Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 12:26:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153316.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_SRR1153316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153316.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 12:26:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	142,741,762
Mapped reads	139,098,449 / 97.45%
Unmapped reads	3,643,313 / 2.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	863,059 / 0.6%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	70,624,479 / 49.48%
Duplication rate	32.6%
Clipped reads	14,353,281 / 10.06%

2.2. ACGT Content

Number/percentage of A's	3,441,639,592 / 25.31%
Number/percentage of C's	3,357,579,446 / 24.69%
Number/percentage of T's	3,472,627,396 / 25.54%
Number/percentage of G's	3,323,060,177 / 24.44%
Number/percentage of N's	2,208,406 / 0.02%
GC Percentage	49.13%

2.3. Coverage

Mean	4.393

Standard Deviation	33.6217

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

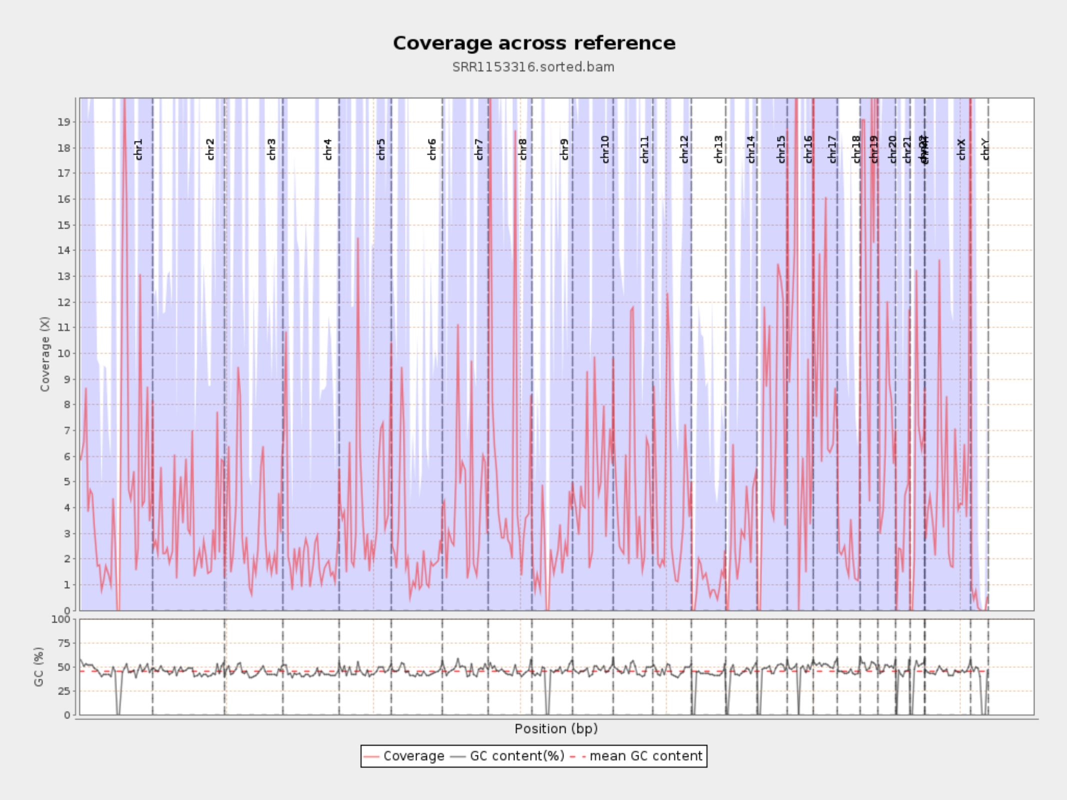
General error rate	0.4%
Mismatches	53,087,149
Insertions	789,552
Mapped reads with at least one insertion	0.56%
Deletions	1,021,679
Mapped reads with at least one deletion	0.72%
Homopolymer indels	45.04%

2.6. Chromosome stats

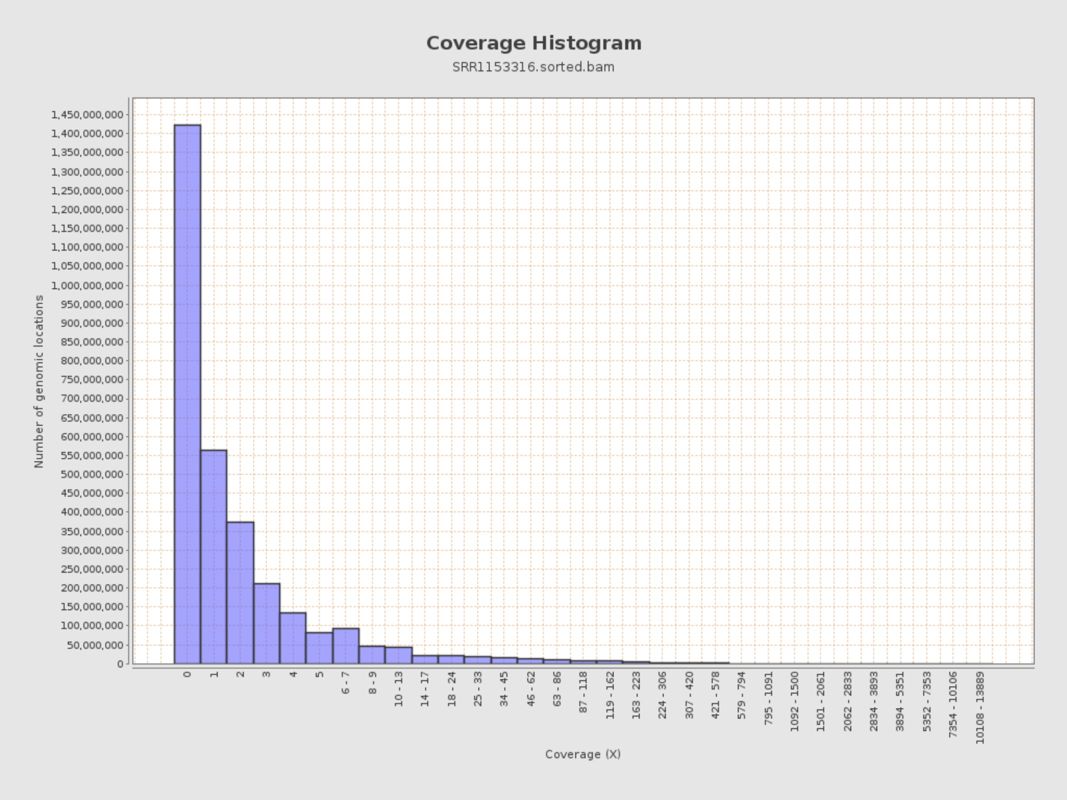
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1256081053	5.0394	31.9866
chr2	243199373	789756266	3.2474	19.1171
chr3	198022430	646839666	3.2665	17.7809
chr4	191154276	454694258	2.3787	22.5597
chr5	180915260	798752489	4.4151	54.0825
chr6	171115067	393241870	2.2981	13.7547
chr7	159138663	666597636	4.1888	47.7078

chr8	146364022	820157831	5.6035	65.0289
chr9	141213431	307438715	2.1771	12.4211
chr10	135534747	698389206	5.1528	26.7085
chr11	135006516	650661063	4.8195	22.676
chr12	133851895	567237125	4.2378	20.6989
chr13	115169878	117139412	1.0171	6.9313
chr14	107349540	319708492	2.9782	15.8846
chr15	102531392	727093628	7.0914	40.1548
chr16	90354753	785433187	8.6928	53.6155
chr17	81195210	749656015	9.2328	46.6326
chr18	78077248	162201220	2.0774	12.1163
chr19	59128983	942865682	15.9459	61.1048
chr20	63025520	459162197	7.2853	35.187
chr21	48129895	178871266	3.7164	32.3243
chr22	51304566	292761497	5.7063	30.6518
chrMT	16571	63928	3.8578	2.5706
chrX	155270560	795785800	5.1252	29.3187
chrY	59373566	18805526	0.3167	14.3185

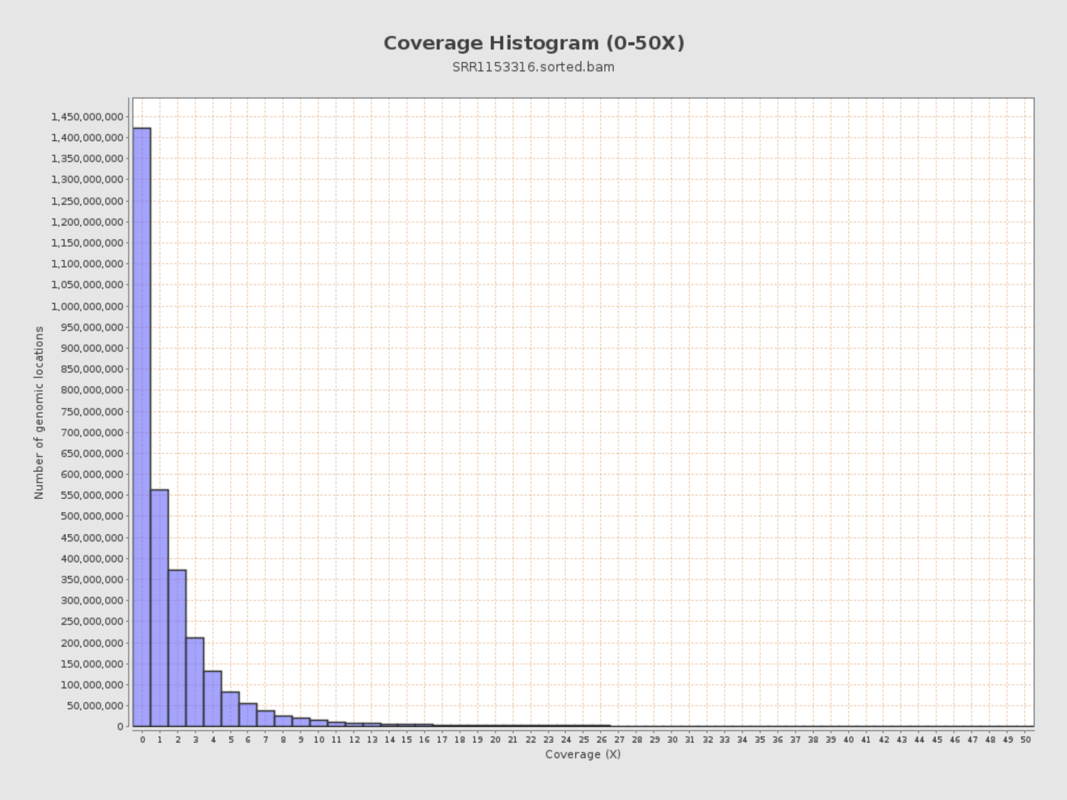
3. Results : Coverage across reference



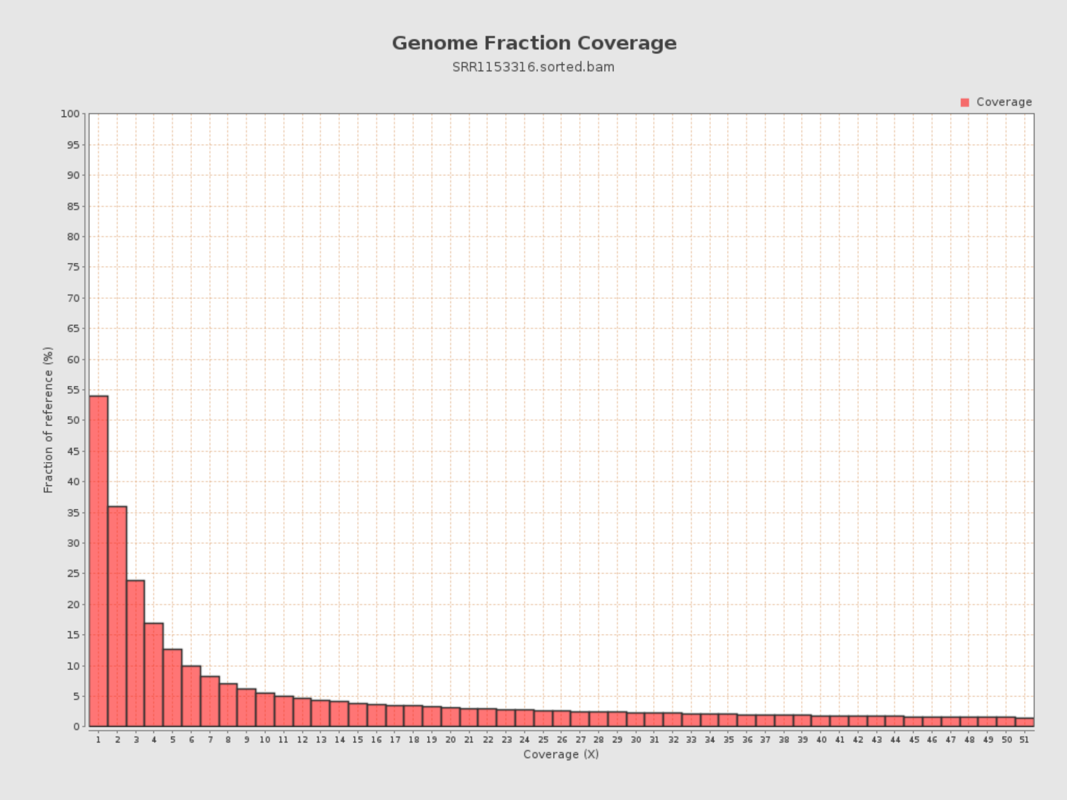
4. Results : Coverage Histogram



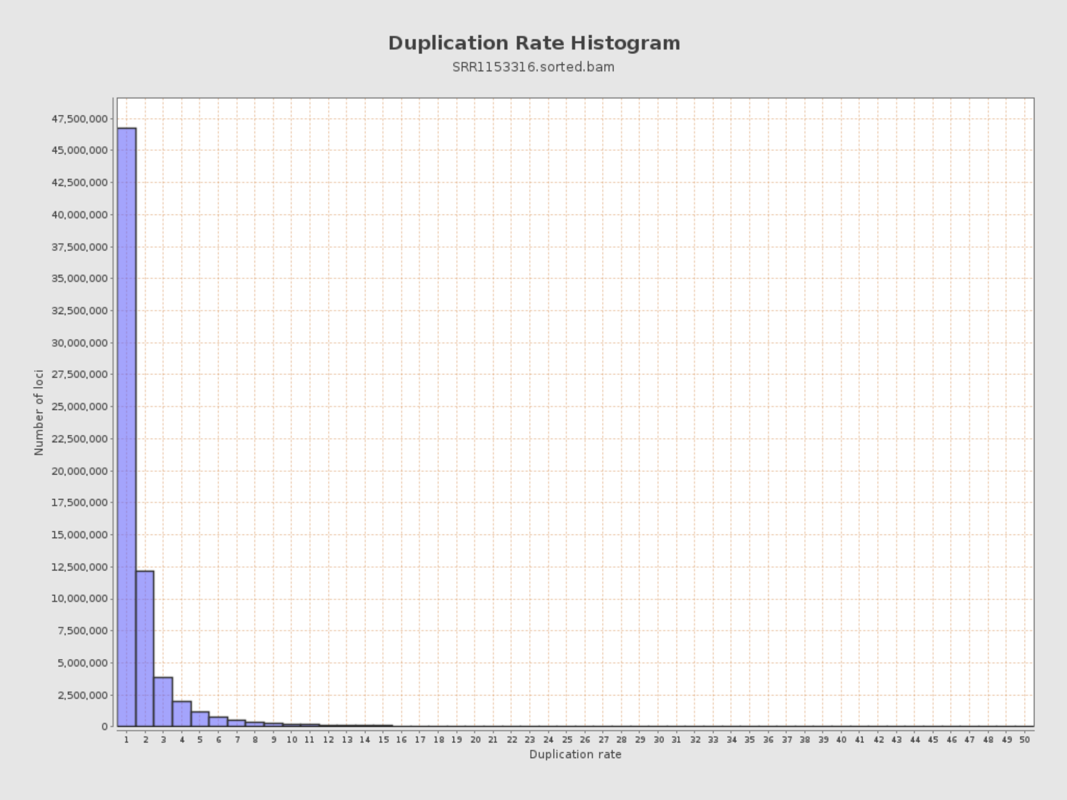
5. Results : Coverage Histogram (0-50X)



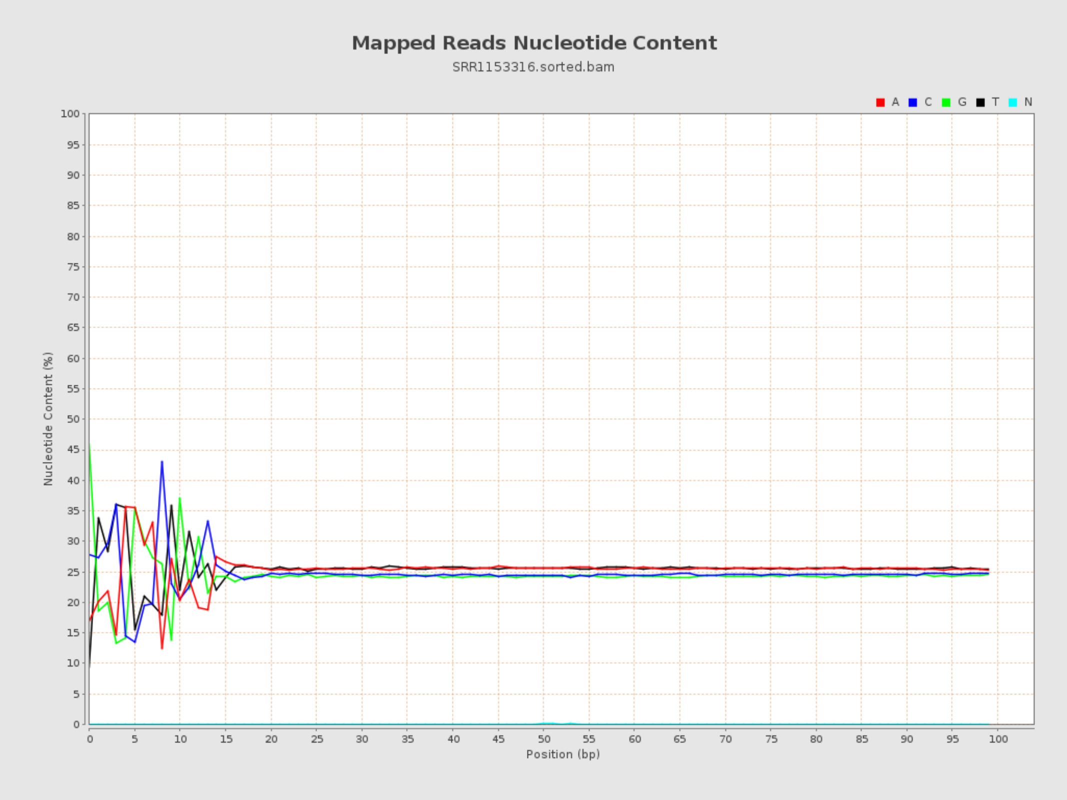
6. Results : Genome Fraction Coverage



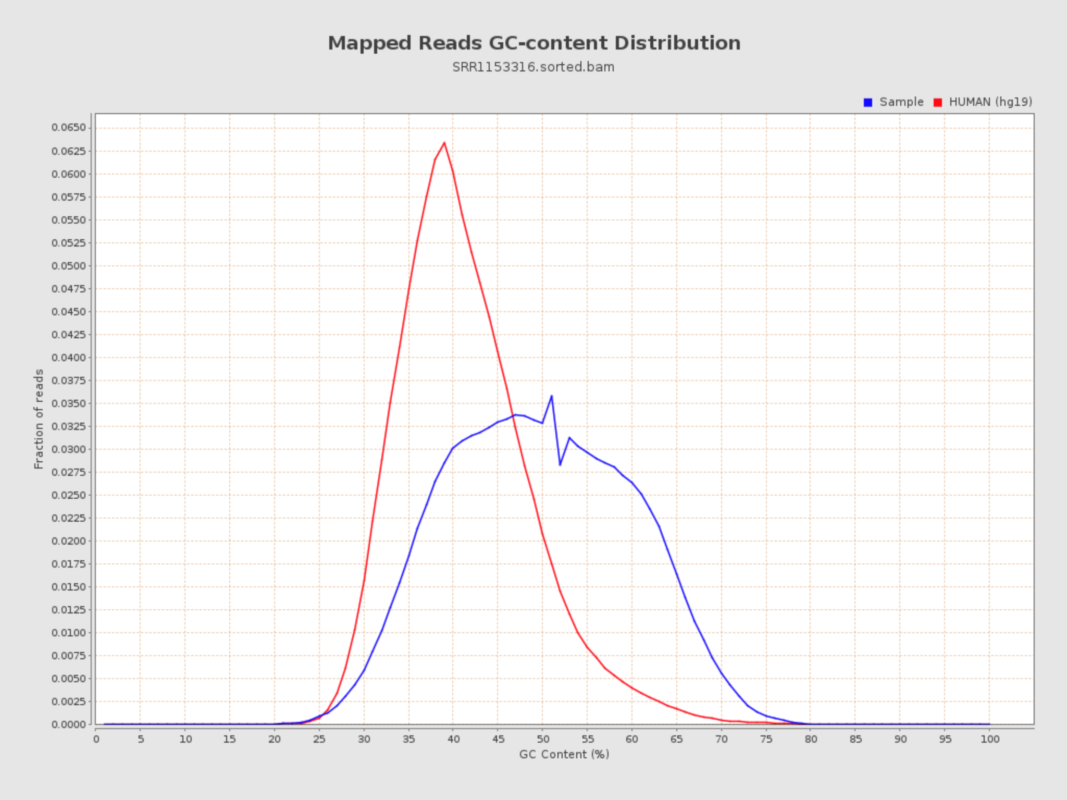
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

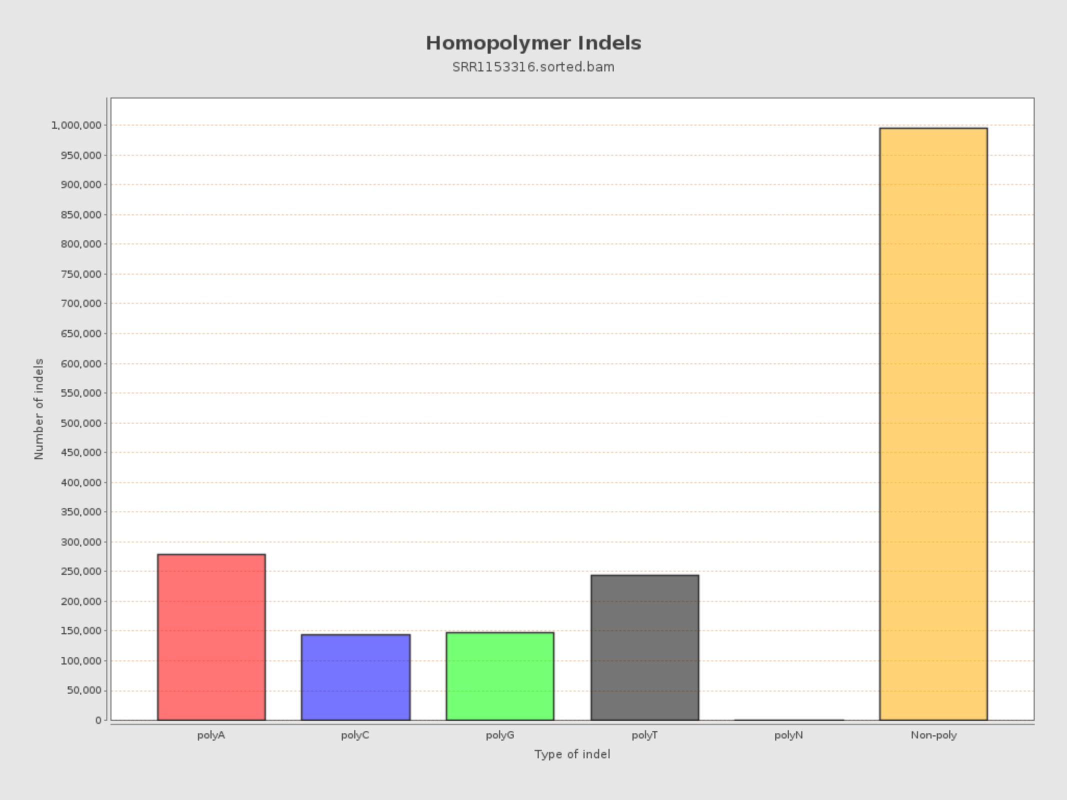


9. Results : Mapped Reads GC-content Distribution

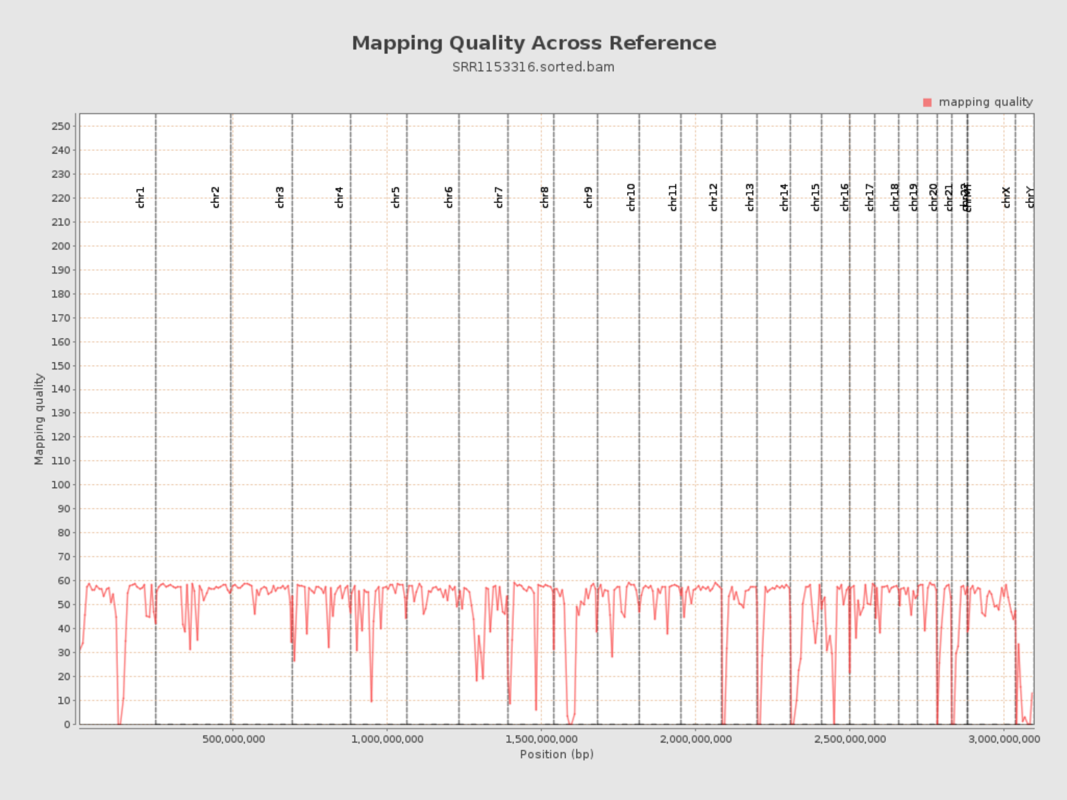


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram