

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 10:41:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153315.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_SRR1153315 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153315.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 10:41:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153315.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,642,644
Mapped reads	51,214,387 / 99.17%
Unmapped reads	428,257 / 0.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	409,054 / 0.79%
Read min/max/mean length	30 / 100 / 100.33
Duplicated reads (estimated)	26,216,979 / 50.77%
Duplication rate	34.29%
Clipped reads	6,730,659 / 13.03%

2.2. ACGT Content

Number/percentage of A's	1,319,367,508 / 26.51%
Number/percentage of C's	1,162,185,643 / 23.35%
Number/percentage of T's	1,347,187,488 / 27.07%
Number/percentage of G's	1,146,293,720 / 23.03%
Number/percentage of N's	1,480,753 / 0.03%
GC Percentage	46.39%

2.3. Coverage

Mean	1.6078

Standard Deviation	15.1364
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2.4. Mapping Quality

Mean Mapping Quality	50.41
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2.5. Mismatches and indels

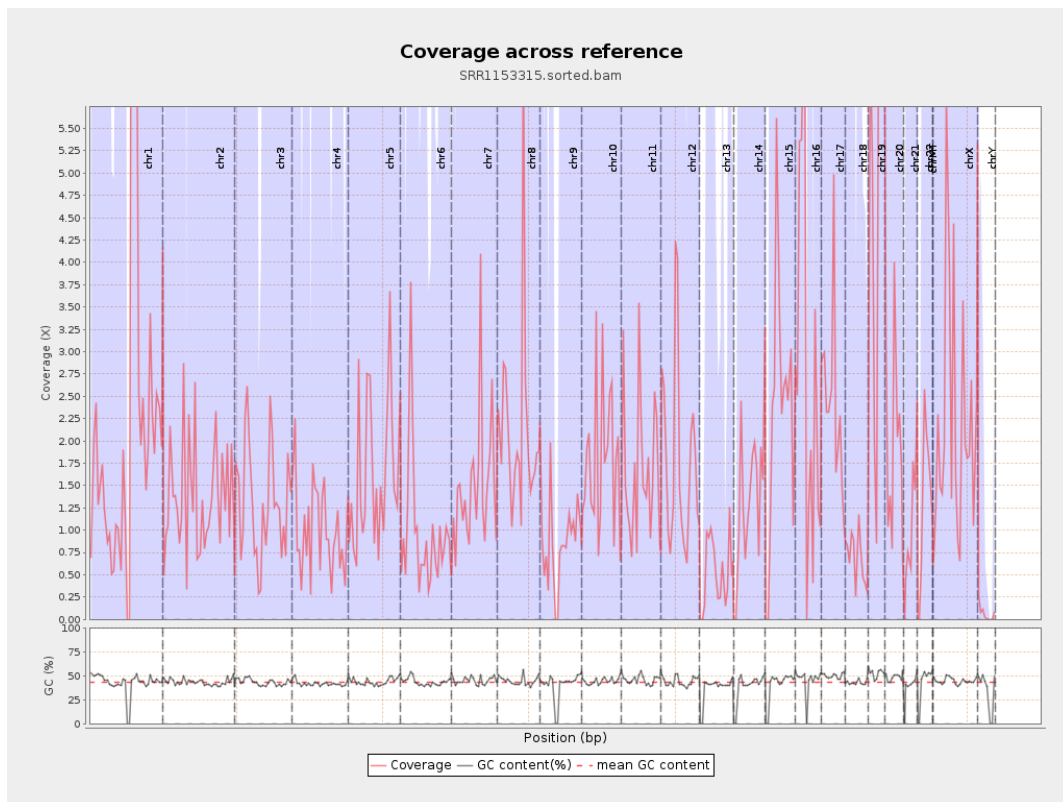
General error rate	0.31%
Mismatches	14,737,805
Insertions	537,913
Mapped reads with at least one insertion	1.04%
Deletions	407,820
Mapped reads with at least one deletion	0.79%
Homopolymer indels	49.66%

2.6. Chromosome stats

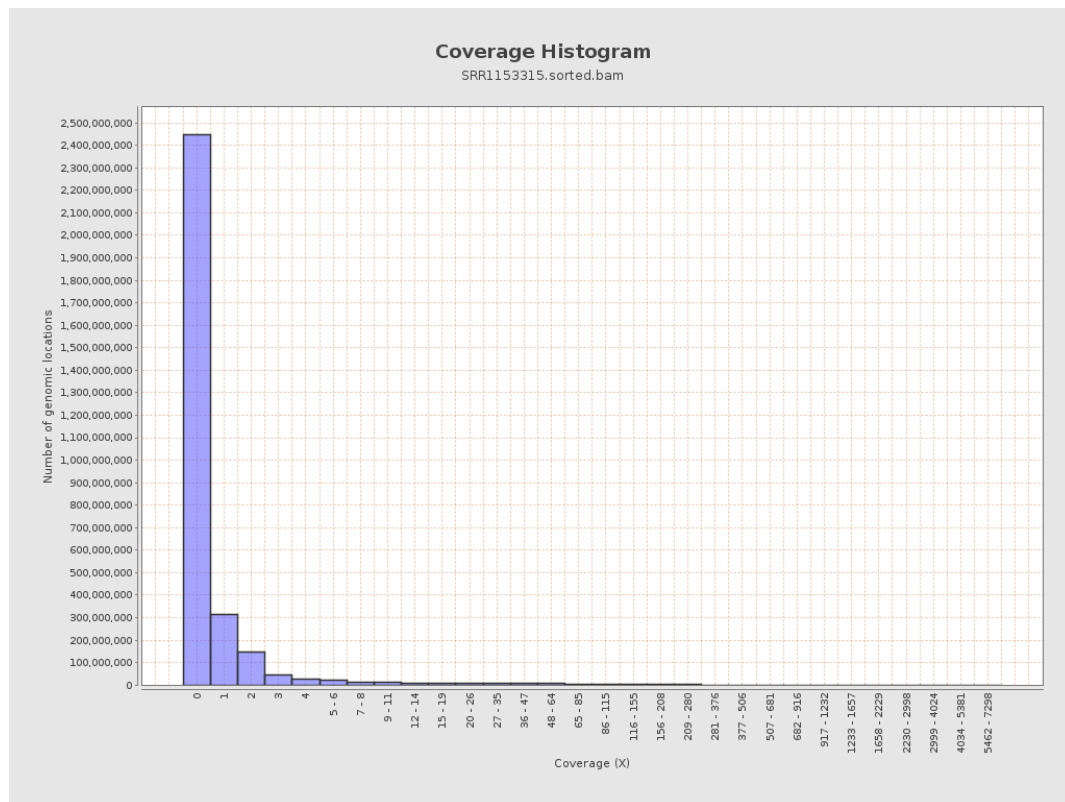
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	549179694	2.2033	21.0331
chr2	243199373	336328393	1.3829	11.3096
chr3	198022430	257779150	1.3018	10.511
chr4	191154276	193260075	1.011	9.6607
chr5	180915260	298867530	1.652	14.3668
chr6	171115067	161963194	0.9465	8.9979
chr7	159138663	233731418	1.4687	12.542

chr8	146364022	312330826	2.1339	25.1731
chr9	141213431	119341331	0.8451	7.9026
chr10	135534747	244185645	1.8016	14.2893
chr11	135006516	225013550	1.6667	12.9198
chr12	133851895	244853876	1.8293	14.4495
chr13	115169878	60990355	0.5296	6.0438
chr14	107349540	138473563	1.2899	11.1397
chr15	102531392	230882243	2.2518	17.1367
chr16	90354753	244568928	2.7068	22.0712
chr17	81195210	199892139	2.4619	16.1296
chr18	78077248	53900157	0.6903	6.6199
chr19	59128983	280144834	4.7379	31.0315
chr20	63025520	123220730	1.9551	17.3905
chr21	48129895	50790201	1.0553	10.0556
chr22	51304566	68367779	1.3326	11.3438
chrMT	16571	9862	0.5951	1.5666
chrX	155270560	345596135	2.2258	20.699
chrY	59373566	3700421	0.0623	2.5626

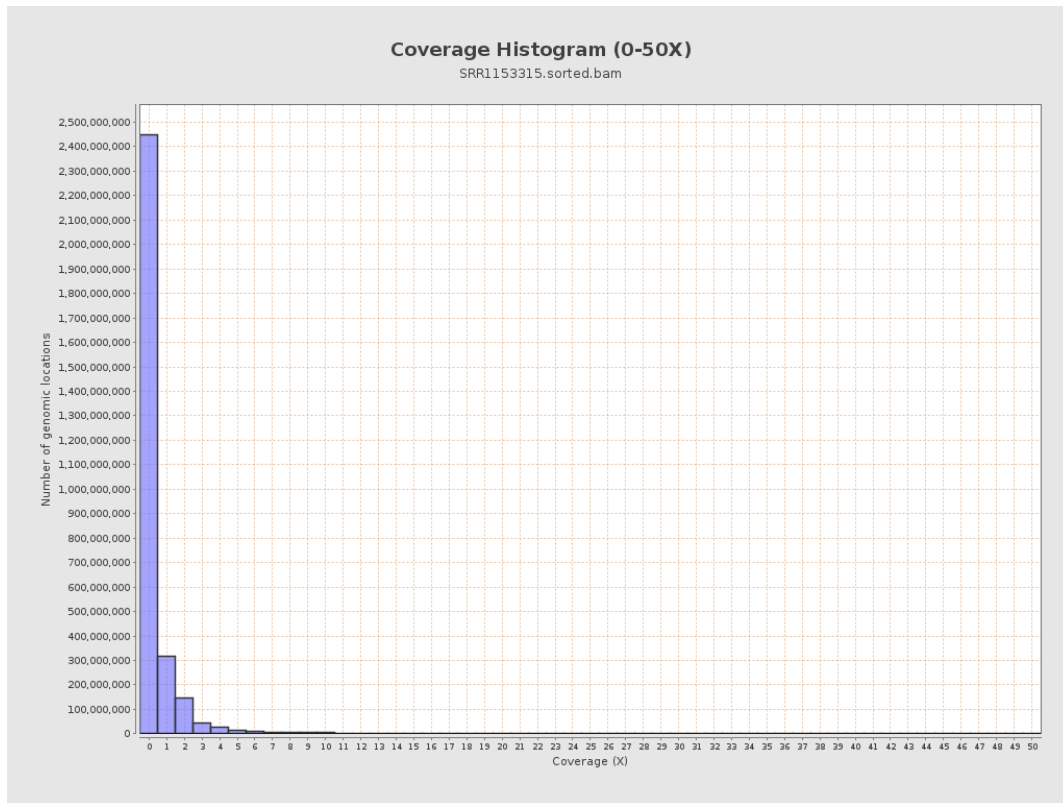
3. Results : Coverage across reference



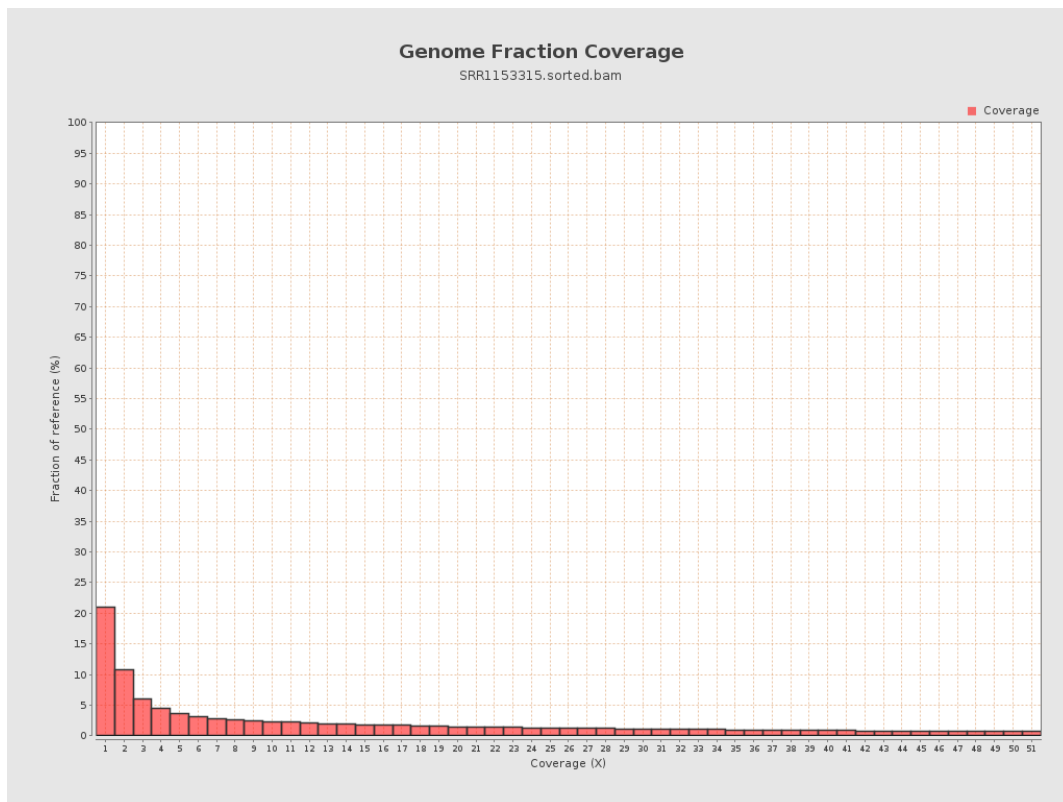
4. Results : Coverage Histogram



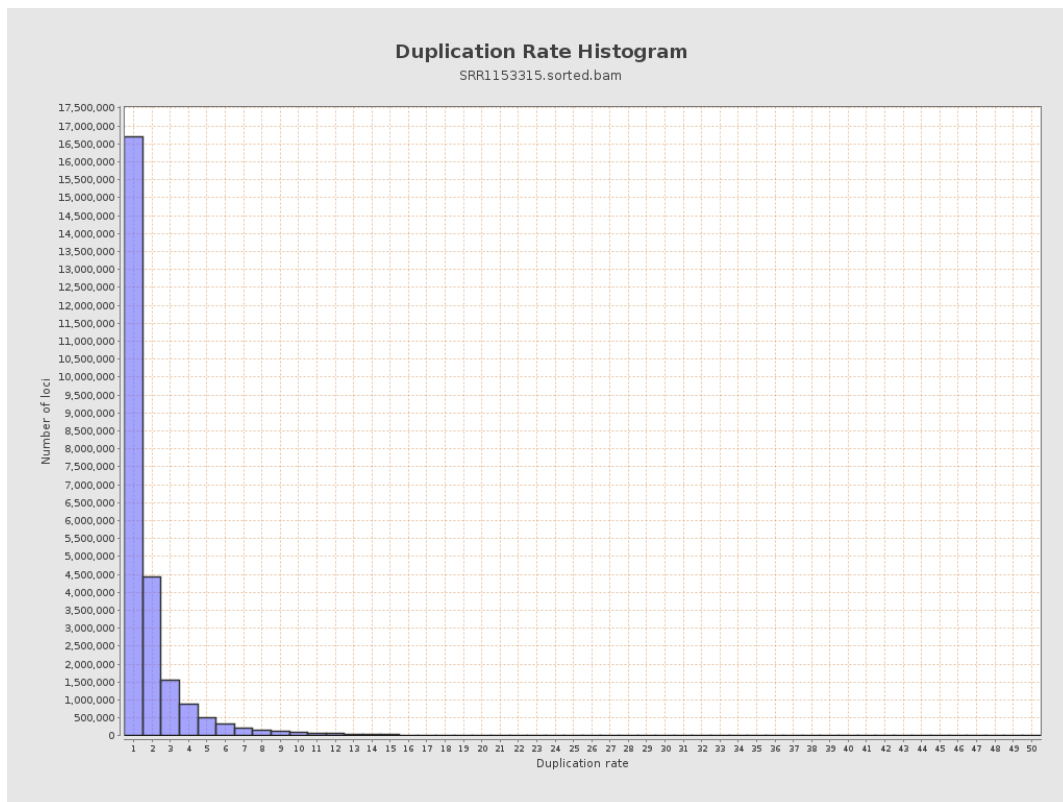
5. Results : Coverage Histogram (0-50X)



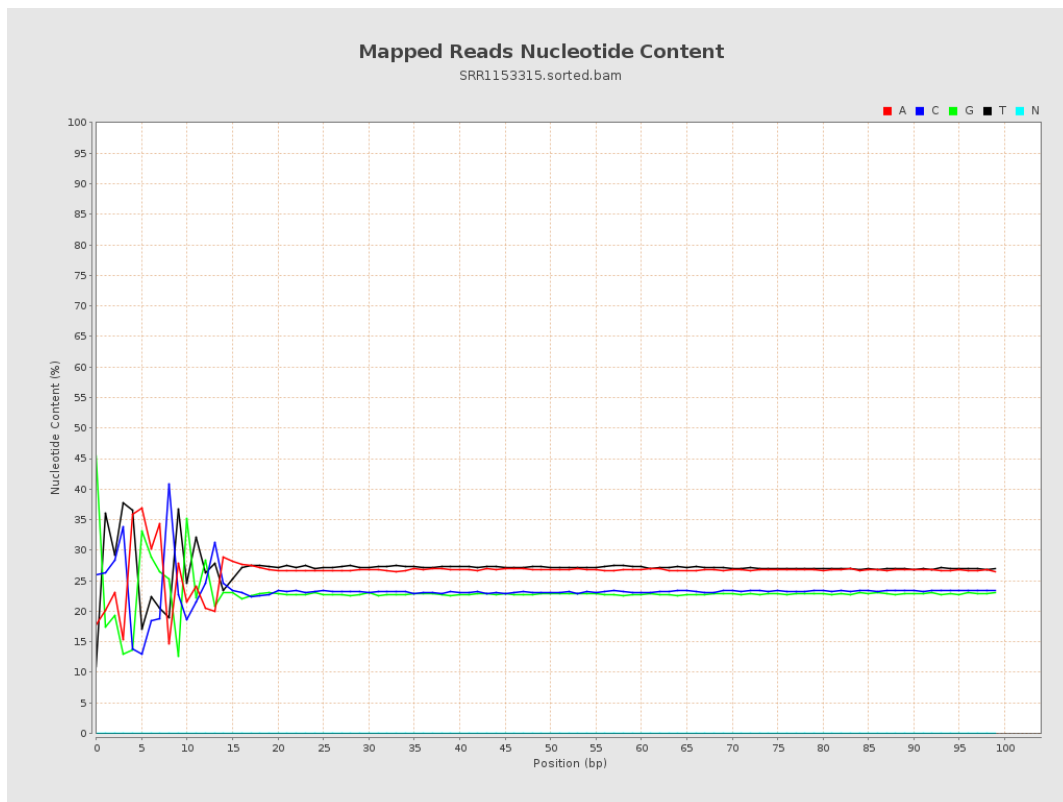
6. Results : Genome Fraction Coverage



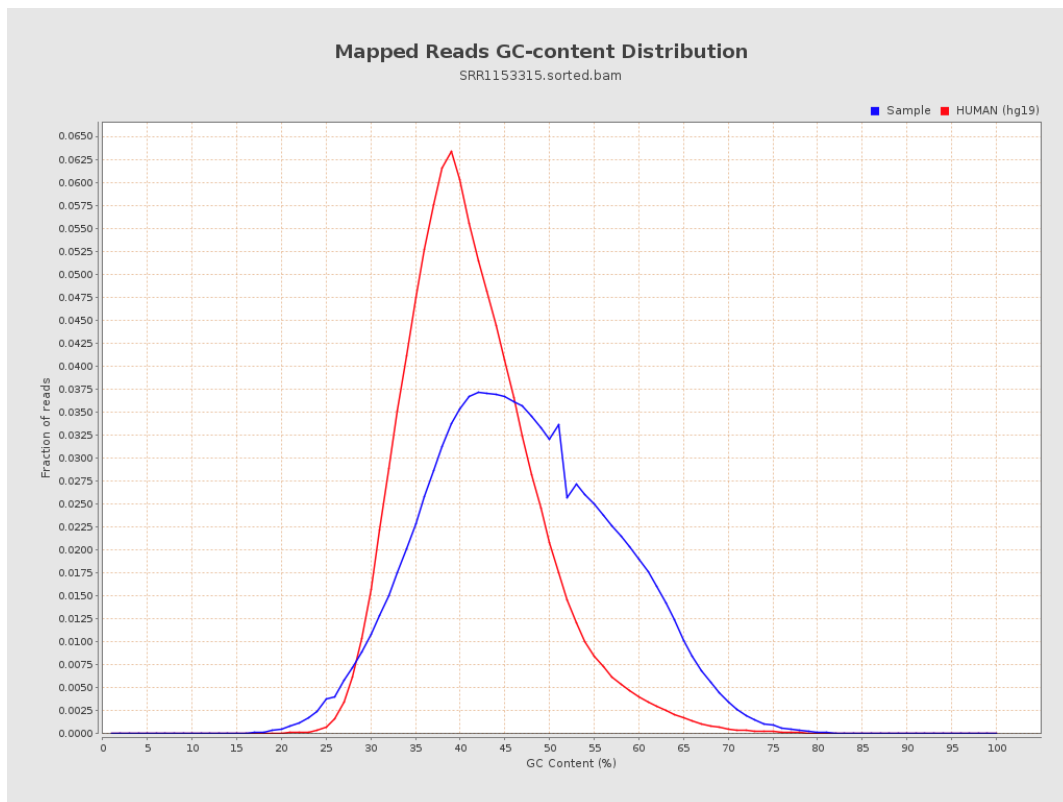
7. Results : Duplication Rate Histogram



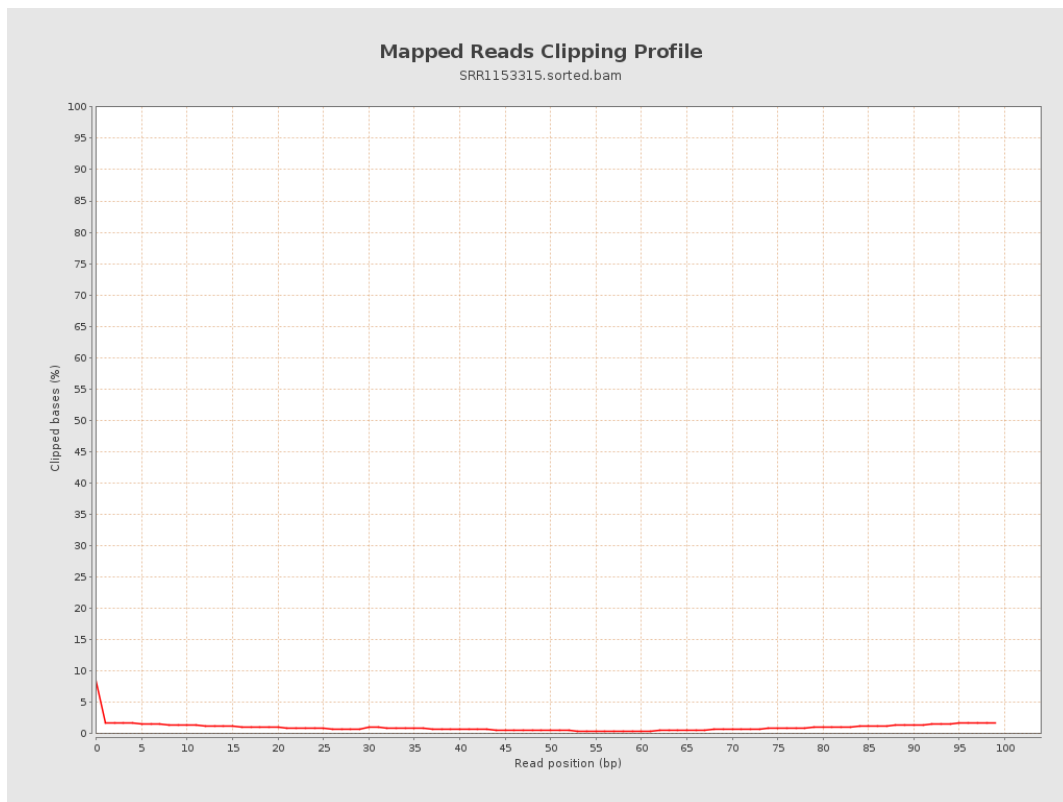
8. Results : Mapped Reads Nucleotide Content



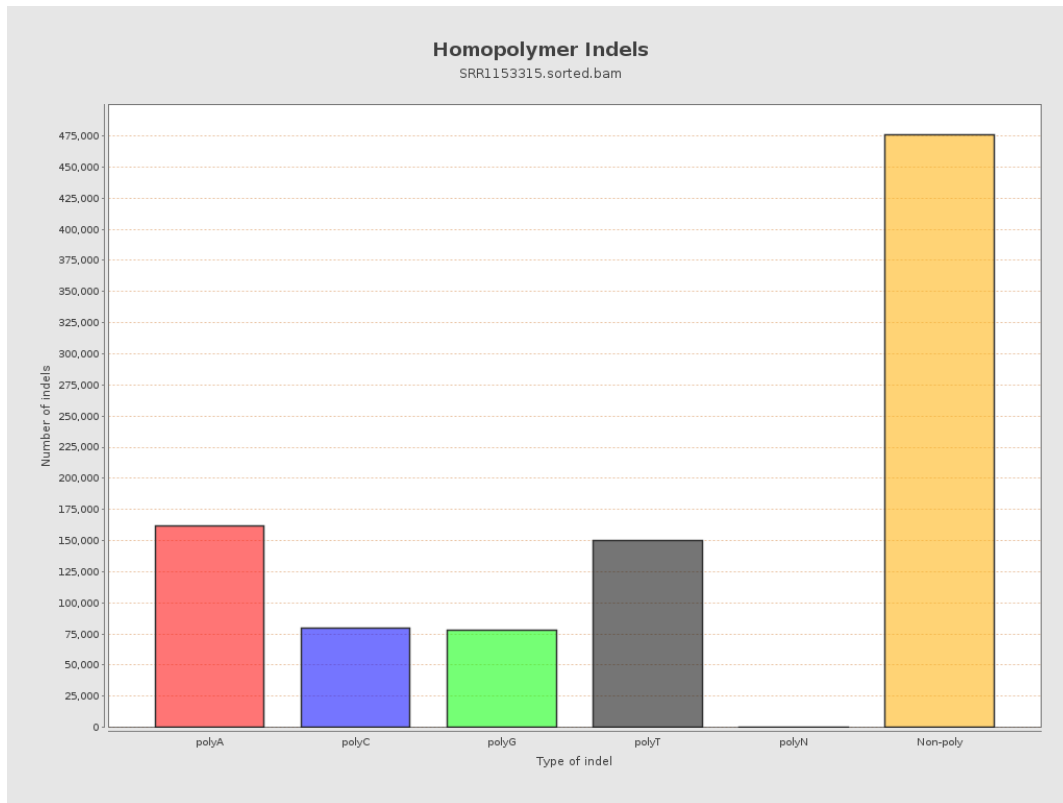
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

