Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:27:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081222.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_SRR3081222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:27:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,144,599
Mapped reads	1,898,793 / 88.54%
Unmapped reads	245,806 / 11.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,705 / 1.2%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	82,829 / 3.86%
Duplication rate	3.68%
Clipped reads	982,995 / 45.84%

2.2. ACGT Content

Number/percentage of A's	35,370,704 / 28.47%
Number/percentage of C's	23,833,461 / 19.18%
Number/percentage of T's	38,265,698 / 30.79%
Number/percentage of G's	26,774,832 / 21.55%
Number/percentage of N's	15,483 / 0.01%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.2998

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

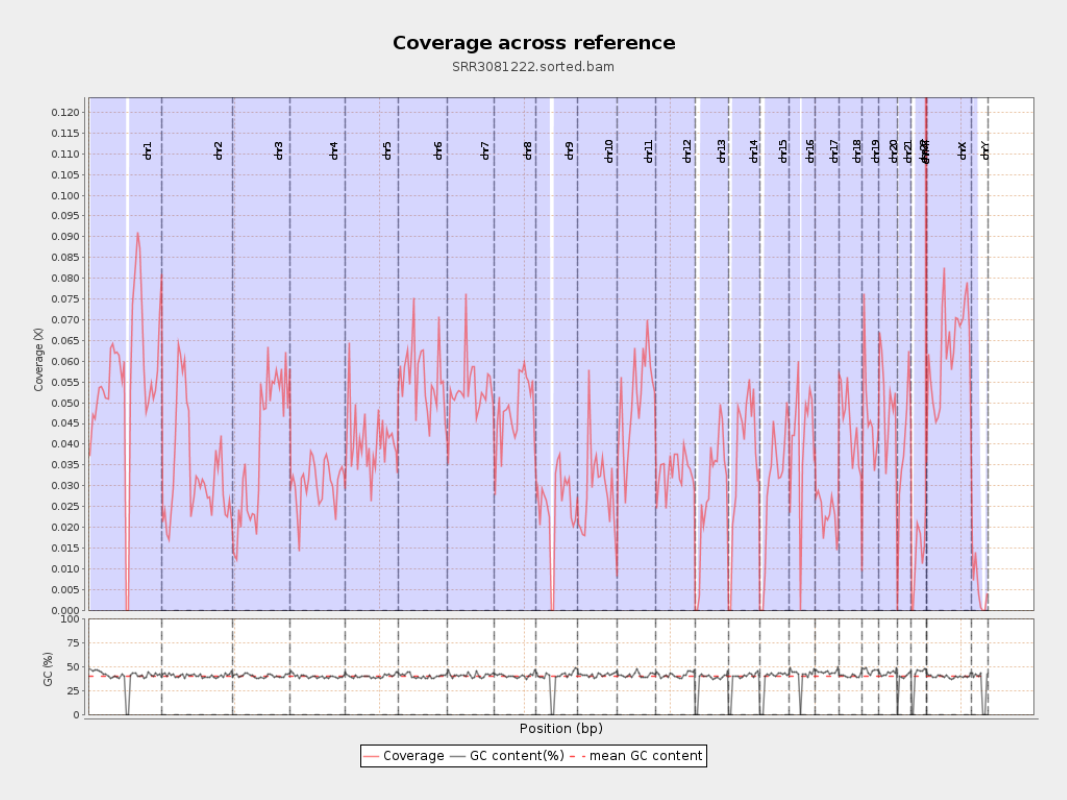
General error rate	0.89%
Mismatches	1,088,319
Insertions	9,022
Mapped reads with at least one insertion	0.47%
Deletions	28,225
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.36%

2.6. Chromosome stats

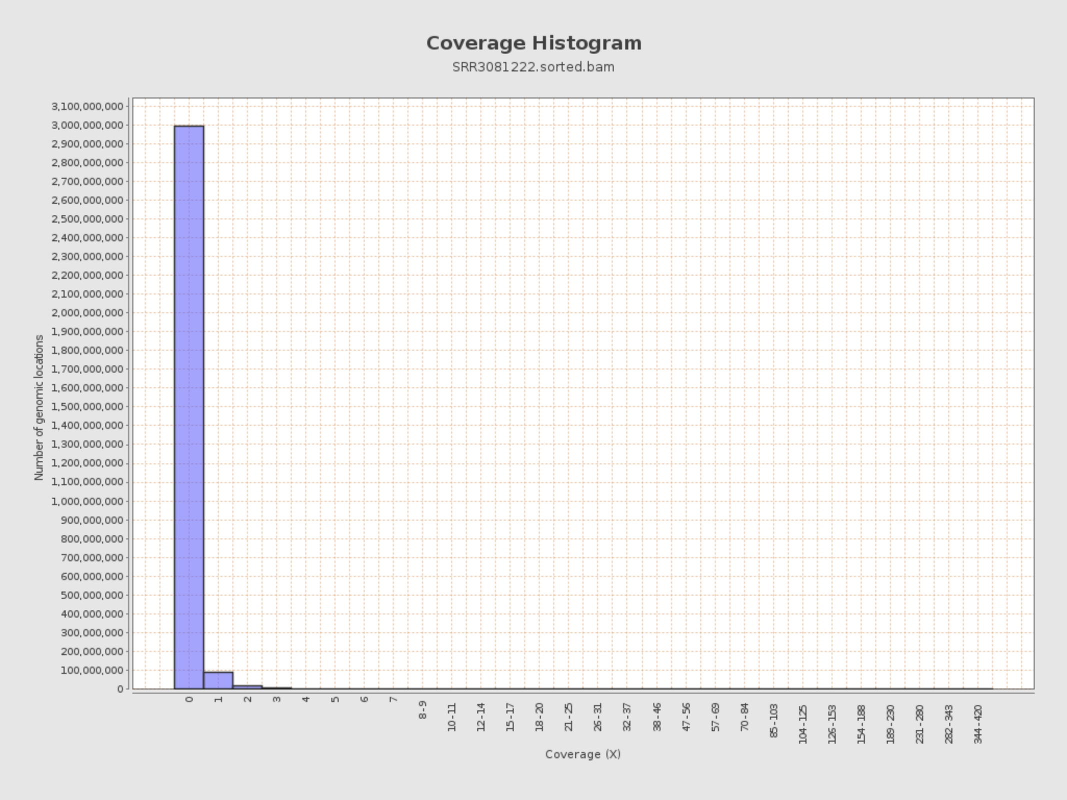
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13878965	0.0557	0.4502
chr2	243199373	8161876	0.0336	0.3187
chr3	198022430	7726071	0.039	0.2352
chr4	191154276	5895580	0.0308	0.2099
chr5	180915260	7290488	0.0403	0.2362
chr6	171115067	9535410	0.0557	0.3182
chr7	159138663	8501578	0.0534	0.4308

chr8	146364022	7028927	0.048	0.3519
chr9	141213431	3517031	0.0249	0.2258
chr10	135534747	3930075	0.029	0.3154
chr11	135006516	6670971	0.0494	0.3325
chr12	133851895	4452561	0.0333	0.2152
chr13	115169878	3231720	0.0281	0.1991
chr14	107349540	3944715	0.0367	0.2296
chr15	102531392	3050483	0.0298	0.2077
chr16	90354753	3748387	0.0415	0.2458
chr17	81195210	1858708	0.0229	0.2031
chr18	78077248	3469462	0.0444	0.3572
chr19	59128983	2735116	0.0463	0.371
chr20	63025520	3137488	0.0498	0.2657
chr21	48129895	1842818	0.0383	0.2372
chr22	51304566	634642	0.0124	0.1275
chrMT	16571	26423	1.5945	1.6175
chrX	155270560	9727457	0.0626	0.3206
chrY	59373566	308766	0.0052	0.1019

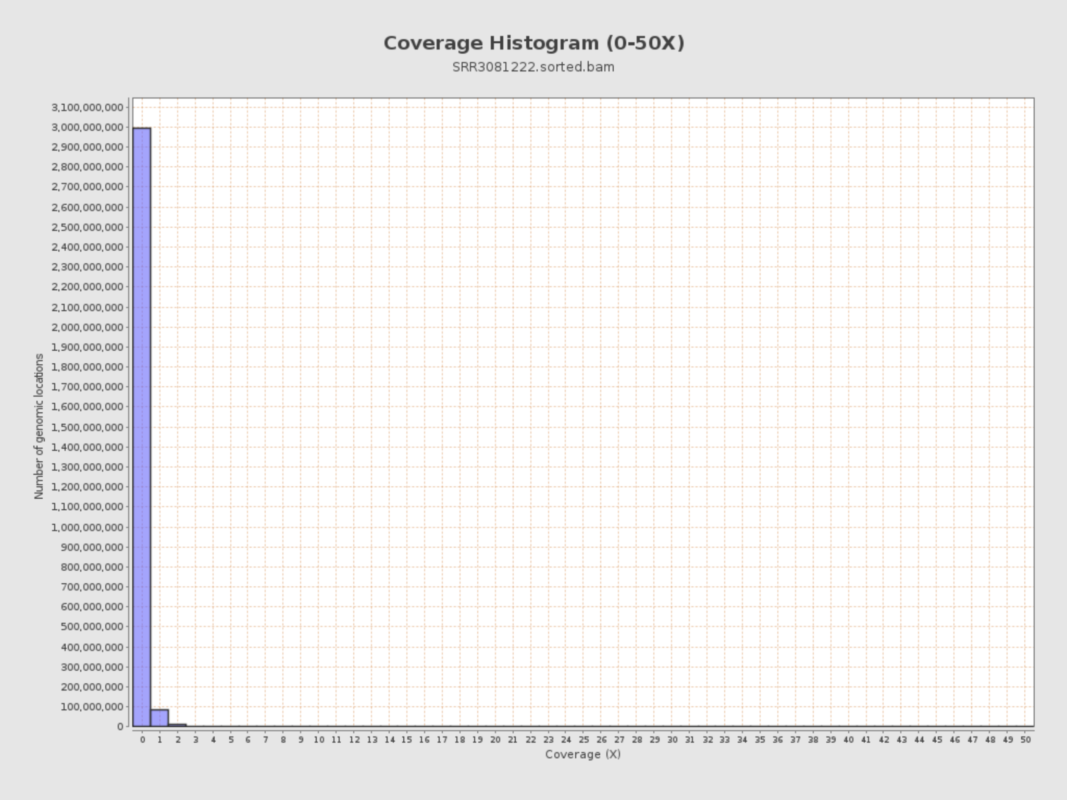
3. Results : Coverage across reference



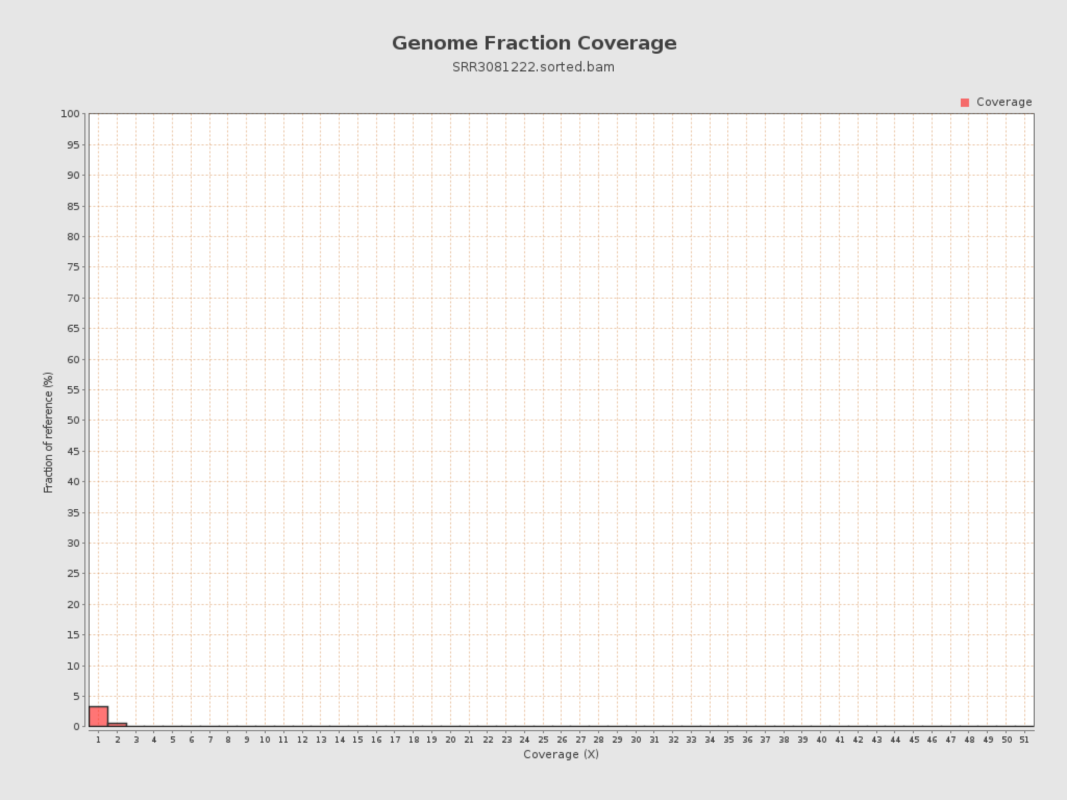
4. Results : Coverage Histogram



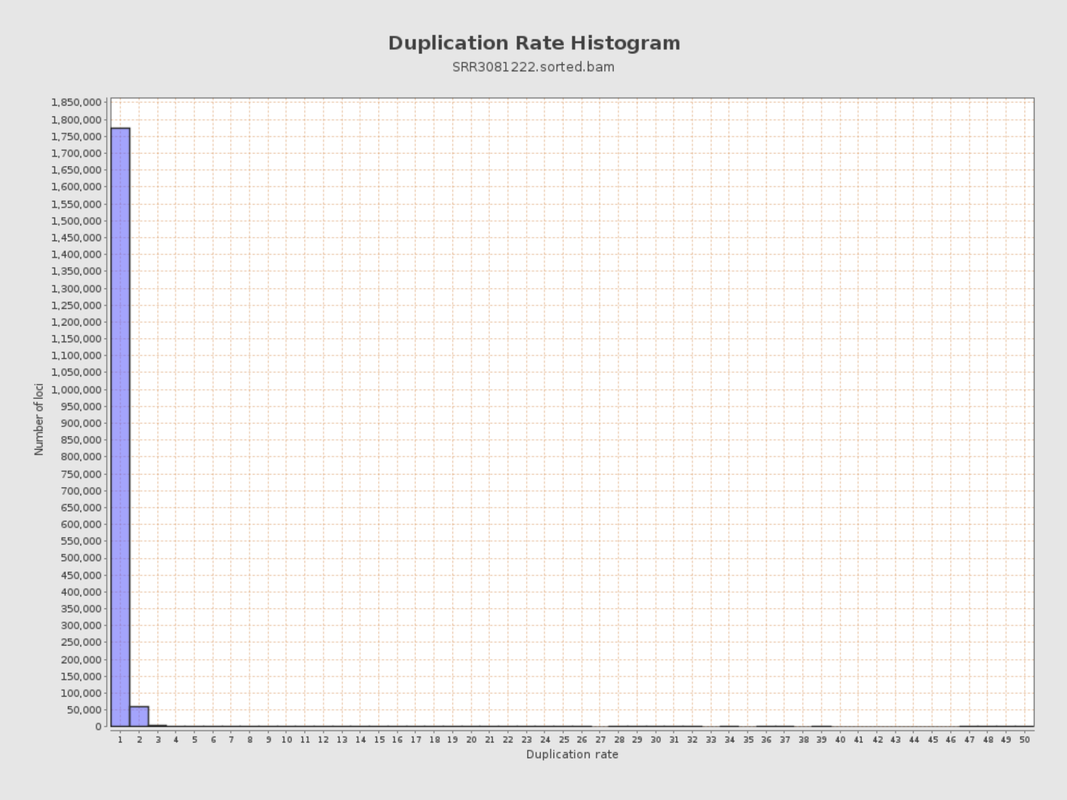
5. Results : Coverage Histogram (0-50X)



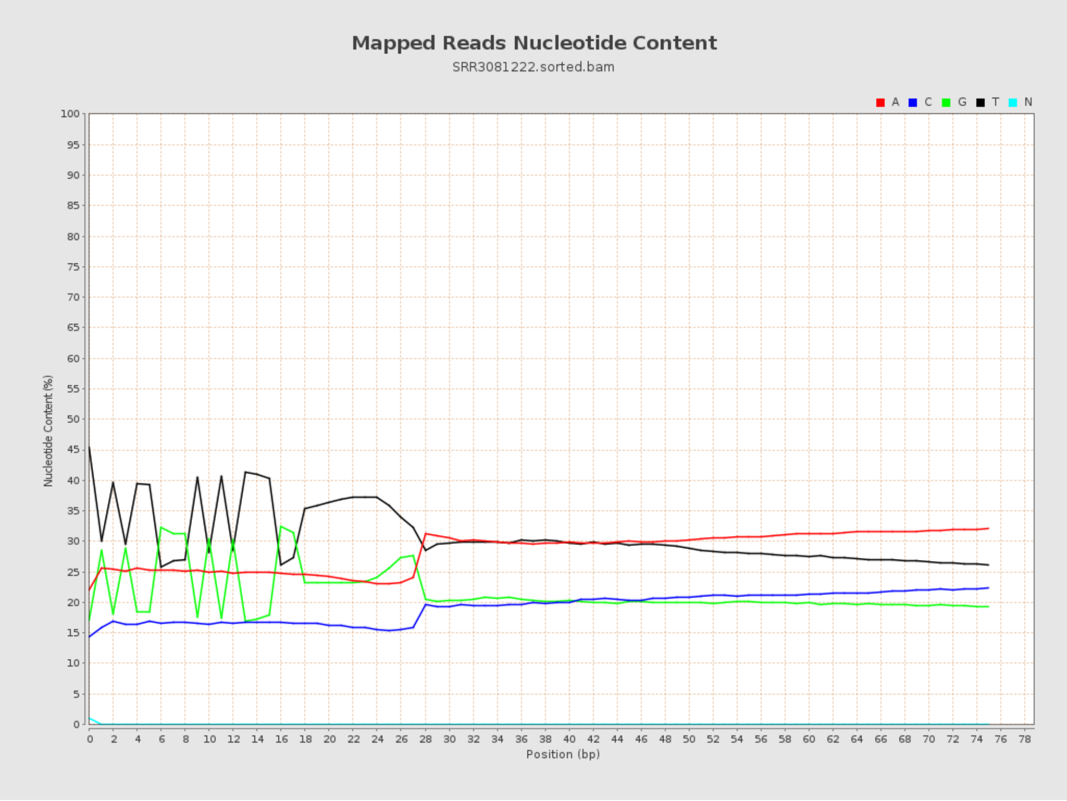
6. Results : Genome Fraction Coverage



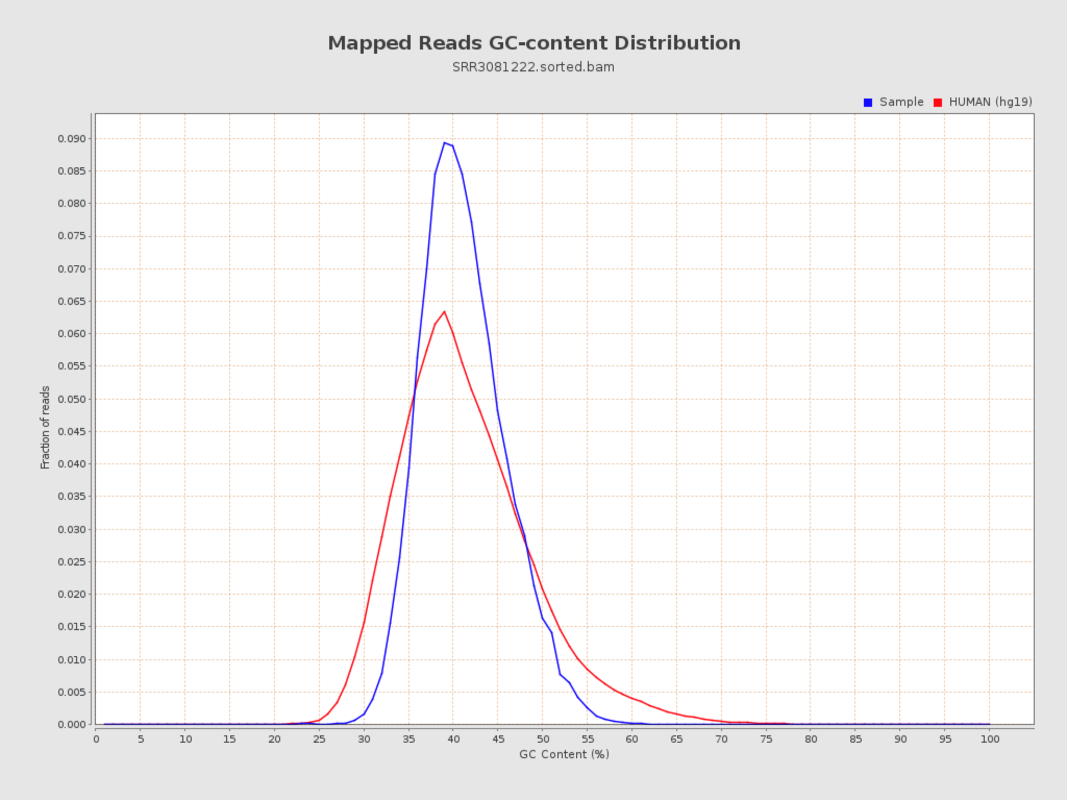
7. Results : Duplication Rate Histogram



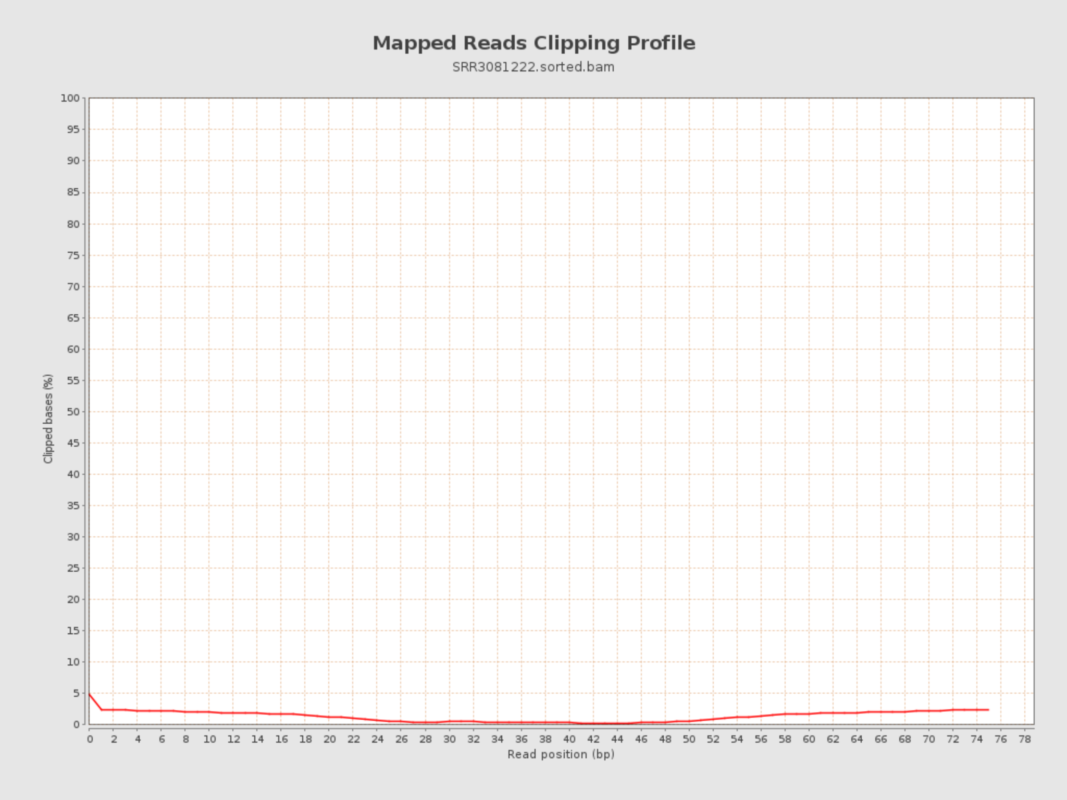
8. Results : Mapped Reads Nucleotide Content



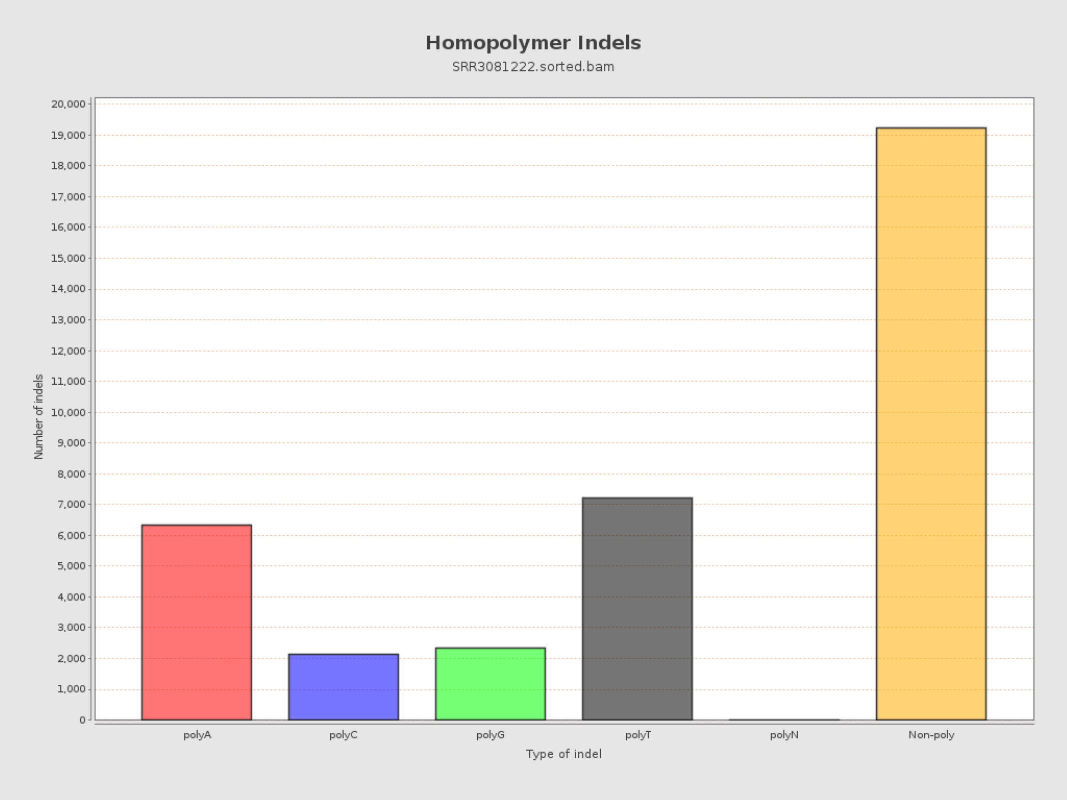
9. Results : Mapped Reads GC-content Distribution



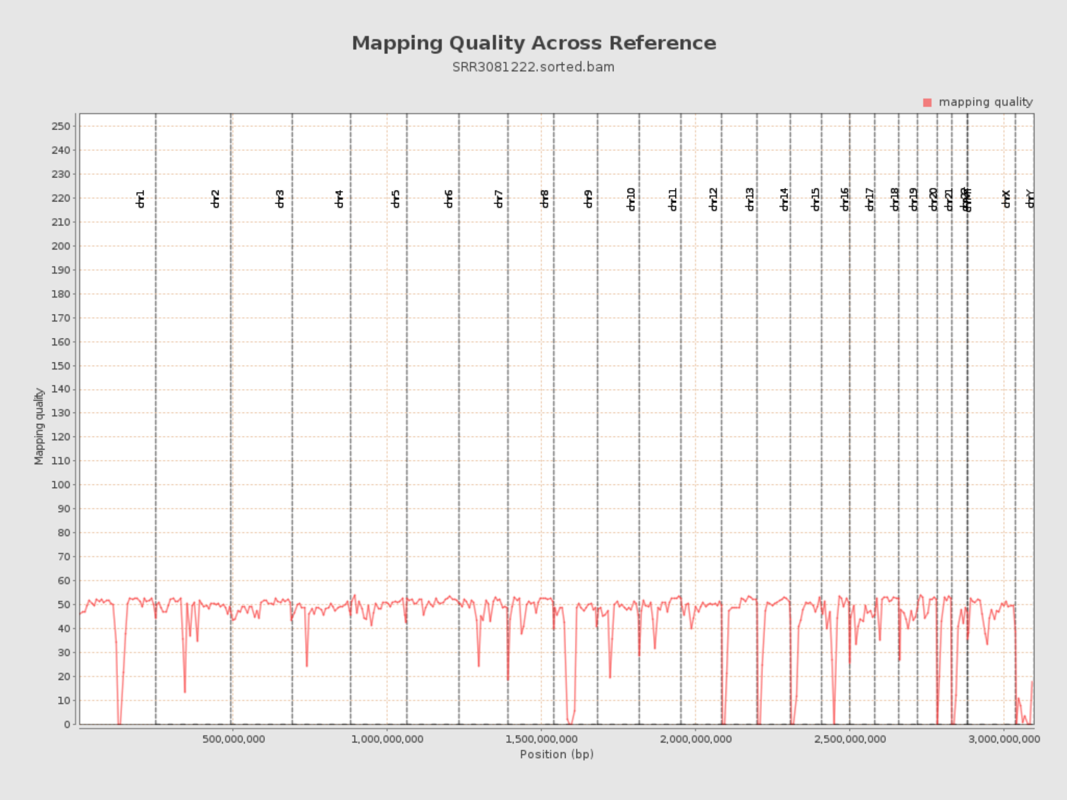
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram