Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 13:11:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153328.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_SRR1153328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 13:11:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,914,276
Mapped reads	43,417,306 / 98.87%
Unmapped reads	496,970 / 1.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	364,829 / 0.83%
Read min/max/mean length	30 / 100 / 100.34
Duplicated reads (estimated)	19,663,185 / 44.78%
Duplication rate	29.78%
Clipped reads	4,936,850 / 11.24%

2.2. ACGT Content

Number/percentage of A's	1,130,101,775 / 26.68%
Number/percentage of C's	981,743,732 / 23.18%
Number/percentage of T's	1,151,282,932 / 27.18%
Number/percentage of G's	971,226,983 / 22.93%
Number/percentage of N's	1,734,125 / 0.04%
GC Percentage	46.1%

2.3. Coverage

Mean	1.3686

Standard Deviation	12.091

2.4. Mapping Quality

Mean Mapping Quality	50.23

2.5. Mismatches and indels

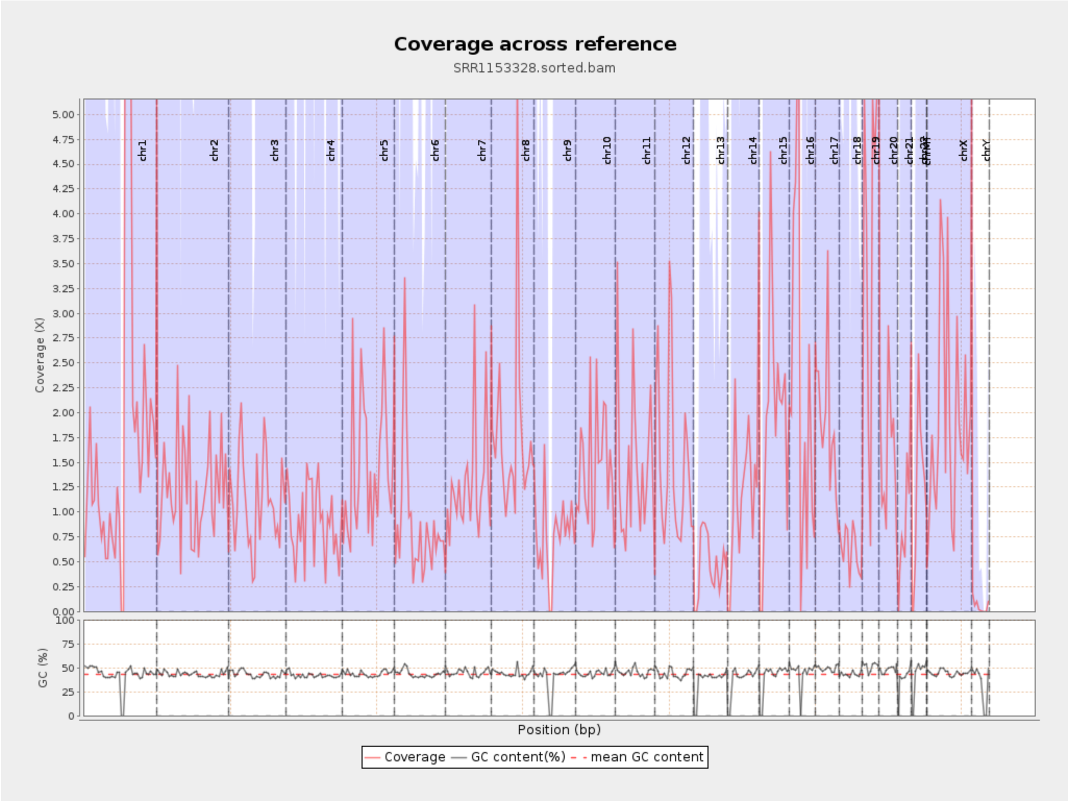
General error rate	0.32%
Mismatches	12,681,376
Insertions	463,322
Mapped reads with at least one insertion	1.05%
Deletions	356,099
Mapped reads with at least one deletion	0.81%
Homopolymer indels	49.3%

2.6. Chromosome stats

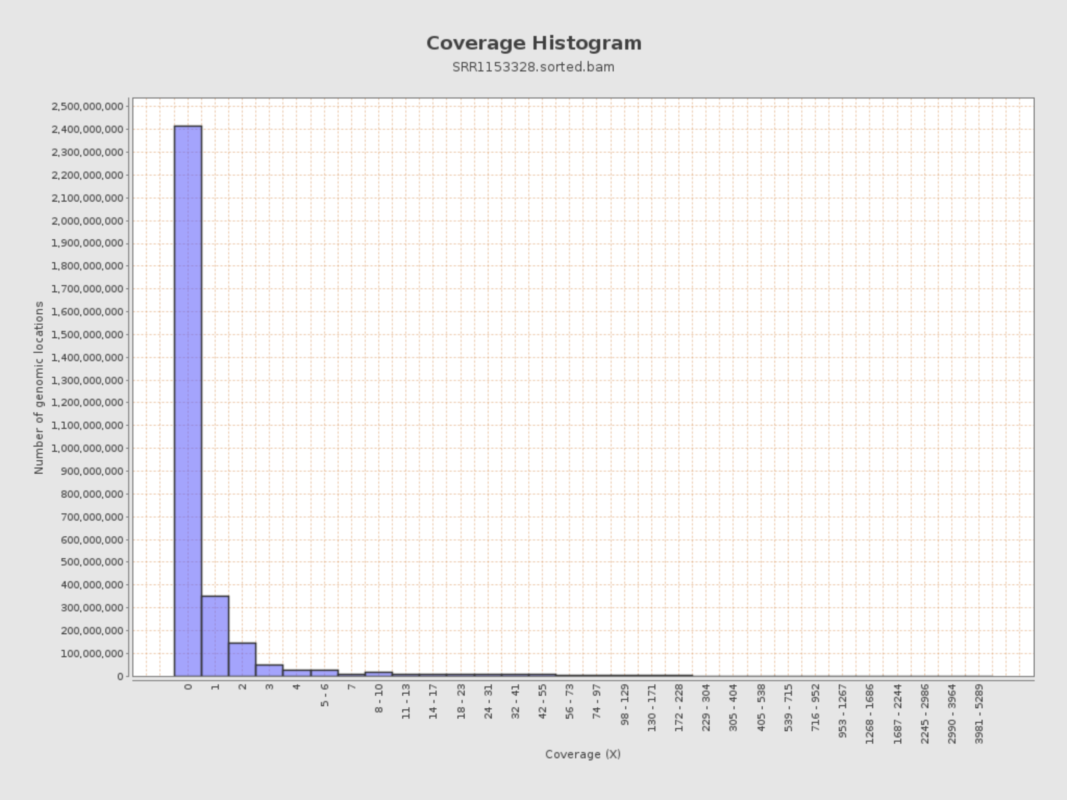
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	454268915	1.8225	15.609
chr2	243199373	298613733	1.2279	9.5802
chr3	198022430	218228782	1.102	9.7487
chr4	191154276	172287497	0.9013	7.4592
chr5	180915260	268627957	1.4848	13.1917
chr6	171115067	146256472	0.8547	7.7919
chr7	159138663	200747579	1.2615	10.4206

chr8	146364022	257886987	1.762	19.7768
chr9	141213431	104576665	0.7406	6.5768
chr10	135534747	198854757	1.4672	10.4864
chr11	135006516	195759064	1.45	10.9735
chr12	133851895	207932031	1.5534	11.1494
chr13	115169878	53144914	0.4614	4.1003
chr14	107349540	127318151	1.186	9.4034
chr15	102531392	190748238	1.8604	13.1949
chr16	90354753	196735031	2.1774	17.5917
chr17	81195210	156232244	1.9242	12.0923
chr18	78077248	48411549	0.62	5.2927
chr19	59128983	222140407	3.7569	23.196
chr20	63025520	99518261	1.579	10.7966
chr21	48129895	48043526	0.9982	12.0461
chr22	51304566	62151640	1.2114	11.1178
chrMT	16571	7108	0.4289	1.1486
chrX	155270560	305090503	1.9649	16.9728
chrY	59373566	3266896	0.055	1.989

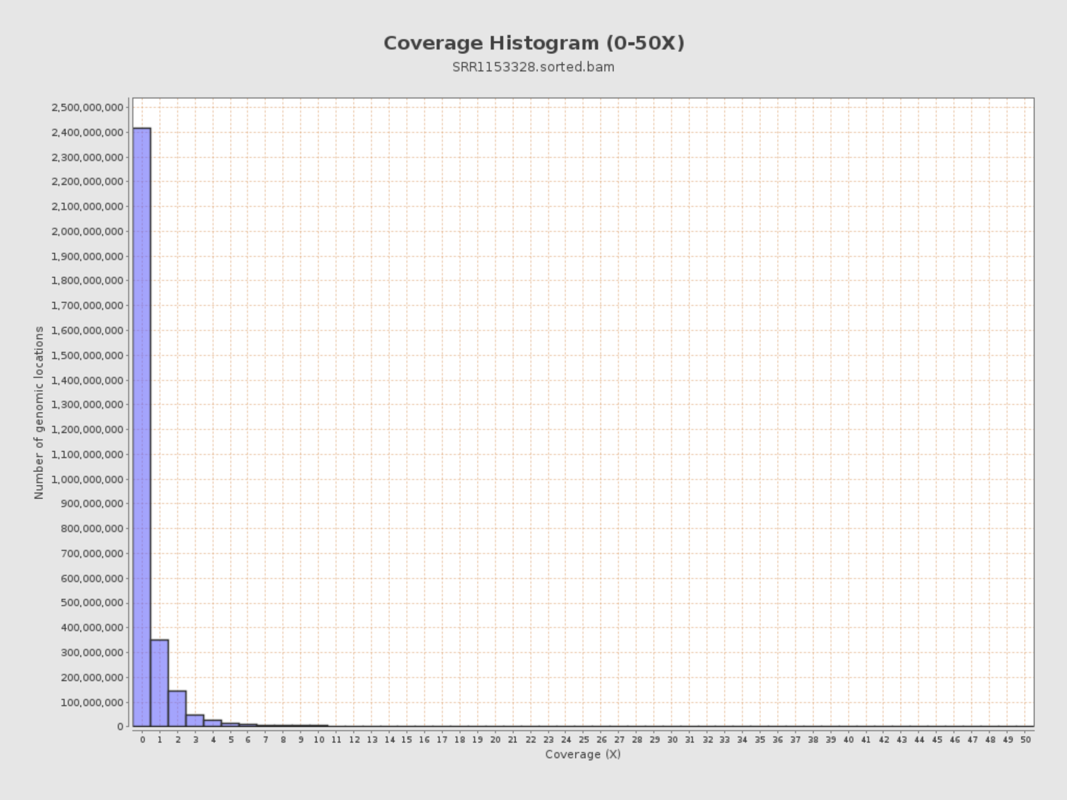
3. Results : Coverage across reference



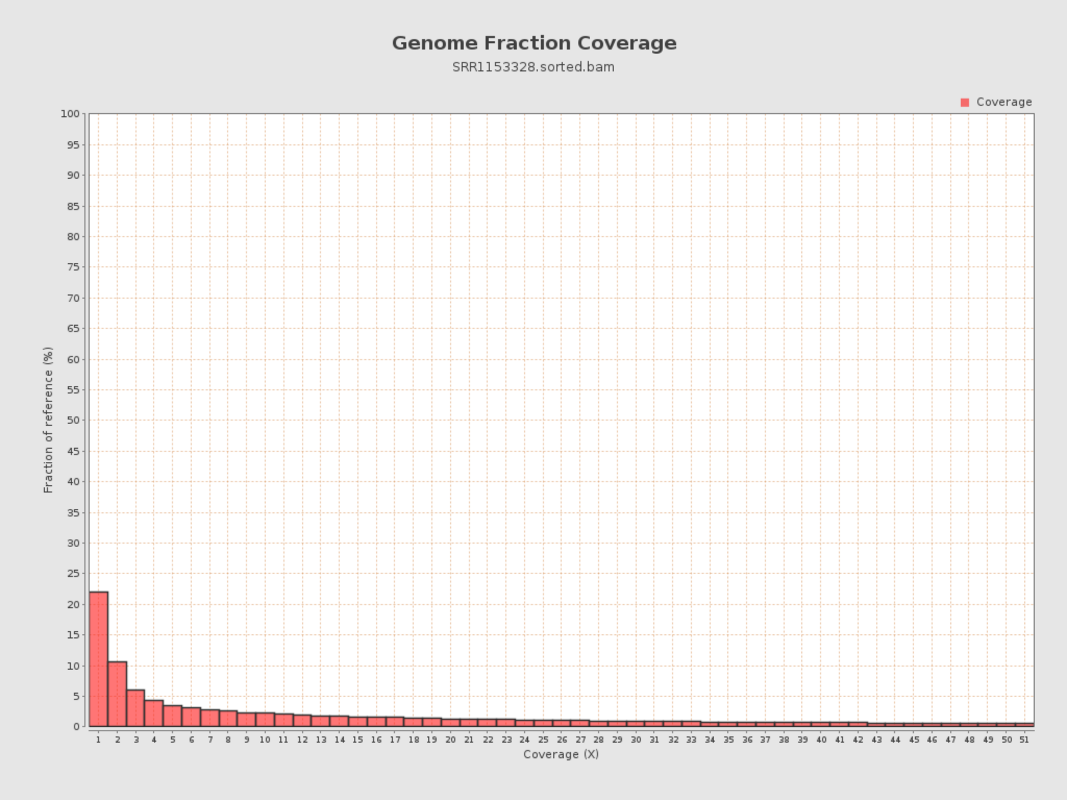
4. Results : Coverage Histogram



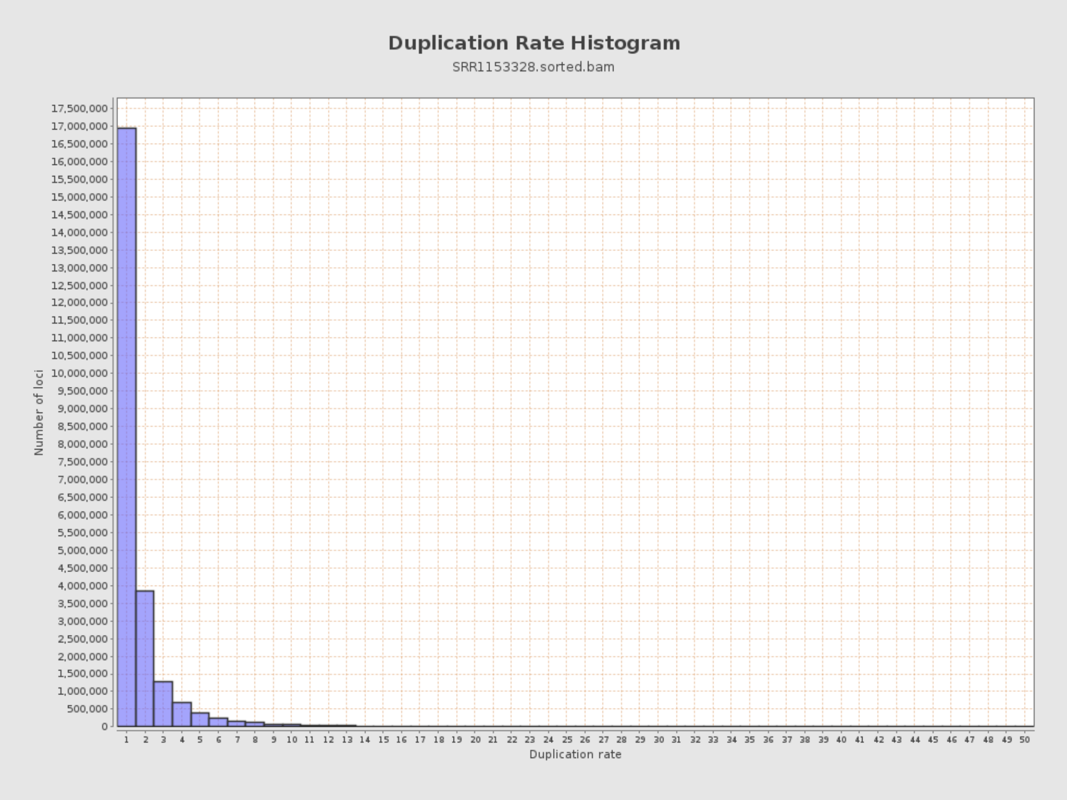
5. Results : Coverage Histogram (0-50X)



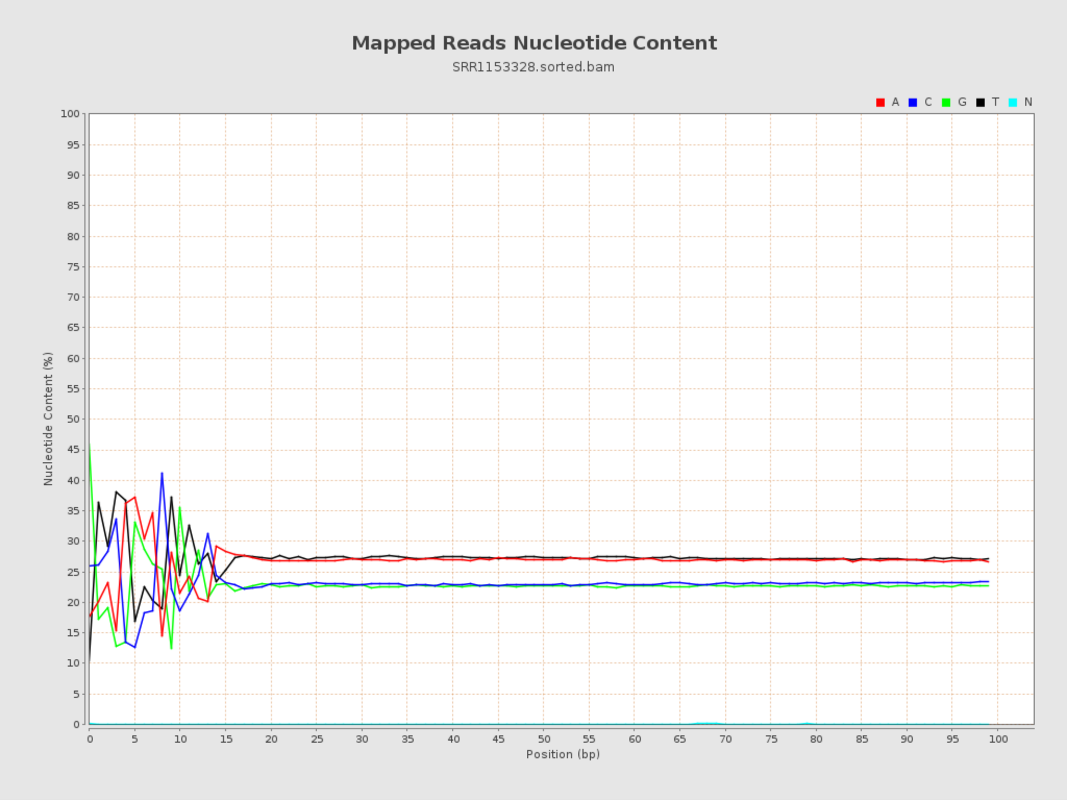
6. Results : Genome Fraction Coverage



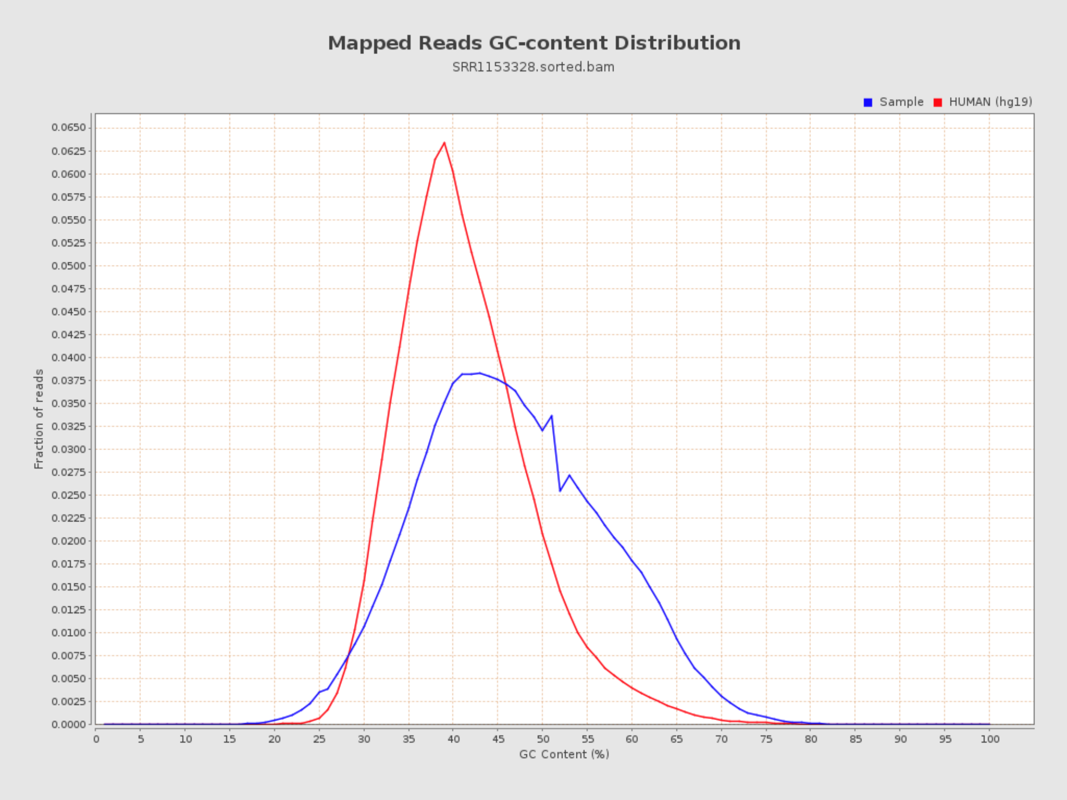
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

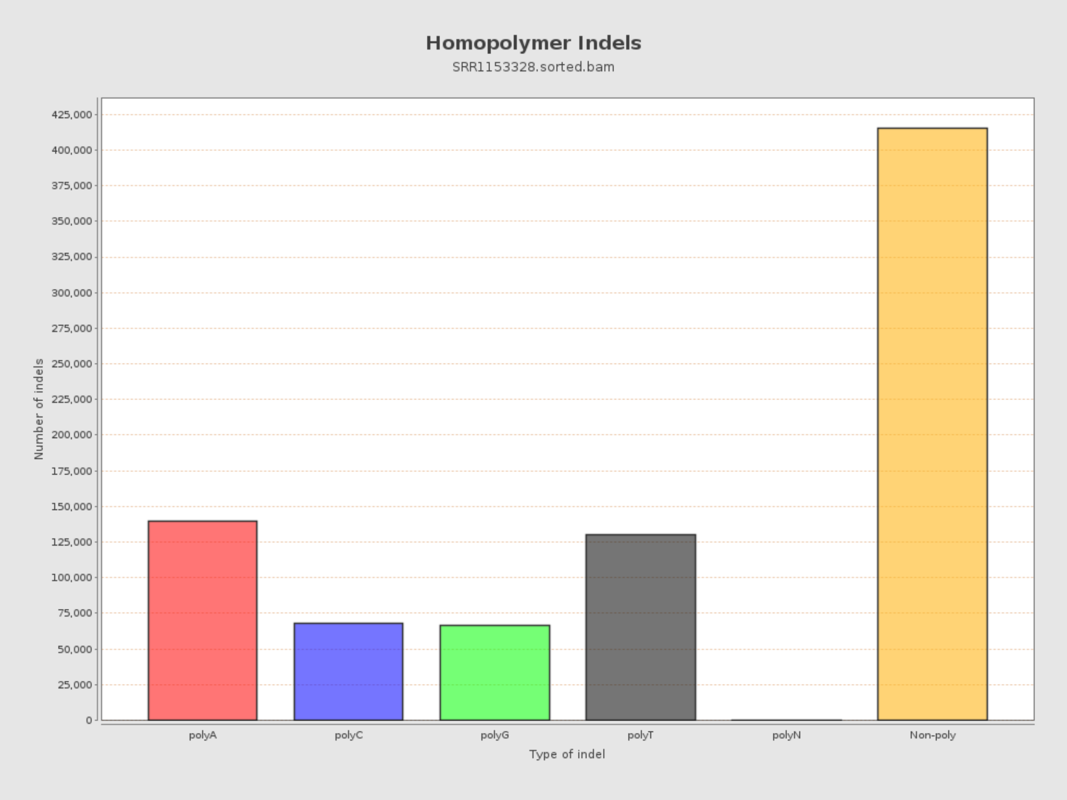


9. Results : Mapped Reads GC-content Distribution

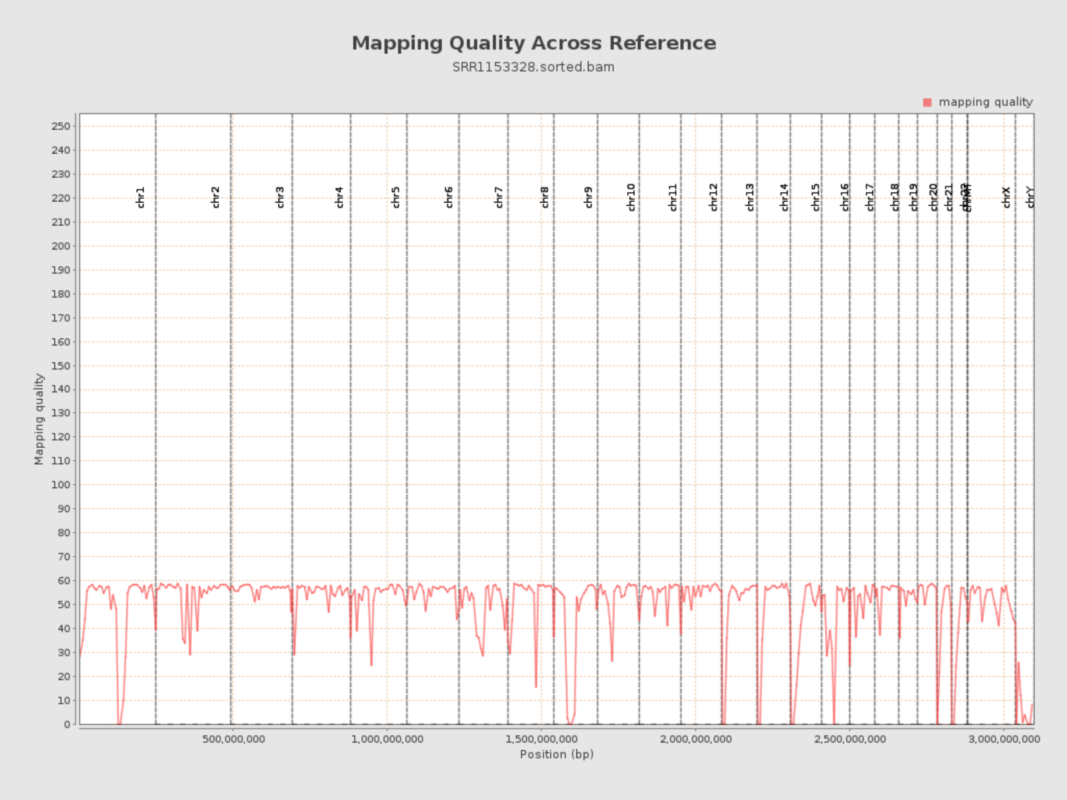


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram