

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:20:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230341.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_SRR6230341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230341.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:20:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,714,254
Mapped reads	2,862,519 / 77.07%
Unmapped reads	851,735 / 22.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,325 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	303,110 / 8.16%
Duplication rate	7.66%
Clipped reads	2,008,761 / 54.08%

2.2. ACGT Content

Number/percentage of A's	43,376,176 / 24.83%
Number/percentage of C's	29,020,705 / 16.61%
Number/percentage of T's	58,124,647 / 33.27%
Number/percentage of G's	43,876,176 / 25.12%
Number/percentage of N's	300,095 / 0.17%
GC Percentage	41.73%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.5465
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2.4. Mapping Quality

Mean Mapping Quality	42.79
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2.5. Mismatches and indels

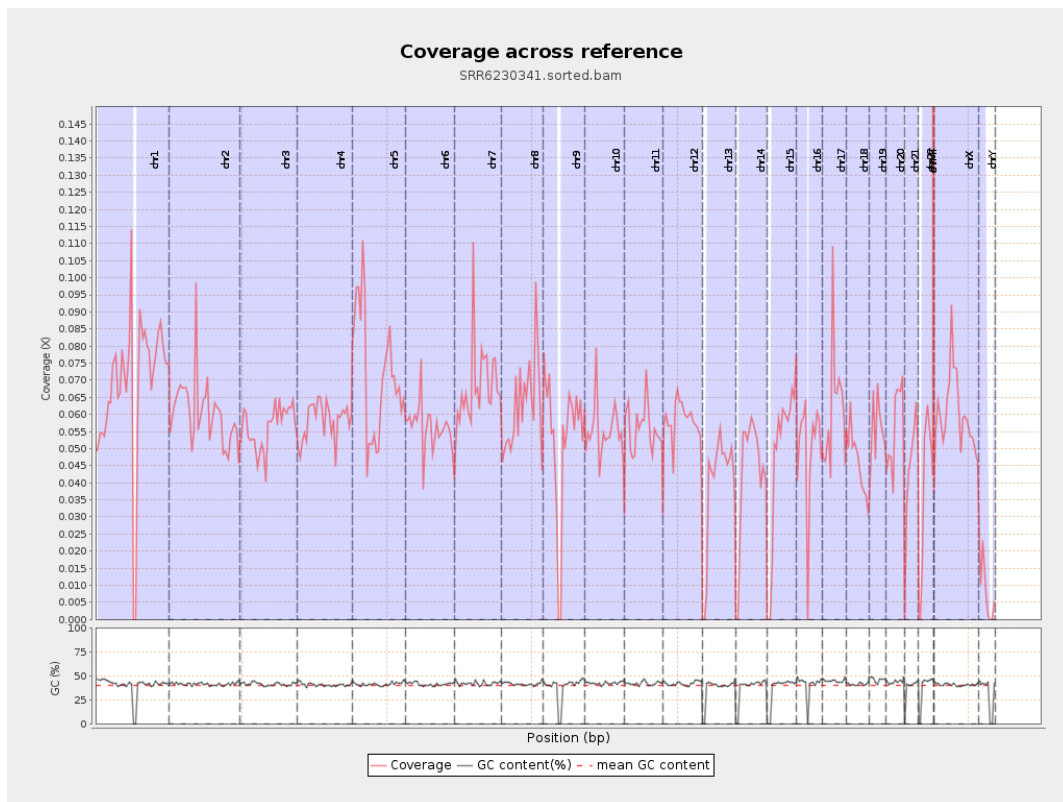
General error rate	1.05%
Mismatches	1,817,325
Insertions	15,181
Mapped reads with at least one insertion	0.53%
Deletions	66,416
Mapped reads with at least one deletion	2.29%
Homopolymer indels	49.99%

2.6. Chromosome stats

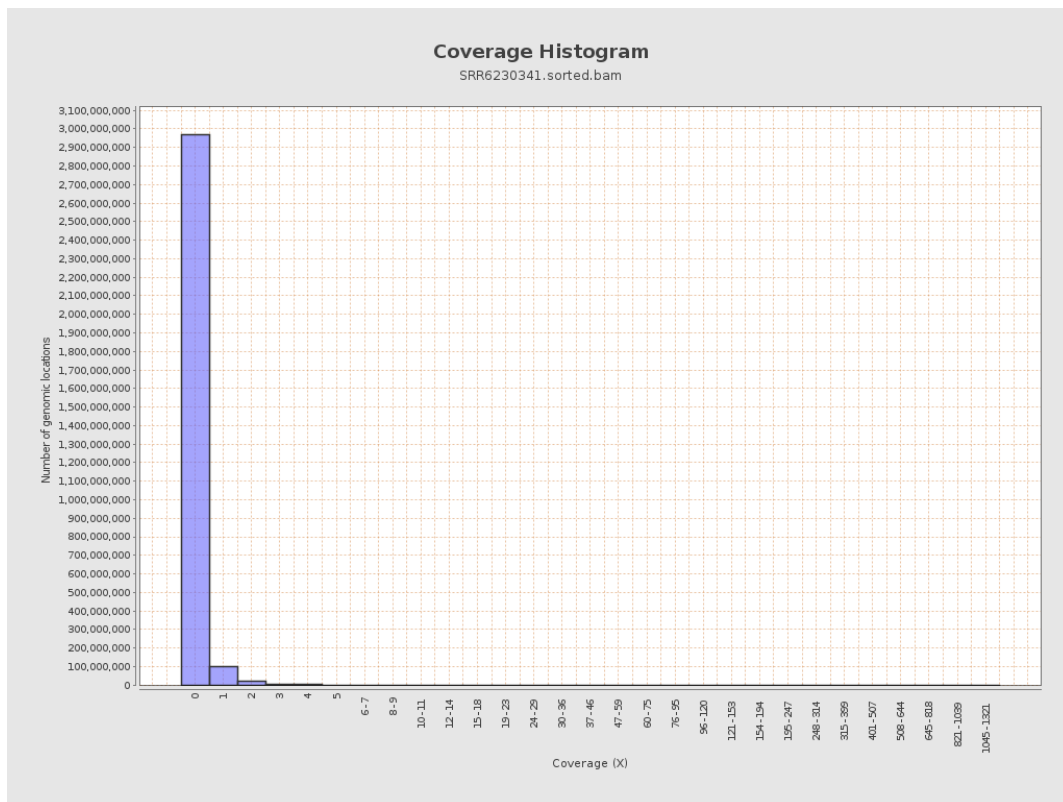
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17072101	0.0685	0.961
chr2	243199373	14698218	0.0604	0.6019
chr3	198022430	11127675	0.0562	0.3259
chr4	191154276	11111789	0.0581	0.3589
chr5	180915260	12930800	0.0715	0.377
chr6	171115067	9598572	0.0561	0.4532
chr7	159138663	10909213	0.0686	0.9966

chr8	146364022	9122443	0.0623	0.4468
chr9	141213431	7388370	0.0523	0.5153
chr10	135534747	7466338	0.0551	0.4568
chr11	135006516	7471140	0.0553	0.5781
chr12	133851895	7788280	0.0582	0.3359
chr13	115169878	4528659	0.0393	0.2708
chr14	107349540	4567968	0.0426	0.3174
chr15	102531392	4898873	0.0478	0.3224
chr16	90354753	4500398	0.0498	0.3294
chr17	81195210	5035013	0.062	0.4165
chr18	78077248	3606416	0.0462	0.7744
chr19	59128983	3302061	0.0558	0.6771
chr20	63025520	3519354	0.0558	0.3514
chr21	48129895	2110966	0.0439	0.3023
chr22	51304566	1917055	0.0374	0.2646
chrMT	16571	394614	23.8135	18.9071
chrX	155270560	9264523	0.0597	0.4069
chrY	59373566	474935	0.008	0.1663

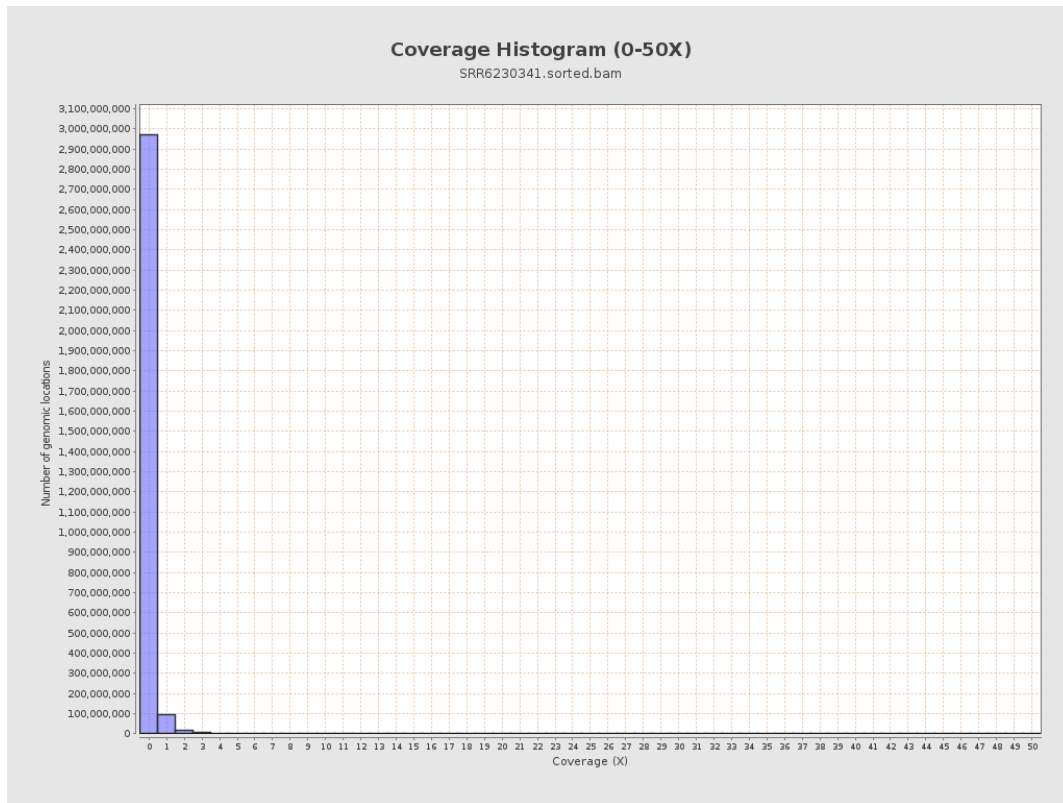
3. Results : Coverage across reference



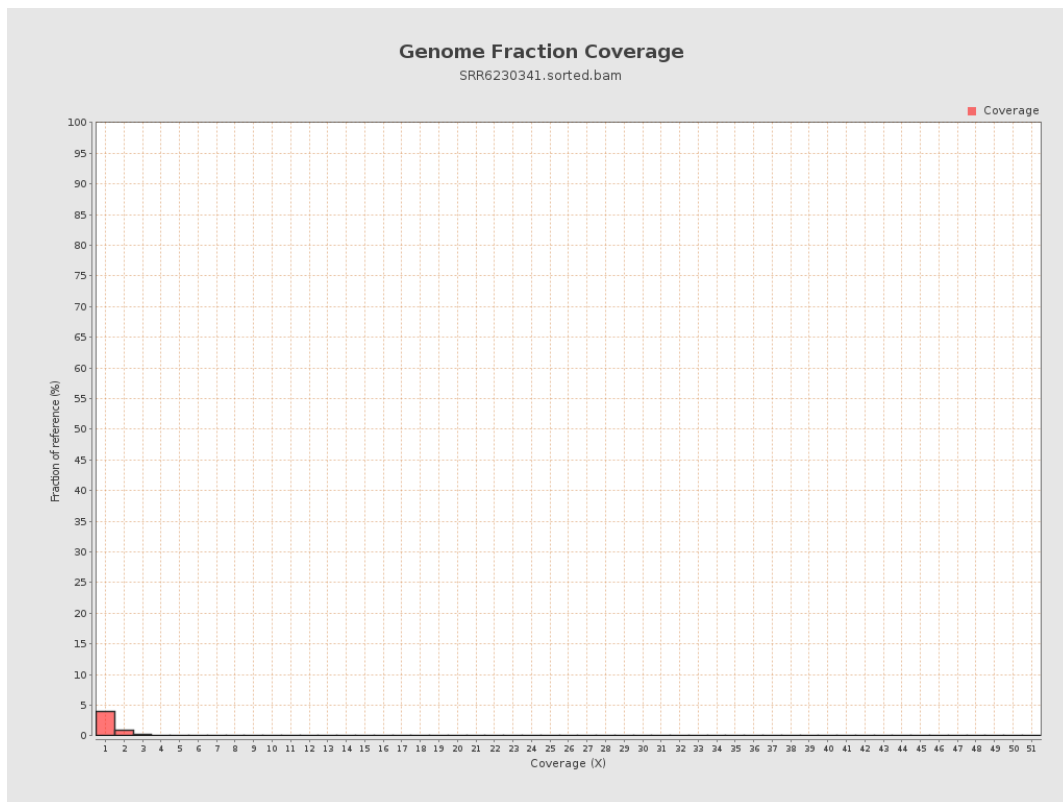
4. Results : Coverage Histogram



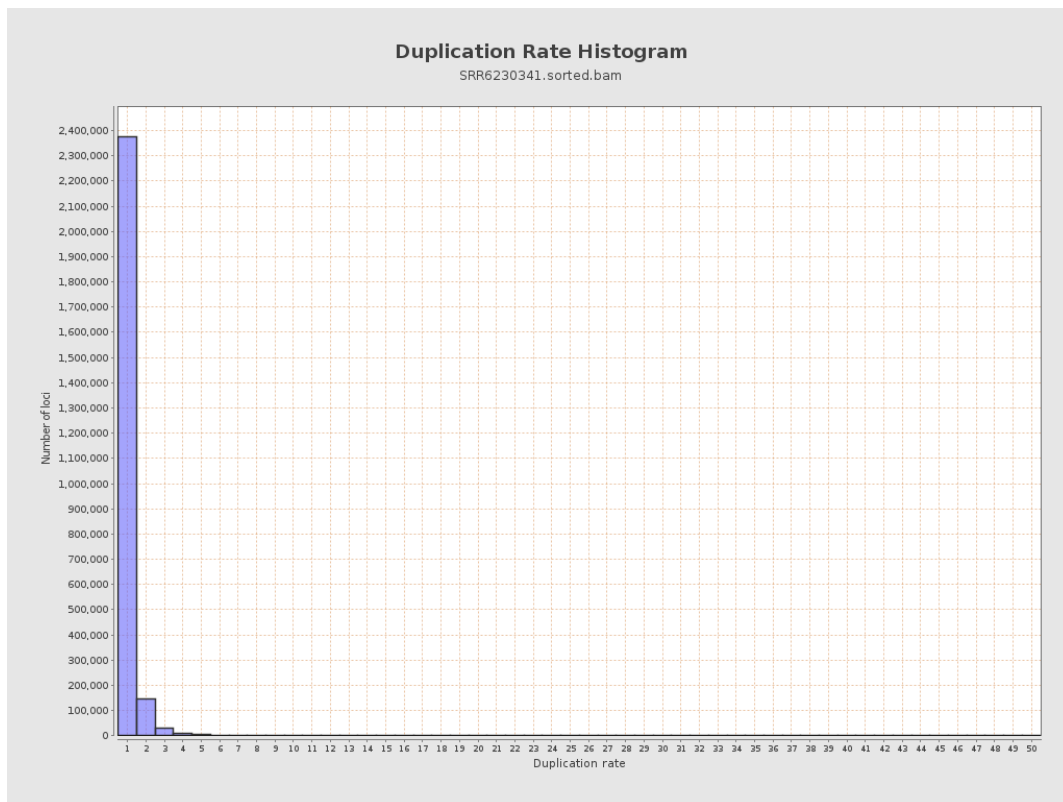
5. Results : Coverage Histogram (0-50X)



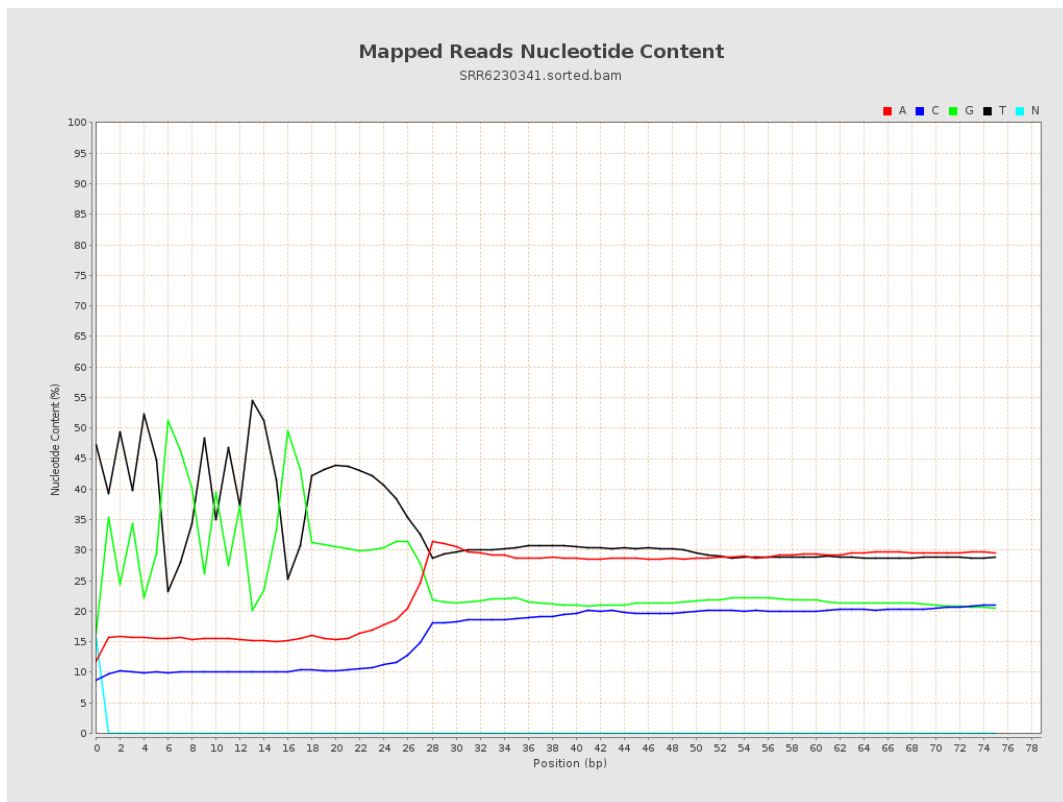
6. Results : Genome Fraction Coverage



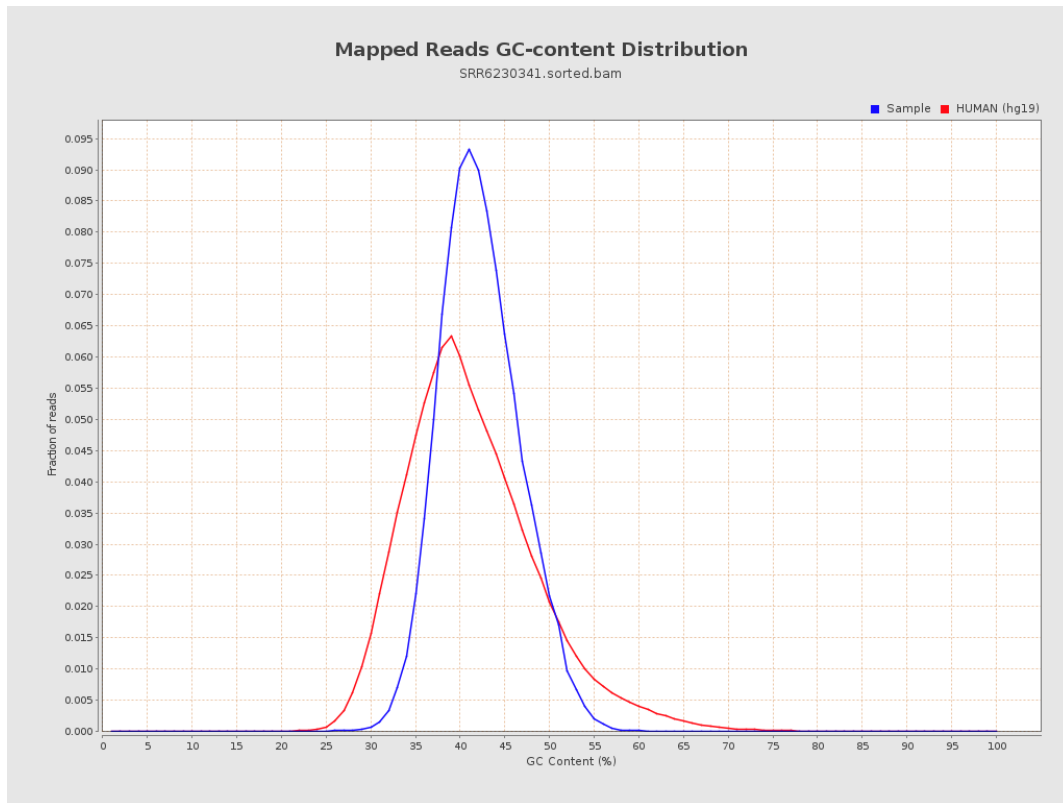
7. Results : Duplication Rate Histogram



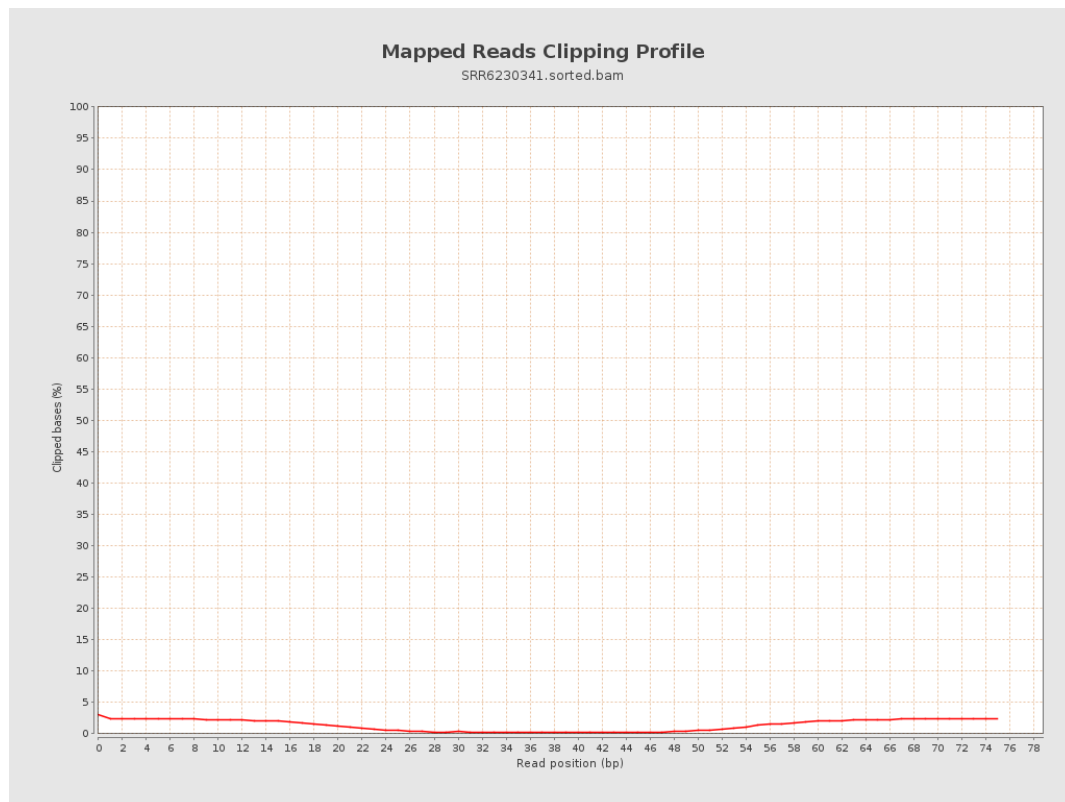
8. Results : Mapped Reads Nucleotide Content



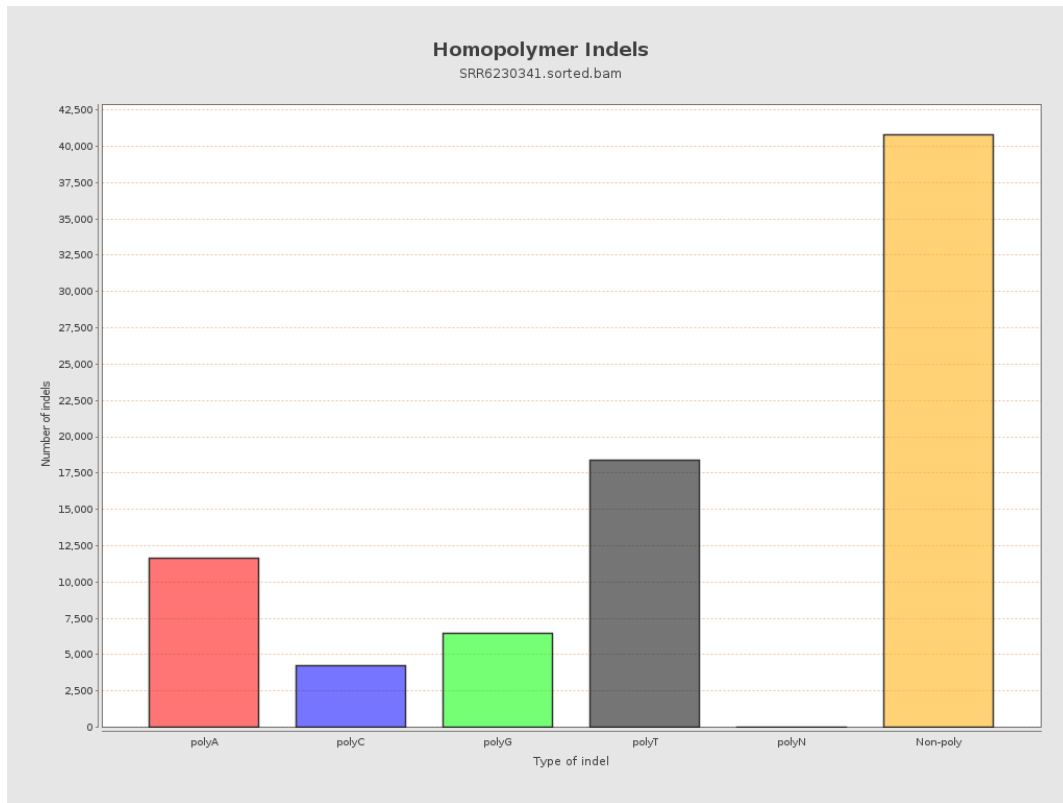
9. Results : Mapped Reads GC-content Distribution



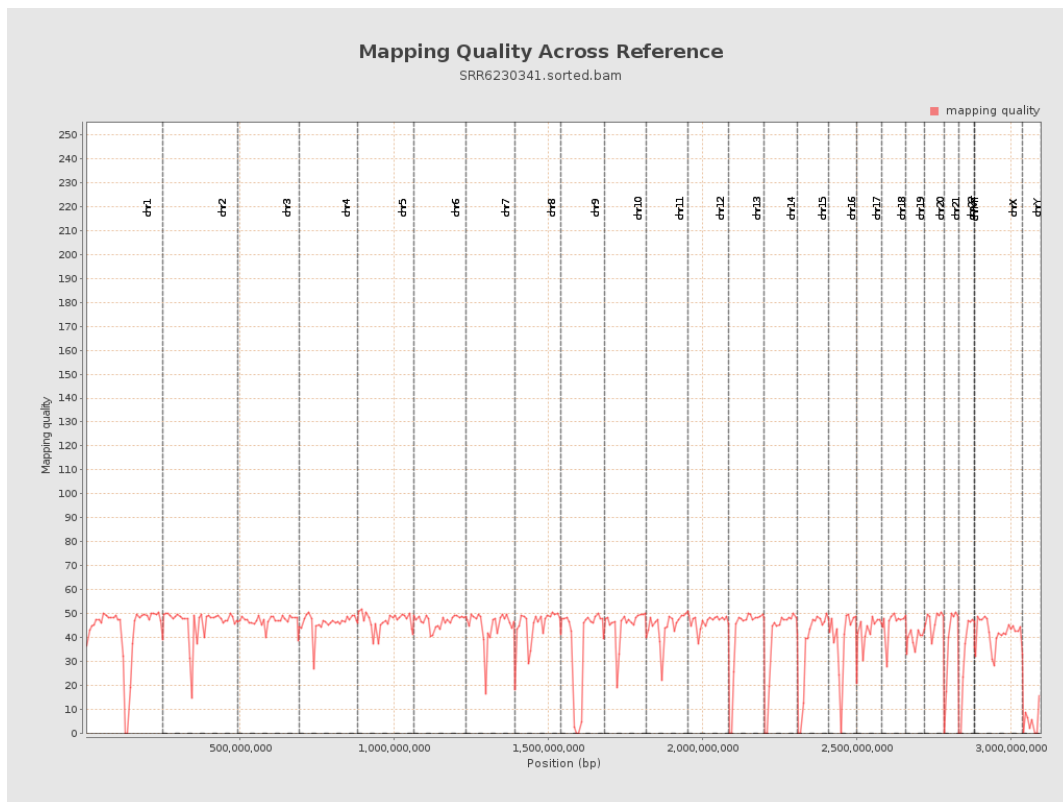
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

