Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 00:36:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153310.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_SRR1153310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153310.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 00:36:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,978,346
Mapped reads	47,599,566 / 99.21%
Unmapped reads	378,780 / 0.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	247,024 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	32,482,389 / 67.7%
Duplication rate	61.16%
Clipped reads	6,565,359 / 13.68%

2.2. ACGT Content

Number/percentage of A's	1,211,691,353 / 26.22%
Number/percentage of C's	1,091,842,679 / 23.63%
Number/percentage of T's	1,246,928,923 / 26.98%
Number/percentage of G's	1,069,267,374 / 23.14%
Number/percentage of N's	1,521,621 / 0.03%
GC Percentage	46.76%

2.3. Coverage

Mean	1.493

Standard Deviation	15.7383

2.4. Mapping Quality

Mean Mapping Quality	50.49

2.5. Mismatches and indels

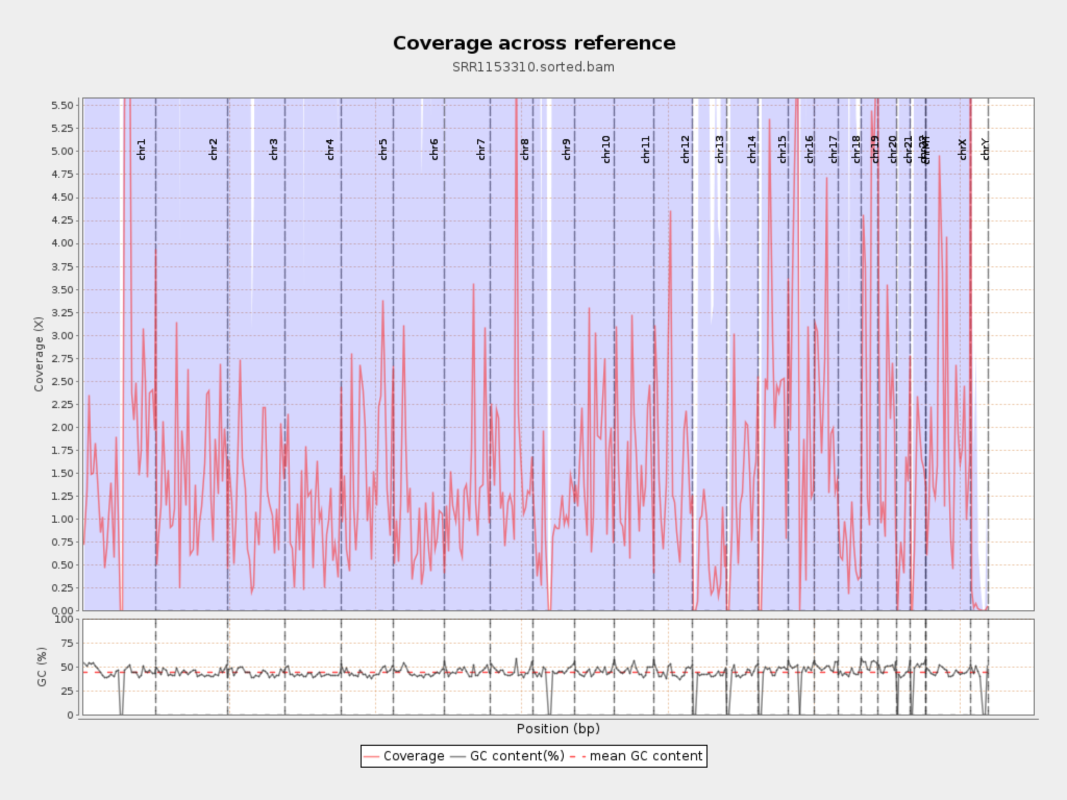
General error rate	0.29%
Mismatches	12,801,766
Insertions	321,377
Mapped reads with at least one insertion	0.67%
Deletions	279,067
Mapped reads with at least one deletion	0.58%
Homopolymer indels	49.7%

2.6. Chromosome stats

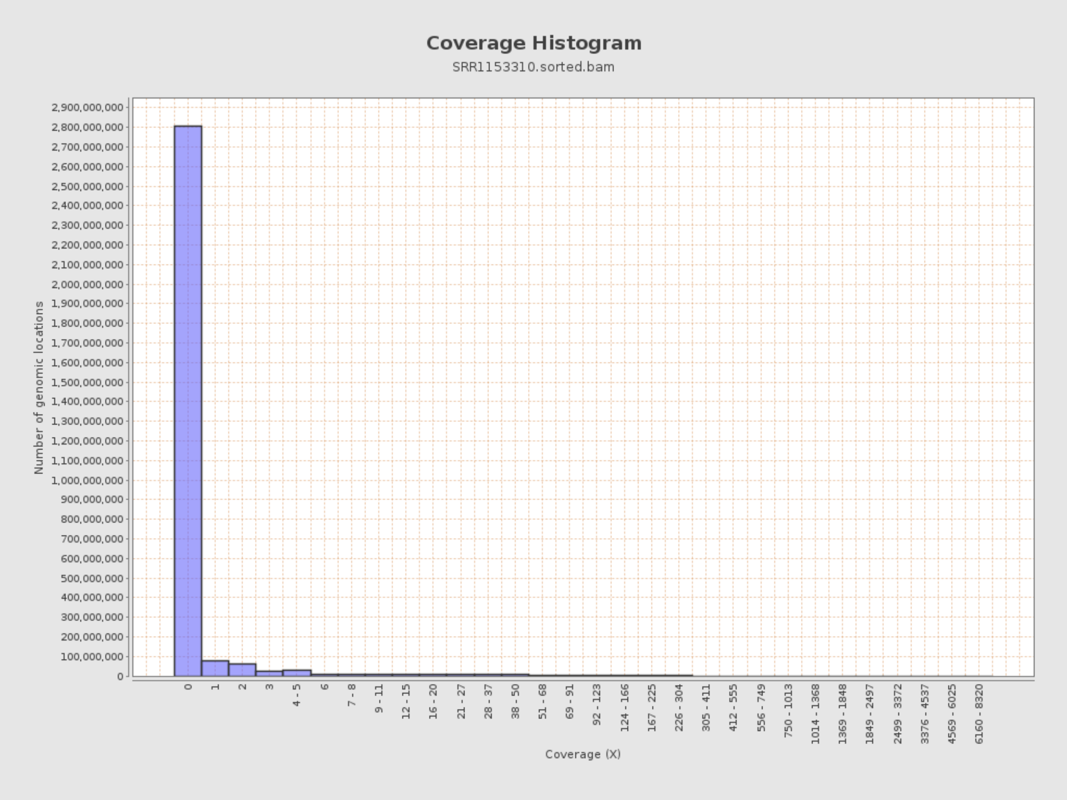
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	490482748	1.9678	18.2381
chr2	243199373	346229429	1.4236	13.4813
chr3	198022430	240020800	1.2121	11.8805
chr4	191154276	190291476	0.9955	11.4882
chr5	180915260	291337606	1.6104	16.4891
chr6	171115067	163436981	0.9551	10.1537
chr7	159138663	212402672	1.3347	13.484

chr8	146364022	244480743	1.6704	26.1451
chr9	141213431	120989577	0.8568	9.2668
chr10	135534747	234176556	1.7278	16.5345
chr11	135006516	215588999	1.5969	14.4134
chr12	133851895	229427999	1.714	14.8789
chr13	115169878	61817201	0.5367	7.6215
chr14	107349540	137134047	1.2775	12.5026
chr15	102531392	213638025	2.0836	18.358
chr16	90354753	215834207	2.3887	22.2627
chr17	81195210	192112481	2.3661	17.4402
chr18	78077248	49756901	0.6373	7.7201
chr19	59128983	223505399	3.78	27.0976
chr20	63025520	121565781	1.9288	19.0264
chr21	48129895	48829565	1.0145	11.5507
chr22	51304566	65739817	1.2814	12.5246
chrMT	16571	20292	1.2245	3.7616
chrX	155270560	310443589	1.9994	21.1889
chrY	59373566	2552914	0.043	1.6521

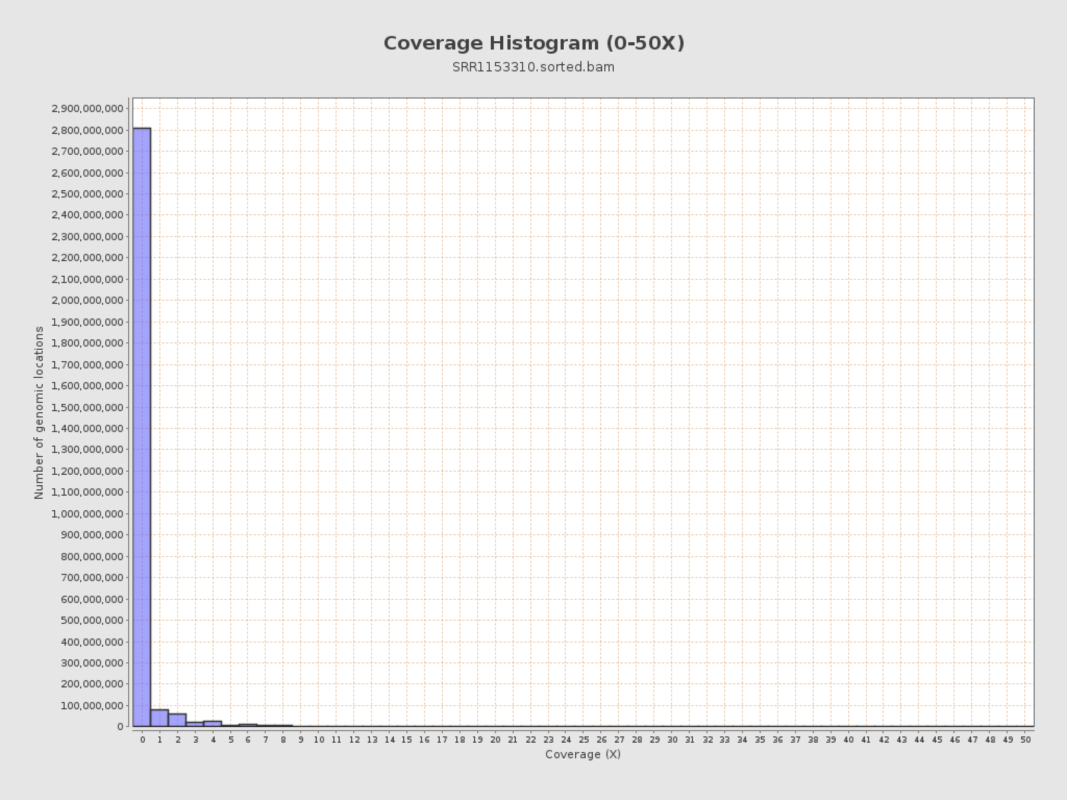
3. Results : Coverage across reference



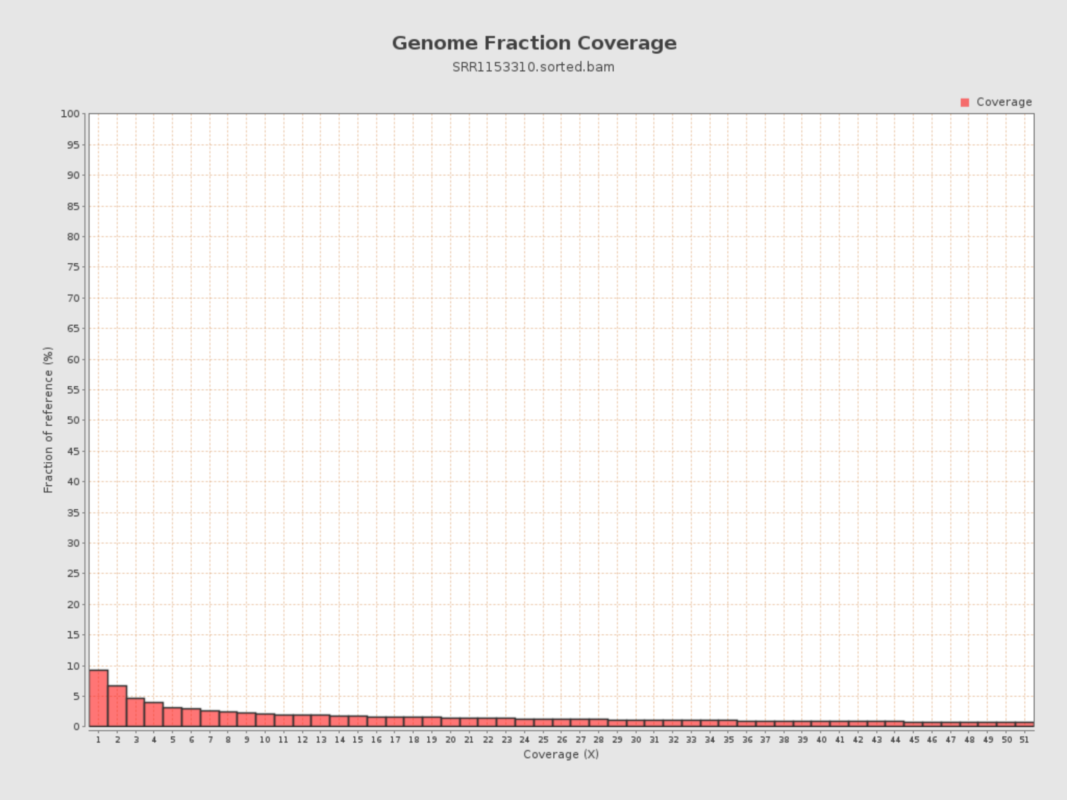
4. Results : Coverage Histogram



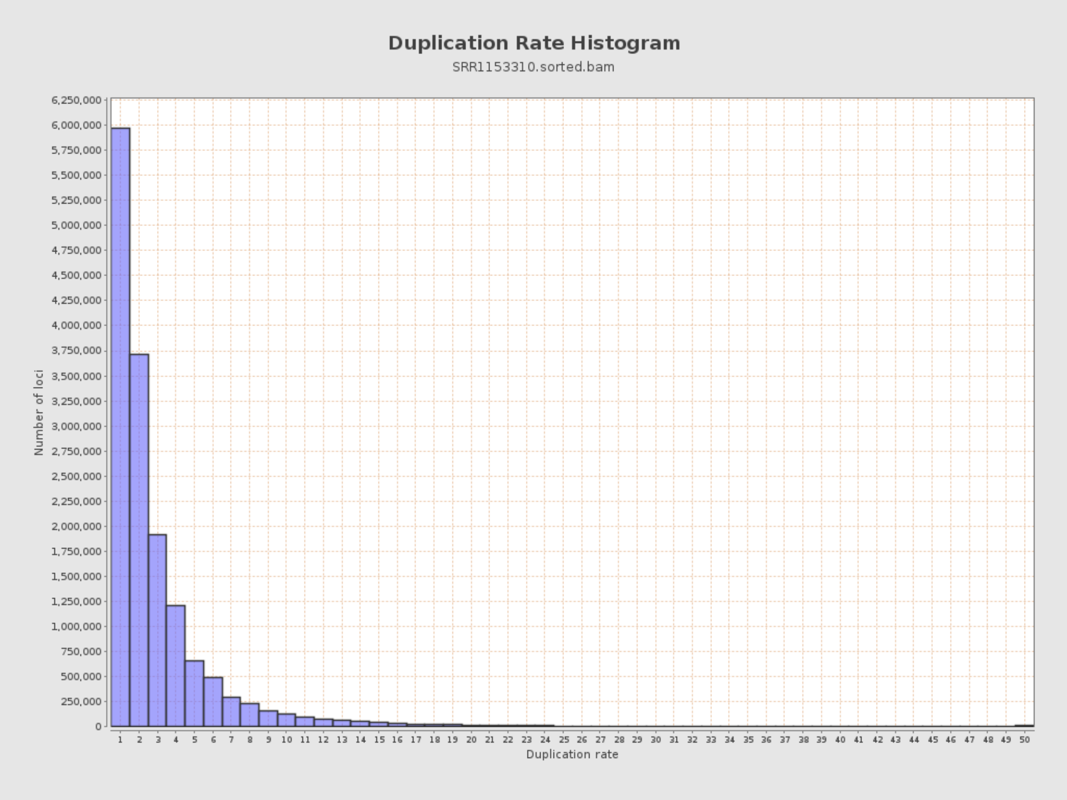
5. Results : Coverage Histogram (0-50X)



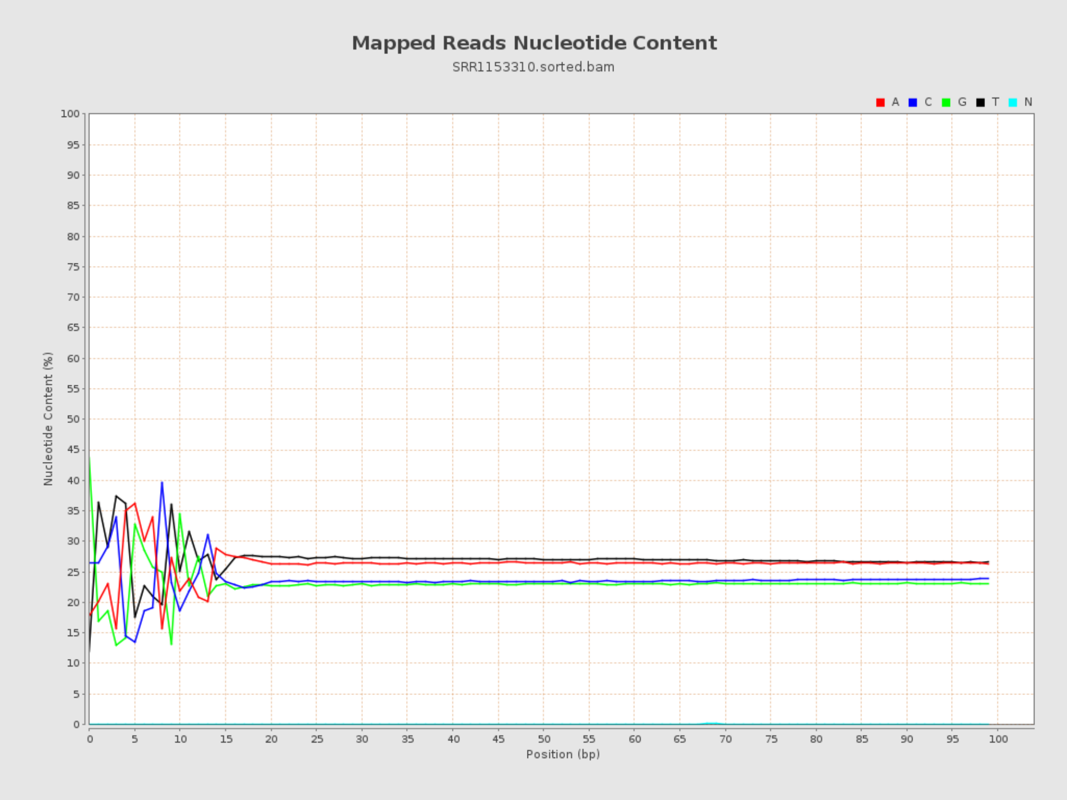
6. Results : Genome Fraction Coverage



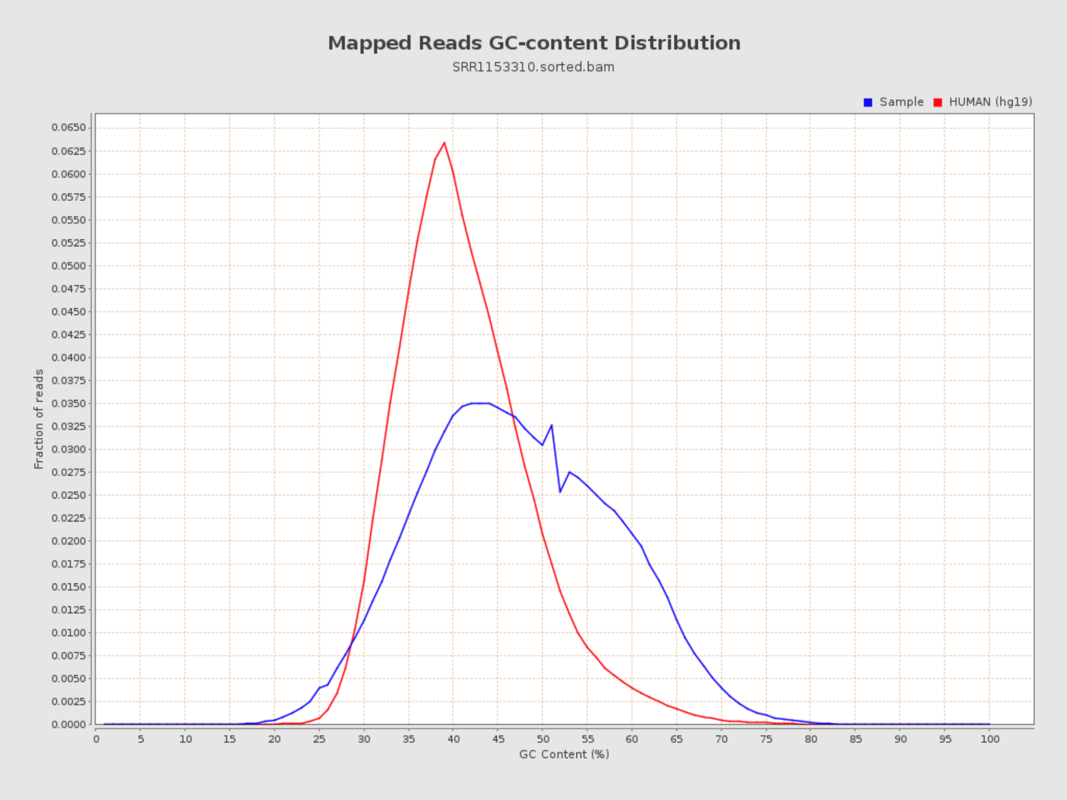
7. Results : Duplication Rate Histogram



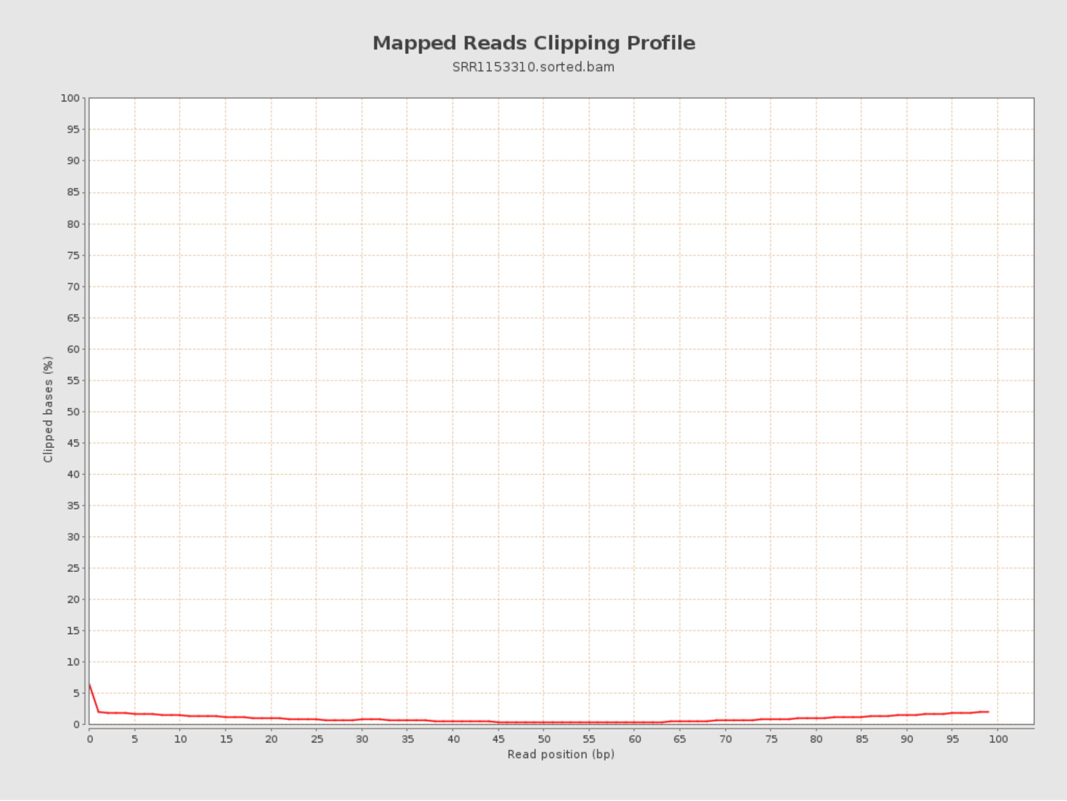
8. Results : Mapped Reads Nucleotide Content



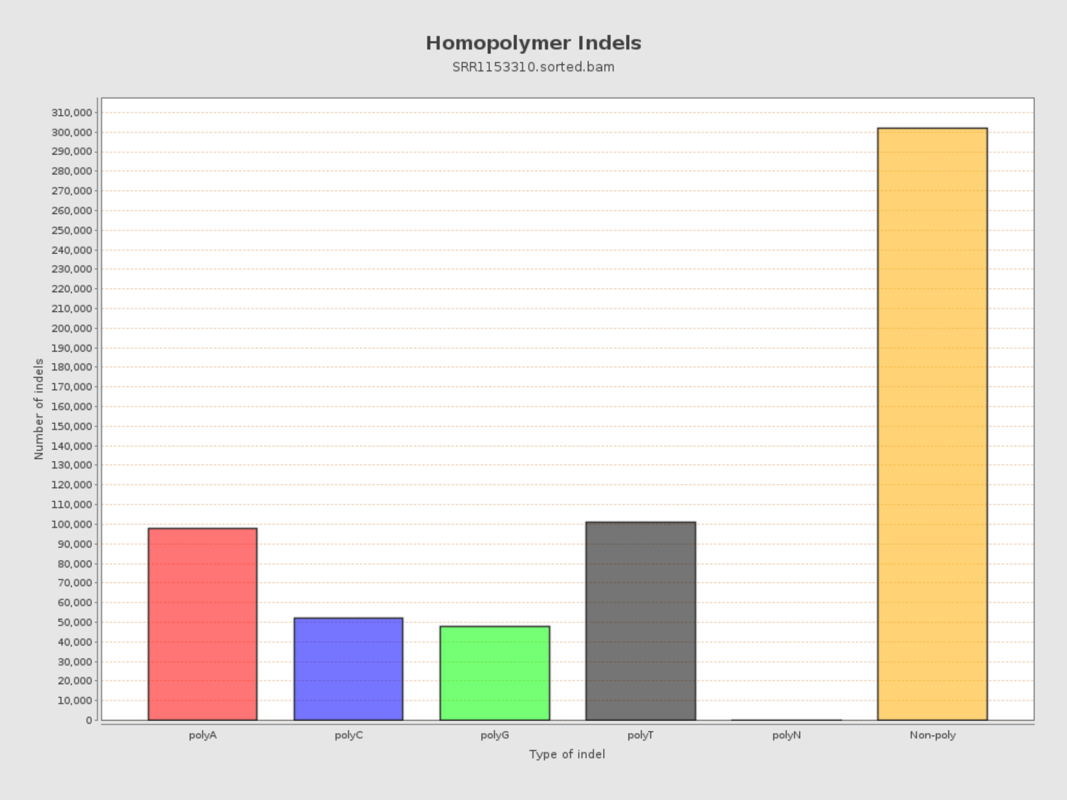
9. Results : Mapped Reads GC-content Distribution



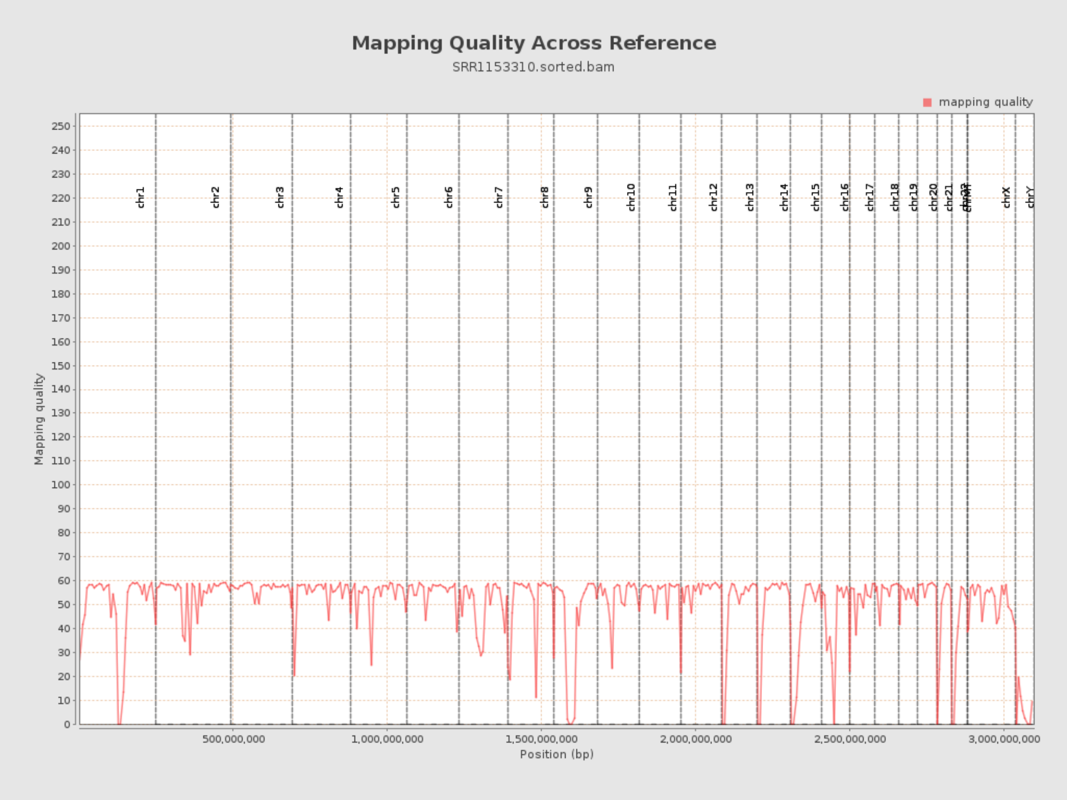
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram