

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 18:50:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153319.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_SRR1153319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 18:50:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,906,248
Mapped reads	56,437,707 / 99.18%
Unmapped reads	468,541 / 0.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	281,461 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	39,020,101 / 68.57%
Duplication rate	60.32%
Clipped reads	7,008,750 / 12.32%

2.2. ACGT Content

Number/percentage of A's	1,451,943,582 / 26.41%
Number/percentage of C's	1,287,936,953 / 23.43%
Number/percentage of T's	1,492,983,546 / 27.16%
Number/percentage of G's	1,262,774,224 / 22.97%
Number/percentage of N's	1,808,155 / 0.03%
GC Percentage	46.4%

2.3. Coverage

Mean	1.7761

Standard Deviation	19.288
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2.4. Mapping Quality

Mean Mapping Quality	50.63
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2.5. Mismatches and indels

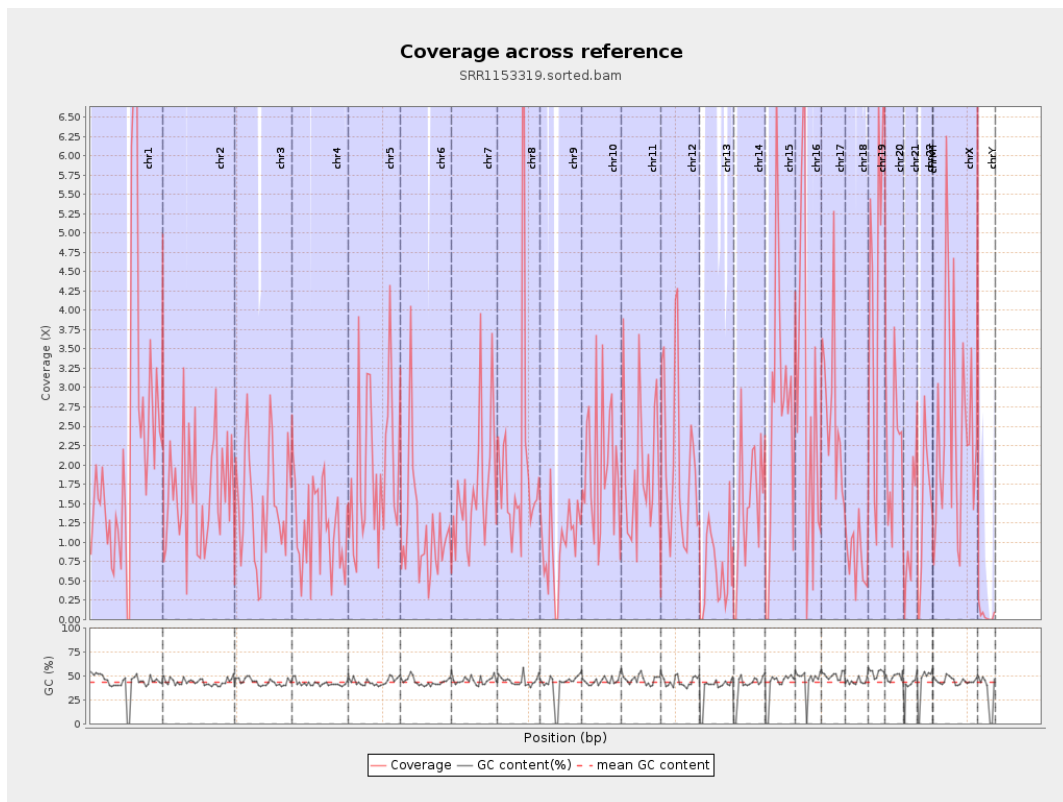
General error rate	0.29%
Mismatches	15,286,396
Insertions	381,696
Mapped reads with at least one insertion	0.67%
Deletions	337,090
Mapped reads with at least one deletion	0.59%
Homopolymer indels	49.57%

2.6. Chromosome stats

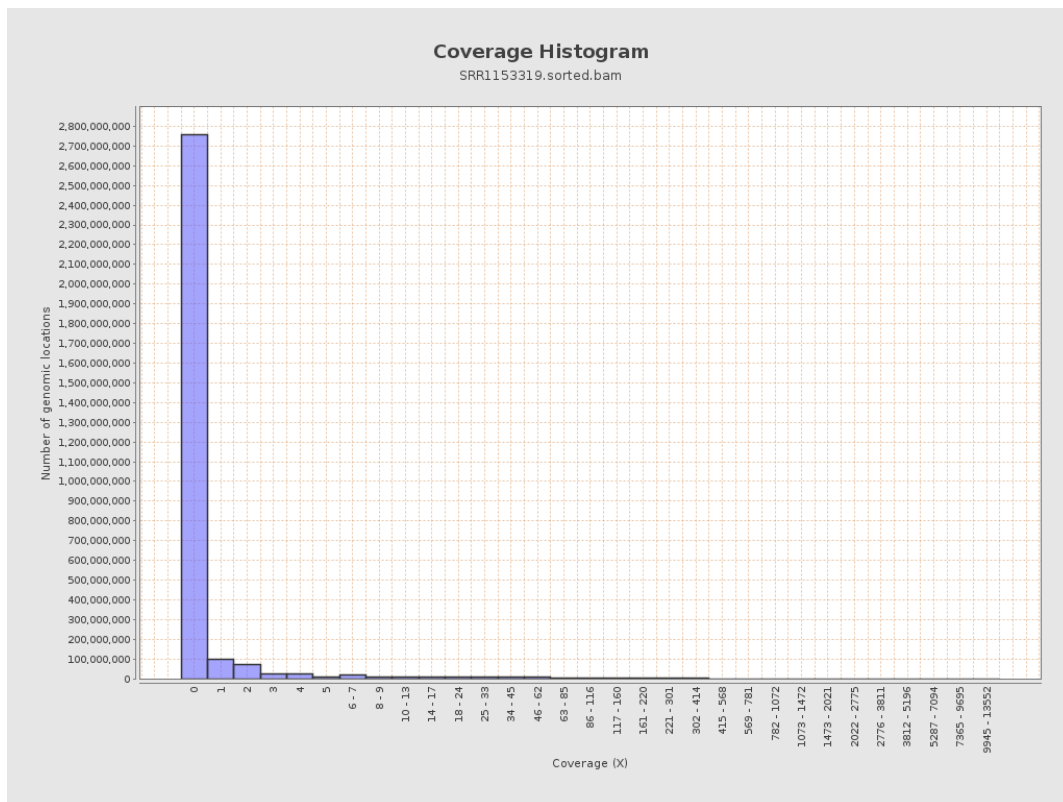
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	553067059	2.2189	20.1981
chr2	243199373	400608654	1.6472	15.3249
chr3	198022430	292004646	1.4746	14.3476
chr4	191154276	225864332	1.1816	13.1039
chr5	180915260	355400413	1.9645	20.0006
chr6	171115067	195015020	1.1397	12.018
chr7	159138663	267648933	1.6819	18.3139

chr8	146364022	301405869	2.0593	39.4609
chr9	141213431	135095549	0.9567	10.3655
chr10	135534747	269973591	1.9919	18.3142
chr11	135006516	259816012	1.9245	16.6958
chr12	133851895	276650317	2.0668	17.5062
chr13	115169878	73825107	0.641	9.1117
chr14	107349540	159346702	1.4844	14.2645
chr15	102531392	266823032	2.6024	23.0786
chr16	90354753	252888654	2.7988	26.3892
chr17	81195210	221723285	2.7307	19.3219
chr18	78077248	62229191	0.797	9.2601
chr19	59128983	260921220	4.4127	30.6974
chr20	63025520	137346552	2.1792	20.2749
chr21	48129895	58039138	1.2059	13.7024
chr22	51304566	74412860	1.4504	13.6844
chrMT	16571	13885	0.8379	3.4788
chrX	155270560	394794074	2.5426	27.0528
chrY	59373566	3216181	0.0542	2.1135

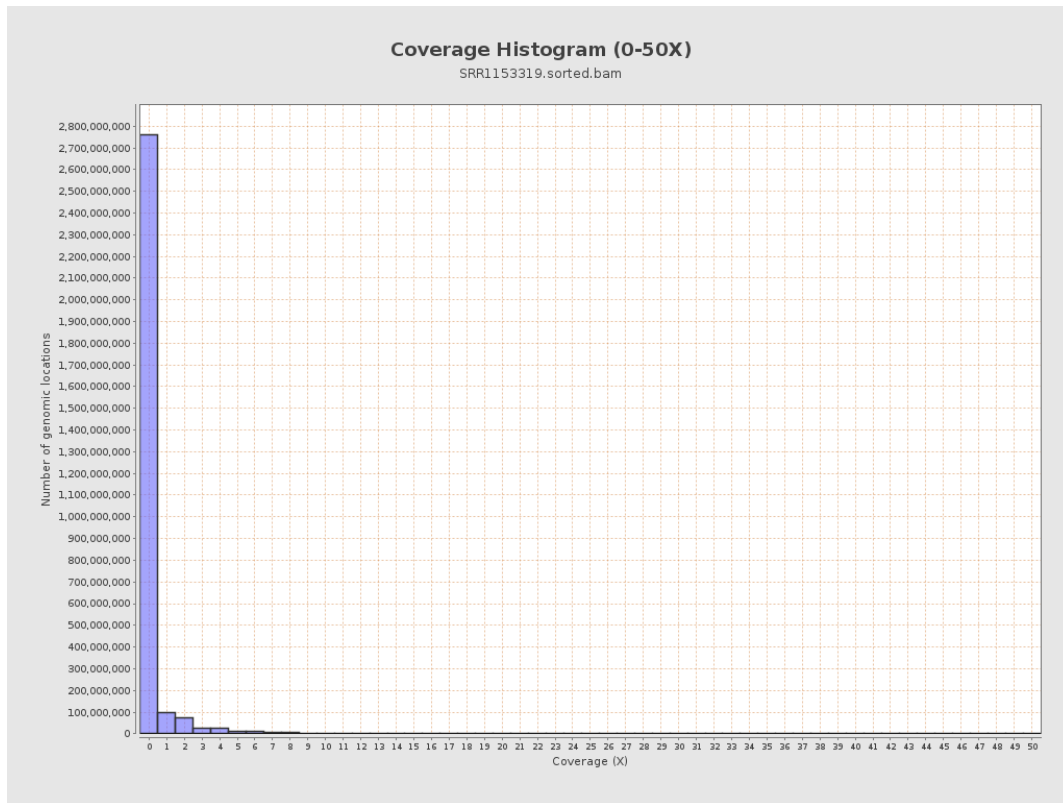
3. Results : Coverage across reference



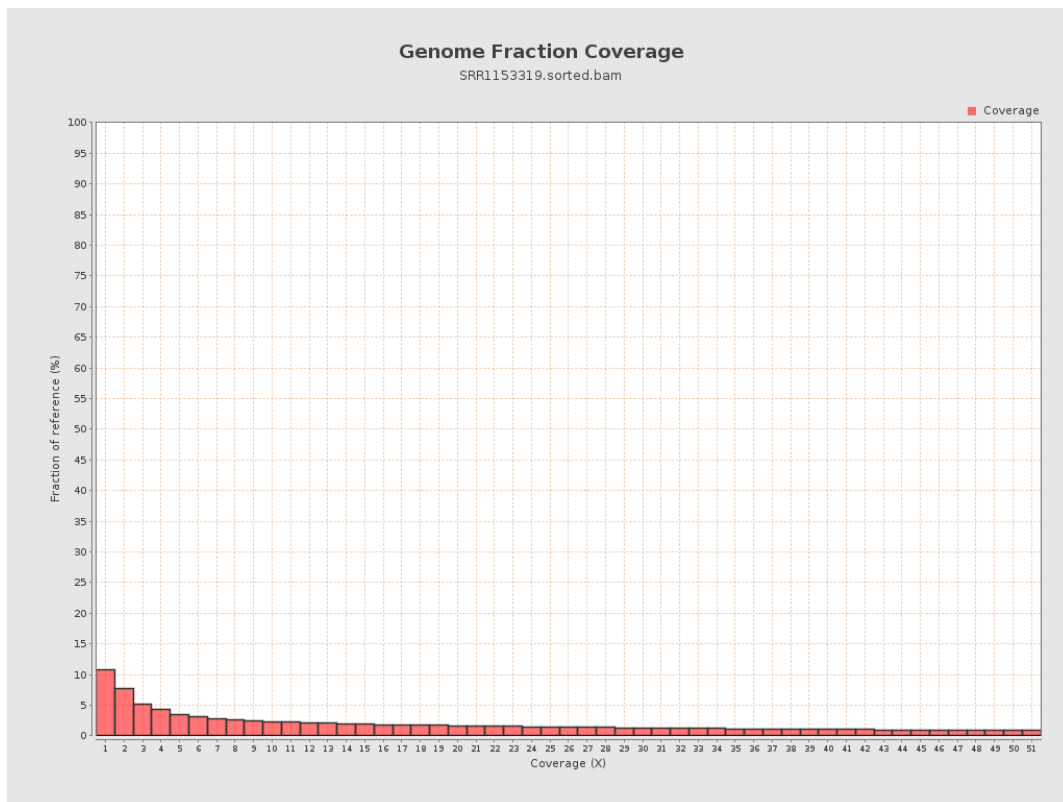
4. Results : Coverage Histogram



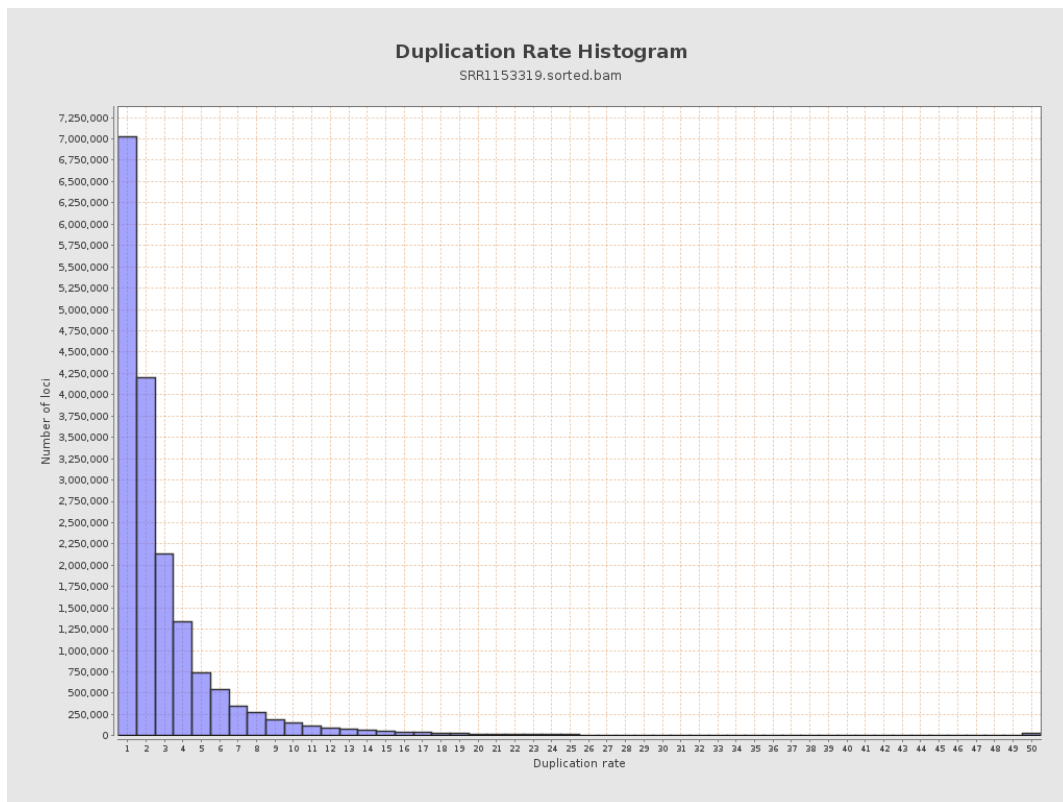
5. Results : Coverage Histogram (0-50X)



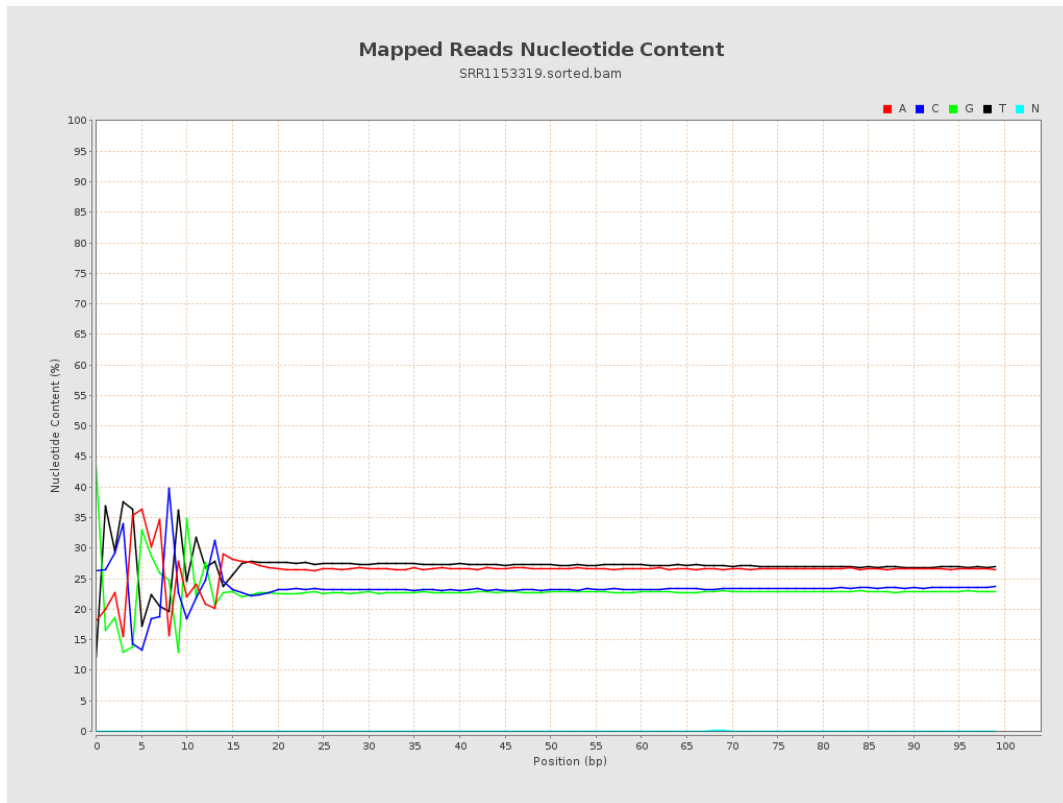
6. Results : Genome Fraction Coverage



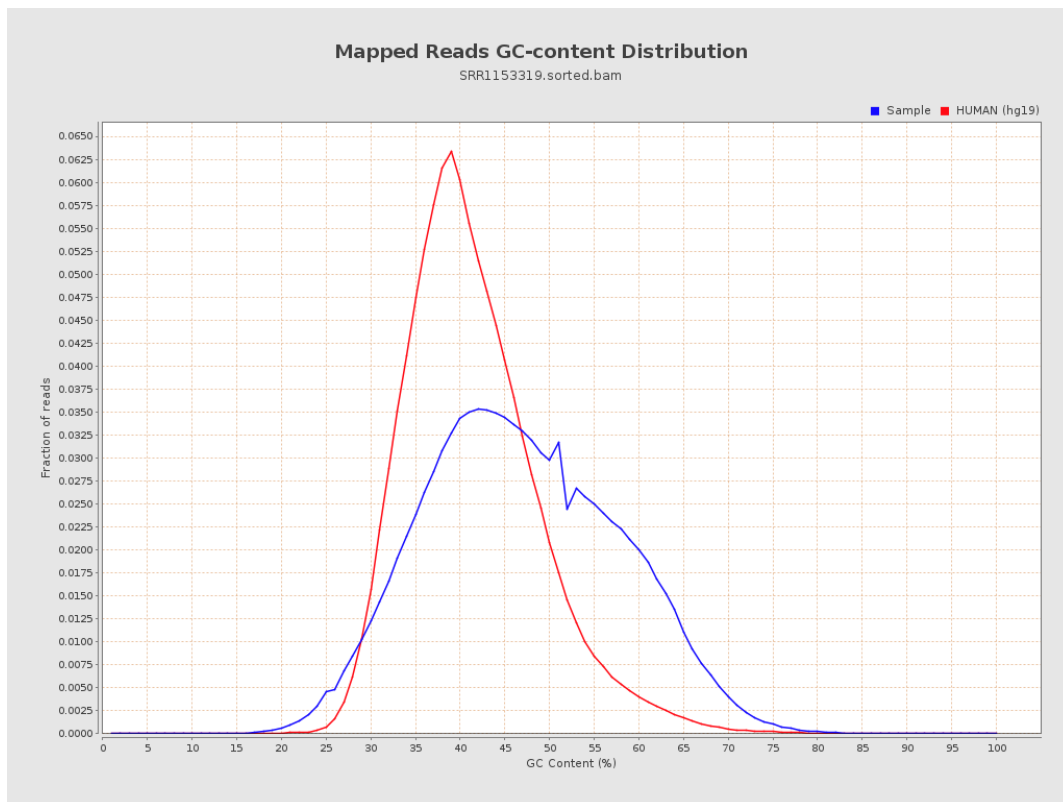
7. Results : Duplication Rate Histogram



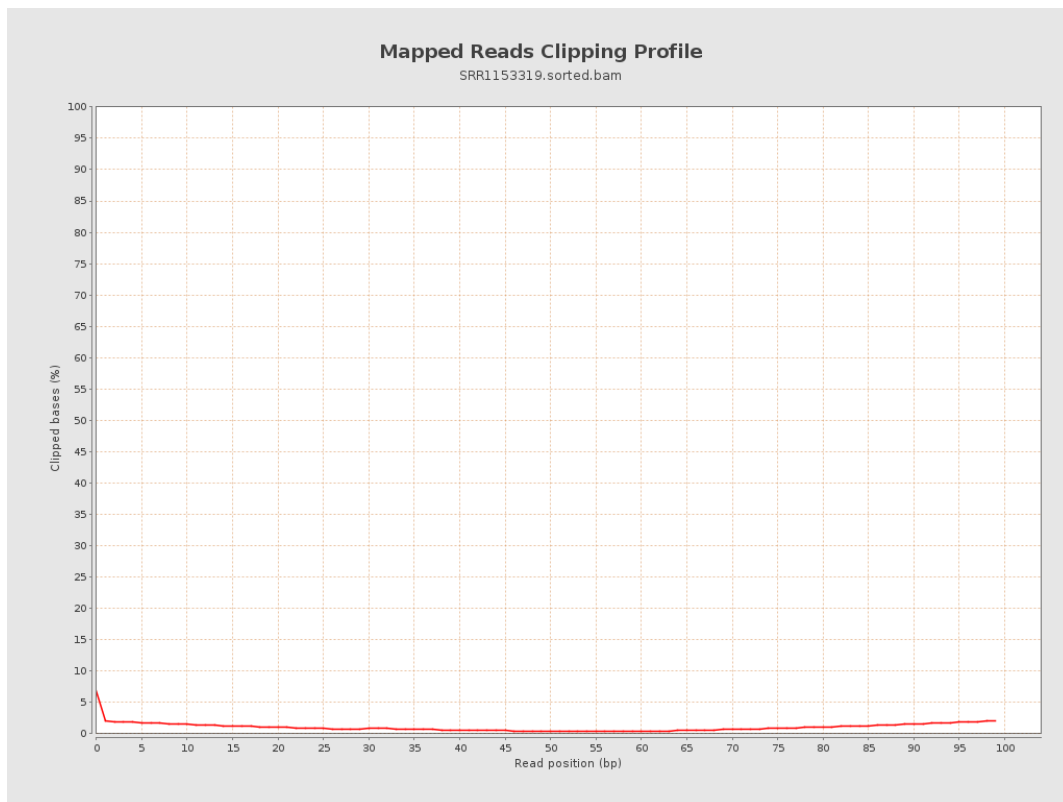
8. Results : Mapped Reads Nucleotide Content



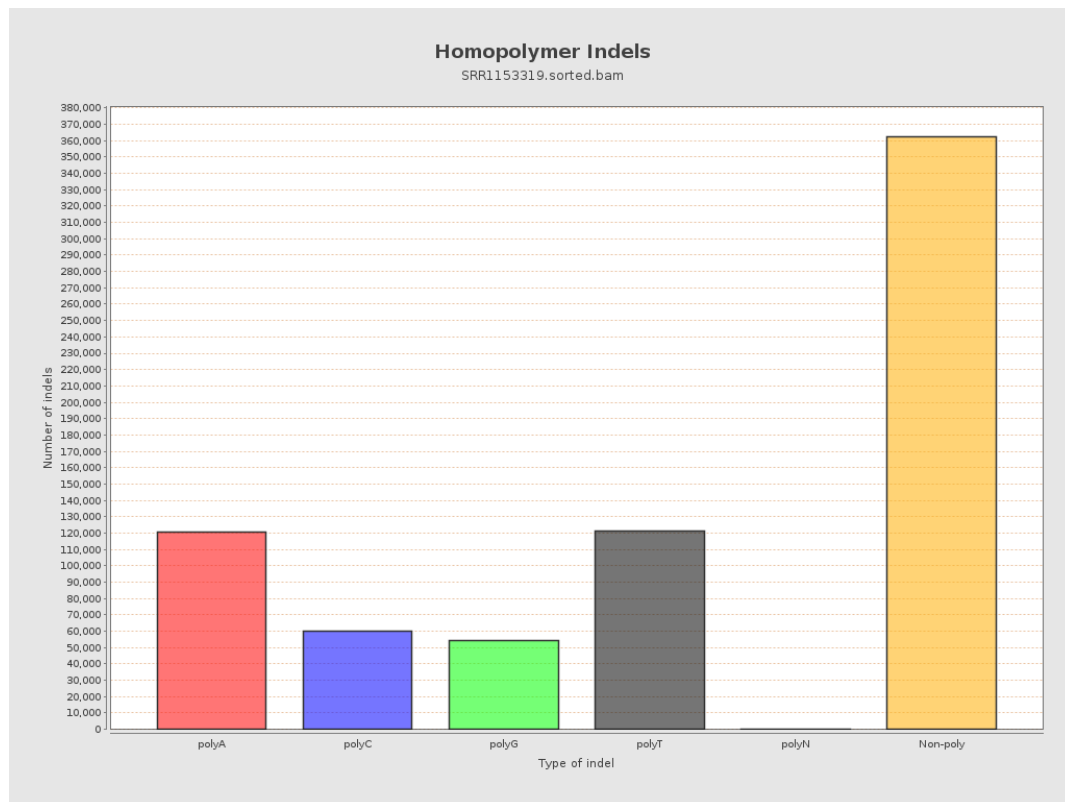
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

