Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 17:30:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153318.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_SRR1153318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 17:30:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	102,650,784
Mapped reads	99,985,242 / 97.4%
Unmapped reads	2,665,542 / 2.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	608,119 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	47,085,401 / 45.87%
Duplication rate	31.27%
Clipped reads	8,301,653 / 8.09%

2.2. ACGT Content

Number/percentage of A's	2,509,039,245 / 25.53%
Number/percentage of C's	2,403,053,469 / 24.46%
Number/percentage of T's	2,530,950,946 / 25.76%
Number/percentage of G's	2,381,333,742 / 24.23%
Number/percentage of N's	1,900,002 / 0.02%
GC Percentage	48.69%

2.3. Coverage

Mean	3.1747

Standard Deviation	25.0237

2.4. Mapping Quality

Mean Mapping Quality	49.3

2.5. Mismatches and indels

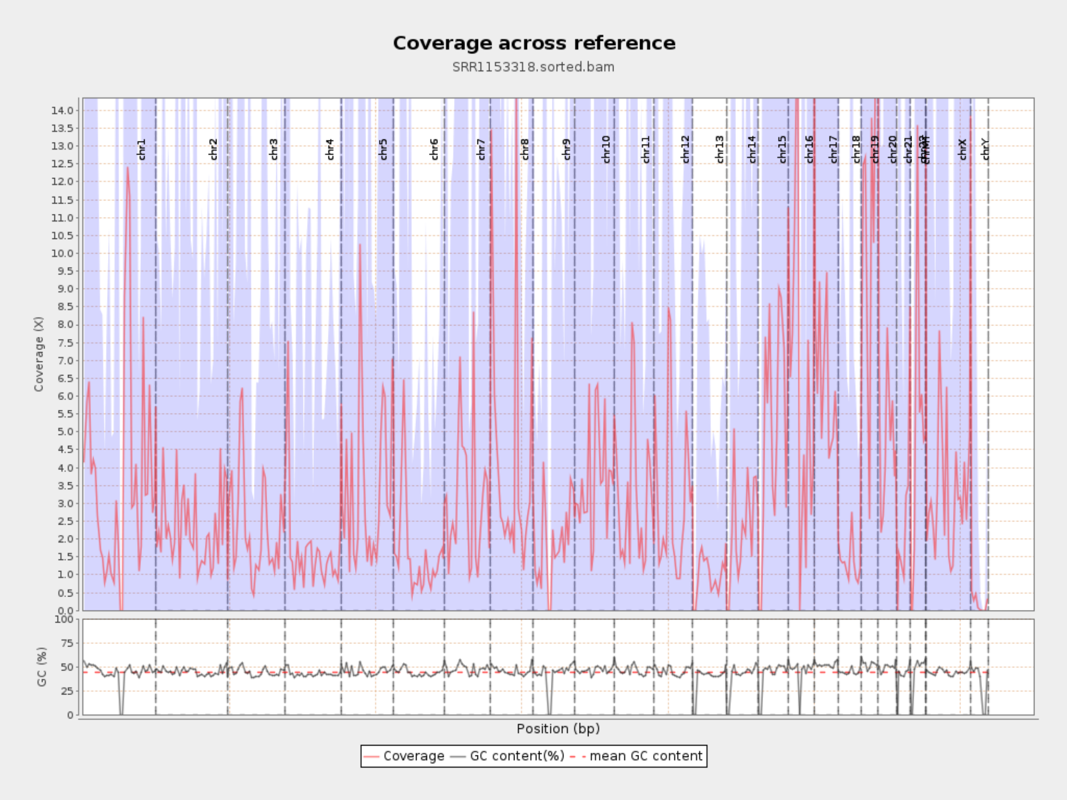
General error rate	0.38%
Mismatches	36,727,876
Insertions	578,784
Mapped reads with at least one insertion	0.57%
Deletions	760,268
Mapped reads with at least one deletion	0.75%
Homopolymer indels	45.66%

2.6. Chromosome stats

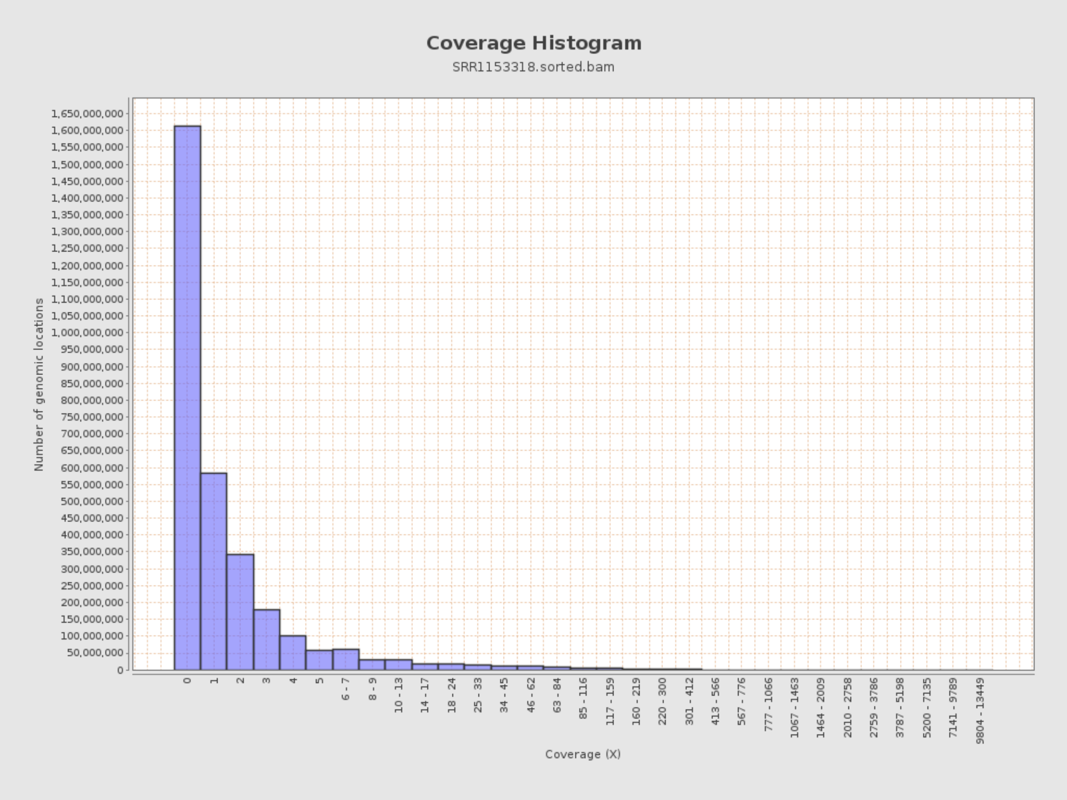
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	915994674	3.675	21.7297
chr2	243199373	559195888	2.2993	12.7316
chr3	198022430	455545997	2.3005	12.6958
chr4	191154276	323224286	1.6909	16.7097
chr5	180915260	624348936	3.4511	50.2229
chr6	171115067	269171017	1.573	10.5303
chr7	159138663	503554242	3.1642	29.8207

chr8	146364022	612745261	4.1864	47.5902
chr9	141213431	259797349	1.8397	10.7724
chr10	135534747	495932019	3.6591	20.114
chr11	135006516	434594689	3.2191	15.101
chr12	133851895	435983367	3.2572	16.4013
chr13	115169878	111793487	0.9707	5.8708
chr14	107349540	247554096	2.3061	13.0129
chr15	102531392	507935045	4.9539	27.6377
chr16	90354753	564123554	6.2434	37.7793
chr17	81195210	521460694	6.4223	30.5386
chr18	78077248	104428488	1.3375	10.7364
chr19	59128983	665101029	11.2483	45.2801
chr20	63025520	296316491	4.7015	21.8991
chr21	48129895	124428668	2.5853	24.6395
chr22	51304566	254904471	4.9685	31.0068
chrMT	16571	217109	13.1017	5.0801
chrX	155270560	527983698	3.4004	18.1999
chrY	59373566	11616709	0.1957	8.9928

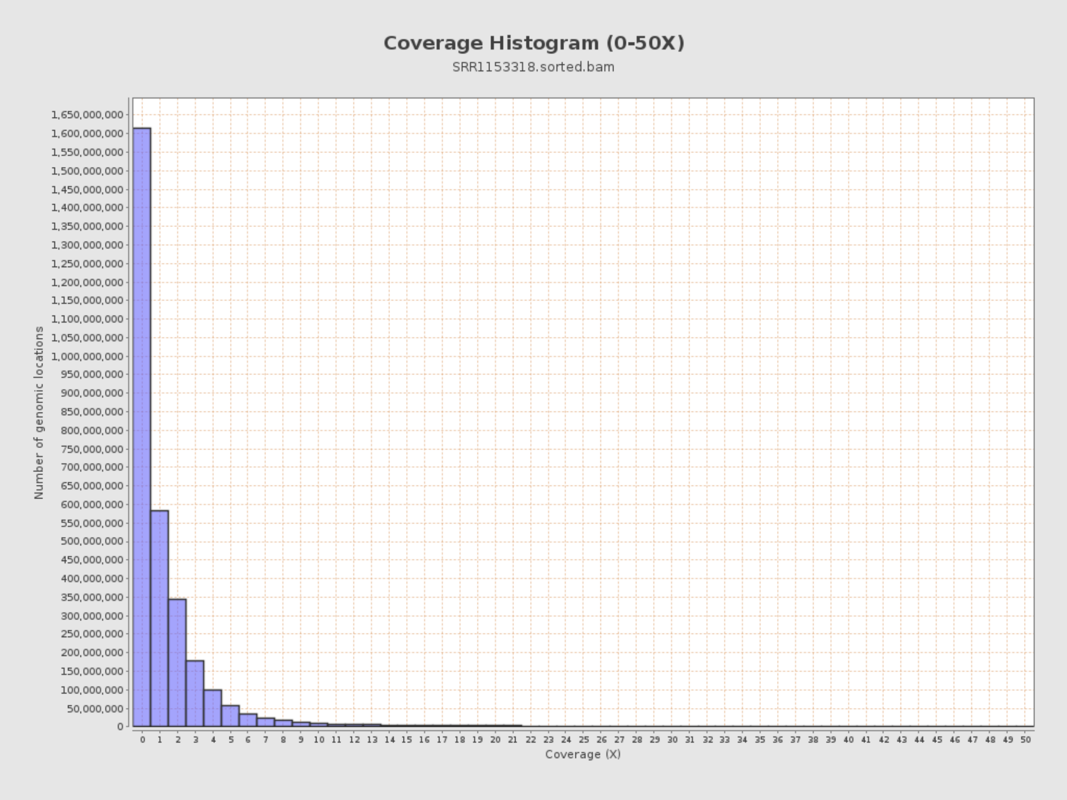
3. Results : Coverage across reference



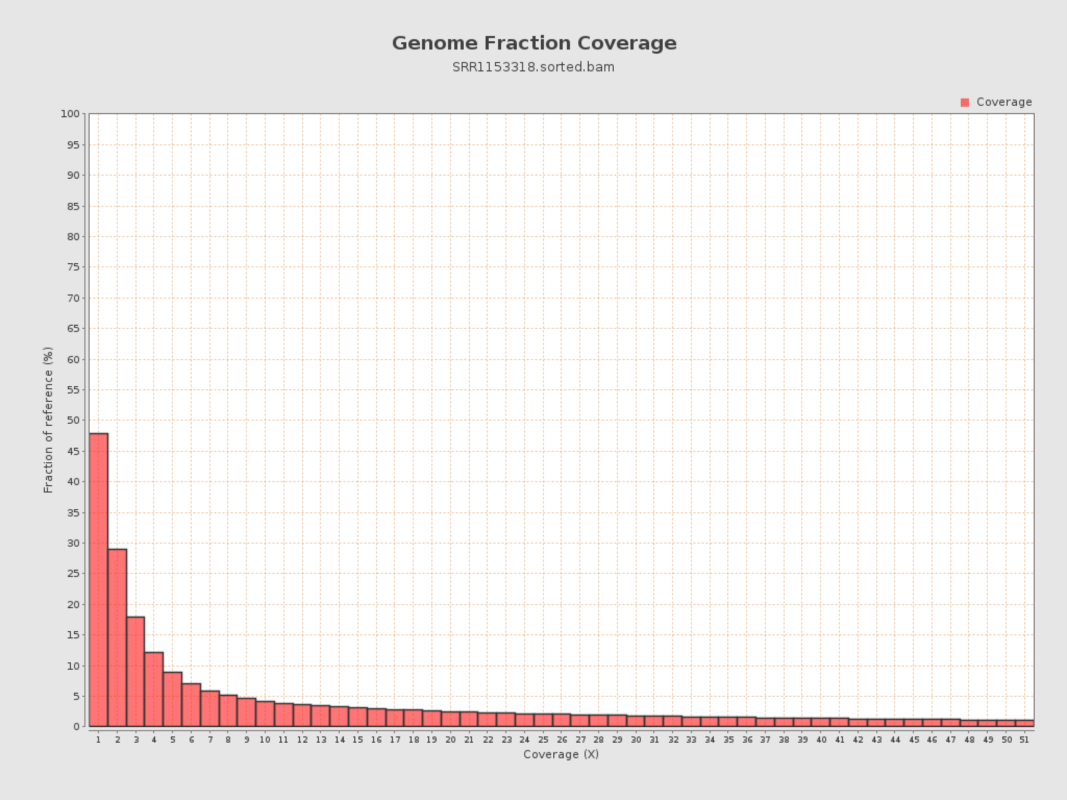
4. Results : Coverage Histogram



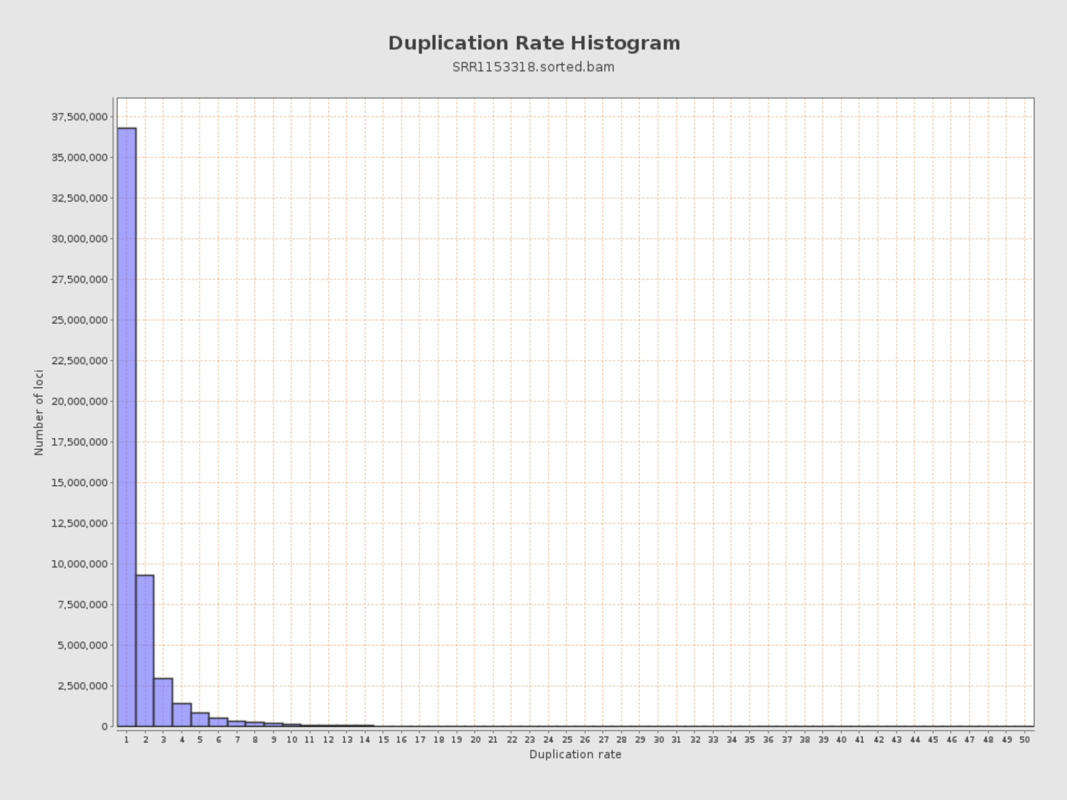
5. Results : Coverage Histogram (0-50X)



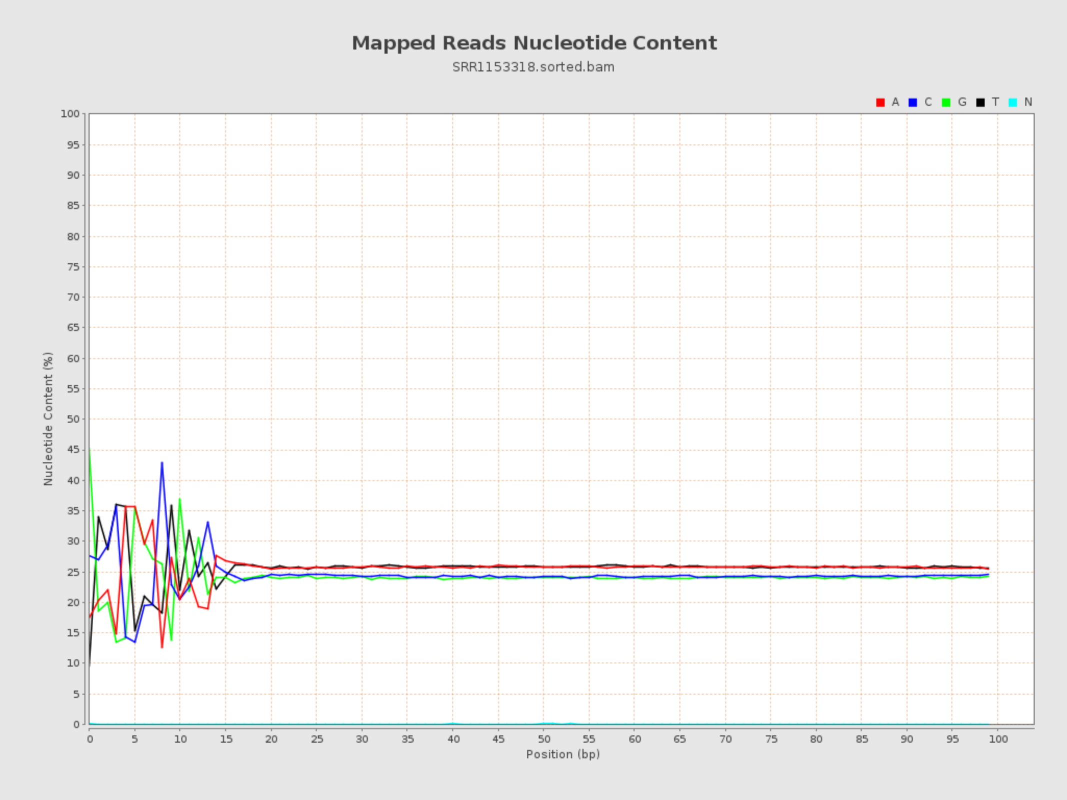
6. Results : Genome Fraction Coverage



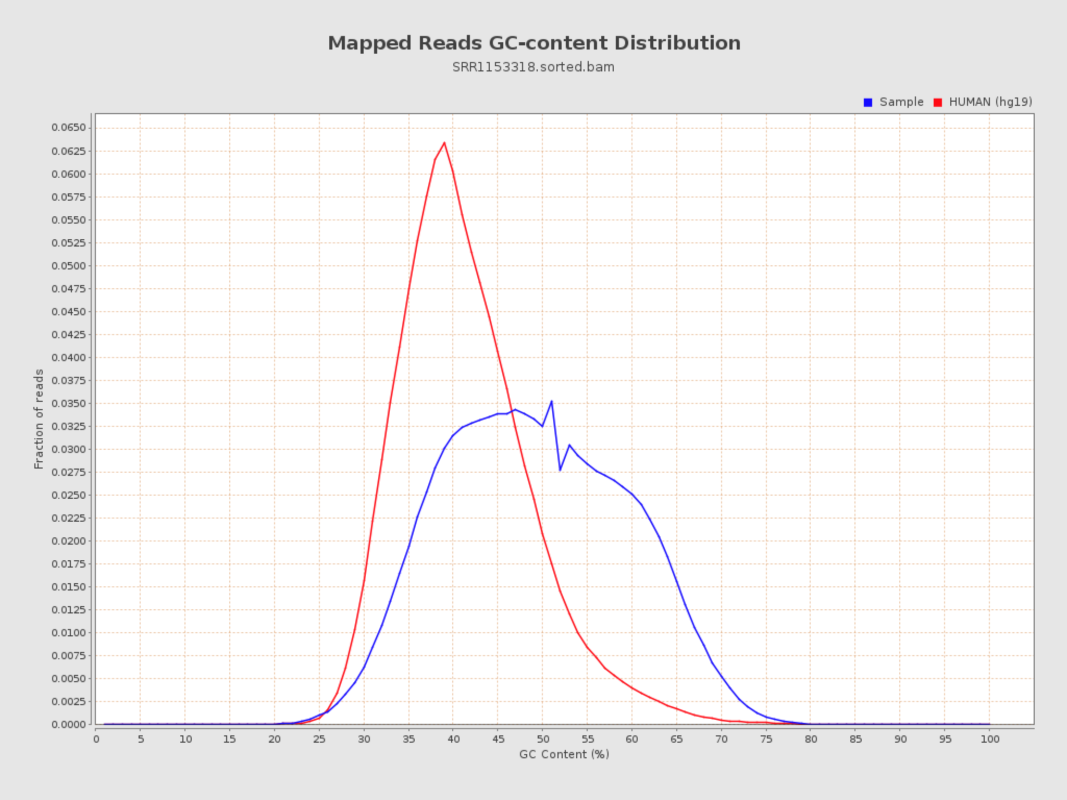
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

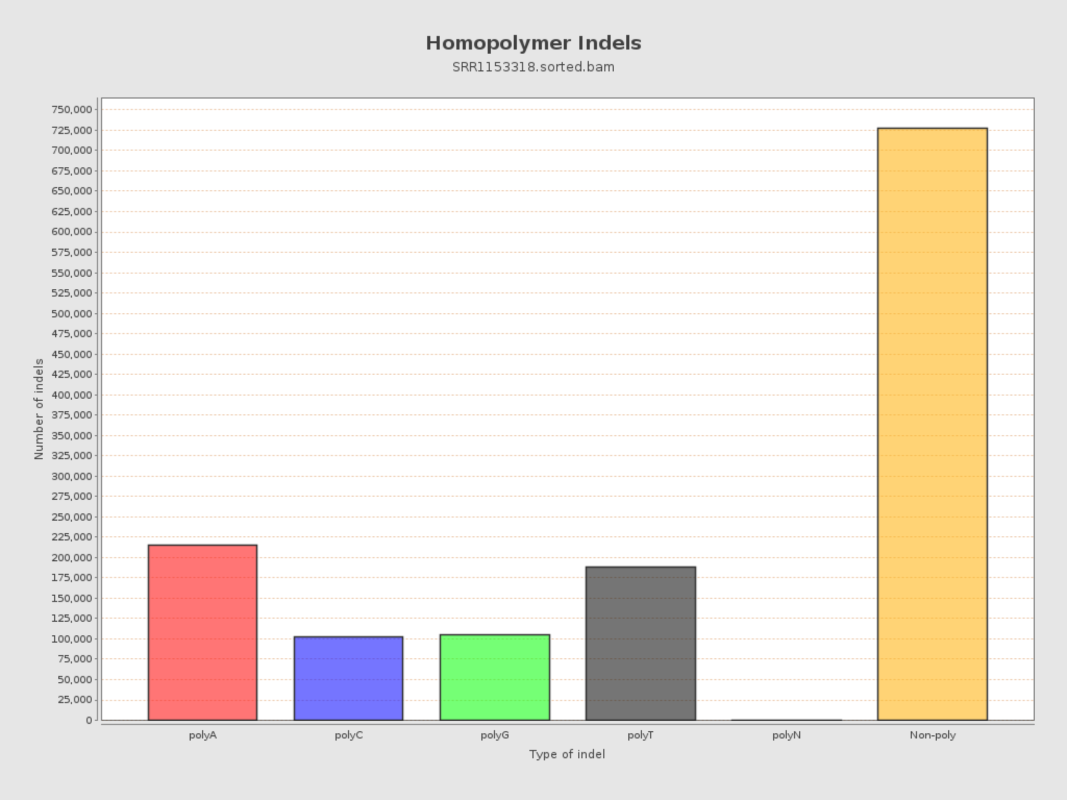


9. Results : Mapped Reads GC-content Distribution

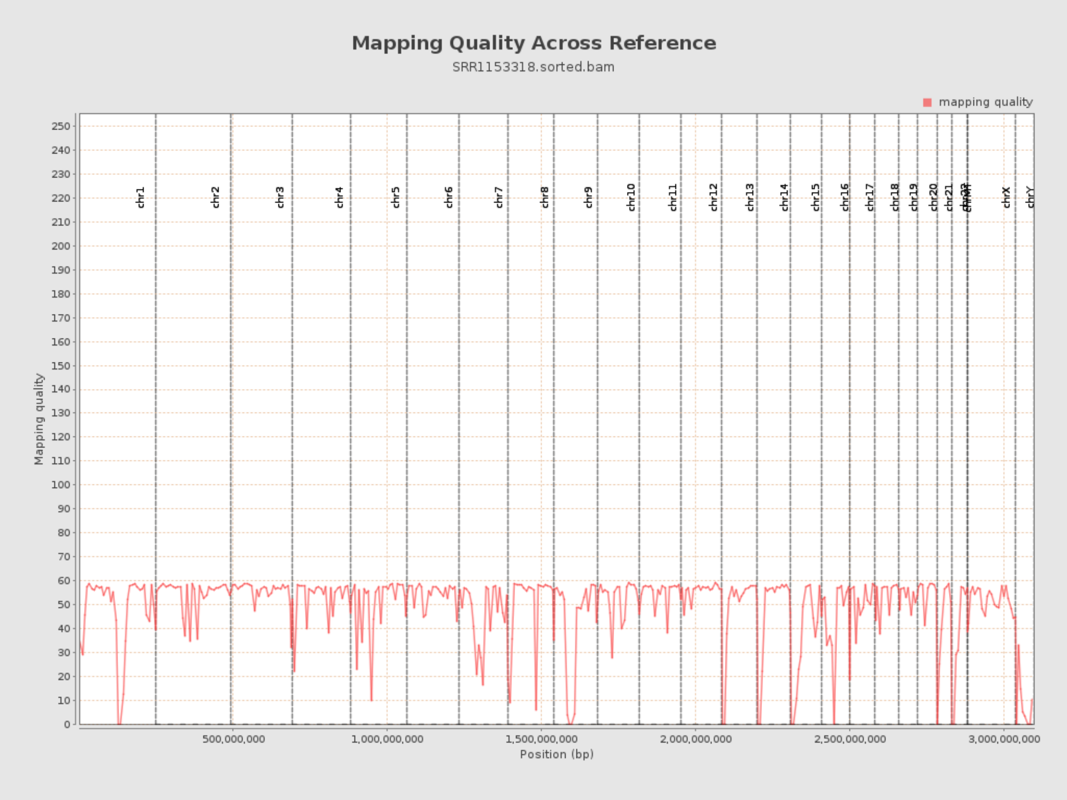


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram