Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:00:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081233.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_SRR3081233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:00:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,117,111
Mapped reads	1,870,328 / 88.34%
Unmapped reads	246,783 / 11.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,969 / 1.13%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	82,815 / 3.91%
Duplication rate	3.8%
Clipped reads	960,134 / 45.35%

2.2. ACGT Content

Number/percentage of A's	35,224,387 / 28.72%
Number/percentage of C's	23,431,259 / 19.1%
Number/percentage of T's	37,807,265 / 30.82%
Number/percentage of G's	26,197,490 / 21.36%
Number/percentage of N's	8,387 / 0.01%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.2869

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

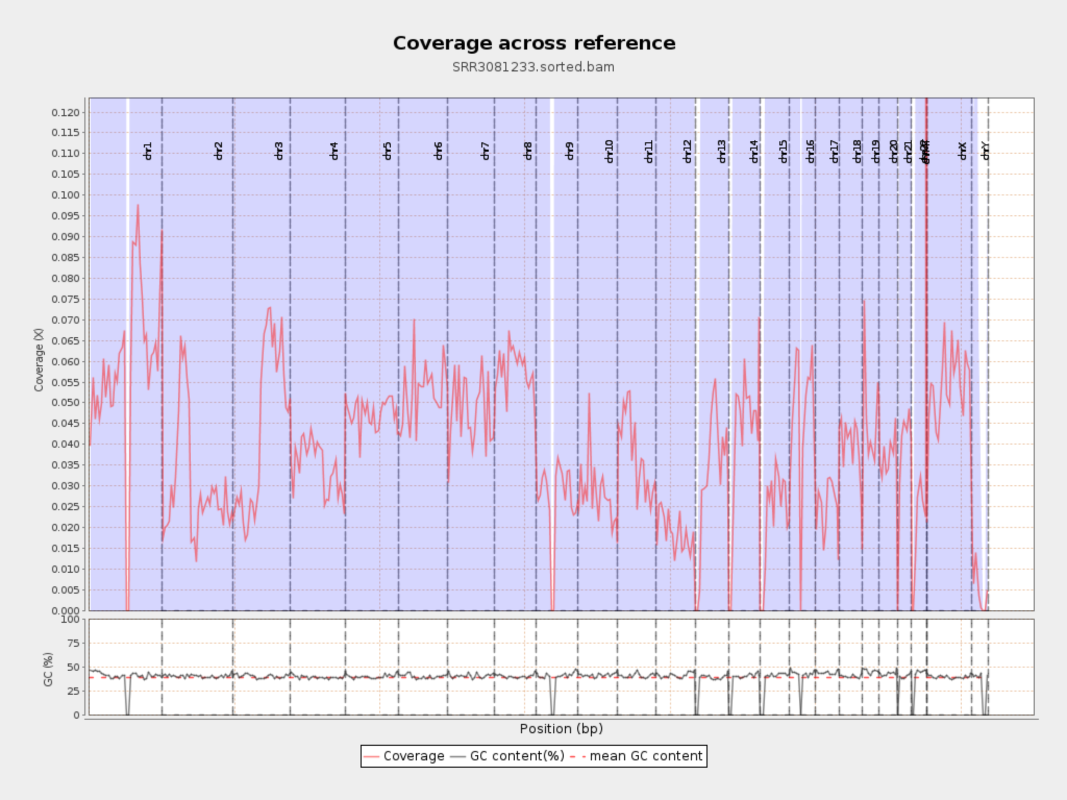
General error rate	0.88%
Mismatches	1,063,007
Insertions	9,055
Mapped reads with at least one insertion	0.48%
Deletions	28,329
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.52%

2.6. Chromosome stats

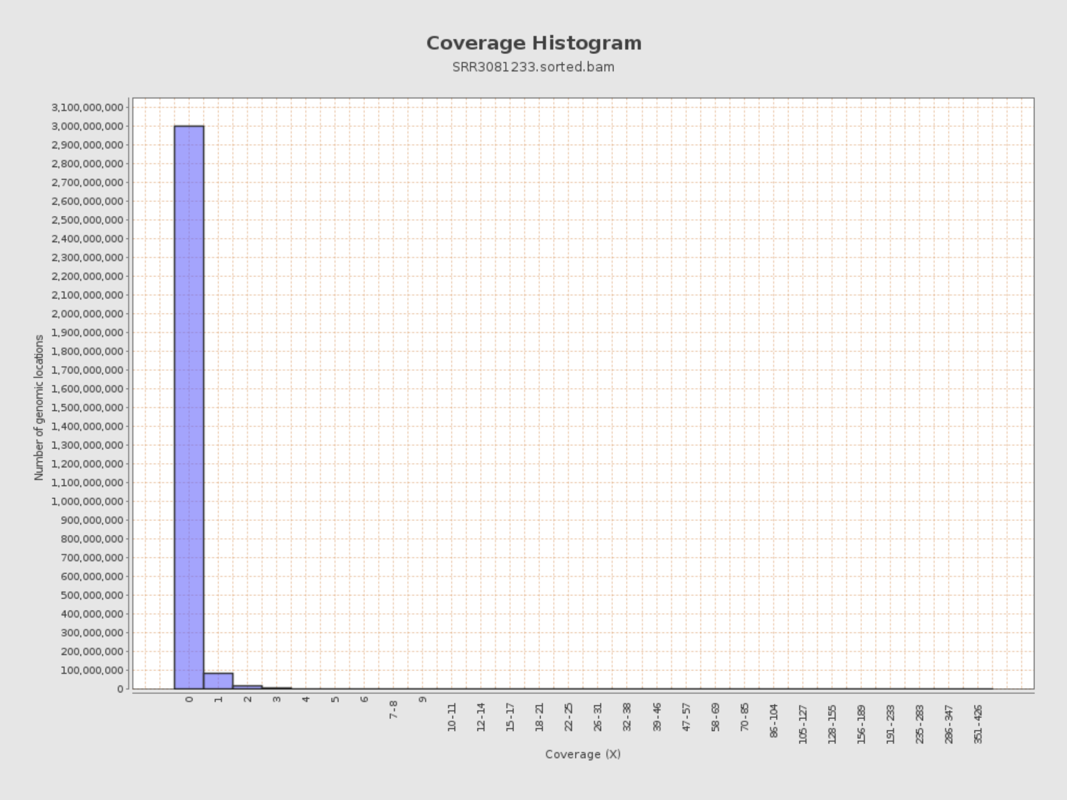
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14562250	0.0584	0.4436
chr2	243199373	7408432	0.0305	0.2865
chr3	198022430	8691421	0.0439	0.2528
chr4	191154276	6601799	0.0345	0.2256
chr5	180915260	8614591	0.0476	0.2605
chr6	171115067	8983661	0.0525	0.3104
chr7	159138663	7675011	0.0482	0.3189

chr8	146364022	8508082	0.0581	0.3861
chr9	141213431	3753380	0.0266	0.2261
chr10	135534747	3846287	0.0284	0.2776
chr11	135006516	5026130	0.0372	0.2947
chr12	133851895	2491745	0.0186	0.1648
chr13	115169878	3816520	0.0331	0.2186
chr14	107349540	4362231	0.0406	0.2451
chr15	102531392	2346261	0.0229	0.1859
chr16	90354753	4293119	0.0475	0.2664
chr17	81195210	2025257	0.0249	0.1997
chr18	78077248	3176720	0.0407	0.3396
chr19	59128983	2693642	0.0456	0.3645
chr20	63025520	2342785	0.0372	0.2335
chr21	48129895	1830435	0.038	0.239
chr22	51304566	987197	0.0192	0.1621
chrMT	16571	41122	2.4816	2.3935
chrX	155270560	8339631	0.0537	0.2877
chrY	59373566	297356	0.005	0.0999

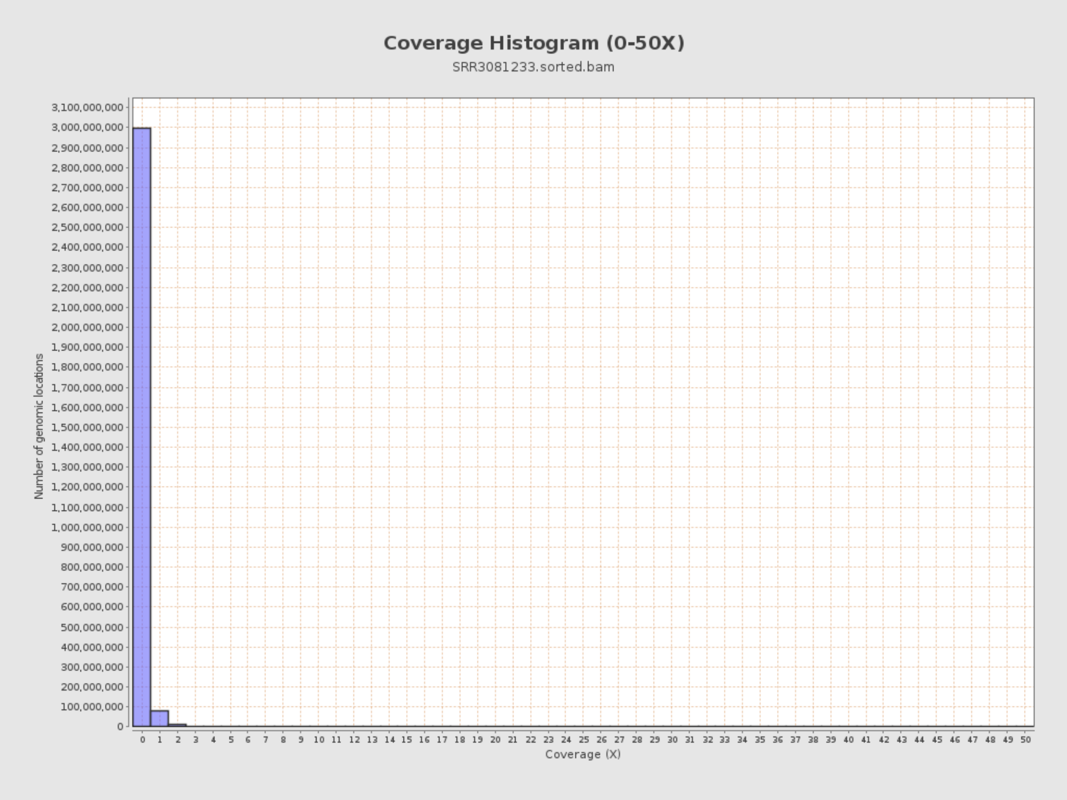
3. Results : Coverage across reference



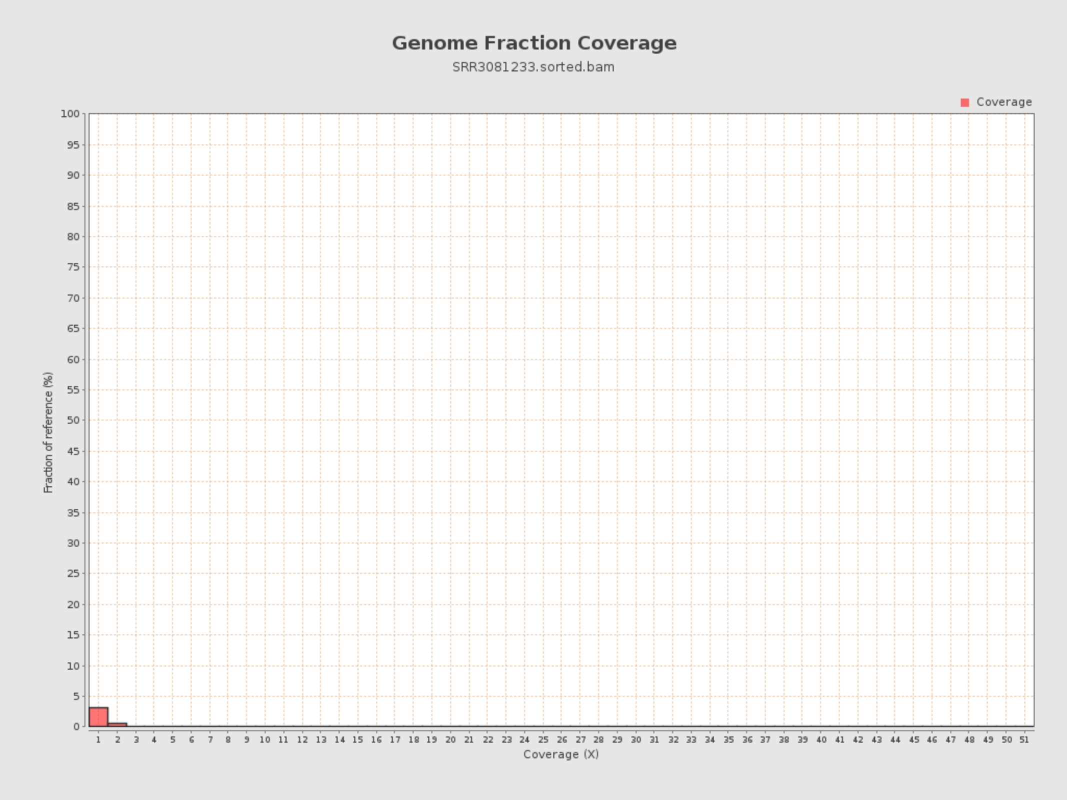
4. Results : Coverage Histogram



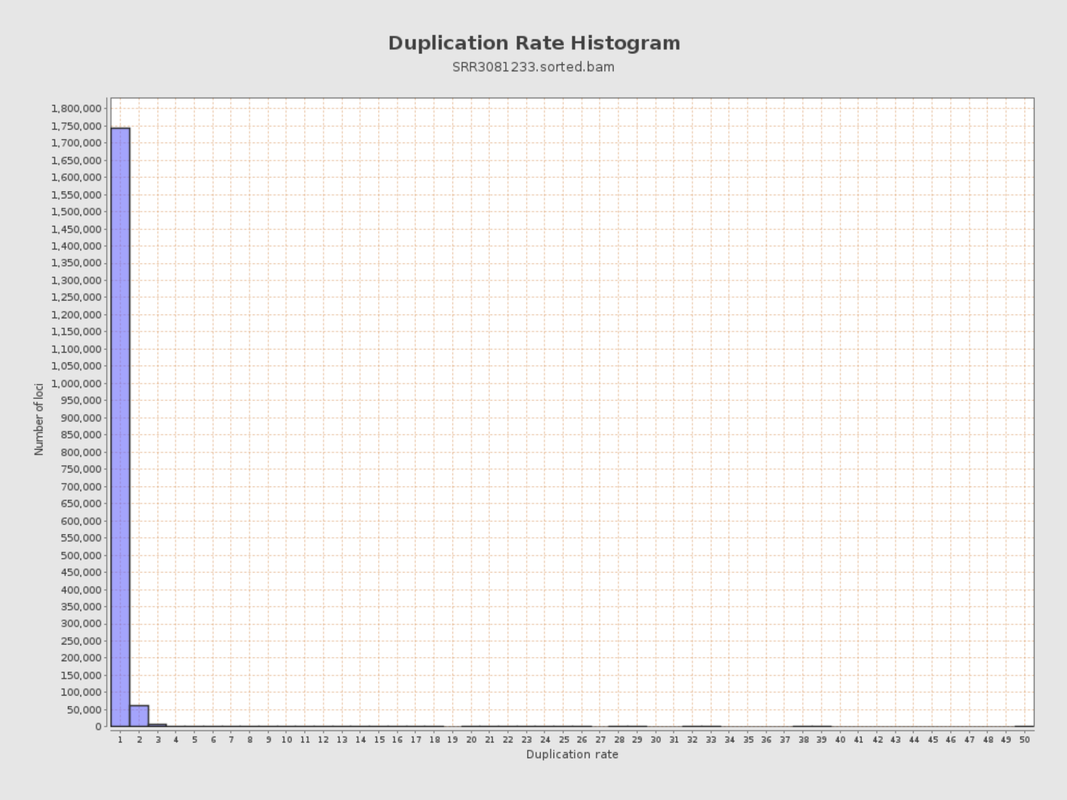
5. Results : Coverage Histogram (0-50X)



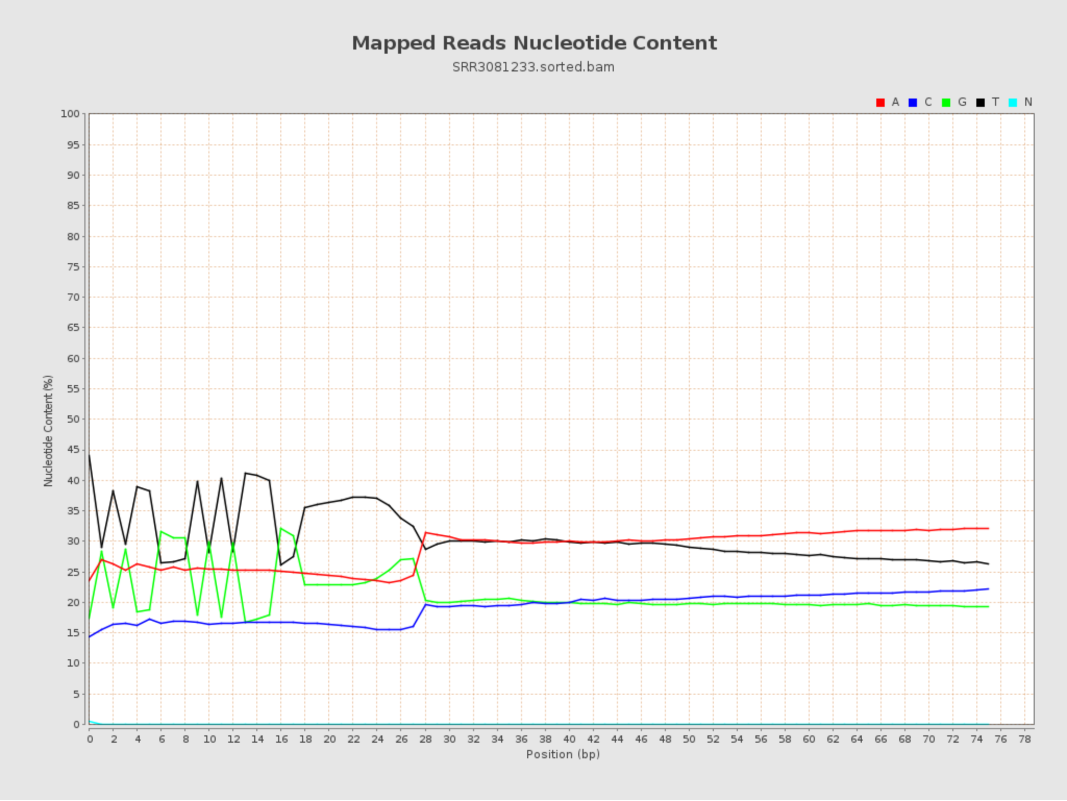
6. Results : Genome Fraction Coverage



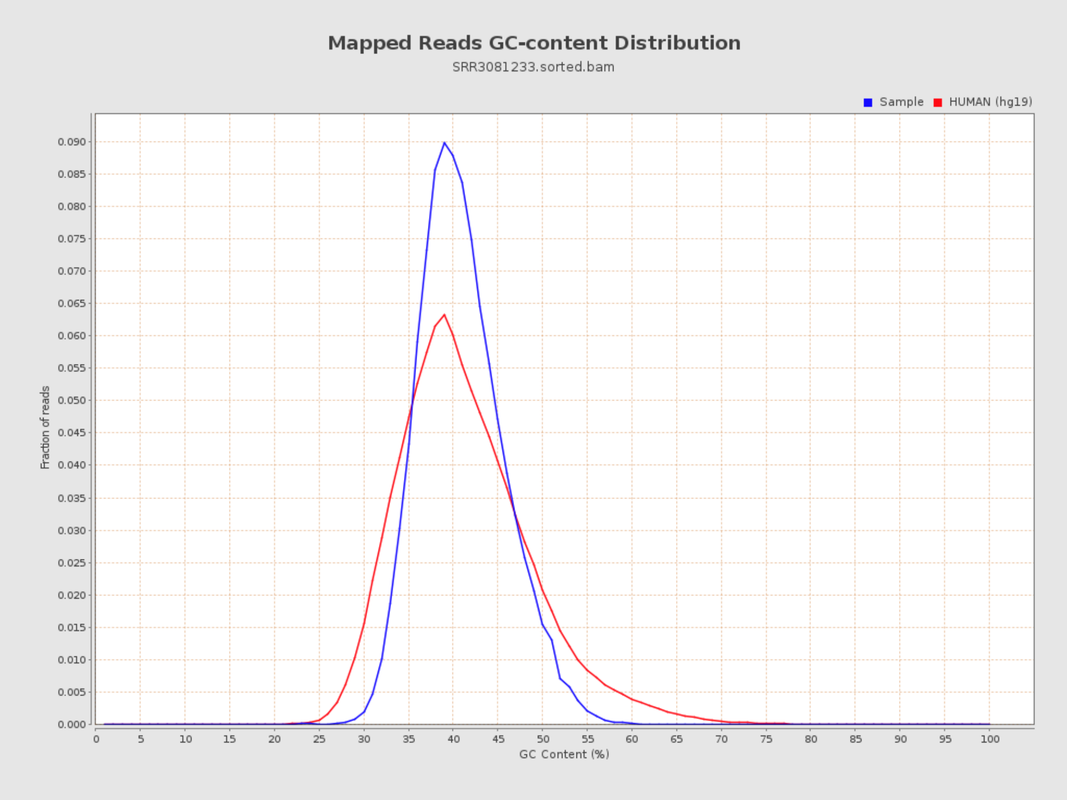
7. Results : Duplication Rate Histogram



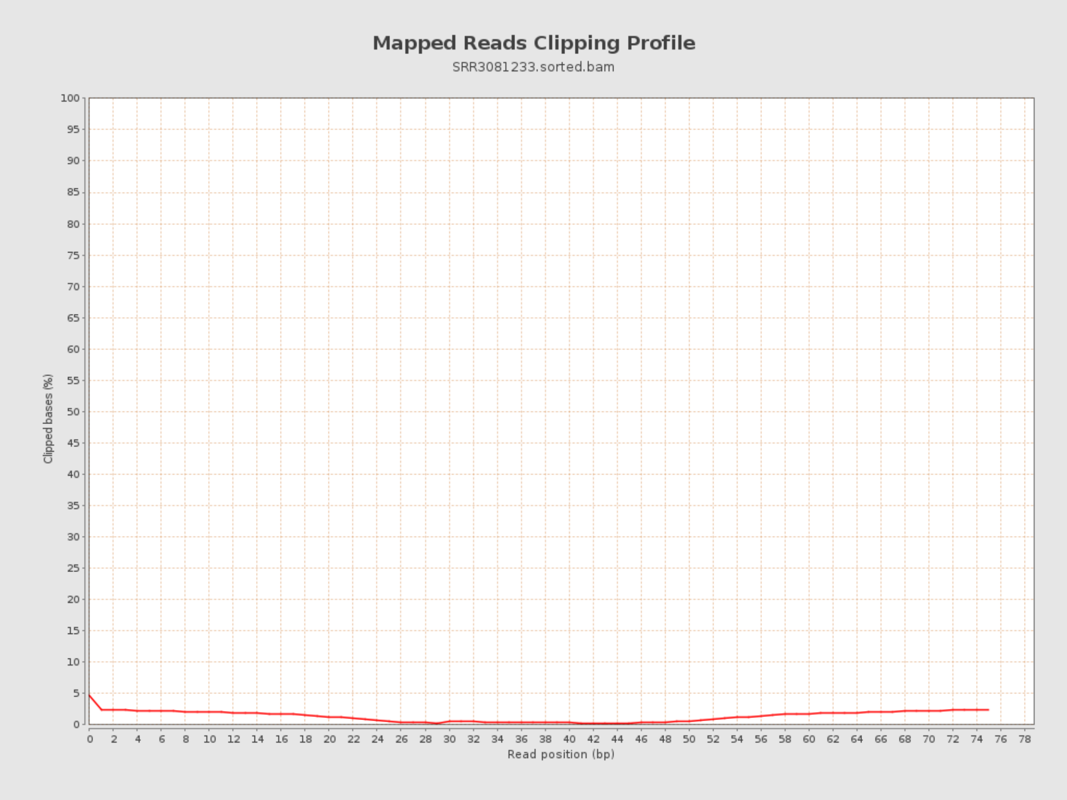
8. Results : Mapped Reads Nucleotide Content



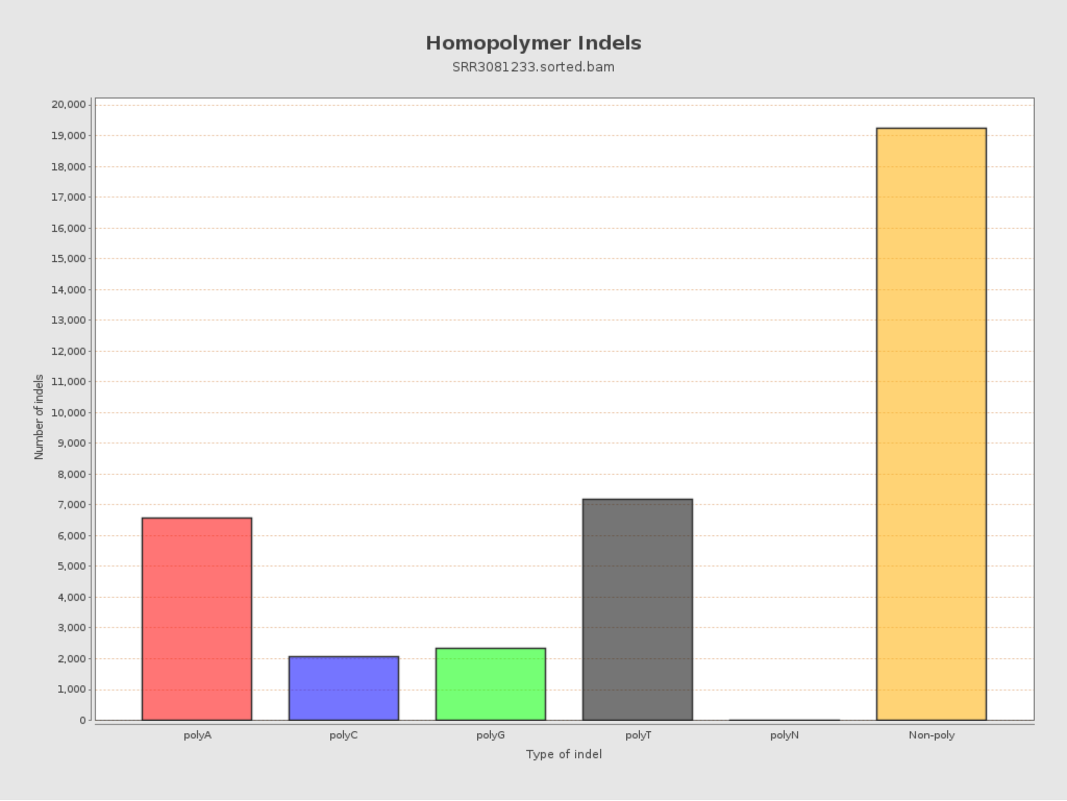
9. Results : Mapped Reads GC-content Distribution



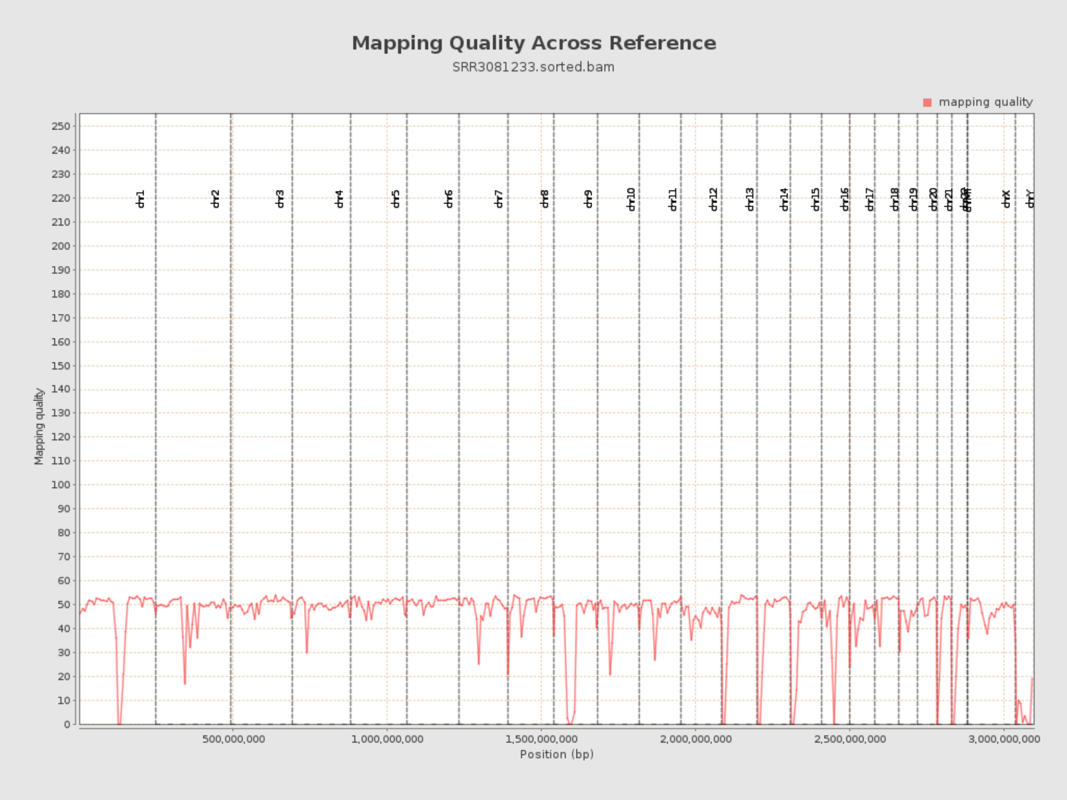
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram