Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 15:05:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163153.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_SRR1163153 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163153.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 15:05:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	80,409,386
Mapped reads	79,612,448 / 99.01%
Unmapped reads	796,938 / 0.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	402,500 / 0.5%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	42,331,547 / 52.65%
Duplication rate	41.71%
Clipped reads	6,633,581 / 8.25%

2.2. ACGT Content

Number/percentage of A's	1,907,833,903 / 24.28%
Number/percentage of C's	2,020,506,689 / 25.72%
Number/percentage of T's	1,914,010,467 / 24.36%
Number/percentage of G's	2,014,106,745 / 25.64%
Number/percentage of N's	261,081 / 0%
GC Percentage	51.35%

2.3. Coverage

Mean	2.5383

Standard Deviation	31.5685

2.4. Mapping Quality

Mean Mapping Quality	49.26

2.5. Mismatches and indels

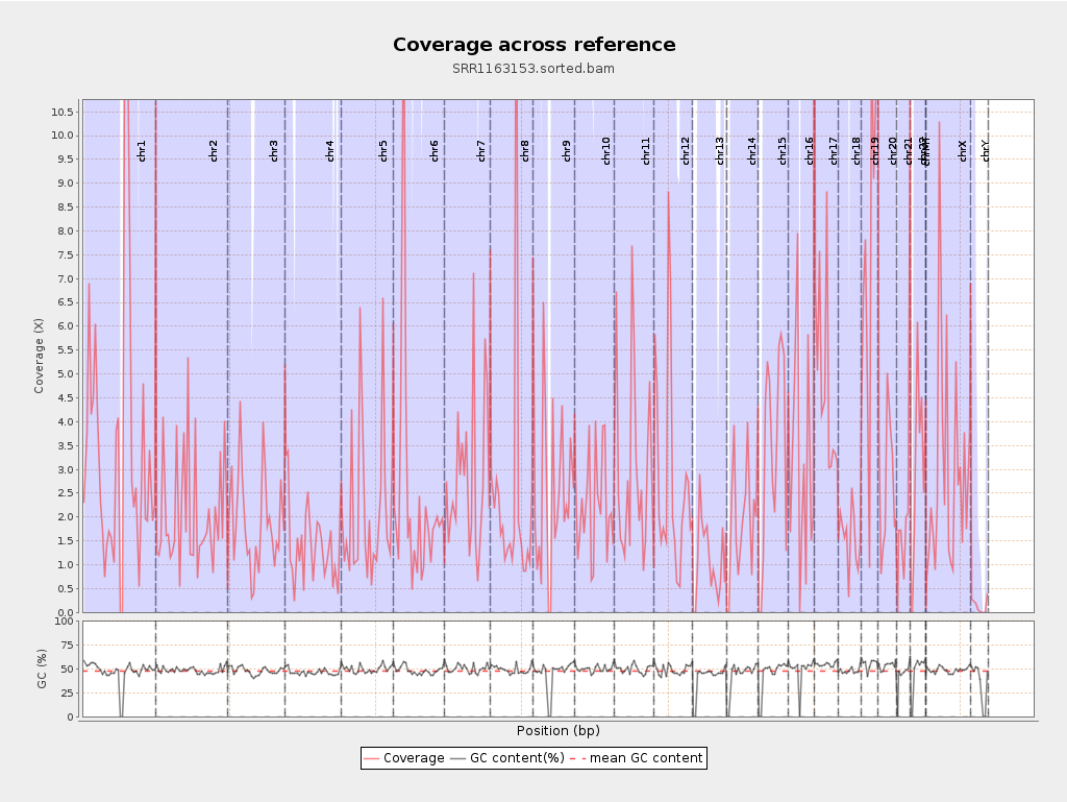
General error rate	0.32%
Mismatches	24,266,042
Insertions	558,113
Mapped reads with at least one insertion	0.69%
Deletions	390,376
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.67%

2.6. Chromosome stats

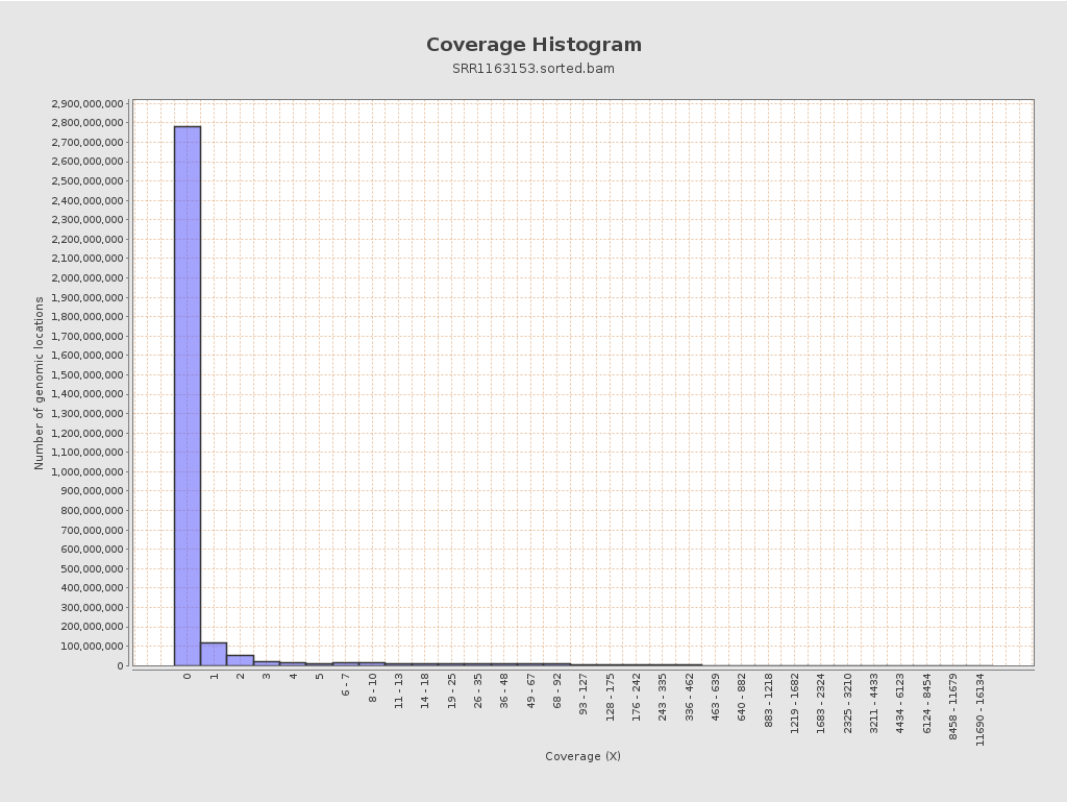
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	853187006	3.423	34.8326
chr2	243199373	500169138	2.0566	23.6535
chr3	198022430	377935060	1.9085	20.2937
chr4	191154276	270590353	1.4156	20.4127
chr5	180915260	397833094	2.199	36.0202
chr6	171115067	400713146	2.3418	29.0447
chr7	159138663	443630667	2.7877	35.0469

chr8	146364022	355379687	2.4281	49.3693
chr9	141213431	339654007	2.4053	31.1201
chr10	135534747	307406639	2.2681	24.5116
chr11	135006516	405657544	3.0047	28.452
chr12	133851895	384560208	2.873	32.6778
chr13	115169878	125231302	1.0874	13.822
chr14	107349540	205001797	1.9097	20.9434
chr15	102531392	335361881	3.2708	28.0983
chr16	90354753	283153494	3.1338	29.7273
chr17	81195210	395317564	4.8687	39.5286
chr18	78077248	122708691	1.5716	17.9496
chr19	59128983	453947544	7.6772	55.1497
chr20	63025520	166486637	2.6416	27.8922
chr21	48129895	116522936	2.421	67.4592
chr22	51304566	152931304	2.9809	29.3348
chrMT	16571	840	0.0507	0.2879
chrX	155270560	456077102	2.9373	36.073
chrY	59373566	8219325	0.1384	8.4023

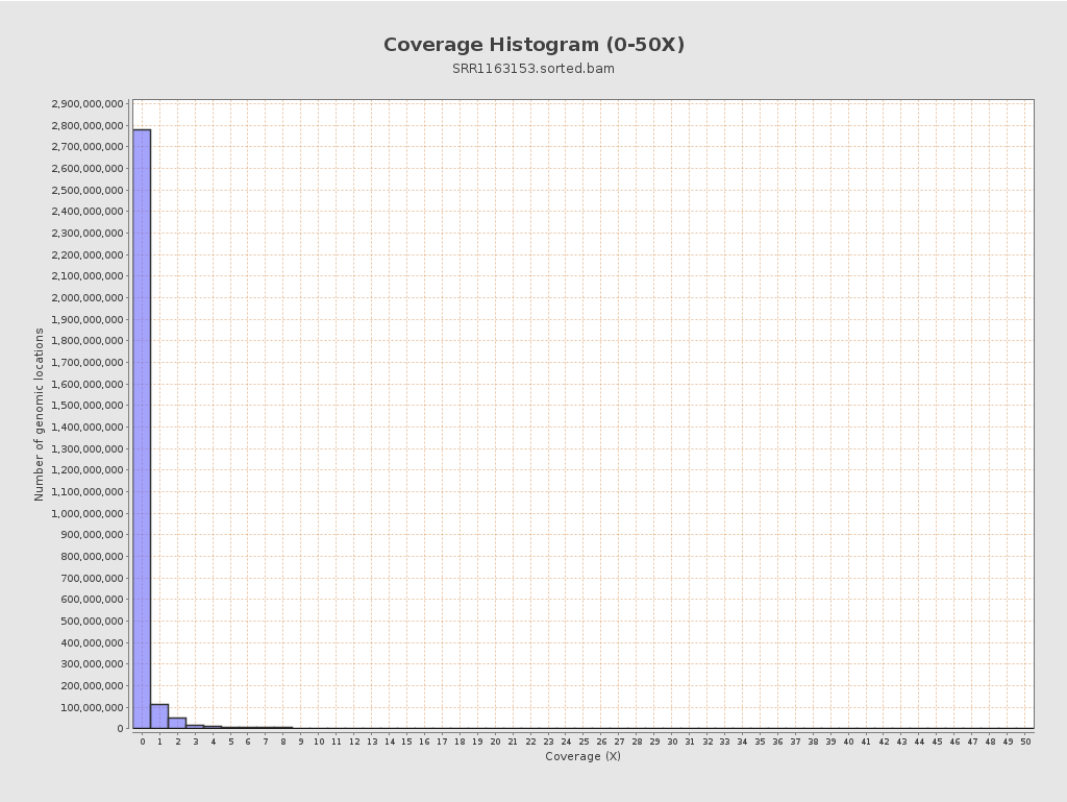
3. Results : Coverage across reference



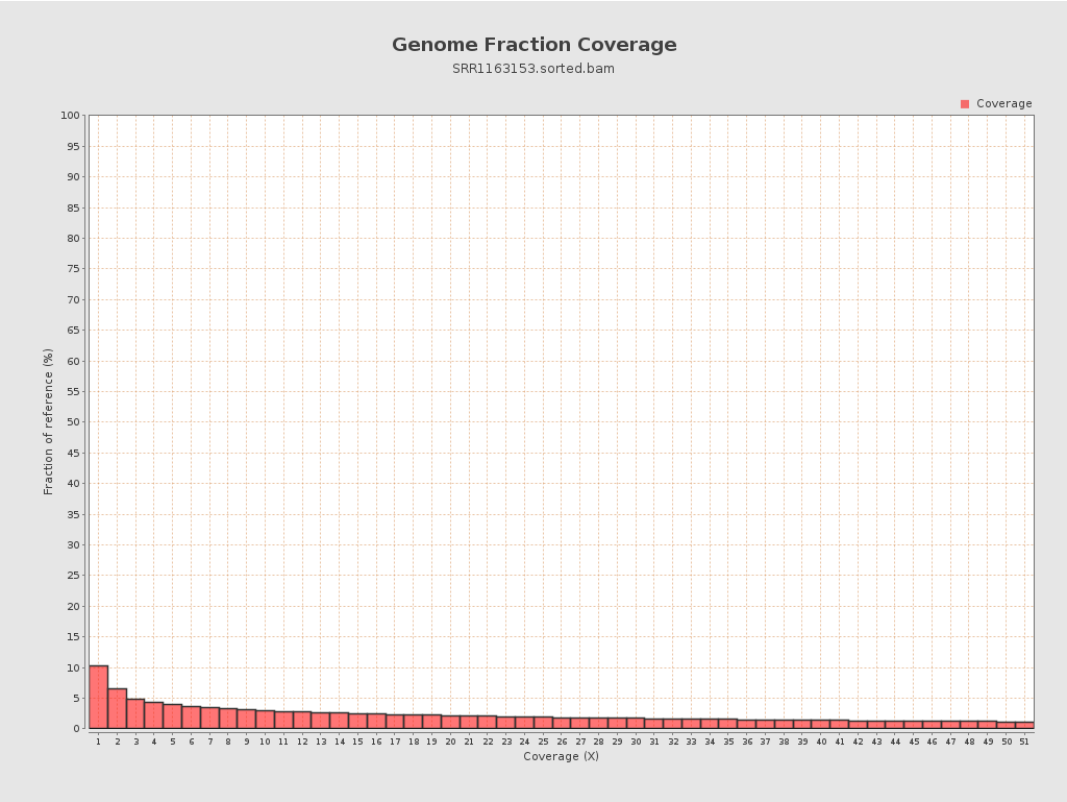
4. Results : Coverage Histogram



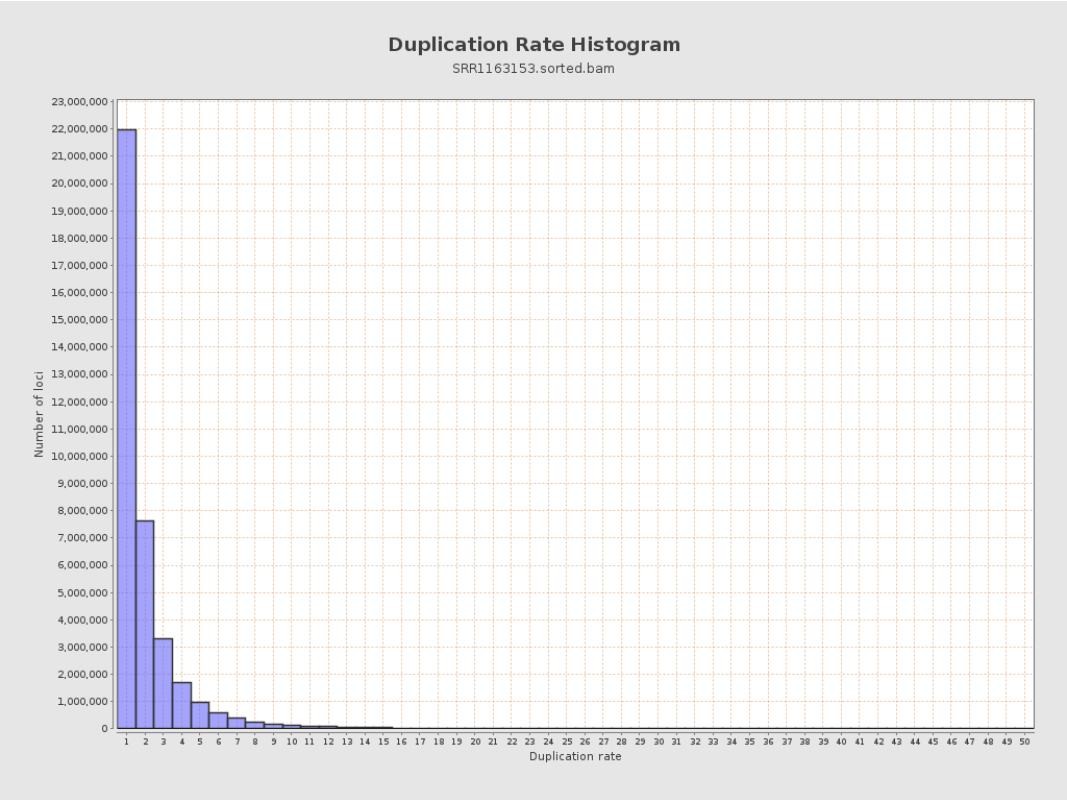
5. Results : Coverage Histogram (0-50X)



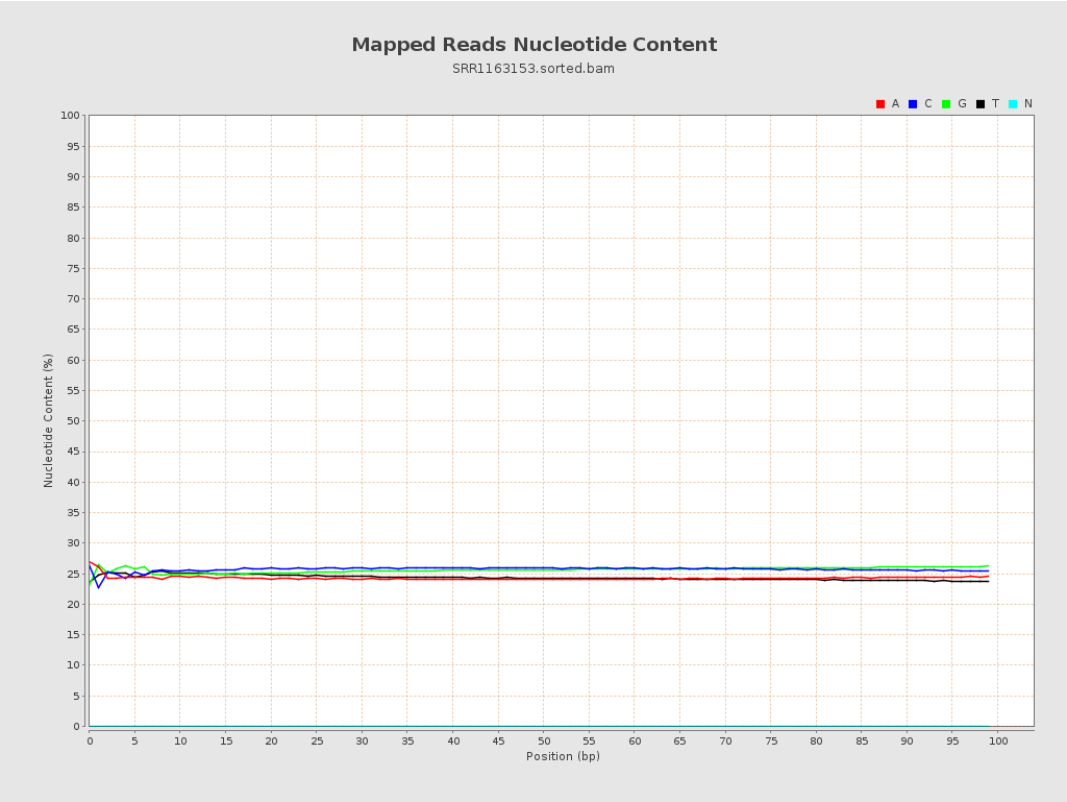
6. Results : Genome Fraction Coverage



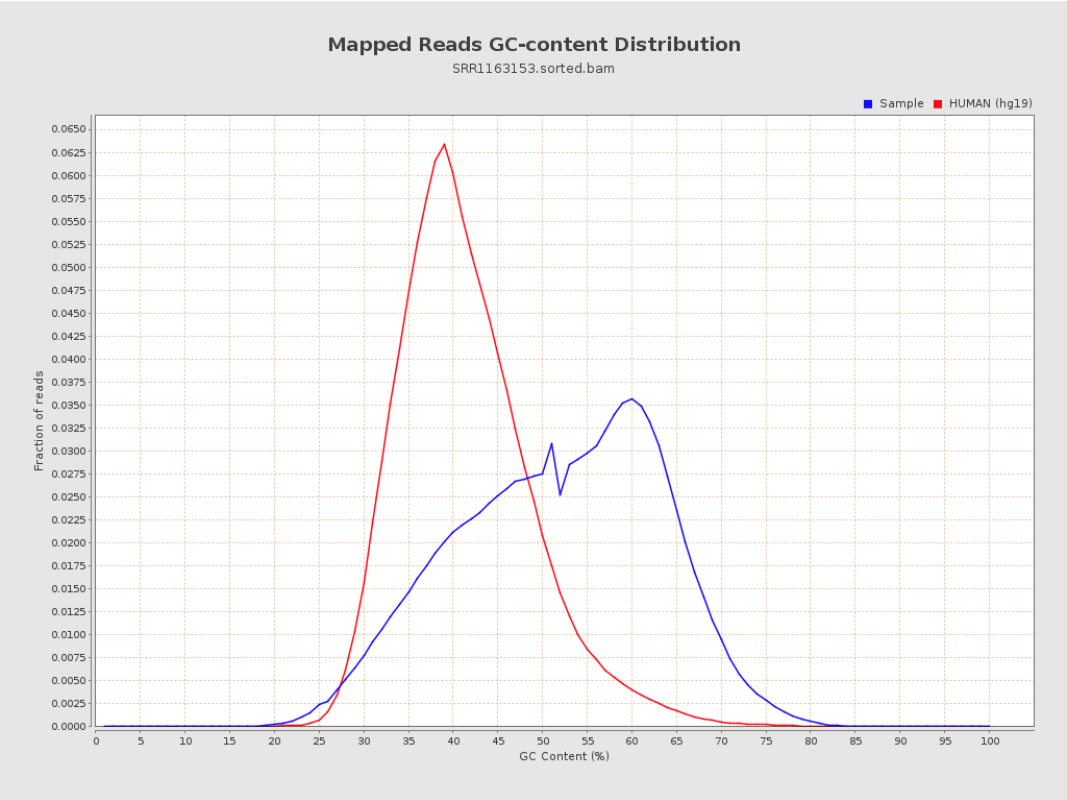
7. Results : Duplication Rate Histogram



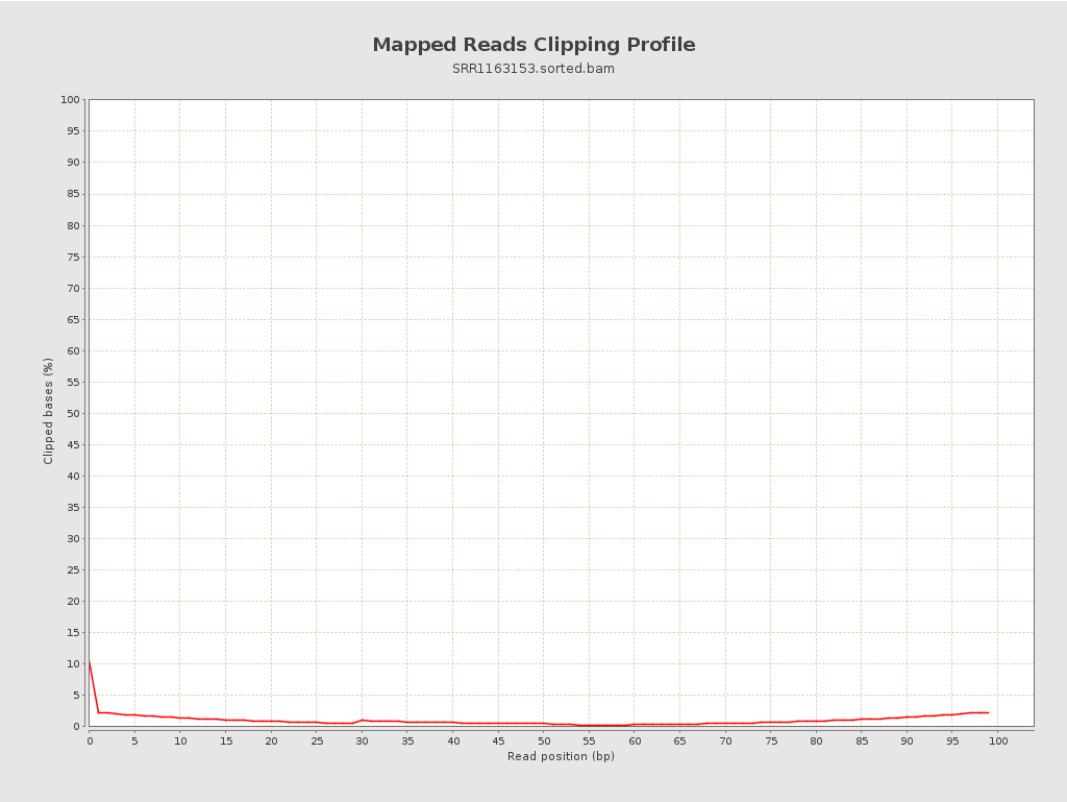
8. Results : Mapped Reads Nucleotide Content



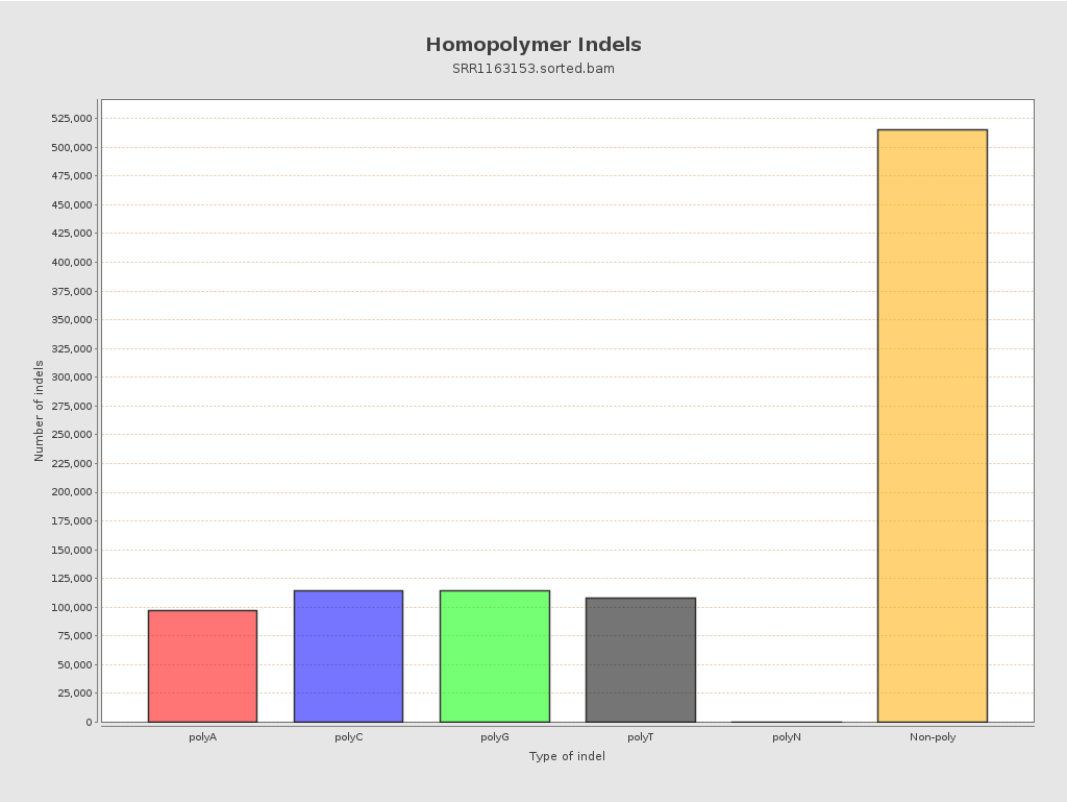
9. Results : Mapped Reads GC-content Distribution



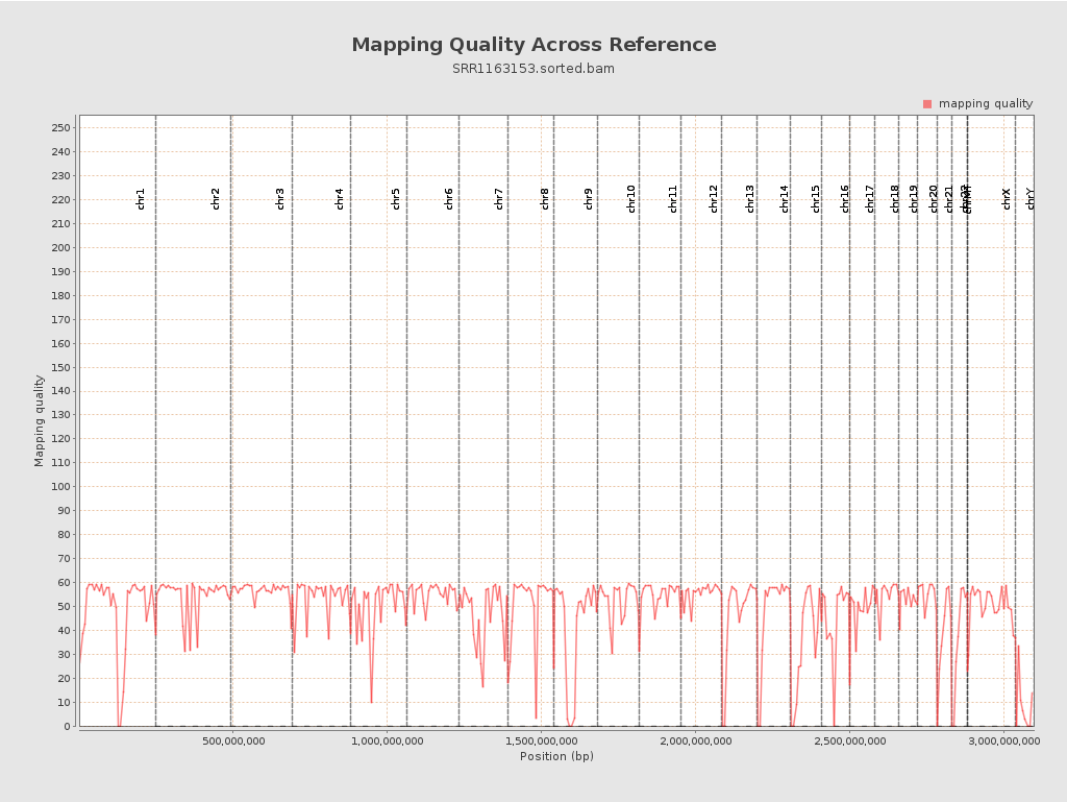
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram