Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 12:51:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514738.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_SRR5514738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 12:51:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	225,727,008
Mapped reads	217,212,695 / 96.23%
Unmapped reads	8,514,313 / 3.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,921,276 / 3.51%
Read min/max/mean length	30 / 100 / 99.82
Duplicated reads (estimated)	175,597,314 / 77.79%
Duplication rate	42.9%
Clipped reads	48,153,528 / 21.33%

2.2. ACGT Content

Number/percentage of A's	5,311,363,168 / 25.99%
Number/percentage of C's	4,803,031,064 / 23.5%
Number/percentage of T's	5,343,138,623 / 26.15%
Number/percentage of G's	4,827,354,515 / 23.62%
Number/percentage of N's	149,361,878 / 0.73%
GC Percentage	47.13%

2.3. Coverage

Mean	6.6056

Standard Deviation	206.0853

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

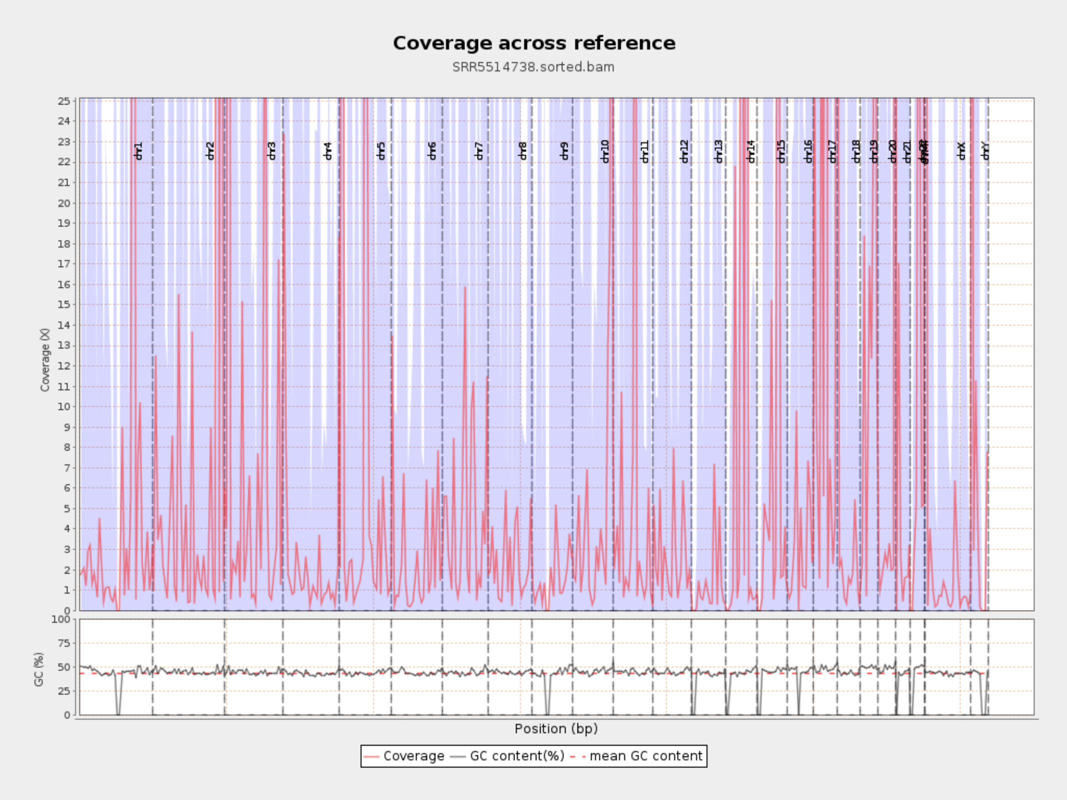
General error rate	1.16%
Mismatches	219,789,283
Insertions	8,659,122
Mapped reads with at least one insertion	3.82%
Deletions	6,280,565
Mapped reads with at least one deletion	2.77%
Homopolymer indels	39.29%

2.6. Chromosome stats

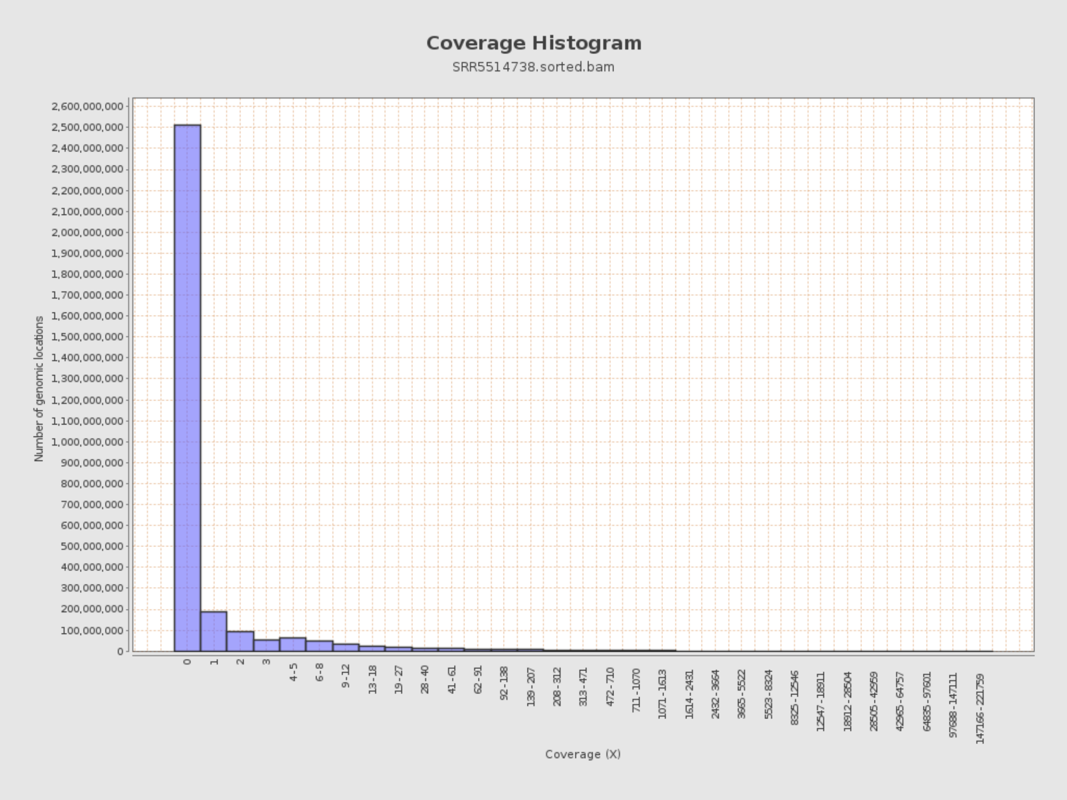
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1191098543	4.7787	145.9574
chr2	243199373	2951618841	12.1366	297.399
chr3	198022430	1908700622	9.6388	201.3722
chr4	191154276	439544383	2.2994	47.2422
chr5	180915260	1652547430	9.1344	183.1301
chr6	171115067	426847155	2.4945	69.2836
chr7	159138663	741189382	4.6575	118.6485

chr8	146364022	356201175	2.4337	34.5534
chr9	141213431	222835090	1.578	67.2424
chr10	135534747	1100343645	8.1185	145.5153
chr11	135006516	784688572	5.8122	134.9896
chr12	133851895	369645683	2.7616	41.8823
chr13	115169878	155479072	1.35	28.1677
chr14	107349540	1346335005	12.5416	141.5864
chr15	102531392	714680353	6.9704	66.7013
chr16	90354753	297346083	3.2909	114.497
chr17	81195210	2180369474	26.8534	300.8367
chr18	78077248	241343348	3.0911	105.6769
chr19	59128983	891890282	15.0838	100.1574
chr20	63025520	451126387	7.1578	124.0664
chr21	48129895	196317562	4.0789	69.0773
chr22	51304566	660363044	12.8714	437.3189
chrMT	16571	33506679	2,022.0071	732.1046
chrX	155270560	547333637	3.525	423.3061
chrY	59373566	587682990	9.8981	698.9816

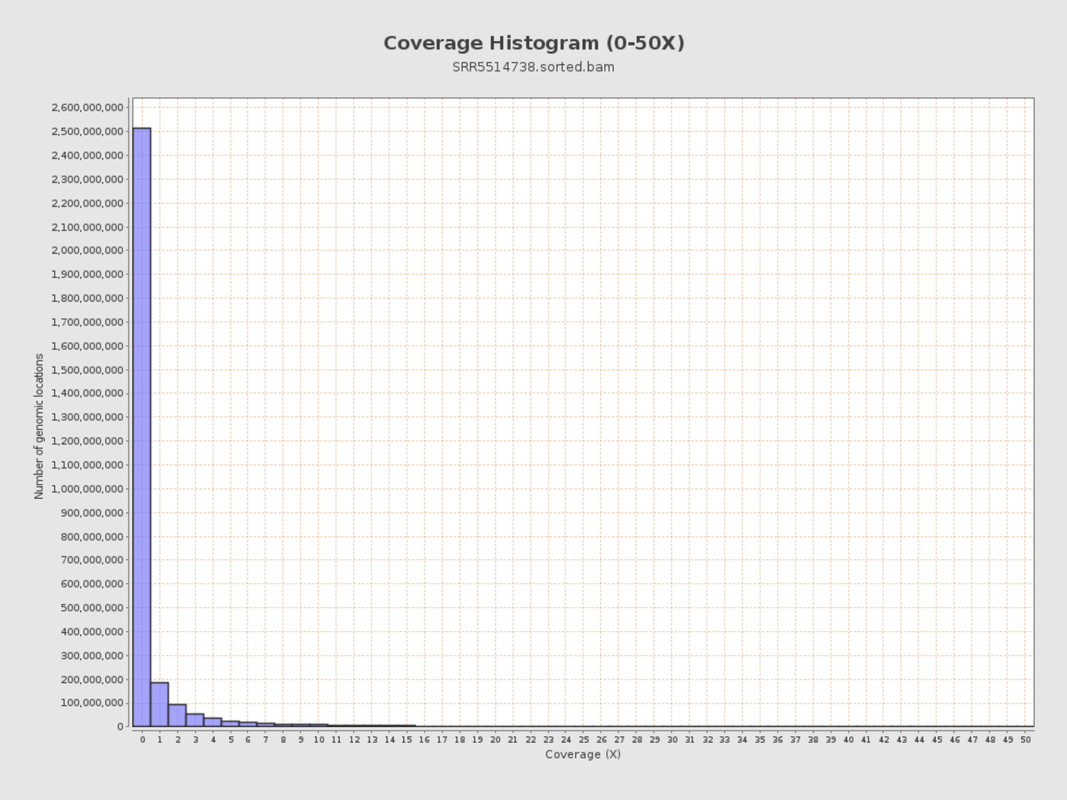
3. Results : Coverage across reference



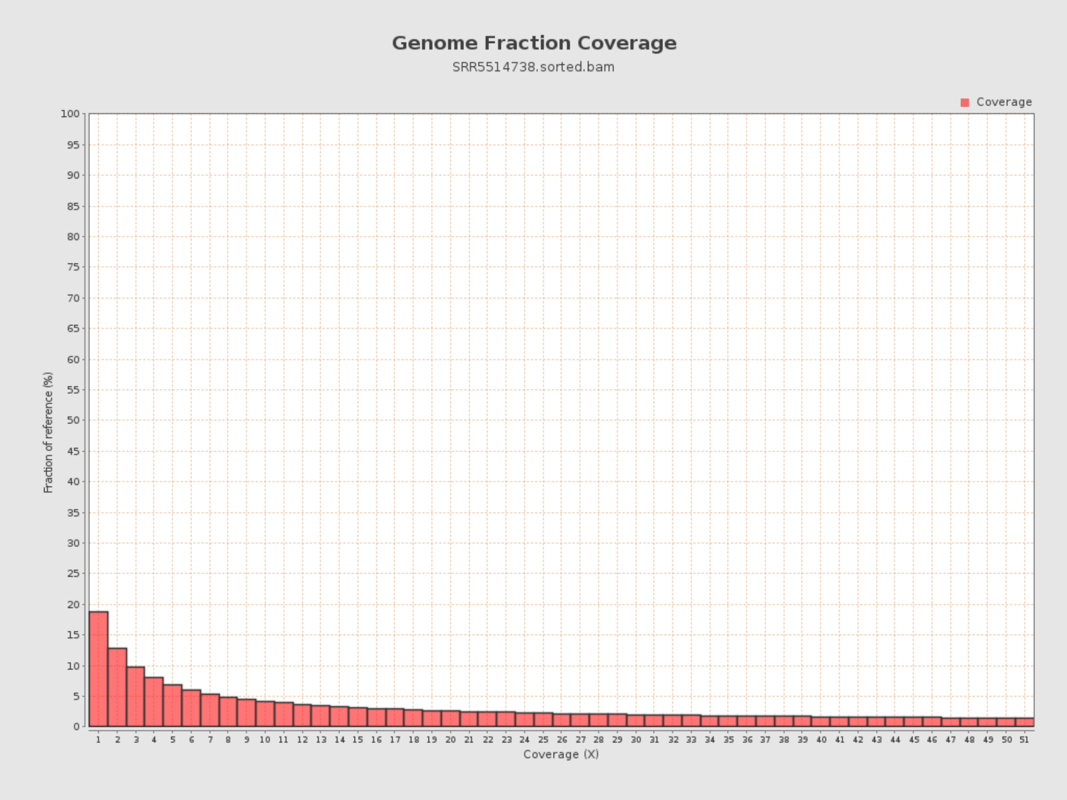
4. Results : Coverage Histogram



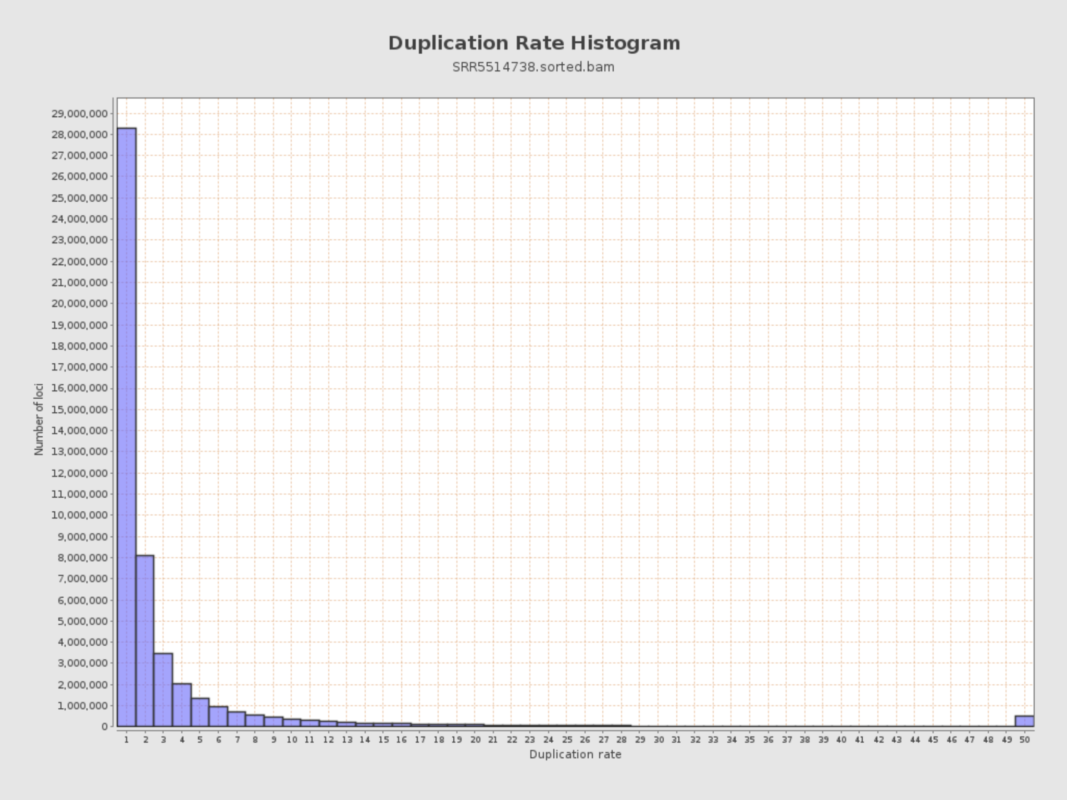
5. Results : Coverage Histogram (0-50X)



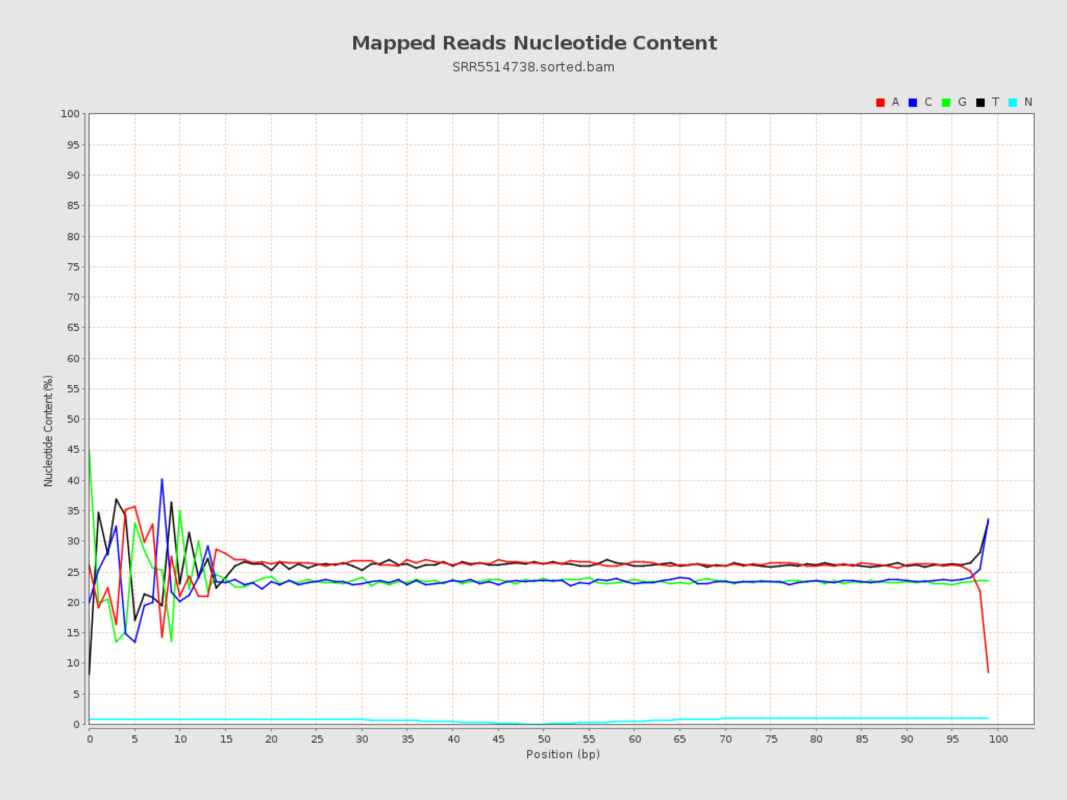
6. Results : Genome Fraction Coverage



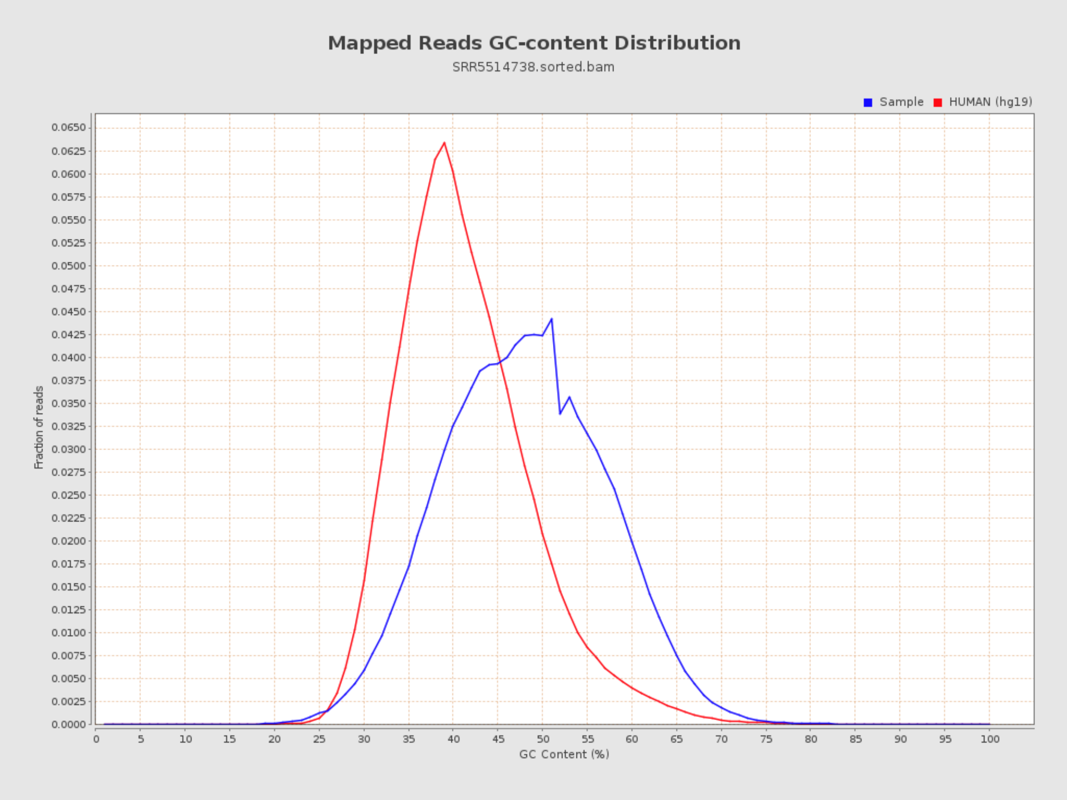
7. Results : Duplication Rate Histogram



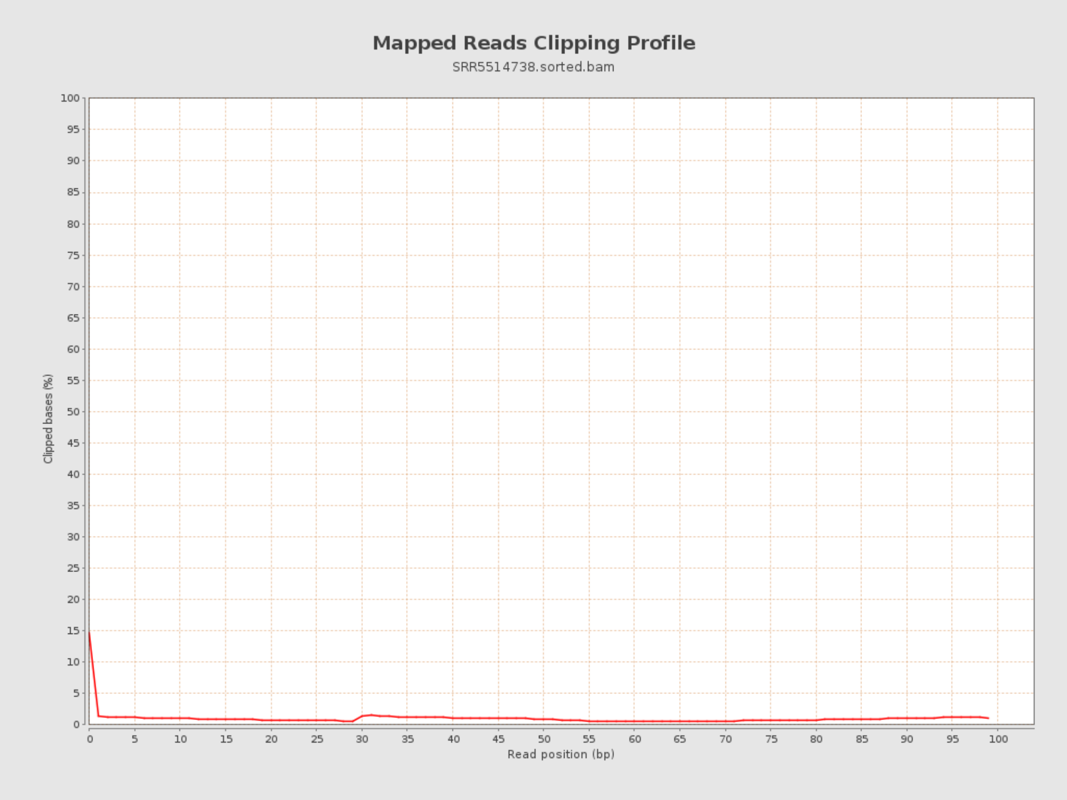
8. Results : Mapped Reads Nucleotide Content



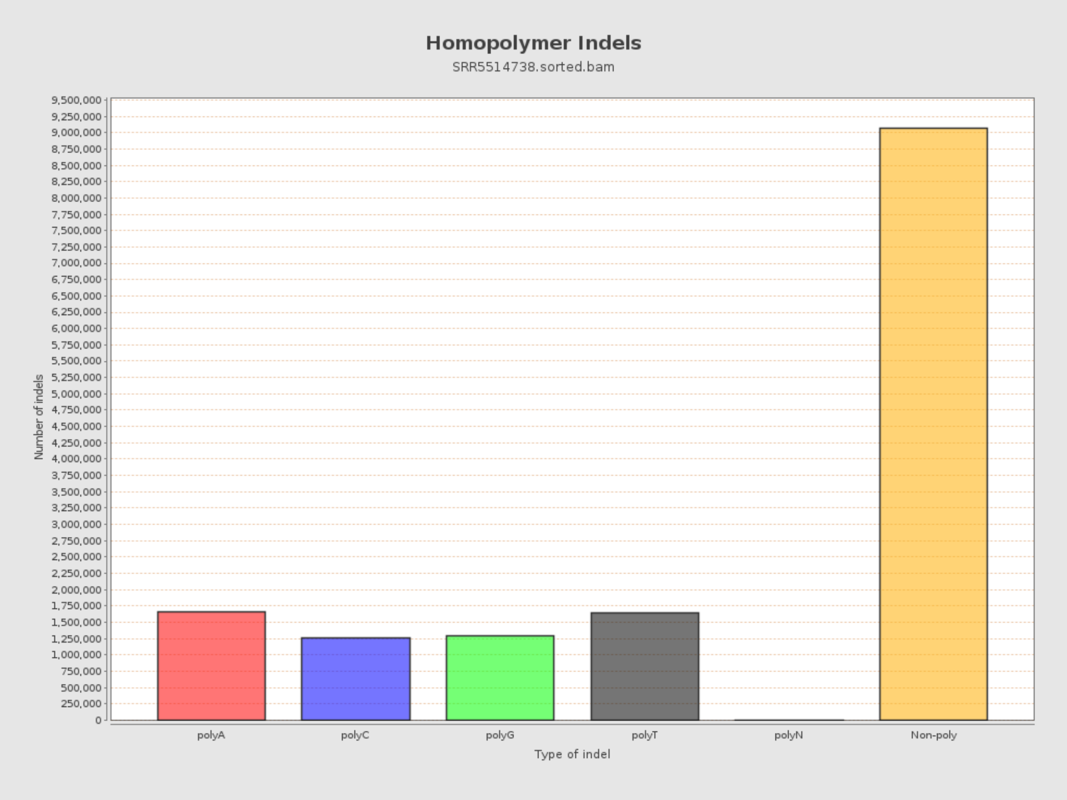
9. Results : Mapped Reads GC-content Distribution



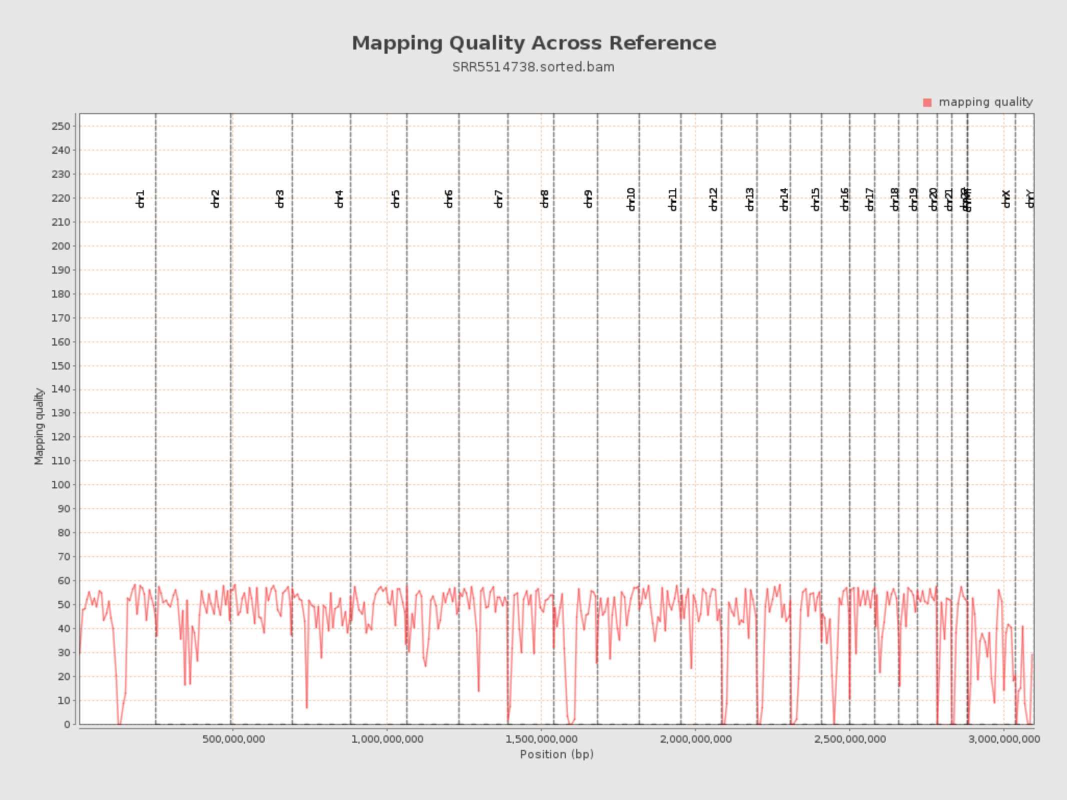
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram