Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 07:31:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153353.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_SRR1153353 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153353.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 07:31:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153353.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,343,454
Mapped reads	63,756,015 / 99.09%
Unmapped reads	587,439 / 0.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	574,195 / 0.89%
Read min/max/mean length	30 / 100 / 100.37
Duplicated reads (estimated)	34,303,506 / 53.31%
Duplication rate	34.73%
Clipped reads	8,293,800 / 12.89%

2.2. ACGT Content

Number/percentage of A's	1,600,063,429 / 25.8%
Number/percentage of C's	1,493,442,712 / 24.08%
Number/percentage of T's	1,631,442,870 / 26.31%
Number/percentage of G's	1,475,209,747 / 23.79%
Number/percentage of N's	1,757,953 / 0.03%
GC Percentage	47.87%

2.3. Coverage

Mean	2.0038

Standard Deviation	20.0299

2.4. Mapping Quality

Mean Mapping Quality	50.43

2.5. Mismatches and indels

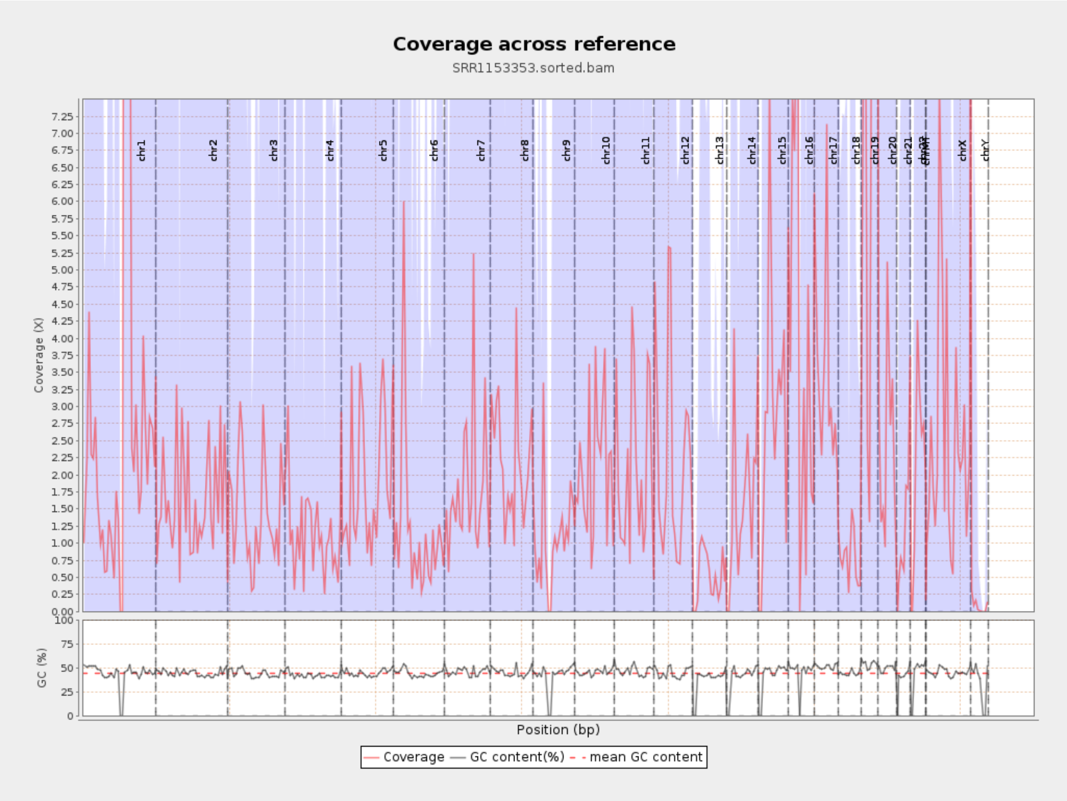
General error rate	0.36%
Mismatches	20,981,845
Insertions	737,834
Mapped reads with at least one insertion	1.14%
Deletions	525,642
Mapped reads with at least one deletion	0.81%
Homopolymer indels	49.01%

2.6. Chromosome stats

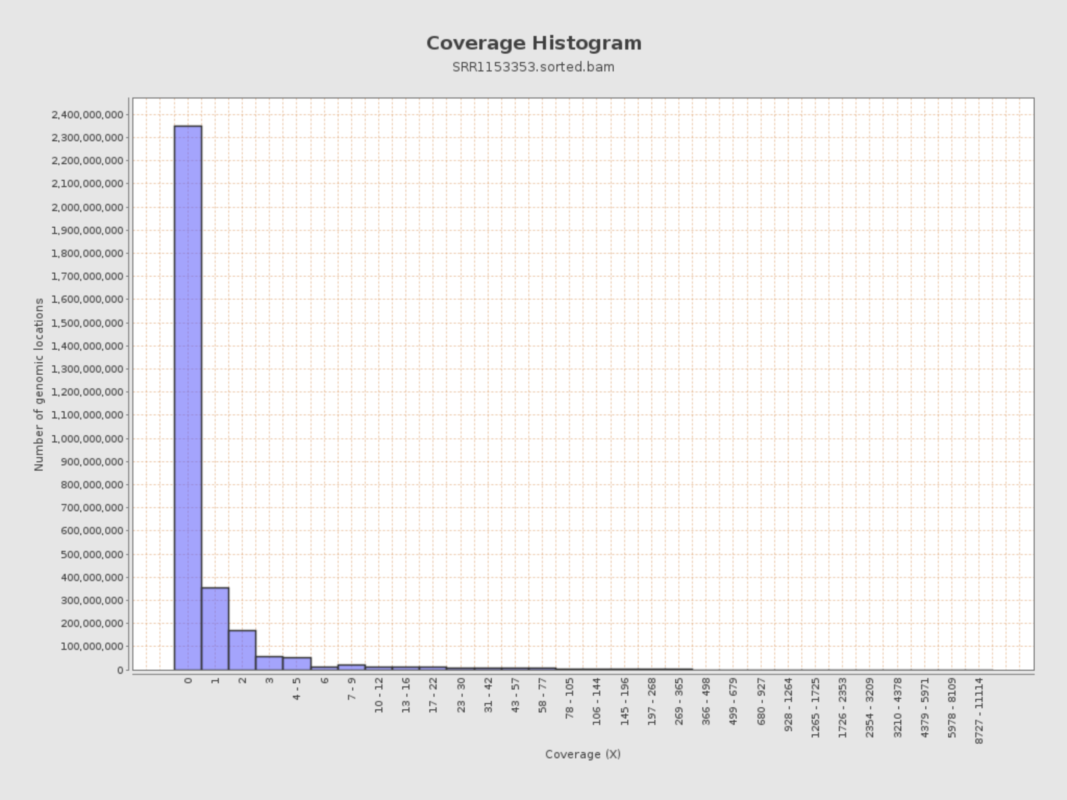
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	770102146	3.0897	37.7792
chr2	243199373	400571587	1.6471	13.3826
chr3	198022430	286099780	1.4448	11.4943
chr4	191154276	218018972	1.1405	11.0898
chr5	180915260	346531599	1.9154	17.1972
chr6	171115067	198992070	1.1629	12.8948
chr7	159138663	282530960	1.7754	15.0768

chr8	146364022	323470887	2.21	20.7022
chr9	141213431	147134430	1.0419	9.7701
chr10	135534747	290258658	2.1416	17.8838
chr11	135006516	281854138	2.0877	16.1653
chr12	133851895	310328125	2.3184	18.4935
chr13	115169878	60587525	0.5261	5.0815
chr14	107349540	166213096	1.5483	12.8357
chr15	102531392	277537789	2.7069	20.4566
chr16	90354753	349734157	3.8707	31.7821
chr17	81195210	286332213	3.5265	23.4016
chr18	78077248	61747334	0.7908	7.9959
chr19	59128983	411692685	6.9626	42.1299
chr20	63025520	150288467	2.3846	19.3327
chr21	48129895	60555356	1.2582	13.0322
chr22	51304566	109814942	2.1405	17.7668
chrMT	16571	2615	0.1578	0.6111
chrX	155270560	407813365	2.6265	26.9544
chrY	59373566	4800626	0.0809	3.5882

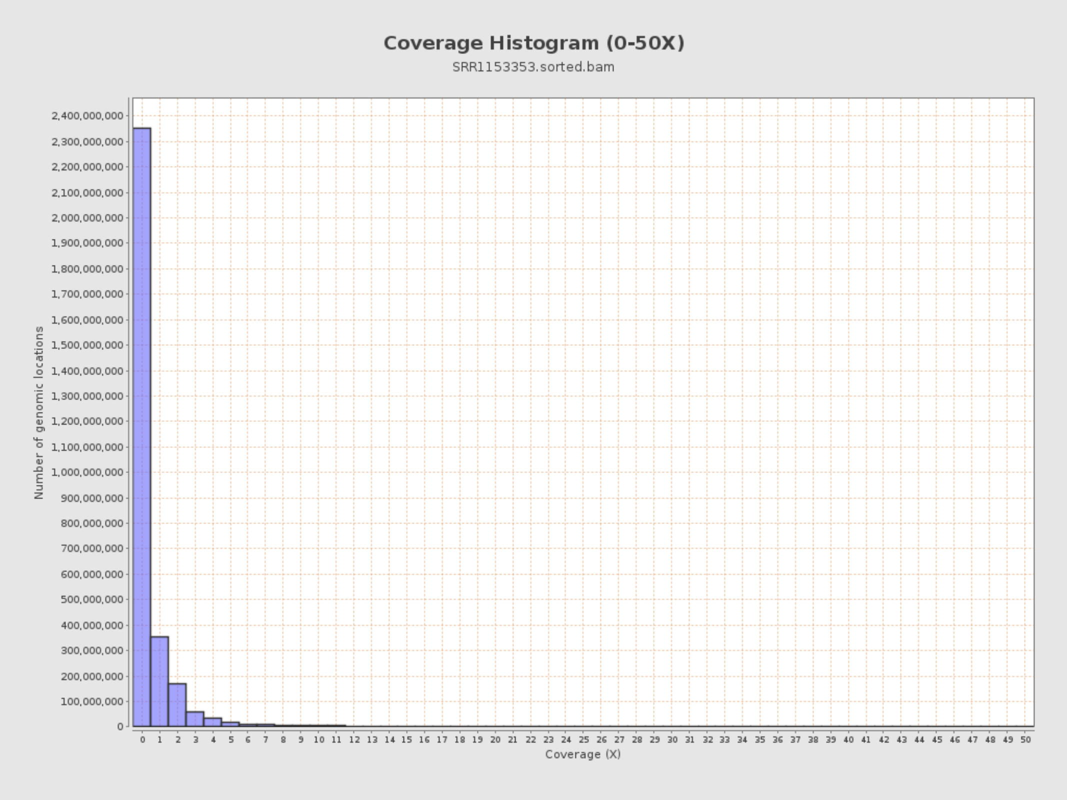
3. Results : Coverage across reference



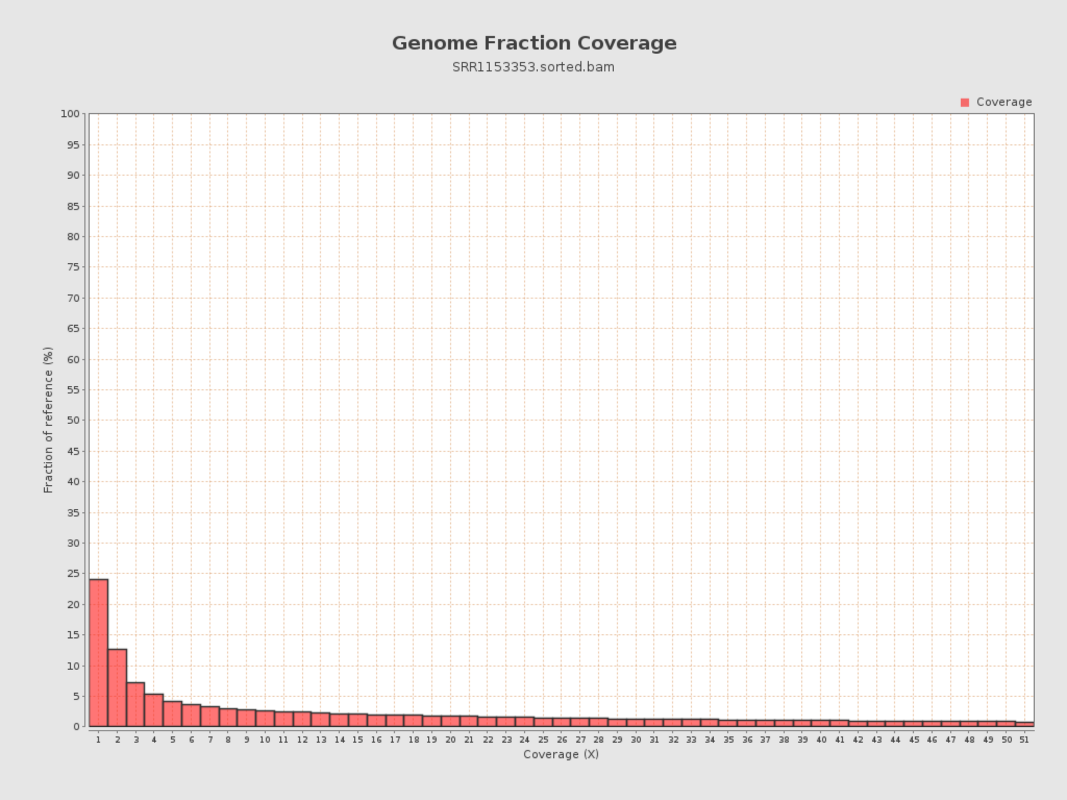
4. Results : Coverage Histogram



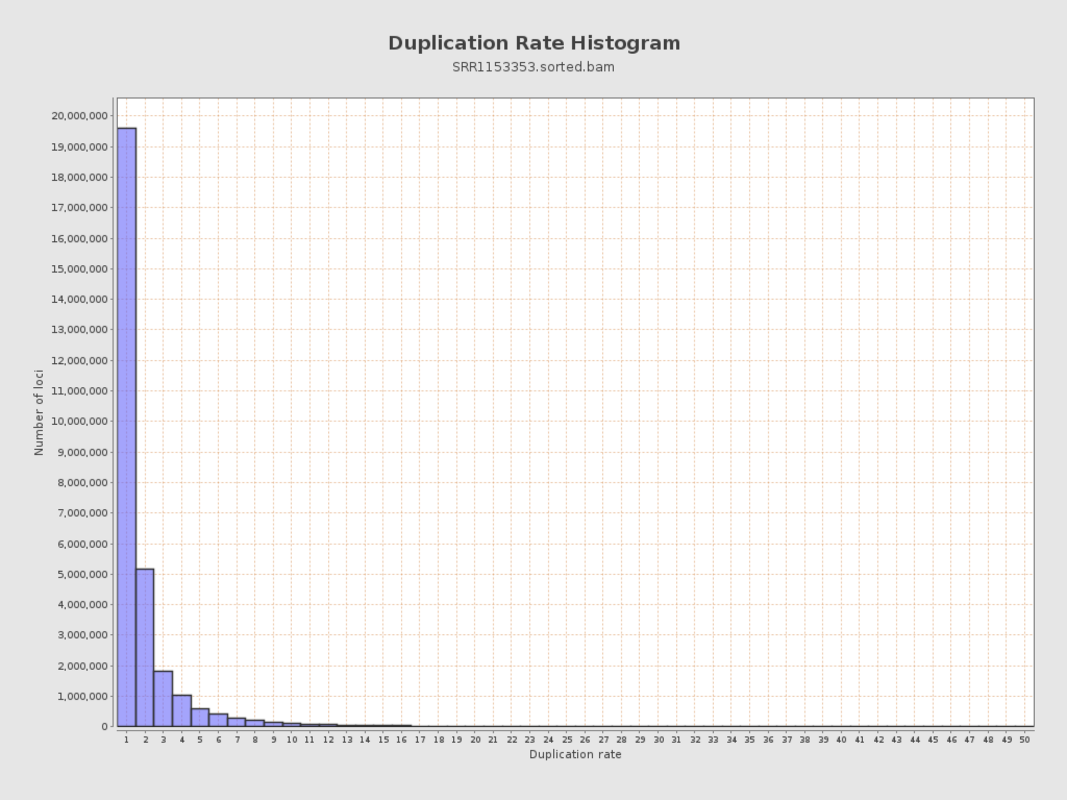
5. Results : Coverage Histogram (0-50X)



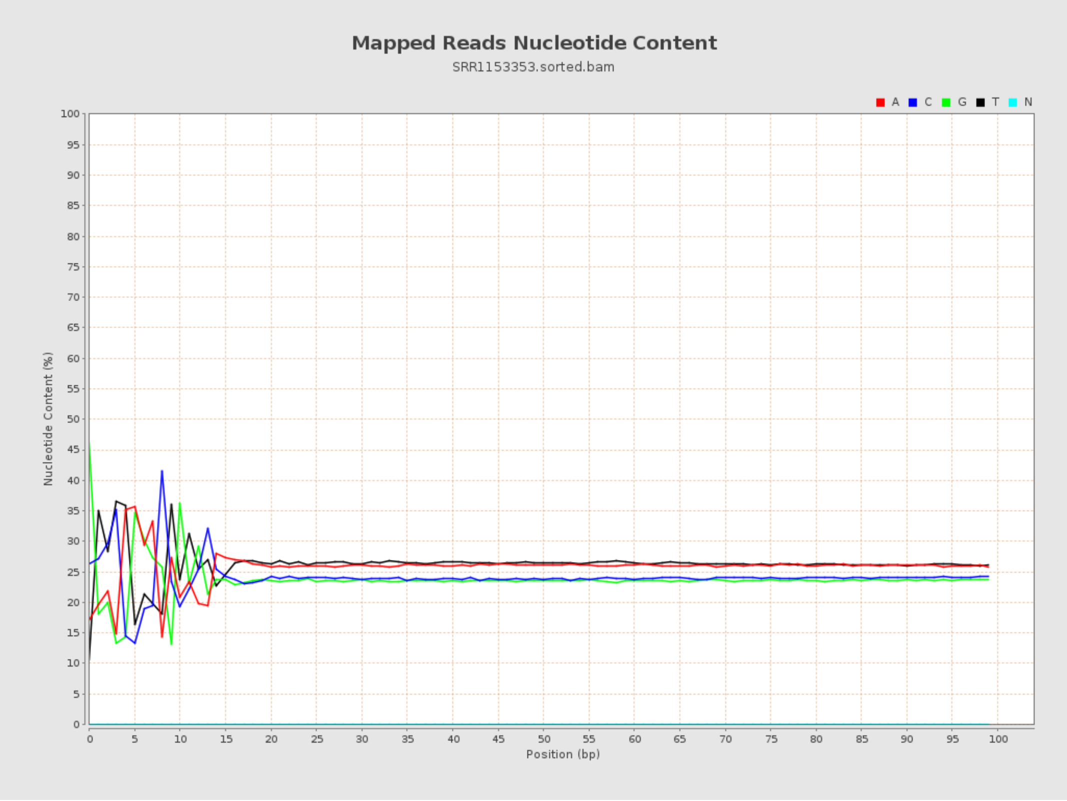
6. Results : Genome Fraction Coverage



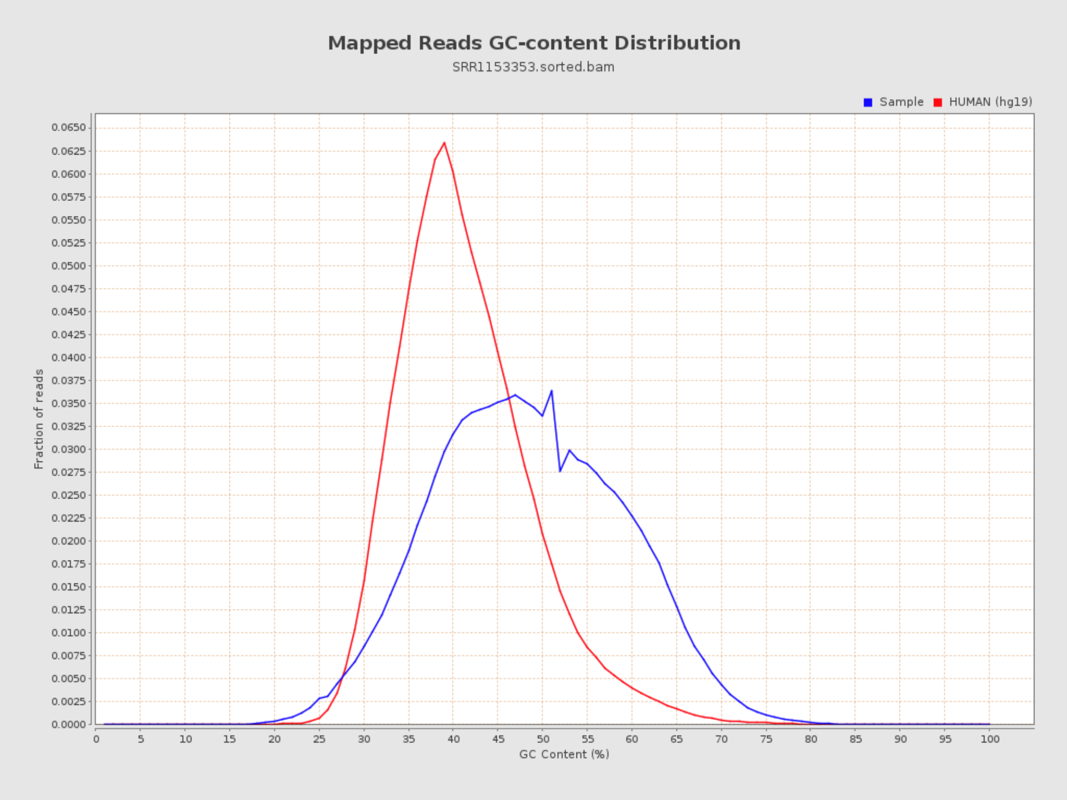
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

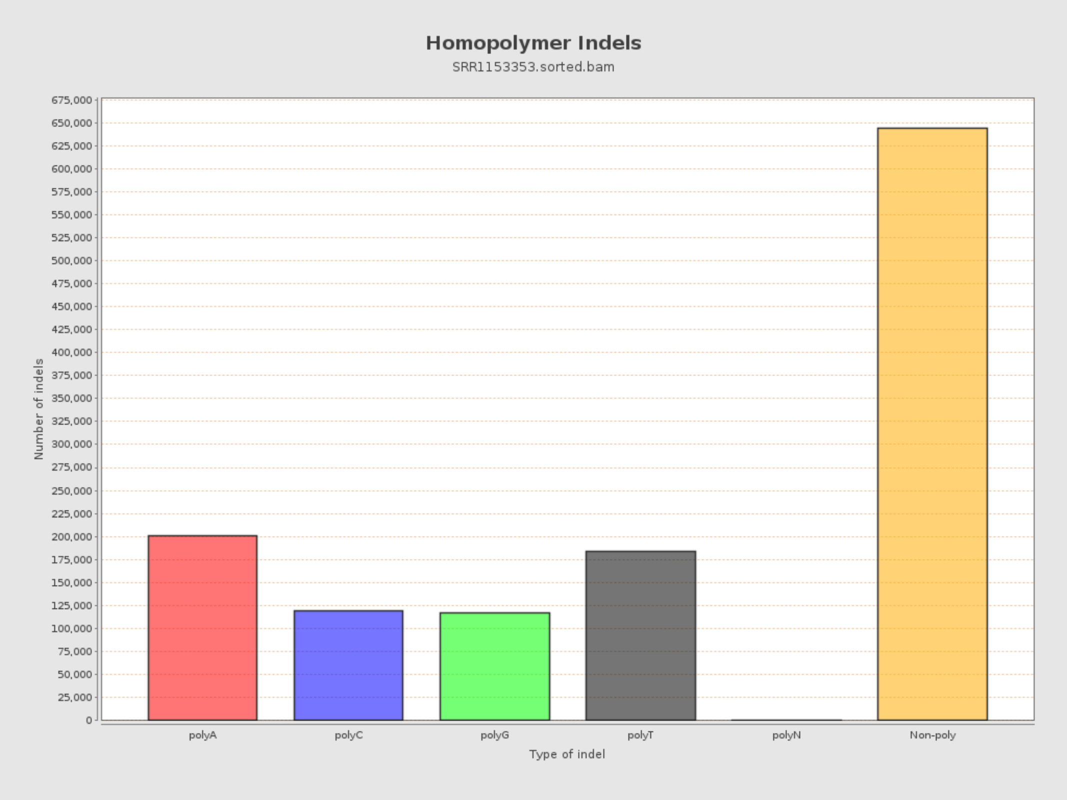


9. Results : Mapped Reads GC-content Distribution

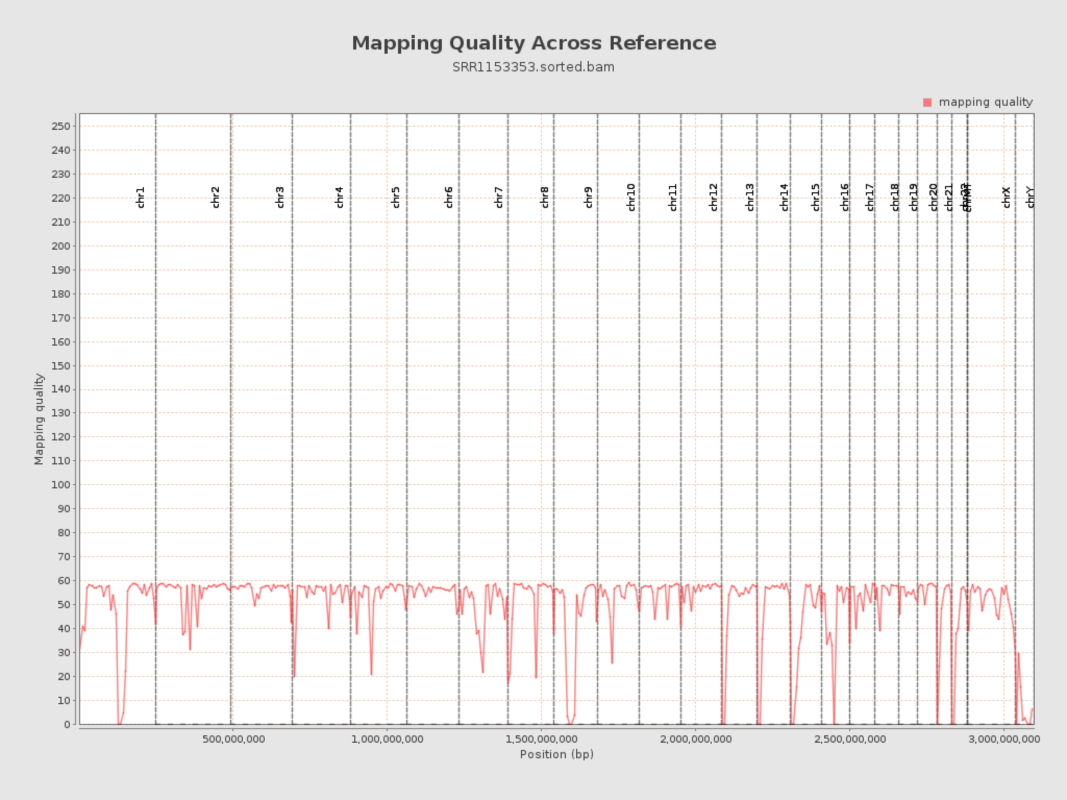


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram