Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:02:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080788.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_SRR3080788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:02:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,976,877
Mapped reads	2,505,059 / 84.15%
Unmapped reads	471,818 / 15.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,007 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	131,618 / 4.42%
Duplication rate	4.38%
Clipped reads	1,434,112 / 48.18%

2.2. ACGT Content

Number/percentage of A's	46,991,295 / 29.35%
Number/percentage of C's	30,898,898 / 19.3%
Number/percentage of T's	48,637,880 / 30.38%
Number/percentage of G's	33,570,489 / 20.97%
Number/percentage of N's	3,233 / 0%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0517

Standard Deviation	0.3627

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

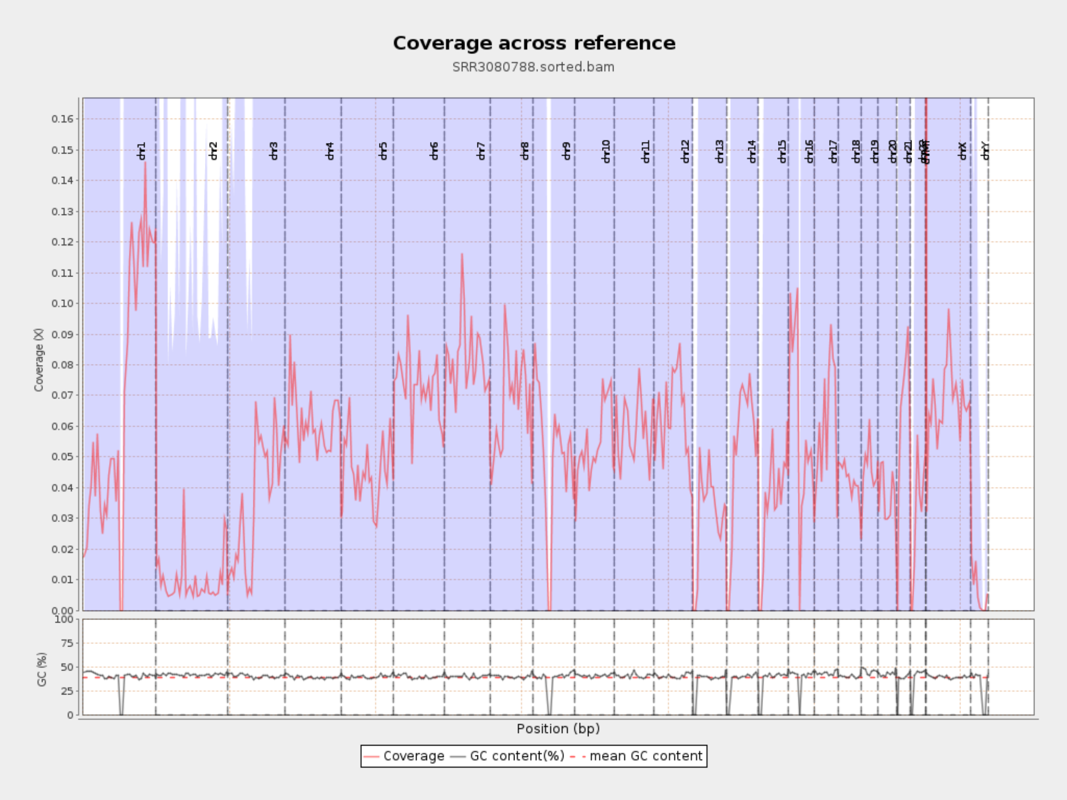
General error rate	0.77%
Mismatches	1,206,905
Insertions	11,838
Mapped reads with at least one insertion	0.47%
Deletions	33,367
Mapped reads with at least one deletion	1.32%
Homopolymer indels	47.2%

2.6. Chromosome stats

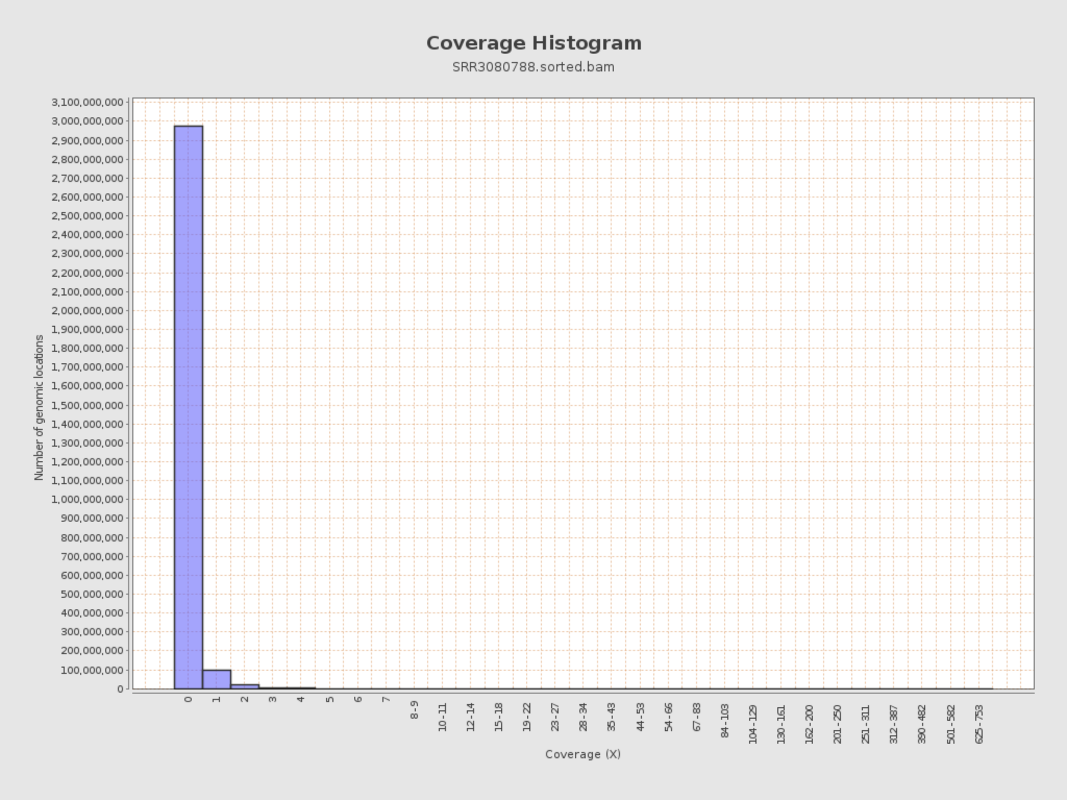
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17315277	0.0695	0.4552
chr2	243199373	2371839	0.0098	0.3432
chr3	198022430	6995803	0.0353	0.2347
chr4	191154276	11667212	0.061	0.315
chr5	180915260	8235597	0.0455	0.2671
chr6	171115067	12559003	0.0734	0.3966
chr7	159138663	13107757	0.0824	0.5803

chr8	146364022	9791876	0.0669	0.555
chr9	141213431	7160382	0.0507	0.3316
chr10	135534747	7435773	0.0549	0.3462
chr11	135006516	7911388	0.0586	0.3402
chr12	133851895	8464316	0.0632	0.3172
chr13	115169878	3601236	0.0313	0.2232
chr14	107349540	5686748	0.053	0.2958
chr15	102531392	3457882	0.0337	0.2372
chr16	90354753	5275441	0.0584	0.3151
chr17	81195210	5065385	0.0624	0.3218
chr18	78077248	3357592	0.043	0.501
chr19	59128983	2745803	0.0464	0.3742
chr20	63025520	2373744	0.0377	0.2426
chr21	48129895	3028091	0.0629	0.3235
chr22	51304566	1542423	0.0301	0.212
chrMT	16571	72078	4.3496	3.4223
chrX	155270560	10566987	0.0681	0.3405
chrY	59373566	364879	0.0061	0.1162

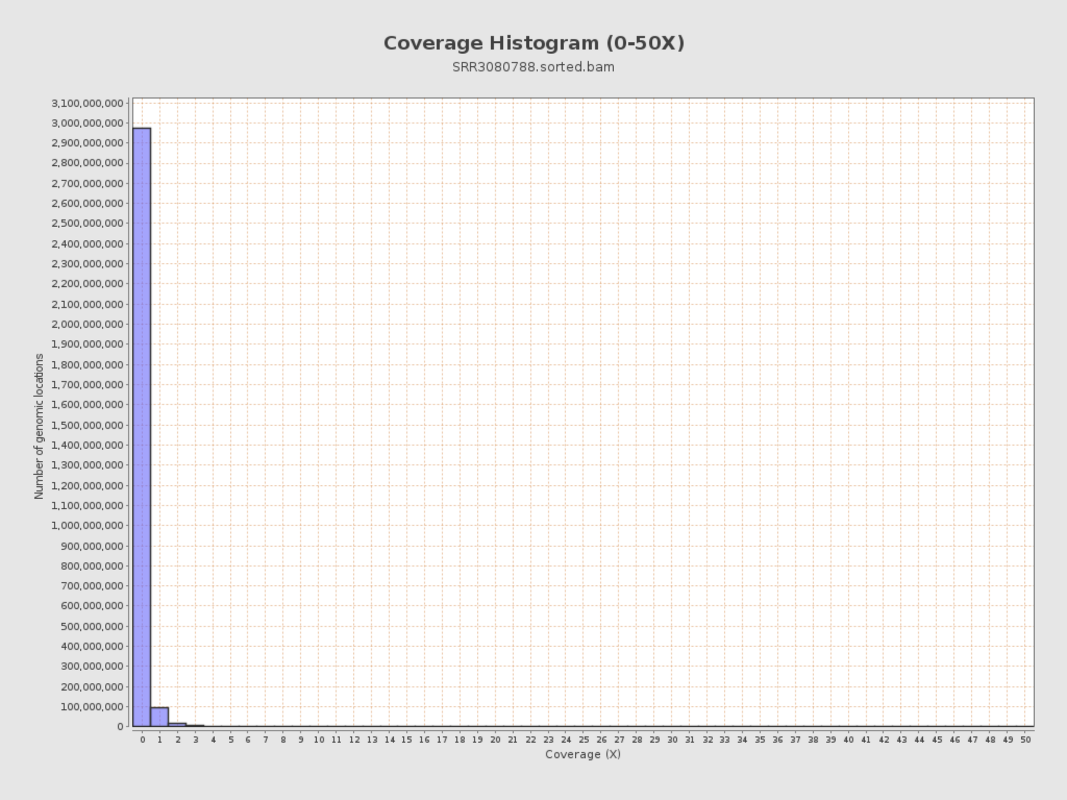
3. Results : Coverage across reference



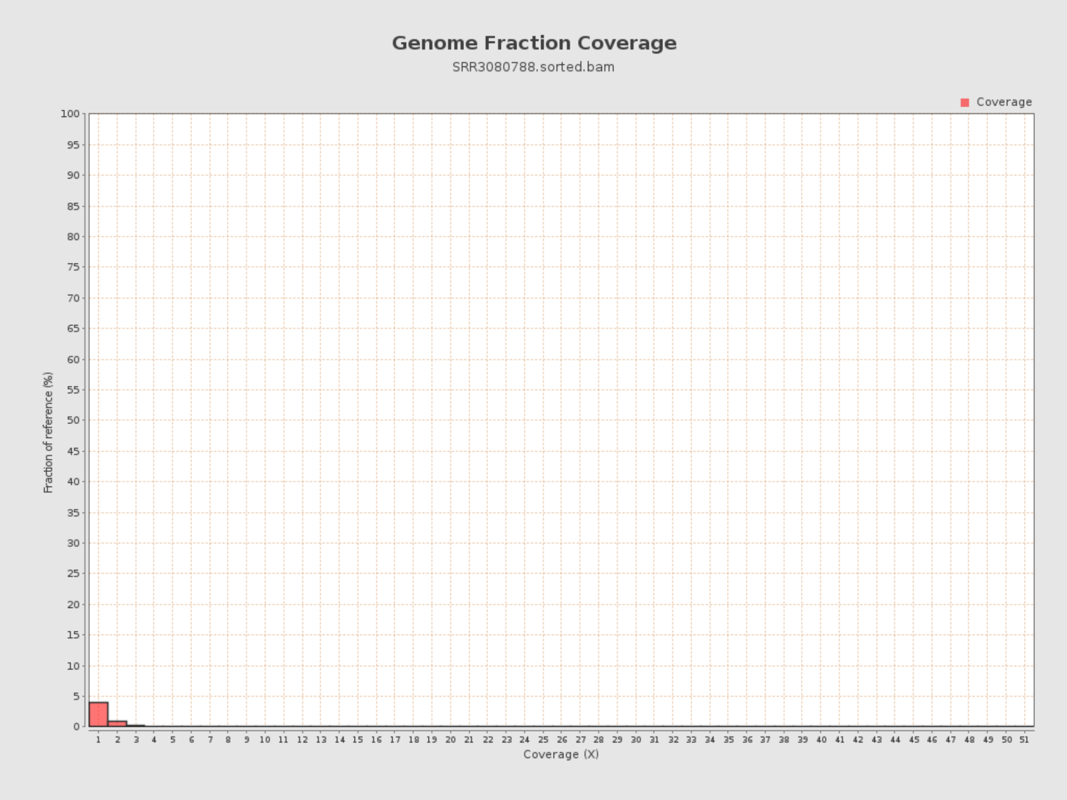
4. Results : Coverage Histogram



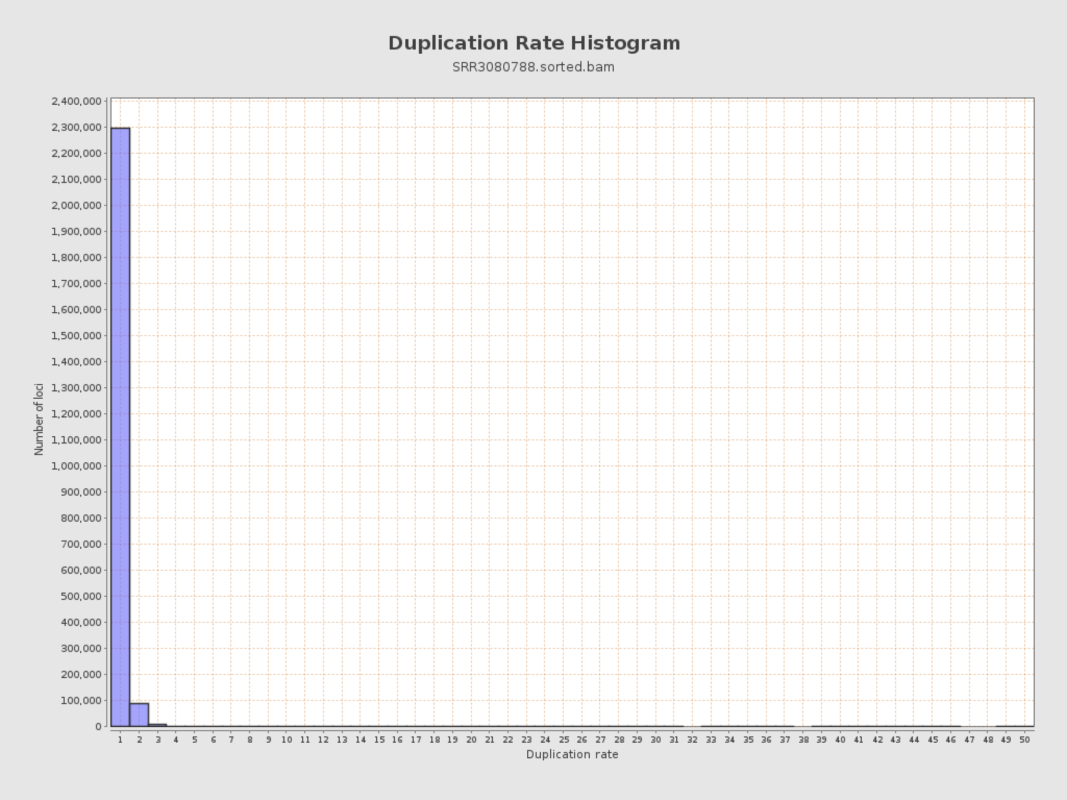
5. Results : Coverage Histogram (0-50X)



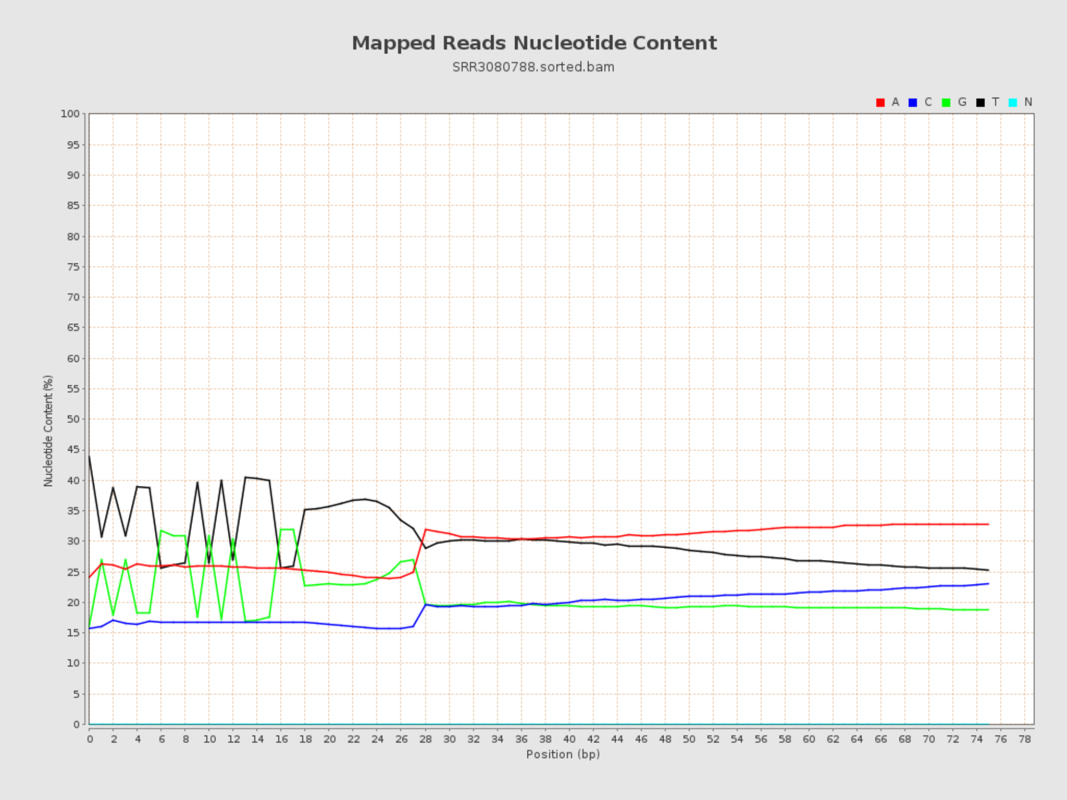
6. Results : Genome Fraction Coverage



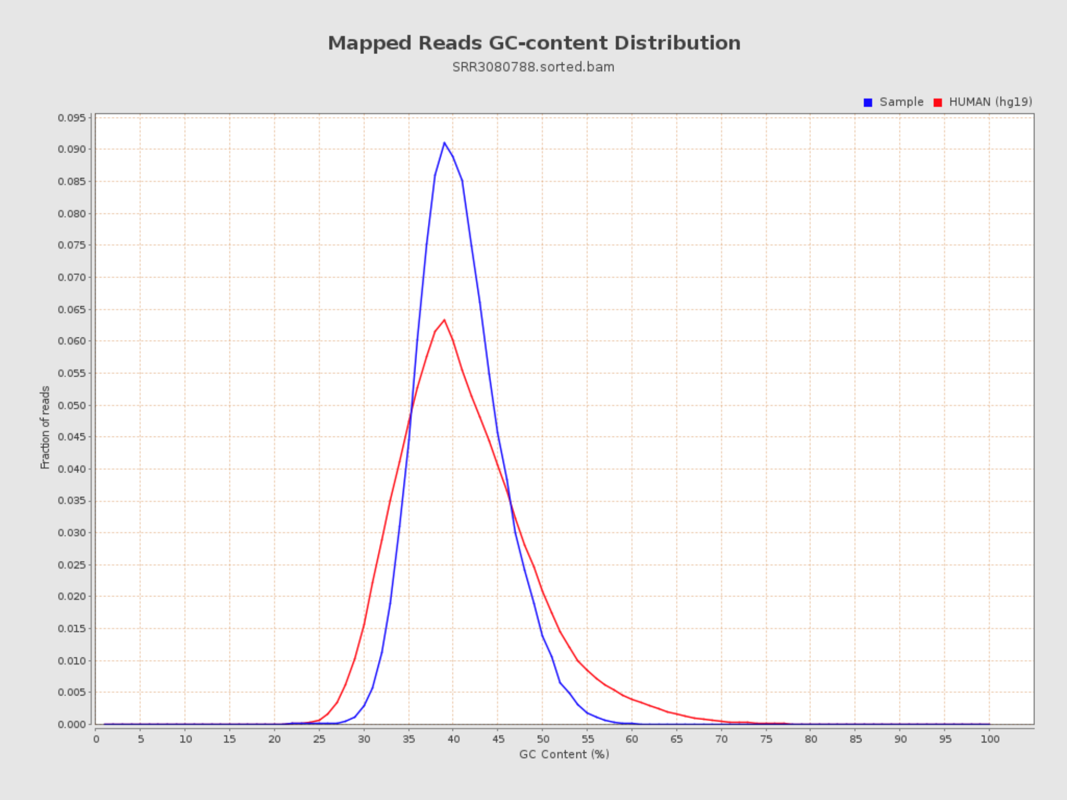
7. Results : Duplication Rate Histogram



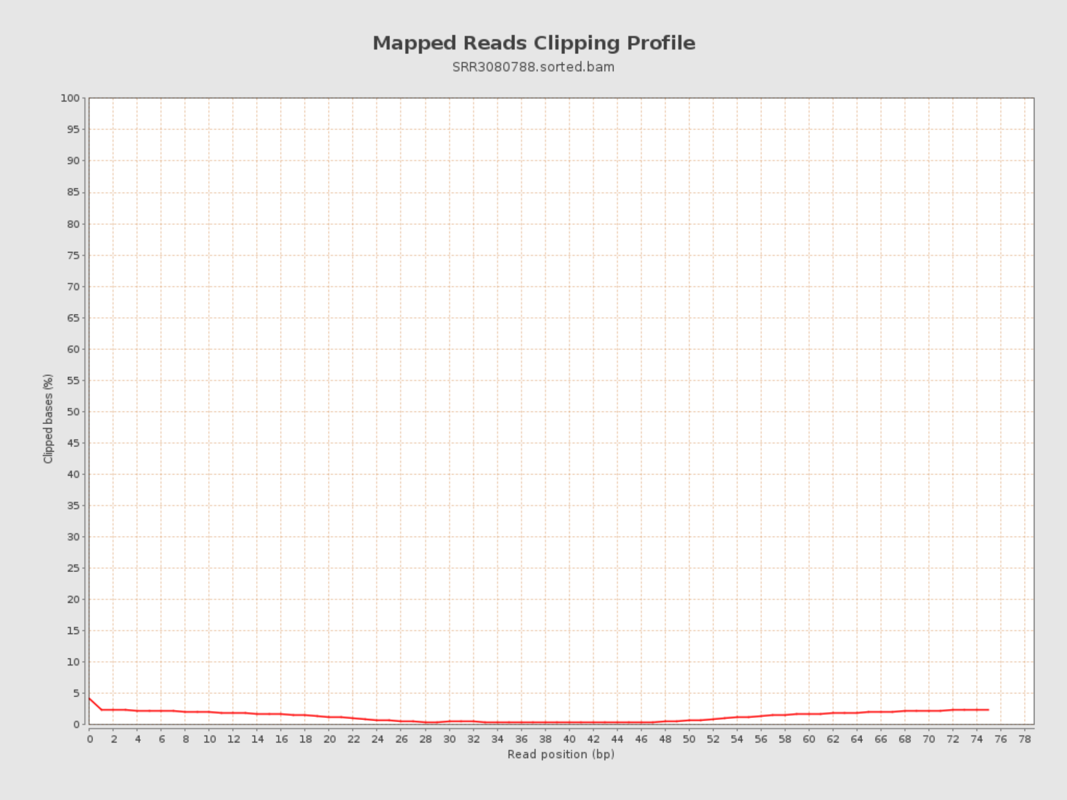
8. Results : Mapped Reads Nucleotide Content



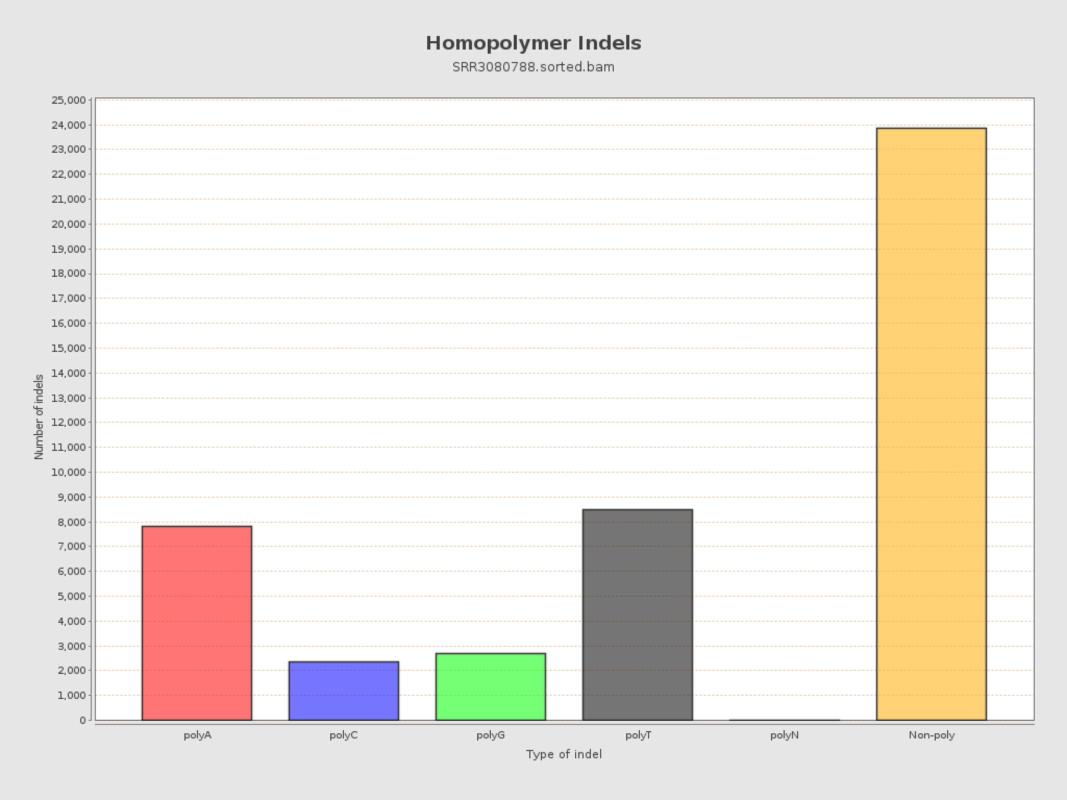
9. Results : Mapped Reads GC-content Distribution



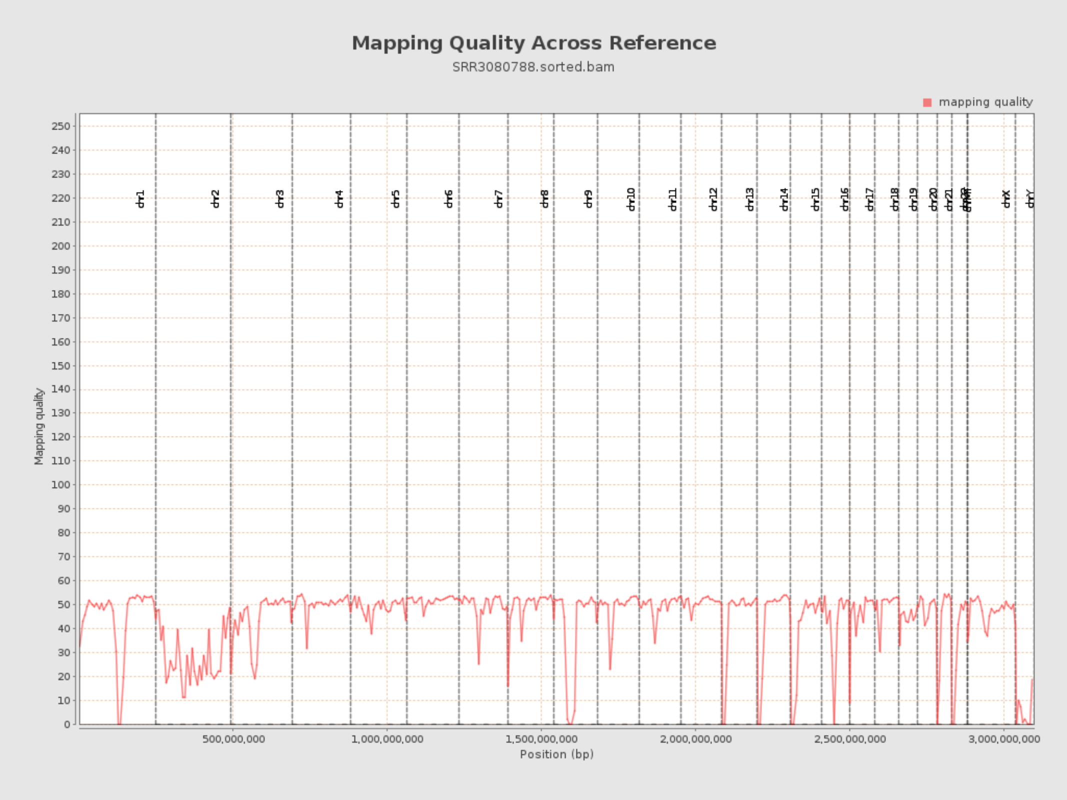
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram