Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 07:50:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153397.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_SRR1153397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153397.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 07:50:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,507,194
Mapped reads	58,983,158 / 99.12%
Unmapped reads	524,036 / 0.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	470,065 / 0.79%
Read min/max/mean length	30 / 100 / 100.32
Duplicated reads (estimated)	29,616,543 / 49.77%
Duplication rate	33.44%
Clipped reads	10,142,675 / 17.04%

2.2. ACGT Content

Number/percentage of A's	1,517,716,746 / 26.84%
Number/percentage of C's	1,303,366,342 / 23.05%
Number/percentage of T's	1,550,103,085 / 27.41%
Number/percentage of G's	1,280,825,306 / 22.65%
Number/percentage of N's	2,484,621 / 0.04%
GC Percentage	45.7%

2.3. Coverage

Mean	1.8269

Standard Deviation	16.5078

2.4. Mapping Quality

Mean Mapping Quality	50.37

2.5. Mismatches and indels

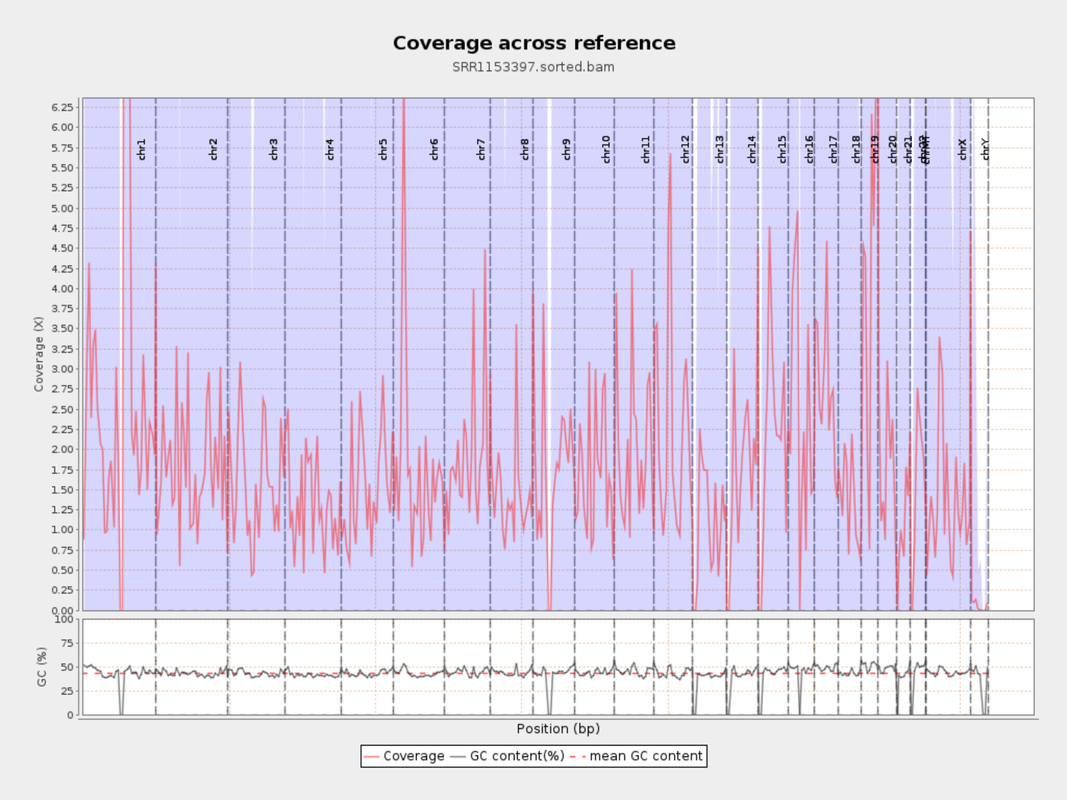
General error rate	0.31%
Mismatches	16,731,575
Insertions	611,806
Mapped reads with at least one insertion	1.03%
Deletions	500,347
Mapped reads with at least one deletion	0.84%
Homopolymer indels	49.41%

2.6. Chromosome stats

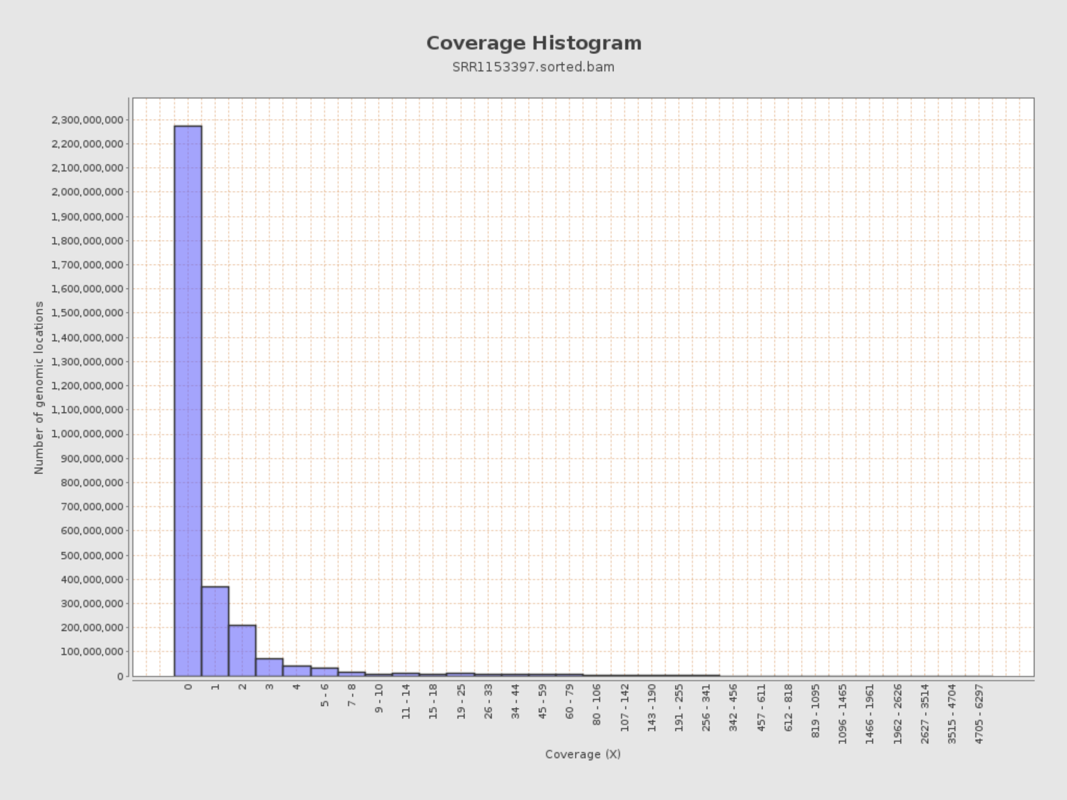
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	703624082	2.823	28.1286
chr2	243199373	437200795	1.7977	14.8617
chr3	198022430	314277184	1.5871	12.8099
chr4	191154276	258067113	1.35	11.7028
chr5	180915260	283449802	1.5668	12.9476
chr6	171115067	306115682	1.7889	15.8962
chr7	159138663	299171359	1.8799	16.8425

chr8	146364022	211185339	1.4429	13.8898
chr9	141213431	238889633	1.6917	15.0528
chr10	135534747	234421650	1.7296	14.0258
chr11	135006516	274069285	2.03	15.8192
chr12	133851895	312715861	2.3363	17.9936
chr13	115169878	125152571	1.0867	10.1904
chr14	107349540	180421559	1.6807	15.6018
chr15	102531392	212036606	2.068	17.1046
chr16	90354753	214843842	2.3778	20.4864
chr17	81195210	229473827	2.8262	18.762
chr18	78077248	109107282	1.3974	11.9585
chr19	59128983	248522742	4.2031	28.6908
chr20	63025520	111867959	1.775	14.2893
chr21	48129895	53182631	1.105	10.761
chr22	51304566	79374334	1.5471	12.9014
chrMT	16571	24721	1.4918	4.0792
chrX	155270560	214952254	1.3844	13.4631
chrY	59373566	3403485	0.0573	3.0814

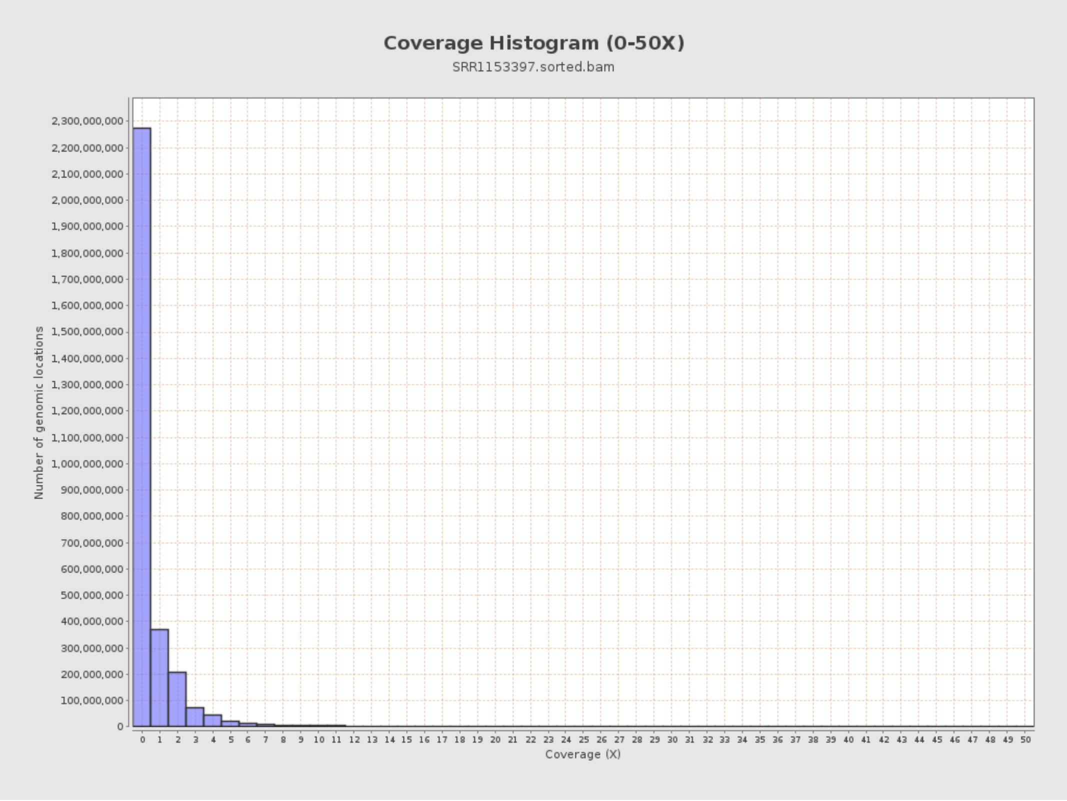
3. Results : Coverage across reference



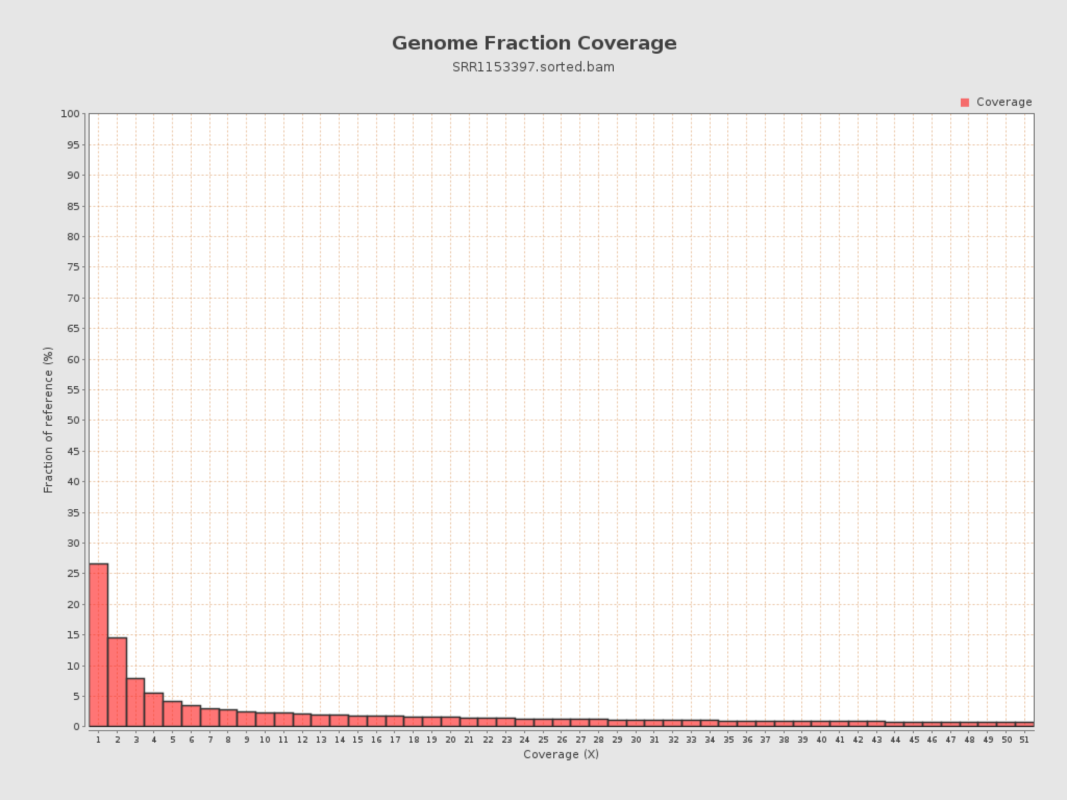
4. Results : Coverage Histogram



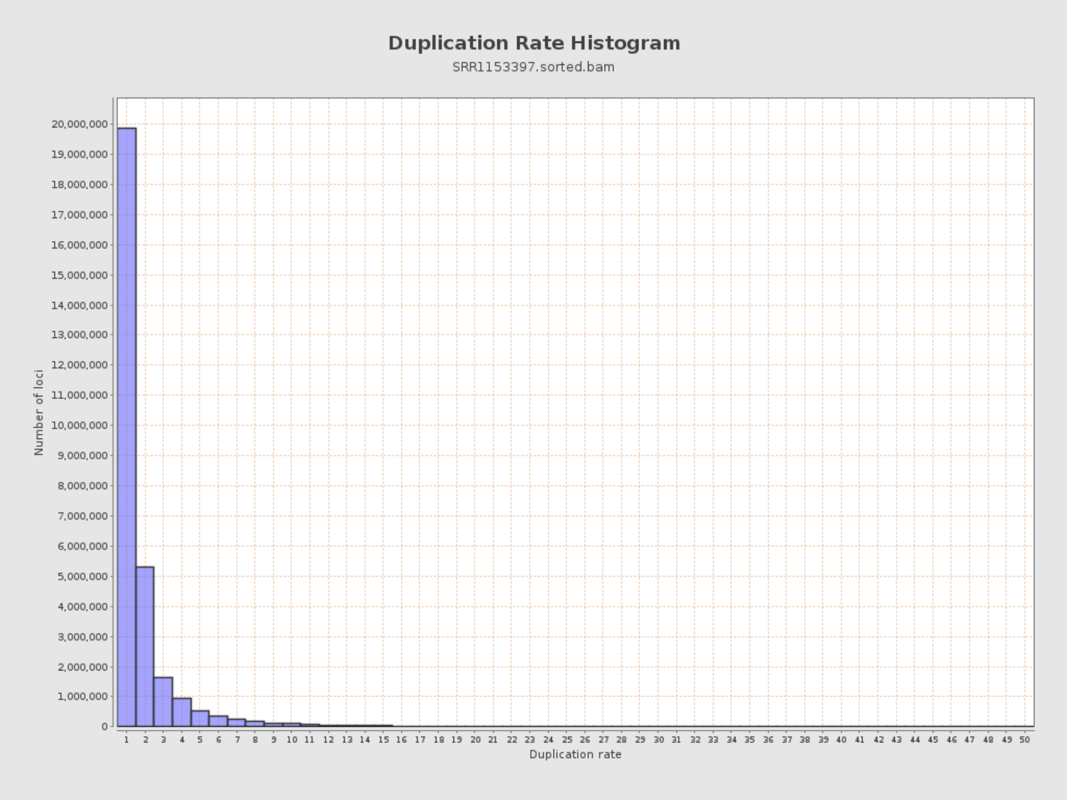
5. Results : Coverage Histogram (0-50X)



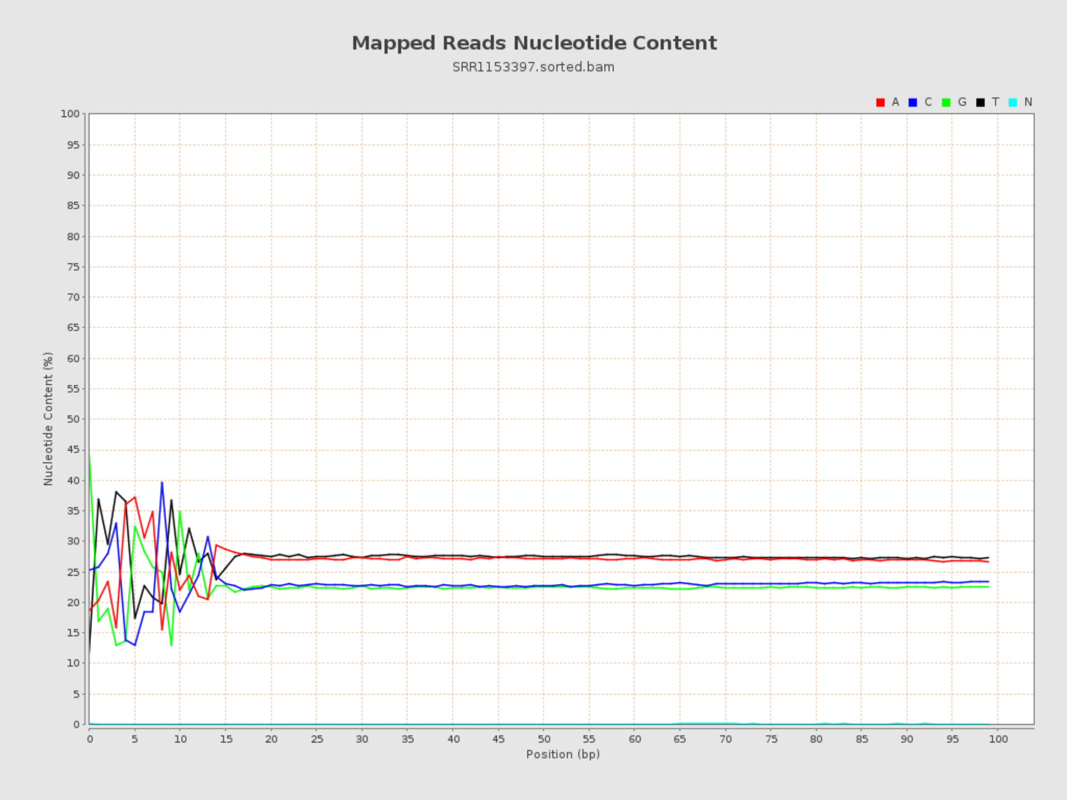
6. Results : Genome Fraction Coverage



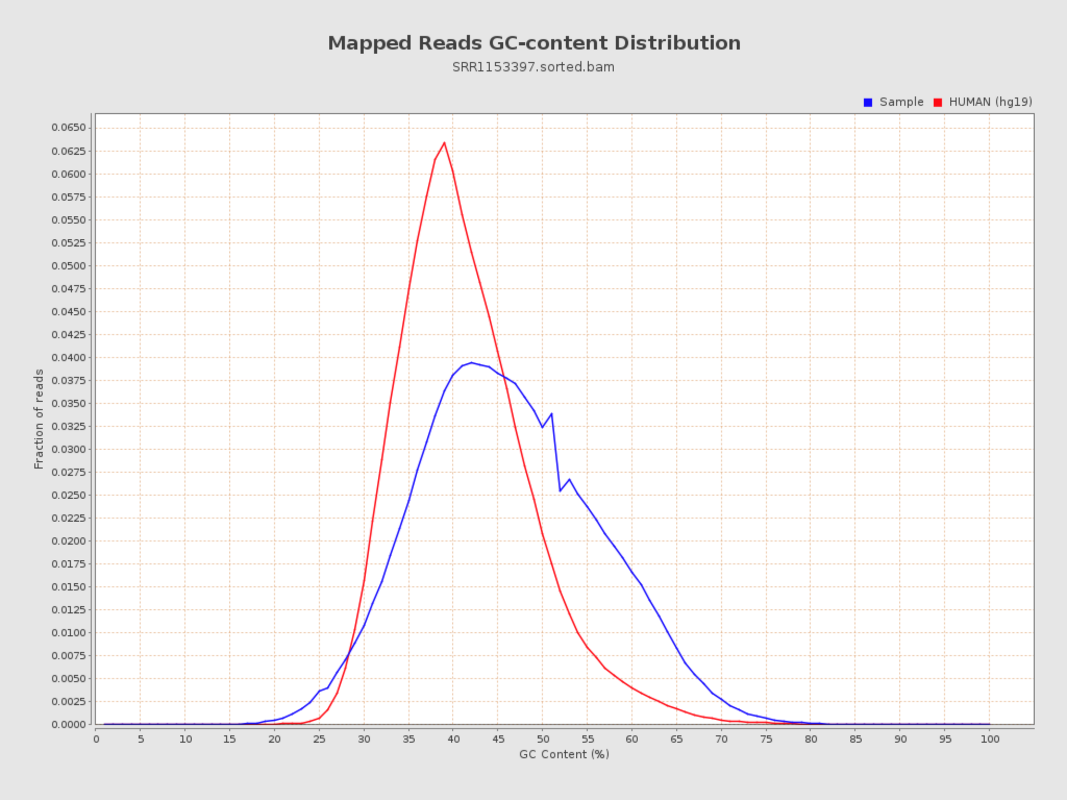
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

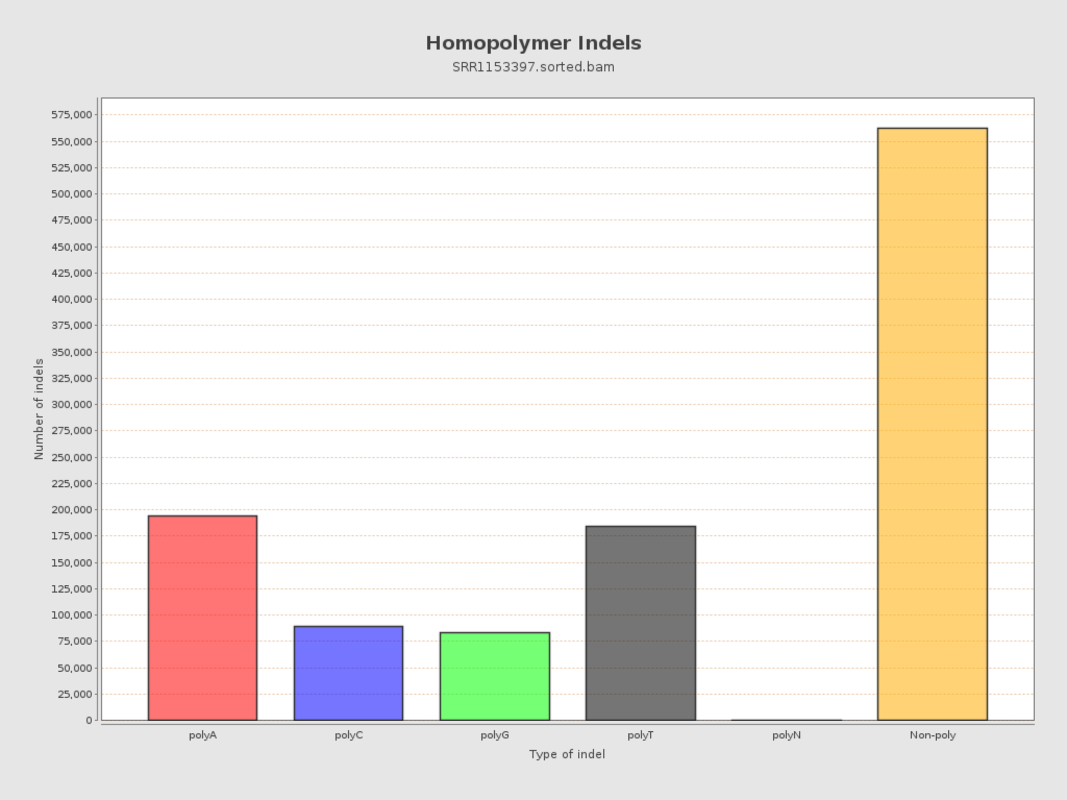


9. Results : Mapped Reads GC-content Distribution

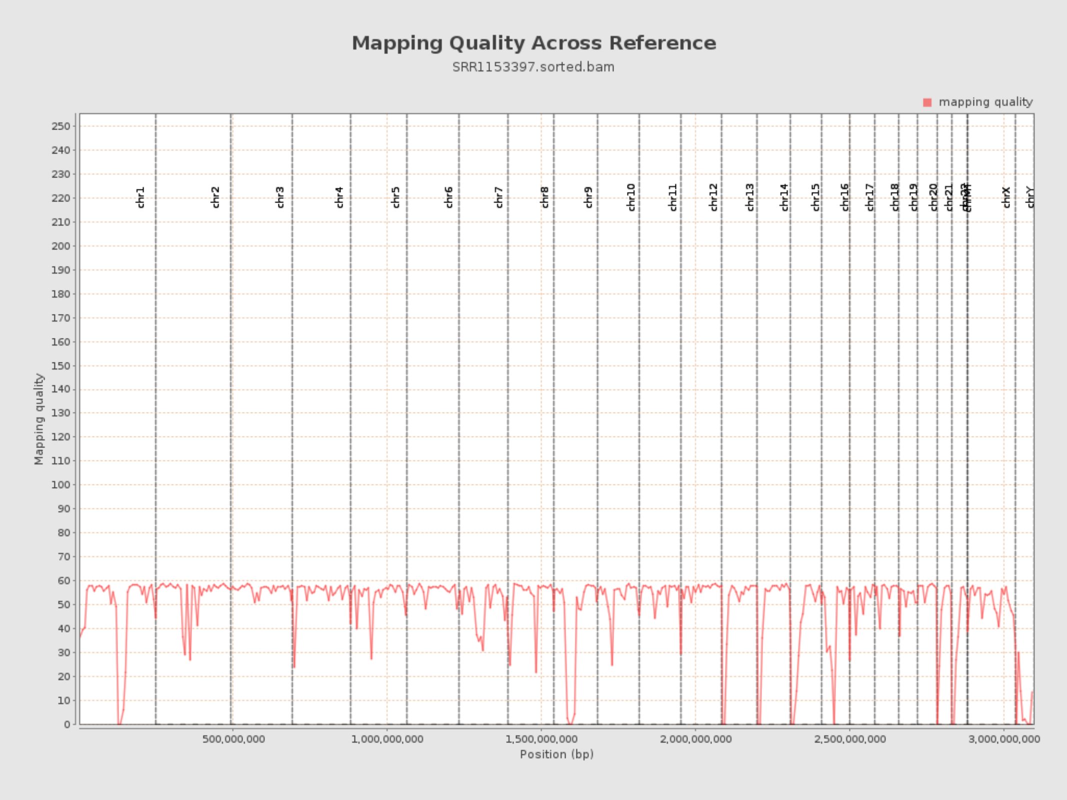


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram