Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:17:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081125.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_SRR3081125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:17:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,225,416
Mapped reads	2,025,561 / 91.02%
Unmapped reads	199,855 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,234 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	79,082 / 3.55%
Duplication rate	3.16%
Clipped reads	819,755 / 36.84%

2.2. ACGT Content

Number/percentage of A's	38,790,642 / 28.23%
Number/percentage of C's	26,122,291 / 19.01%
Number/percentage of T's	42,741,165 / 31.11%
Number/percentage of G's	29,744,049 / 21.65%
Number/percentage of N's	1,604 / 0%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0444

Standard Deviation	0.3467

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

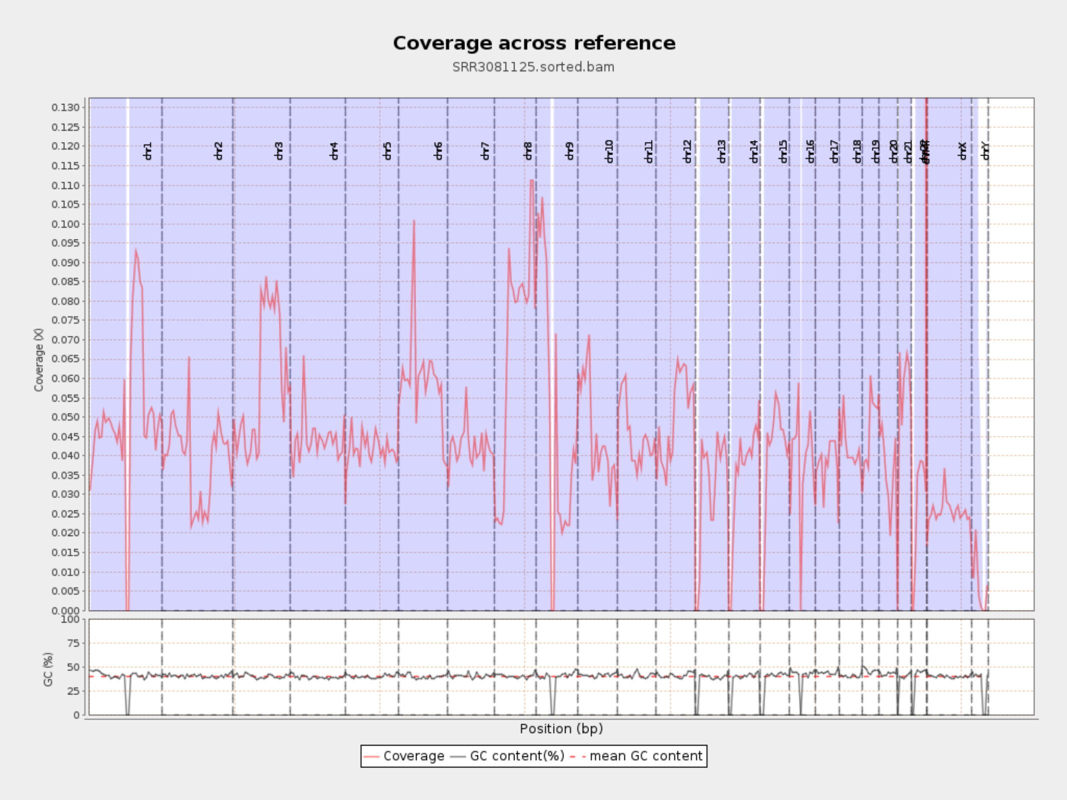
General error rate	0.87%
Mismatches	1,175,875
Insertions	10,516
Mapped reads with at least one insertion	0.51%
Deletions	29,447
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.34%

2.6. Chromosome stats

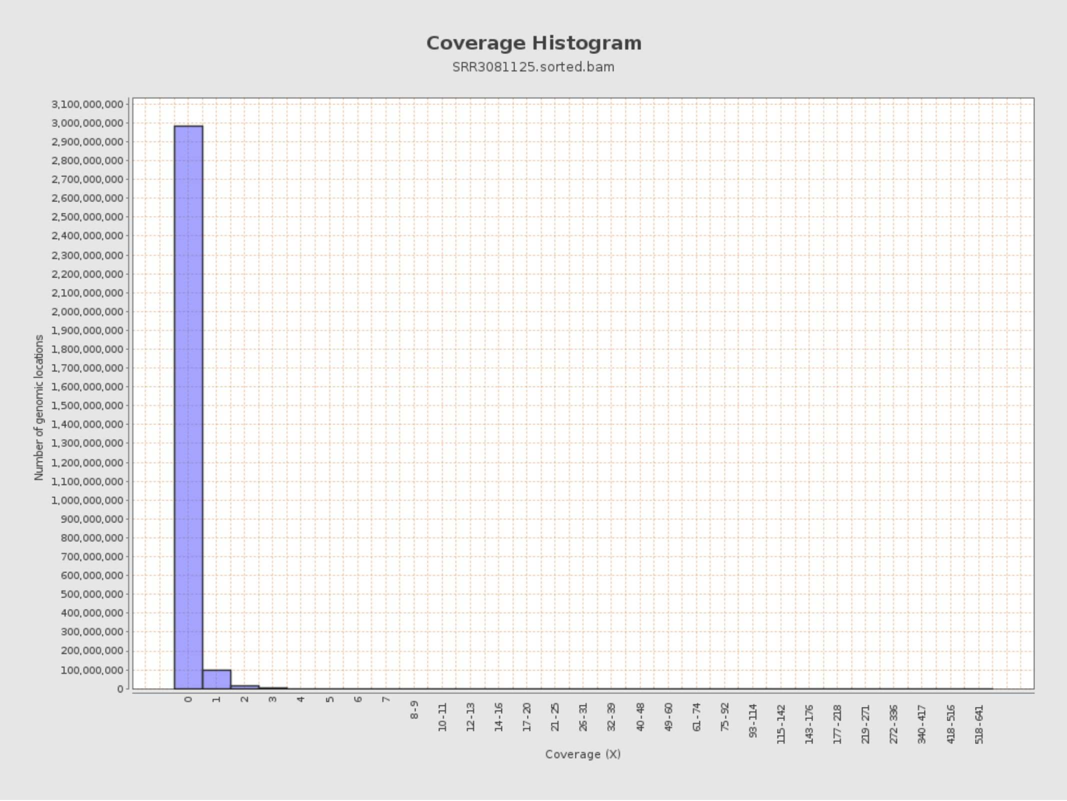
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12617142	0.0506	0.495
chr2	243199373	9493324	0.039	0.3738
chr3	198022430	11707979	0.0591	0.2831
chr4	191154276	8435584	0.0441	0.2623
chr5	180915260	7553907	0.0418	0.2381
chr6	171115067	10266233	0.06	0.3869
chr7	159138663	6771656	0.0426	0.3705

chr8	146364022	10116802	0.0691	0.4183
chr9	141213431	6899222	0.0489	0.4301
chr10	135534747	6257605	0.0462	0.3321
chr11	135006516	6085407	0.0451	0.2868
chr12	133851895	6708510	0.0501	0.2725
chr13	115169878	3617186	0.0314	0.2032
chr14	107349540	3699473	0.0345	0.2802
chr15	102531392	3916927	0.0382	0.23
chr16	90354753	3484434	0.0386	0.2866
chr17	81195210	3070090	0.0378	0.2284
chr18	78077248	3299019	0.0423	0.747
chr19	59128983	2790392	0.0472	0.3781
chr20	63025520	2285542	0.0363	0.2341
chr21	48129895	2608081	0.0542	0.3221
chr22	51304566	1304712	0.0254	0.1817
chrMT	16571	143048	8.6324	5.8257
chrX	155270560	3960892	0.0255	0.2093
chrY	59373566	359192	0.006	0.1466

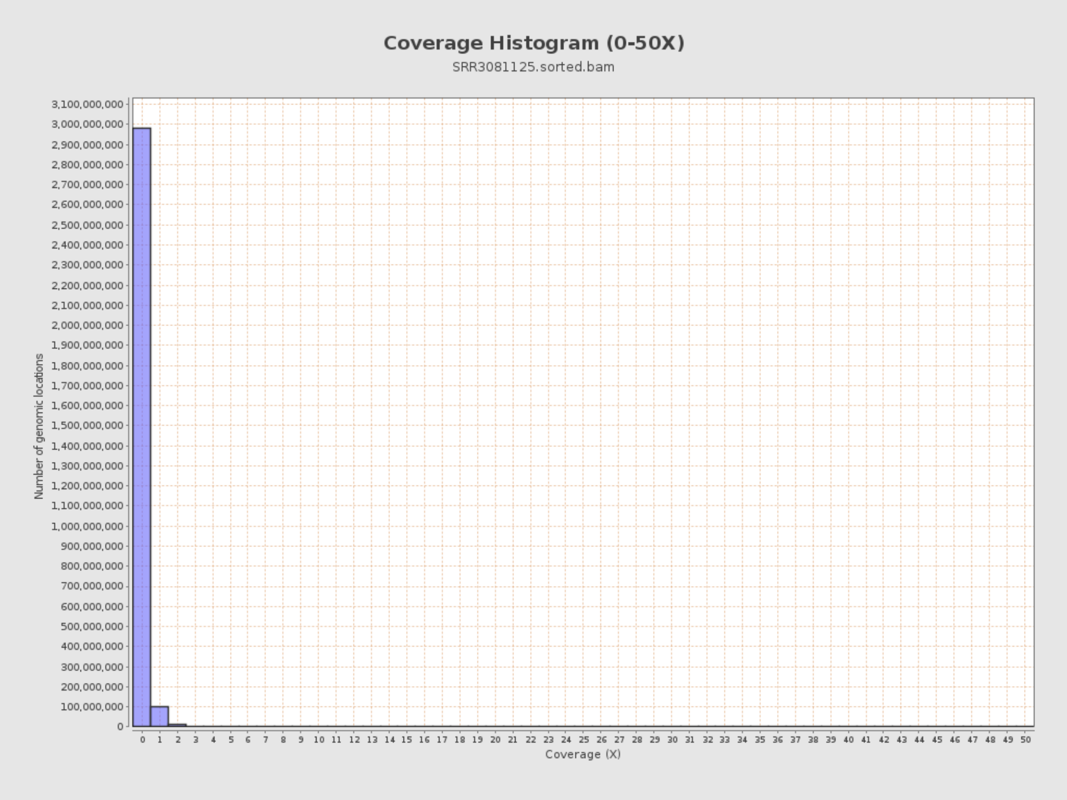
3. Results : Coverage across reference



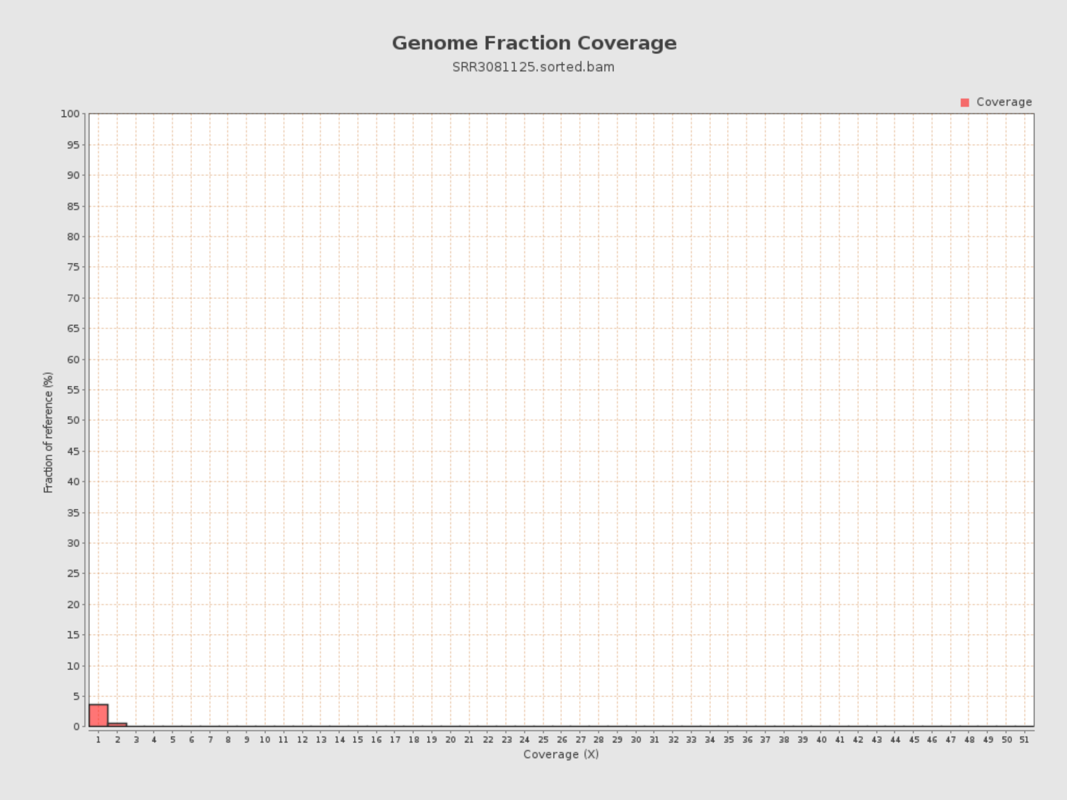
4. Results : Coverage Histogram



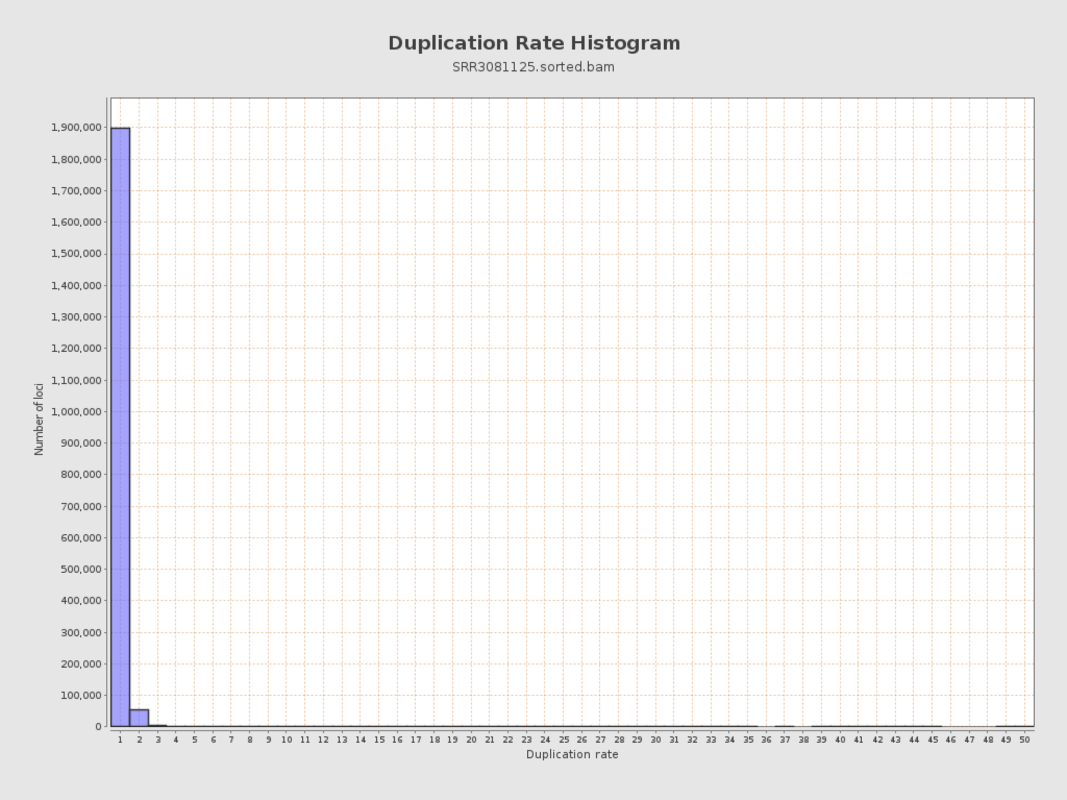
5. Results : Coverage Histogram (0-50X)



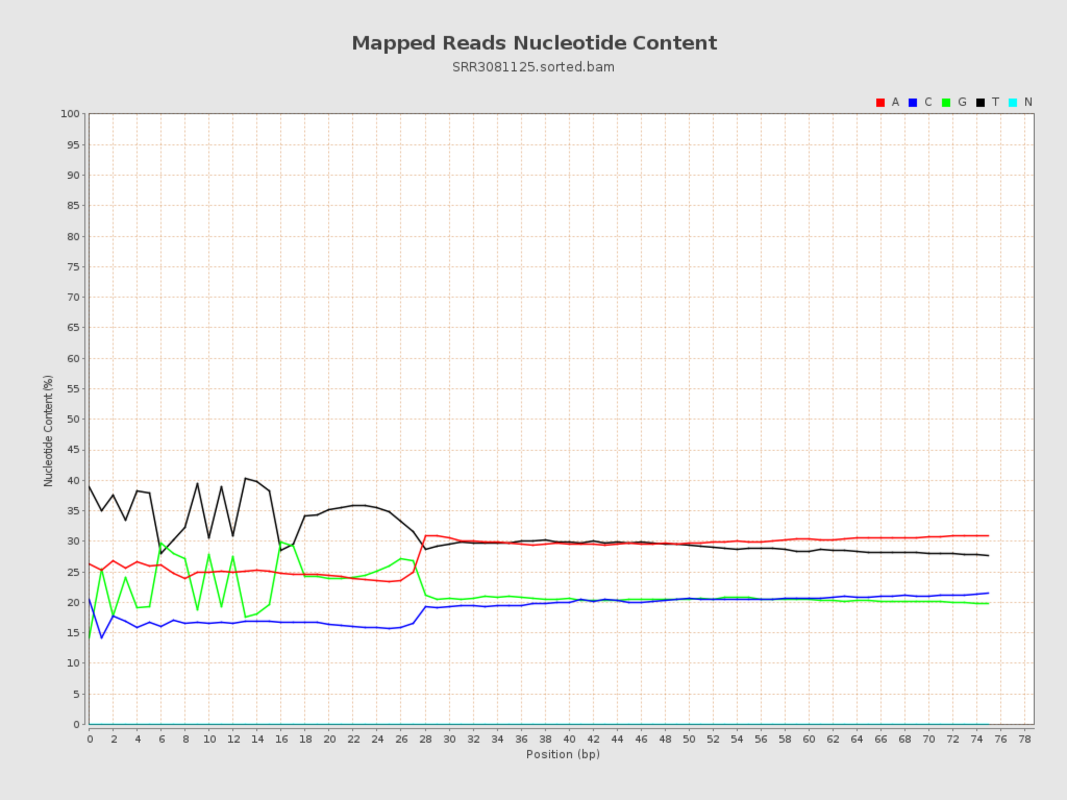
6. Results : Genome Fraction Coverage



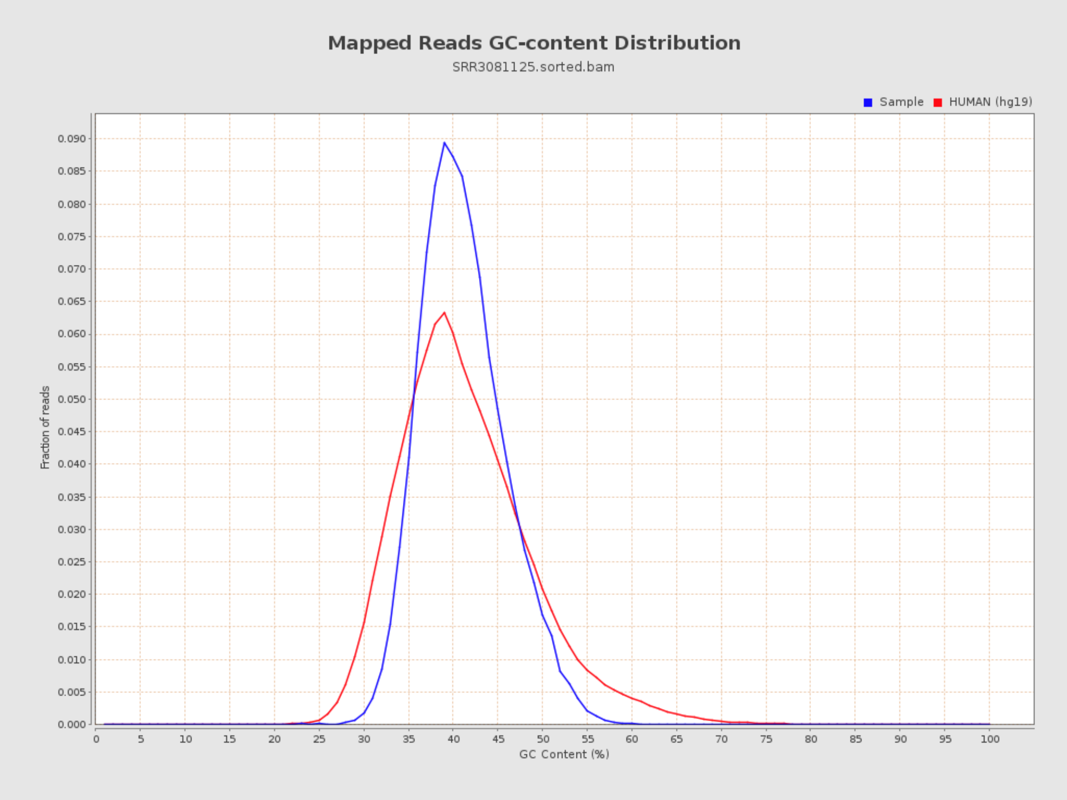
7. Results : Duplication Rate Histogram



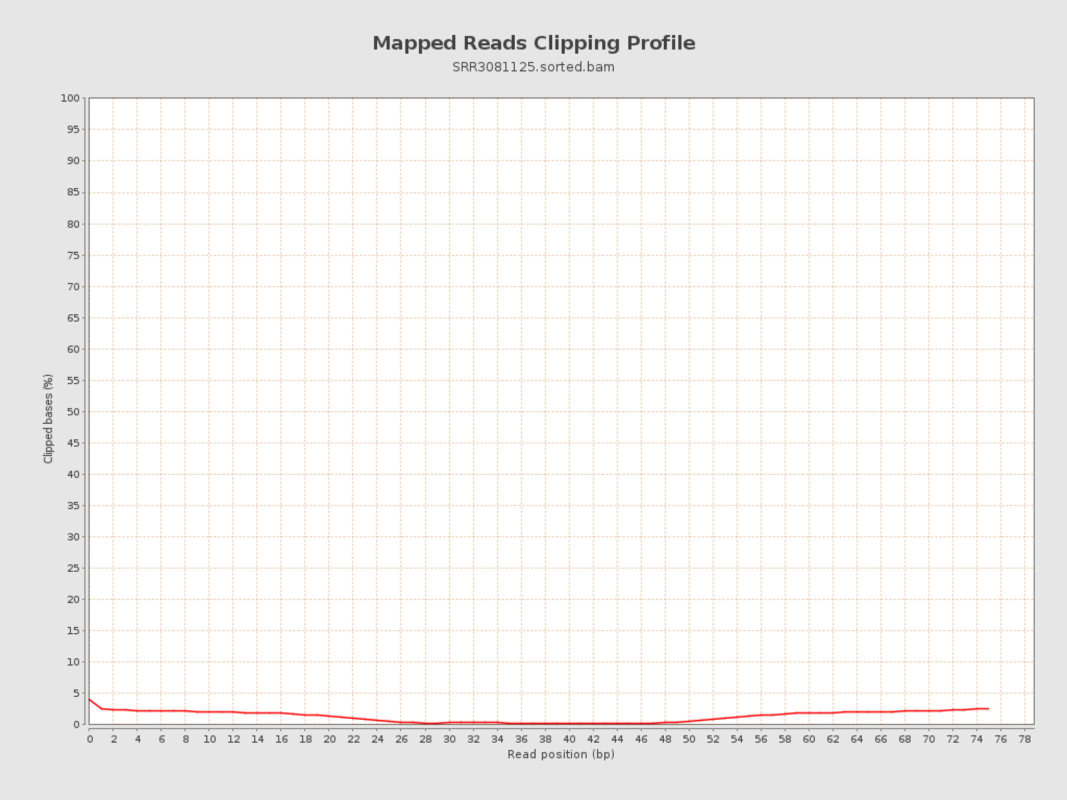
8. Results : Mapped Reads Nucleotide Content



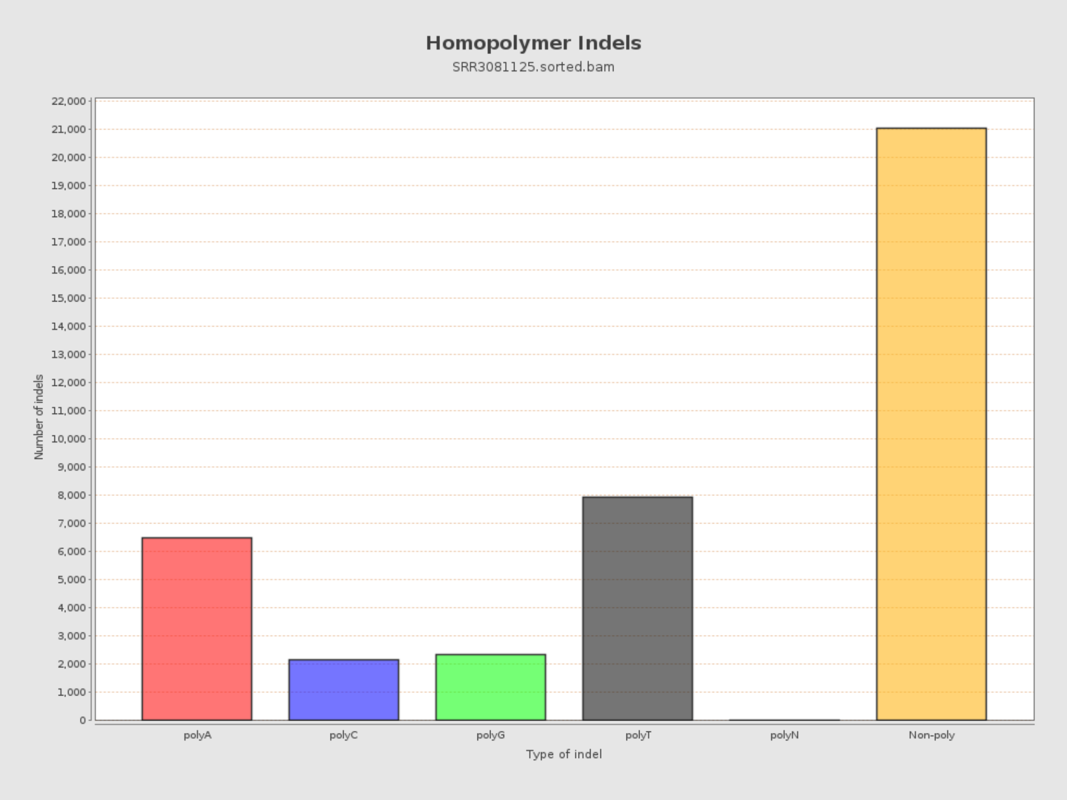
9. Results : Mapped Reads GC-content Distribution



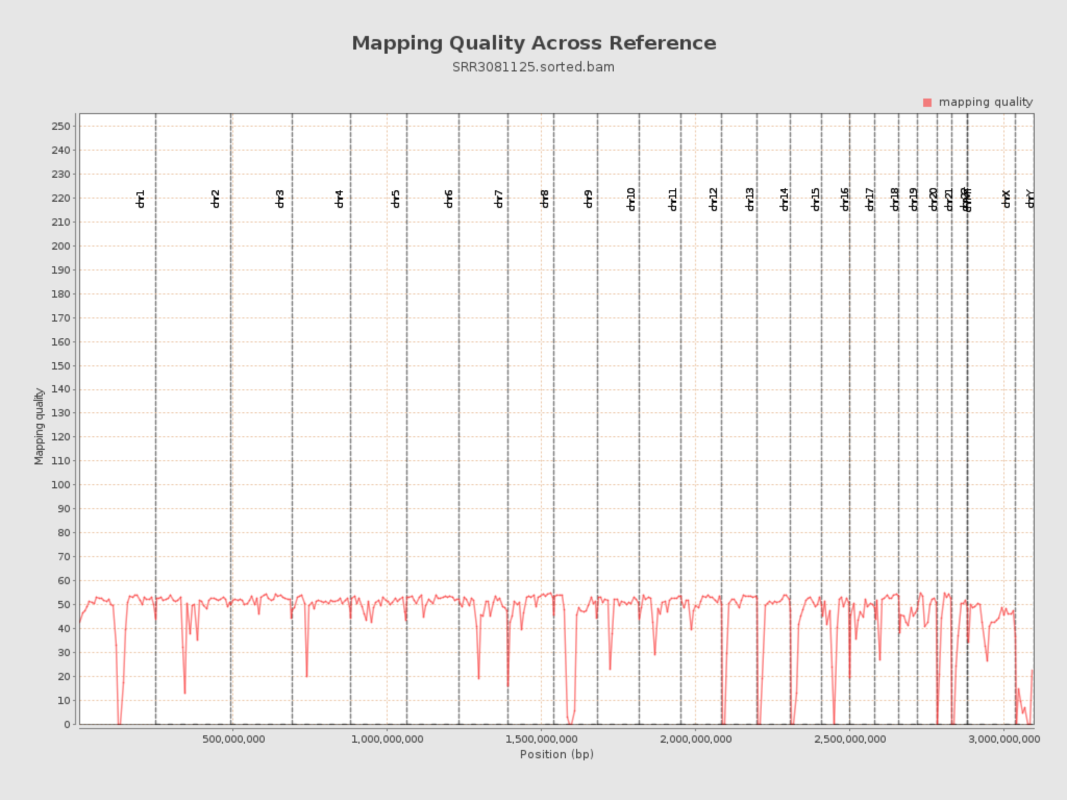
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram