

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/13 21:37:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153308.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_SRR1153308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153308.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 13 21:37:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	359,585,682
Mapped reads	350,634,981 / 97.51%
Unmapped reads	8,950,701 / 2.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,346,630 / 0.65%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	275,819,167 / 76.7%
Duplication rate	64.6%
Clipped reads	20,366,023 / 5.66%

2.2. ACGT Content

Number/percentage of A's	7,704,826,094 / 22.15%
Number/percentage of C's	9,690,251,305 / 27.86%
Number/percentage of T's	7,796,565,847 / 22.42%
Number/percentage of G's	9,584,057,270 / 27.56%
Number/percentage of N's	5,472,577 / 0.02%
GC Percentage	55.42%

2.3. Coverage

Mean	11.2367

Standard Deviation	145.7144
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2.4. Mapping Quality

Mean Mapping Quality	48.44
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2.5. Mismatches and indels

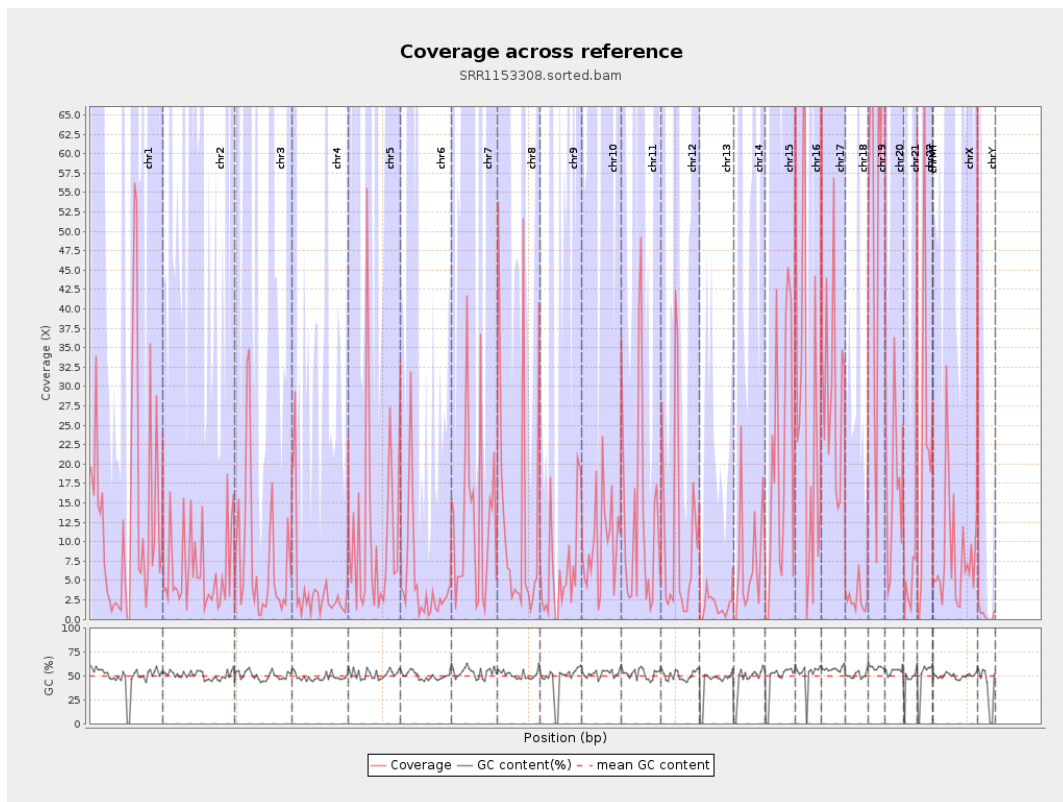
General error rate	0.38%
Mismatches	129,582,594
Insertions	1,432,256
Mapped reads with at least one insertion	0.4%
Deletions	1,566,303
Mapped reads with at least one deletion	0.44%
Homopolymer indels	40.75%

2.6. Chromosome stats

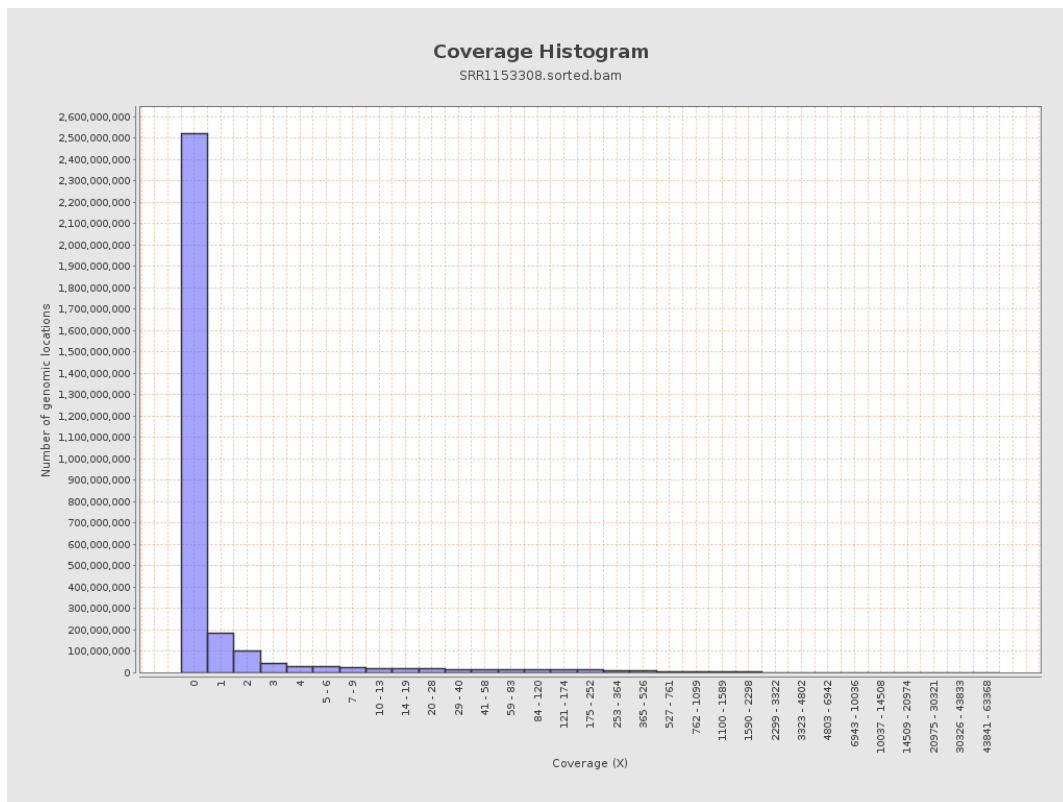
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3249265928	13.0361	129.0399
chr2	243199373	1539873194	6.3317	67.1689
chr3	198022430	1546272969	7.8086	86.2843
chr4	191154276	778067671	4.0704	76.8066
chr5	180915260	2011705790	11.1196	259.8577
chr6	171115067	790525087	4.6198	57.1837
chr7	159138663	2006986069	12.6116	225.2504

chr8	146364022	1812403583	12.3828	206.241
chr9	141213431	893610130	6.3281	64.1831
chr10	135534747	1333757564	9.8407	94.1277
chr11	135006516	1736379247	12.8614	108.4685
chr12	133851895	1495773311	11.1748	100.4371
chr13	115169878	206165163	1.7901	24.1808
chr14	107349540	786162891	7.3234	70.495
chr15	102531392	1999241626	19.4988	174.4826
chr16	90354753	2452467876	27.1427	232.5309
chr17	81195210	2372077880	29.2145	206.902
chr18	78077248	200503382	2.568	38.7351
chr19	59128983	3417541905	57.7981	298.6392
chr20	63025520	1032827258	16.3874	140.6822
chr21	48129895	506861459	10.5311	291.3904
chr22	51304566	1129926748	22.0239	178.3448
chrMT	16571	63709	3.8446	3.1603
chrX	155270560	1453388421	9.3604	92.6379
chrY	59373566	33522910	0.5646	32.5056

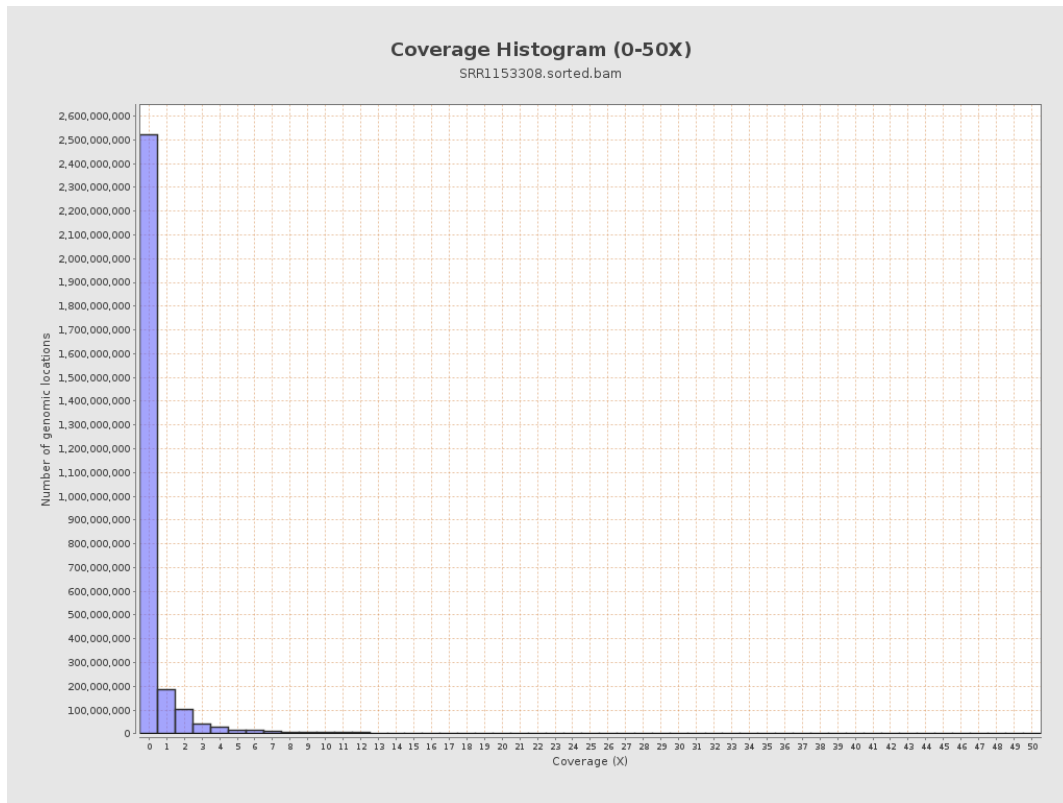
3. Results : Coverage across reference



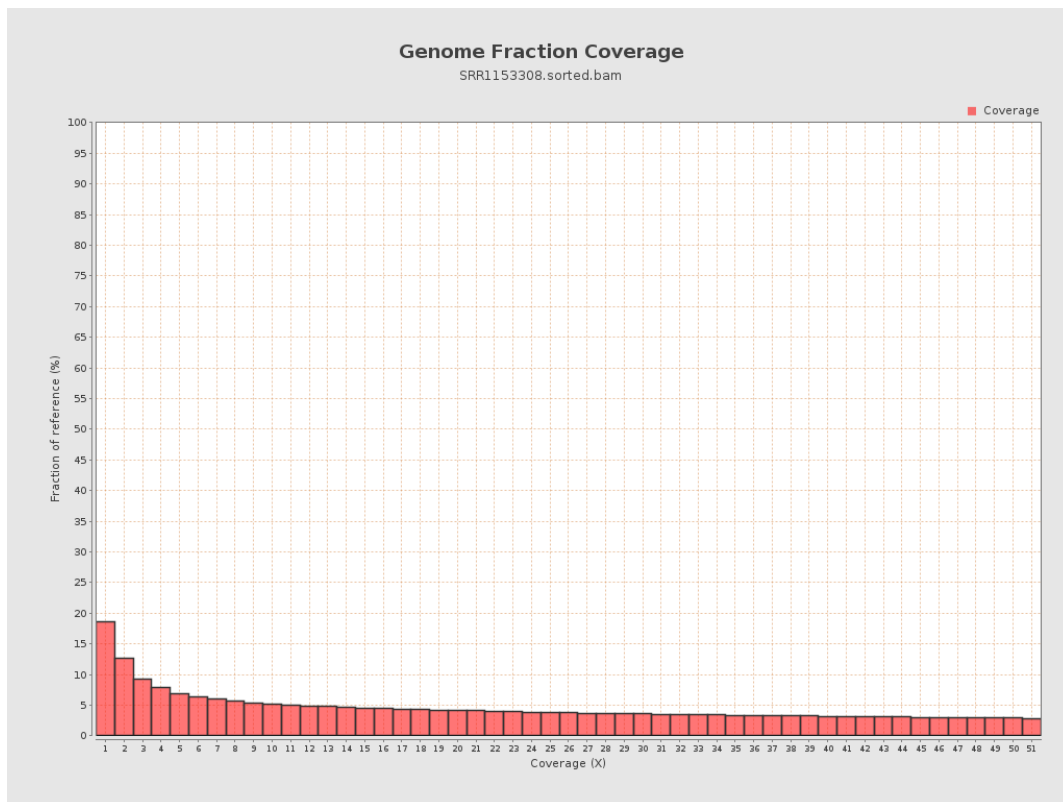
4. Results : Coverage Histogram



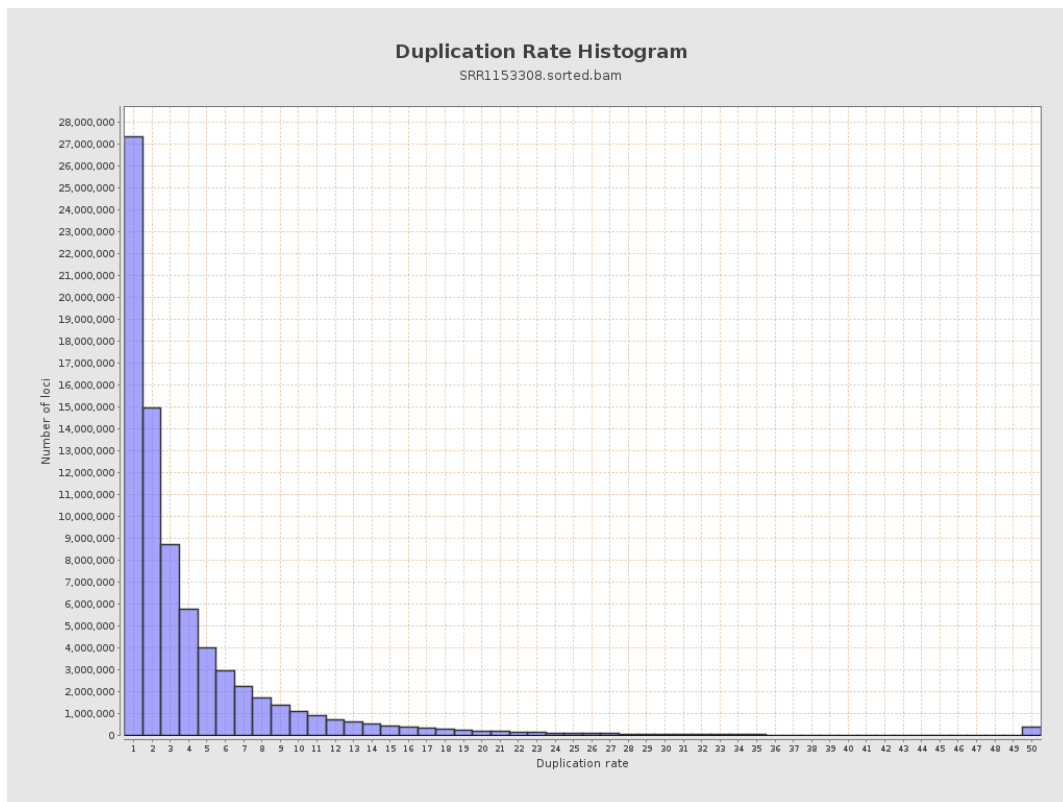
5. Results : Coverage Histogram (0-50X)



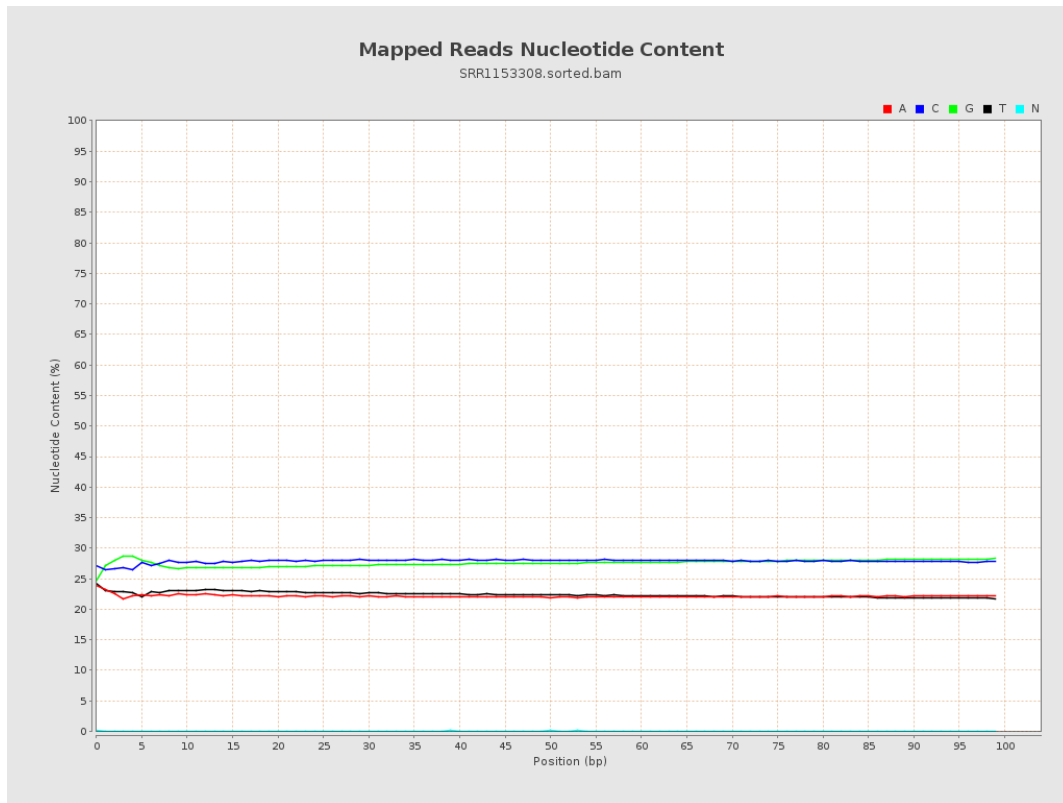
6. Results : Genome Fraction Coverage



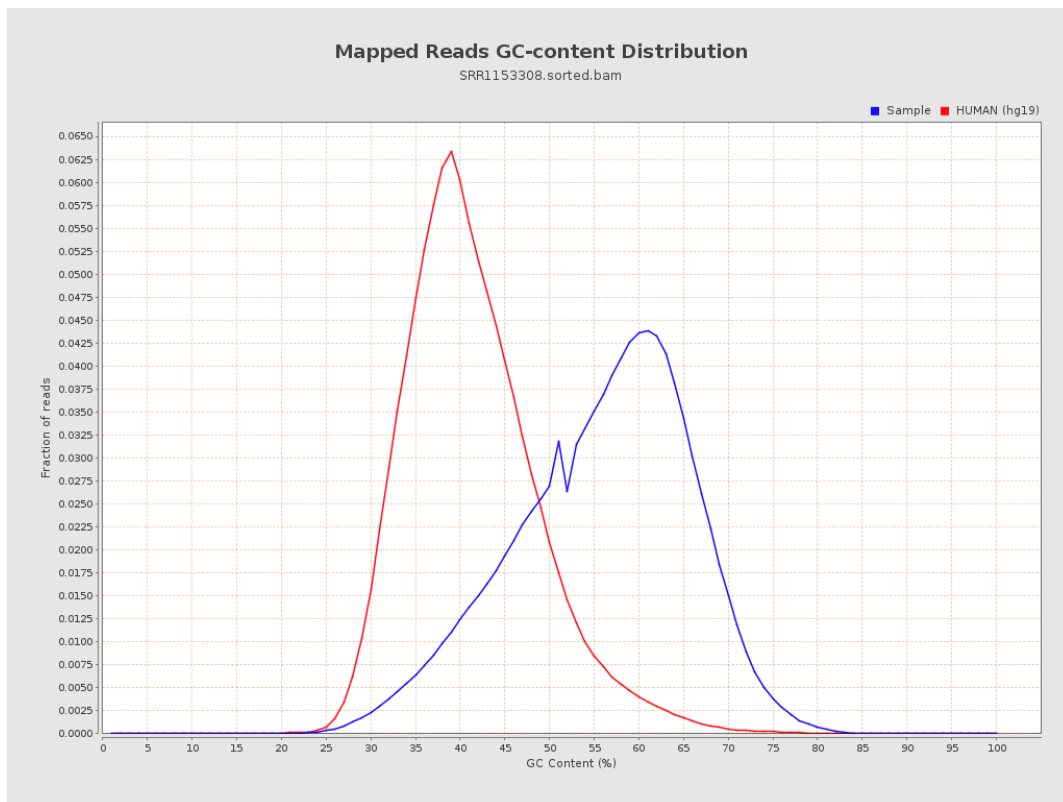
7. Results : Duplication Rate Histogram



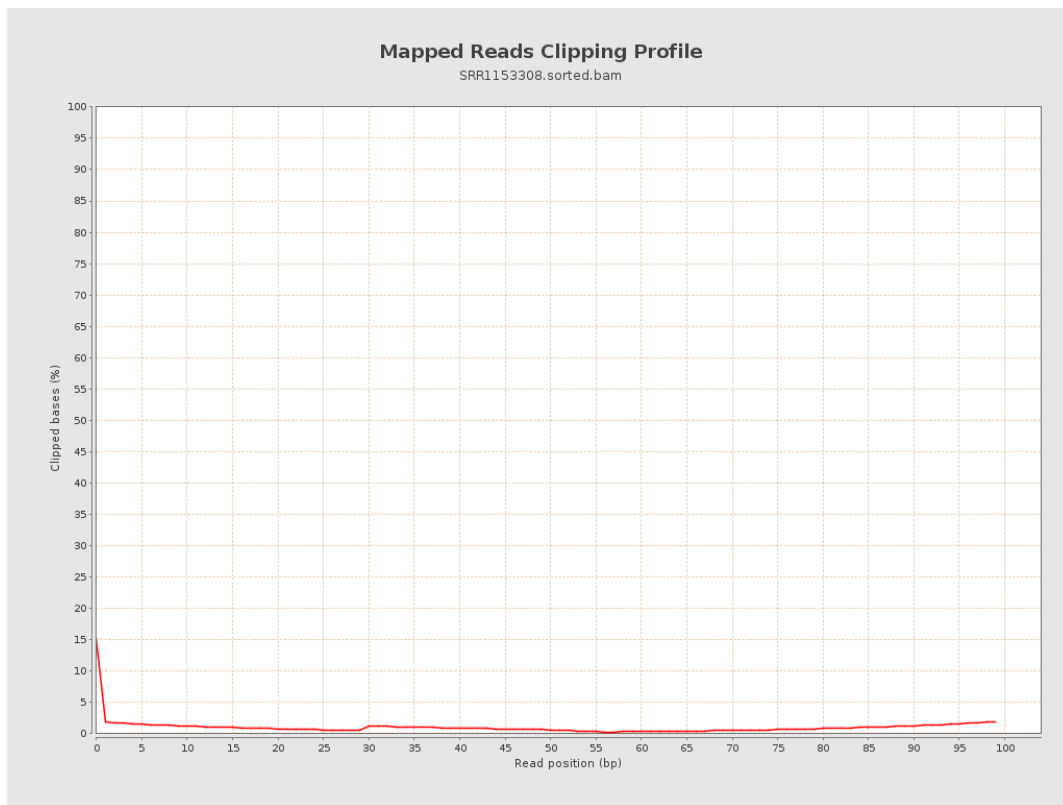
8. Results : Mapped Reads Nucleotide Content



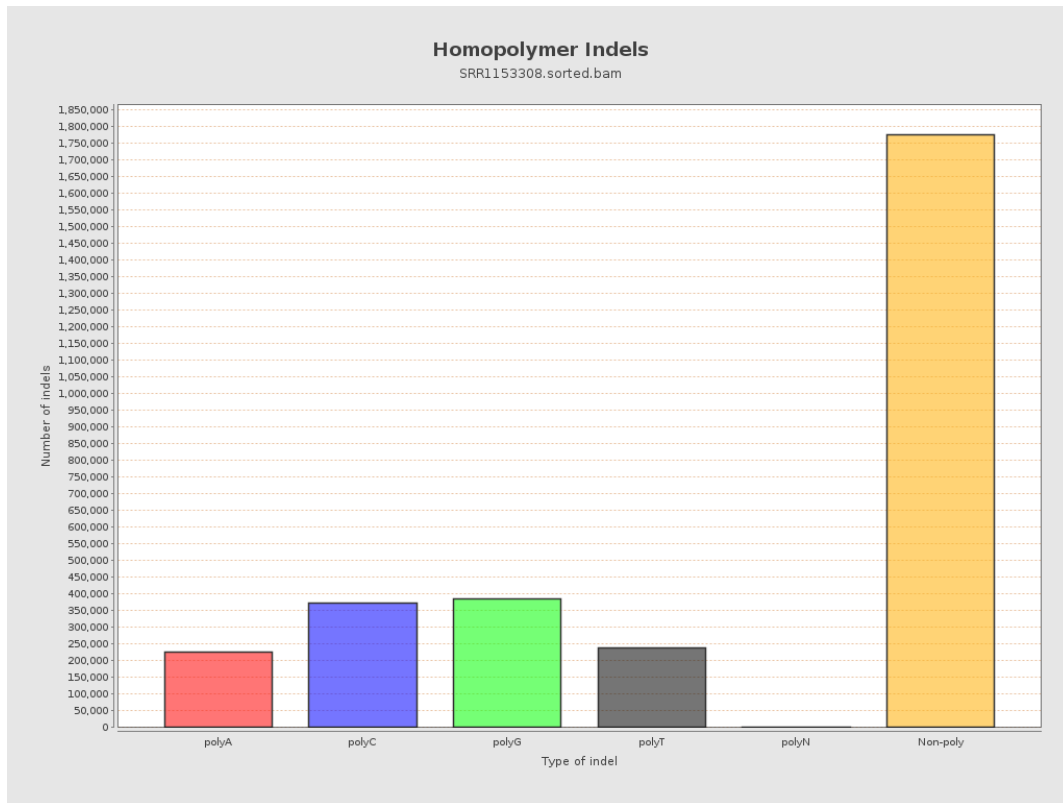
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

