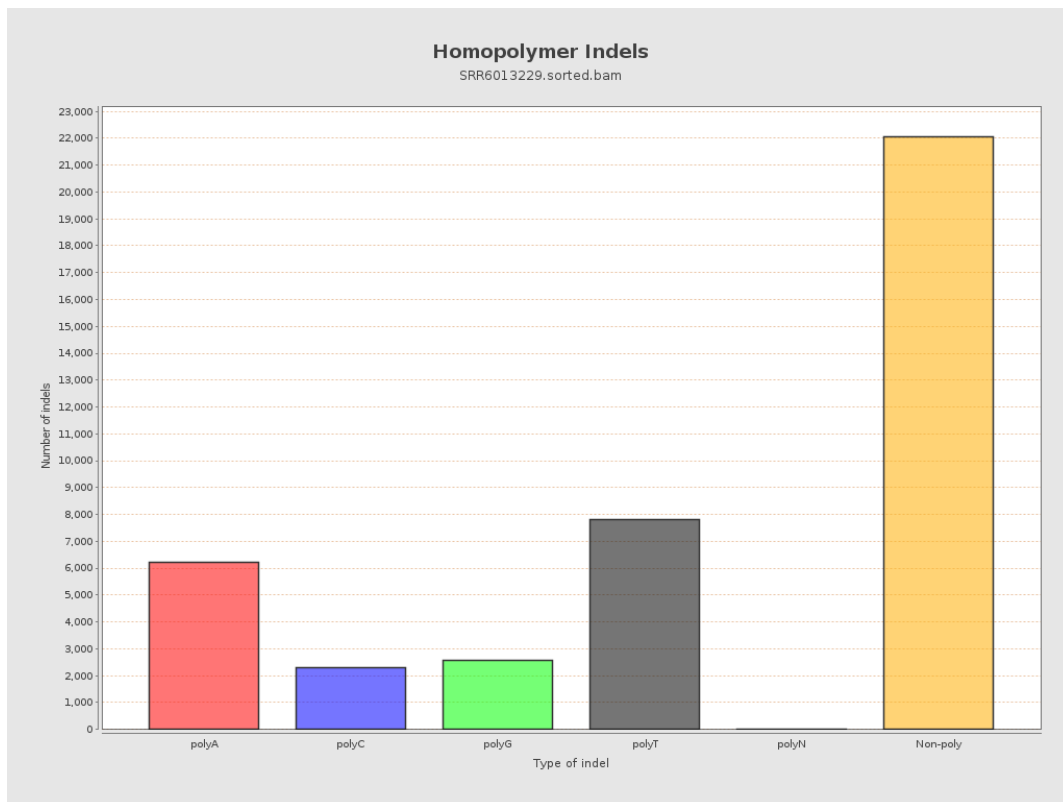
9. Results : Mapped Reads GC-content Distribution



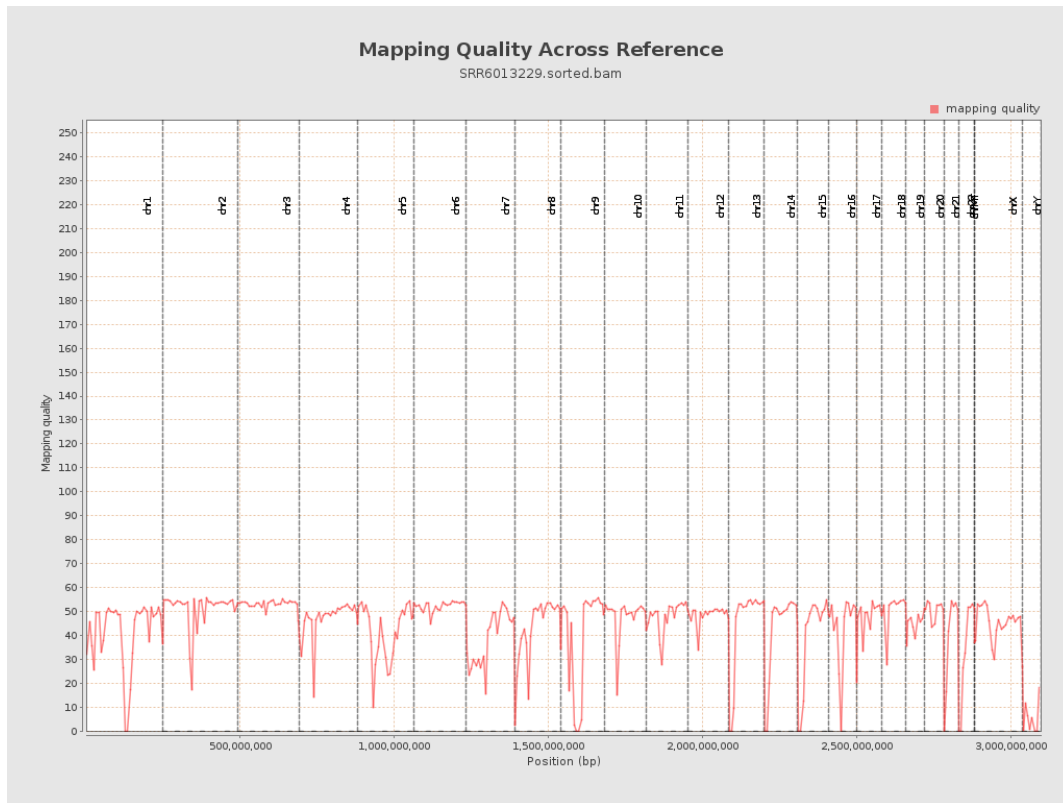
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

