Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 15:11:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153317.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_SRR1153317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 15:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	187,284,870
Mapped reads	184,215,667 / 98.36%
Unmapped reads	3,069,203 / 1.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,114,244 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	147,178,893 / 78.59%
Duplication rate	70.03%
Clipped reads	16,805,713 / 8.97%

2.2. ACGT Content

Number/percentage of A's	4,005,598,466 / 22.07%
Number/percentage of C's	5,077,151,578 / 27.98%
Number/percentage of T's	4,019,879,177 / 22.15%
Number/percentage of G's	5,038,406,983 / 27.77%
Number/percentage of N's	5,322,416 / 0.03%
GC Percentage	55.74%

2.3. Coverage

Mean	5.8625

Standard Deviation	75.2194

2.4. Mapping Quality

Mean Mapping Quality	48.51

2.5. Mismatches and indels

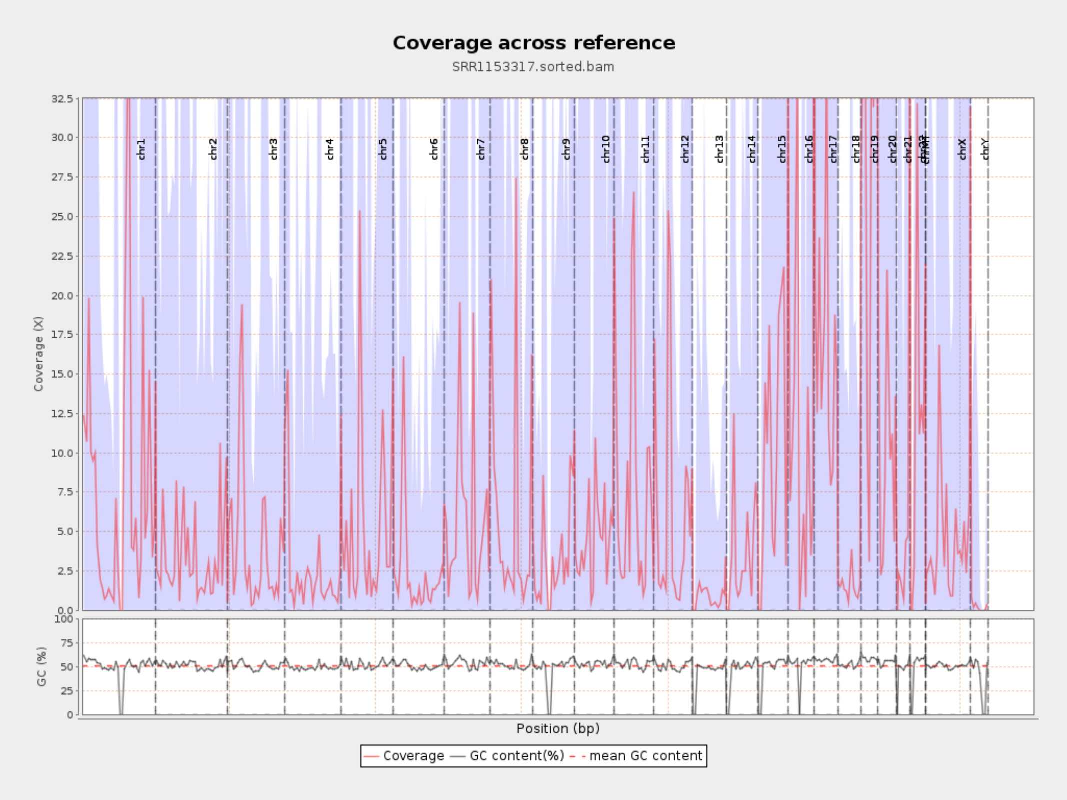
General error rate	0.43%
Mismatches	76,076,072
Insertions	687,154
Mapped reads with at least one insertion	0.37%
Deletions	794,037
Mapped reads with at least one deletion	0.42%
Homopolymer indels	38.79%

2.6. Chromosome stats

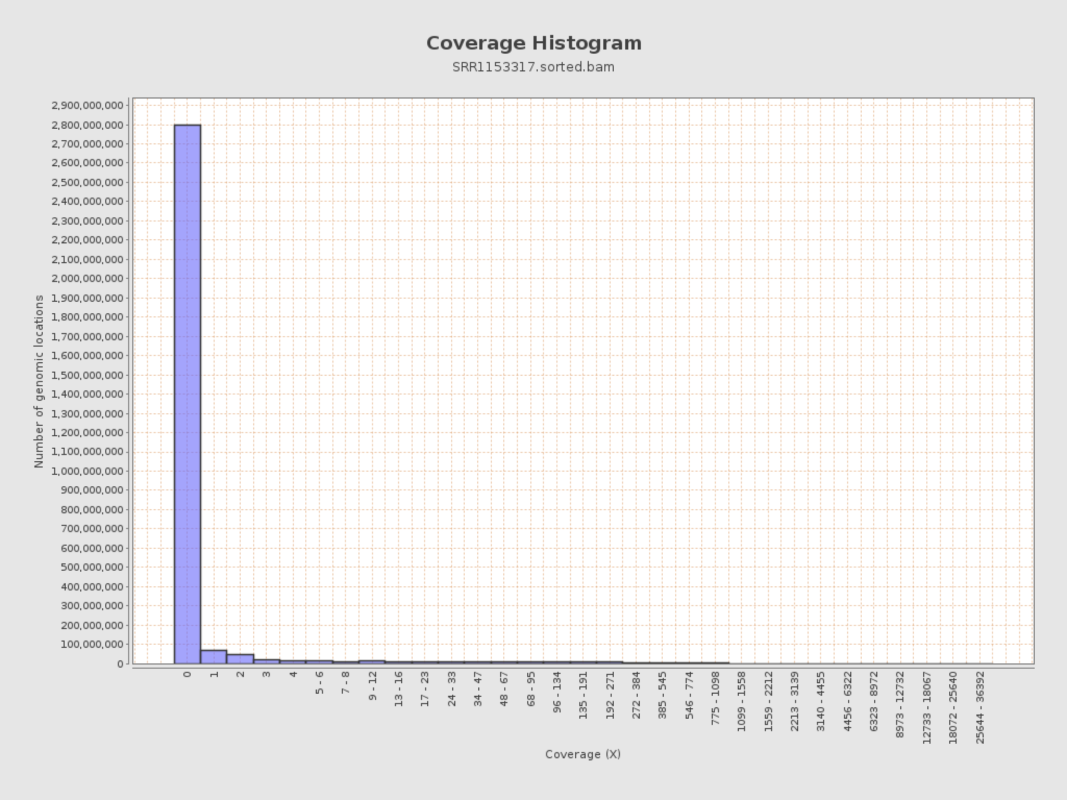
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1945404823	7.805	77.2507
chr2	243199373	818687086	3.3663	37.5542
chr3	198022430	812104992	4.1011	44.0486
chr4	191154276	467342915	2.4448	48.2723
chr5	180915260	968172036	5.3515	119.7341
chr6	171115067	400345102	2.3396	27.3966
chr7	159138663	928693472	5.8358	96.888

chr8	146364022	859214232	5.8704	102.2658
chr9	141213431	445466543	3.1546	31.5255
chr10	135534747	612994355	4.5228	48.2201
chr11	135006516	1069361024	7.9208	68.0322
chr12	133851895	881307769	6.5842	63.6939
chr13	115169878	98307731	0.8536	14.0745
chr14	107349540	384442835	3.5812	37.7804
chr15	102531392	1024148606	9.9886	104.5672
chr16	90354753	975783088	10.7995	91.3448
chr17	81195210	1391680076	17.1399	121.7547
chr18	78077248	119402324	1.5293	22.0798
chr19	59128983	1720299517	29.094	151.3417
chr20	63025520	600709572	9.5312	81.3444
chr21	48129895	287982440	5.9834	179.973
chr22	51304566	590558967	11.5108	91.7497
chrMT	16571	6223	0.3755	0.8897
chrX	155270560	732361264	4.7167	48.021
chrY	59373566	13759391	0.2317	10.9418

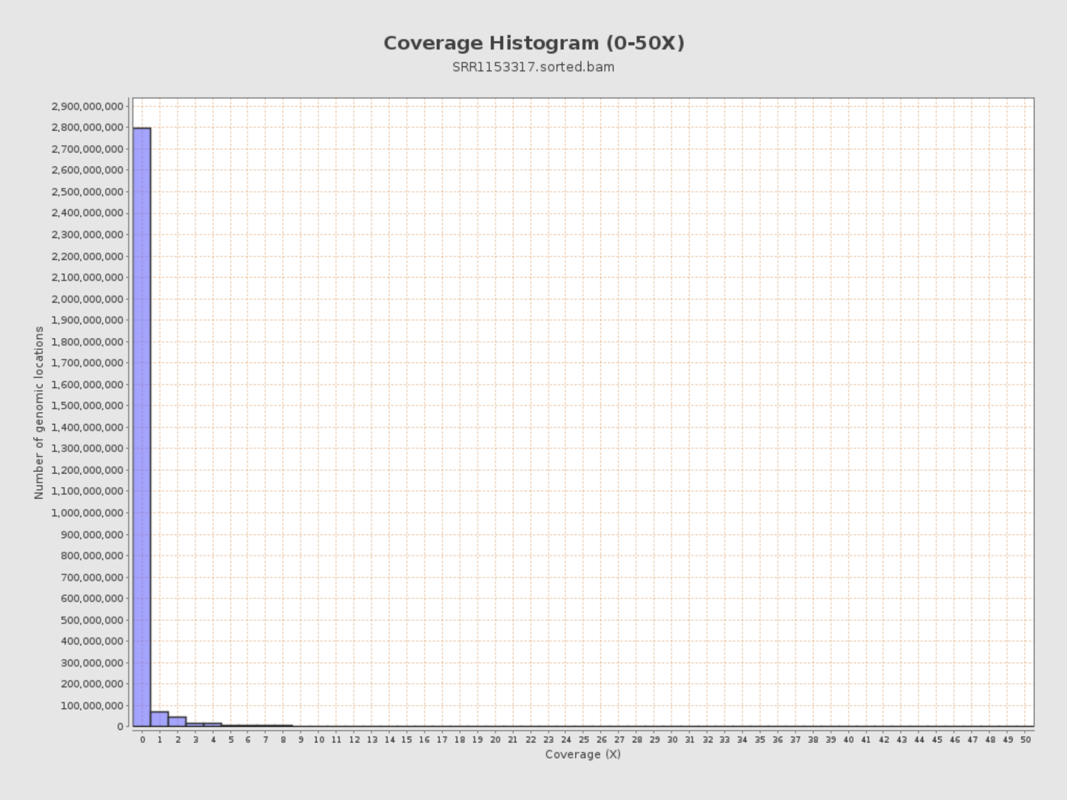
3. Results : Coverage across reference



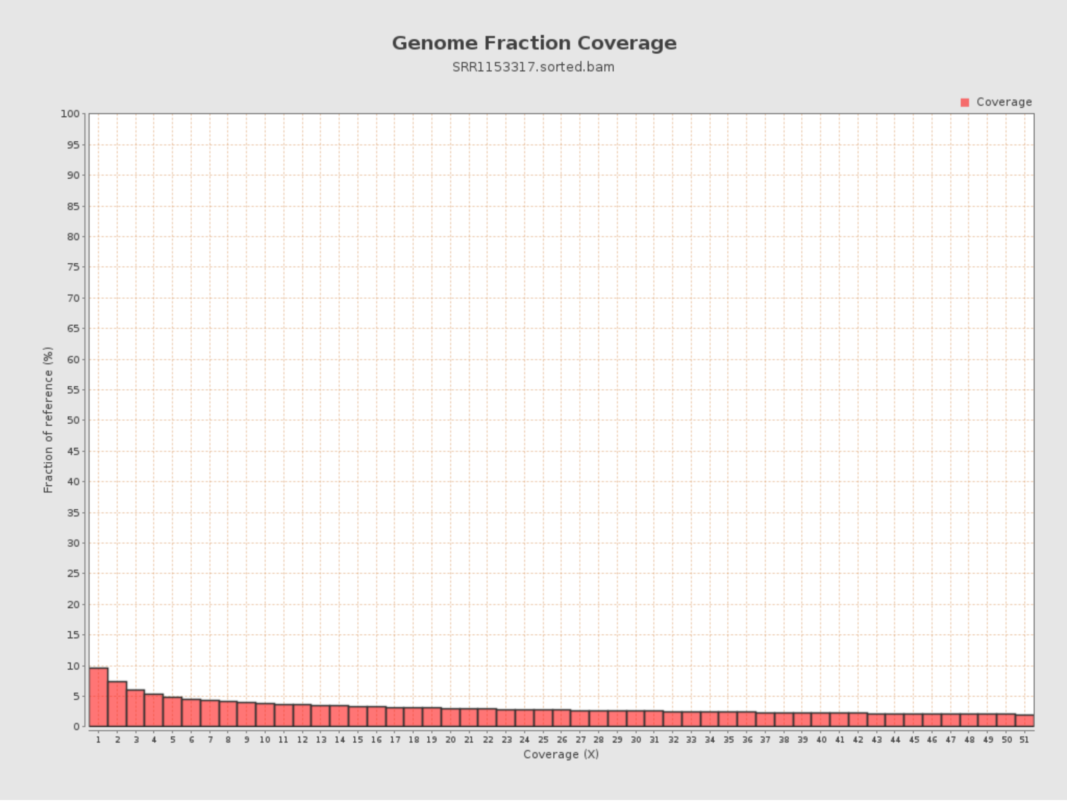
4. Results : Coverage Histogram



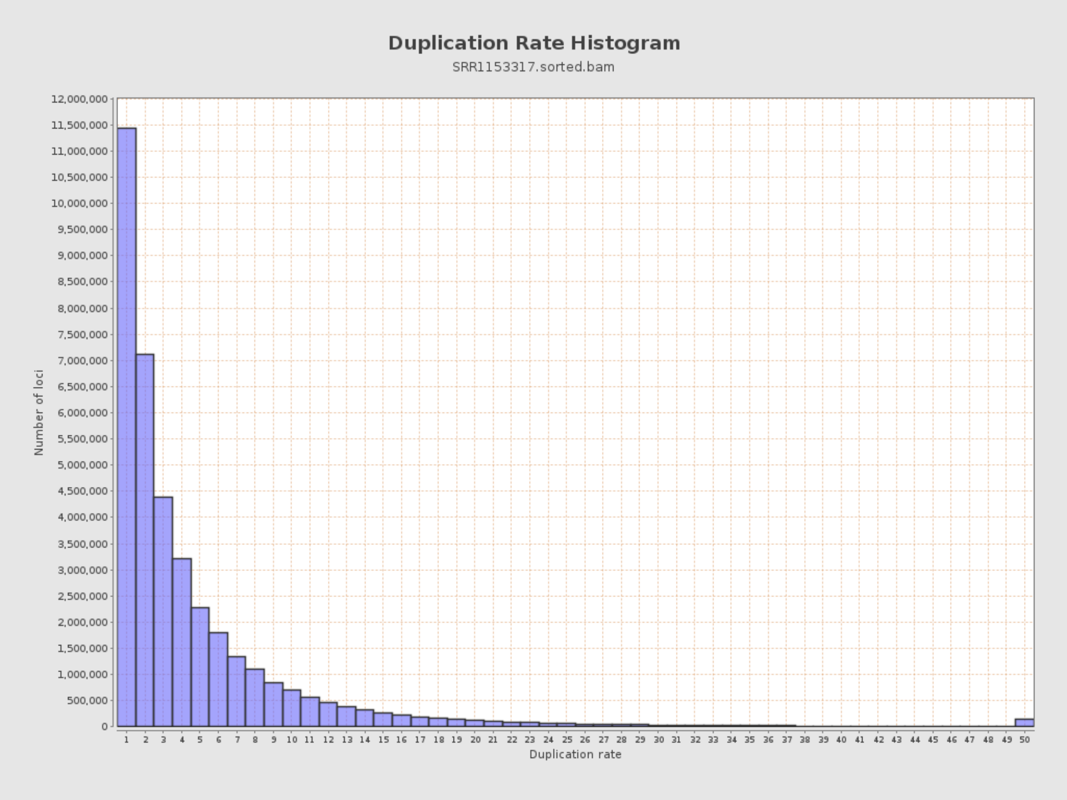
5. Results : Coverage Histogram (0-50X)



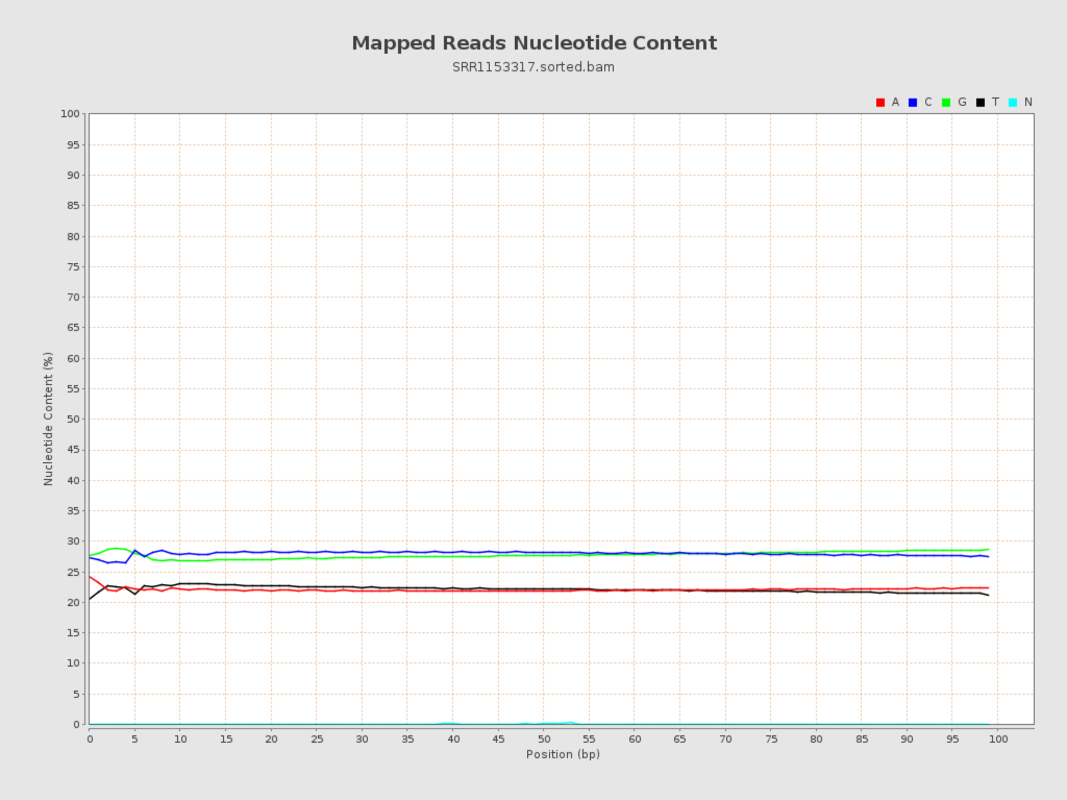
6. Results : Genome Fraction Coverage



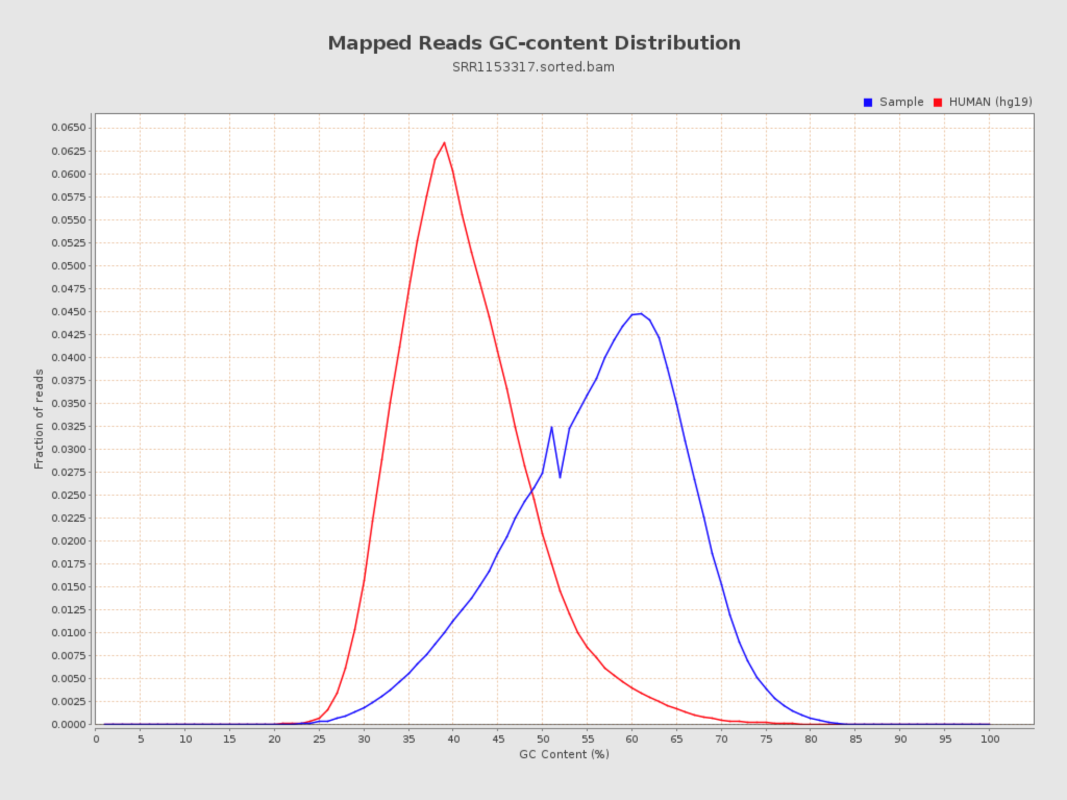
7. Results : Duplication Rate Histogram



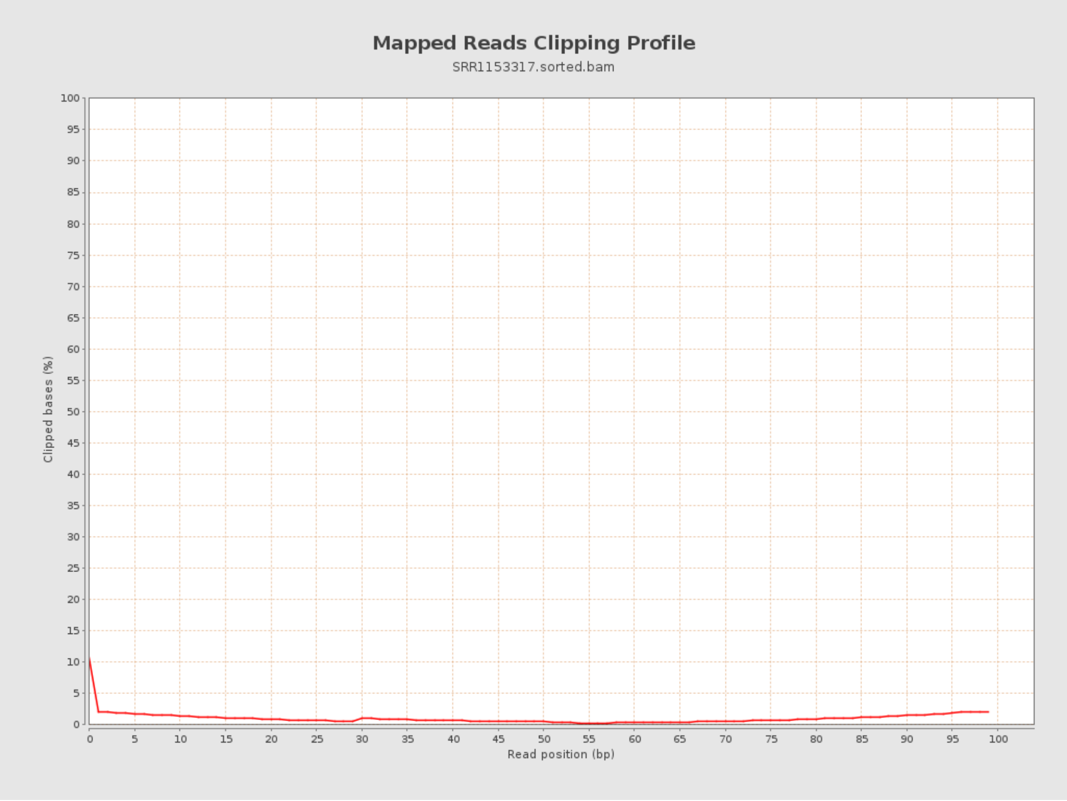
8. Results : Mapped Reads Nucleotide Content



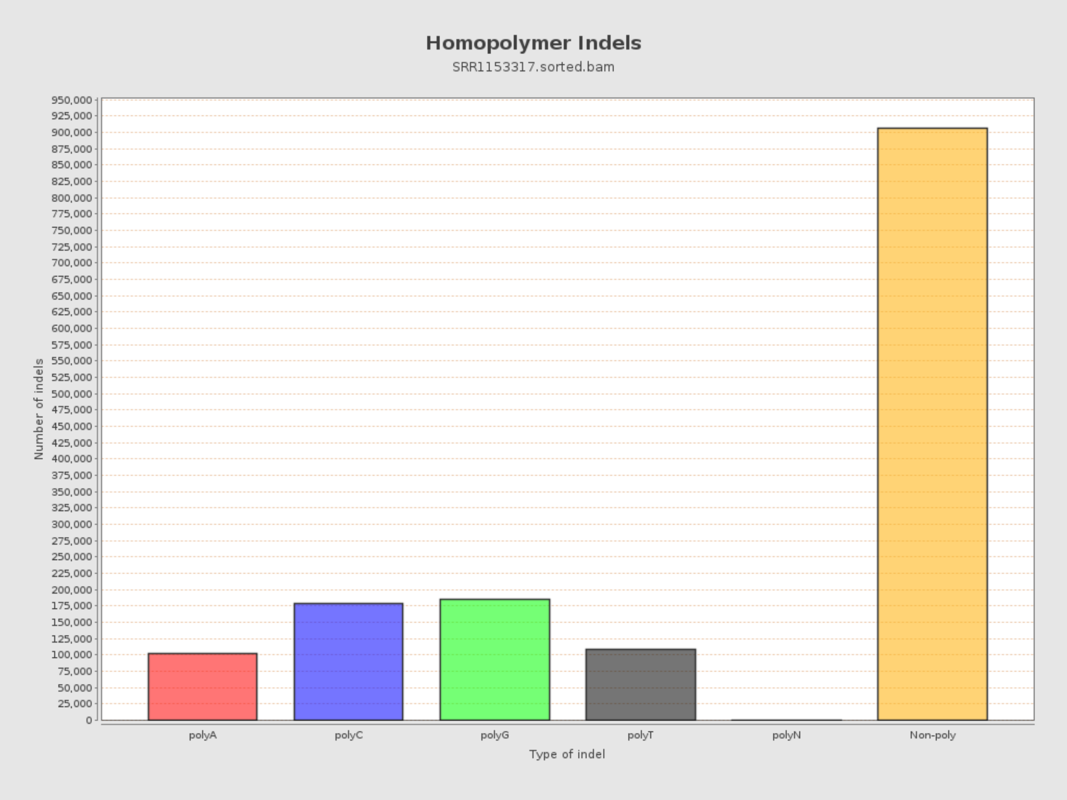
9. Results : Mapped Reads GC-content Distribution



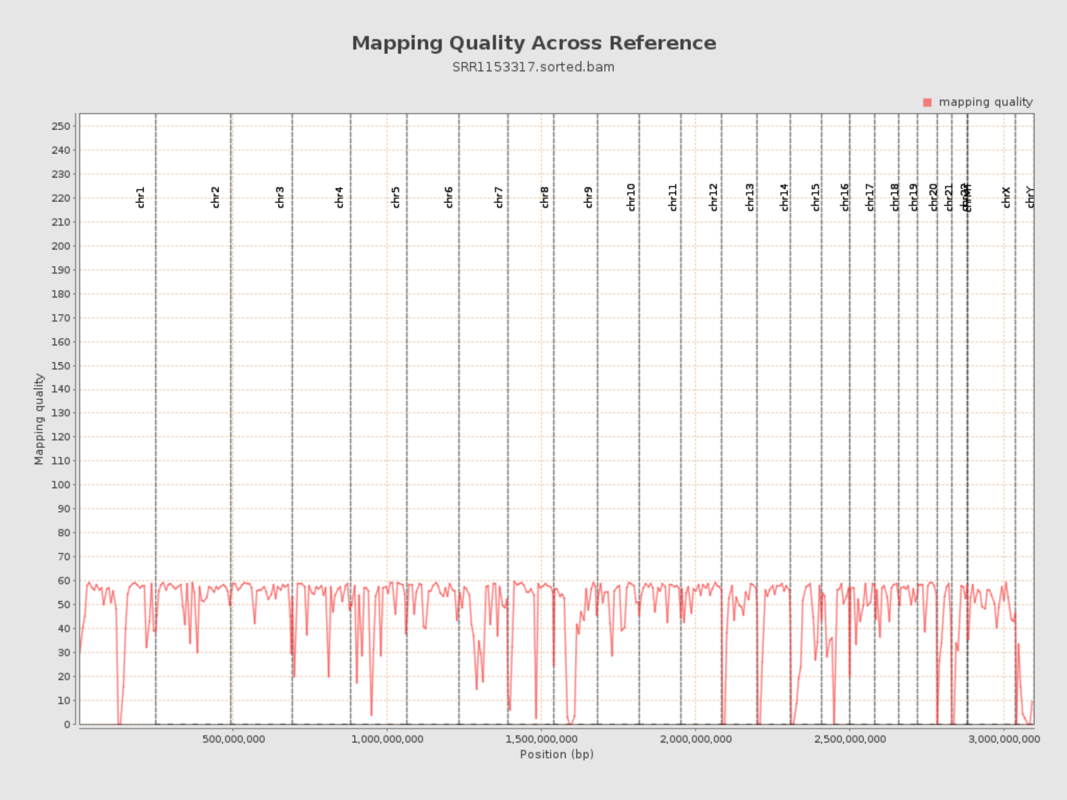
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram