

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 12:40:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153400.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_SRR1153400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153400.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 12:40:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	243,865,252
Mapped reads	229,978,073 / 94.31%
Unmapped reads	13,887,179 / 5.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	168,103 / 0.07%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	123,101,950 / 50.48%
Duplication rate	42.37%
Clipped reads	18,456,002 / 7.57%

2.2. ACGT Content

Number/percentage of A's	5,700,416,872 / 25.26%
Number/percentage of C's	5,608,316,445 / 24.86%
Number/percentage of T's	5,616,677,948 / 24.89%
Number/percentage of G's	5,613,173,940 / 24.88%
Number/percentage of N's	24,355,430 / 0.11%
GC Percentage	49.73%

2.3. Coverage

Mean	7.2896

Standard Deviation	61.8869
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2.4. Mapping Quality

Mean Mapping Quality	48.88
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2.5. Mismatches and indels

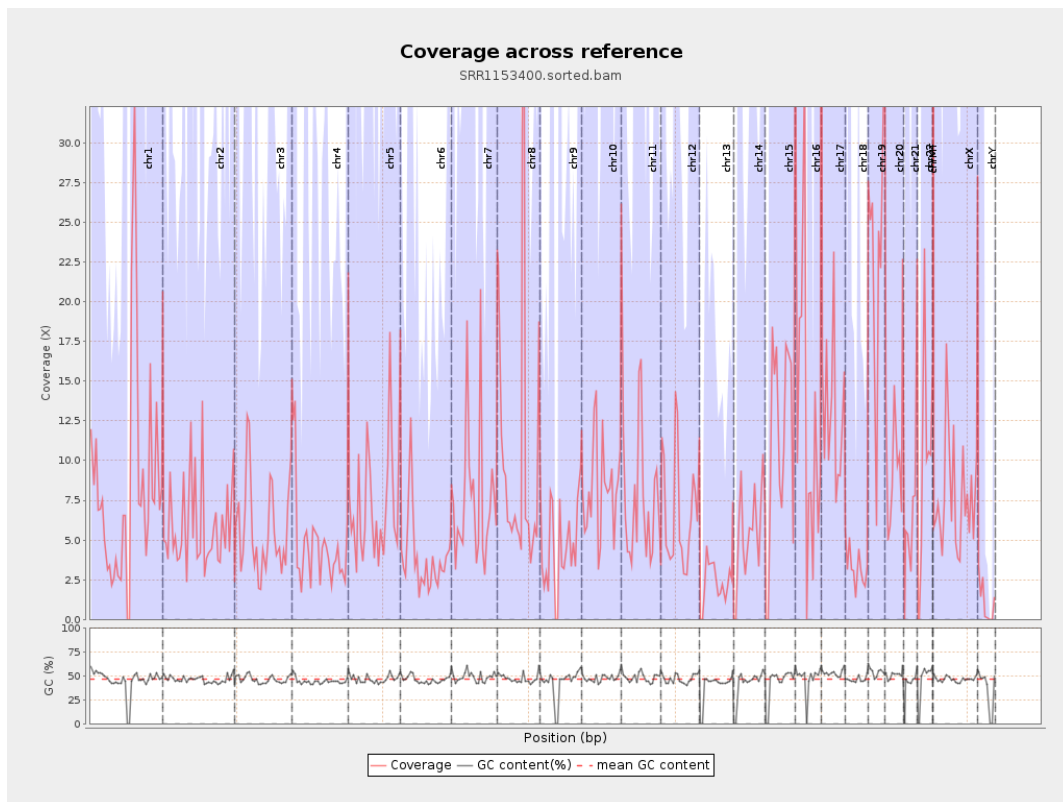
General error rate	0.61%
Mismatches	135,978,425
Insertions	1,096,377
Mapped reads with at least one insertion	0.46%
Deletions	1,409,761
Mapped reads with at least one deletion	0.6%
Homopolymer indels	40.03%

2.6. Chromosome stats

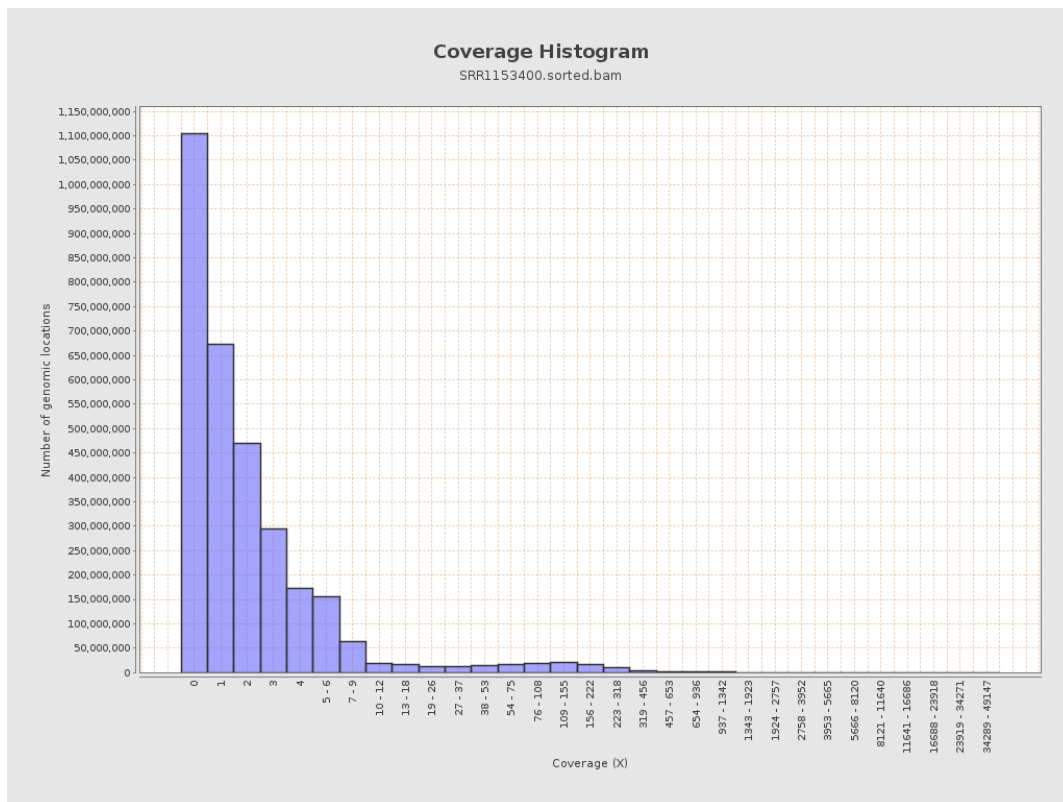
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2055992385	8.2487	63.2113
chr2	243199373	1440730320	5.9241	46.5297
chr3	198022430	1129819604	5.7055	40.2068
chr4	191154276	878544896	4.596	34.5207
chr5	180915260	1349579575	7.4597	58.0888
chr6	171115067	656406028	3.8361	21.6817
chr7	159138663	1214266884	7.6302	102.8739

chr8	146364022	1523816334	10.4111	158.7
chr9	141213431	632399253	4.4783	28.0636
chr10	135534747	1106488894	8.1639	61.1833
chr11	135006516	1046493230	7.7514	37.422
chr12	133851895	922241736	6.89	31.8861
chr13	115169878	276816522	2.4035	15.0013
chr14	107349540	579078581	5.3943	31.5995
chr15	102531392	1136410439	11.0835	61.5935
chr16	90354753	1226695555	13.5764	72.6933
chr17	81195210	1054826214	12.9912	72.2882
chr18	78077248	251471577	3.2208	29.0157
chr19	59128983	1345742548	22.7594	81.3577
chr20	63025520	621534172	9.8616	46.2651
chr21	48129895	339219973	7.048	55.1328
chr22	51304566	489660723	9.5442	52.3667
chrMT	16571	1921088	115.9307	39.6953
chrX	155270560	1224907043	7.8889	43.1204
chrY	59373566	61397207	1.0341	50.6968

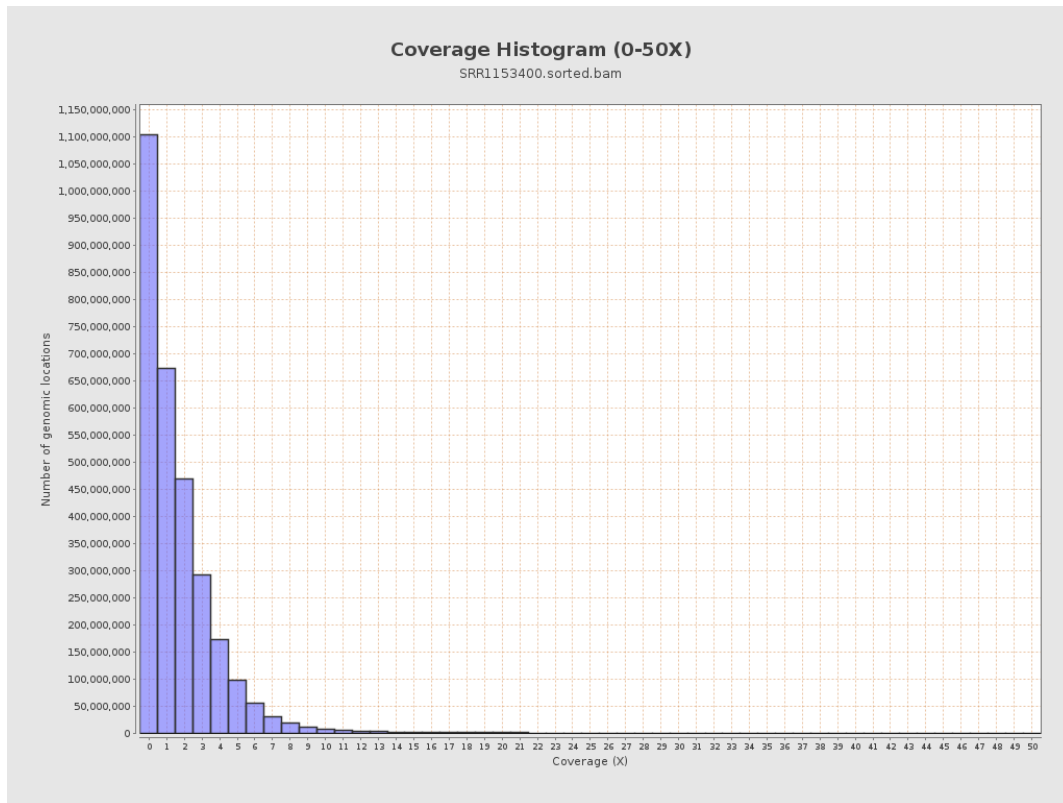
3. Results : Coverage across reference



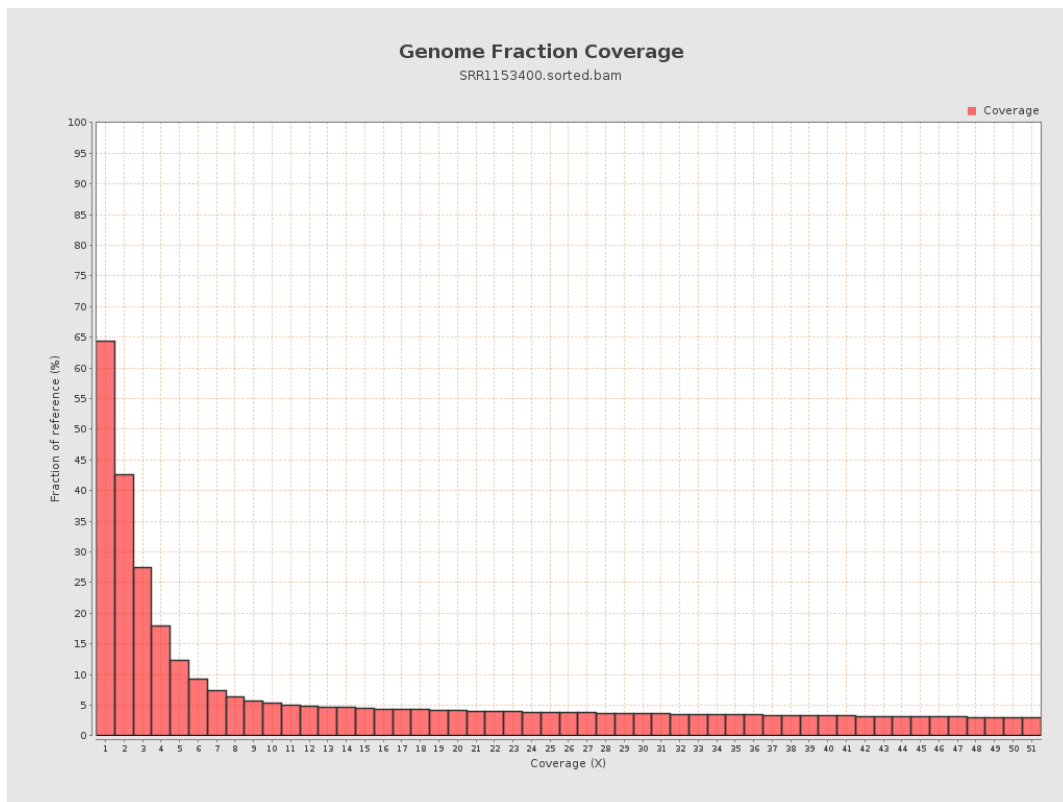
4. Results : Coverage Histogram



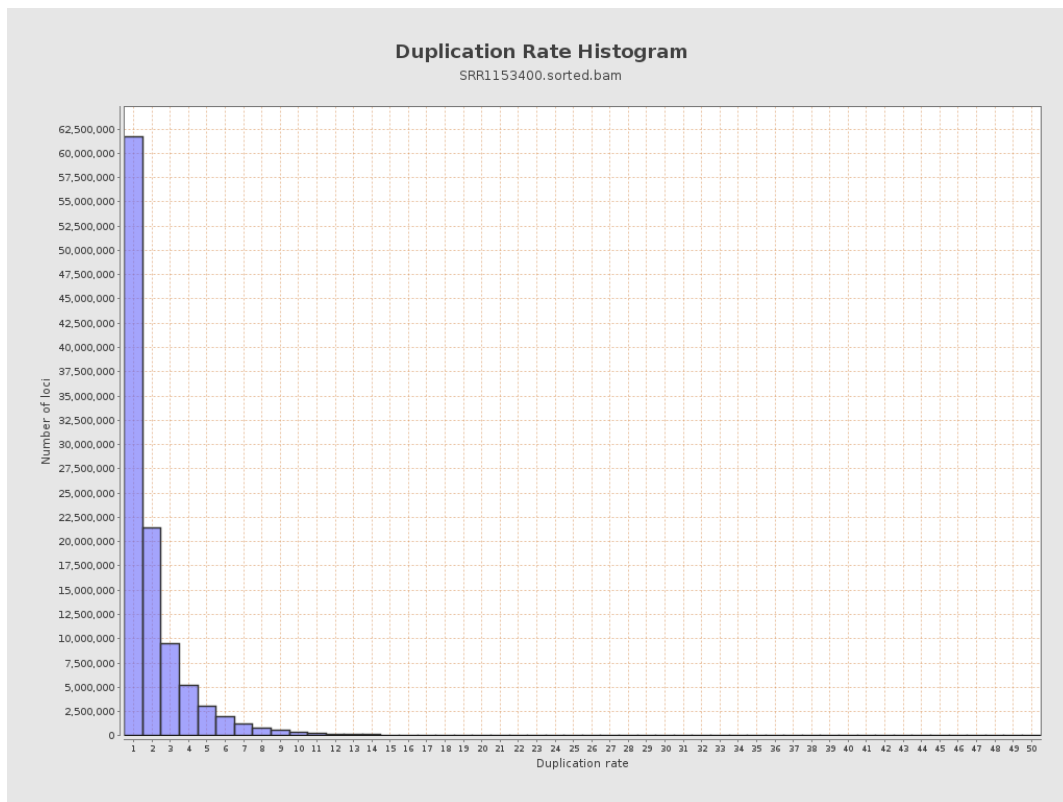
5. Results : Coverage Histogram (0-50X)



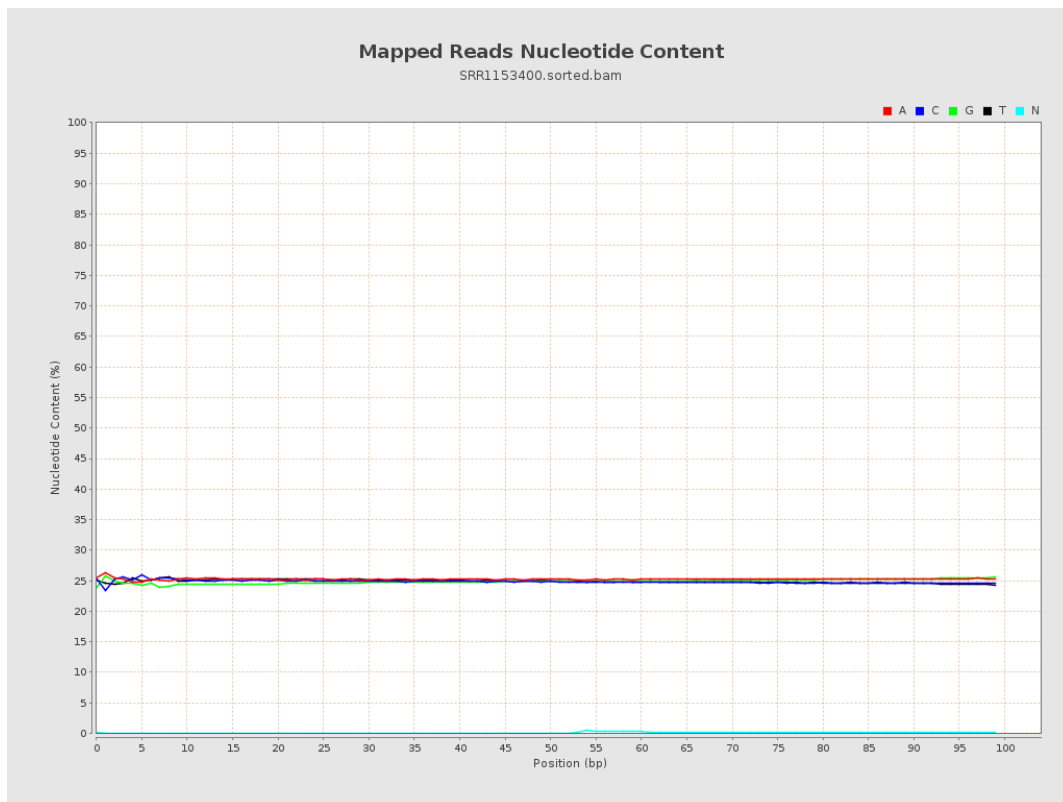
6. Results : Genome Fraction Coverage



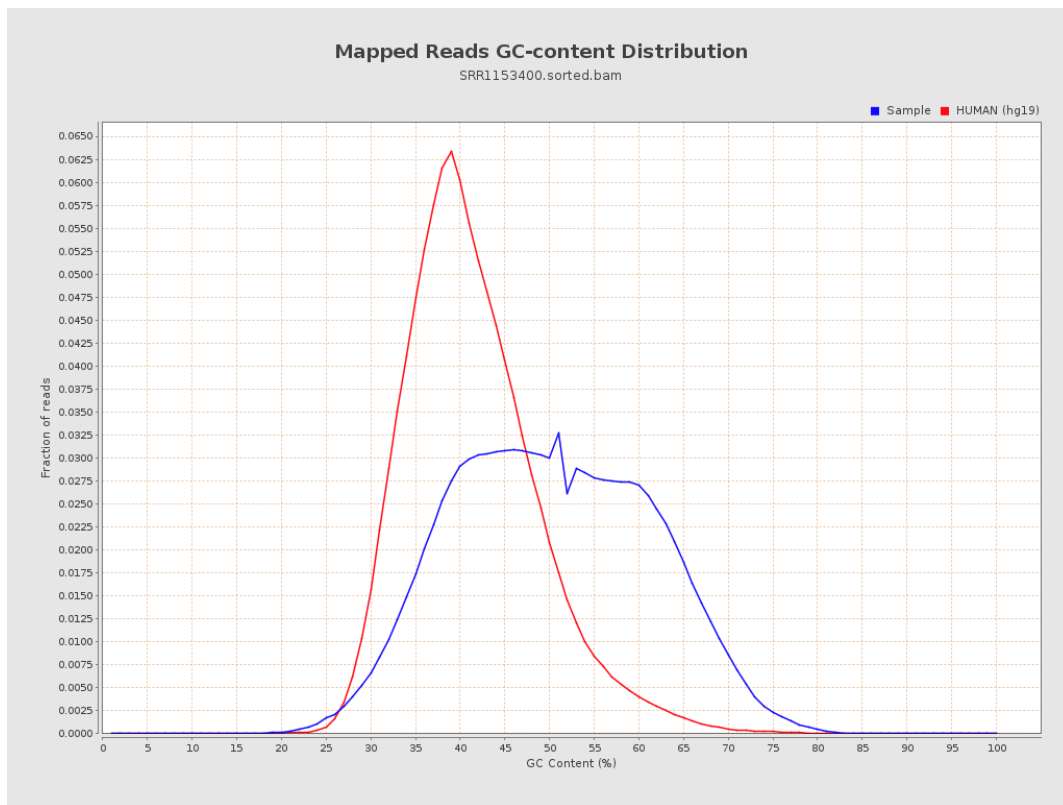
7. Results : Duplication Rate Histogram



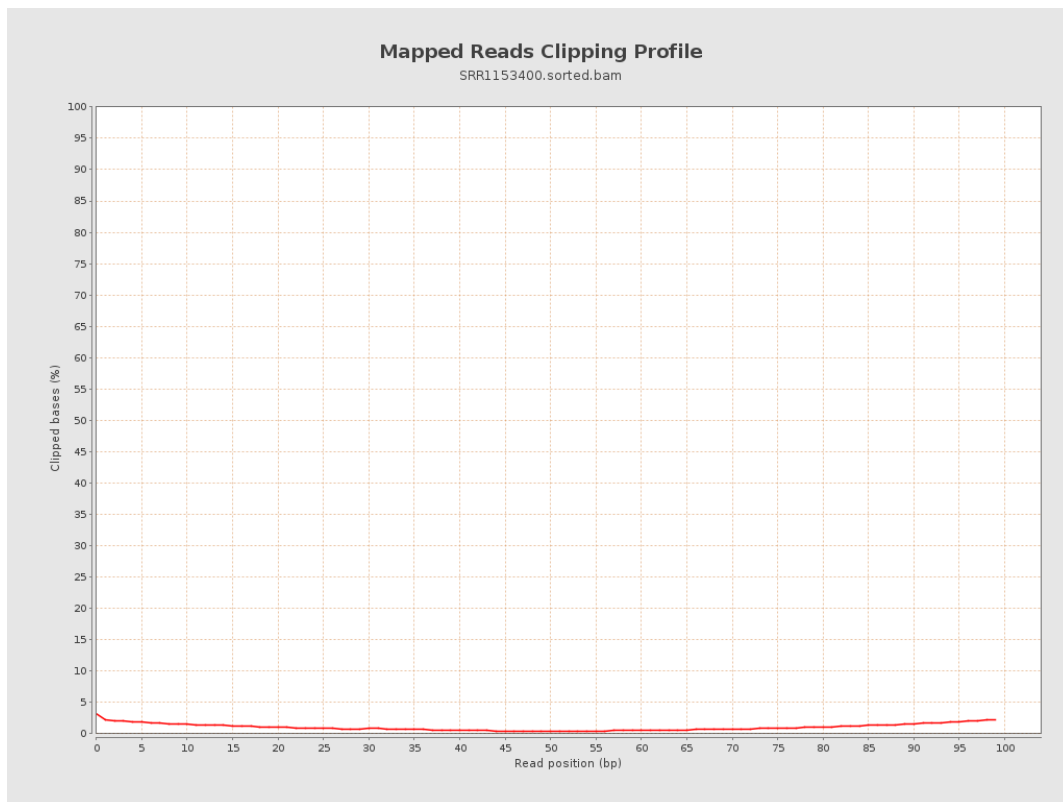
8. Results : Mapped Reads Nucleotide Content



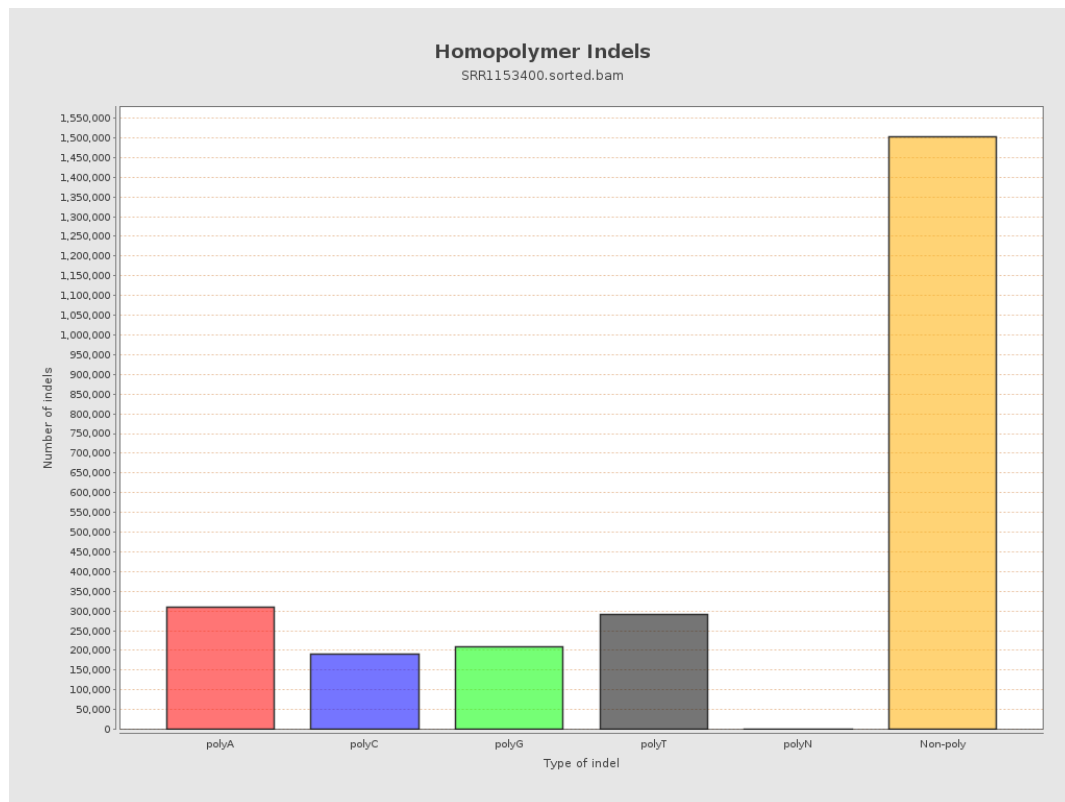
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

