Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:09:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818806.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_SRR1818806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:09:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,575,976
Mapped reads	3,485,125 / 97.46%
Unmapped reads	90,851 / 2.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,350 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,774,103 / 49.61%
Duplication rate	42.16%
Clipped reads	3,487,850 / 97.54%

2.2. ACGT Content

Number/percentage of A's	68,717,171 / 29%
Number/percentage of C's	49,965,644 / 21.09%
Number/percentage of T's	68,597,063 / 28.95%
Number/percentage of G's	49,653,406 / 20.96%
Number/percentage of N's	14,798 / 0.01%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0766

Standard Deviation	0.921

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

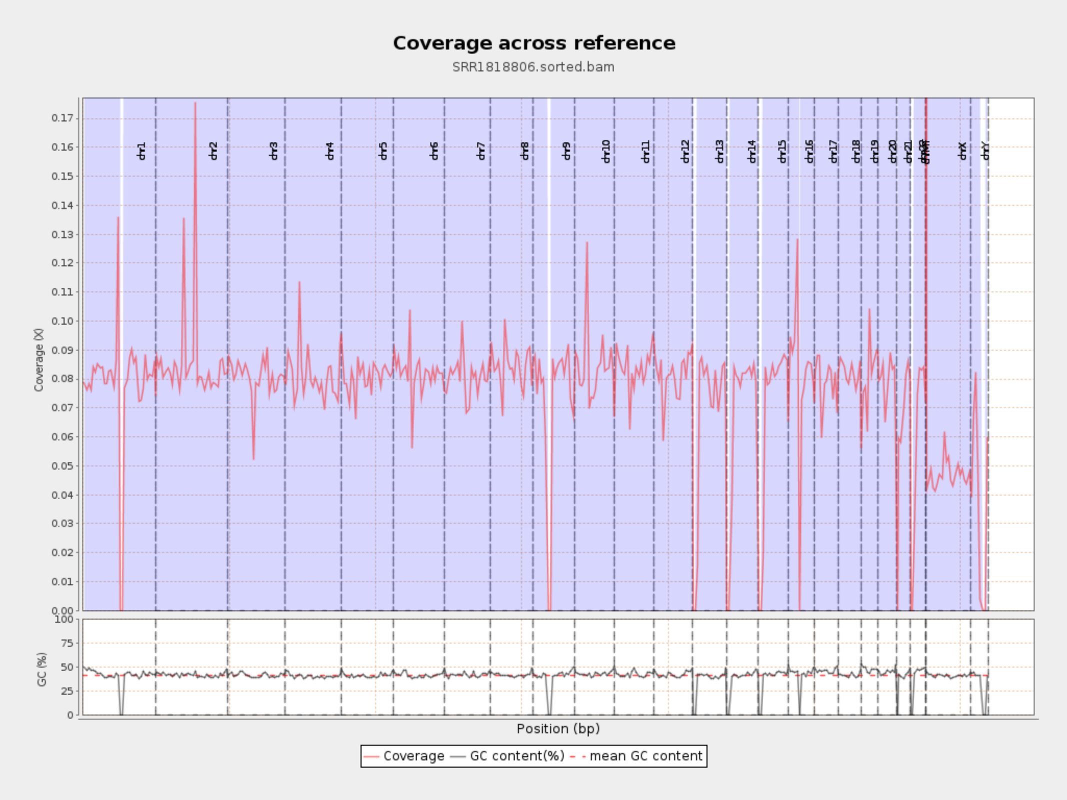
General error rate	0.53%
Mismatches	1,190,372
Insertions	30,811
Mapped reads with at least one insertion	0.88%
Deletions	58,832
Mapped reads with at least one deletion	1.67%
Homopolymer indels	39.05%

2.6. Chromosome stats

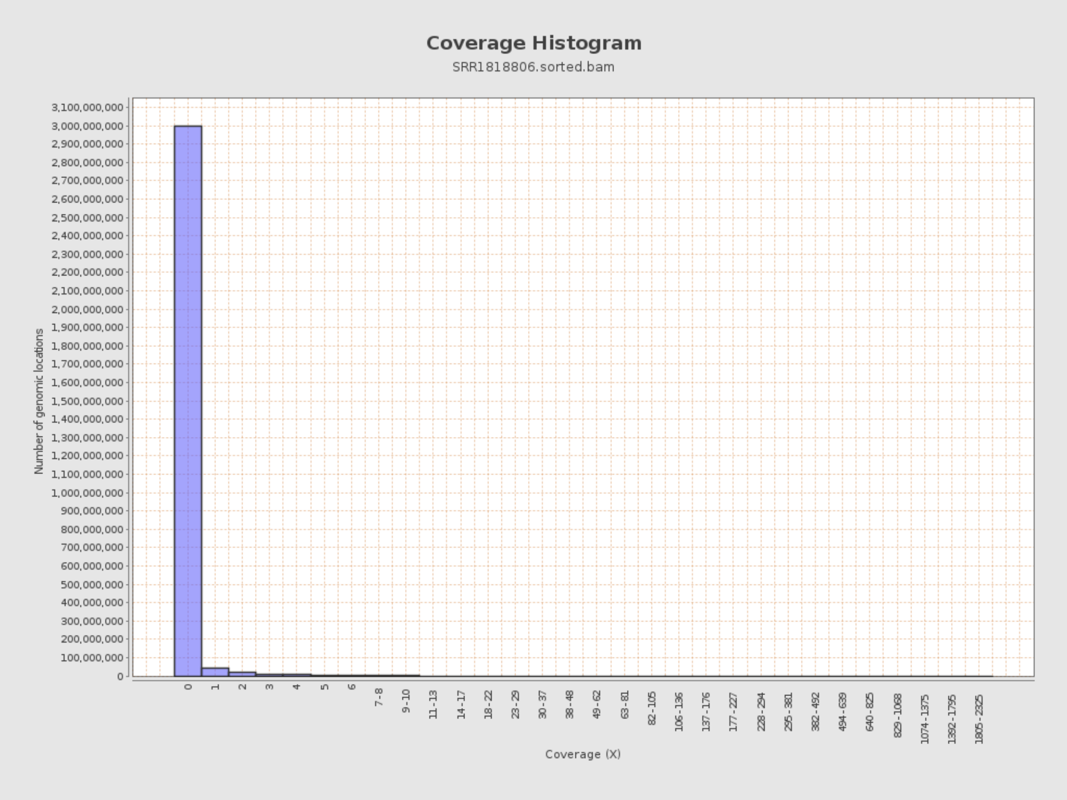
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19445989	0.078	1.4537
chr2	243199373	21048508	0.0865	1.5964
chr3	198022430	15963959	0.0806	0.5774
chr4	191154276	15527595	0.0812	0.7316
chr5	180915260	14616846	0.0808	0.6188
chr6	171115067	14022824	0.0819	0.6859
chr7	159138663	12896668	0.081	0.7607

chr8	146364022	12310443	0.0841	0.7042
chr9	141213431	10175977	0.0721	0.7171
chr10	135534747	11446159	0.0845	0.9996
chr11	135006516	11261712	0.0834	0.6843
chr12	133851895	10885786	0.0813	0.6345
chr13	115169878	7660575	0.0665	0.5278
chr14	107349540	7284511	0.0679	0.6473
chr15	102531392	6857614	0.0669	0.5328
chr16	90354753	7211778	0.0798	1.0852
chr17	81195210	6440949	0.0793	0.6368
chr18	78077248	6430604	0.0824	0.9364
chr19	59128983	4805443	0.0813	1.1763
chr20	63025520	5005143	0.0794	0.6146
chr21	48129895	3144889	0.0653	0.5591
chr22	51304566	2868790	0.0559	0.5549
chrMT	16571	175939	10.6173	9.8018
chrX	155270560	7307238	0.0471	0.5321
chrY	59373566	2249847	0.0379	1.7084

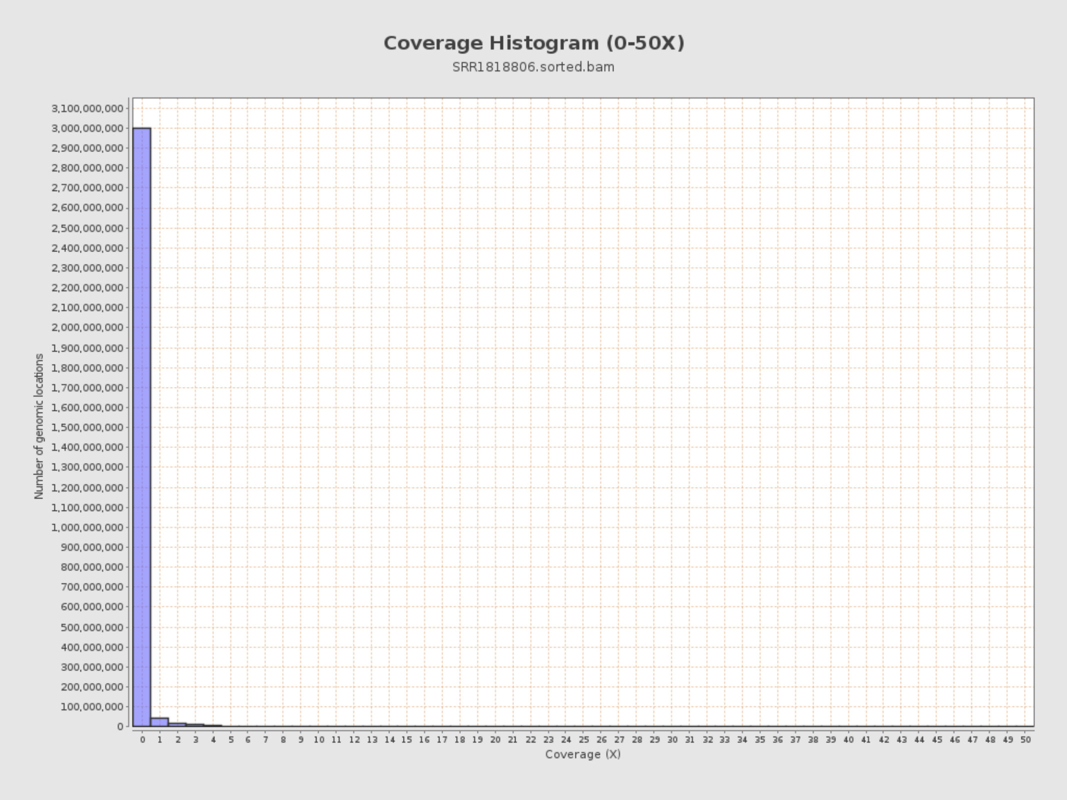
3. Results : Coverage across reference



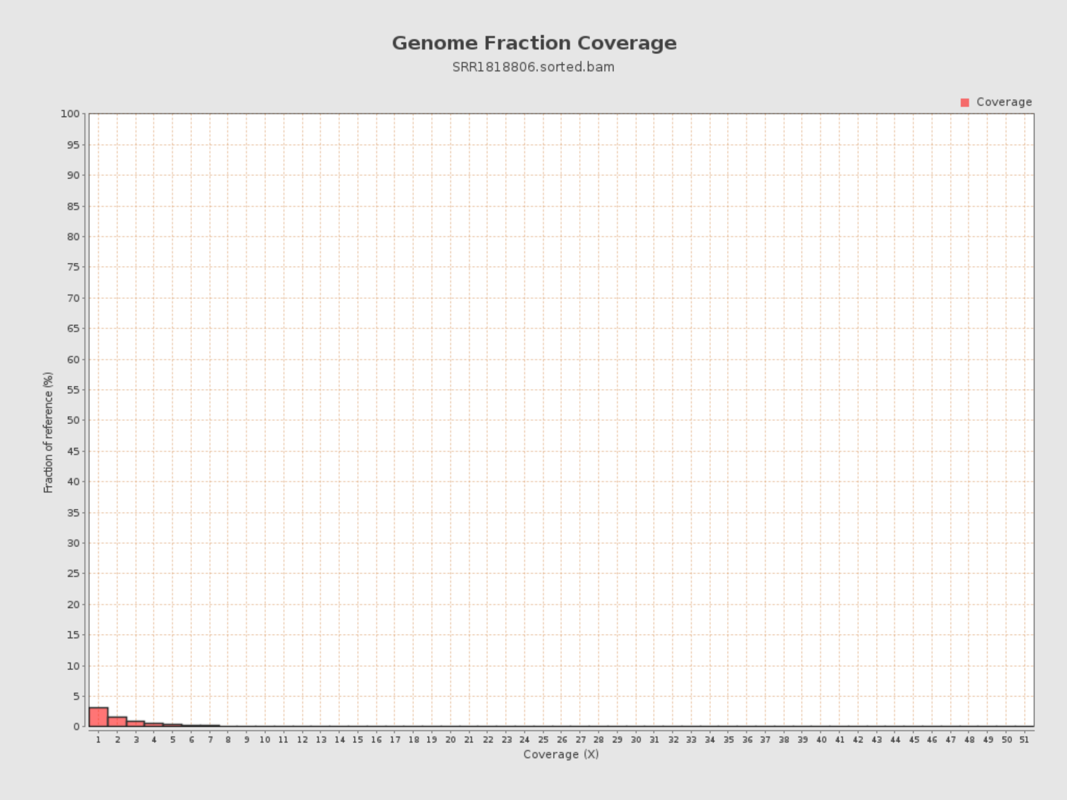
4. Results : Coverage Histogram



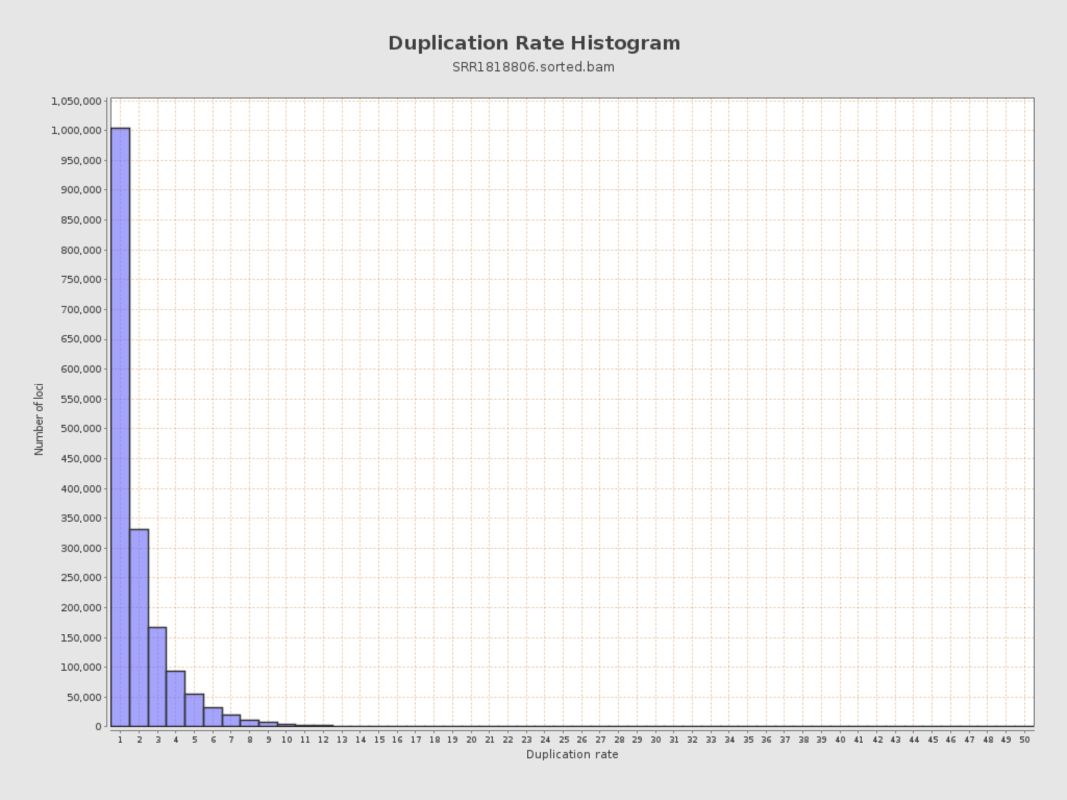
5. Results : Coverage Histogram (0-50X)



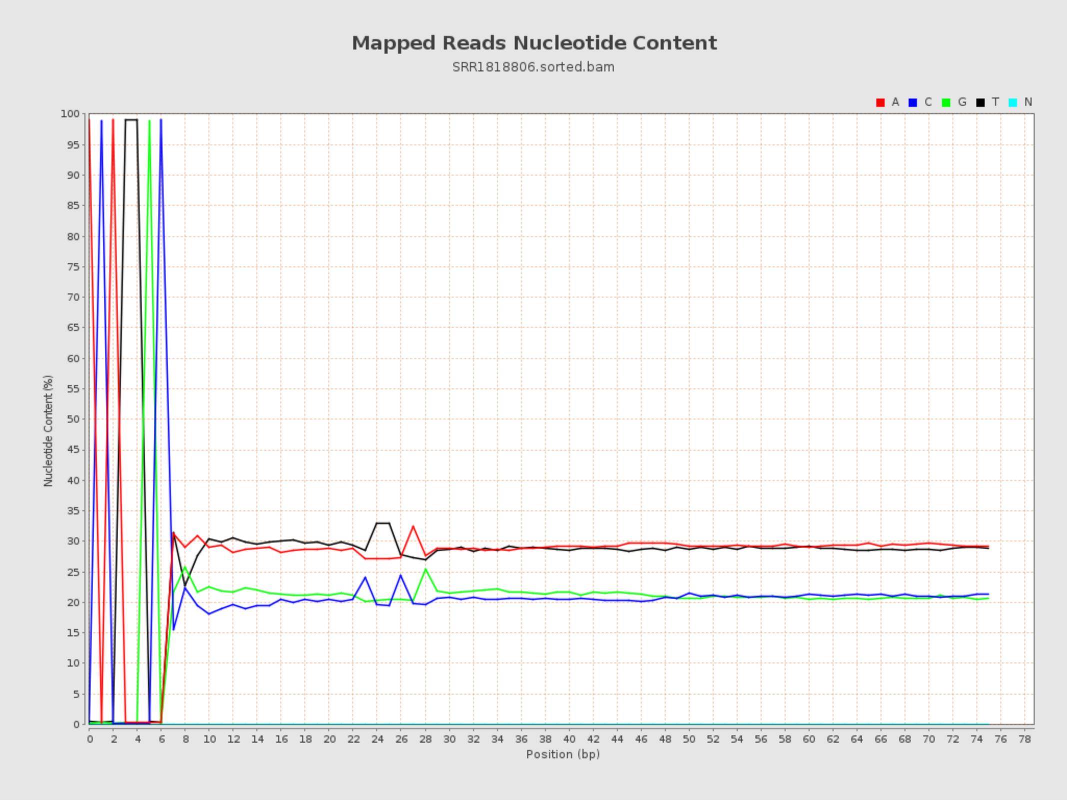
6. Results : Genome Fraction Coverage



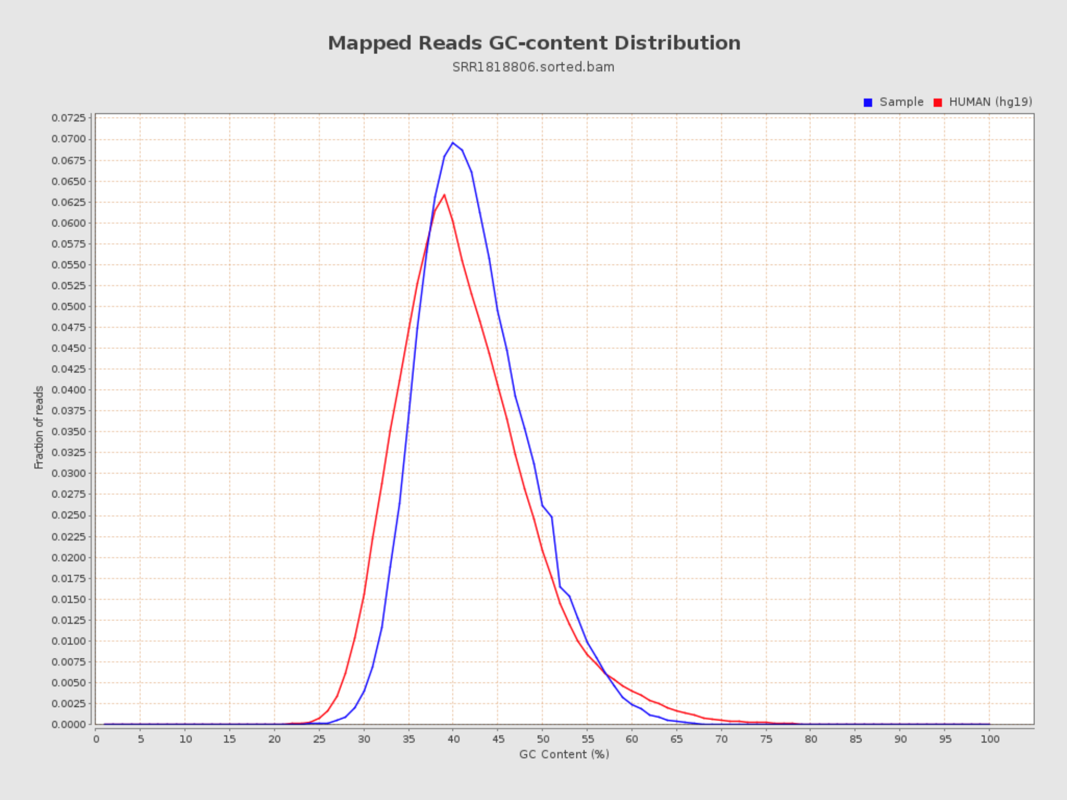
7. Results : Duplication Rate Histogram



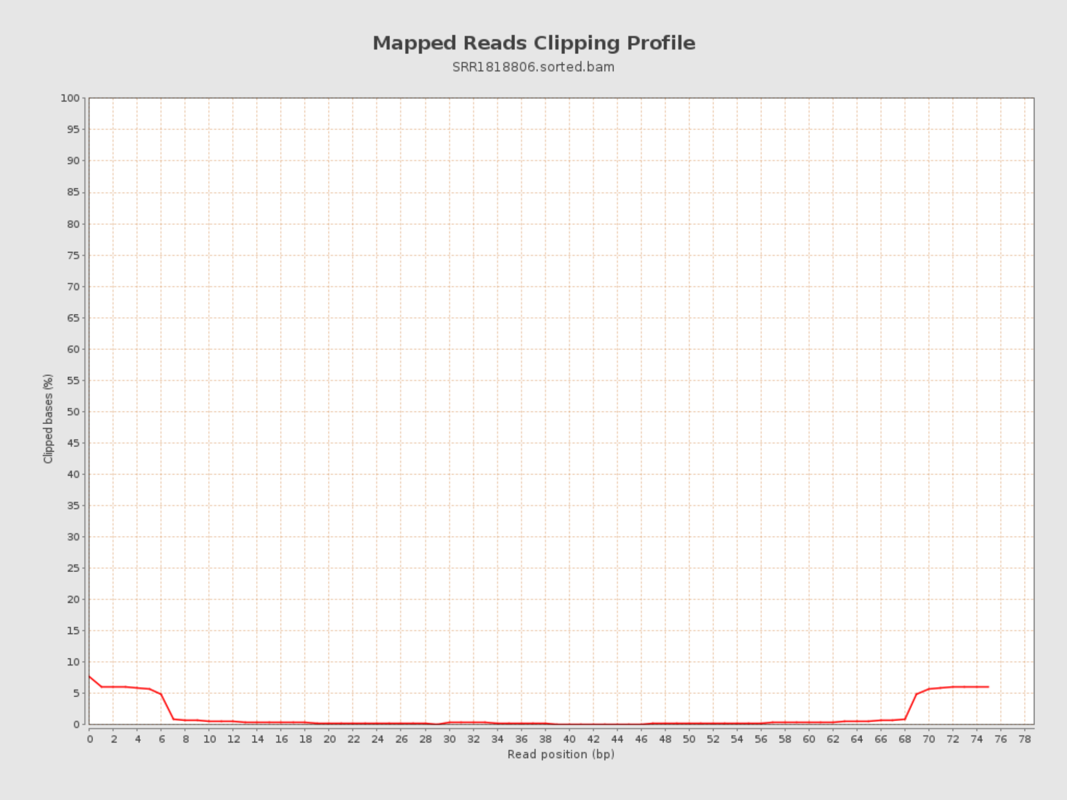
8. Results : Mapped Reads Nucleotide Content



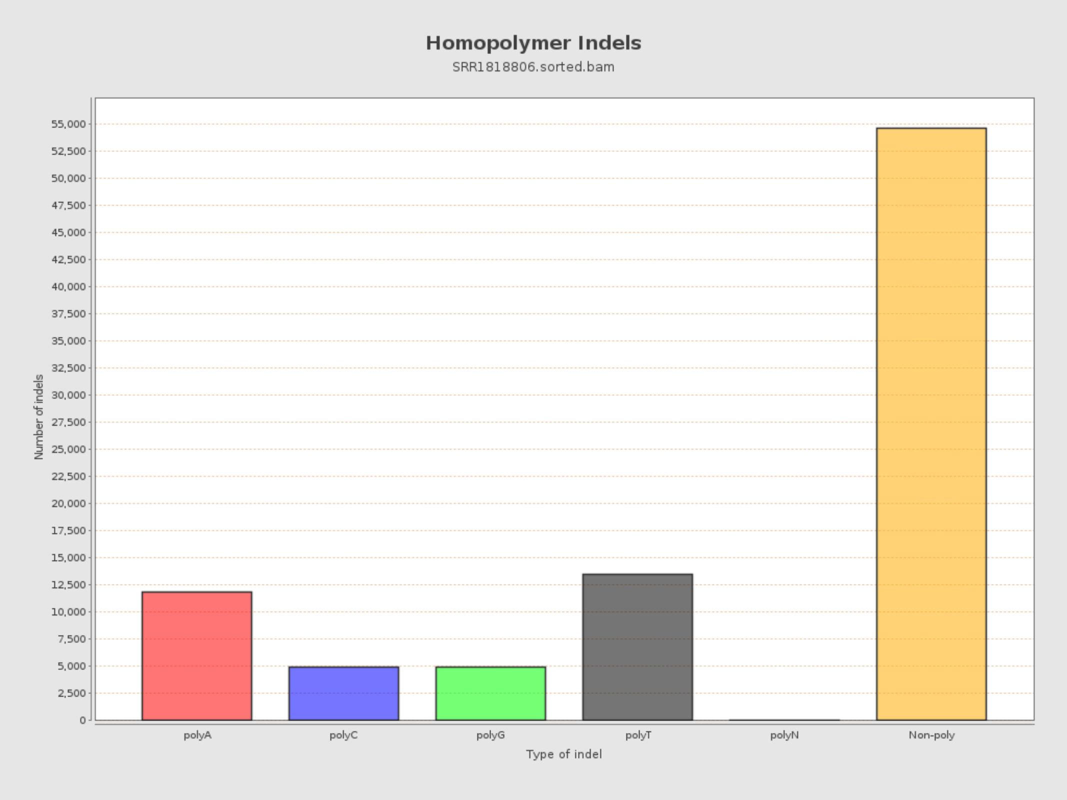
9. Results : Mapped Reads GC-content Distribution



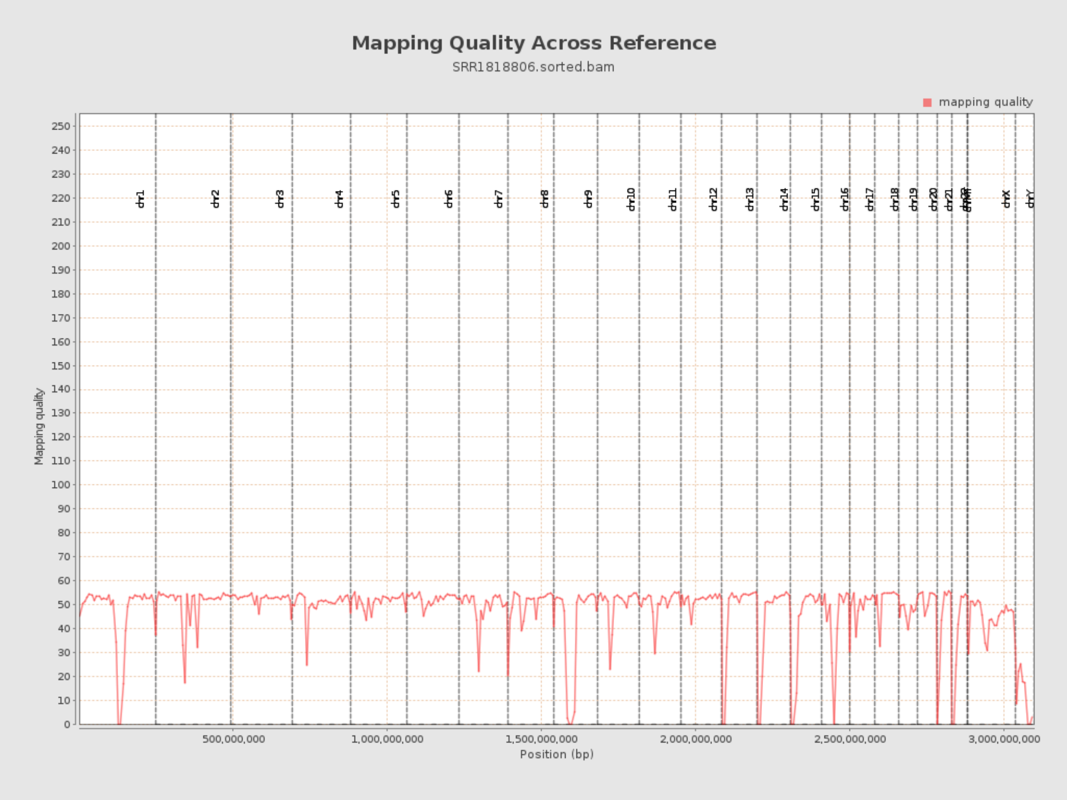
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram