

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/13 23:47:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153309.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_SRR1153309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153309.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 13 23:47:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	153,430,650
Mapped reads	148,564,384 / 96.83%
Unmapped reads	4,866,266 / 3.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	910,919 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	78,666,238 / 51.27%
Duplication rate	34.1%
Clipped reads	12,947,105 / 8.44%

2.2. ACGT Content

Number/percentage of A's	3,672,684,365 / 25.18%
Number/percentage of C's	3,619,302,074 / 24.81%
Number/percentage of T's	3,710,500,245 / 25.44%
Number/percentage of G's	3,581,580,902 / 24.55%
Number/percentage of N's	3,088,912 / 0.02%
GC Percentage	49.36%

2.3. Coverage

Mean	4.7129

Standard Deviation	36.8994
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2.4. Mapping Quality

Mean Mapping Quality	49.34
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2.5. Mismatches and indels

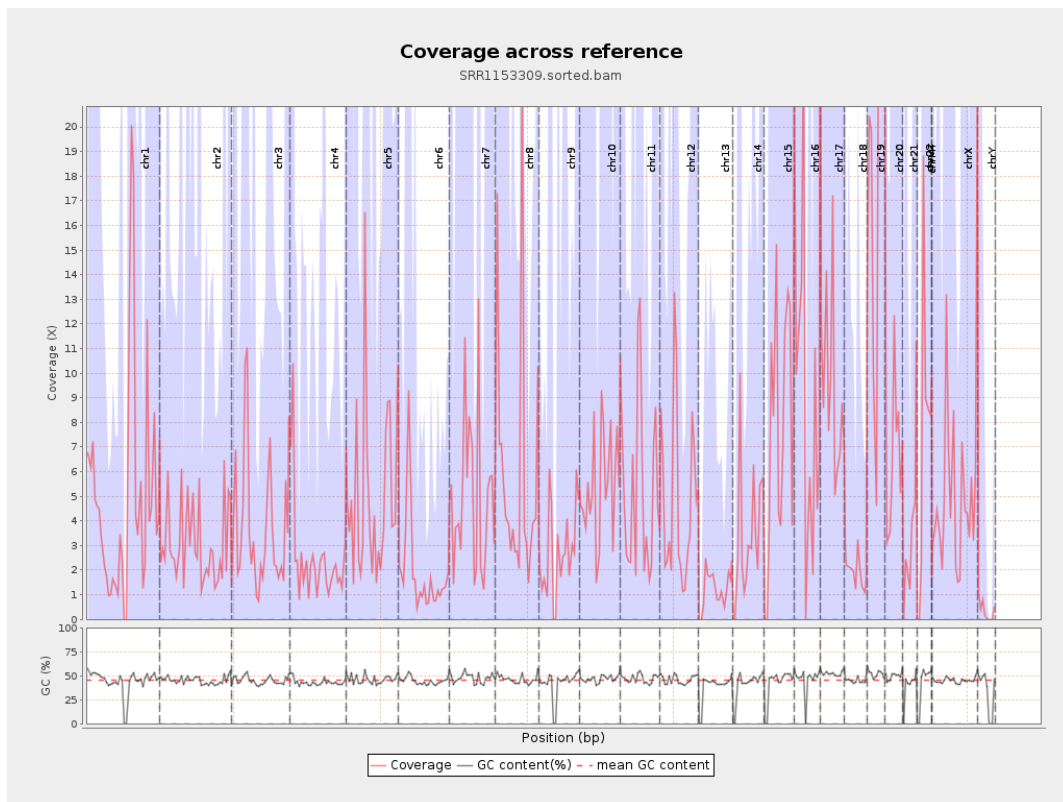
General error rate	0.41%
Mismatches	58,113,405
Insertions	833,023
Mapped reads with at least one insertion	0.55%
Deletions	1,082,561
Mapped reads with at least one deletion	0.72%
Homopolymer indels	45.31%

2.6. Chromosome stats

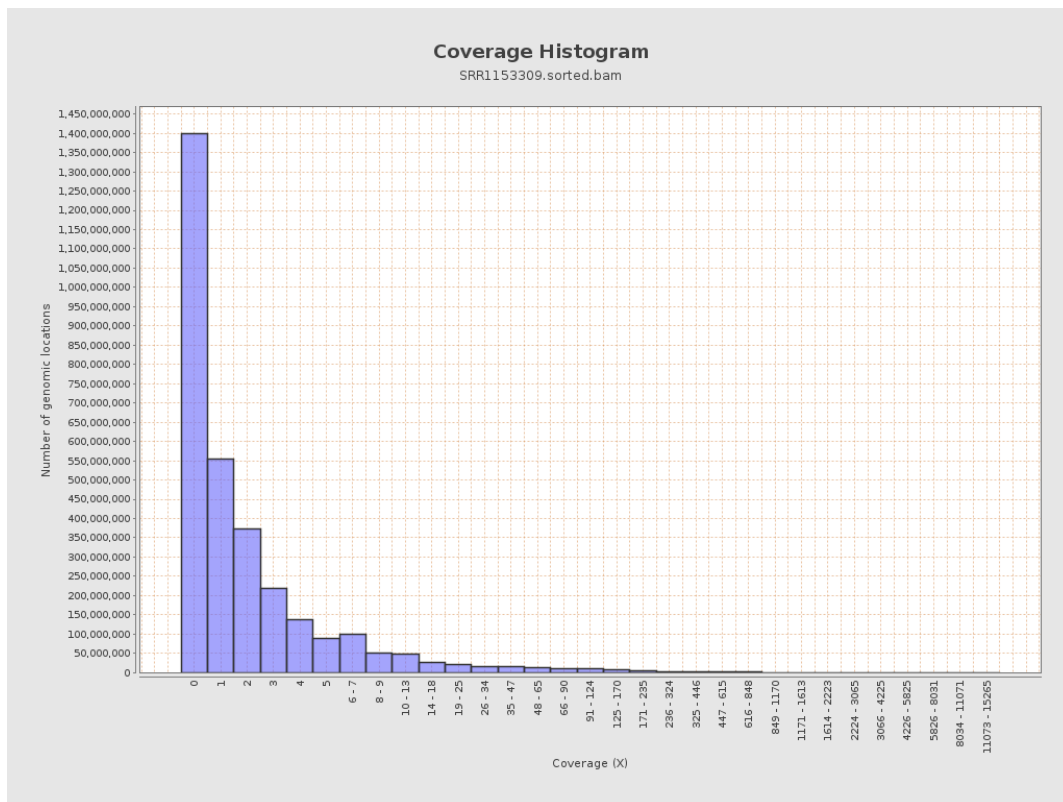
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1232758350	4.9459	31.4178
chr2	243199373	748581678	3.0781	17.2874
chr3	198022430	745741302	3.7659	21.0466
chr4	191154276	463932586	2.427	22.9714
chr5	180915260	923237476	5.1031	70.8233
chr6	171115067	324983852	1.8992	13.5519
chr7	159138663	785164858	4.9338	41.4019

chr8	146364022	854329434	5.837	69.4969
chr9	141213431	392115064	2.7768	17.0103
chr10	135534747	737771877	5.4434	28.6394
chr11	135006516	731487493	5.4182	27.2818
chr12	133851895	649494284	4.8523	24.2046
chr13	115169878	142332457	1.2358	8.4924
chr14	107349540	359320783	3.3472	19.5849
chr15	102531392	757757308	7.3905	42.6237
chr16	90354753	832735473	9.2163	54.5705
chr17	81195210	766880703	9.4449	46.7561
chr18	78077248	152519523	1.9534	11.7839
chr19	59128983	1202292469	20.3334	82.4514
chr20	63025520	437329615	6.9389	32.7666
chr21	48129895	166489977	3.4592	30.6878
chr22	51304566	382890132	7.4631	41.5899
chrMT	16571	26879	1.6221	2.1467
chrX	155270560	779897069	5.0228	28.2677
chrY	59373566	19489588	0.3283	13.1187

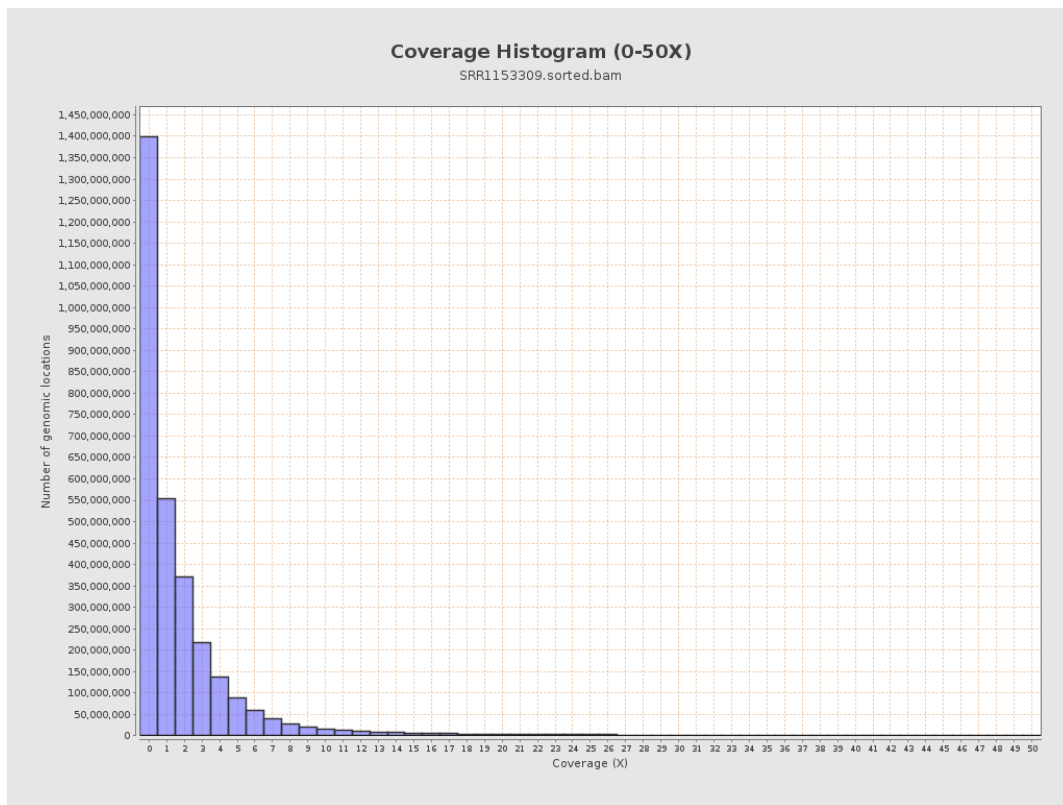
3. Results : Coverage across reference



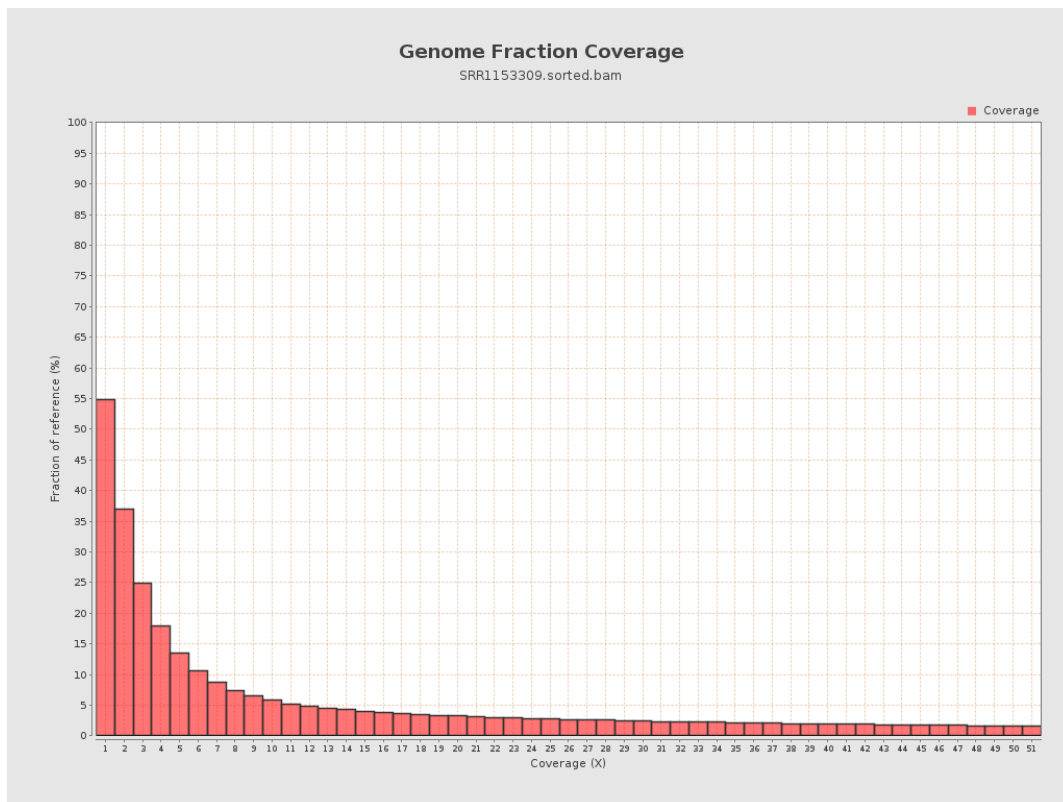
4. Results : Coverage Histogram



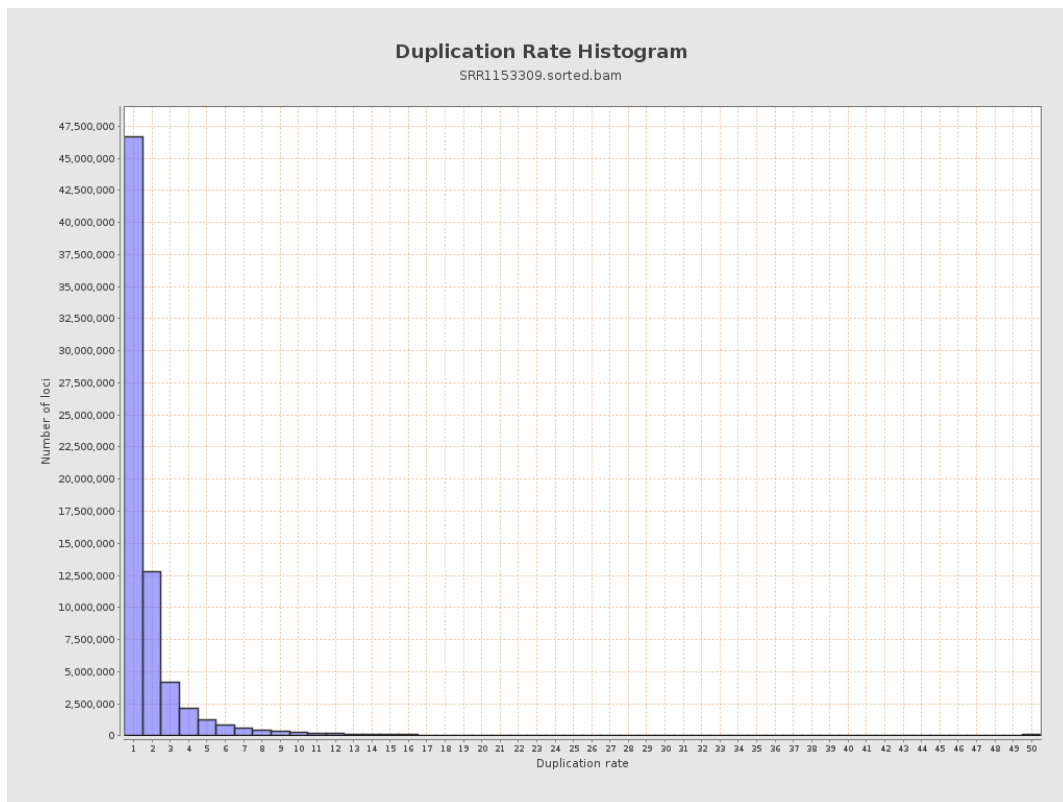
5. Results : Coverage Histogram (0-50X)



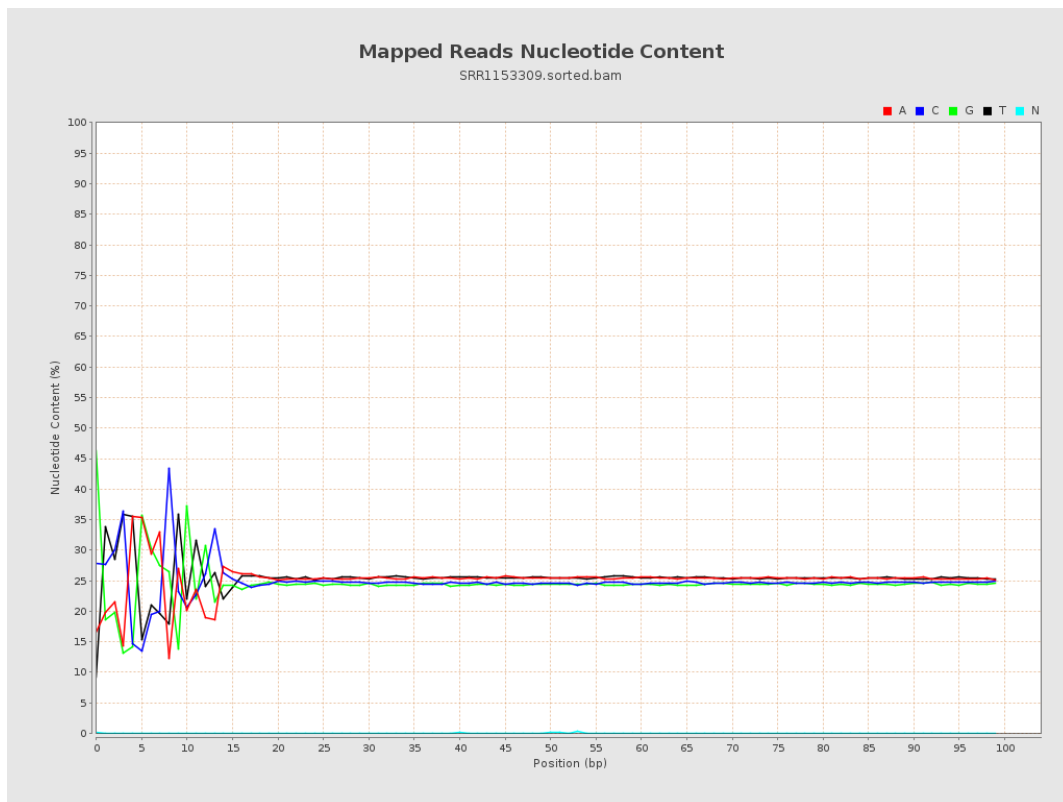
6. Results : Genome Fraction Coverage



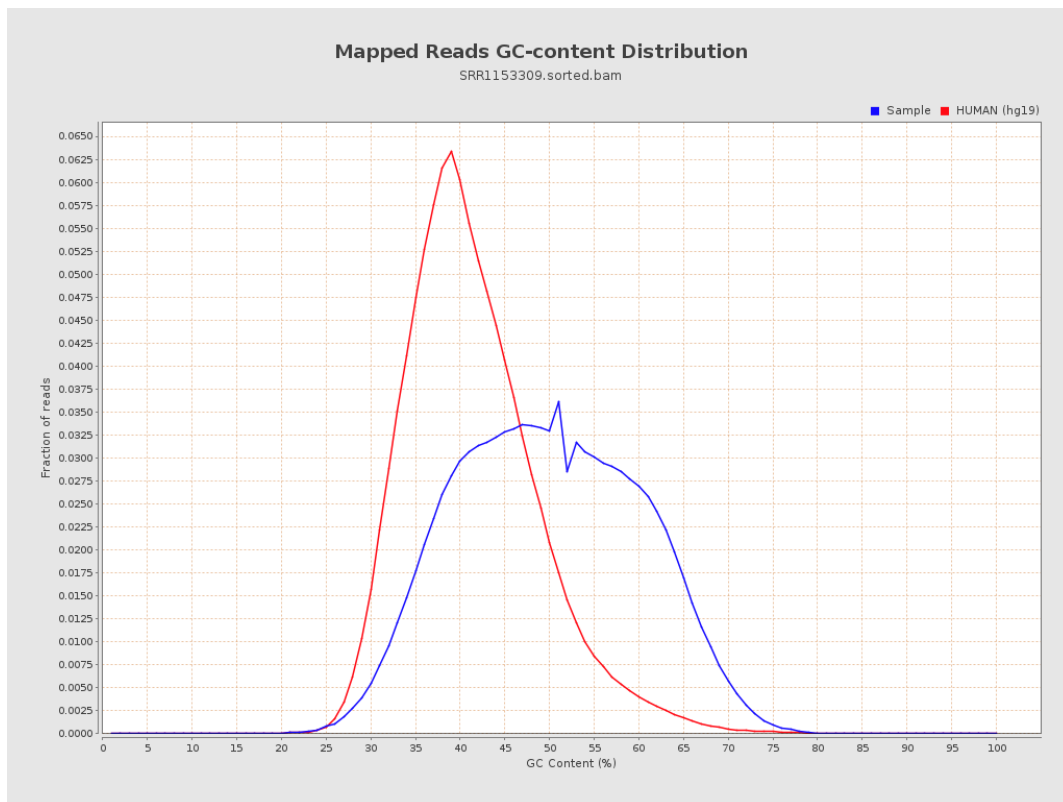
7. Results : Duplication Rate Histogram



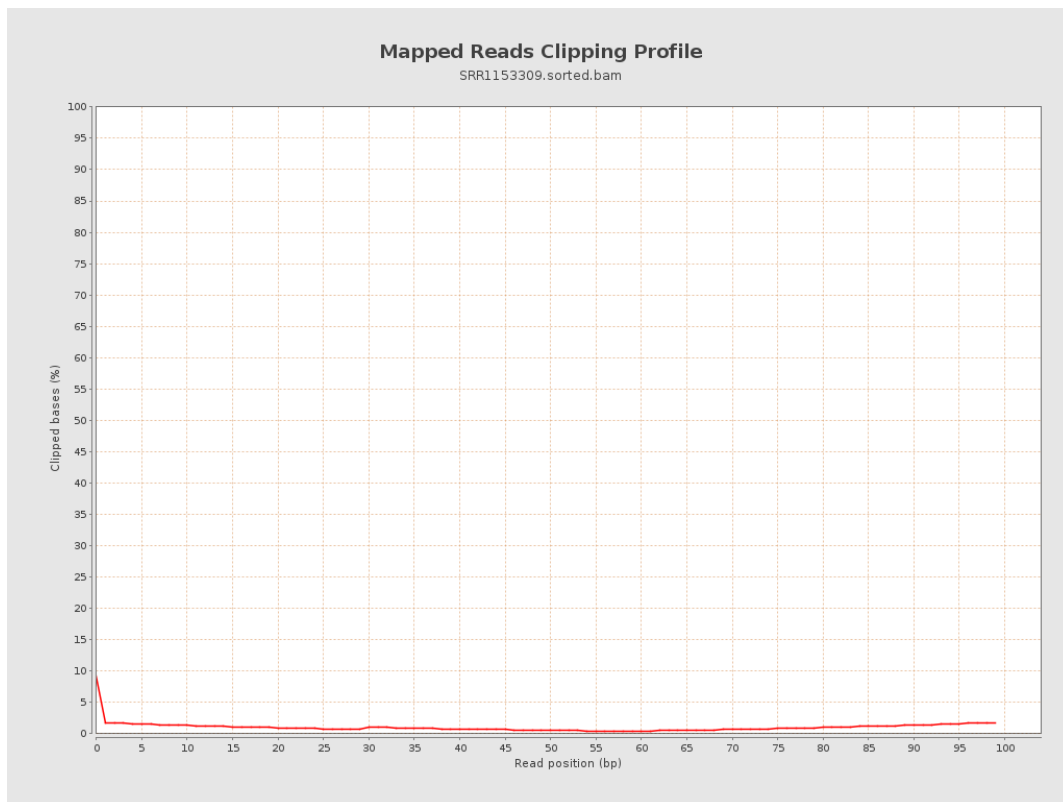
8. Results : Mapped Reads Nucleotide Content



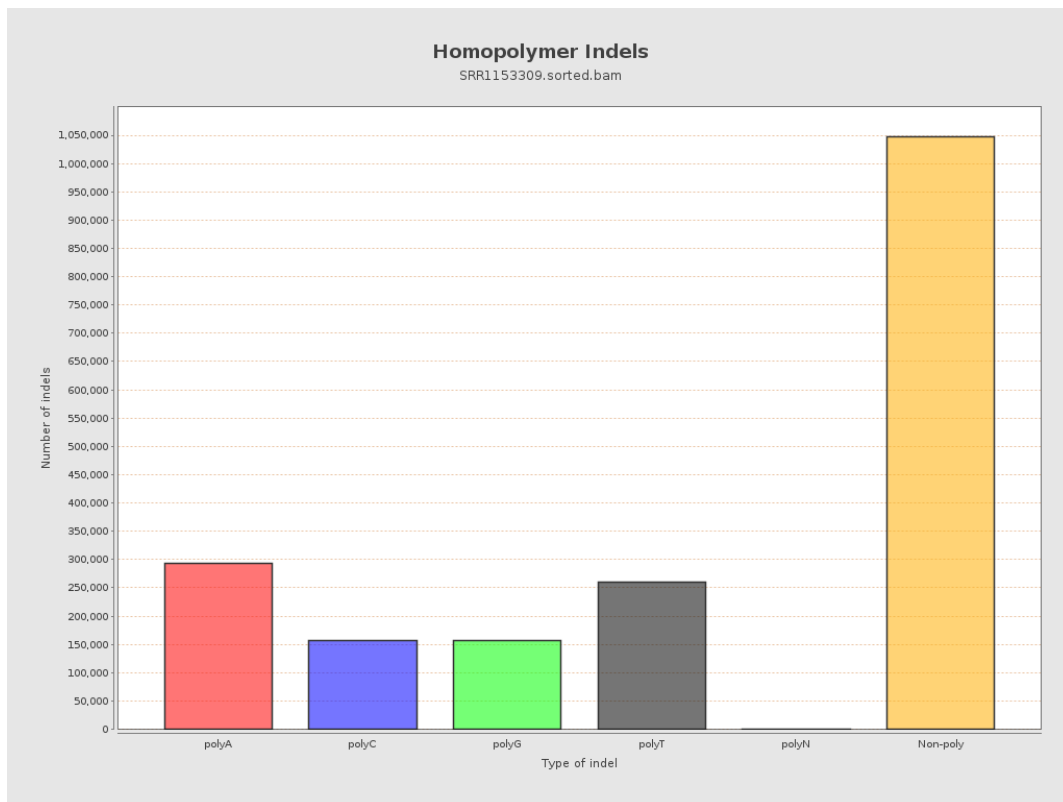
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

