Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:14:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818986.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_SRR1818986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818986.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:14:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,479,058
Mapped reads	2,445,135 / 98.63%
Unmapped reads	33,923 / 1.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,340 / 1.59%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	1,199,510 / 48.39%
Duplication rate	41.75%
Clipped reads	2,469,642 / 99.62%

2.2. ACGT Content

Number/percentage of A's	64,463,933 / 28.53%
Number/percentage of C's	49,012,323 / 21.69%
Number/percentage of T's	63,905,498 / 28.28%
Number/percentage of G's	48,568,723 / 21.49%
Number/percentage of N's	10,213 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.073

Standard Deviation	0.8638

2.4. Mapping Quality

Mean Mapping Quality	49.01

2.5. Mismatches and indels

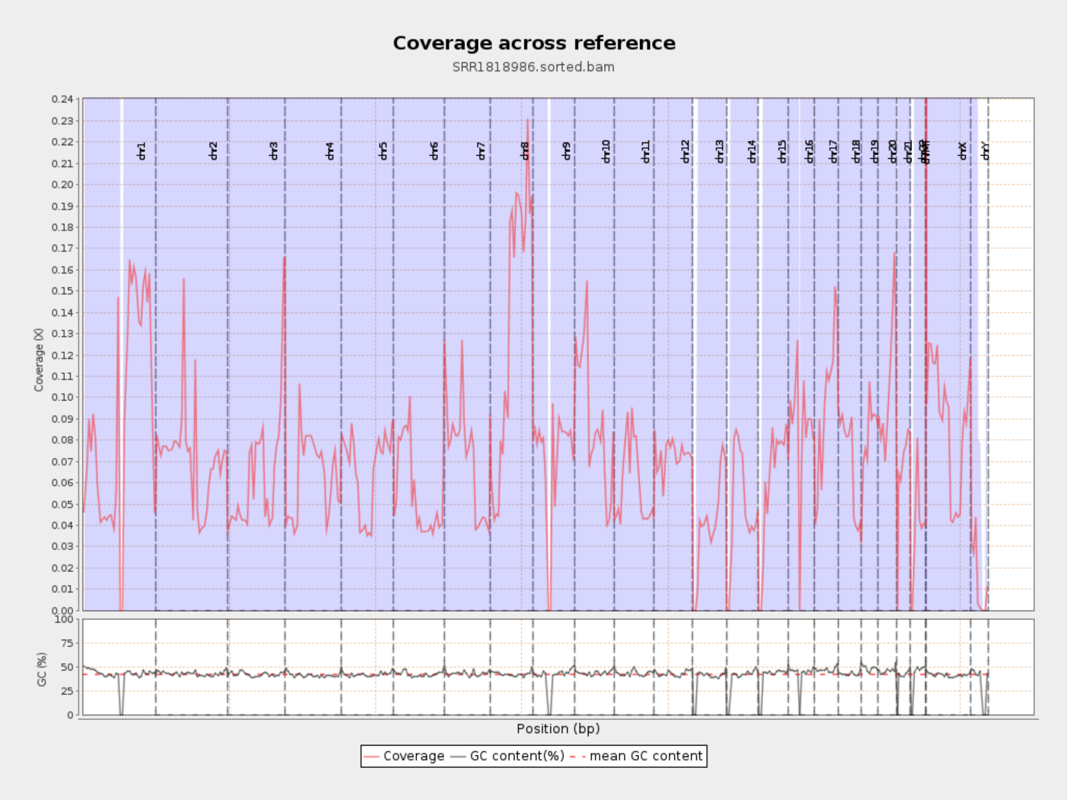
General error rate	0.67%
Mismatches	1,429,888
Insertions	35,399
Mapped reads with at least one insertion	1.4%
Deletions	72,810
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.93%

2.6. Chromosome stats

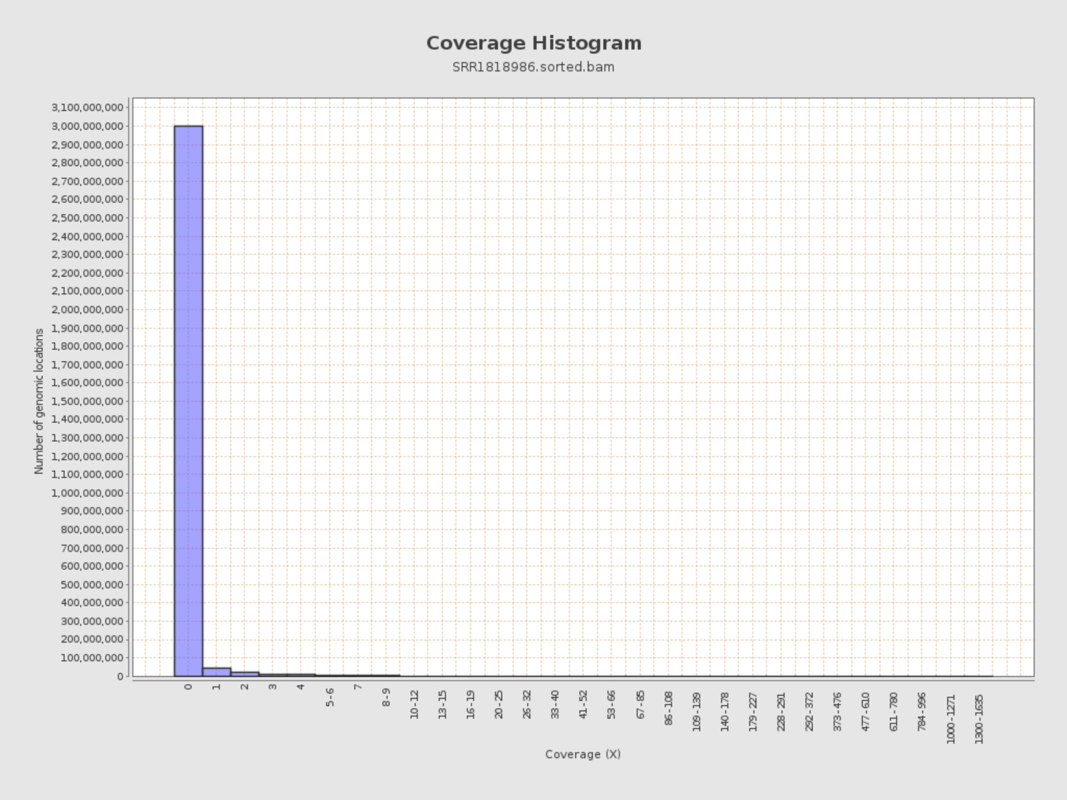
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22414944	0.0899	1.5064
chr2	243199373	17590519	0.0723	1.2414
chr3	198022430	12666046	0.064	0.4933
chr4	191154276	12126277	0.0634	0.5759
chr5	180915260	11997763	0.0663	0.5223
chr6	171115067	9392200	0.0549	0.5514
chr7	159138663	11462554	0.072	1.0522

chr8	146364022	20112567	0.1374	0.8227
chr9	141213431	9975525	0.0706	0.858
chr10	135534747	12065746	0.089	0.9913
chr11	135006516	8022433	0.0594	0.5758
chr12	133851895	9831899	0.0735	0.5425
chr13	115169878	4723779	0.041	0.3906
chr14	107349540	5208102	0.0485	0.4586
chr15	102531392	6015944	0.0587	0.477
chr16	90354753	7598389	0.0841	1.0002
chr17	81195210	7808667	0.0962	0.7038
chr18	78077248	5494693	0.0704	0.9705
chr19	59128983	4888371	0.0827	1.4071
chr20	63025520	6769488	0.1074	0.6905
chr21	48129895	3218892	0.0669	0.5533
chr22	51304566	1862593	0.0363	0.4164
chrMT	16571	128604	7.7608	7.0419
chrX	155270560	13879243	0.0894	0.6845
chrY	59373566	840798	0.0142	0.8744

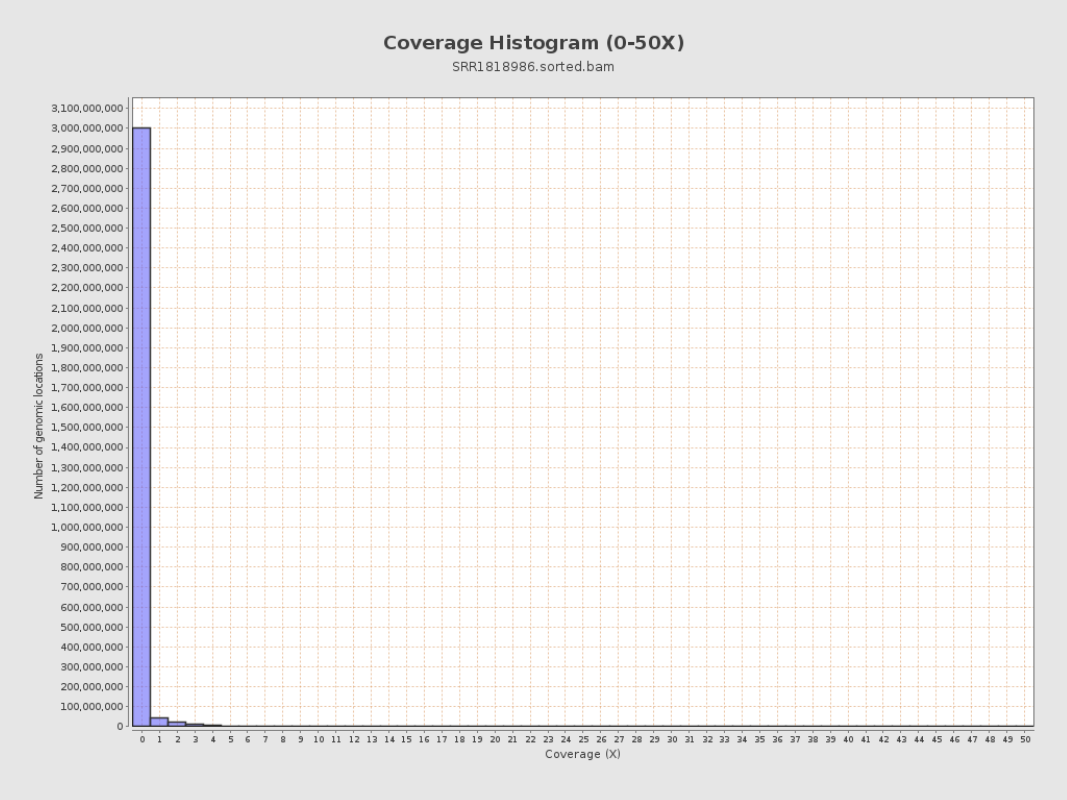
3. Results : Coverage across reference



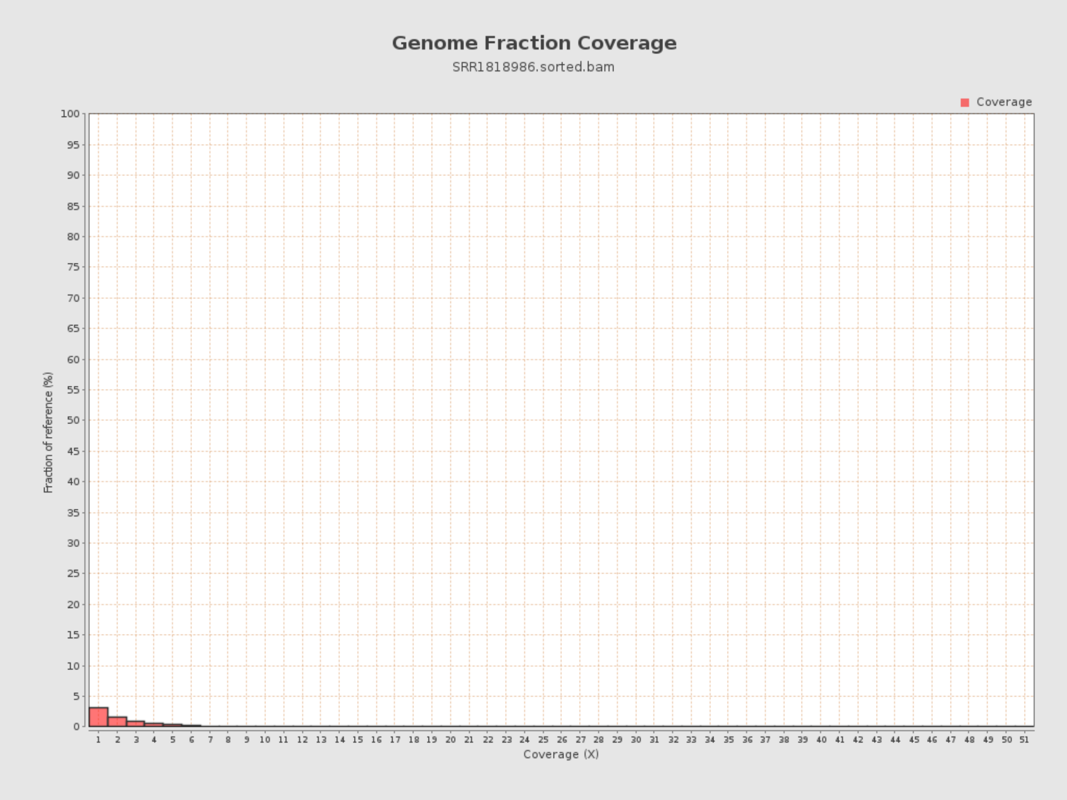
4. Results : Coverage Histogram



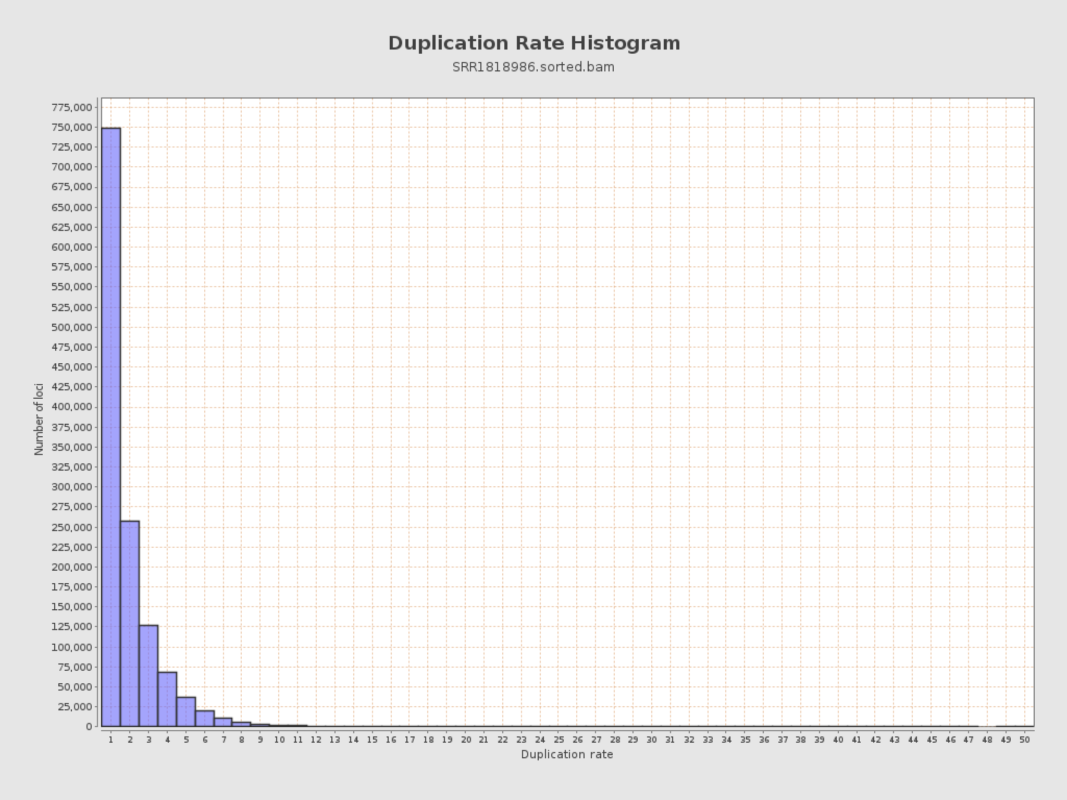
5. Results : Coverage Histogram (0-50X)



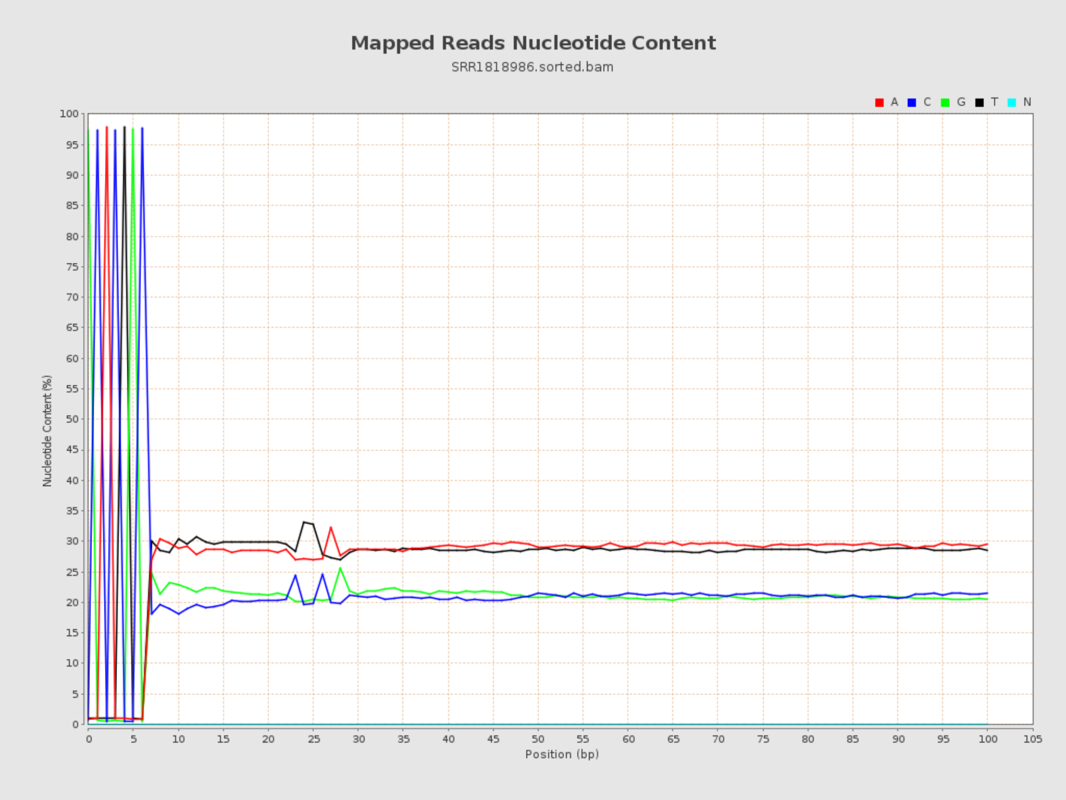
6. Results : Genome Fraction Coverage



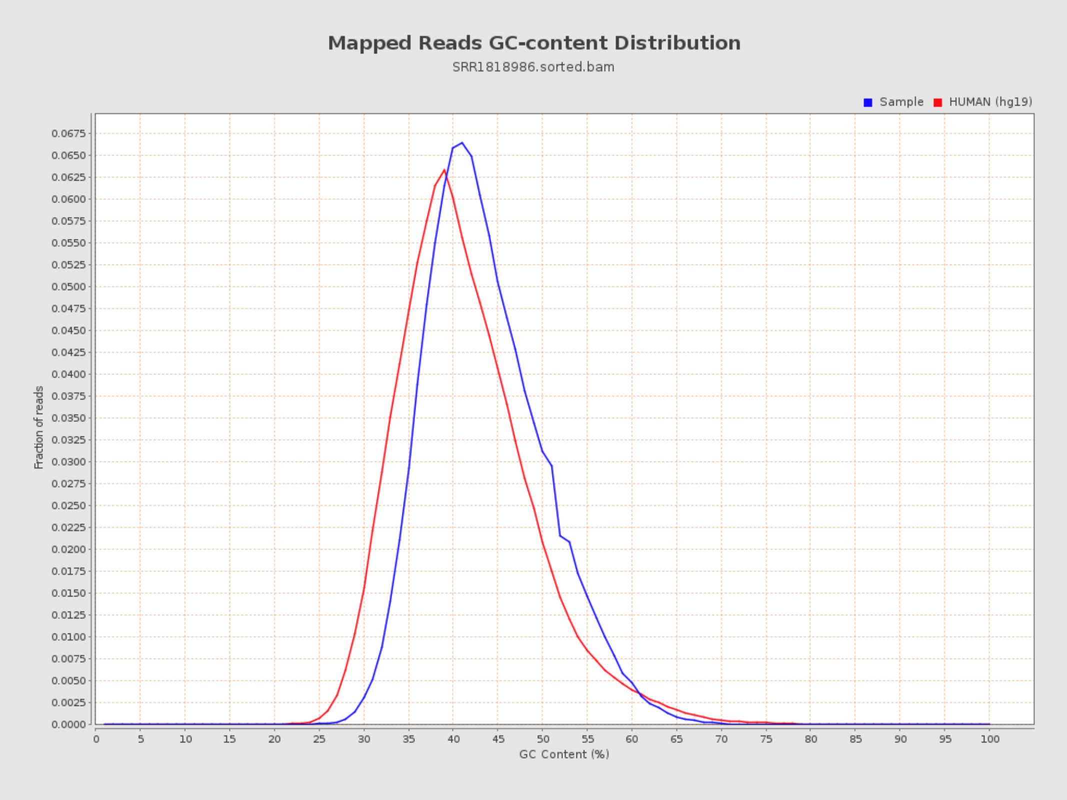
7. Results : Duplication Rate Histogram



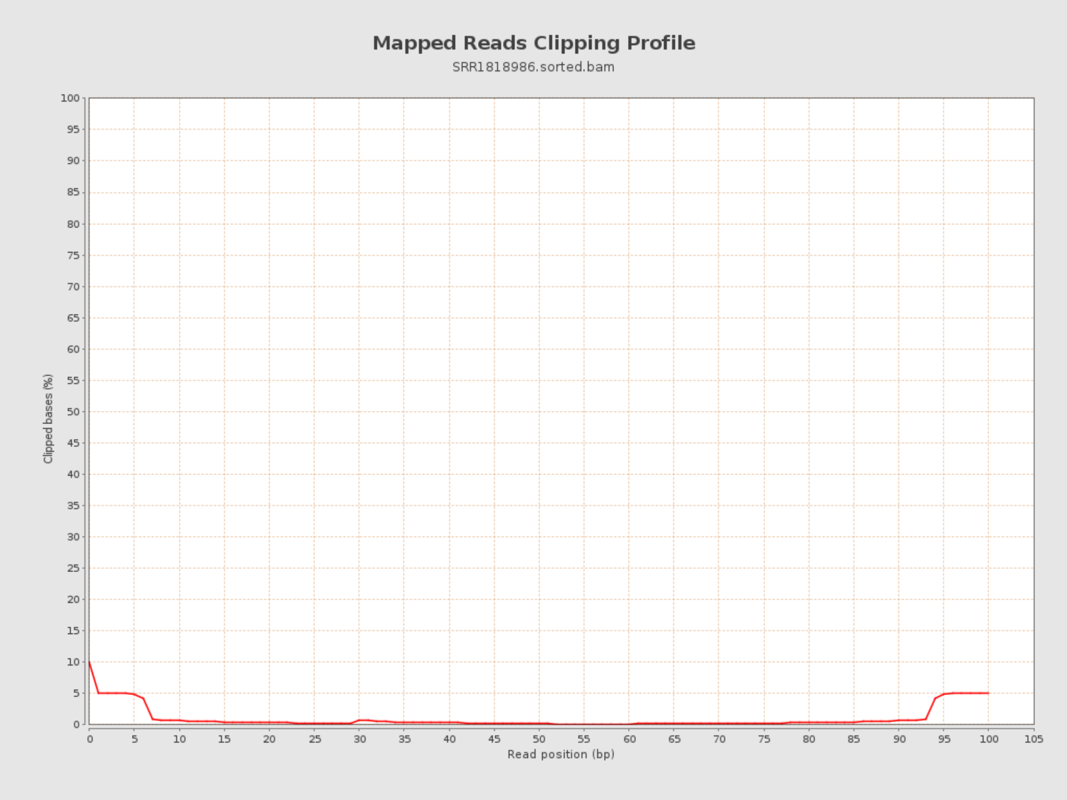
8. Results : Mapped Reads Nucleotide Content



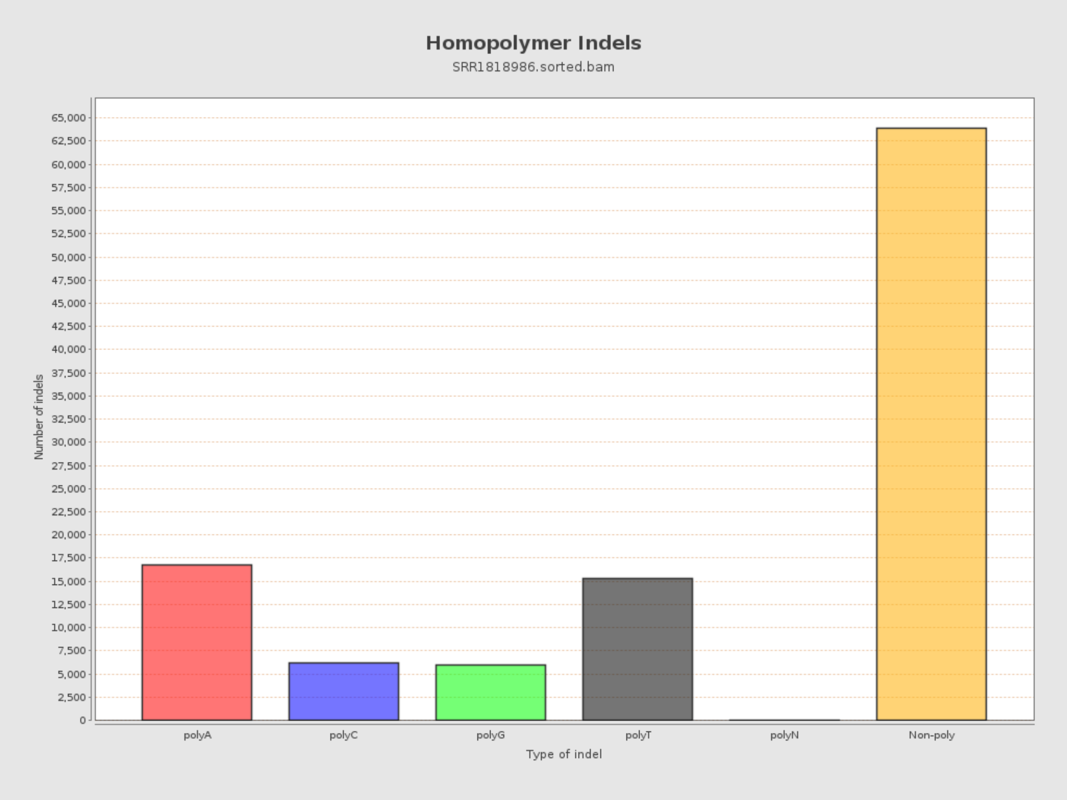
9. Results : Mapped Reads GC-content Distribution



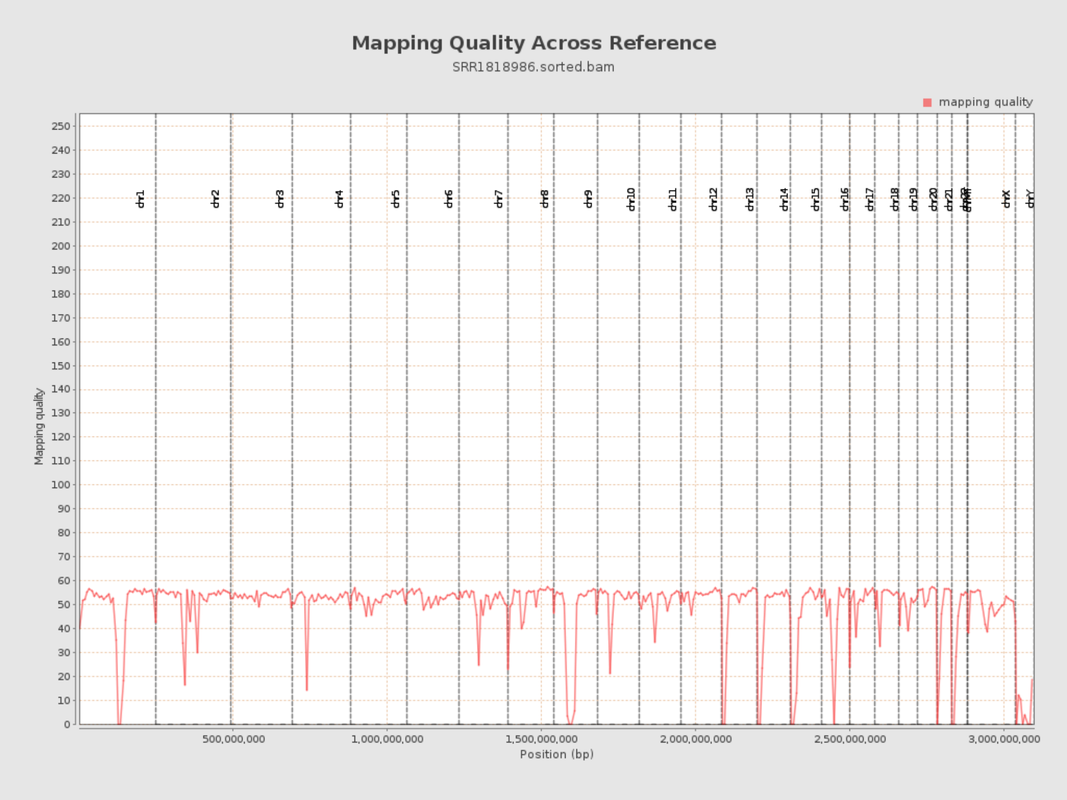
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram