Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 09:03:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153314.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_SRR1153314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 09:03:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	147,553,632
Mapped reads	143,160,278 / 97.02%
Unmapped reads	4,393,354 / 2.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	932,835 / 0.63%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	92,900,735 / 62.96%
Duplication rate	53.03%
Clipped reads	13,815,071 / 9.36%

2.2. ACGT Content

Number/percentage of A's	3,189,277,977 / 22.63%
Number/percentage of C's	3,859,002,037 / 27.39%
Number/percentage of T's	3,196,991,389 / 22.69%
Number/percentage of G's	3,830,039,595 / 27.18%
Number/percentage of N's	15,354,020 / 0.11%
GC Percentage	54.57%

2.3. Coverage

Mean	4.5522

Standard Deviation	55.9808

2.4. Mapping Quality

Mean Mapping Quality	48.46

2.5. Mismatches and indels

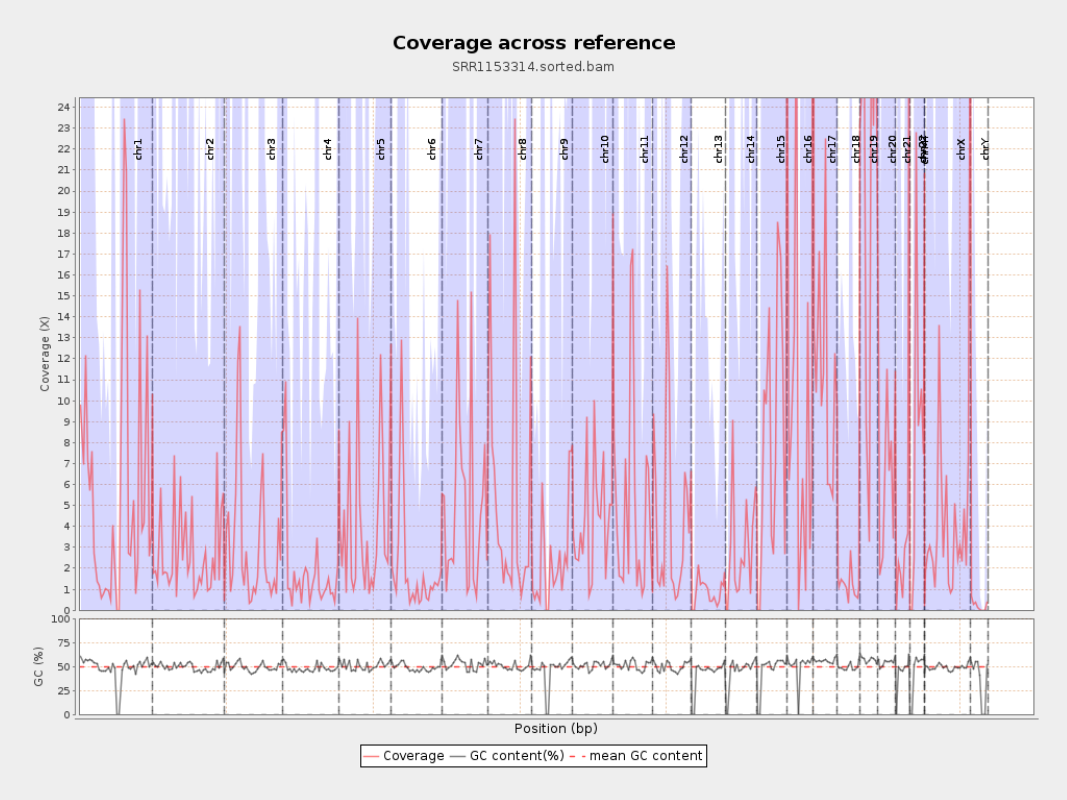
General error rate	0.63%
Mismatches	88,238,613
Insertions	584,962
Mapped reads with at least one insertion	0.4%
Deletions	654,276
Mapped reads with at least one deletion	0.45%
Homopolymer indels	40.67%

2.6. Chromosome stats

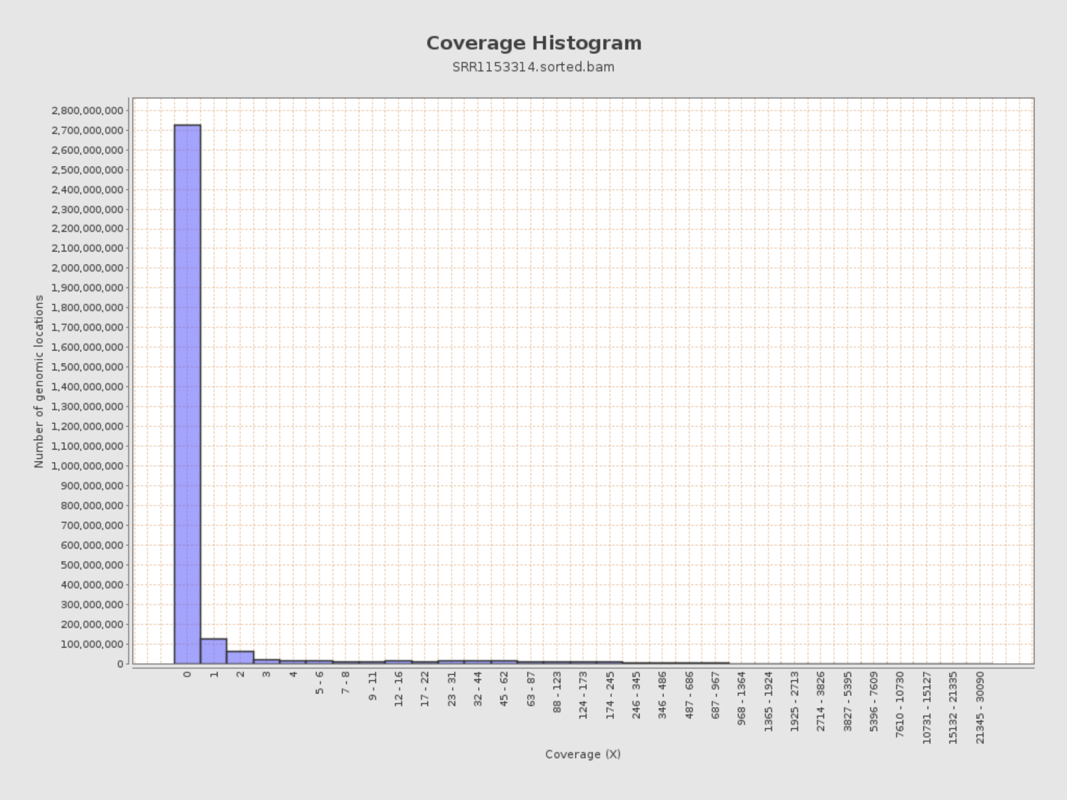
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1401548591	5.623	56.3232
chr2	243199373	661456712	2.7198	27.859
chr3	198022430	633544874	3.1994	34.4969
chr4	191154276	353447701	1.849	32.9536
chr5	180915260	781255765	4.3184	91.5376
chr6	171115067	331039619	1.9346	22.4606
chr7	159138663	790854489	4.9696	68.8602

chr8	146364022	743118901	5.0772	82.1473
chr9	141213431	347081483	2.4579	24.341
chr10	135534747	586130170	4.3246	42.3446
chr11	135006516	733478781	5.4329	46.2448
chr12	133851895	580421798	4.3363	36.6899
chr13	115169878	102376247	0.8889	12.5722
chr14	107349540	309946523	2.8873	29.4195
chr15	102531392	815222494	7.951	68.9758
chr16	90354753	891613297	9.8679	84.9332
chr17	81195210	919041729	11.3189	77.8992
chr18	78077248	94043713	1.2045	15.6446
chr19	59128983	1262886069	21.3582	109.365
chr20	63025520	418890491	6.6464	54.8043
chr21	48129895	225730521	4.69	141.2956
chr22	51304566	445903428	8.6913	66.5803
chrMT	16571	2902	0.1751	0.5075
chrX	155270560	650436461	4.1891	40.0576
chrY	59373566	12867985	0.2167	11.6834

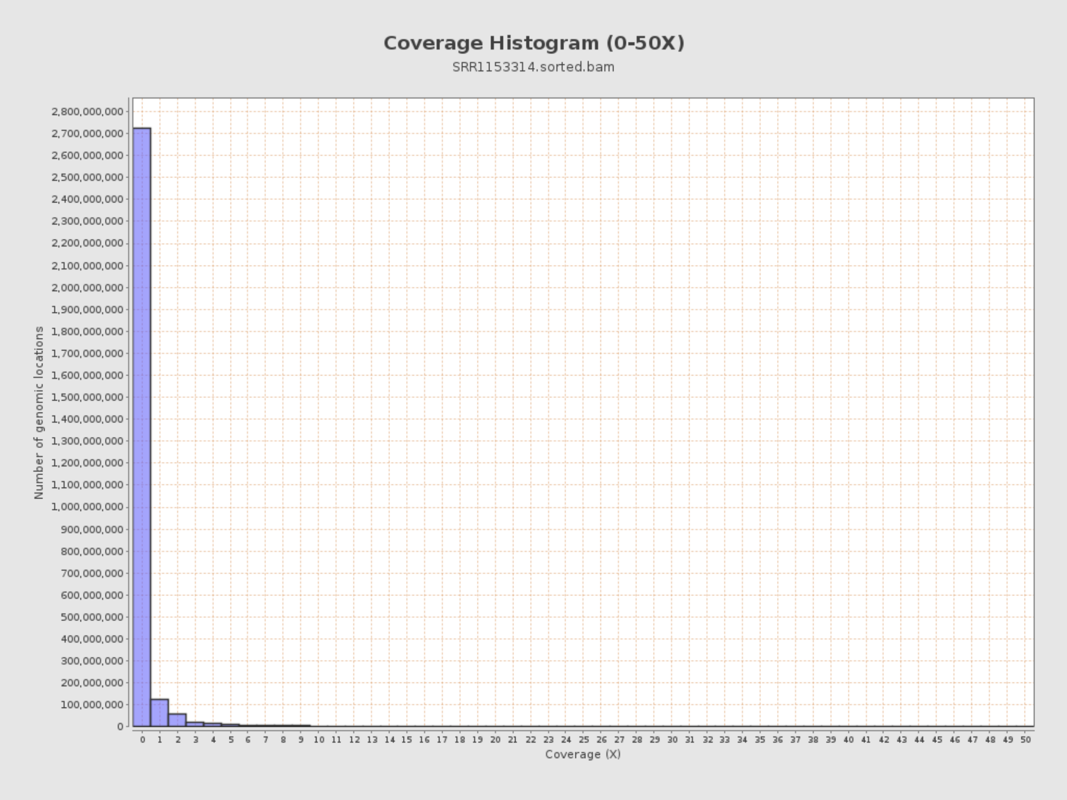
3. Results : Coverage across reference



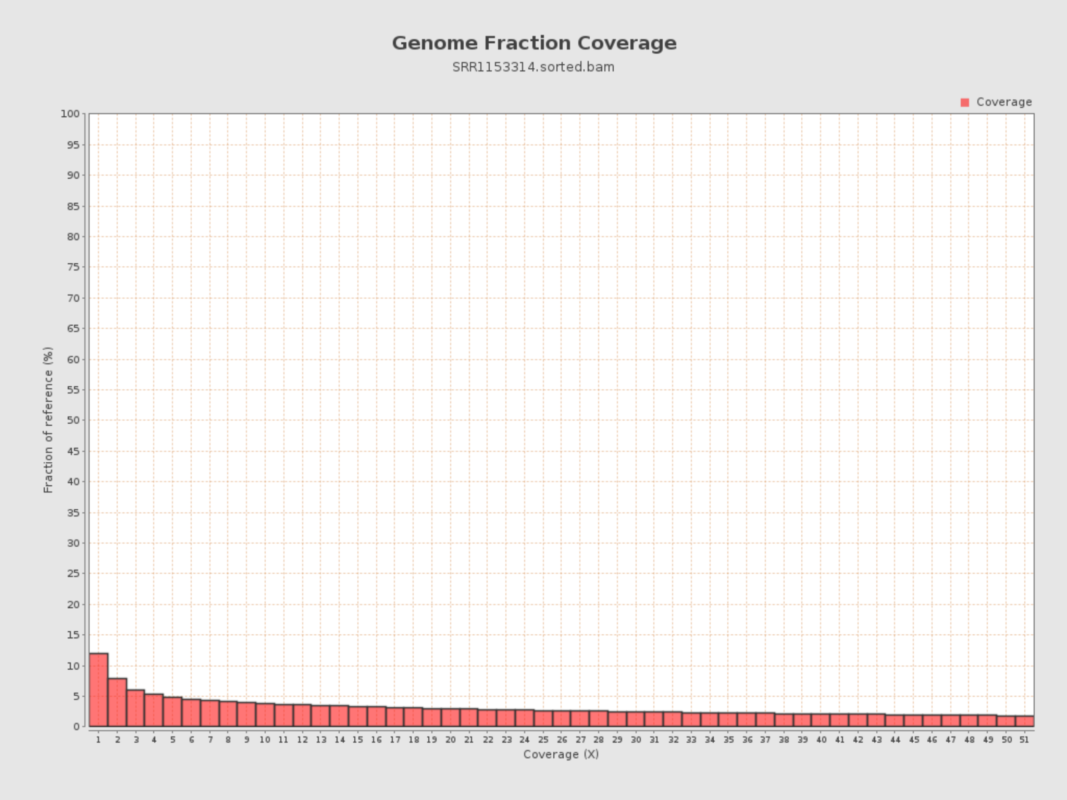
4. Results : Coverage Histogram



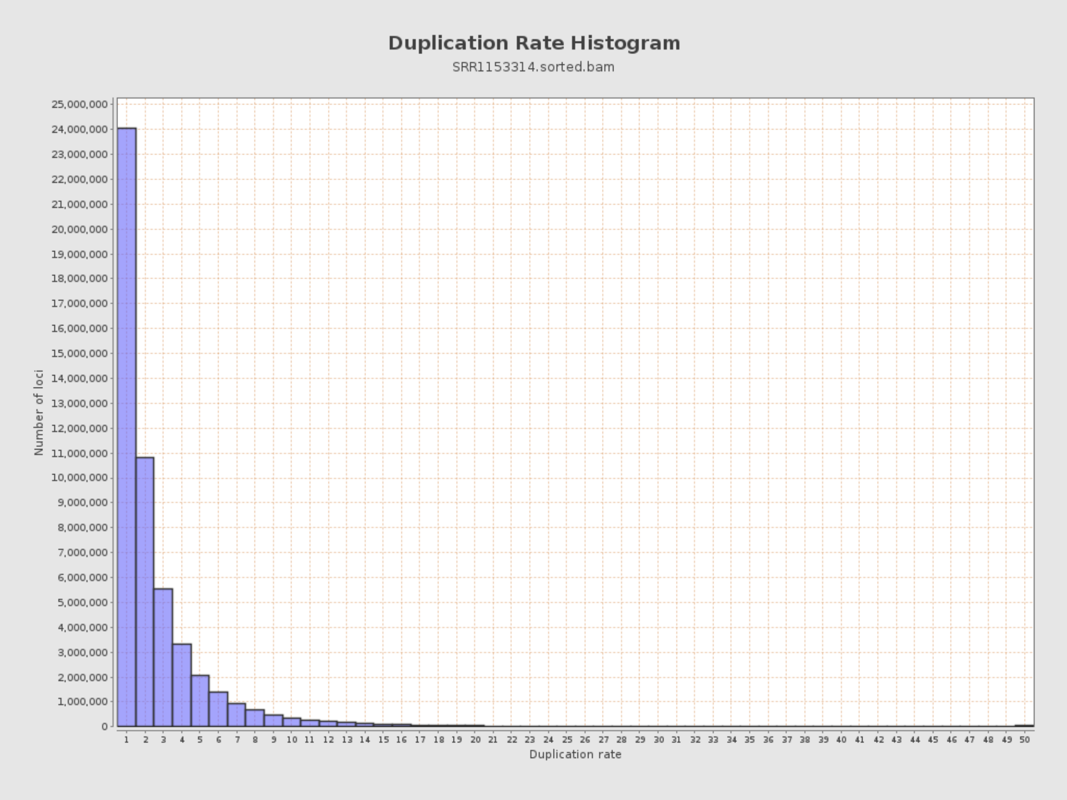
5. Results : Coverage Histogram (0-50X)



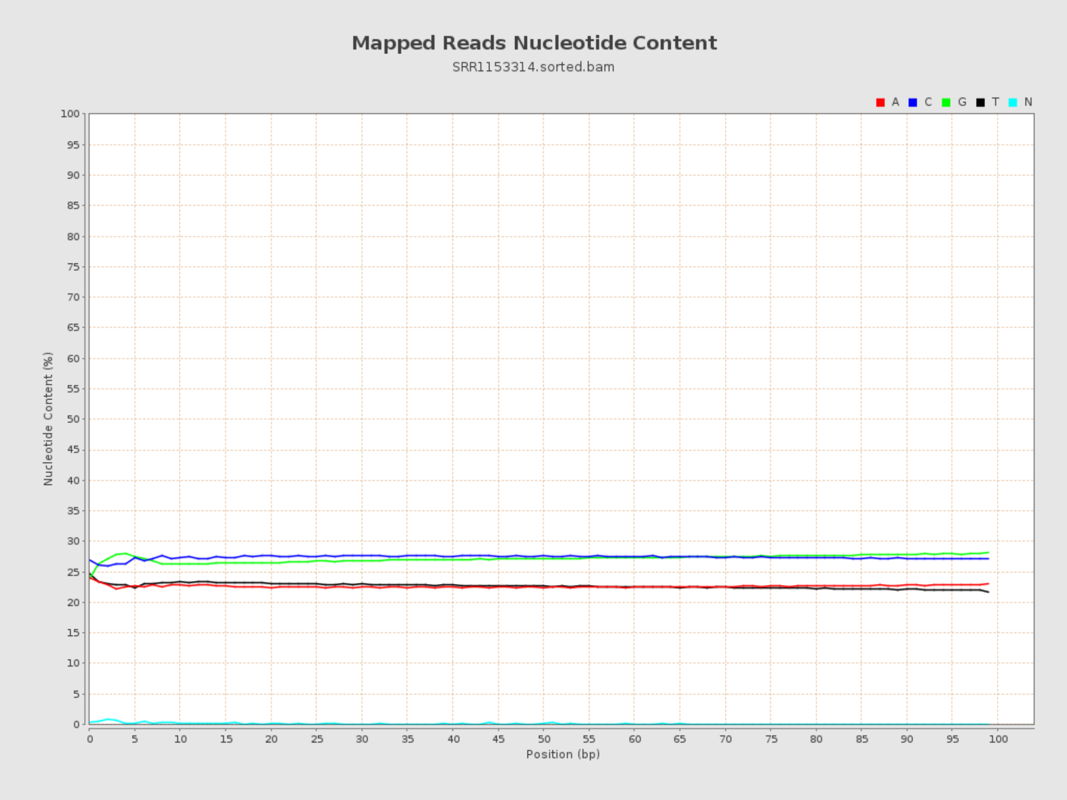
6. Results : Genome Fraction Coverage



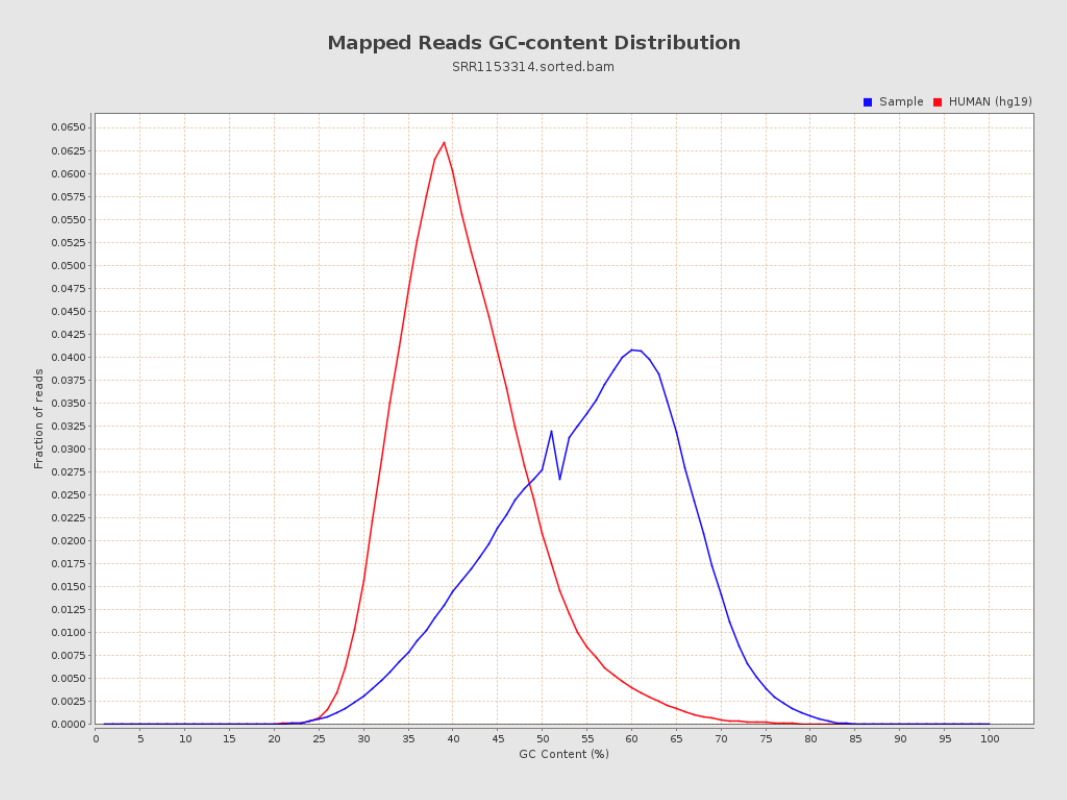
7. Results : Duplication Rate Histogram



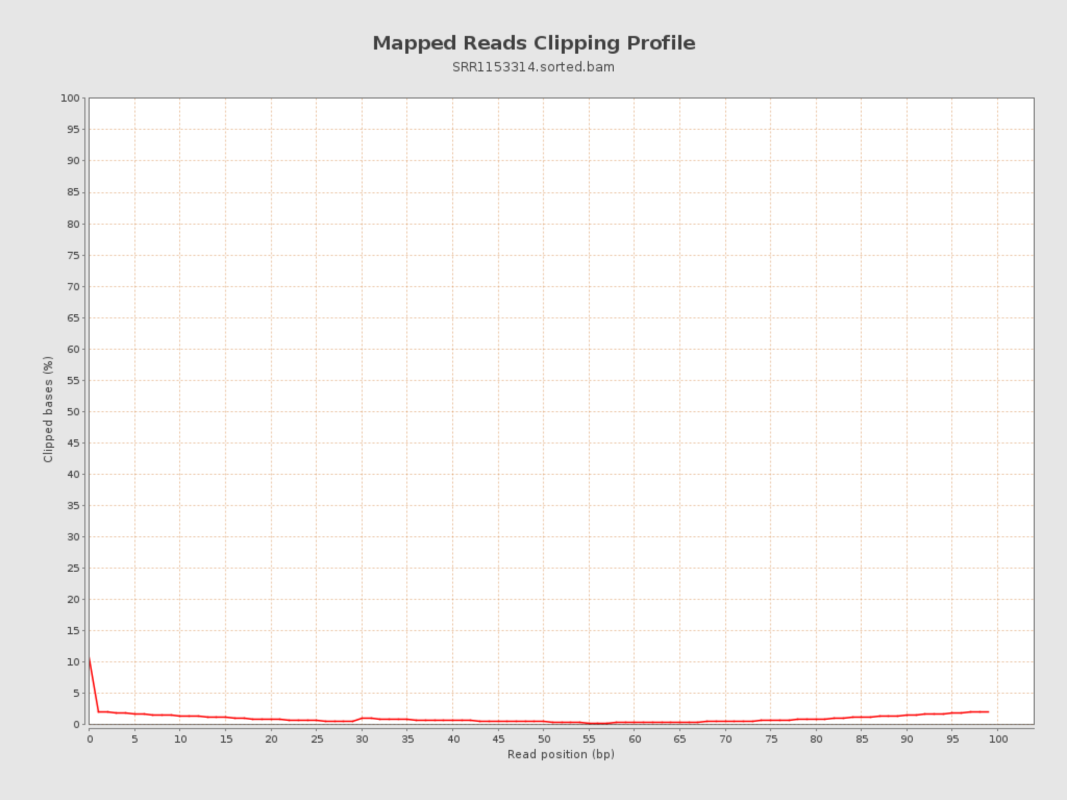
8. Results : Mapped Reads Nucleotide Content



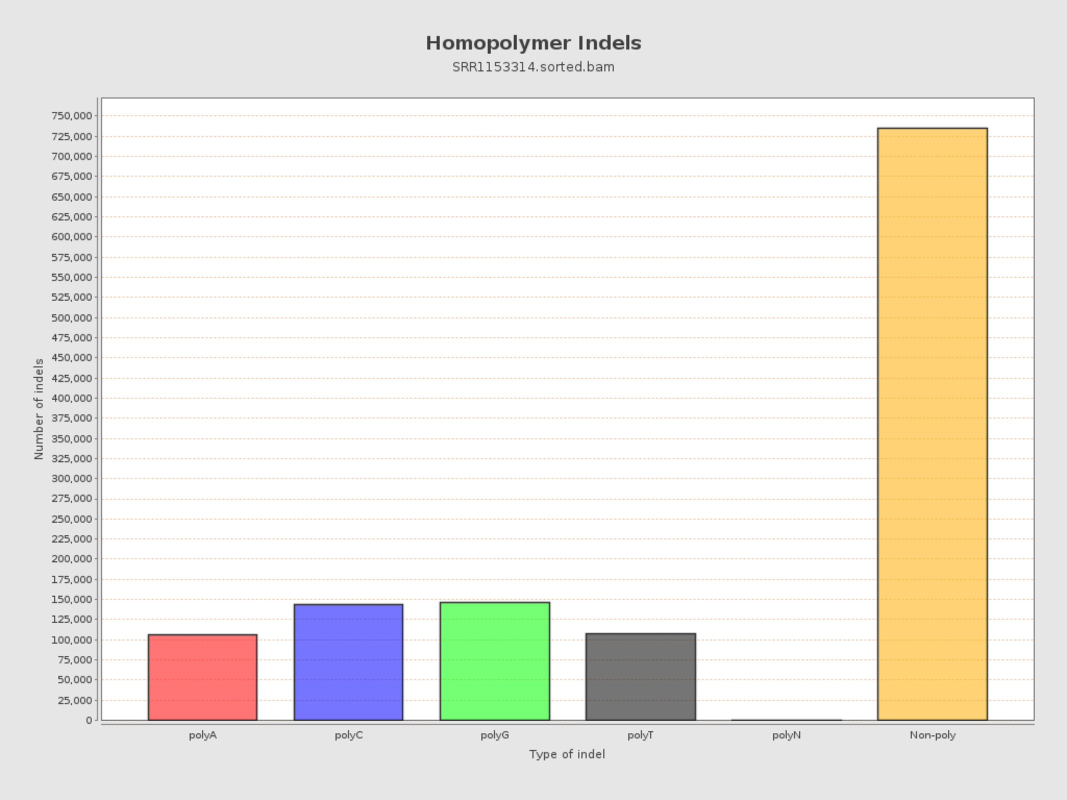
9. Results : Mapped Reads GC-content Distribution



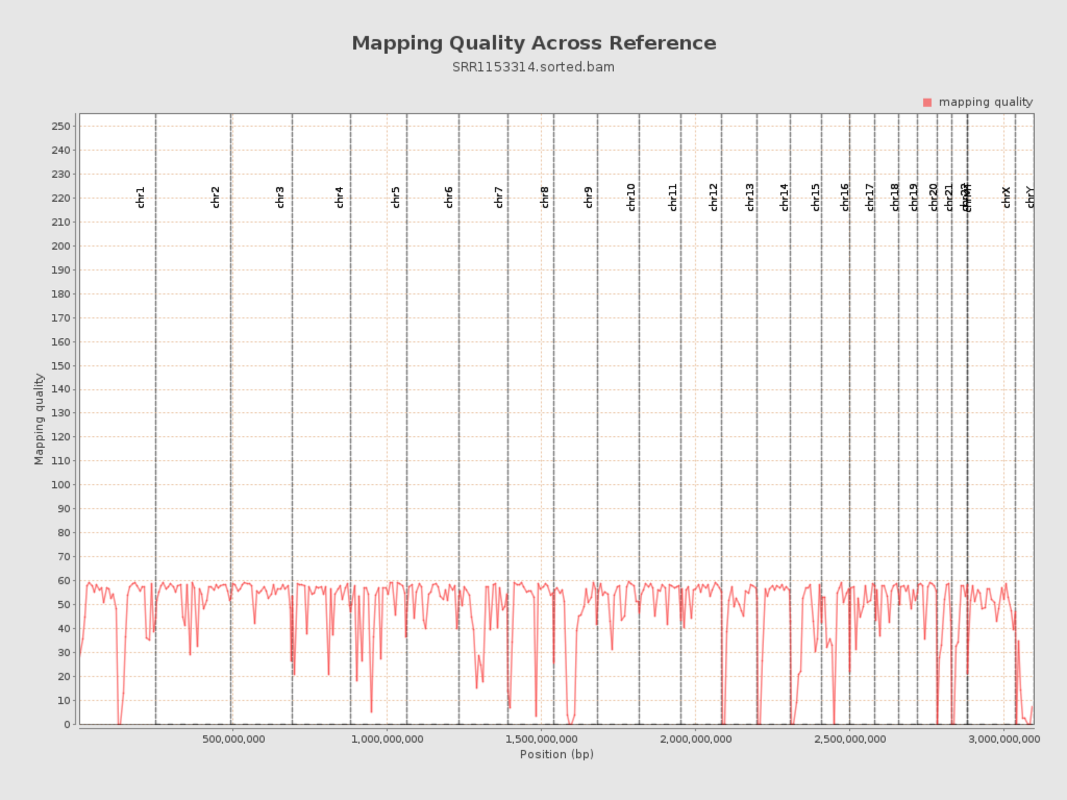
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram