Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/15 00:07:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153322.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_SRR1153322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 15 00:07:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,447,490
Mapped reads	43,842,672 / 98.64%
Unmapped reads	604,818 / 1.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	421,757 / 0.95%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	19,471,510 / 43.81%
Duplication rate	29.17%
Clipped reads	4,905,874 / 11.04%

2.2. ACGT Content

Number/percentage of A's	1,142,254,333 / 26.66%
Number/percentage of C's	994,220,746 / 23.2%
Number/percentage of T's	1,160,135,771 / 27.07%
Number/percentage of G's	986,873,382 / 23.03%
Number/percentage of N's	1,720,100 / 0.04%
GC Percentage	46.23%

2.3. Coverage

Mean	1.3845

Standard Deviation	11.7796

2.4. Mapping Quality

Mean Mapping Quality	50.17

2.5. Mismatches and indels

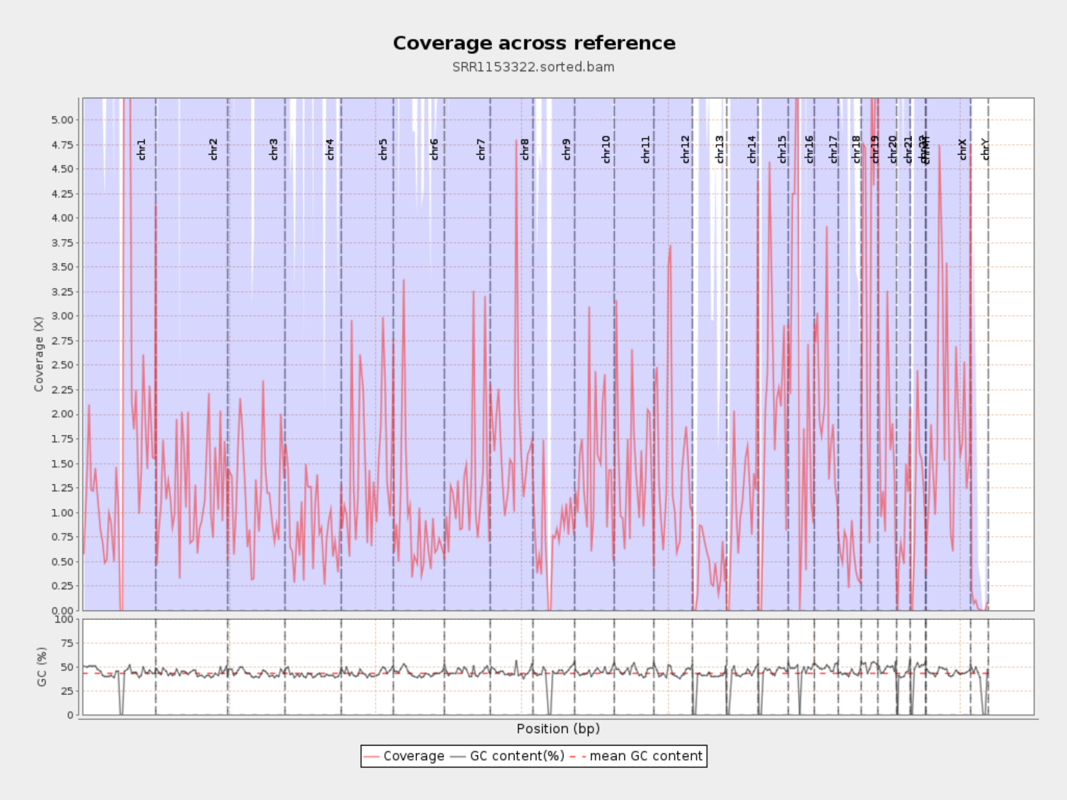
General error rate	0.35%
Mismatches	14,183,569
Insertions	485,545
Mapped reads with at least one insertion	1.09%
Deletions	377,970
Mapped reads with at least one deletion	0.85%
Homopolymer indels	49.24%

2.6. Chromosome stats

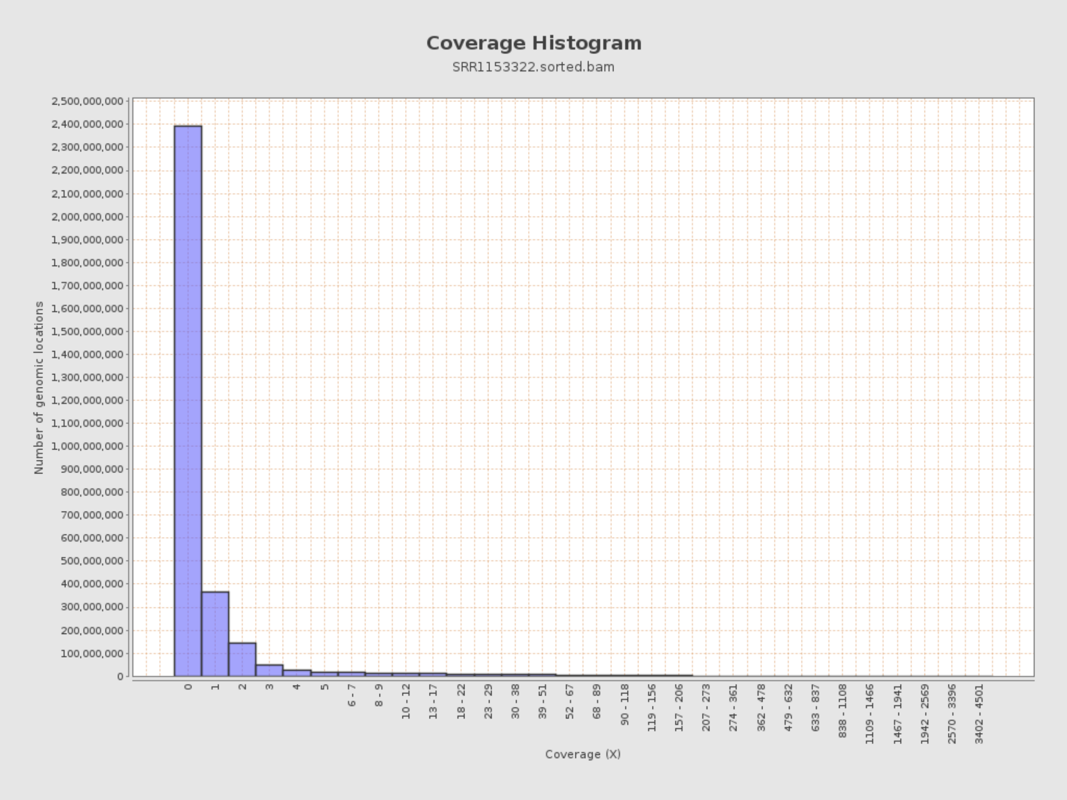
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	475502401	1.9077	17.281
chr2	243199373	297843776	1.2247	8.8766
chr3	198022430	232318887	1.1732	8.5682
chr4	191154276	163580809	0.8558	6.821
chr5	180915260	268626205	1.4848	12.3753
chr6	171115067	146713786	0.8574	7.0863
chr7	159138663	201055703	1.2634	10.2552

chr8	146364022	256054949	1.7494	18.0999
chr9	141213431	105019884	0.7437	6.1277
chr10	135534747	203064137	1.4982	10.1916
chr11	135006516	198774641	1.4723	9.9571
chr12	133851895	210645271	1.5737	11.4677
chr13	115169878	49299894	0.4281	3.8723
chr14	107349540	117365868	1.0933	8.5618
chr15	102531392	197099658	1.9223	13.4358
chr16	90354753	206193039	2.282	17.7724
chr17	81195210	171491868	2.1121	13.0749
chr18	78077248	43194885	0.5532	5.0164
chr19	59128983	233631795	3.9512	23.5373
chr20	63025520	100528881	1.5951	10.8238
chr21	48129895	43501841	0.9038	9.2568
chr22	51304566	58948953	1.149	8.9013
chrMT	16571	6093	0.3677	0.9503
chrX	155270560	302312634	1.947	15.8474
chrY	59373566	3241737	0.0546	1.8706

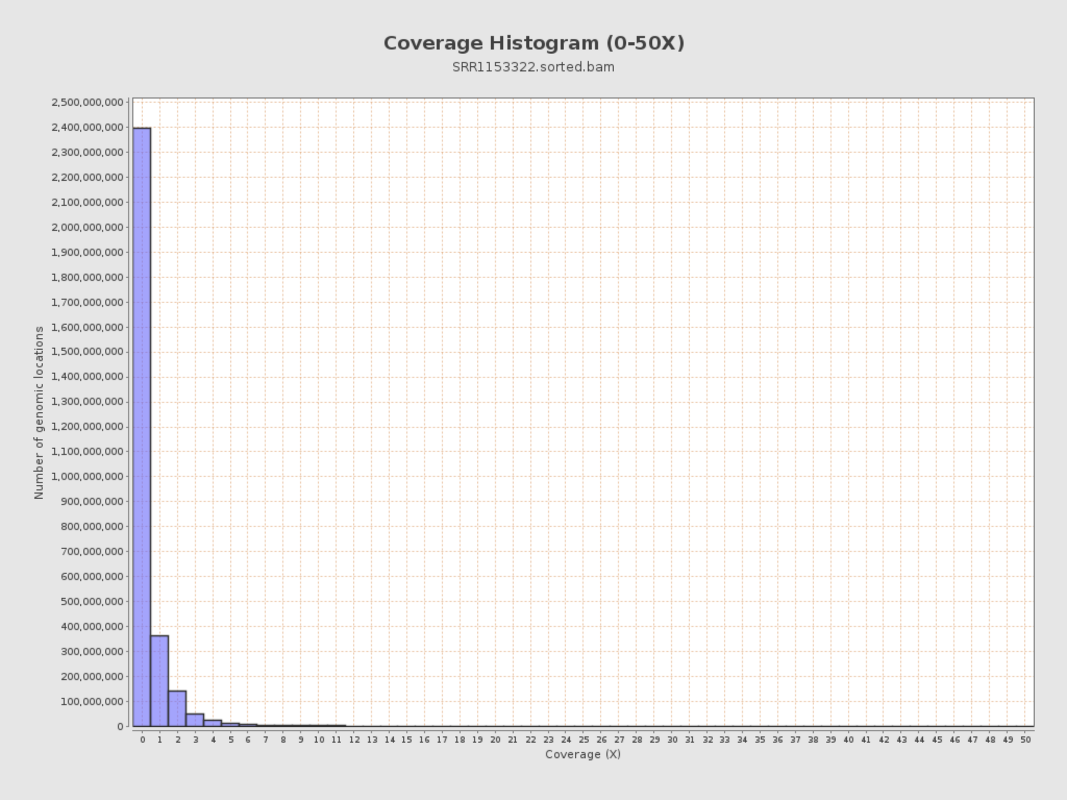
3. Results : Coverage across reference



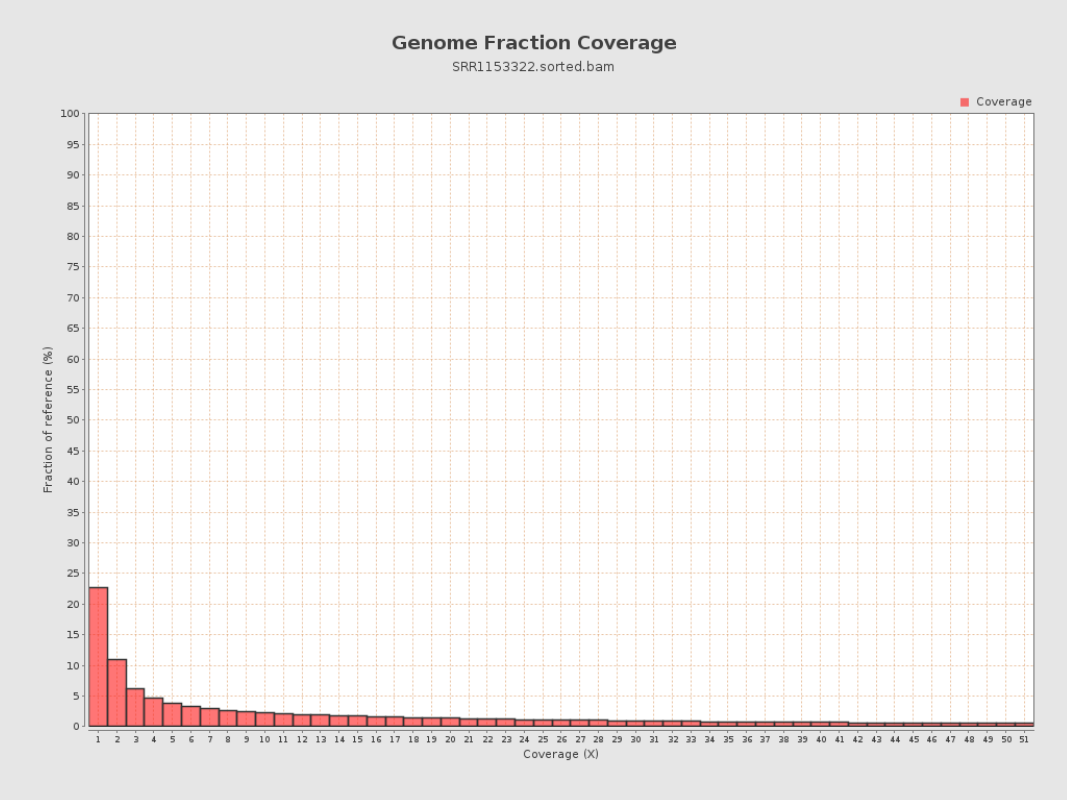
4. Results : Coverage Histogram



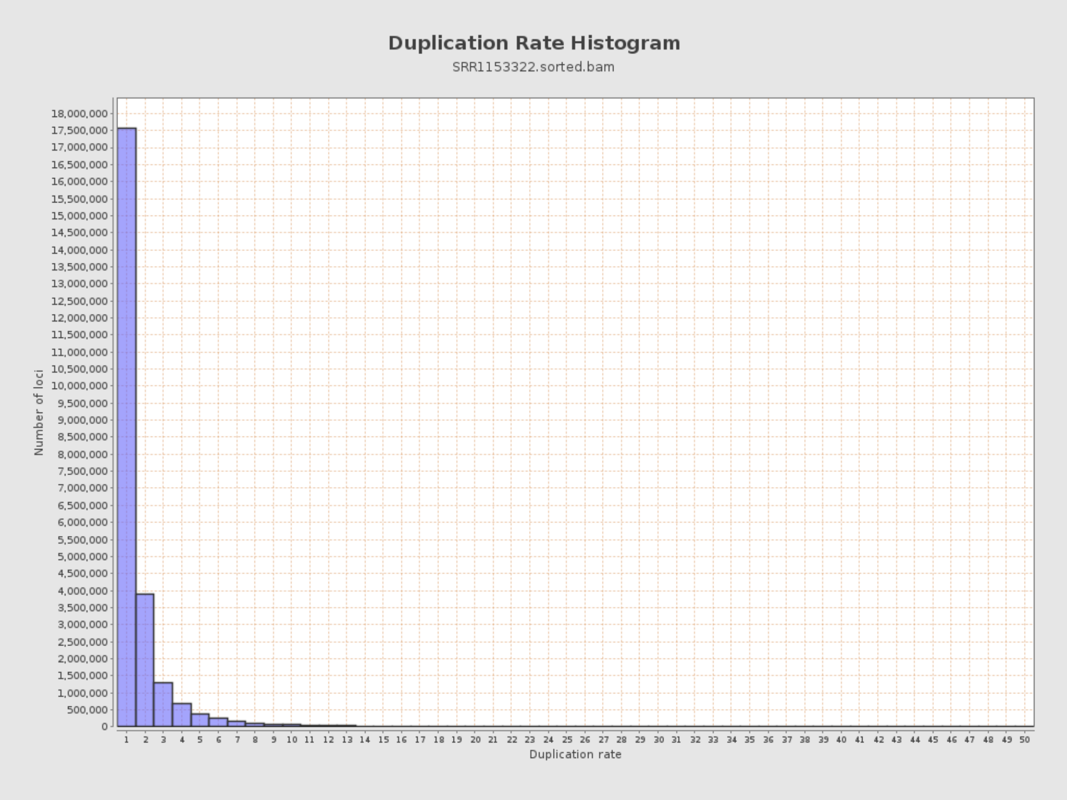
5. Results : Coverage Histogram (0-50X)



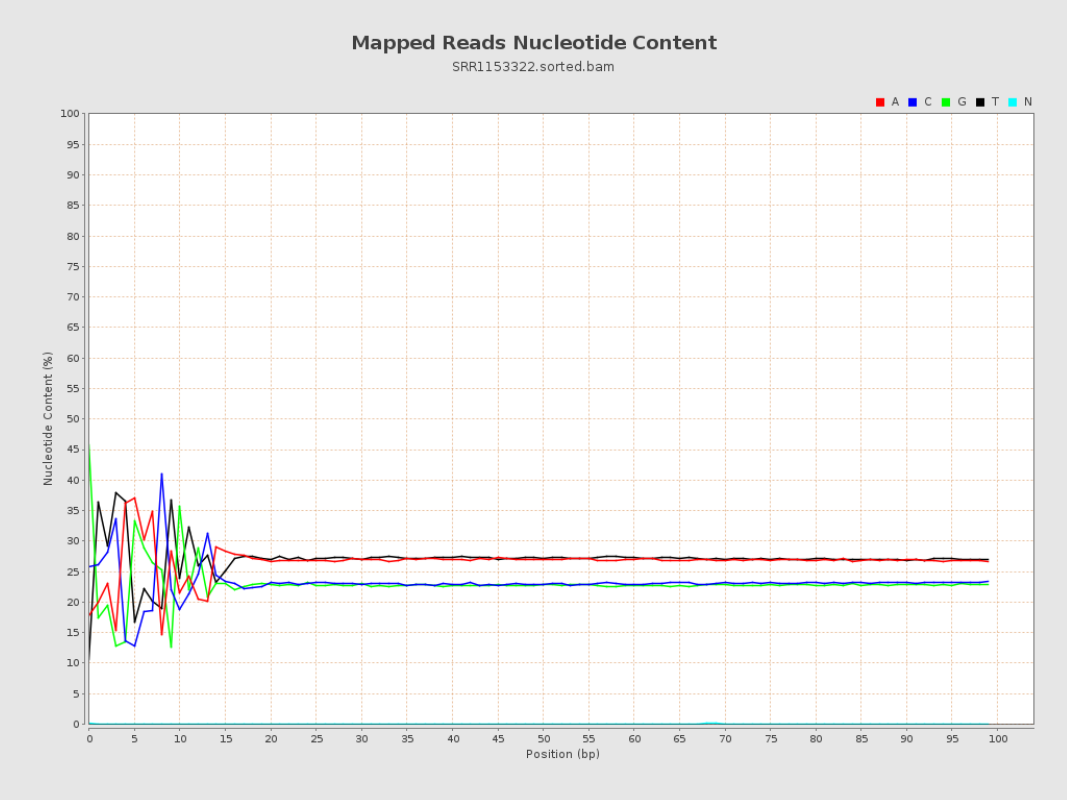
6. Results : Genome Fraction Coverage



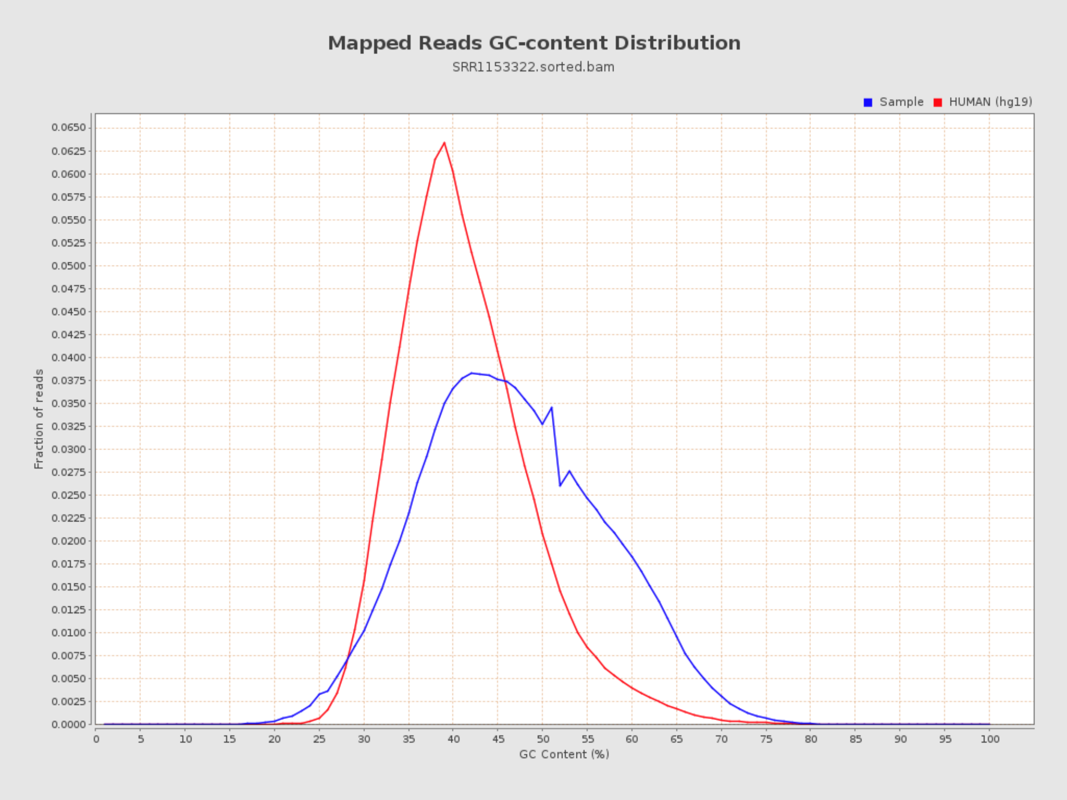
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

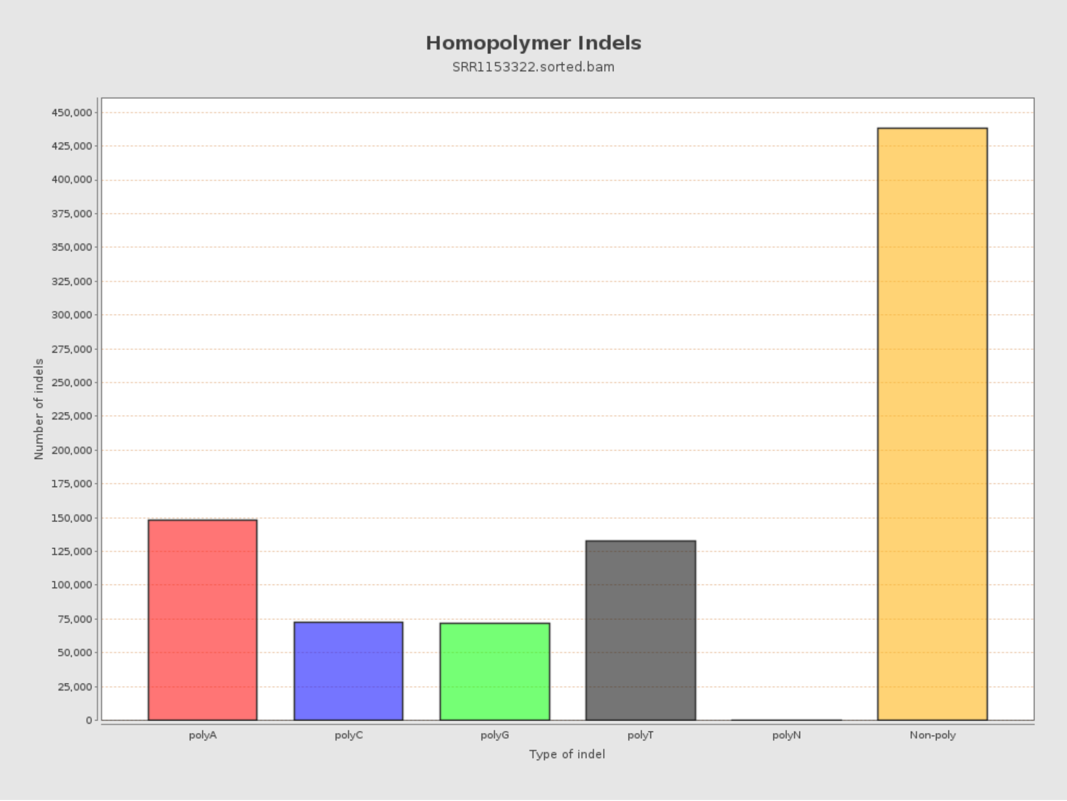


9. Results : Mapped Reads GC-content Distribution

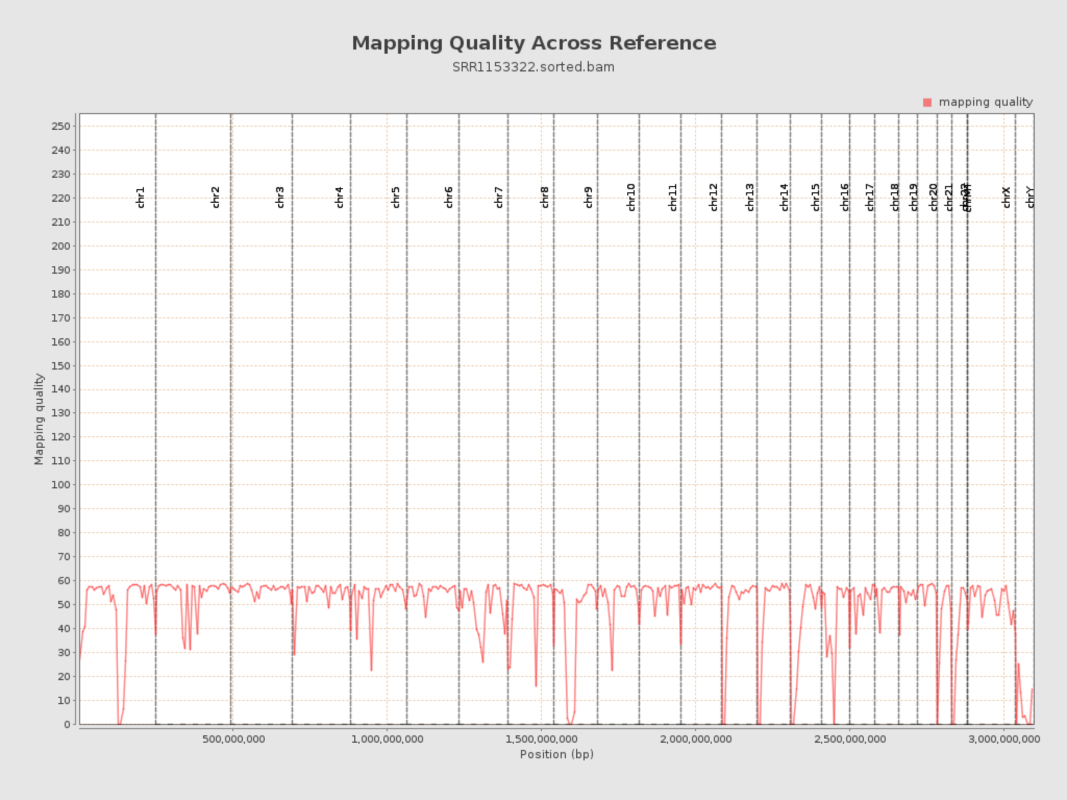


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram