Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 20:24:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153382.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_SRR1153382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153382.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 20:24:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	52,668,876
Mapped reads	52,174,893 / 99.06%
Unmapped reads	493,983 / 0.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	403,680 / 0.77%
Read min/max/mean length	30 / 100 / 100.31
Duplicated reads (estimated)	25,395,232 / 48.22%
Duplication rate	32.85%
Clipped reads	9,034,727 / 17.15%

2.2. ACGT Content

Number/percentage of A's	1,345,138,092 / 26.91%
Number/percentage of C's	1,149,713,830 / 23%
Number/percentage of T's	1,372,652,042 / 27.46%
Number/percentage of G's	1,129,529,667 / 22.59%
Number/percentage of N's	2,196,175 / 0.04%
GC Percentage	45.59%

2.3. Coverage

Mean	1.6152

Standard Deviation	14.3626

2.4. Mapping Quality

Mean Mapping Quality	50.08

2.5. Mismatches and indels

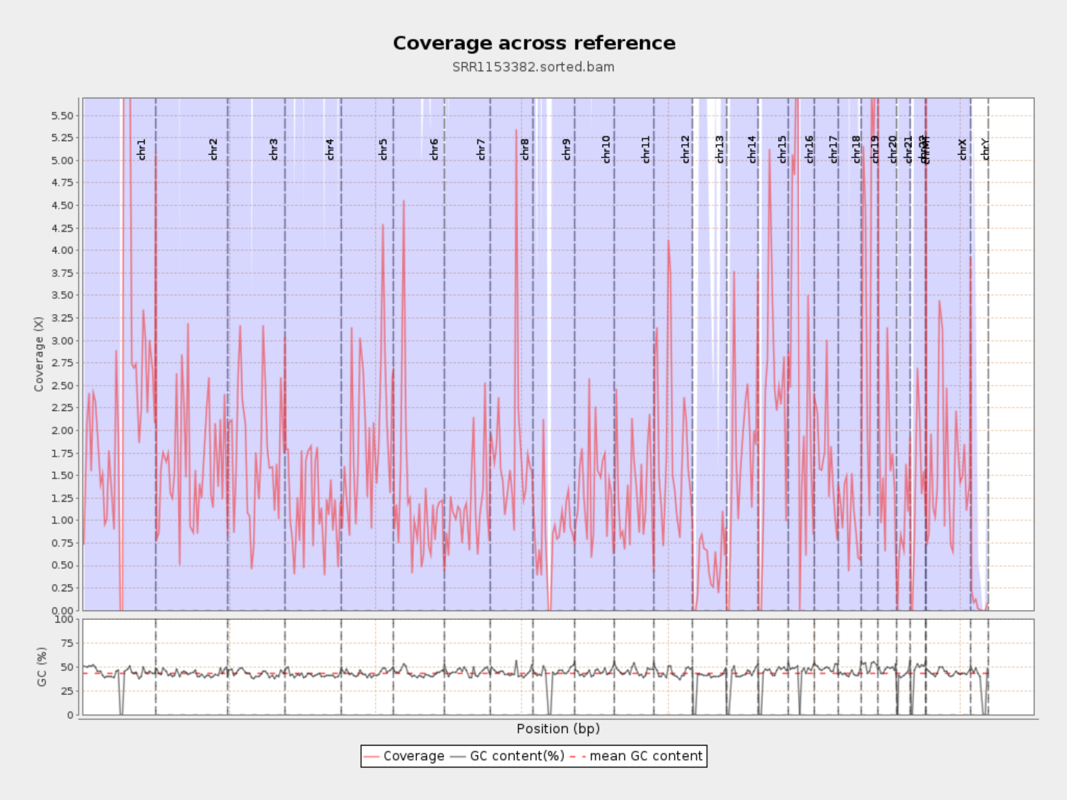
General error rate	0.31%
Mismatches	14,880,012
Insertions	542,133
Mapped reads with at least one insertion	1.03%
Deletions	439,564
Mapped reads with at least one deletion	0.83%
Homopolymer indels	49.68%

2.6. Chromosome stats

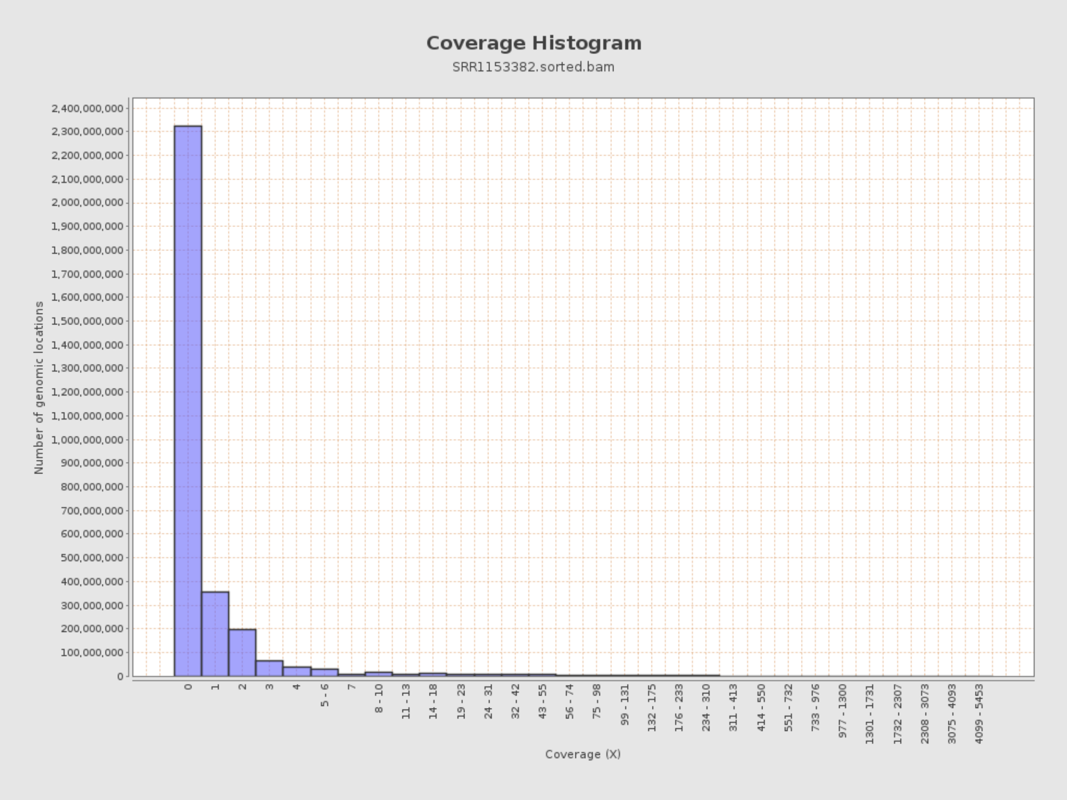
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	654085420	2.6242	22.7042
chr2	243199373	397848708	1.6359	12.5646
chr3	198022430	344980393	1.7421	13.3358
chr4	191154276	225131559	1.1777	10.0144
chr5	180915260	355319846	1.964	15.883
chr6	171115067	202600075	1.184	11.1834
chr7	159138663	179853436	1.1302	10.3999

chr8	146364022	259099165	1.7702	20.0506
chr9	141213431	116794724	0.8271	8.6793
chr10	135534747	186504359	1.3761	10.8759
chr11	135006516	177216373	1.3127	9.9354
chr12	133851895	253516573	1.894	14.5662
chr13	115169878	57506735	0.4993	4.8487
chr14	107349540	183492605	1.7093	13.0689
chr15	102531392	222444950	2.1695	16.1607
chr16	90354753	240659776	2.6635	22.3761
chr17	81195210	140877989	1.7351	11.9716
chr18	78077248	81770846	1.0473	9.412
chr19	59128983	254368354	4.3019	27.3733
chr20	63025520	99185794	1.5737	12.554
chr21	48129895	46474164	0.9656	8.7286
chr22	51304566	67639789	1.3184	11.2465
chrMT	16571	102273	6.1718	17.3067
chrX	155270560	249050090	1.604	13.4403
chrY	59373566	3629675	0.0611	2.5038

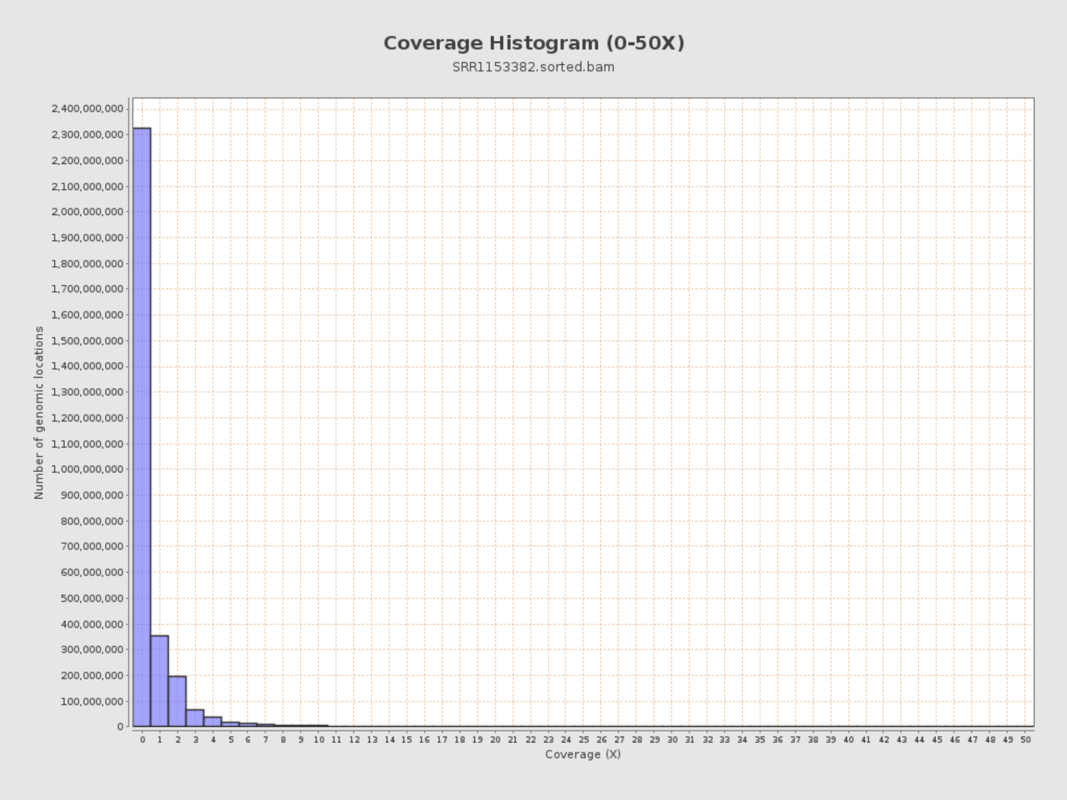
3. Results : Coverage across reference



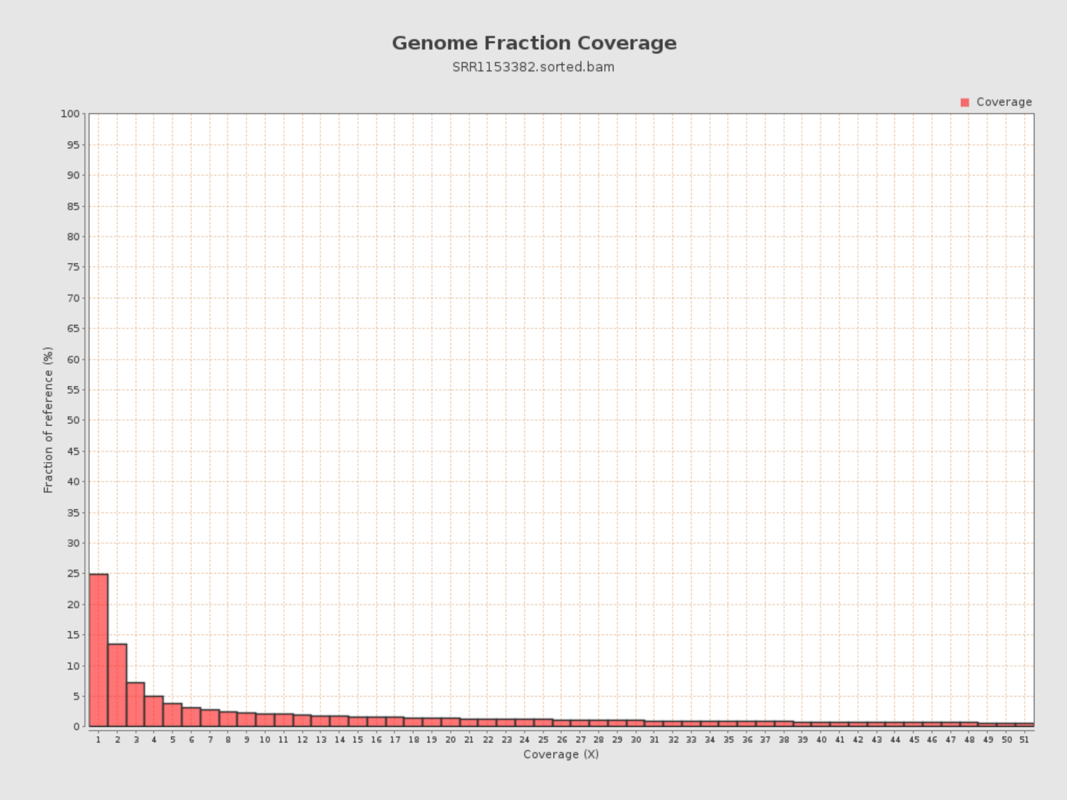
4. Results : Coverage Histogram



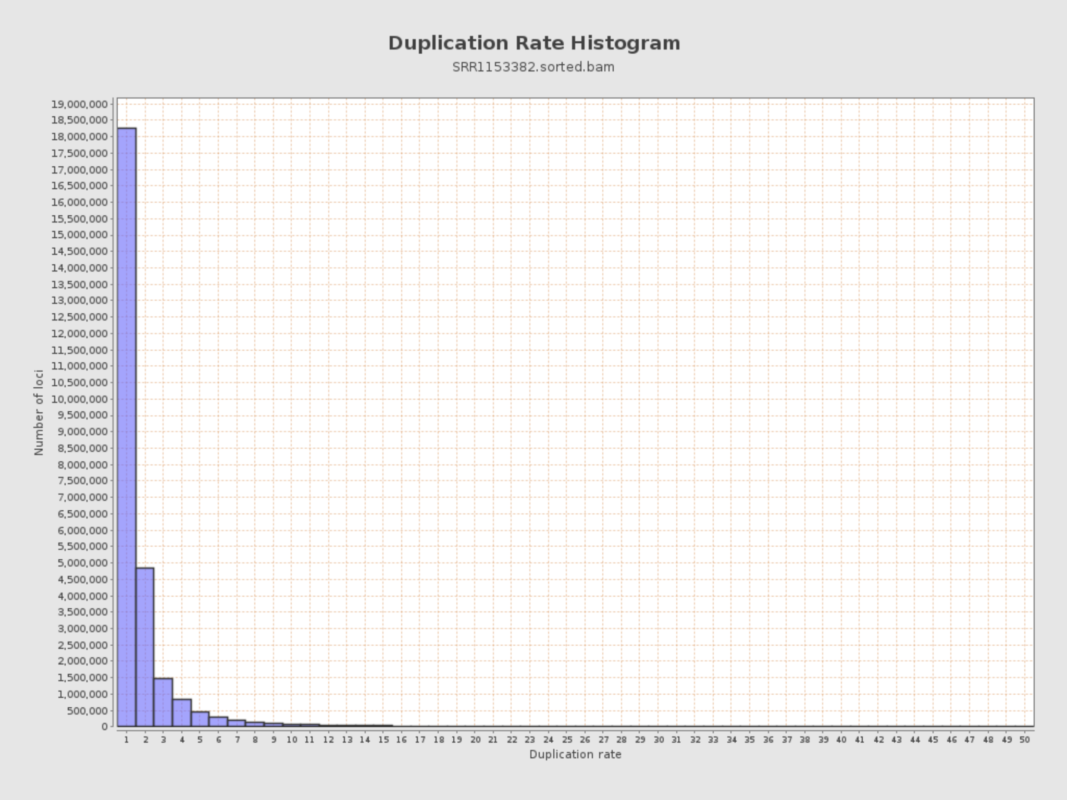
5. Results : Coverage Histogram (0-50X)



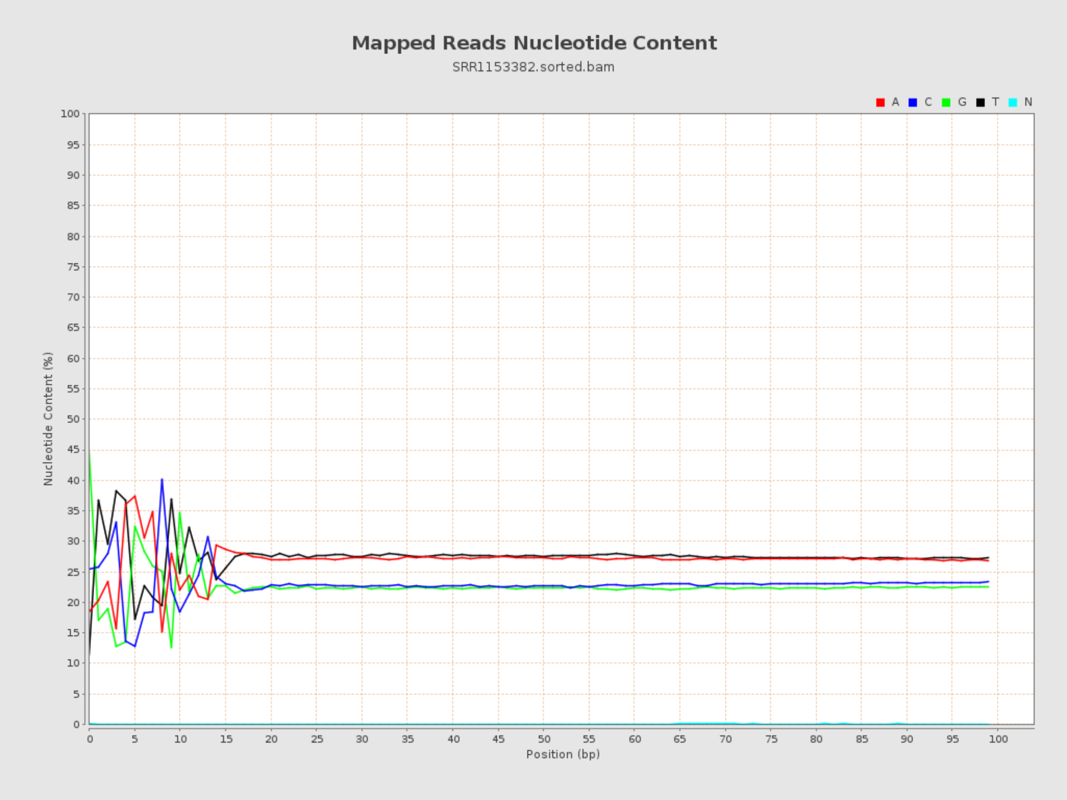
6. Results : Genome Fraction Coverage



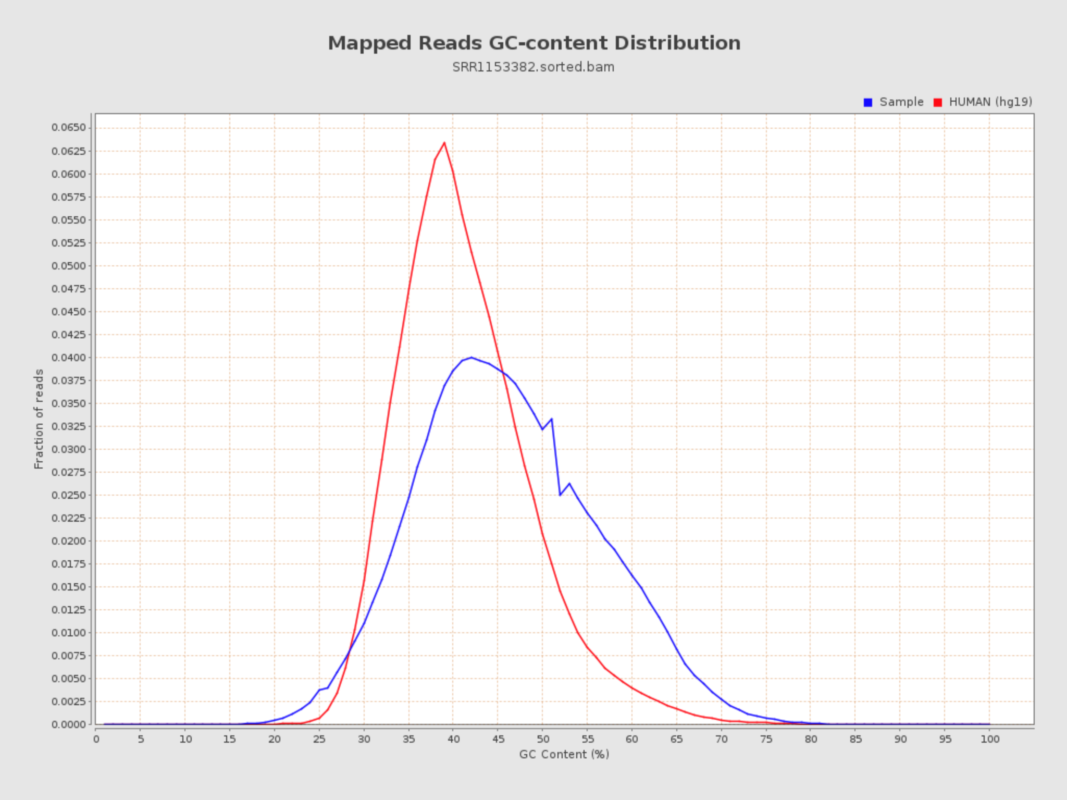
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

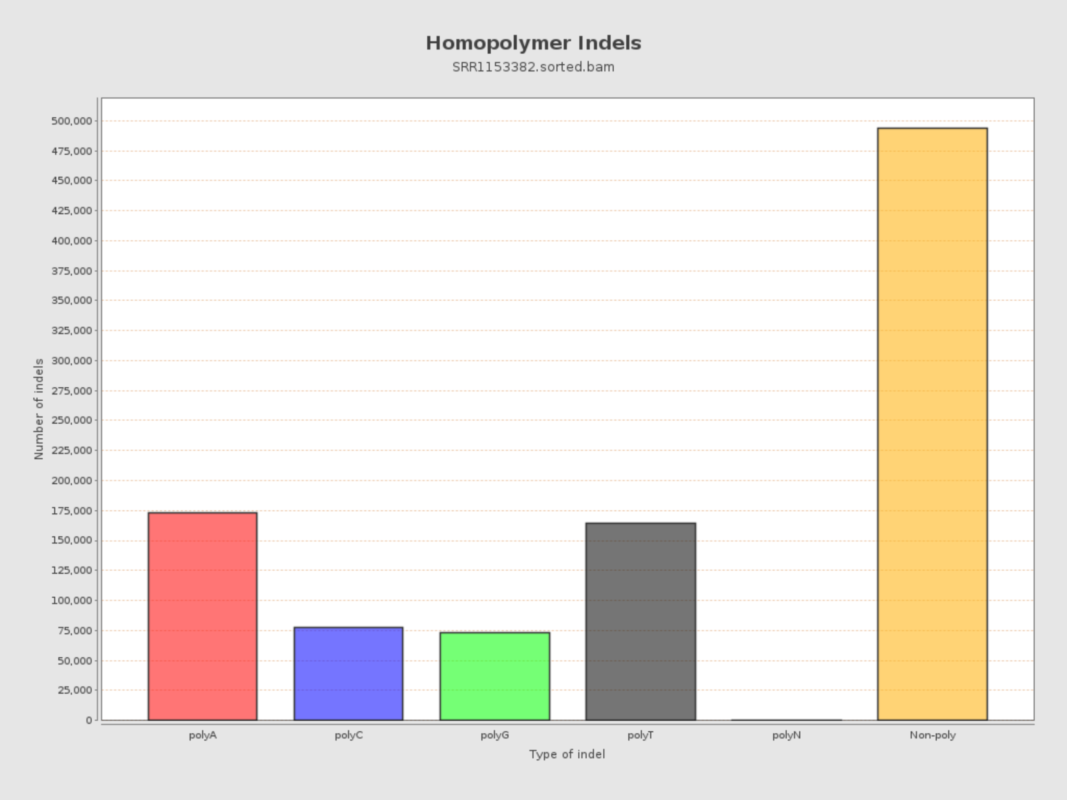


9. Results : Mapped Reads GC-content Distribution

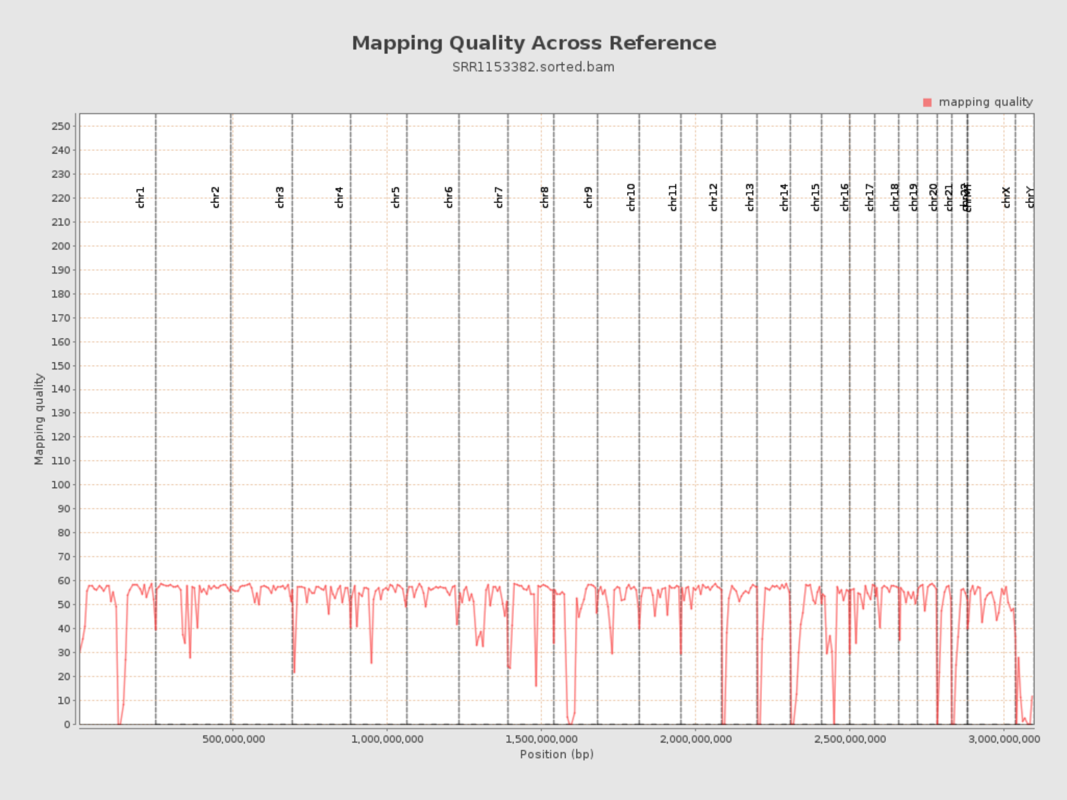


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram