

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 04:50:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153348.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_SRR1153348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153348.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 04:50:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,426,706
Mapped reads	42,165,874 / 99.39%
Unmapped reads	260,832 / 0.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	278,325 / 0.66%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	24,824,732 / 58.51%
Duplication rate	44.6%
Clipped reads	17,194,857 / 40.53%

2.2. ACGT Content

Number/percentage of A's	994,305,208 / 26.57%
Number/percentage of C's	881,598,513 / 23.56%
Number/percentage of T's	1,019,804,477 / 27.25%
Number/percentage of G's	845,275,470 / 22.59%
Number/percentage of N's	1,044,112 / 0.03%
GC Percentage	46.15%

2.3. Coverage

Mean	1.209

Standard Deviation	14.9324
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2.4. Mapping Quality

Mean Mapping Quality	50.01
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2.5. Mismatches and indels

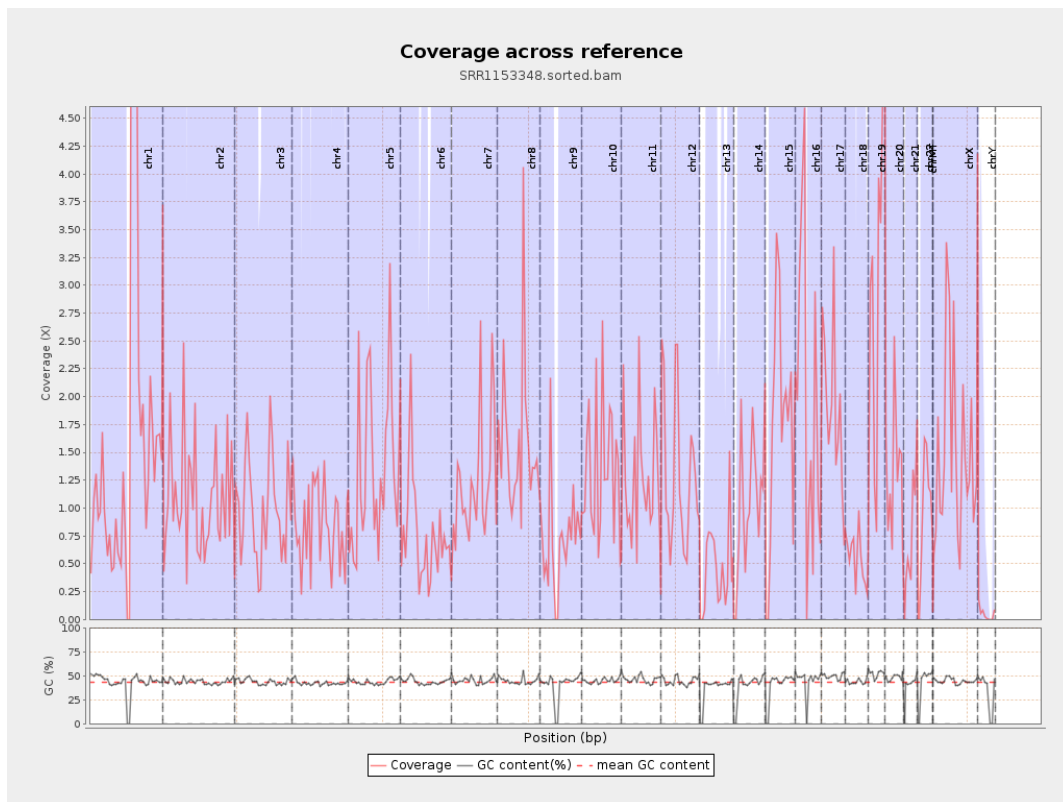
General error rate	0.24%
Mismatches	8,274,116
Insertions	378,424
Mapped reads with at least one insertion	0.89%
Deletions	288,540
Mapped reads with at least one deletion	0.68%
Homopolymer indels	48.98%

2.6. Chromosome stats

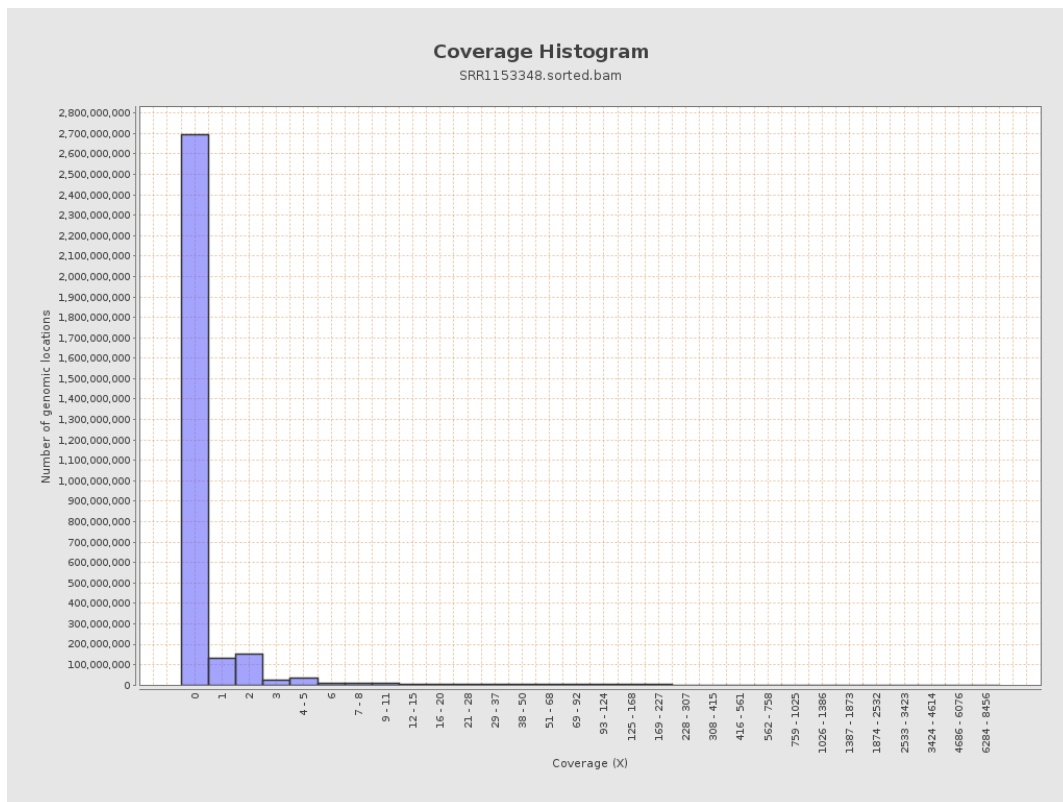
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	393384404	1.5783	18.7459
chr2	243199373	264672277	1.0883	12.0762
chr3	198022430	194844059	0.9839	11.0806
chr4	191154276	161312687	0.8439	12.0407
chr5	180915260	247404269	1.3675	16.3032
chr6	171115067	127033520	0.7424	9.3252
chr7	159138663	192607902	1.2103	16.9205

chr8	146364022	232277711	1.587	21.0336
chr9	141213431	99911813	0.7075	10.1724
chr10	135534747	185191067	1.3664	14.7429
chr11	135006516	171186229	1.268	14.0445
chr12	133851895	177989420	1.3297	15.15
chr13	115169878	52741325	0.4579	8.5421
chr14	107349540	108588810	1.0115	12.1478
chr15	102531392	172255778	1.68	18.8058
chr16	90354753	172859843	1.9131	19.6808
chr17	81195210	158836840	1.9562	18.7898
chr18	78077248	43197870	0.5533	7.6938
chr19	59128983	176355965	2.9826	24.4861
chr20	63025520	83662589	1.3274	14.1765
chr21	48129895	37296368	0.7749	10.0013
chr22	51304566	48605110	0.9474	13.1569
chrMT	16571	1057	0.0638	0.375
chrX	155270560	237558455	1.53	17.7472
chrY	59373566	2841133	0.0479	2.191

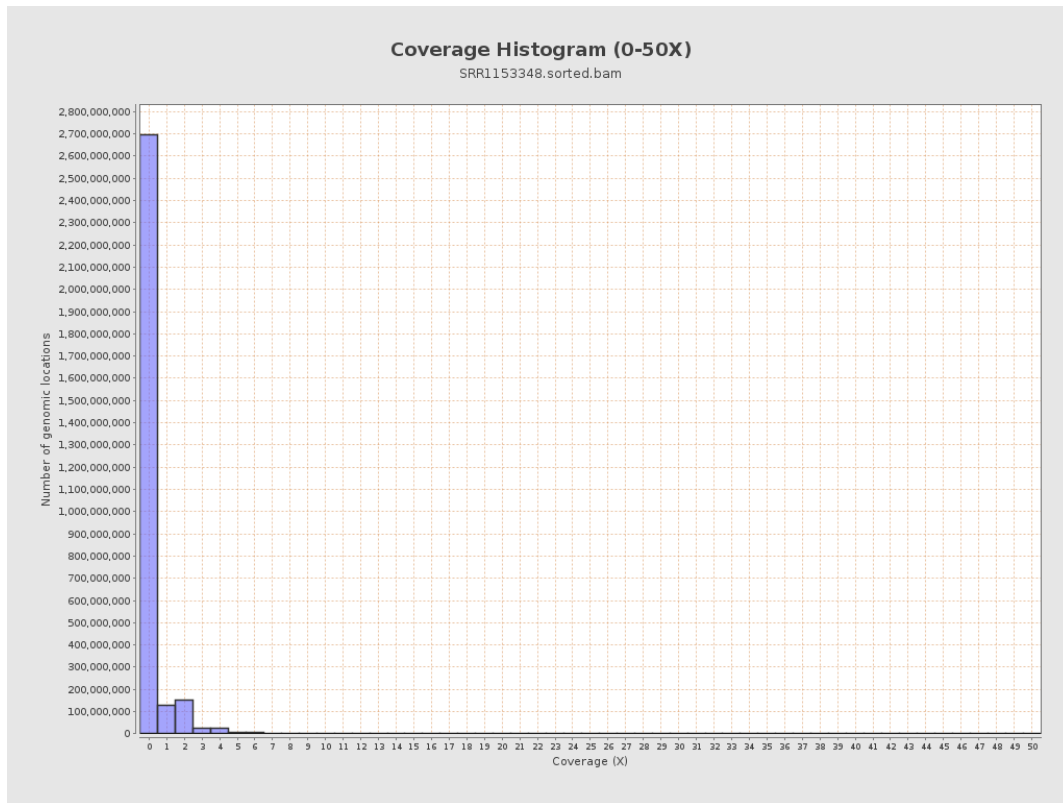
3. Results : Coverage across reference



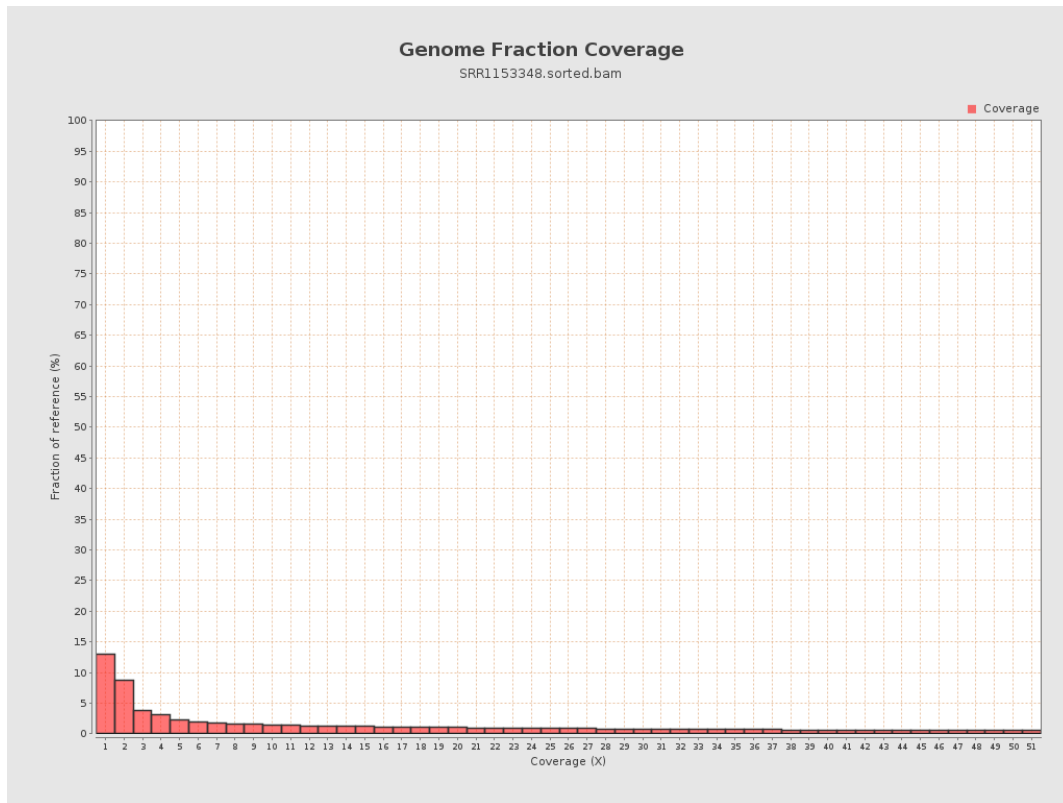
4. Results : Coverage Histogram



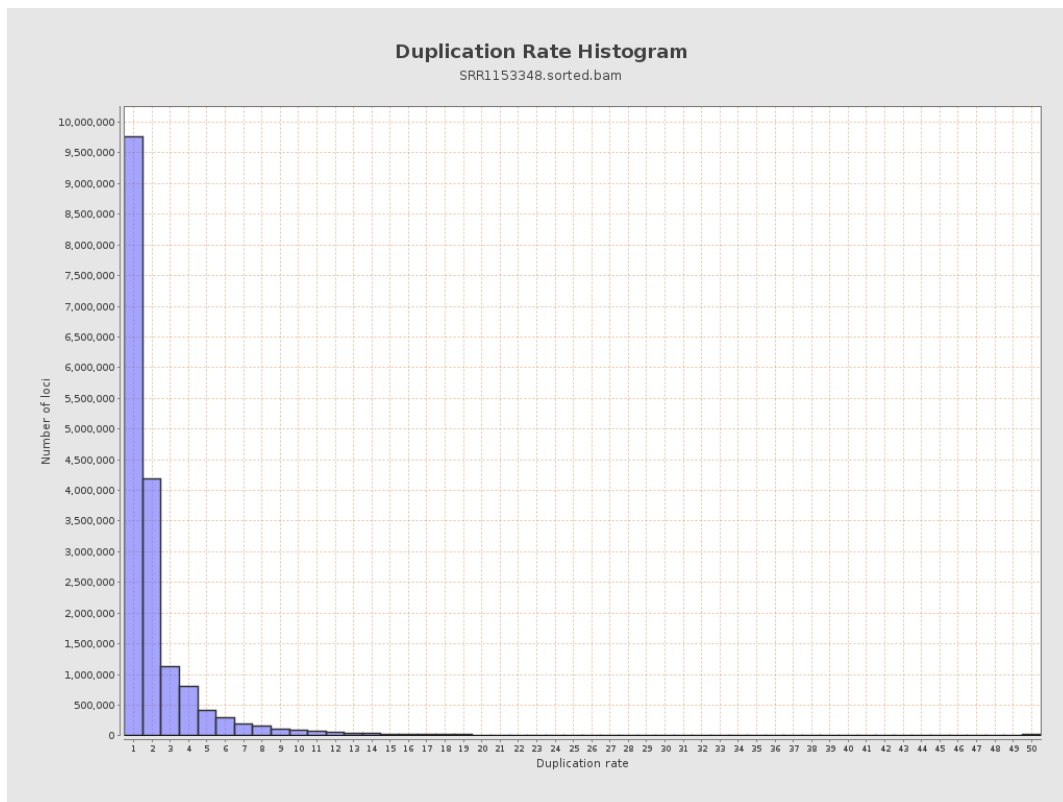
5. Results : Coverage Histogram (0-50X)



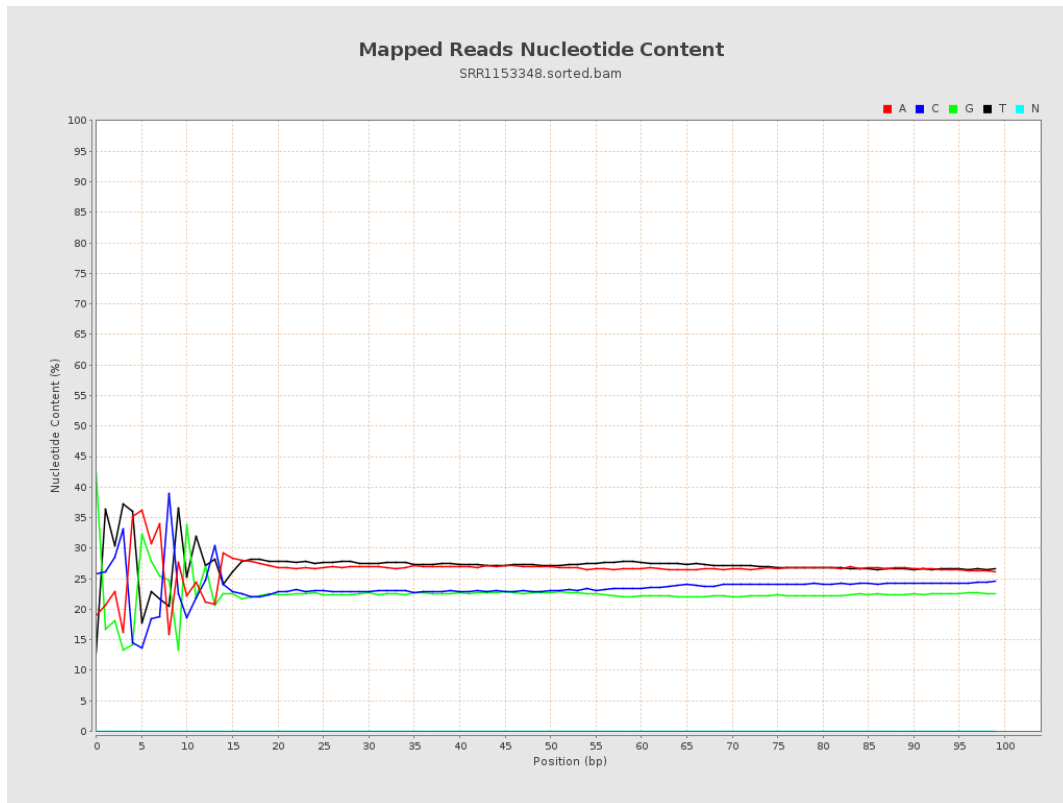
6. Results : Genome Fraction Coverage



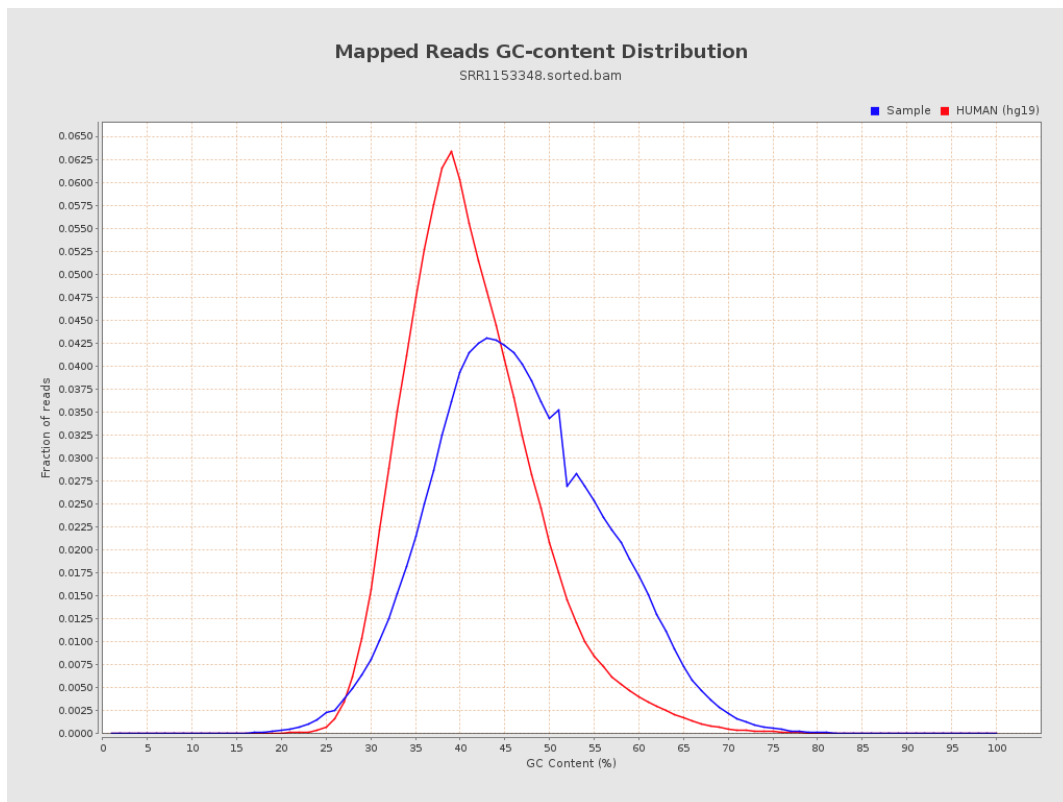
7. Results : Duplication Rate Histogram



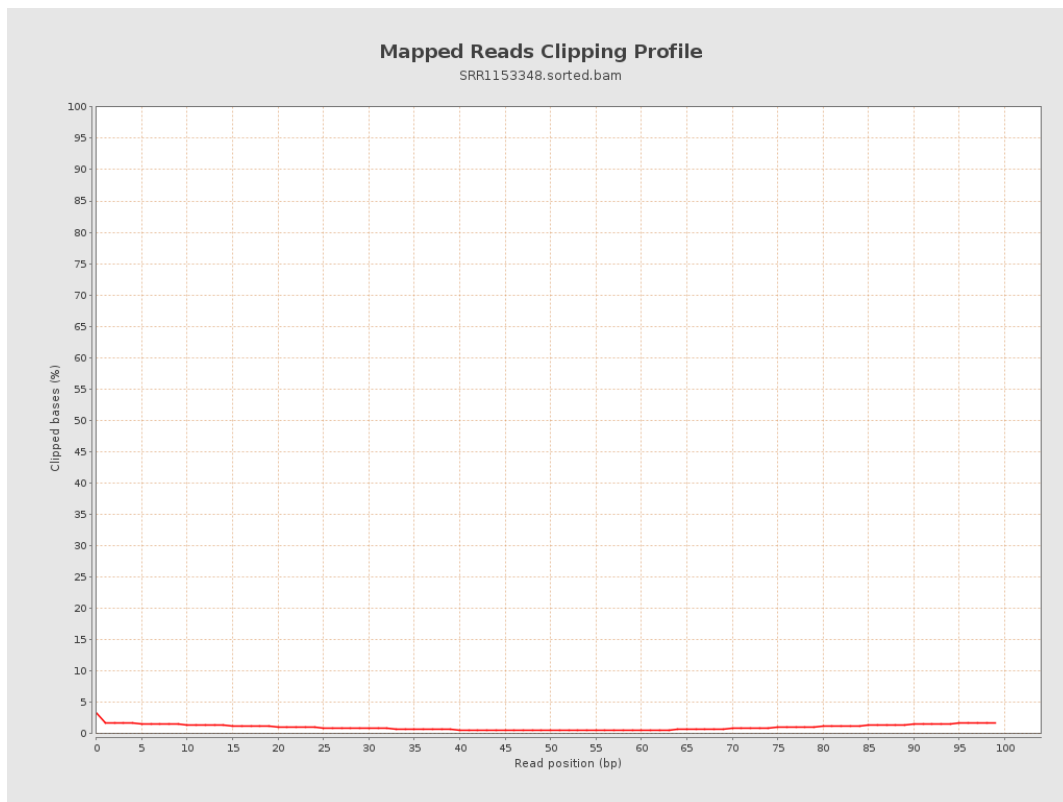
8. Results : Mapped Reads Nucleotide Content



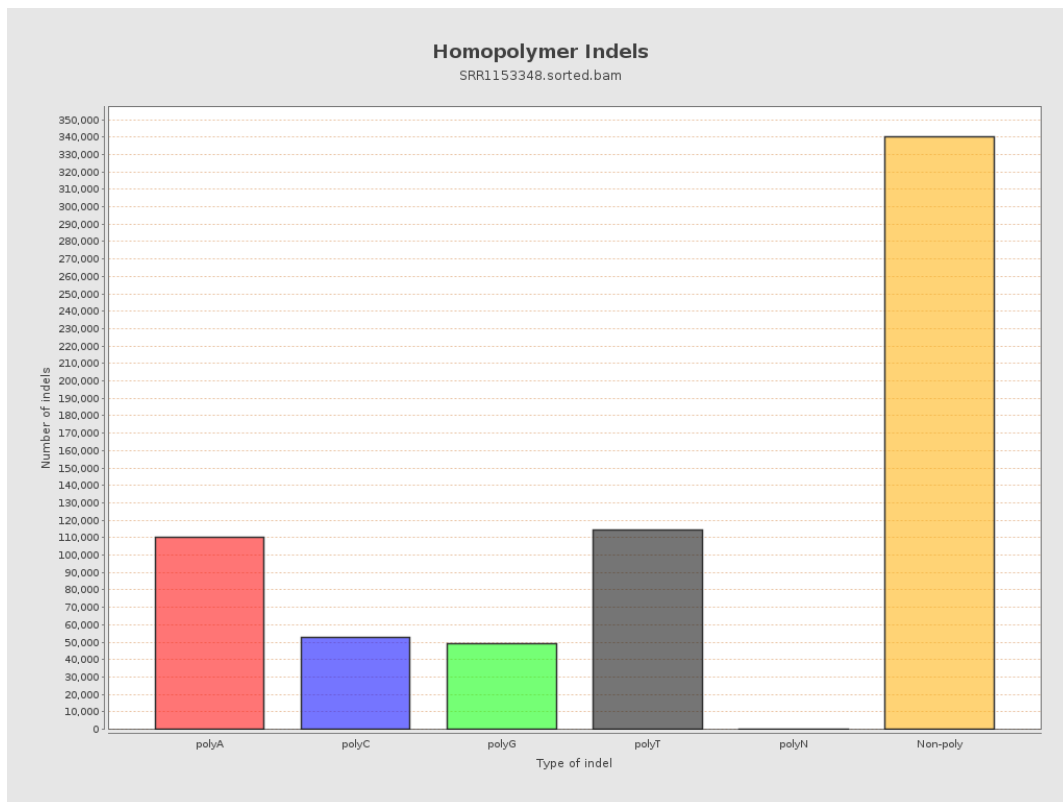
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

