Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 05:09:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153394.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_SRR1153394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153394.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 05:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,870,600
Mapped reads	44,516,209 / 99.21%
Unmapped reads	354,391 / 0.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	246,361 / 0.55%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	25,324,014 / 56.44%
Duplication rate	44.83%
Clipped reads	22,189,716 / 49.45%

2.2. ACGT Content

Number/percentage of A's	1,006,980,332 / 26.64%
Number/percentage of C's	891,756,020 / 23.59%
Number/percentage of T's	1,037,595,598 / 27.45%
Number/percentage of G's	842,378,652 / 22.28%
Number/percentage of N's	1,629,148 / 0.04%
GC Percentage	45.87%

2.3. Coverage

Mean	1.2214

Standard Deviation	14.3119

2.4. Mapping Quality

Mean Mapping Quality	49.74

2.5. Mismatches and indels

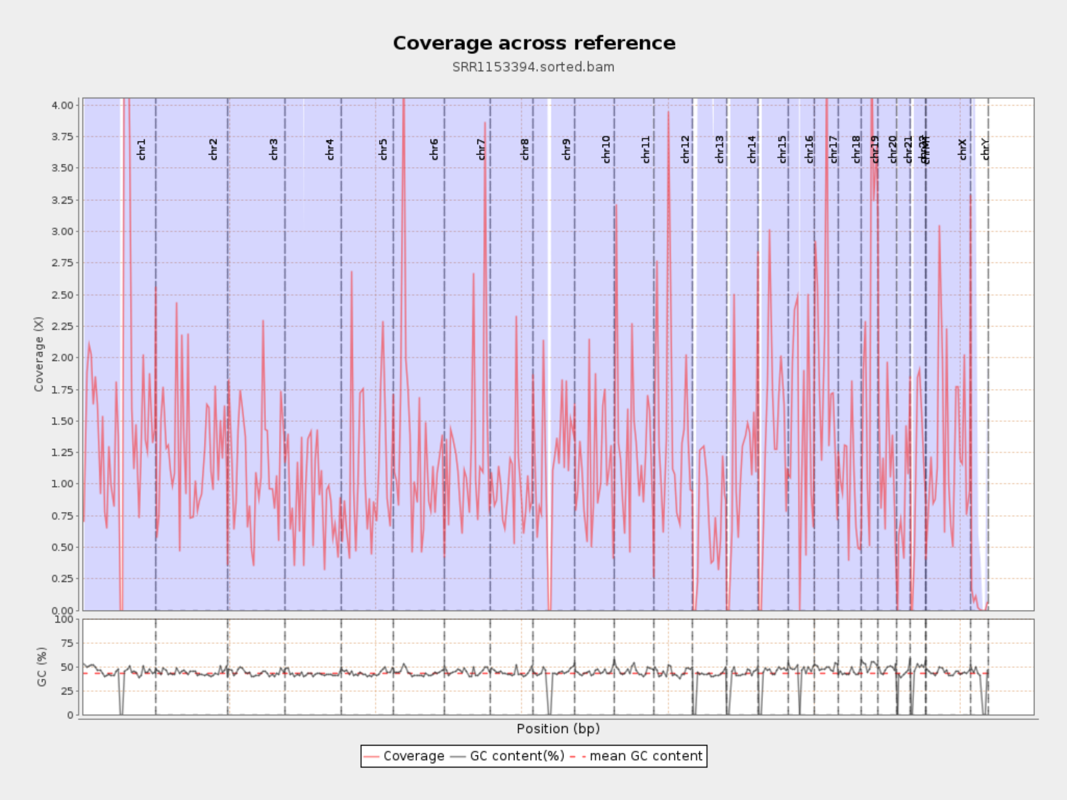
General error rate	0.24%
Mismatches	8,529,018
Insertions	389,368
Mapped reads with at least one insertion	0.87%
Deletions	334,807
Mapped reads with at least one deletion	0.74%
Homopolymer indels	49.54%

2.6. Chromosome stats

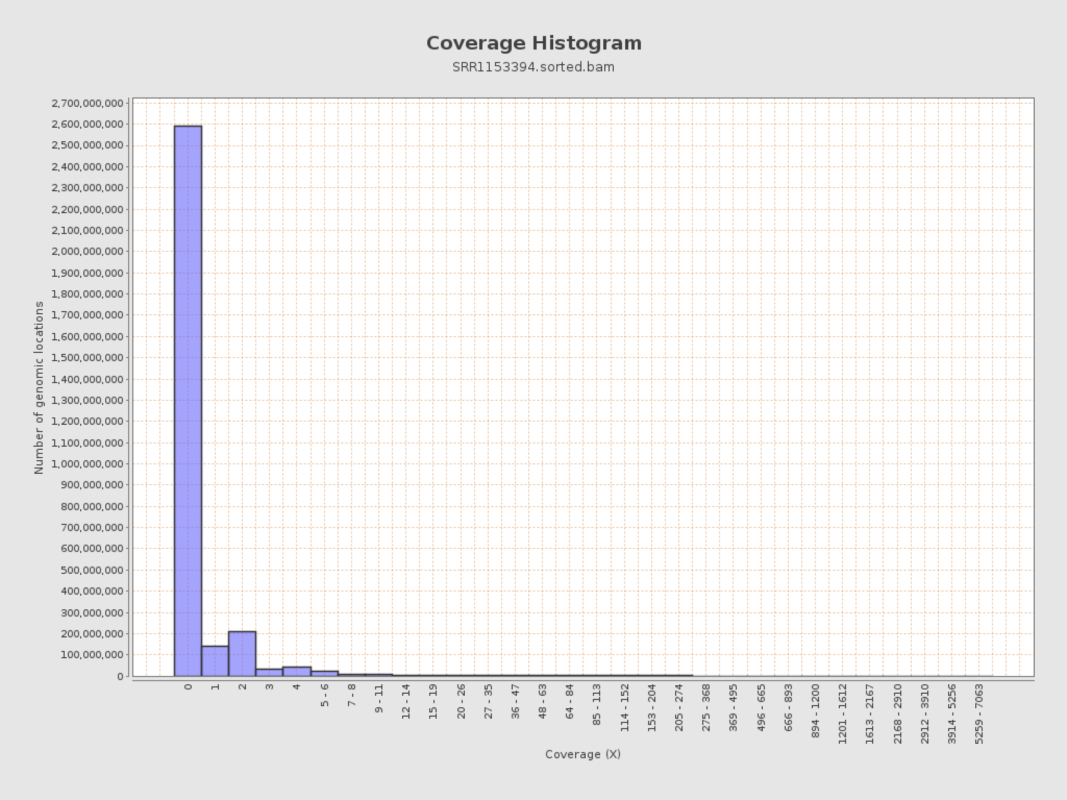
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	404670924	1.6236	17.8467
chr2	243199373	304560876	1.2523	14.3021
chr3	198022430	224911178	1.1358	12.4863
chr4	191154276	172445048	0.9021	10.129
chr5	180915260	200298453	1.1071	13.091
chr6	171115067	217561405	1.2714	14.6316
chr7	159138663	201624505	1.267	17.8749

chr8	146364022	144130201	0.9847	11.8611
chr9	141213431	160708610	1.1381	13.4256
chr10	135534747	152492371	1.1251	11.9852
chr11	135006516	176897601	1.3103	13.8345
chr12	133851895	203237051	1.5184	17.9589
chr13	115169878	81659913	0.709	8.9044
chr14	107349540	118688190	1.1056	13.7981
chr15	102531392	135721585	1.3237	13.6634
chr16	90354753	124969244	1.3831	14.7063
chr17	81195210	164771308	2.0293	18.6264
chr18	78077248	76893381	0.9848	12.3597
chr19	59128983	140967483	2.3841	23.3132
chr20	63025520	71201628	1.1297	12.0525
chr21	48129895	41974997	0.8721	15.0396
chr22	51304566	55362481	1.0791	11.6598
chrMT	16571	6684	0.4034	1.5249
chrX	155270560	202183111	1.3021	14.6402
chrY	59373566	3091321	0.0521	2.3679

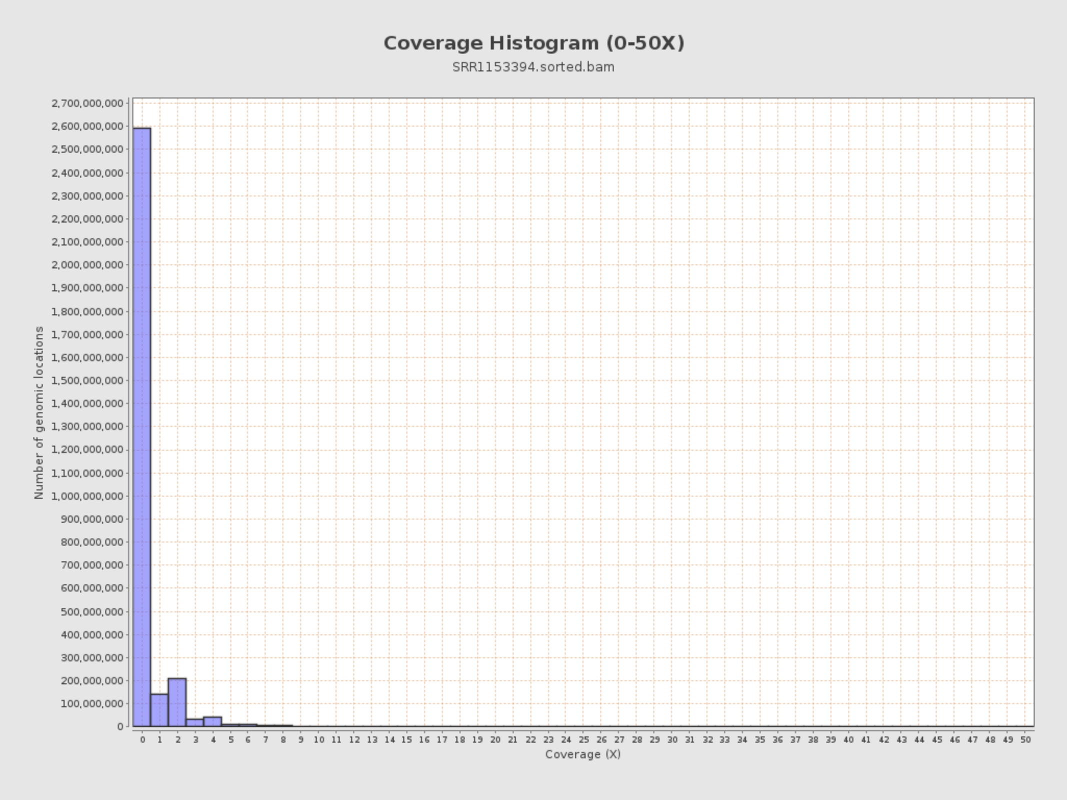
3. Results : Coverage across reference



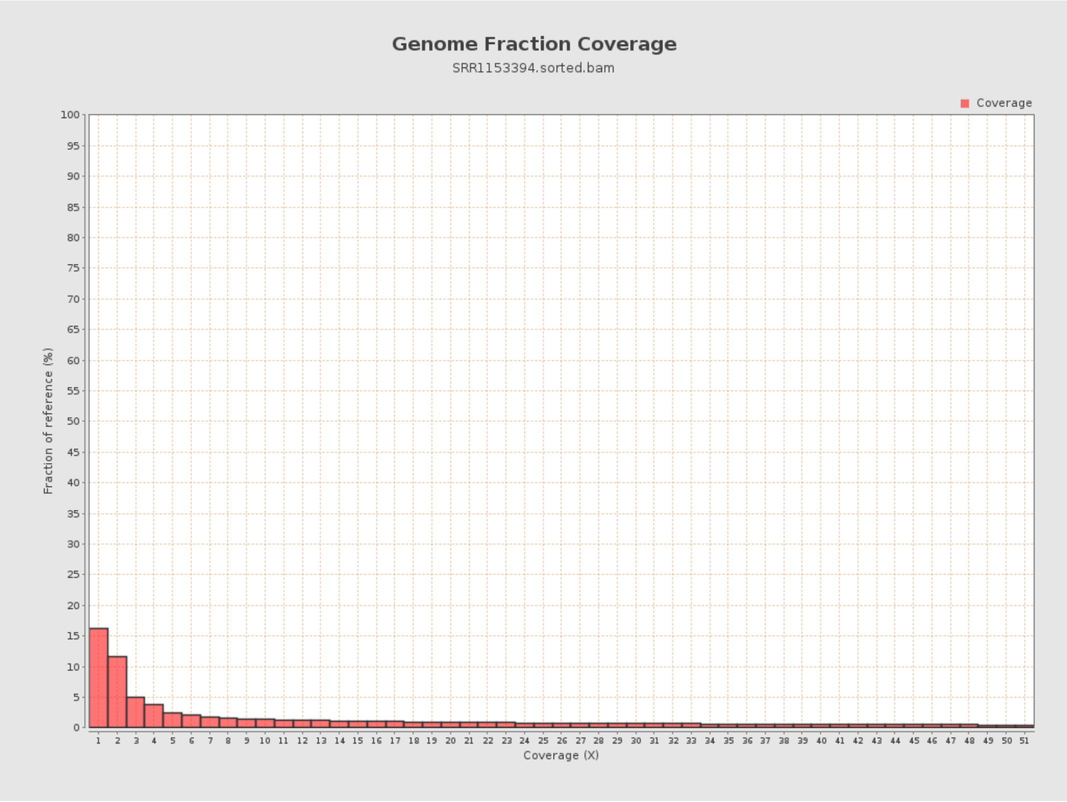
4. Results : Coverage Histogram



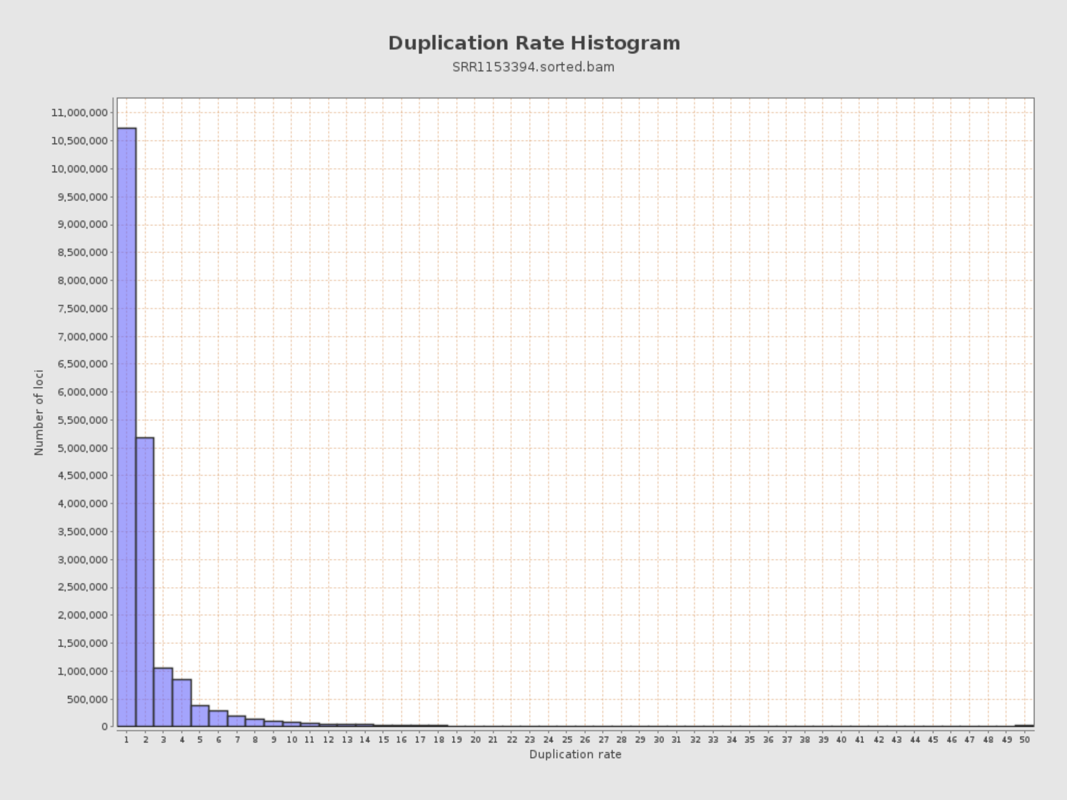
5. Results : Coverage Histogram (0-50X)



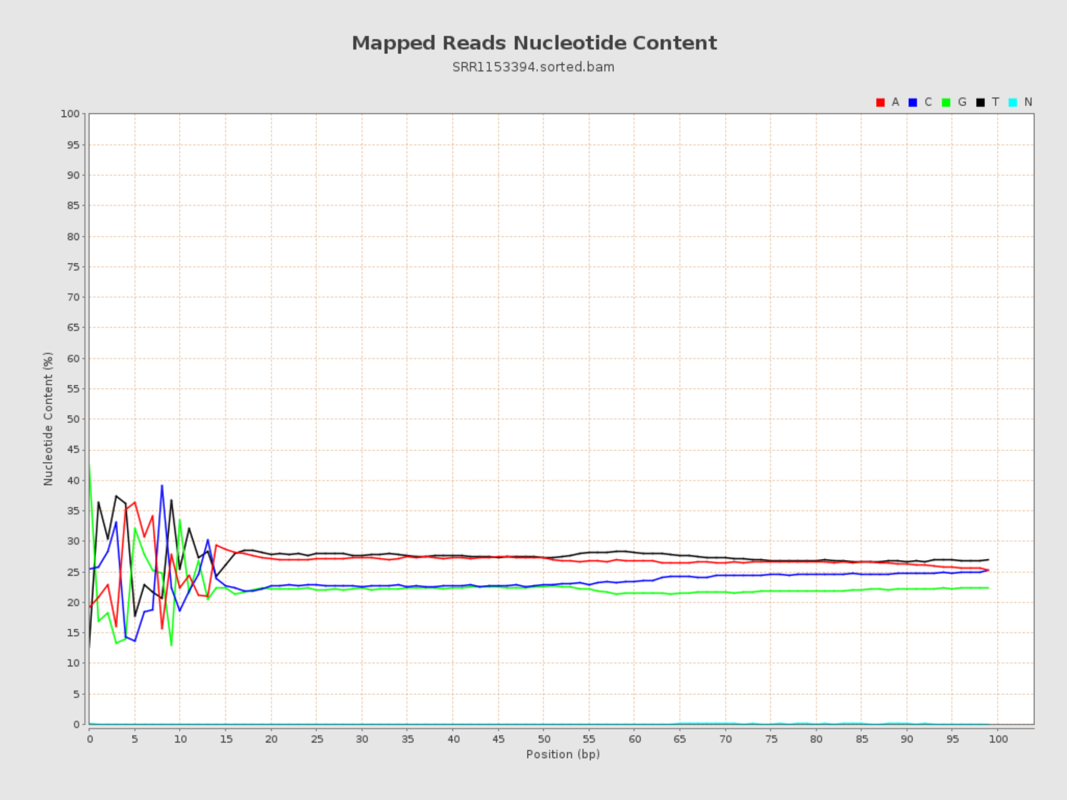
6. Results : Genome Fraction Coverage



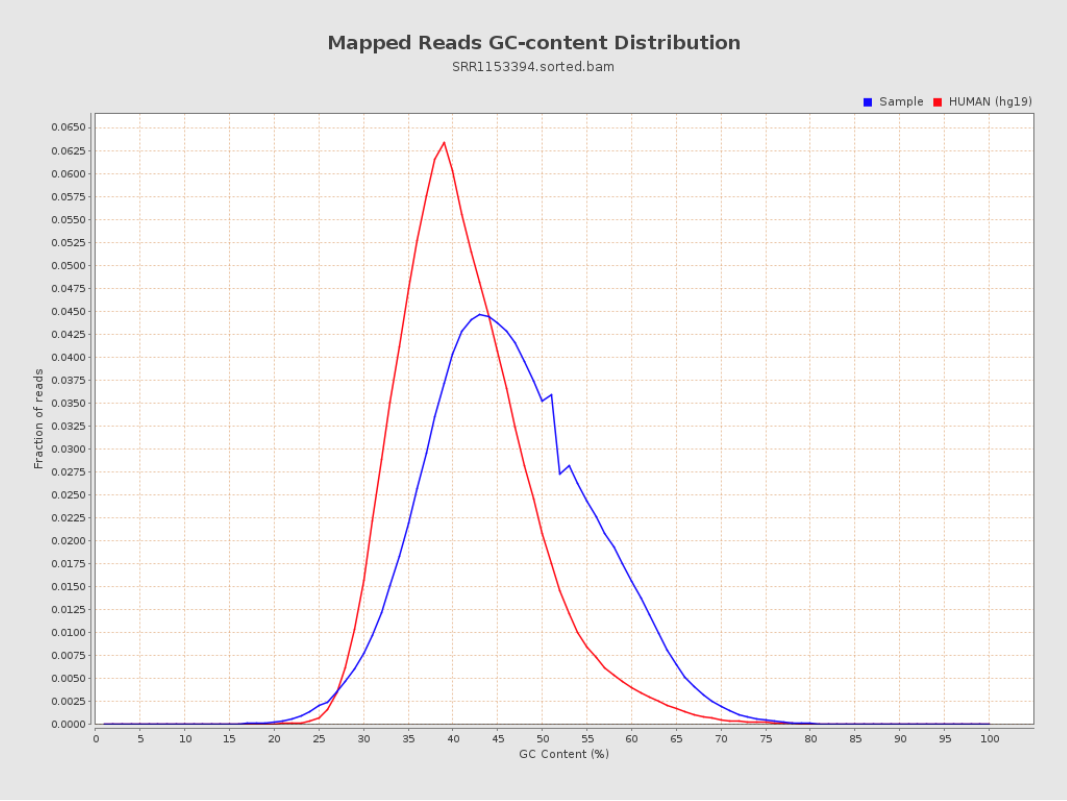
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

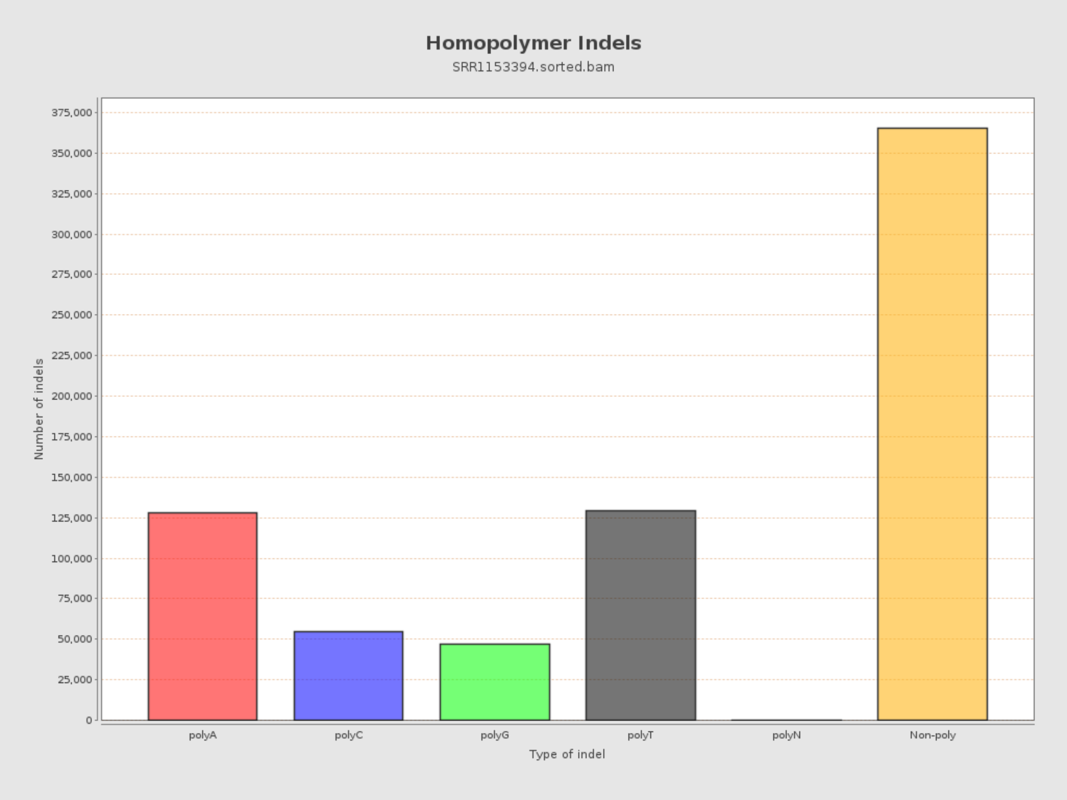


9. Results : Mapped Reads GC-content Distribution

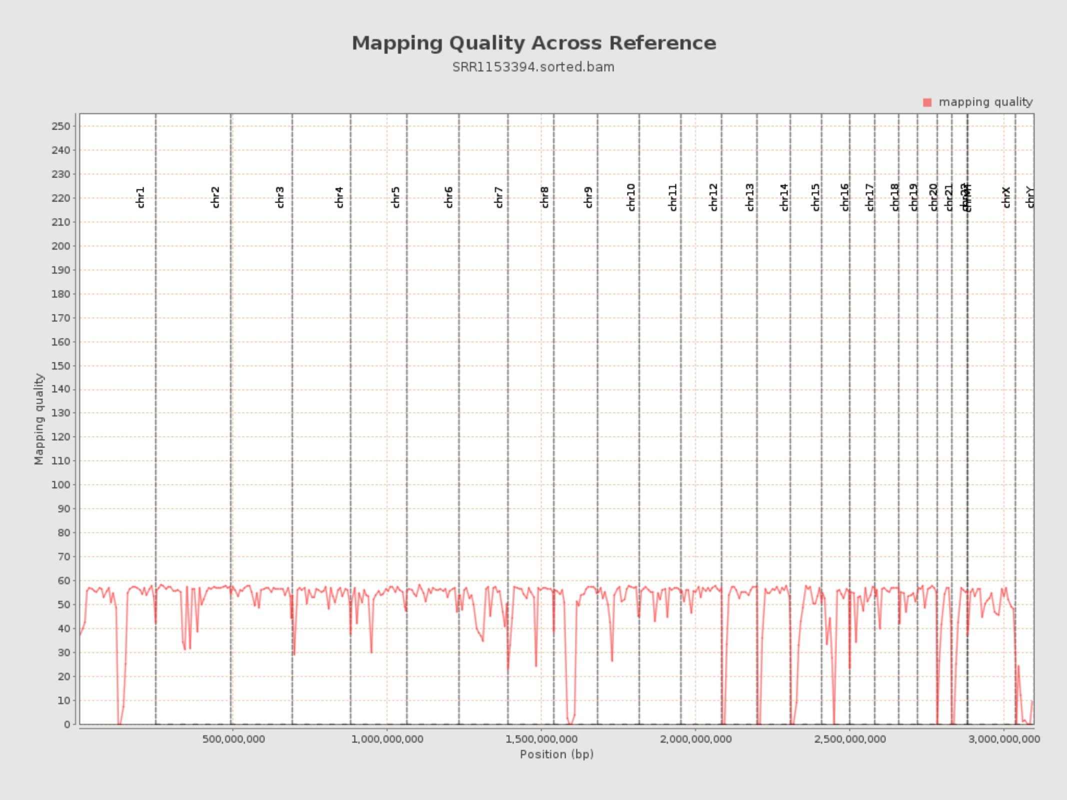


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram