

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 19:29:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153334.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_SRR1153334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 19:29:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	224,415,324
Mapped reads	219,638,547 / 97.87%
Unmapped reads	4,776,777 / 2.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,612,490 / 0.72%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	169,859,666 / 75.69%
Duplication rate	66.3%
Clipped reads	20,441,224 / 9.11%

2.2. ACGT Content

Number/percentage of A's	4,771,505,091 / 22.04%
Number/percentage of C's	6,061,976,550 / 28%
Number/percentage of T's	4,806,170,549 / 22.2%
Number/percentage of G's	6,002,569,238 / 27.73%
Number/percentage of N's	6,392,804 / 0.03%
GC Percentage	55.73%

2.3. Coverage

Mean	6.9939

Standard Deviation	94.0284
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2.4. Mapping Quality

Mean Mapping Quality	48.62
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2.5. Mismatches and indels

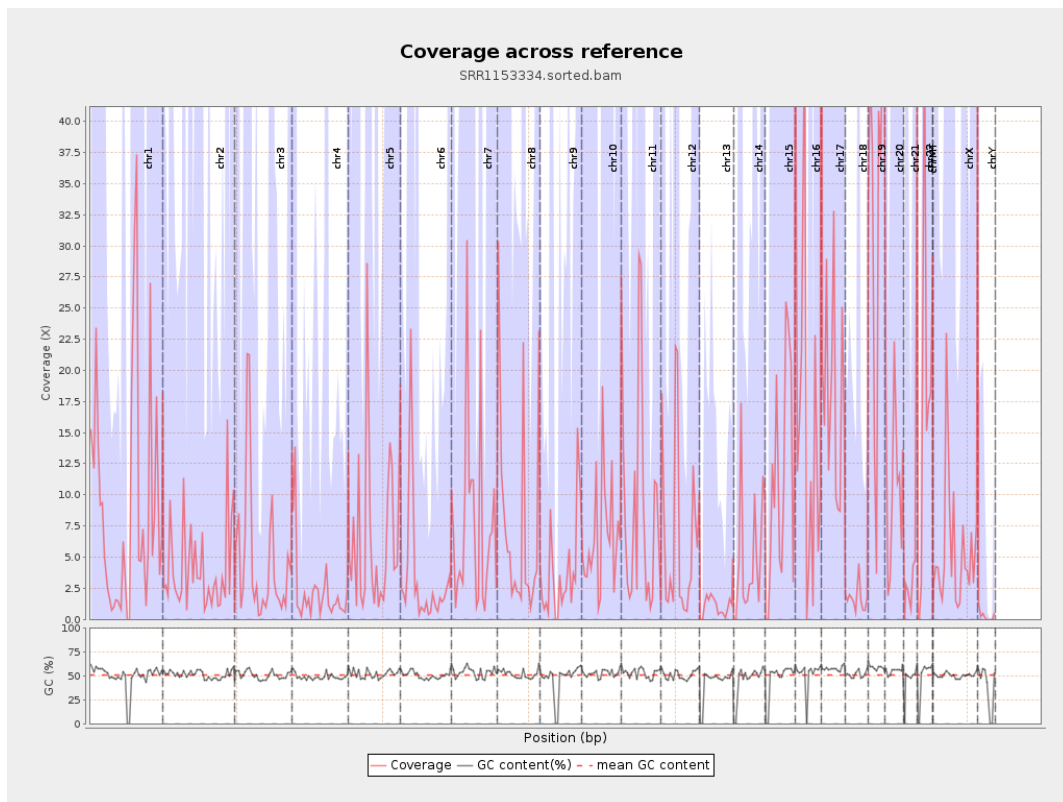
General error rate	0.41%
Mismatches	86,545,386
Insertions	816,982
Mapped reads with at least one insertion	0.37%
Deletions	922,053
Mapped reads with at least one deletion	0.41%
Homopolymer indels	39.55%

2.6. Chromosome stats

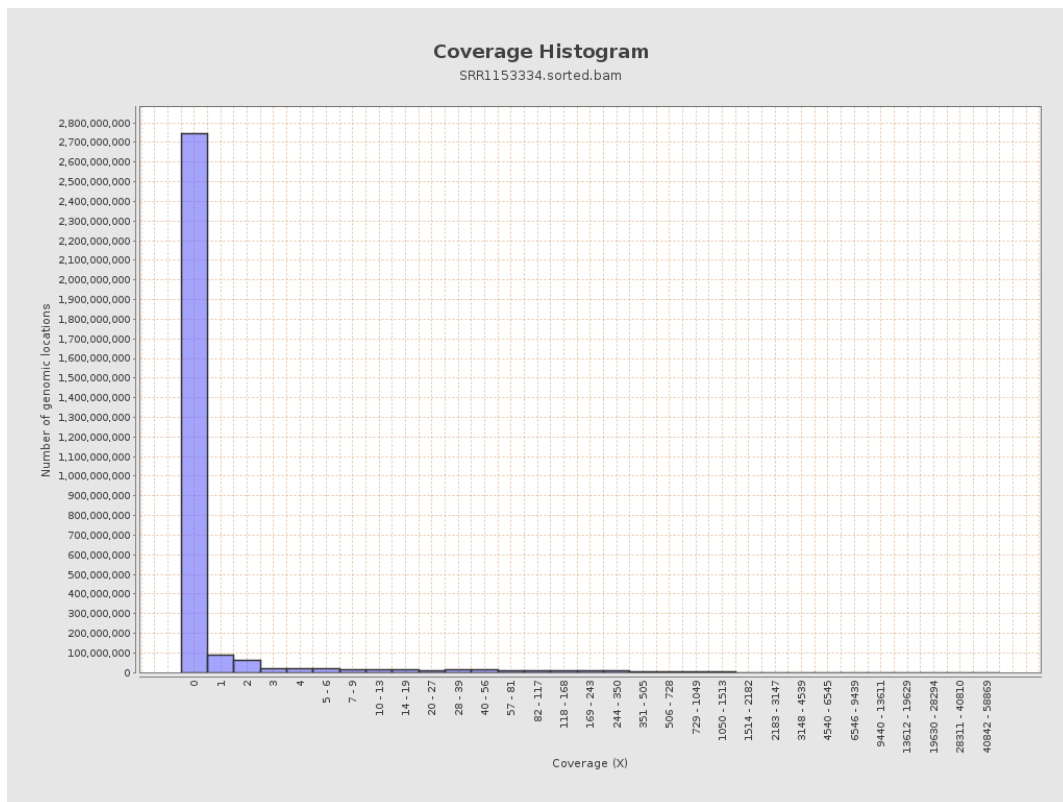
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2241570888	8.9932	94.9093
chr2	243199373	980637543	4.0322	47.6492
chr3	198022430	921231670	4.6522	54.8691
chr4	191154276	420578280	2.2002	41.7873
chr5	180915260	1198868350	6.6267	162.6026
chr6	171115067	540400404	3.1581	42.6437
chr7	159138663	1205985853	7.5782	142.8576

chr8	146364022	1075745045	7.3498	109.4033
chr9	141213431	521964052	3.6963	49.4873
chr10	135534747	897473415	6.6217	69.0189
chr11	135006516	1181122631	8.7486	82.6474
chr12	133851895	906804800	6.7747	64.4682
chr13	115169878	126777004	1.1008	15.8366
chr14	107349540	520632471	4.8499	51.4626
chr15	102531392	1098719740	10.7159	102.3409
chr16	90354753	1486334456	16.45	135.2832
chr17	81195210	1469380738	18.0969	139.4512
chr18	78077248	128487627	1.6456	27.3768
chr19	59128983	1961127131	33.1669	189.6672
chr20	63025520	651471214	10.3366	91.864
chr21	48129895	319448675	6.6372	201.1793
chr22	51304566	849377870	16.5556	144.1949
chrMT	16571	2091	0.1262	0.453
chrX	155270560	929563130	5.9867	63.6673
chrY	59373566	17421990	0.2934	12.5291

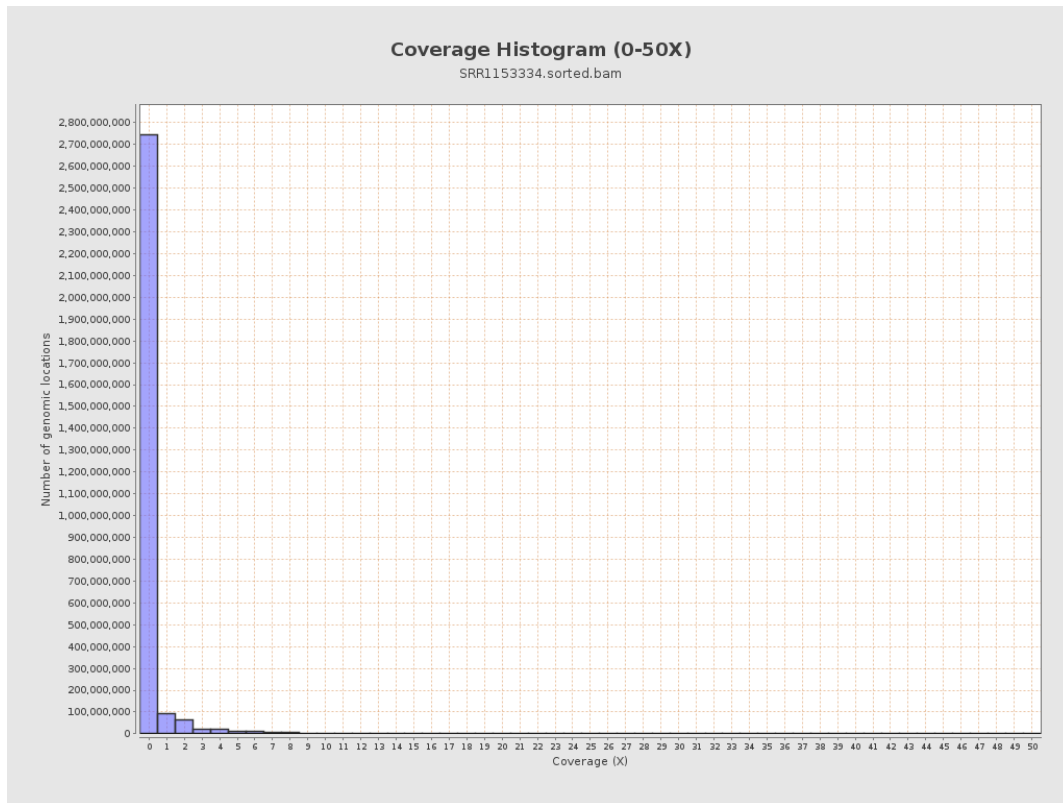
3. Results : Coverage across reference



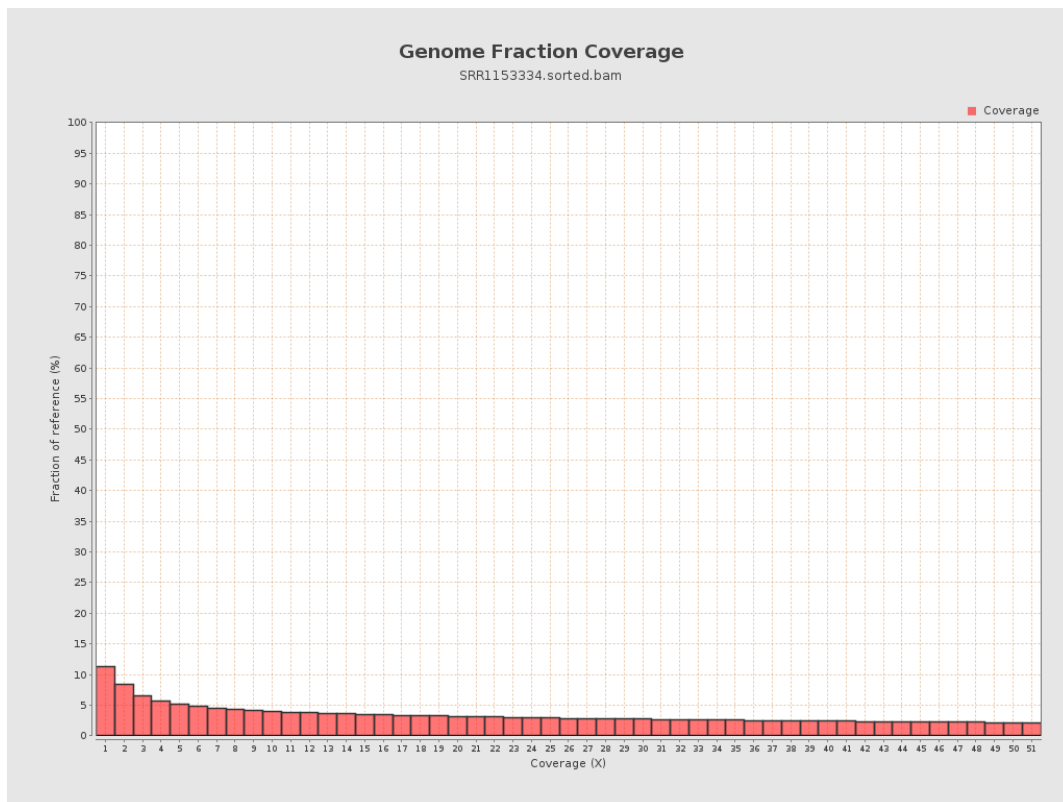
4. Results : Coverage Histogram



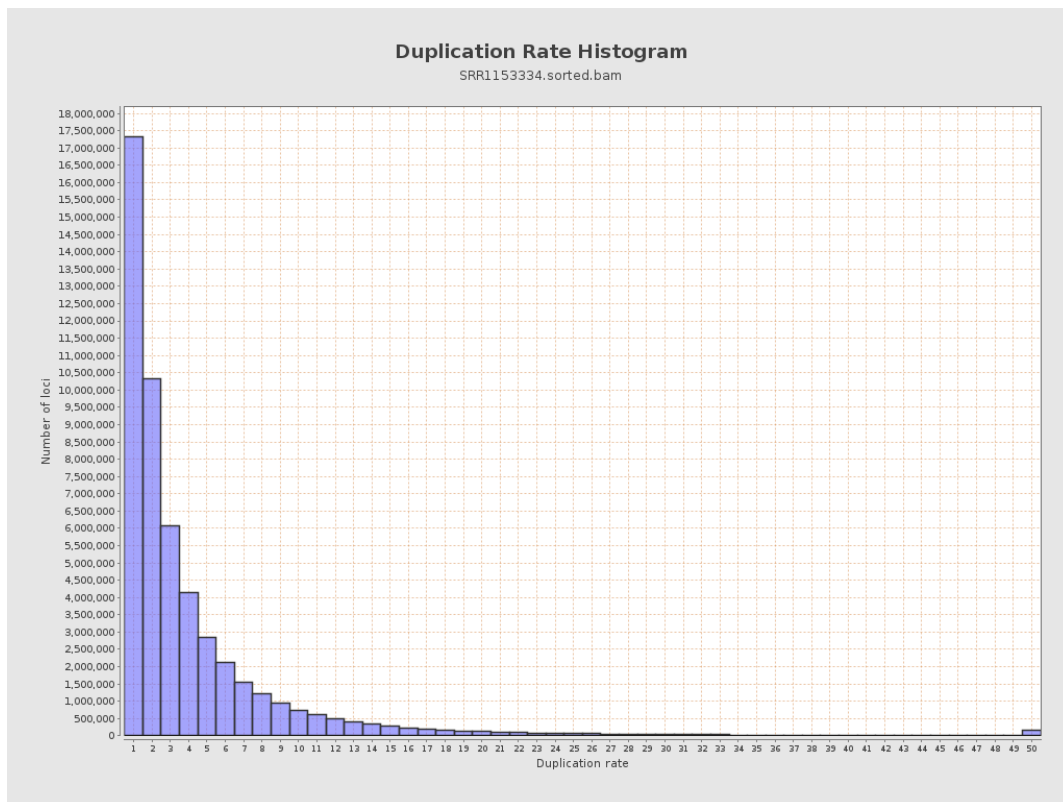
5. Results : Coverage Histogram (0-50X)



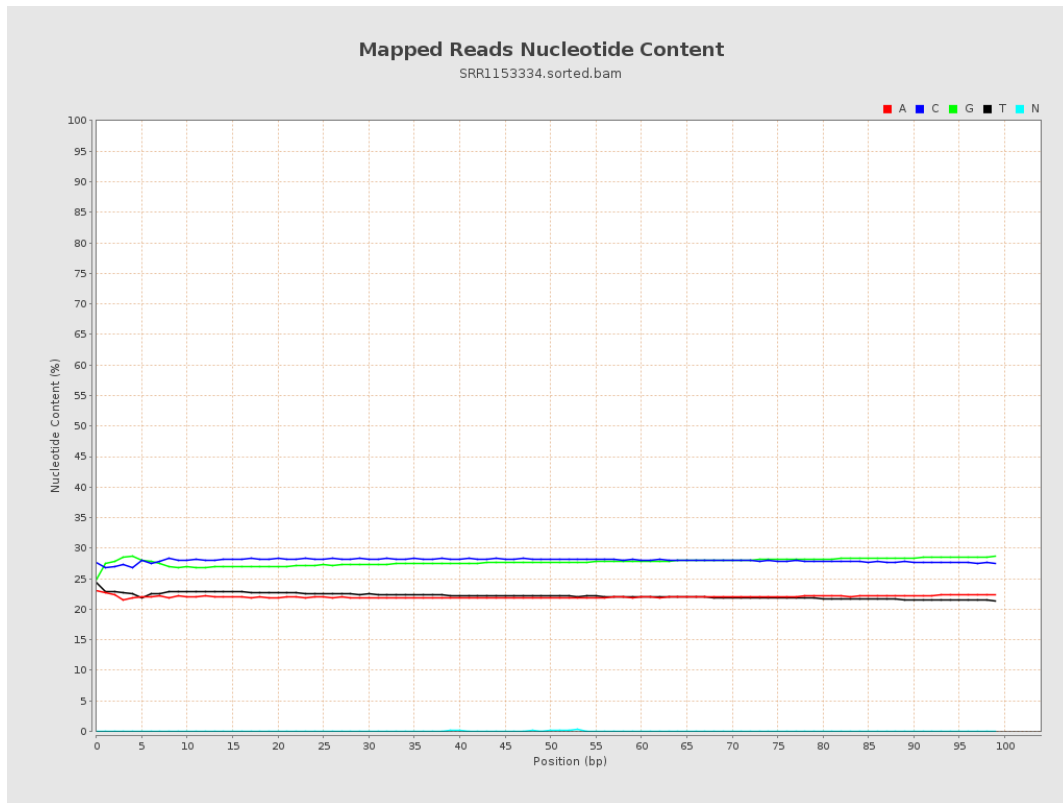
6. Results : Genome Fraction Coverage



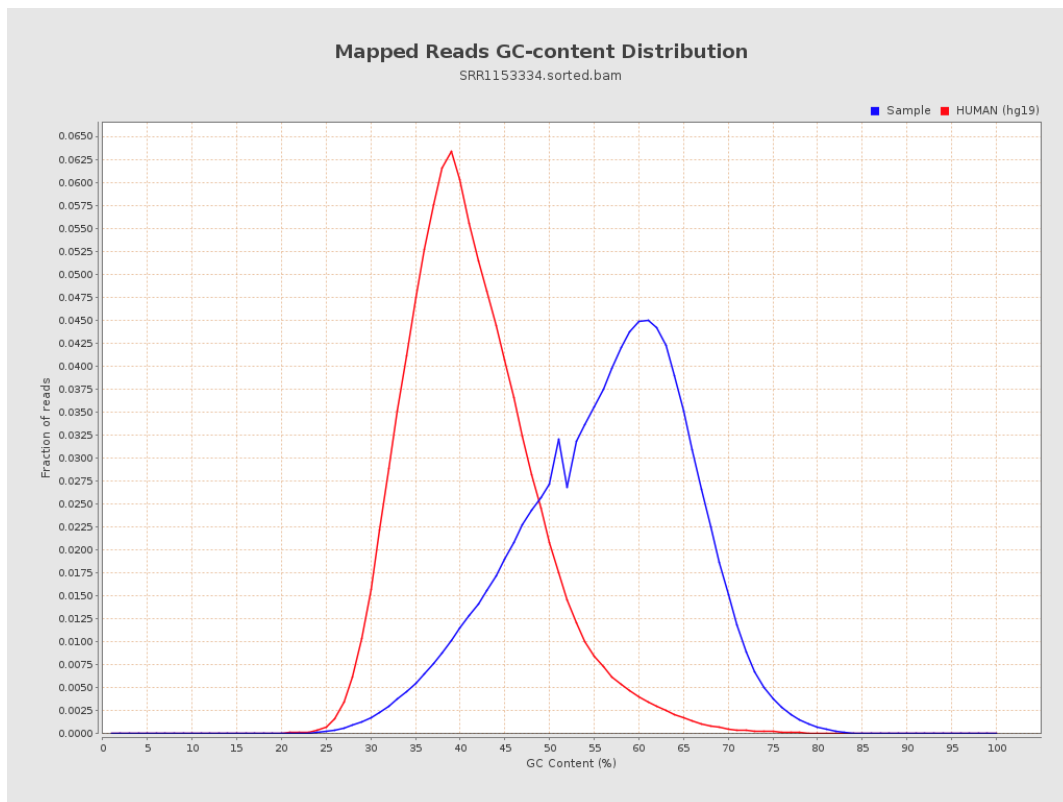
7. Results : Duplication Rate Histogram



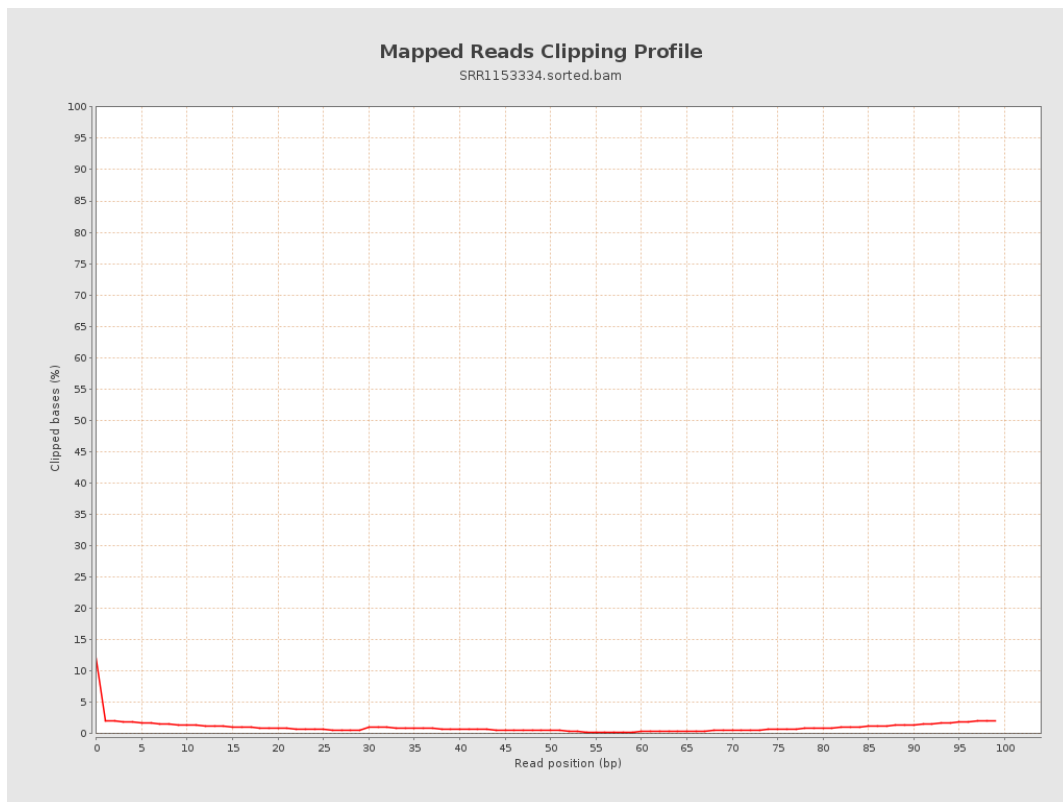
8. Results : Mapped Reads Nucleotide Content



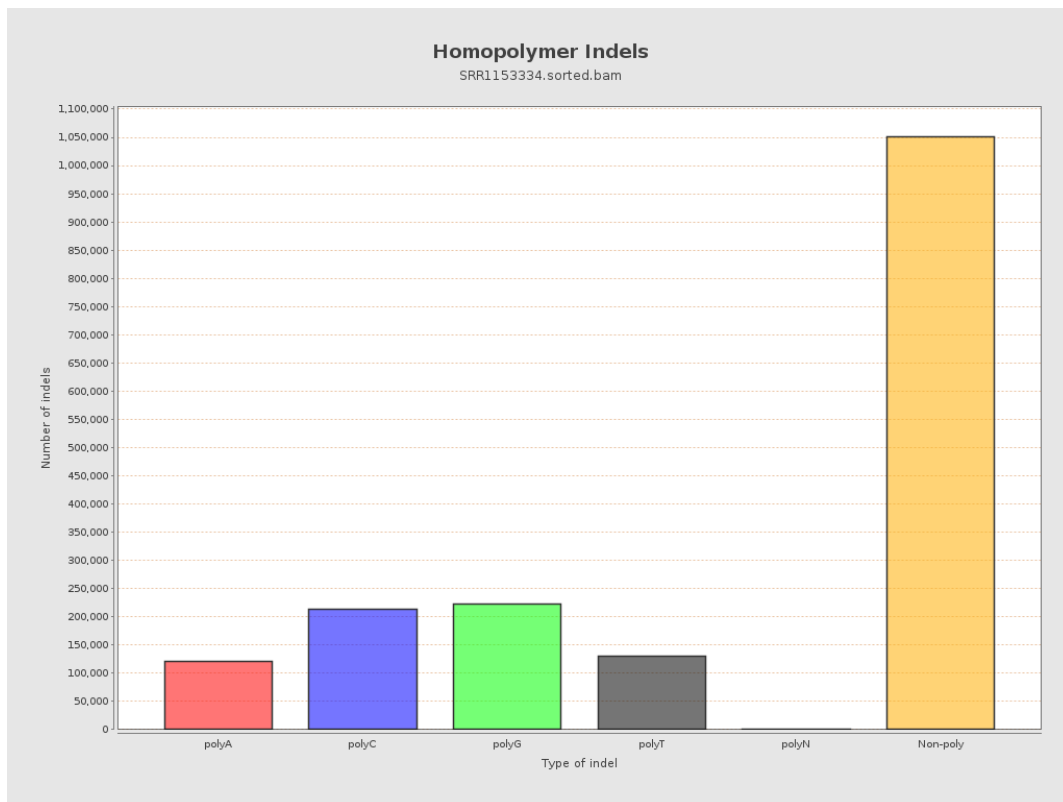
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

