Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 13:40:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153371.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_SRR1153371 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153371.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 13:40:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153371.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,367,754
Mapped reads	43,048,183 / 99.26%
Unmapped reads	319,571 / 0.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	364,821 / 0.84%
Read min/max/mean length	30 / 100 / 100.35
Duplicated reads (estimated)	20,232,087 / 46.65%
Duplication rate	31.48%
Clipped reads	6,099,986 / 14.07%

2.2. ACGT Content

Number/percentage of A's	1,118,000,718 / 26.81%
Number/percentage of C's	961,178,952 / 23.05%
Number/percentage of T's	1,140,636,922 / 27.36%
Number/percentage of G's	948,106,821 / 22.74%
Number/percentage of N's	1,670,326 / 0.04%
GC Percentage	45.79%

2.3. Coverage

Mean	1.3471

Standard Deviation	12.418

2.4. Mapping Quality

Mean Mapping Quality	50.21

2.5. Mismatches and indels

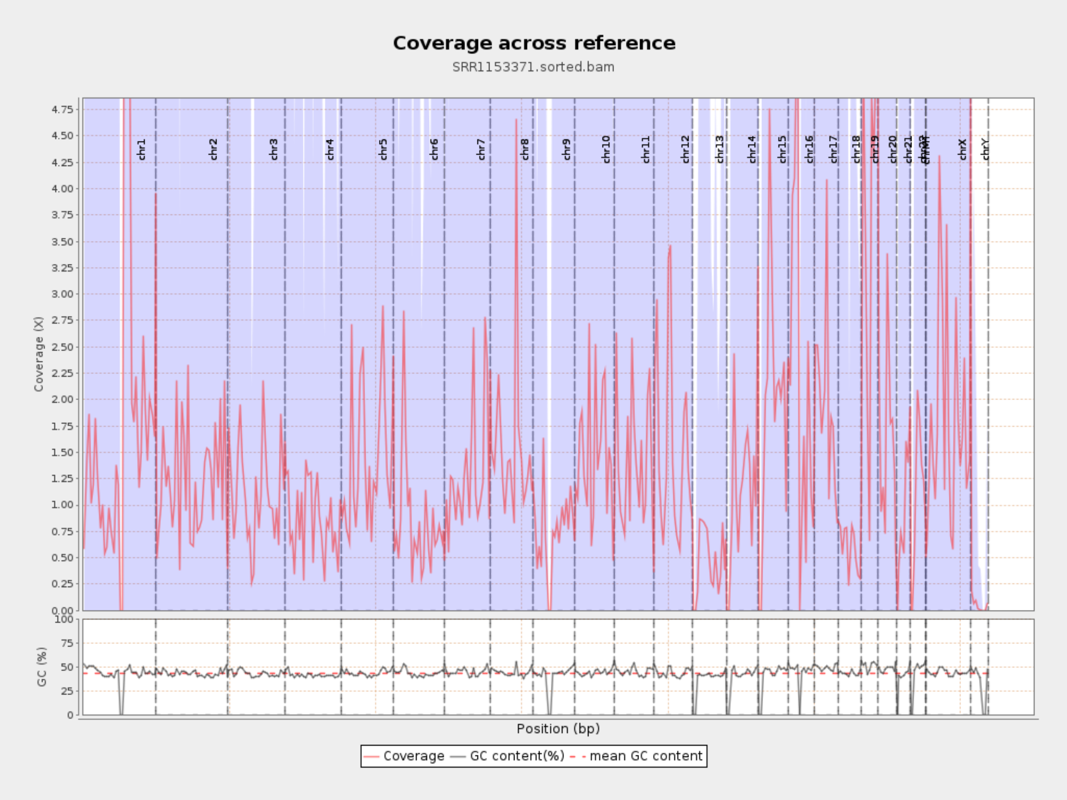
General error rate	0.29%
Mismatches	11,238,932
Insertions	462,031
Mapped reads with at least one insertion	1.06%
Deletions	350,577
Mapped reads with at least one deletion	0.8%
Homopolymer indels	49.81%

2.6. Chromosome stats

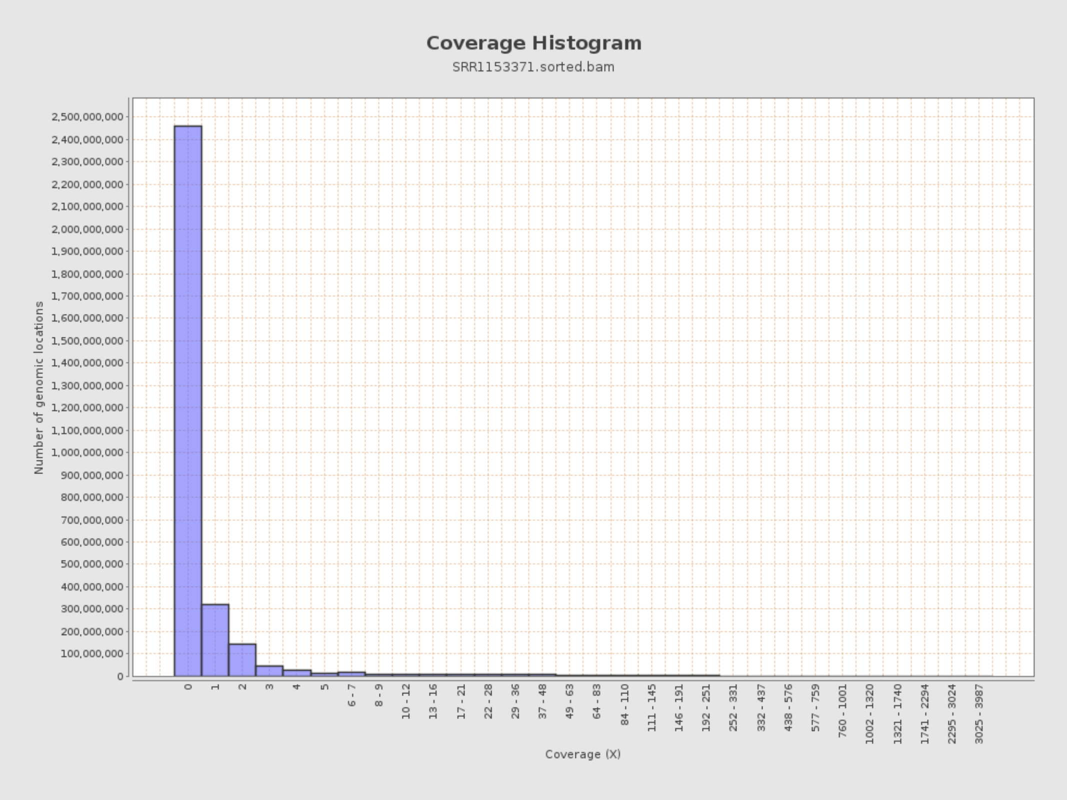
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	456194810	1.8303	17.3277
chr2	243199373	301172370	1.2384	10.033
chr3	198022430	219538849	1.1087	9.1767
chr4	191154276	165221689	0.8643	7.1512
chr5	180915260	262049887	1.4485	12.3059
chr6	171115067	140571489	0.8215	7.188
chr7	159138663	205129531	1.289	15.2884

chr8	146364022	227173653	1.5521	17.353
chr9	141213431	103558344	0.7333	6.6707
chr10	135534747	203615072	1.5023	11.5657
chr11	135006516	191819902	1.4208	10.5581
chr12	133851895	212382366	1.5867	12.5572
chr13	115169878	53929077	0.4683	4.7134
chr14	107349540	119104061	1.1095	9.5119
chr15	102531392	193691426	1.8891	14.3336
chr16	90354753	194976994	2.1579	18.3455
chr17	81195210	163773127	2.017	13.2258
chr18	78077248	46795407	0.5993	5.5066
chr19	59128983	216599255	3.6632	24.364
chr20	63025520	101118251	1.6044	12.1961
chr21	48129895	45828795	0.9522	8.9598
chr22	51304566	56193034	1.0953	9.6091
chrMT	16571	8323	0.5023	1.3874
chrX	155270560	286993559	1.8483	15.8405
chrY	59373566	2894745	0.0488	1.8748

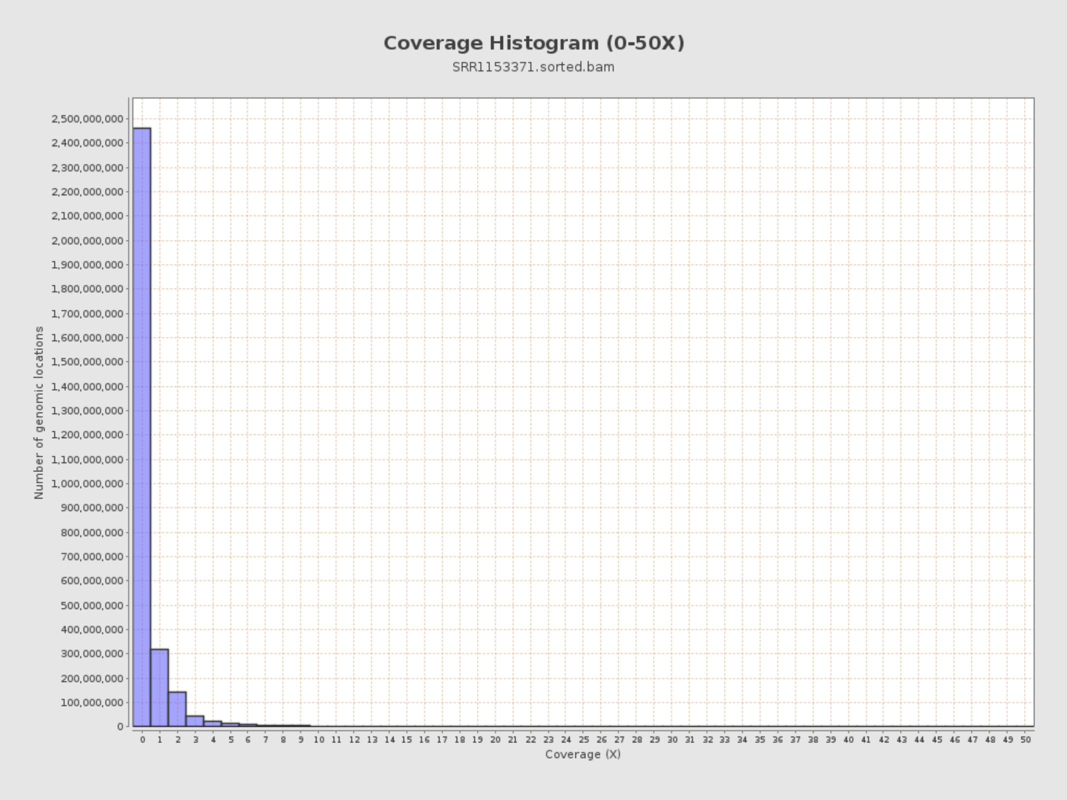
3. Results : Coverage across reference



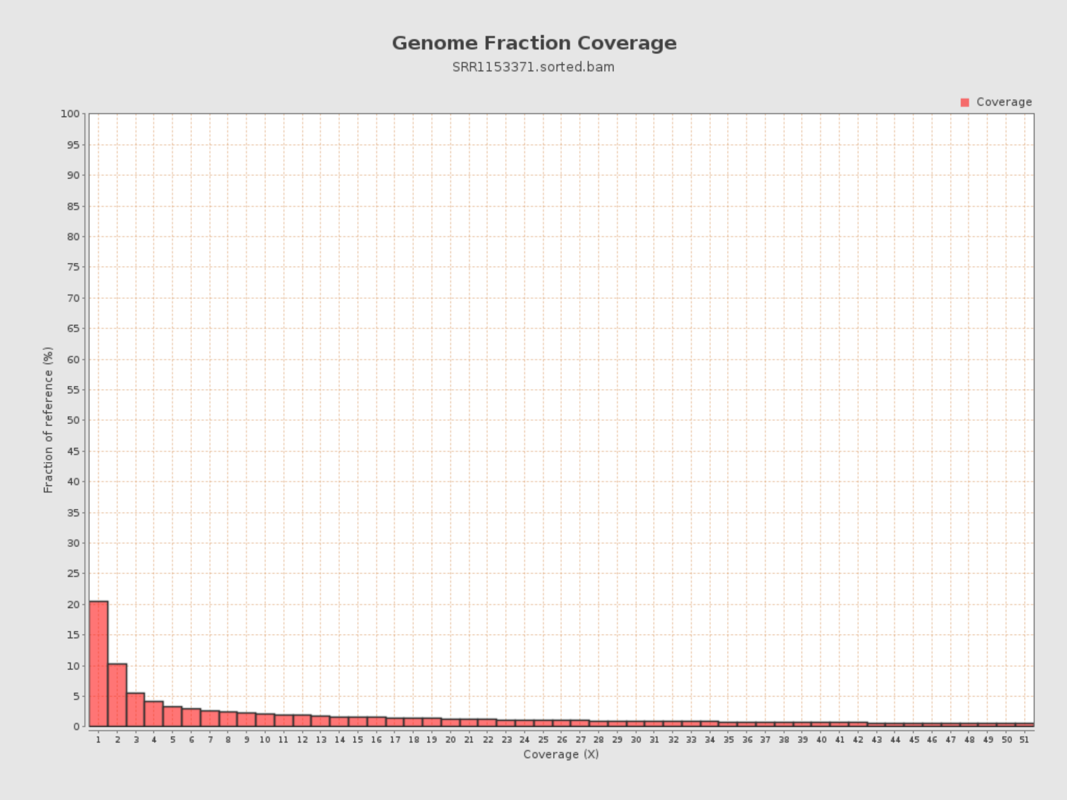
4. Results : Coverage Histogram



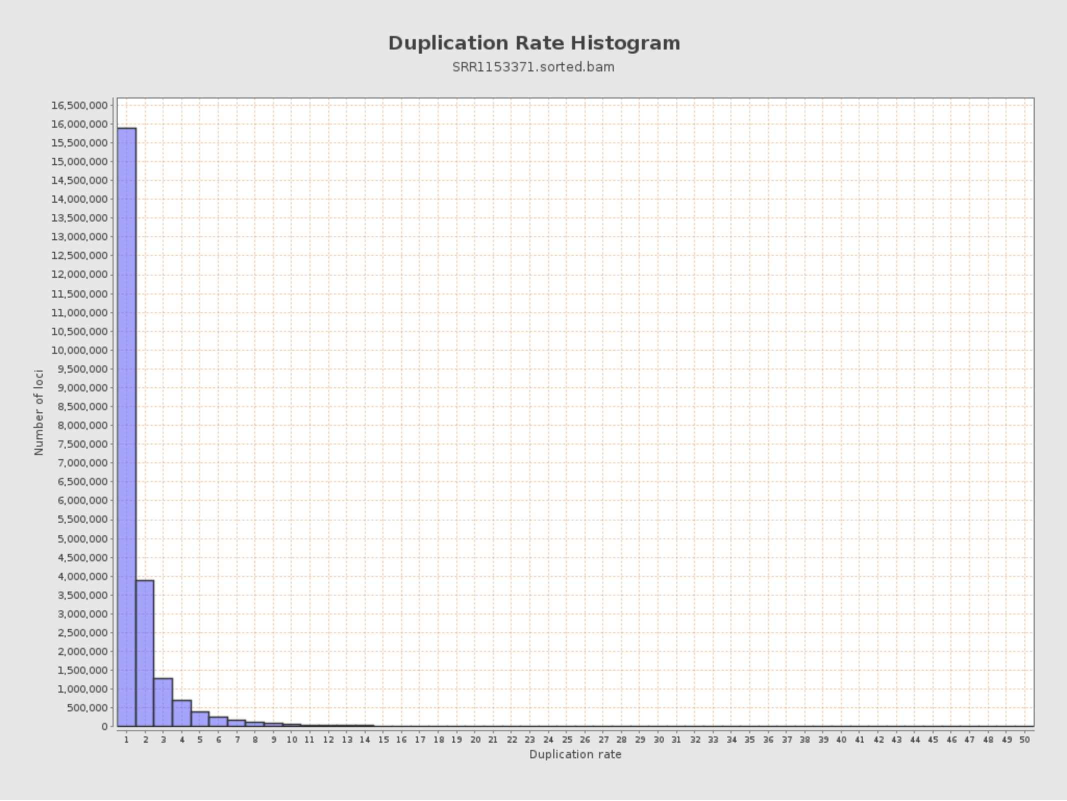
5. Results : Coverage Histogram (0-50X)



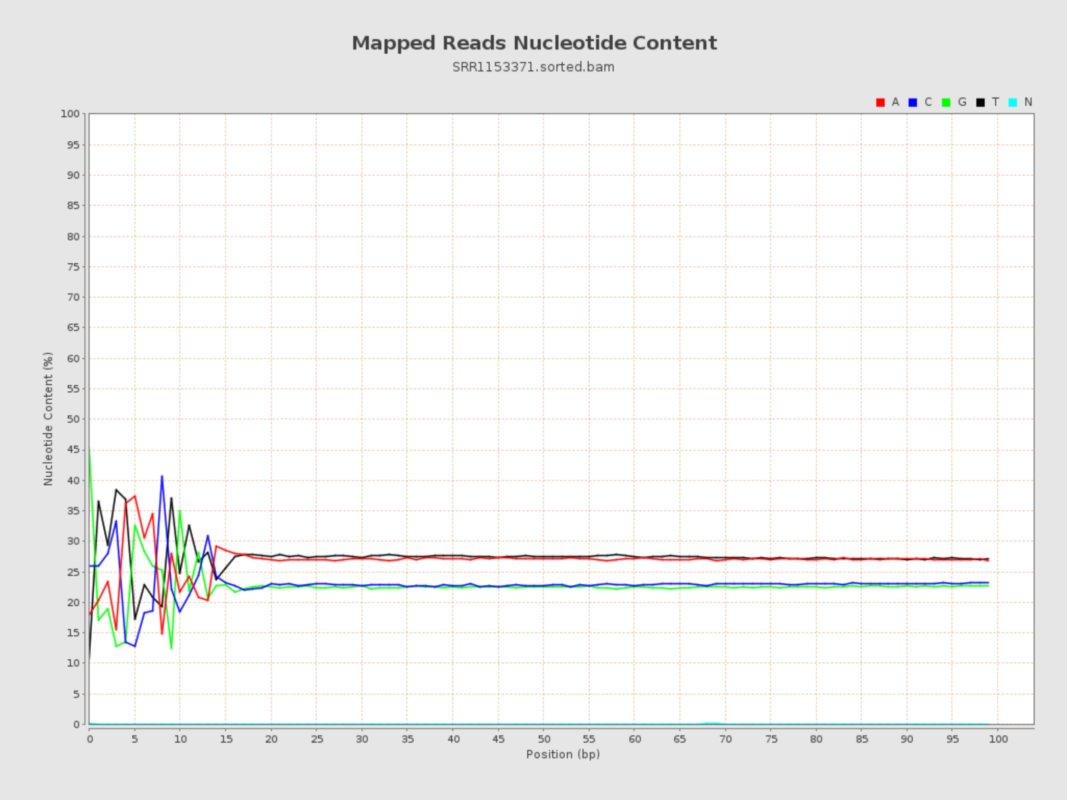
6. Results : Genome Fraction Coverage



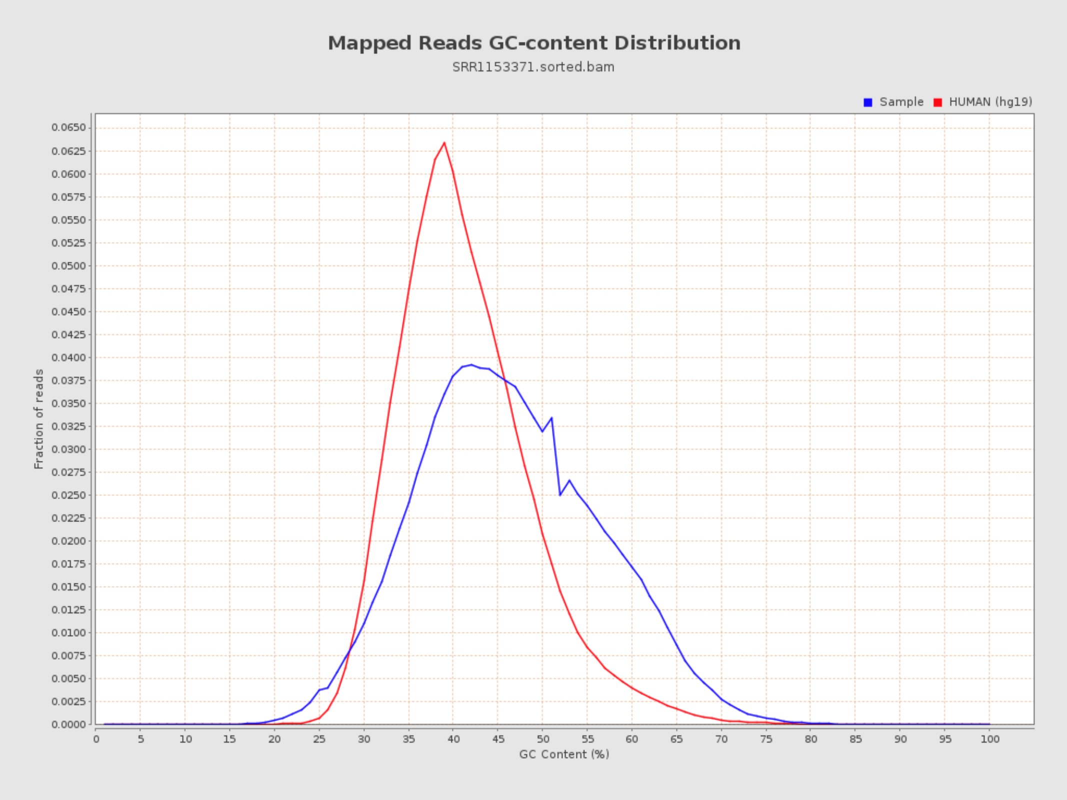
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

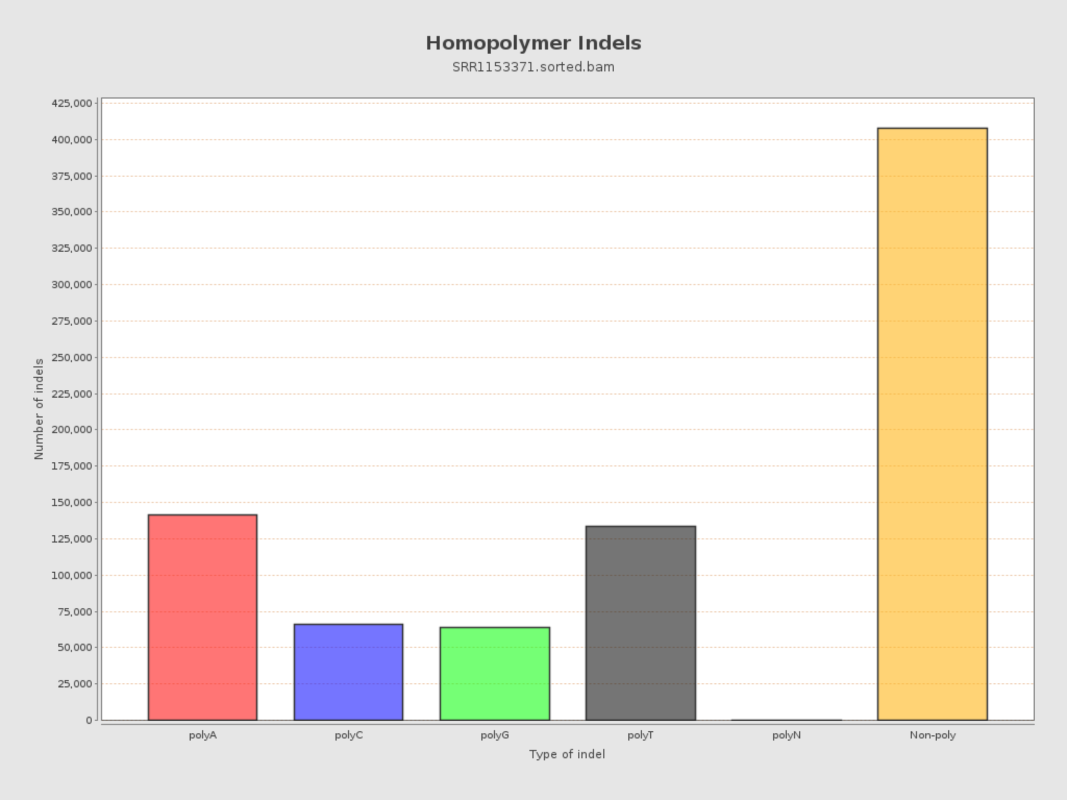


9. Results : Mapped Reads GC-content Distribution

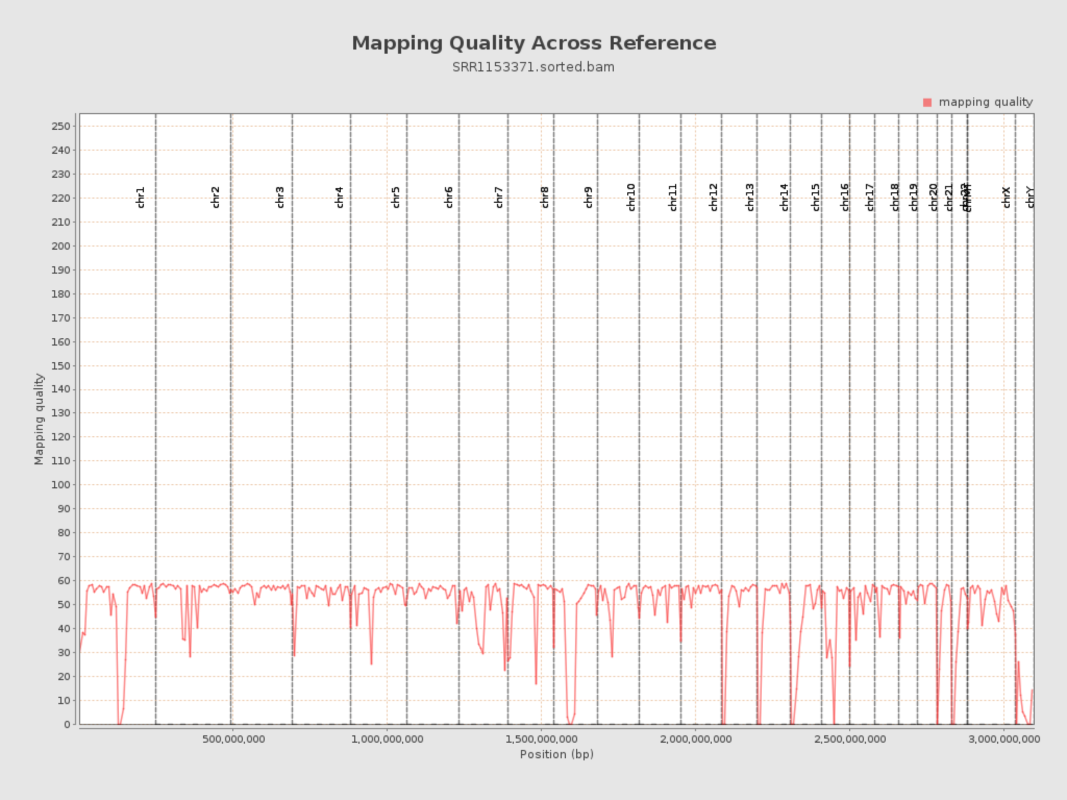


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram