Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:29:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081117.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_SRR3081117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:29:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,496,705
Mapped reads	2,315,270 / 92.73%
Unmapped reads	181,435 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,835 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	119,086 / 4.77%
Duplication rate	3.35%
Clipped reads	836,631 / 33.51%

2.2. ACGT Content

Number/percentage of A's	45,830,371 / 28.78%
Number/percentage of C's	29,887,817 / 18.77%
Number/percentage of T's	49,828,124 / 31.29%
Number/percentage of G's	33,691,636 / 21.16%
Number/percentage of N's	1,803 / 0%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0515

Standard Deviation	0.6212

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

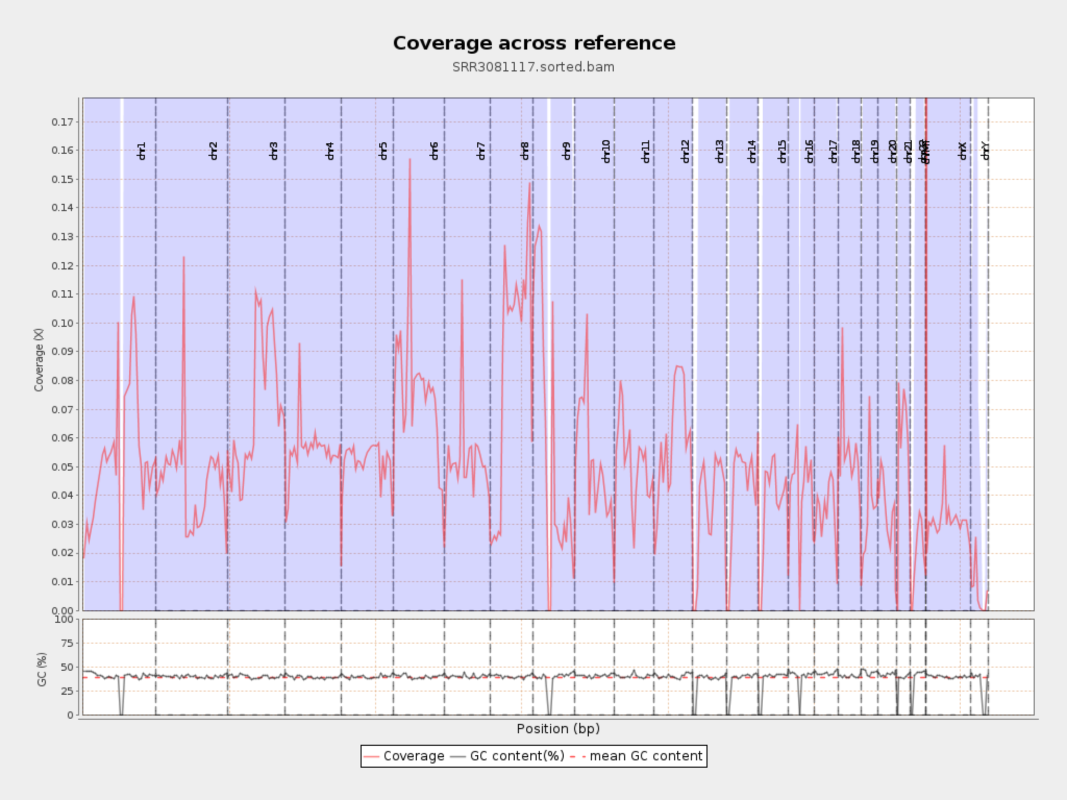
General error rate	0.9%
Mismatches	1,401,026
Insertions	12,479
Mapped reads with at least one insertion	0.53%
Deletions	34,239
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.22%

2.6. Chromosome stats

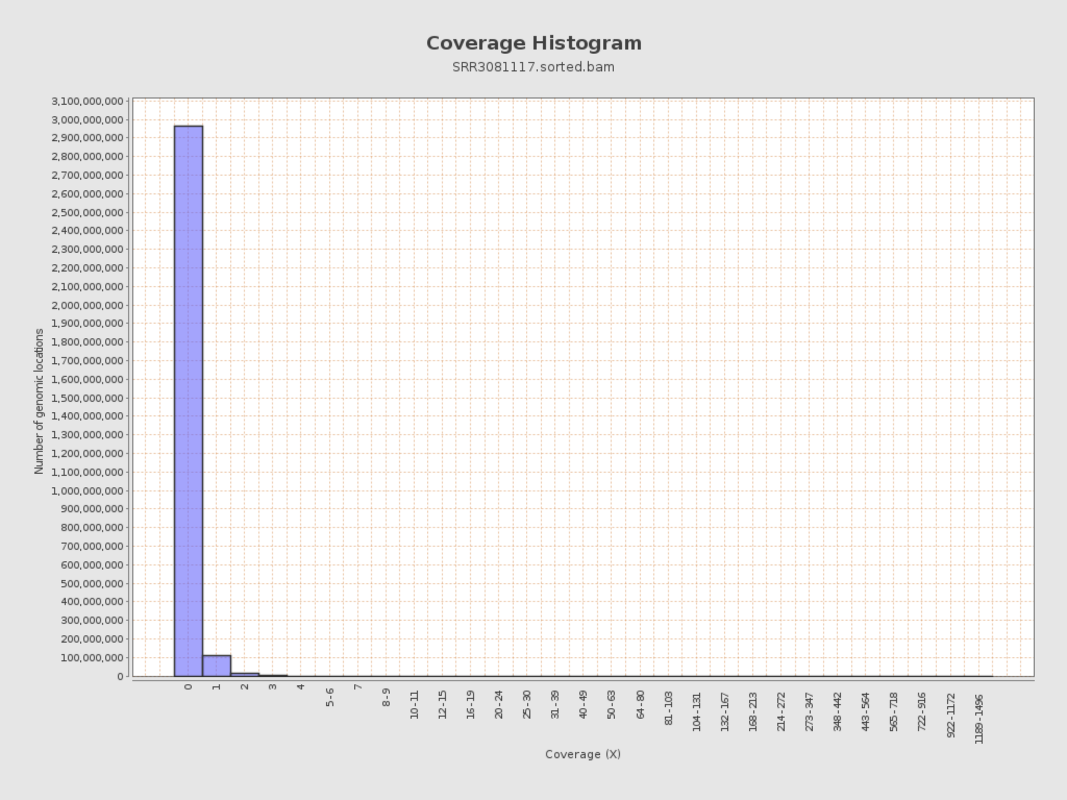
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13008662	0.0522	1.0081
chr2	243199373	11070137	0.0455	0.6825
chr3	198022430	14027042	0.0708	0.316
chr4	191154276	10669299	0.0558	0.3218
chr5	180915260	9311019	0.0515	0.2733
chr6	171115067	13417560	0.0784	0.6369
chr7	159138663	8352122	0.0525	0.8646

chr8	146364022	12748741	0.0871	0.685
chr9	141213431	8074389	0.0572	0.8188
chr10	135534747	7025928	0.0518	0.5164
chr11	135006516	6942852	0.0514	0.5112
chr12	133851895	7876056	0.0588	0.3397
chr13	115169878	4135636	0.0359	0.2168
chr14	107349540	4490264	0.0418	0.4548
chr15	102531392	3728682	0.0364	0.2296
chr16	90354753	3664372	0.0406	0.4258
chr17	81195210	2847971	0.0351	0.2597
chr18	78077248	4389082	0.0562	1.6594
chr19	59128983	2109559	0.0357	0.742
chr20	63025520	2247248	0.0357	0.2852
chr21	48129895	2767527	0.0575	0.4331
chr22	51304566	998483	0.0195	0.1594
chrMT	16571	127052	7.6671	4.5723
chrX	155270560	4874851	0.0314	0.3031
chrY	59373566	396304	0.0067	0.1929

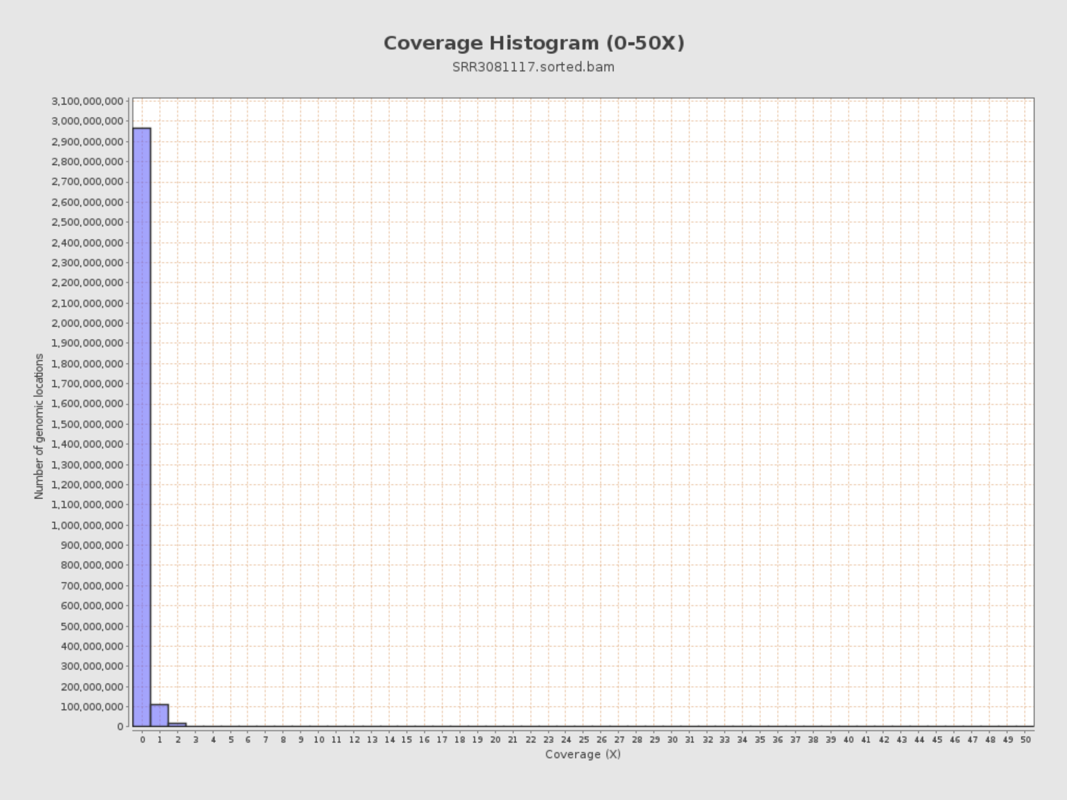
3. Results : Coverage across reference



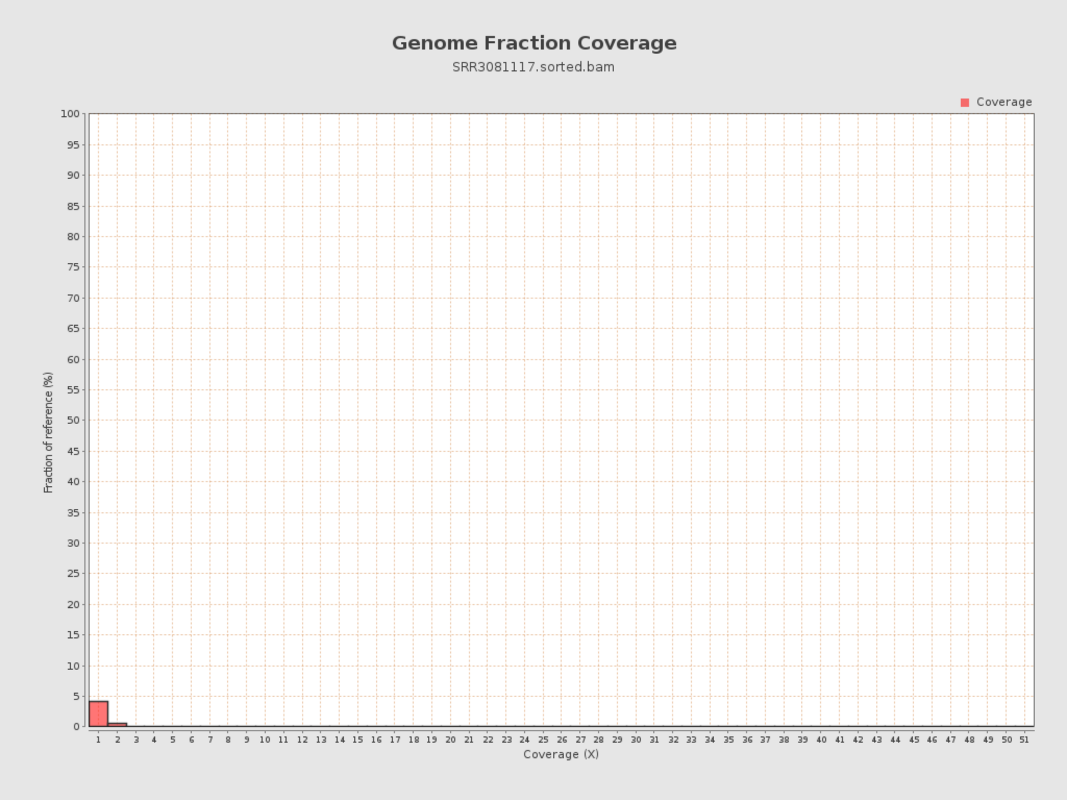
4. Results : Coverage Histogram



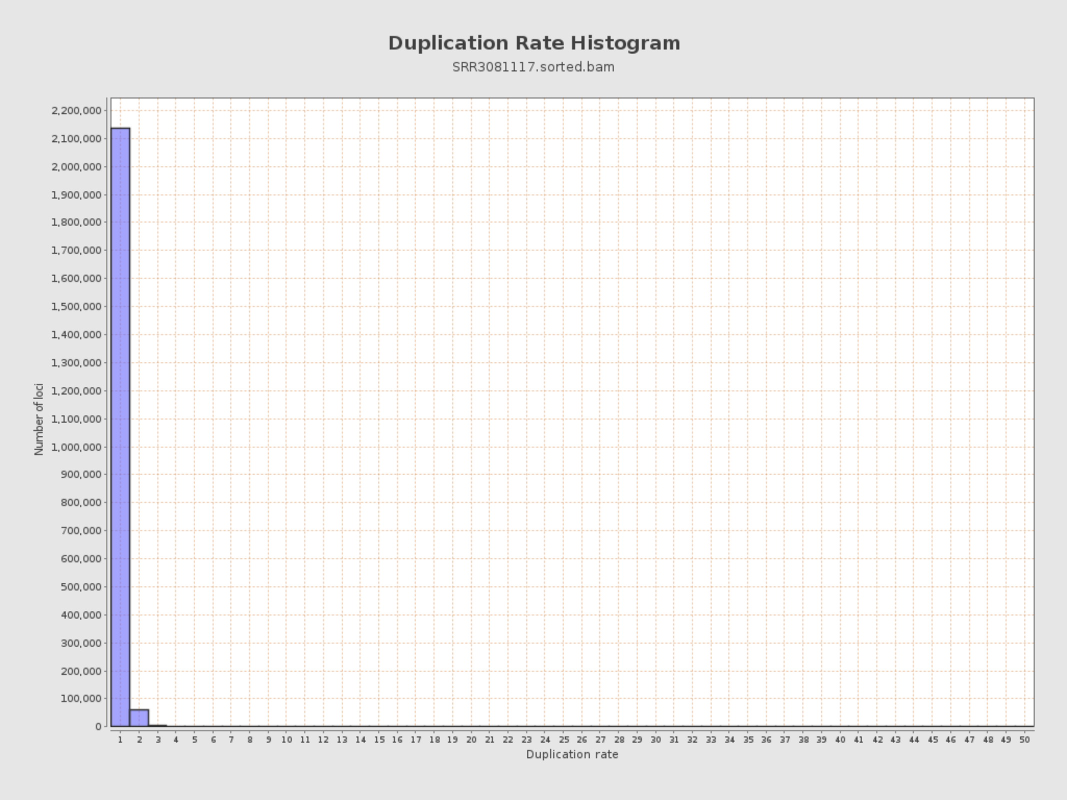
5. Results : Coverage Histogram (0-50X)



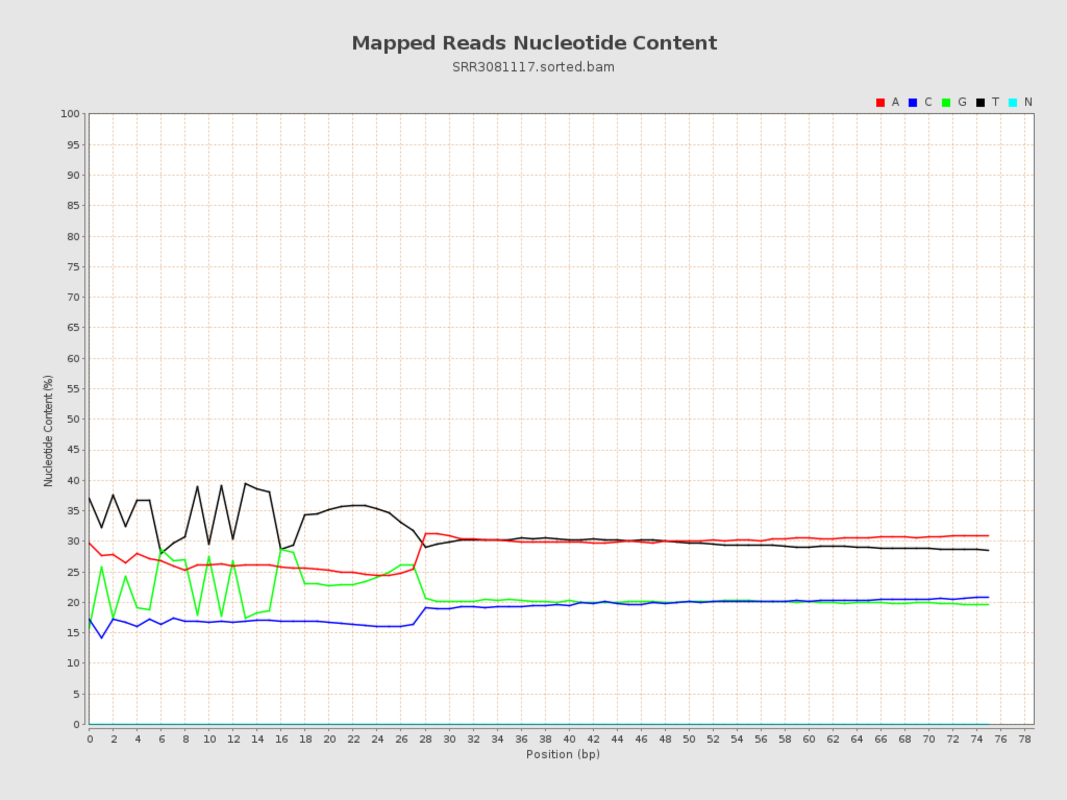
6. Results : Genome Fraction Coverage



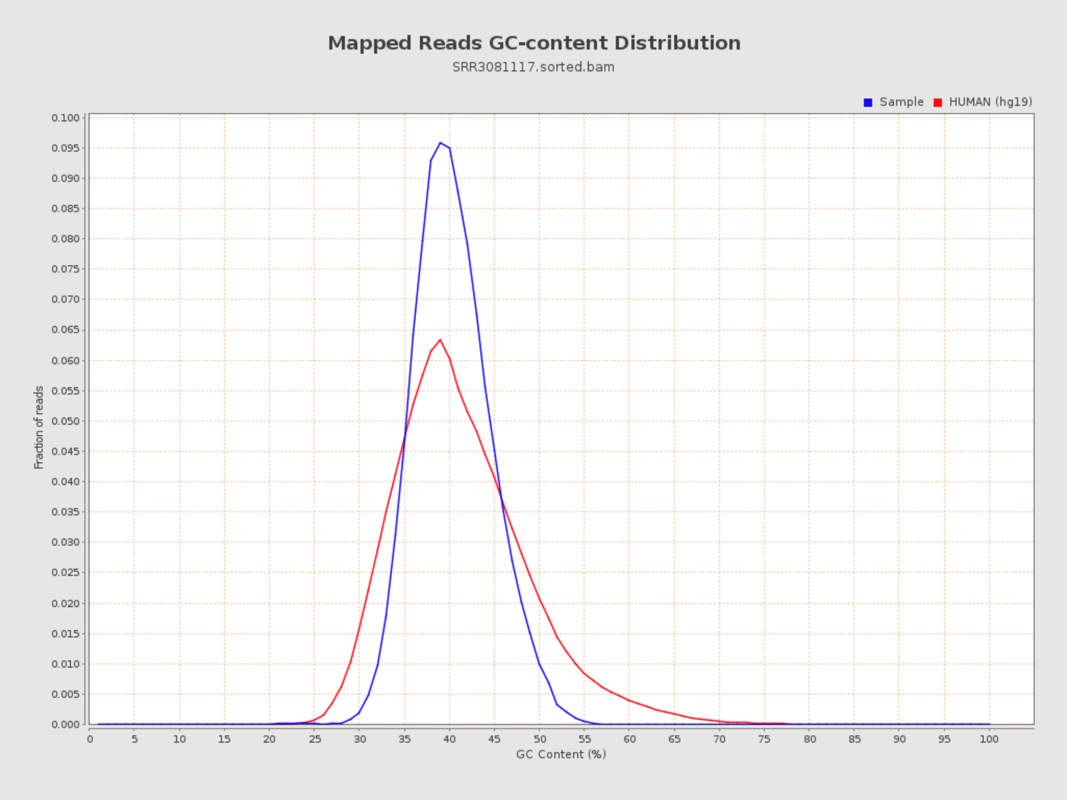
7. Results : Duplication Rate Histogram



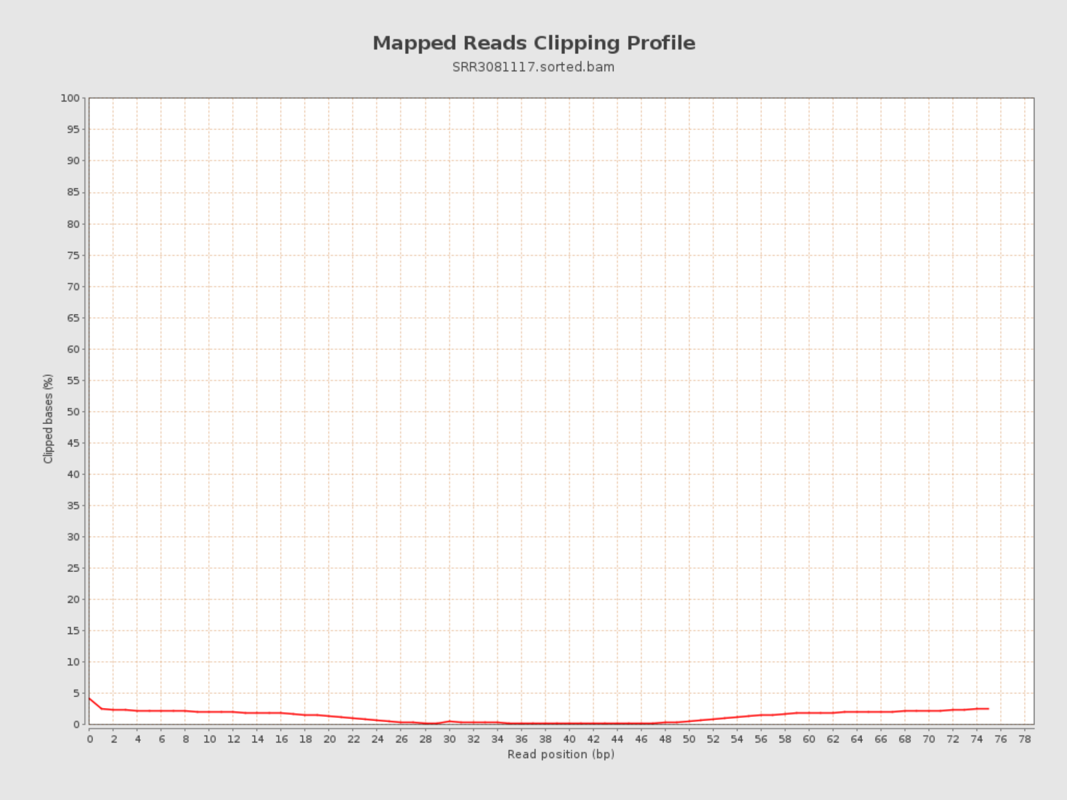
8. Results : Mapped Reads Nucleotide Content



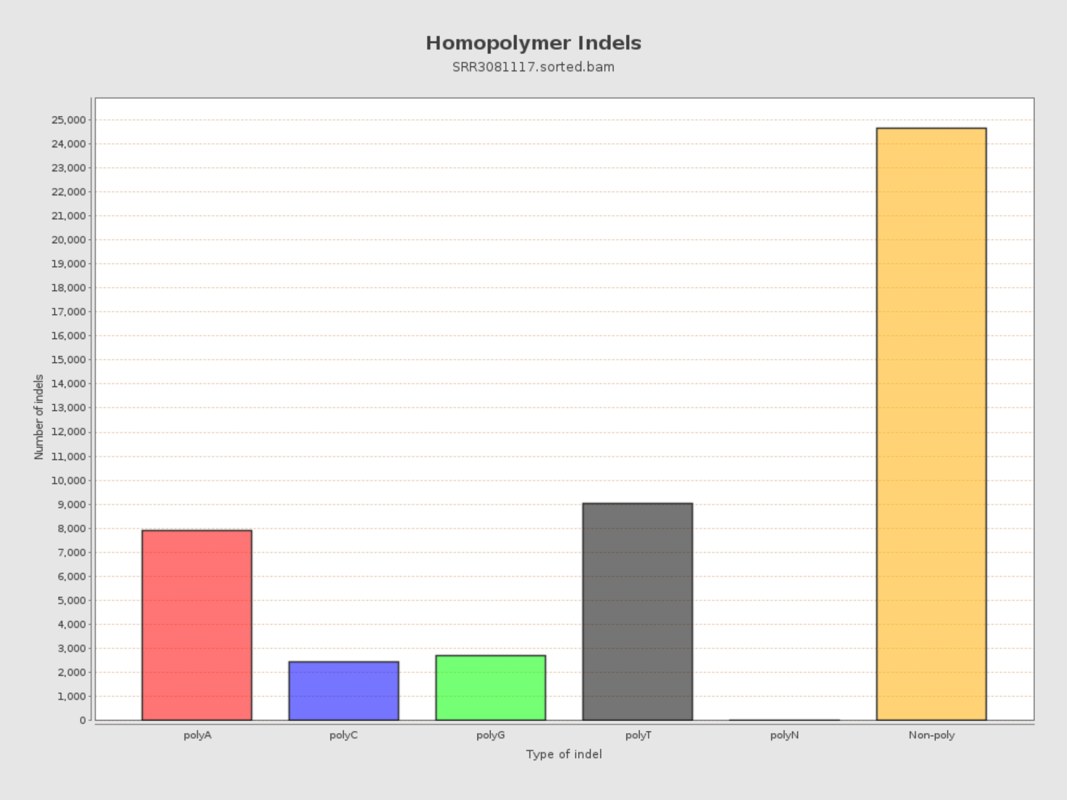
9. Results : Mapped Reads GC-content Distribution



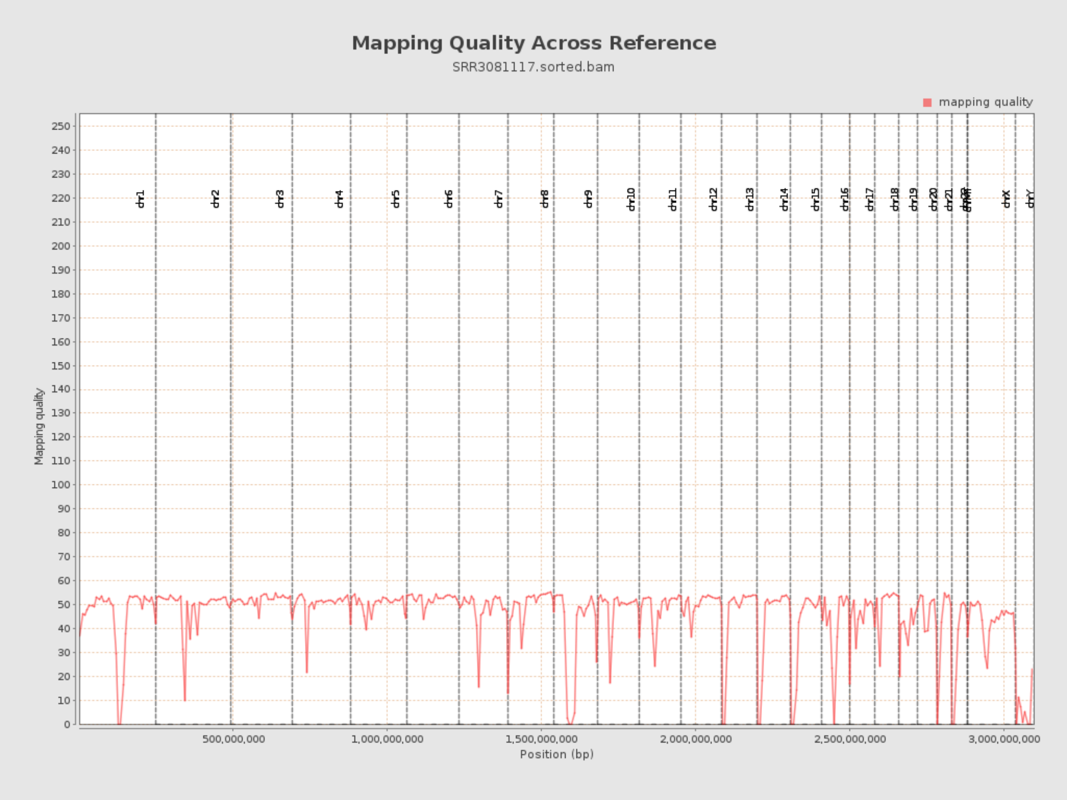
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram