Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 01:35:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153391.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_SRR1153391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153391.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 01:35:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,131,220
Mapped reads	32,910,554 / 99.33%
Unmapped reads	220,666 / 0.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	255,549 / 0.77%
Read min/max/mean length	30 / 100 / 100.32
Duplicated reads (estimated)	13,999,416 / 42.25%
Duplication rate	28.48%
Clipped reads	4,330,393 / 13.07%

2.2. ACGT Content

Number/percentage of A's	861,937,924 / 26.97%
Number/percentage of C's	732,207,538 / 22.91%
Number/percentage of T's	879,227,219 / 27.51%
Number/percentage of G's	721,929,834 / 22.59%
Number/percentage of N's	1,180,687 / 0.04%
GC Percentage	45.49%

2.3. Coverage

Mean	1.0328

Standard Deviation	9.6825

2.4. Mapping Quality

Mean Mapping Quality	50.54

2.5. Mismatches and indels

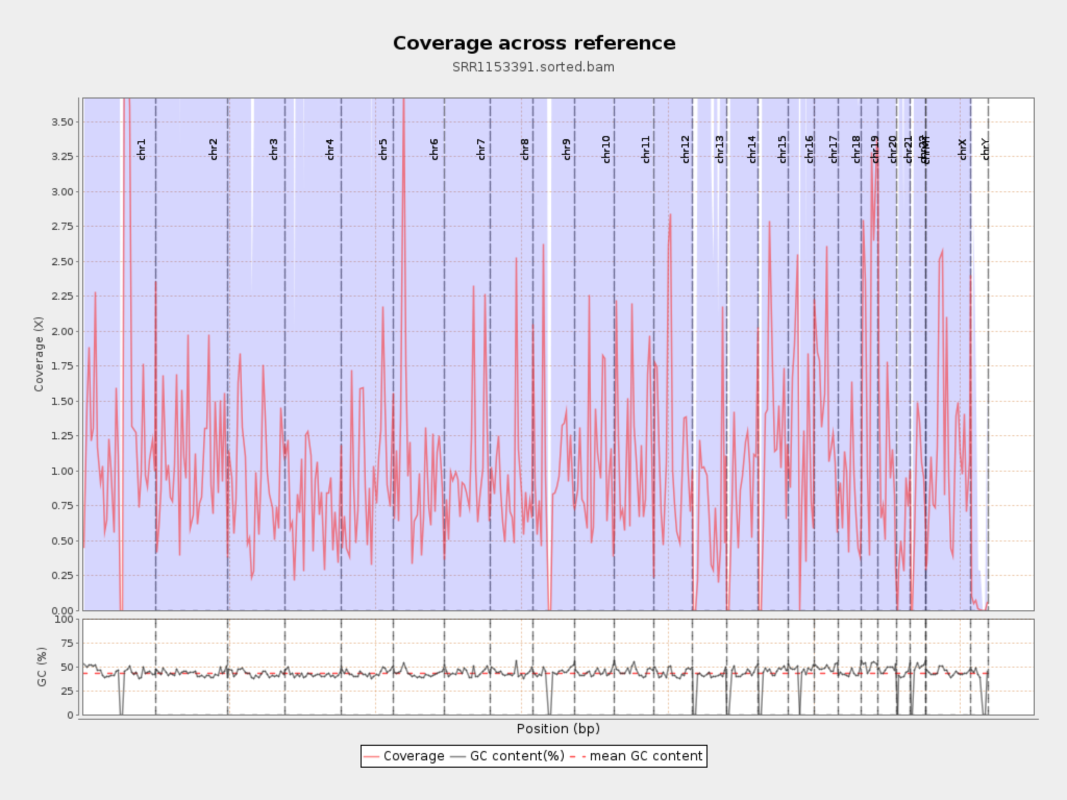
General error rate	0.27%
Mismatches	8,181,444
Insertions	339,551
Mapped reads with at least one insertion	1.02%
Deletions	283,837
Mapped reads with at least one deletion	0.85%
Homopolymer indels	49.87%

2.6. Chromosome stats

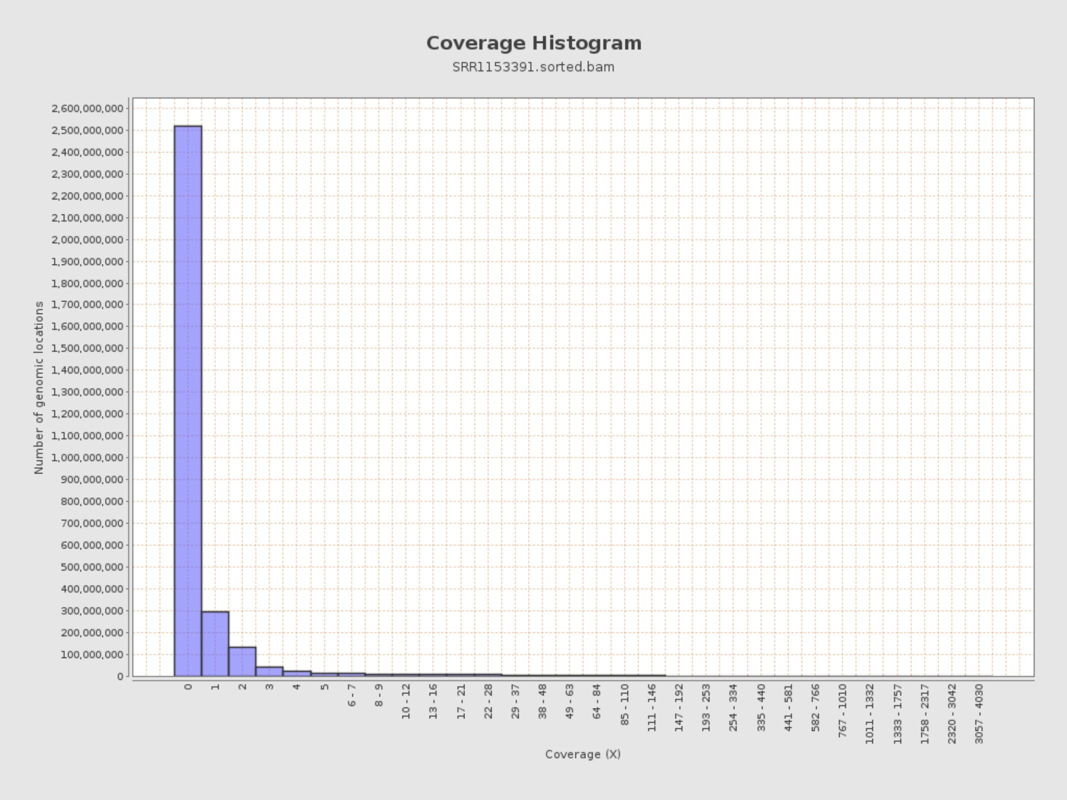
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	337878085	1.3556	11.8879
chr2	243199373	258178568	1.0616	9.0305
chr3	198022430	184510579	0.9318	8.4417
chr4	191154276	148972452	0.7793	7.1021
chr5	180915260	177137155	0.9791	9.206
chr6	171115067	179458293	1.0488	9.4389
chr7	159138663	160303536	1.0073	9.2686

chr8	146364022	131302007	0.8971	10.1859
chr9	141213431	132889262	0.9411	10.0159
chr10	135534747	143154701	1.0562	9.0011
chr11	135006516	155160361	1.1493	9.6112
chr12	133851895	160970238	1.2026	9.5878
chr13	115169878	78073527	0.6779	9.8751
chr14	107349540	91065704	0.8483	7.4686
chr15	102531392	120531354	1.1756	10.415
chr16	90354753	103783091	1.1486	9.0281
chr17	81195210	123330113	1.5189	11.0726
chr18	78077248	65269286	0.836	7.7868
chr19	59128983	131009973	2.2157	18.4813
chr20	63025520	61420466	0.9745	8.9093
chr21	48129895	26358334	0.5476	5.039
chr22	51304566	42399193	0.8264	7.7095
chrMT	16571	4766	0.2876	1.0116
chrX	155270560	181858504	1.1712	11.8587
chrY	59373566	2069635	0.0349	1.3324

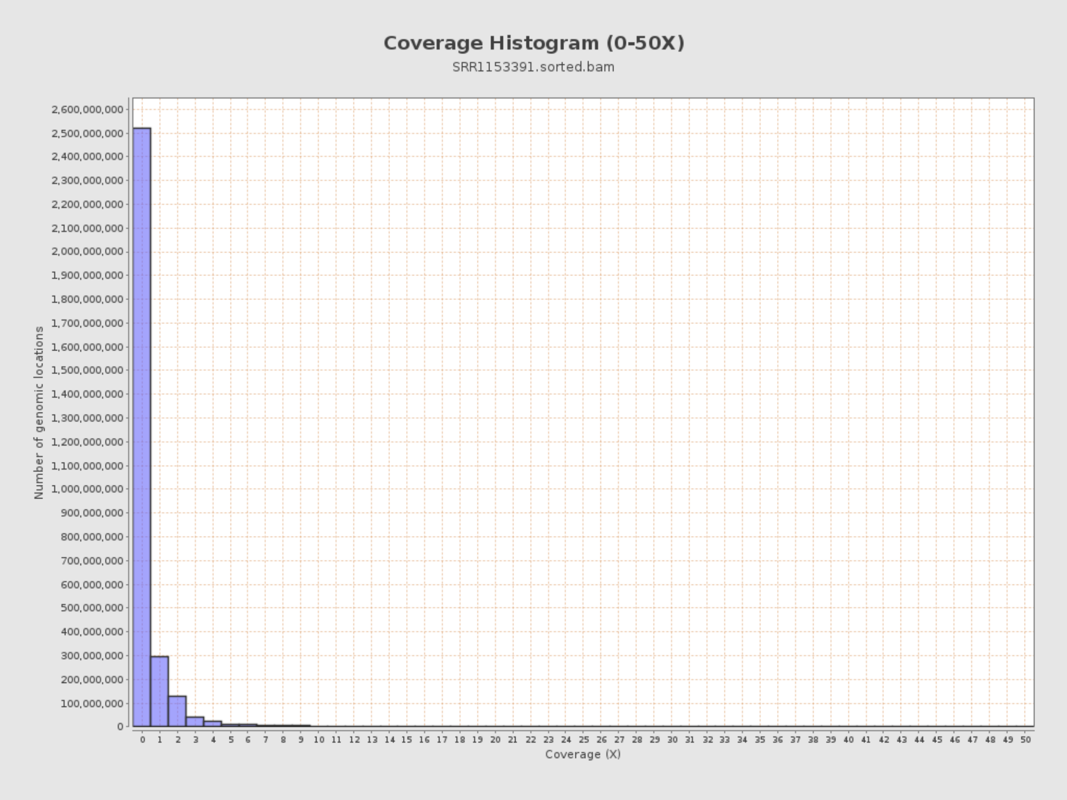
3. Results : Coverage across reference



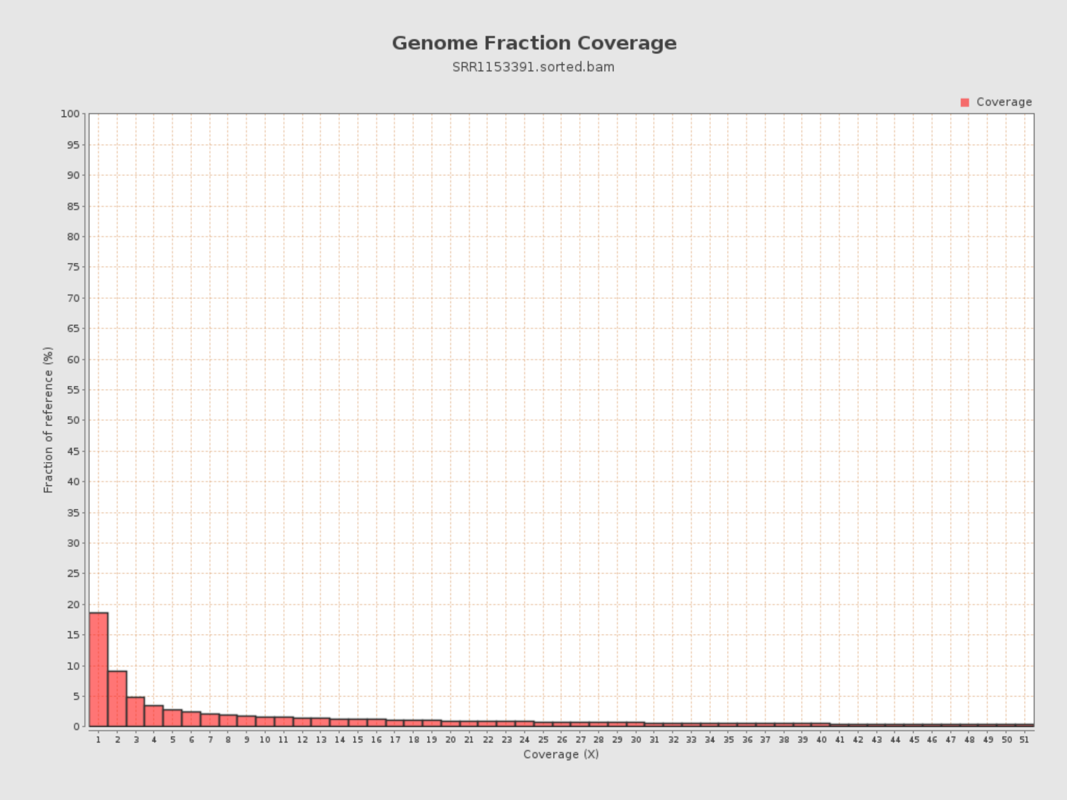
4. Results : Coverage Histogram



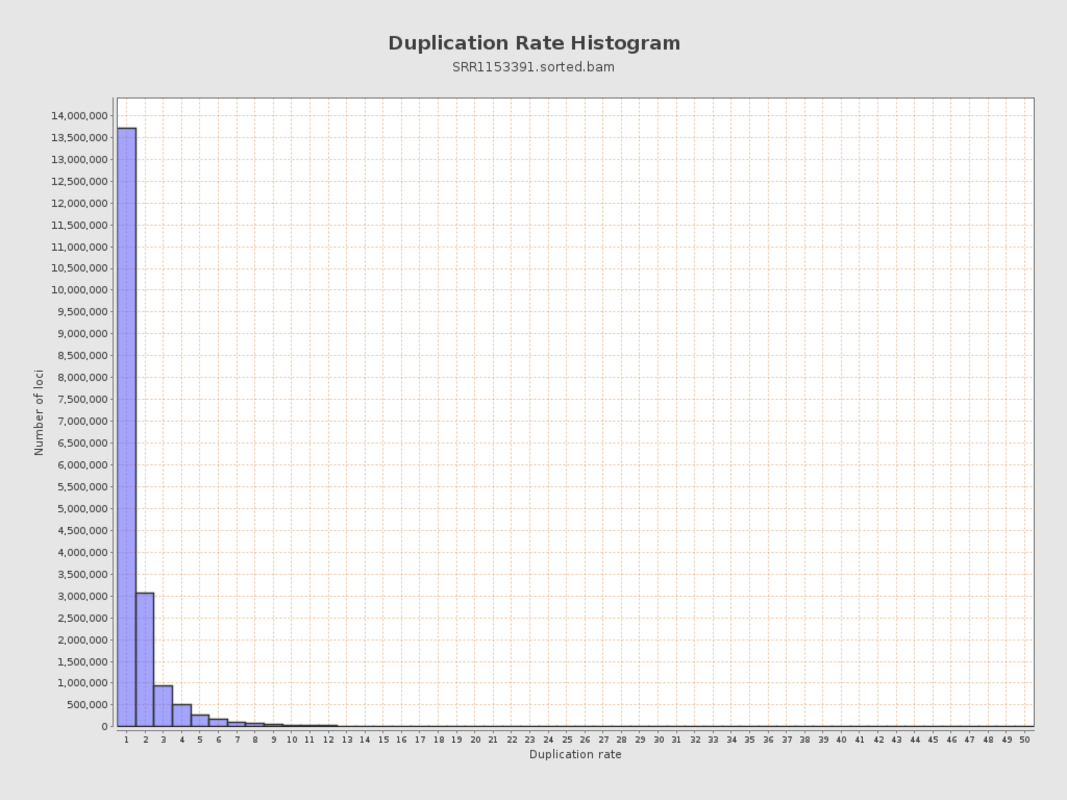
5. Results : Coverage Histogram (0-50X)



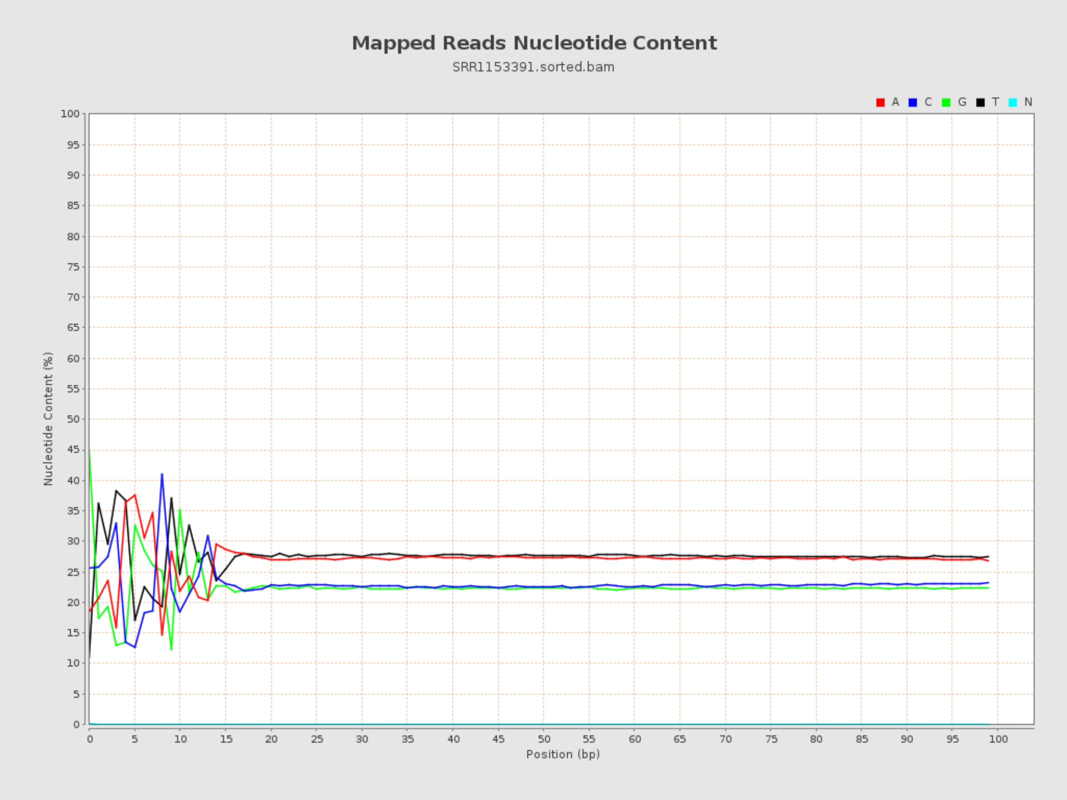
6. Results : Genome Fraction Coverage



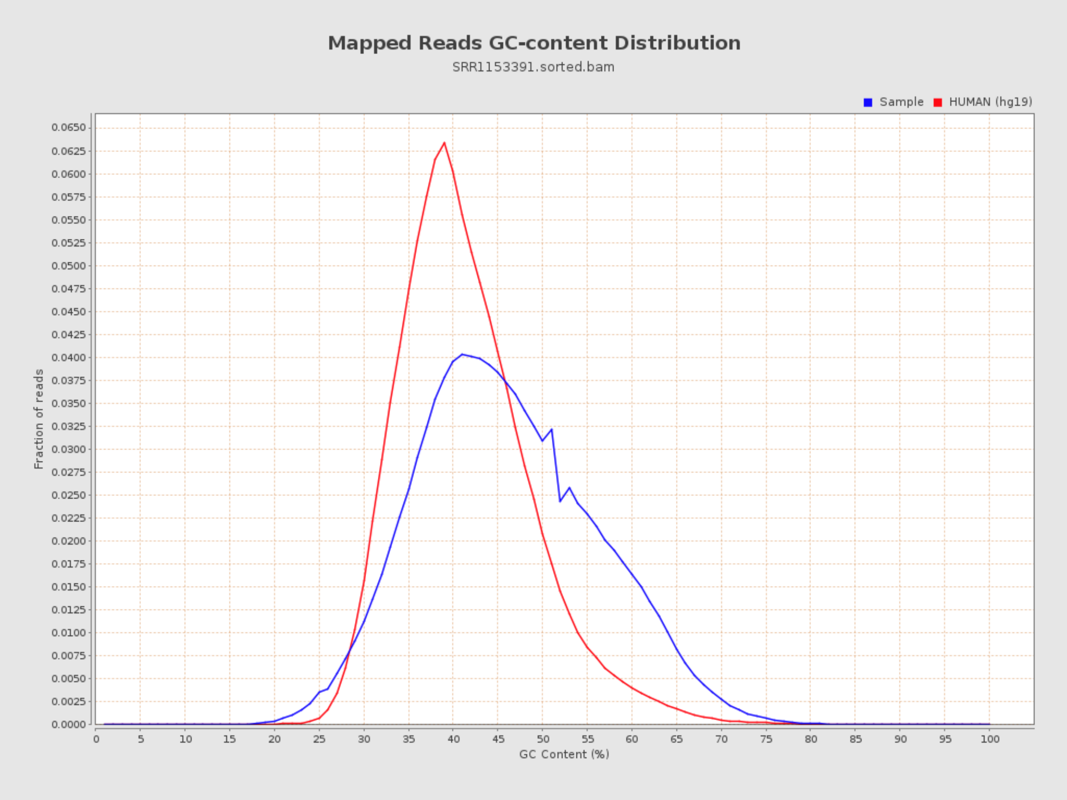
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

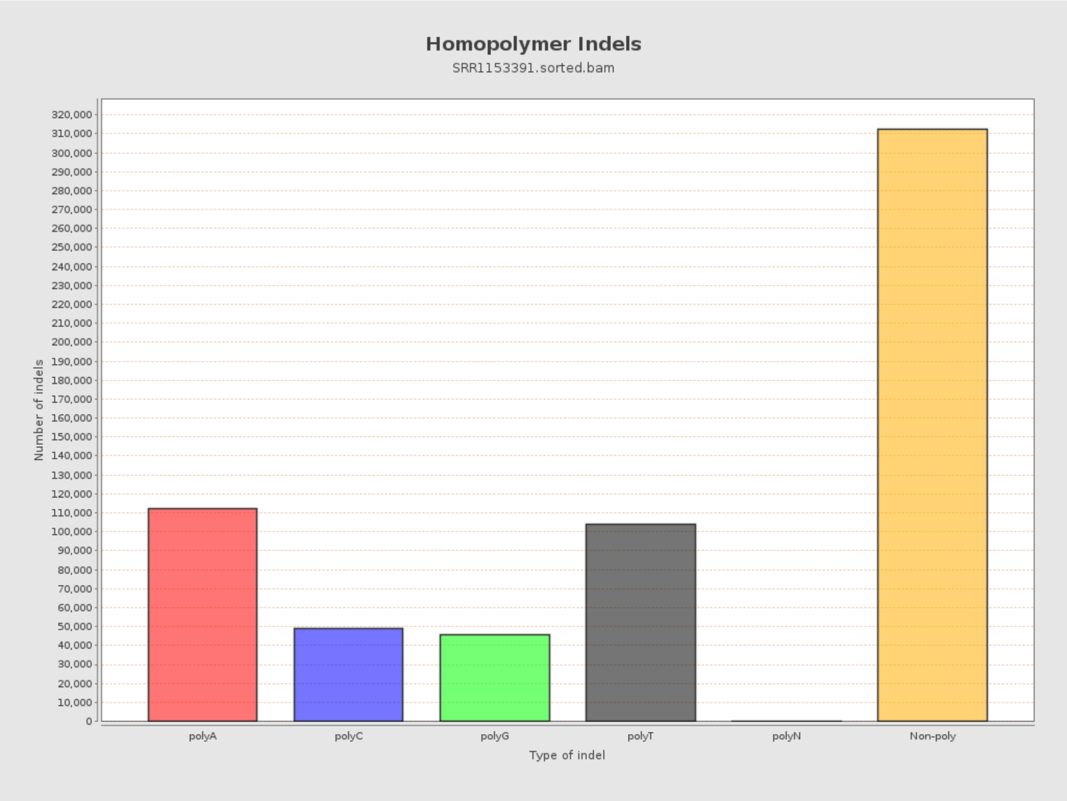


9. Results : Mapped Reads GC-content Distribution

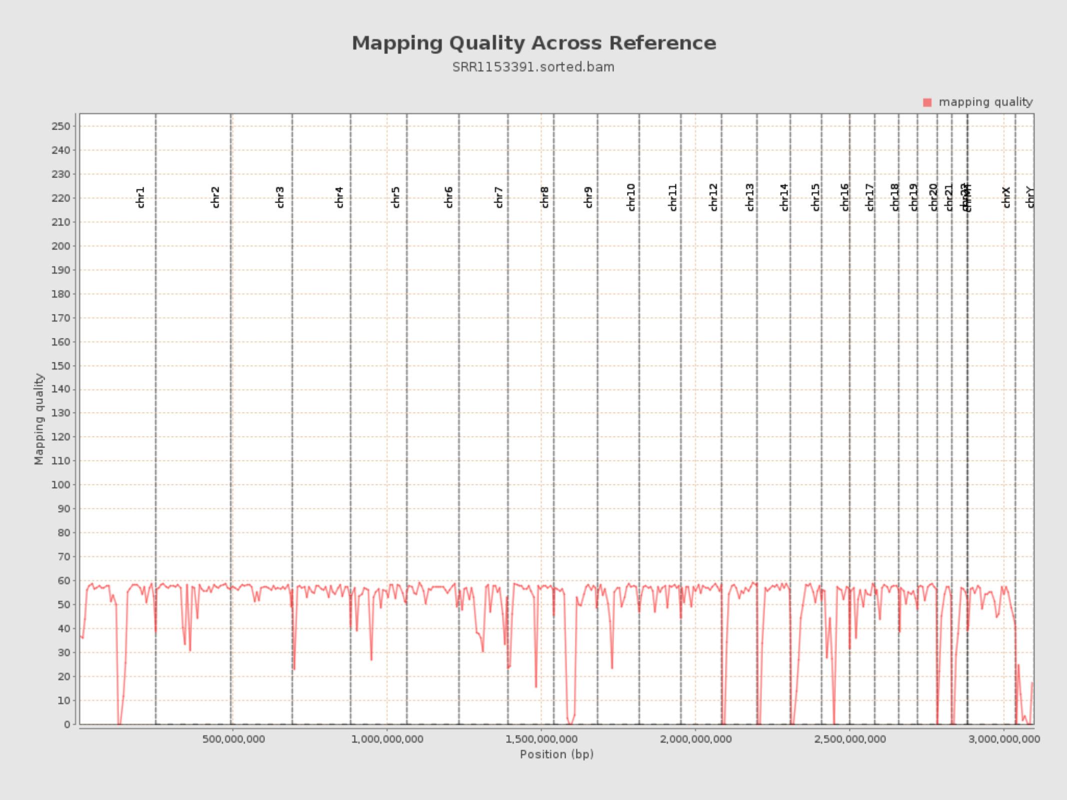


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram