Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:41:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080555.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_SRR3080555 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080555.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:40:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080555.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,691,393
Mapped reads	2,222,594 / 82.58%
Unmapped reads	468,799 / 17.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,065 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	109,700 / 4.08%
Duplication rate	4.33%
Clipped reads	1,045,420 / 38.84%

2.2. ACGT Content

Number/percentage of A's	40,272,500 / 27.34%
Number/percentage of C's	26,066,765 / 17.7%
Number/percentage of T's	48,177,921 / 32.71%
Number/percentage of G's	32,662,678 / 22.17%
Number/percentage of N's	119,482 / 0.08%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.319

2.4. Mapping Quality

Mean Mapping Quality	47.63

2.5. Mismatches and indels

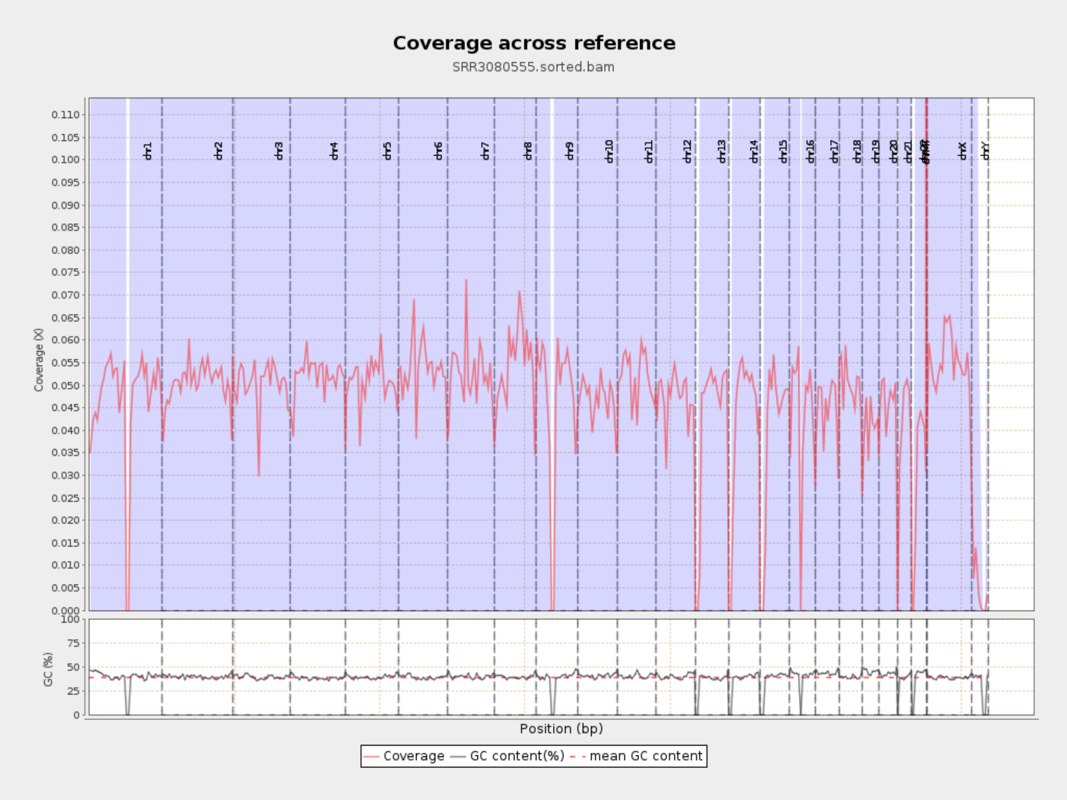
General error rate	0.89%
Mismatches	1,292,898
Insertions	12,011
Mapped reads with at least one insertion	0.54%
Deletions	34,496
Mapped reads with at least one deletion	1.54%
Homopolymer indels	49.04%

2.6. Chromosome stats

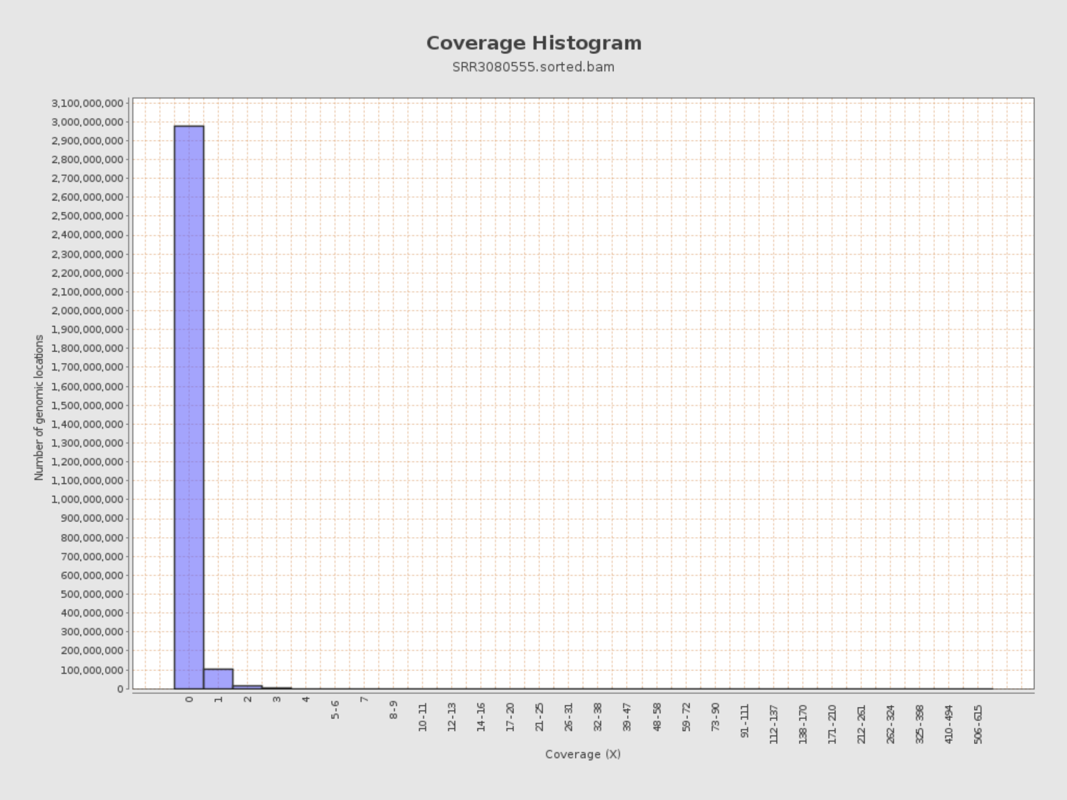
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11704256	0.047	0.3833
chr2	243199373	12289241	0.0505	0.3277
chr3	198022430	10006712	0.0505	0.2641
chr4	191154276	9959813	0.0521	0.2742
chr5	180915260	9238342	0.0511	0.2656
chr6	171115067	9219669	0.0539	0.3122
chr7	159138663	8410451	0.0528	0.5188

chr8	146364022	7986046	0.0546	0.4532
chr9	141213431	6502475	0.046	0.3083
chr10	135534747	6401828	0.0472	0.2917
chr11	135006516	6987328	0.0518	0.2923
chr12	133851895	6273126	0.0469	0.2579
chr13	115169878	4819135	0.0418	0.2414
chr14	107349540	4500777	0.0419	0.25
chr15	102531392	4019119	0.0392	0.2327
chr16	90354753	3943784	0.0436	0.2607
chr17	81195210	3601117	0.0444	0.261
chr18	78077248	3943325	0.0505	0.4653
chr19	59128983	2406939	0.0407	0.3125
chr20	63025520	2910614	0.0462	0.2558
chr21	48129895	1891883	0.0393	0.2413
chr22	51304566	1470565	0.0287	0.1971
chrMT	16571	37135	2.241	3.594
chrX	155270560	8515121	0.0548	0.2887
chrY	59373566	316760	0.0053	0.111

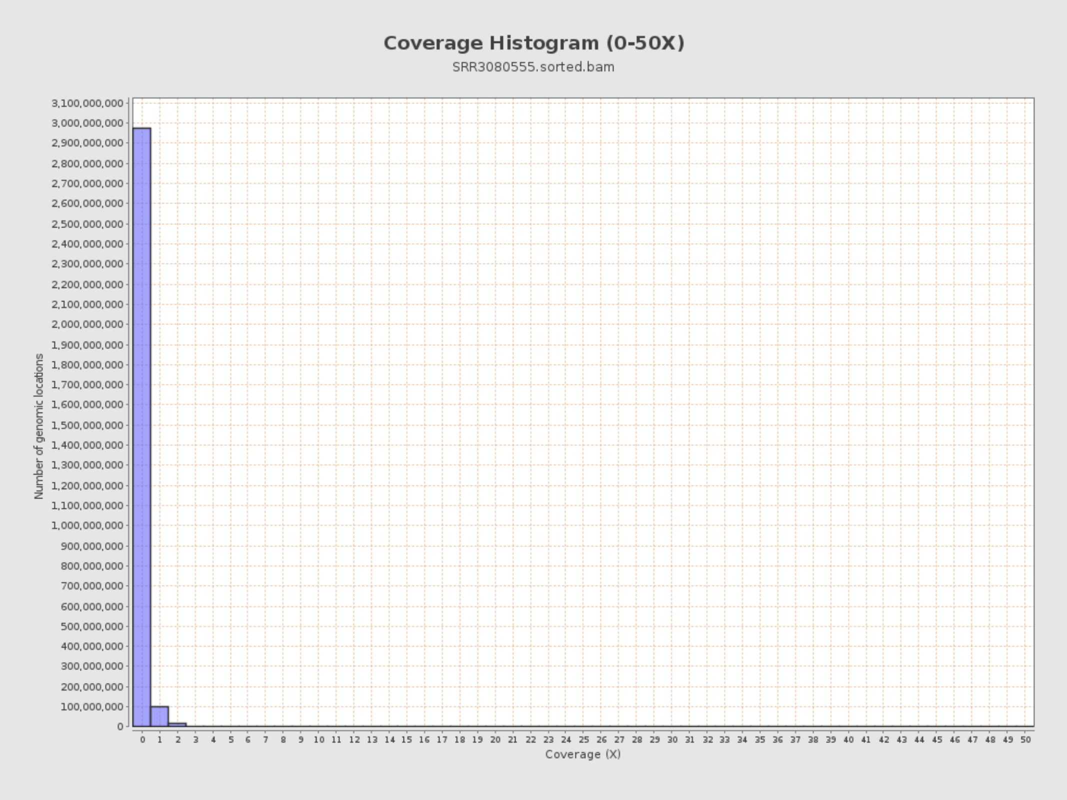
3. Results : Coverage across reference



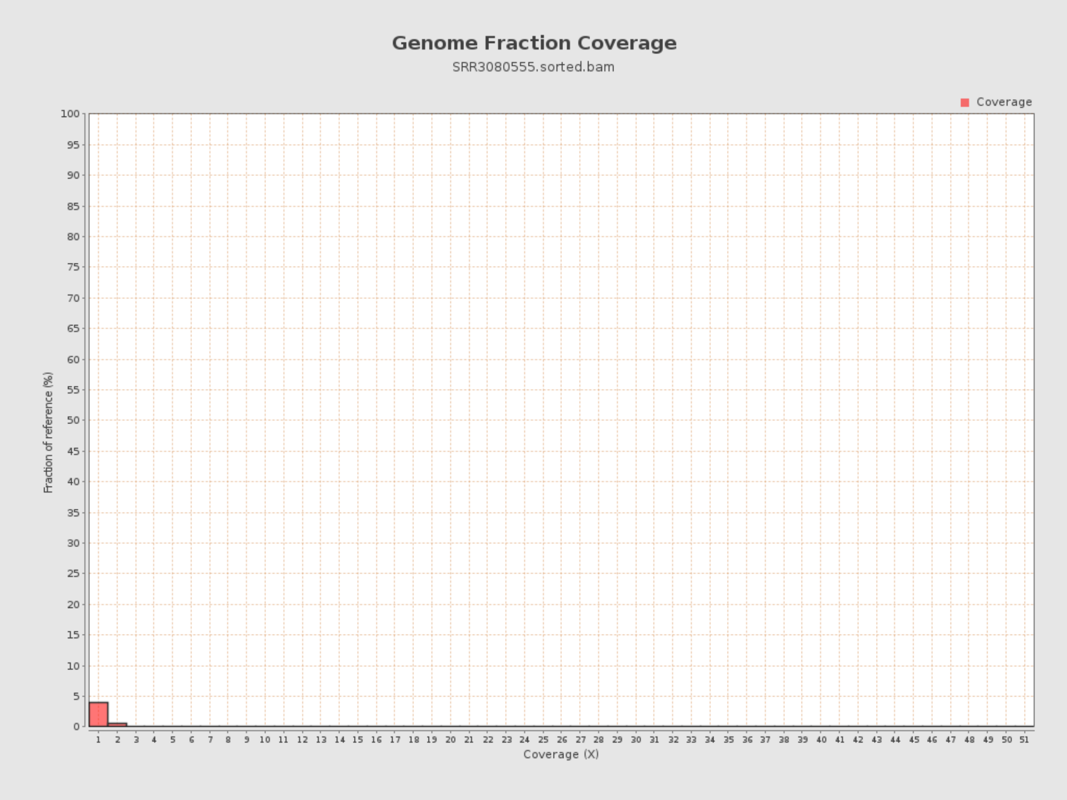
4. Results : Coverage Histogram



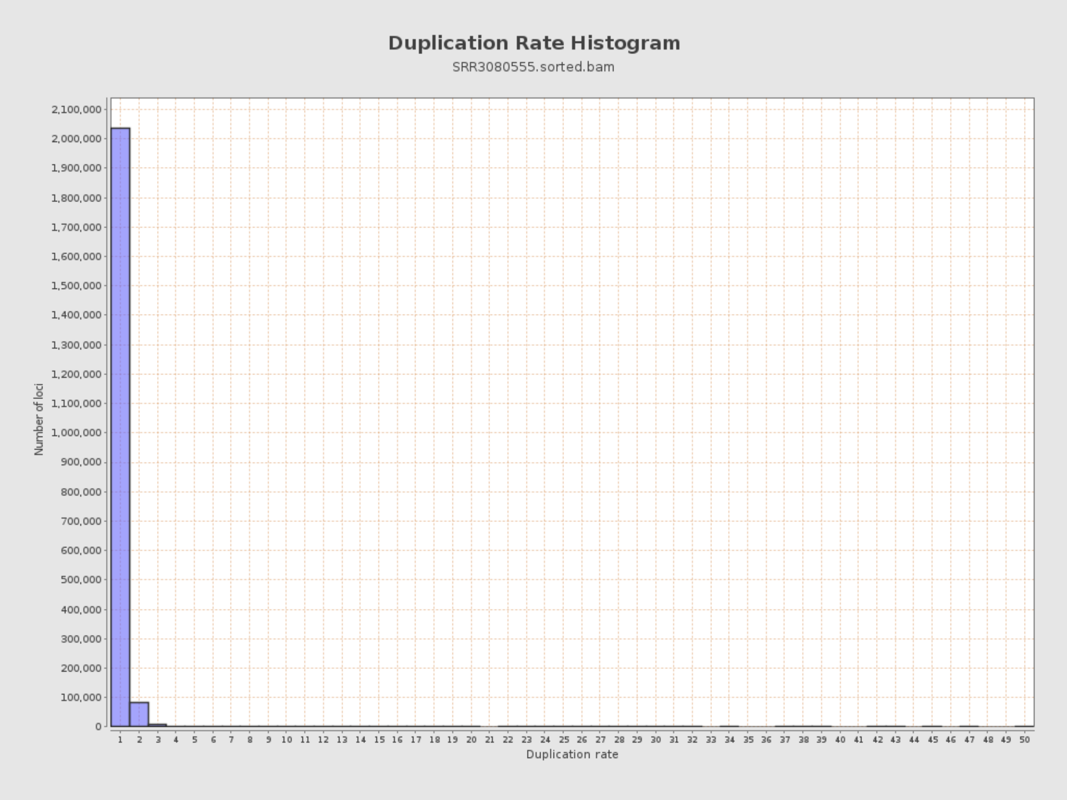
5. Results : Coverage Histogram (0-50X)



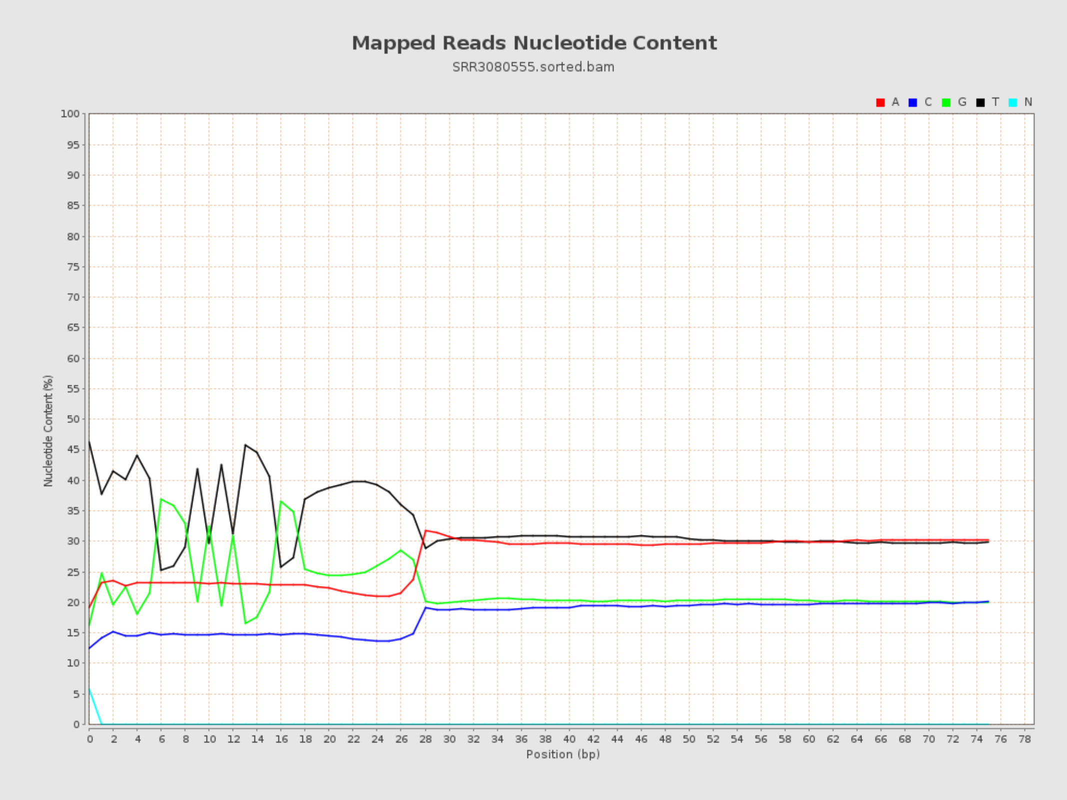
6. Results : Genome Fraction Coverage



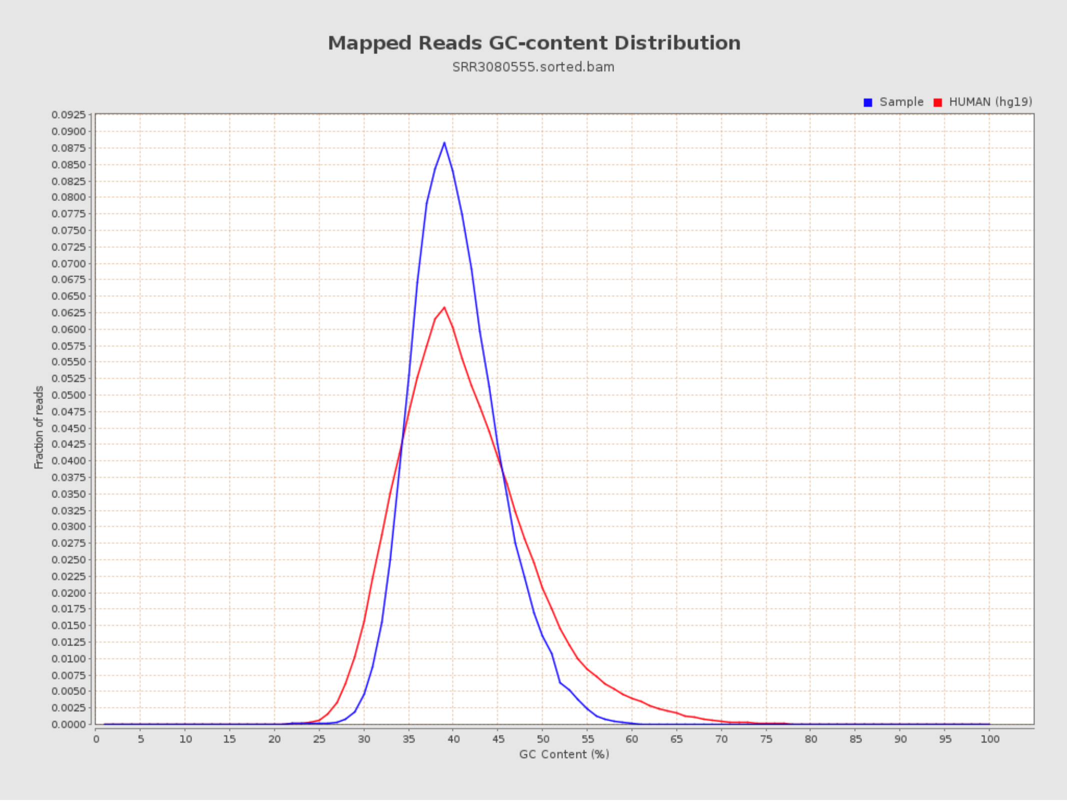
7. Results : Duplication Rate Histogram



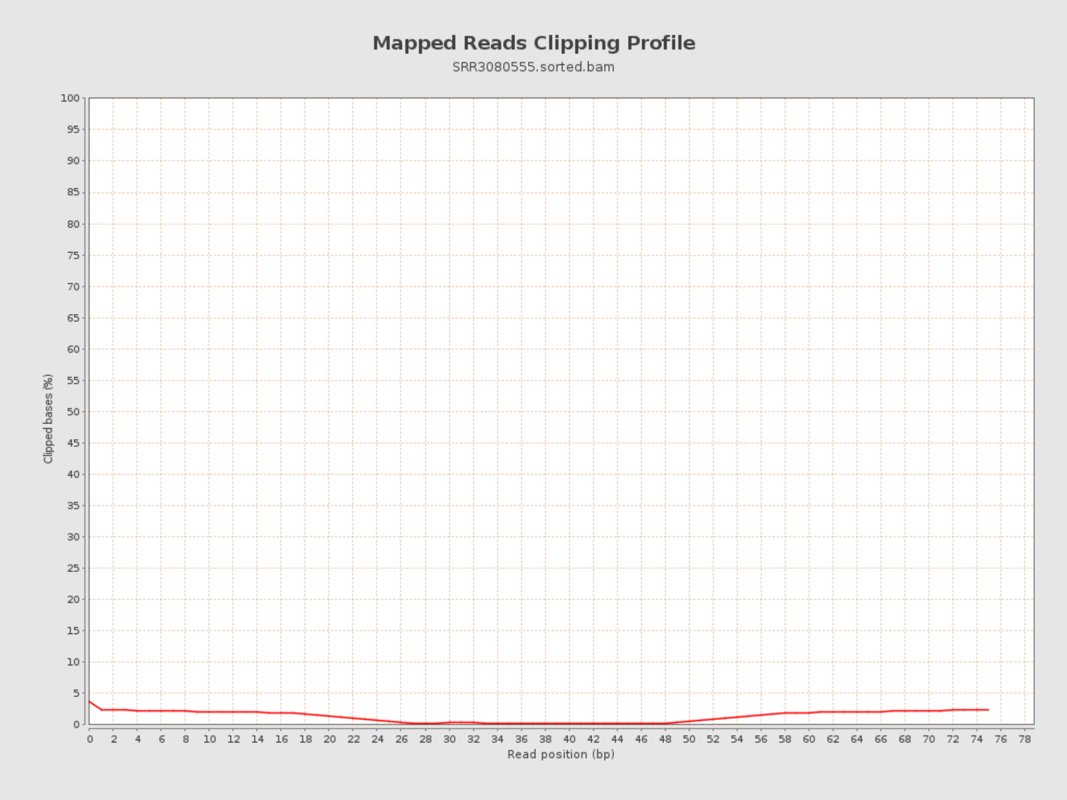
8. Results : Mapped Reads Nucleotide Content



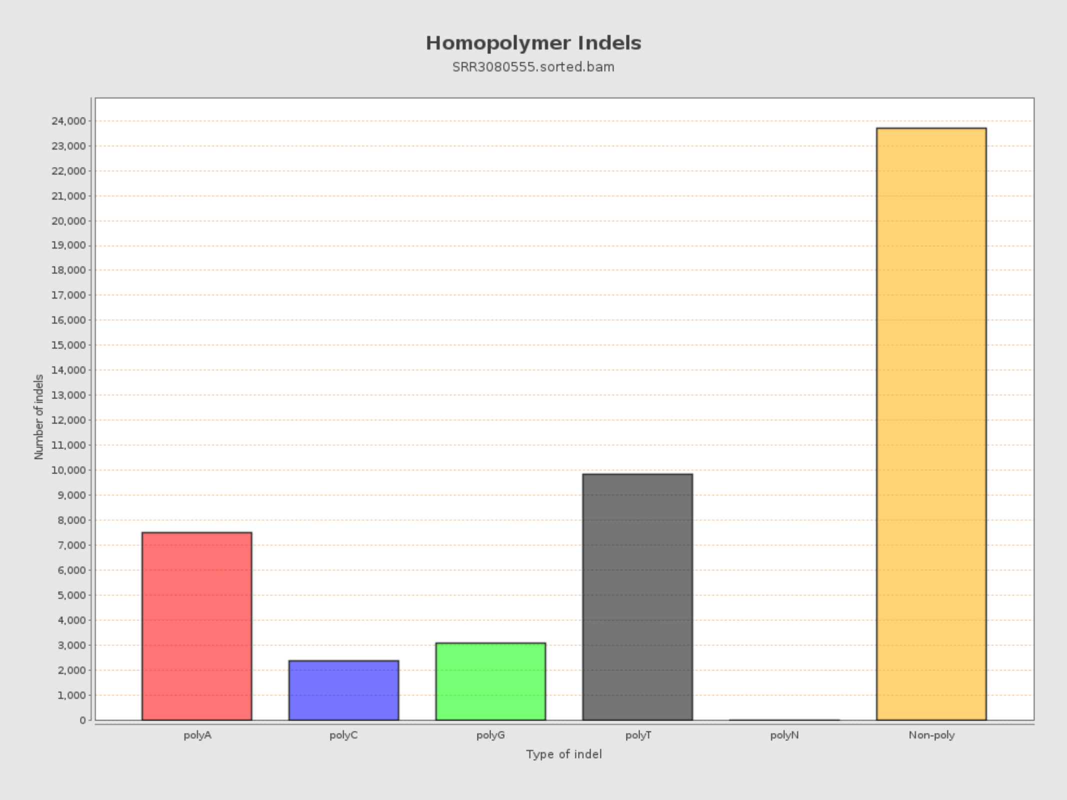
9. Results : Mapped Reads GC-content Distribution



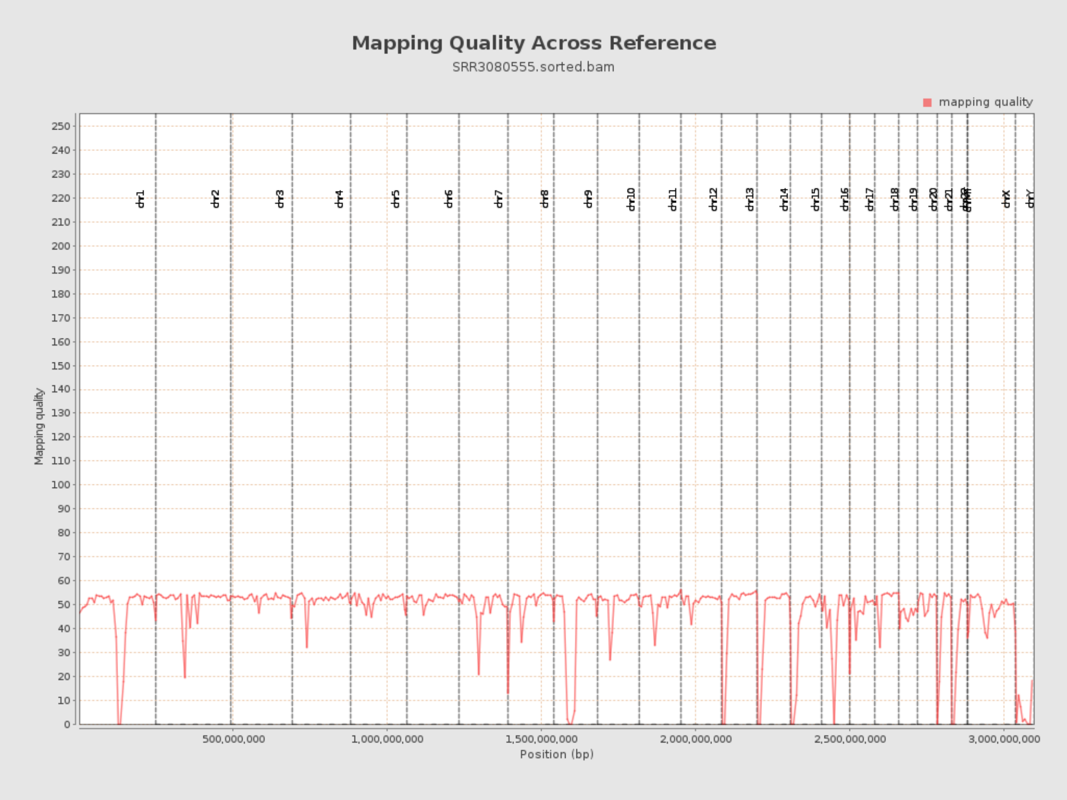
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram