Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:59:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818996.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_SRR1818996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818996.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:59:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,641,396
Mapped reads	2,603,643 / 98.57%
Unmapped reads	37,753 / 1.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,320 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	1,354,377 / 51.28%
Duplication rate	43.6%
Clipped reads	2,630,435 / 99.59%

2.2. ACGT Content

Number/percentage of A's	70,253,247 / 29.17%
Number/percentage of C's	52,109,020 / 21.64%
Number/percentage of T's	68,184,972 / 28.32%
Number/percentage of G's	50,242,580 / 20.86%
Number/percentage of N's	12,952 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0778

Standard Deviation	0.9238

2.4. Mapping Quality

Mean Mapping Quality	49.12

2.5. Mismatches and indels

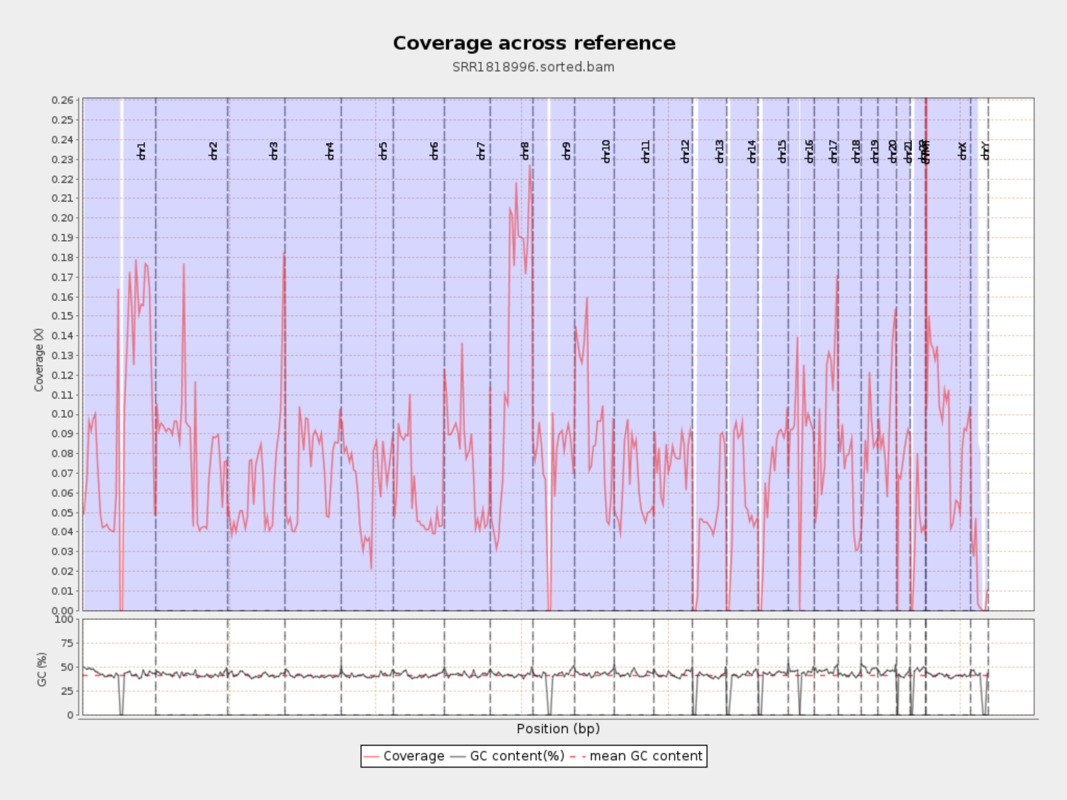
General error rate	0.66%
Mismatches	1,519,382
Insertions	36,157
Mapped reads with at least one insertion	1.35%
Deletions	78,251
Mapped reads with at least one deletion	2.94%
Homopolymer indels	41.57%

2.6. Chromosome stats

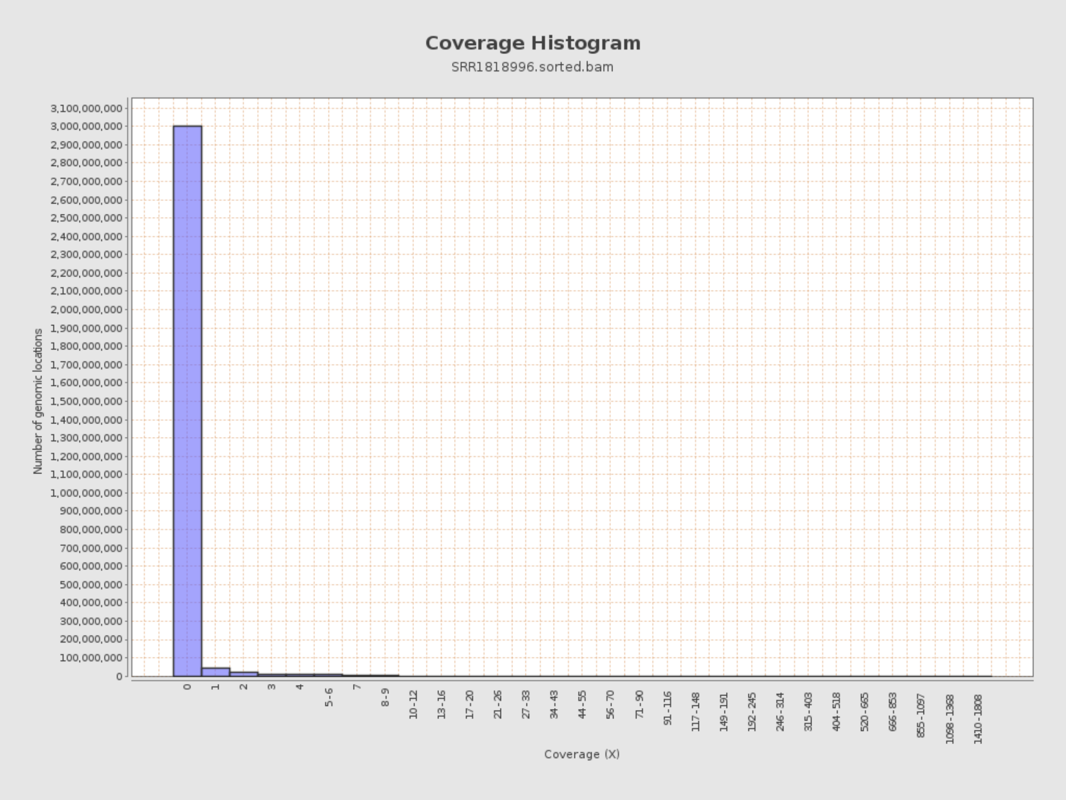
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24103698	0.0967	1.6582
chr2	243199373	20209025	0.0831	1.2997
chr3	198022430	13034782	0.0658	0.5287
chr4	191154276	14142098	0.074	0.6288
chr5	180915260	11933467	0.066	0.5512
chr6	171115067	10258573	0.06	0.5932
chr7	159138663	12310895	0.0774	1.1276

chr8	146364022	20377347	0.1392	0.8733
chr9	141213431	10438010	0.0739	0.8642
chr10	135534747	13163602	0.0971	1.0832
chr11	135006516	8370864	0.062	0.6136
chr12	133851895	10387722	0.0776	0.5882
chr13	115169878	5380575	0.0467	0.4392
chr14	107349540	6082385	0.0567	0.5174
chr15	102531392	6572300	0.0641	0.5216
chr16	90354753	8083058	0.0895	1.0705
chr17	81195210	8210053	0.1011	0.7449
chr18	78077248	5124378	0.0656	0.9525
chr19	59128983	4953788	0.0838	1.4362
chr20	63025520	6471939	0.1027	0.7127
chr21	48129895	3497840	0.0727	0.6025
chr22	51304566	1901328	0.0371	0.4431
chrMT	16571	45471	2.744	3.9784
chrX	155270560	15001303	0.0966	0.7572
chrY	59373566	894083	0.0151	0.9469

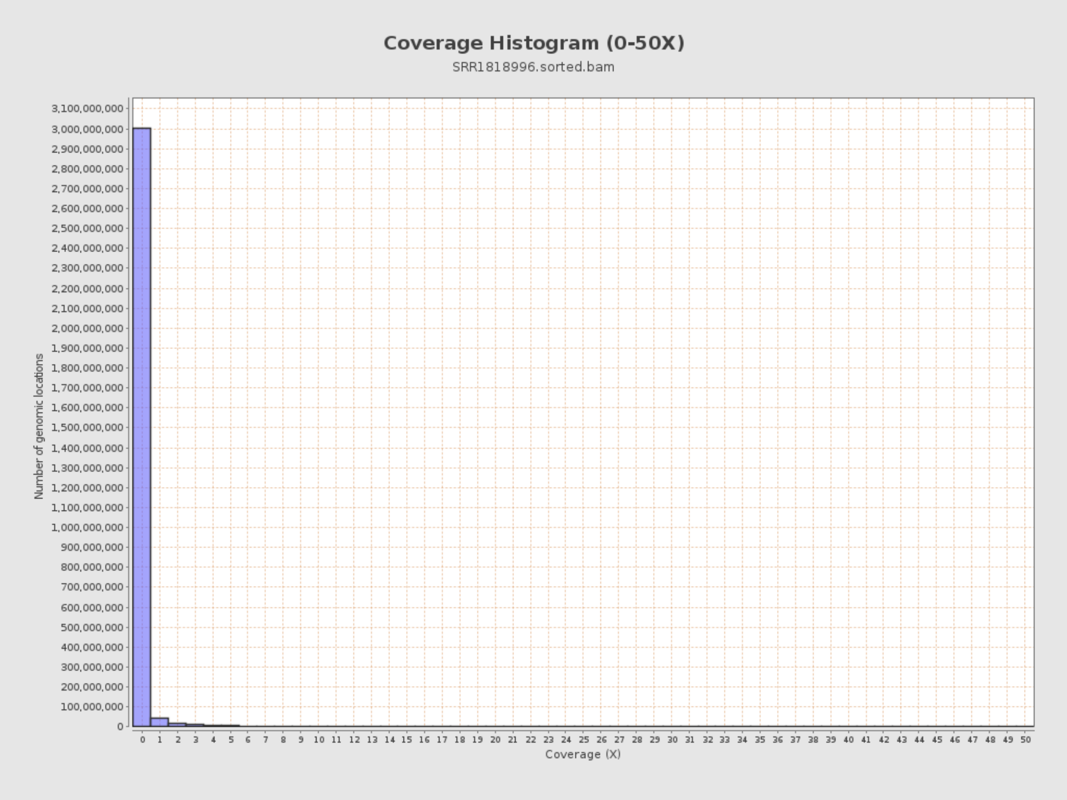
3. Results : Coverage across reference



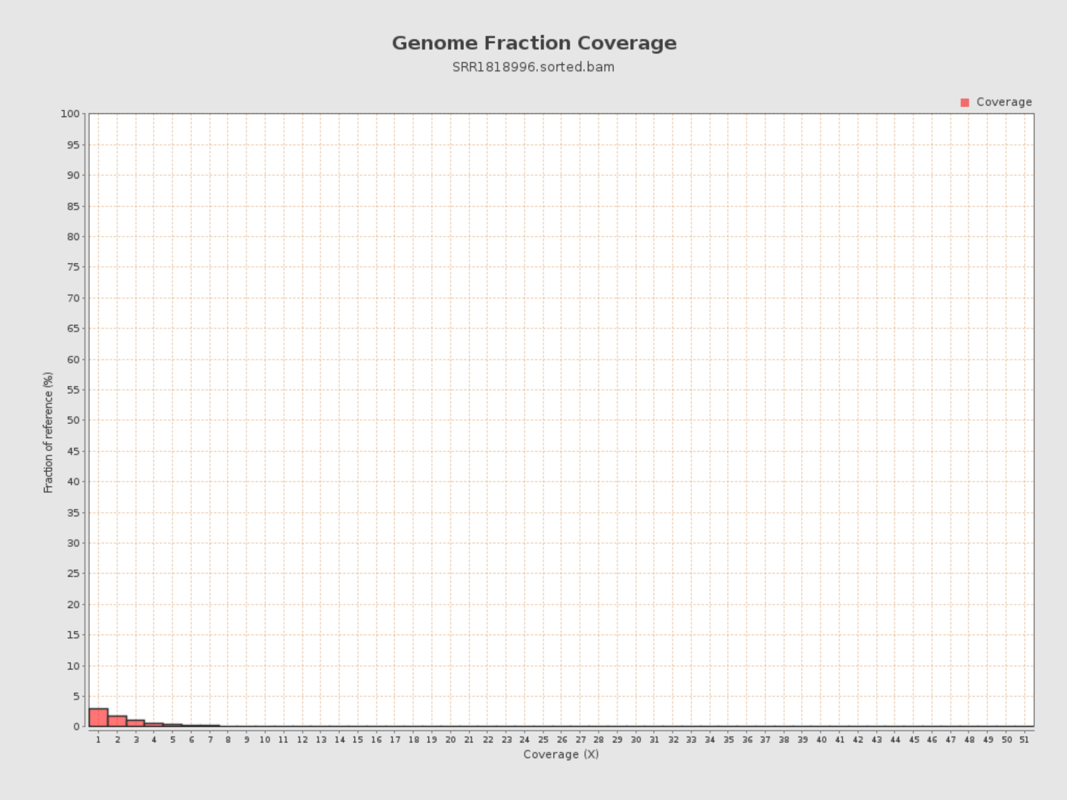
4. Results : Coverage Histogram



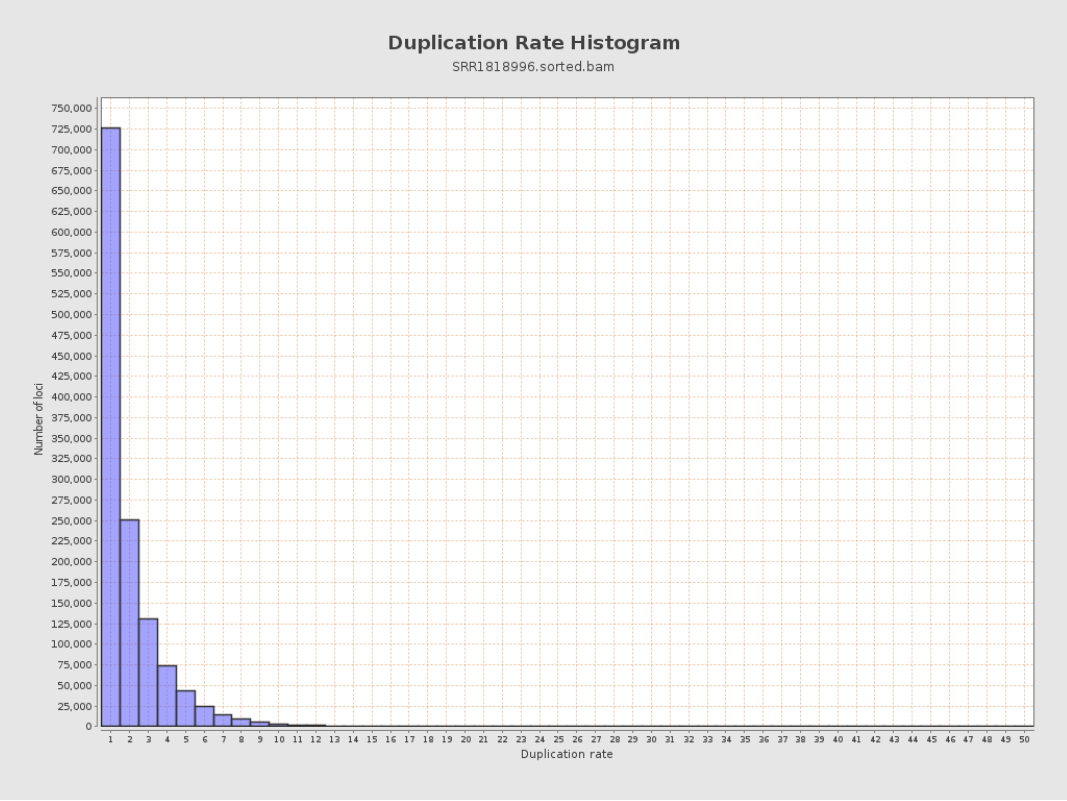
5. Results : Coverage Histogram (0-50X)



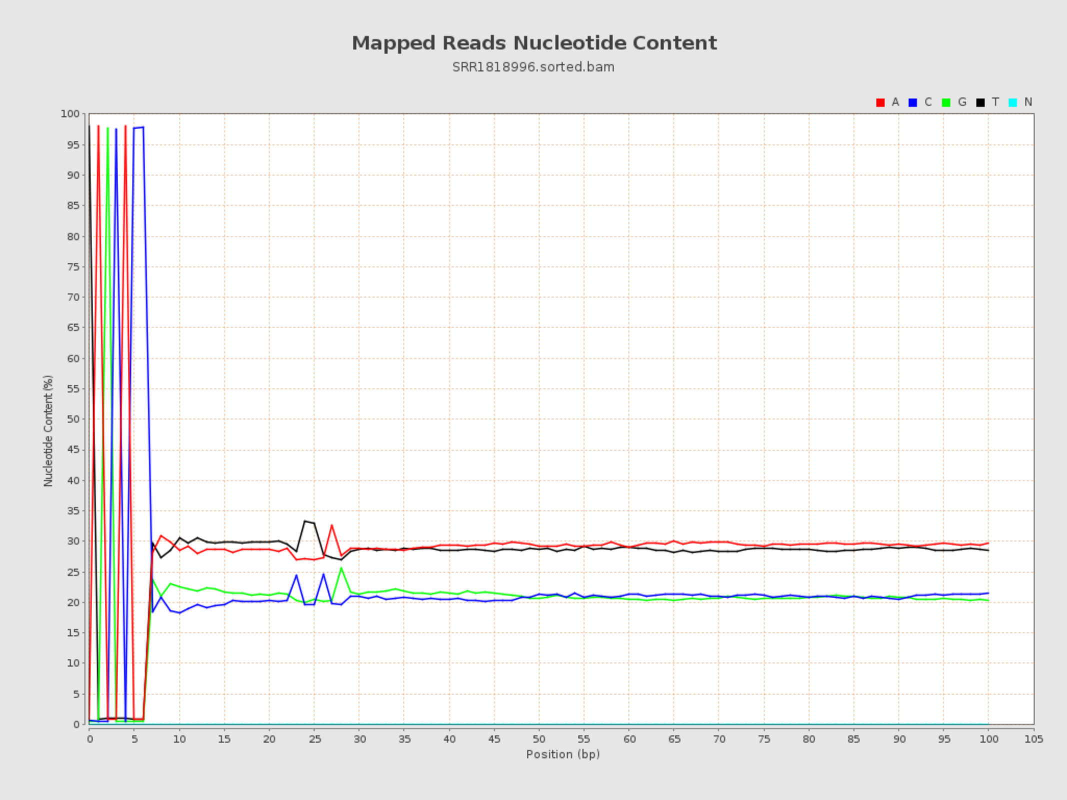
6. Results : Genome Fraction Coverage



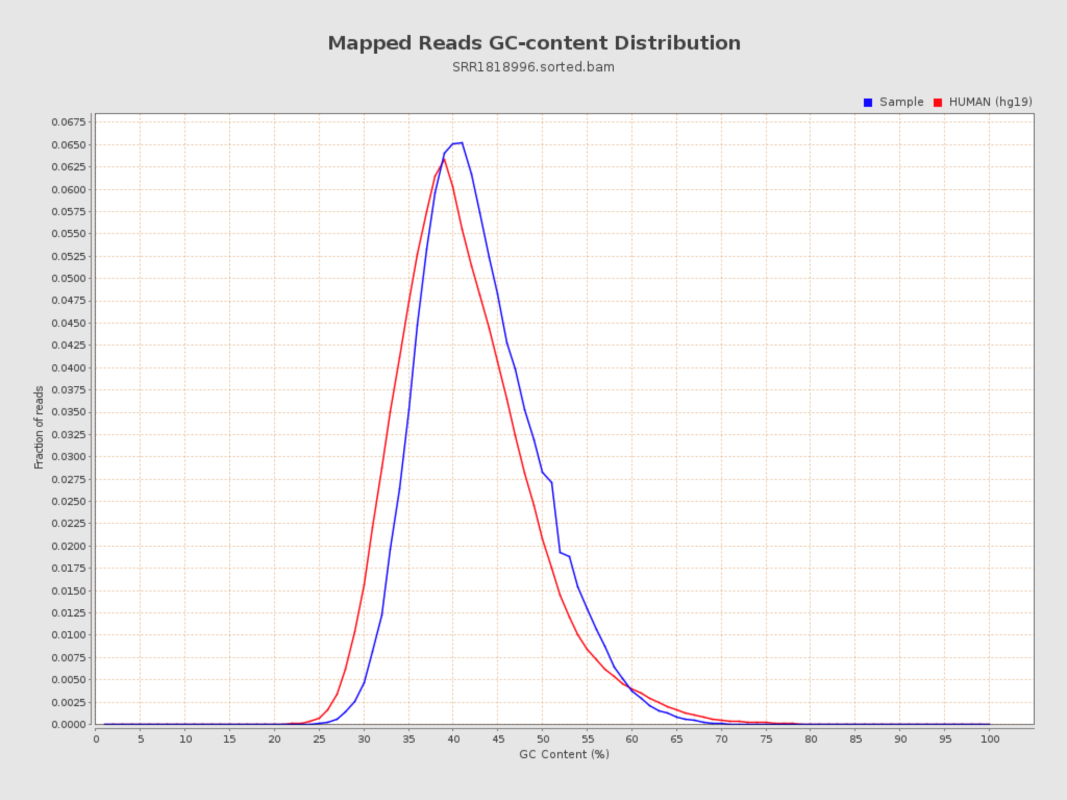
7. Results : Duplication Rate Histogram



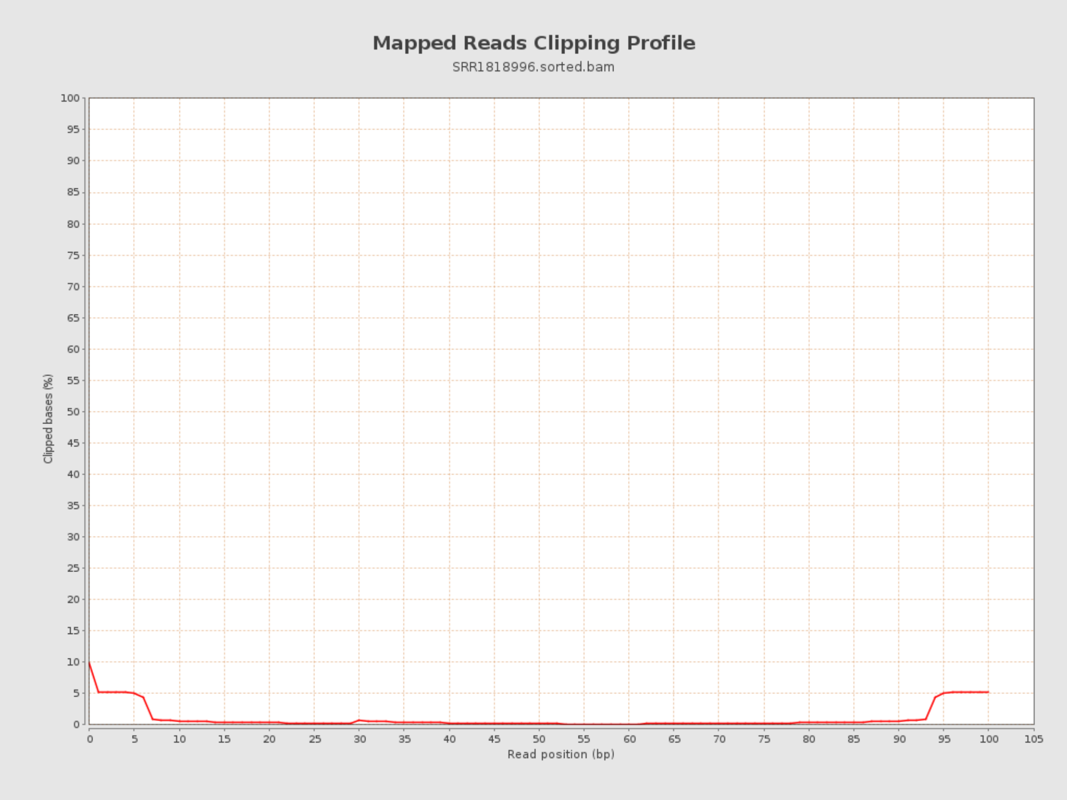
8. Results : Mapped Reads Nucleotide Content



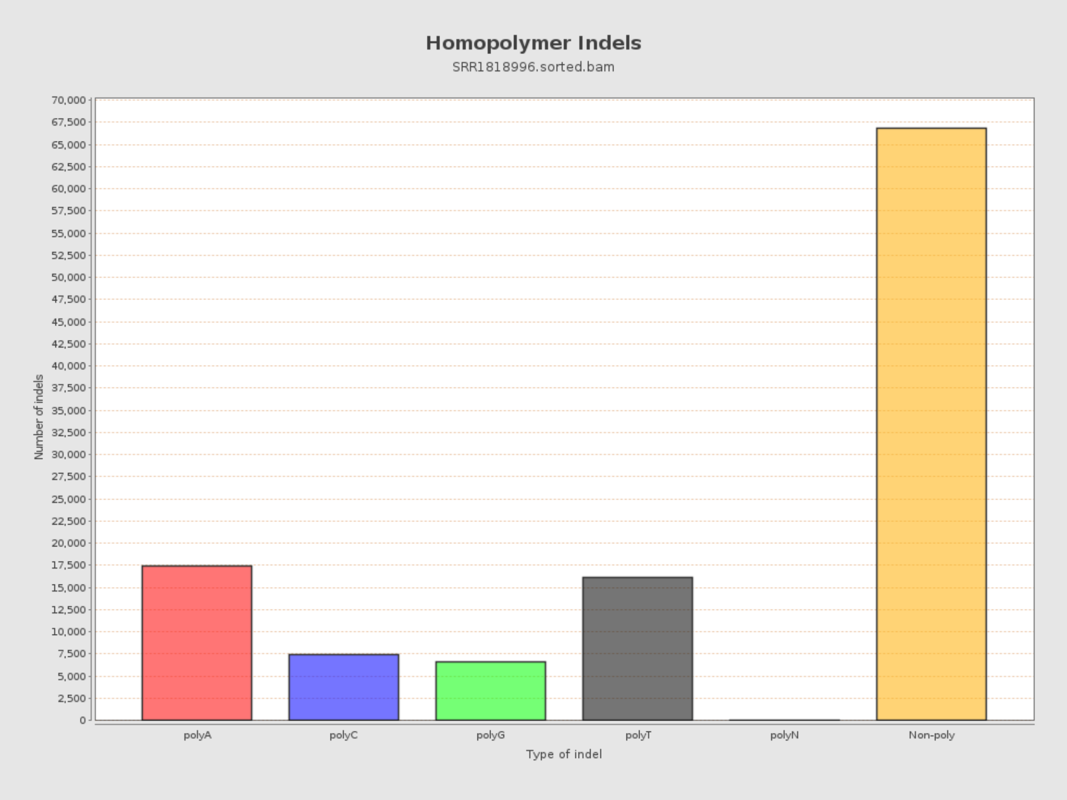
9. Results : Mapped Reads GC-content Distribution



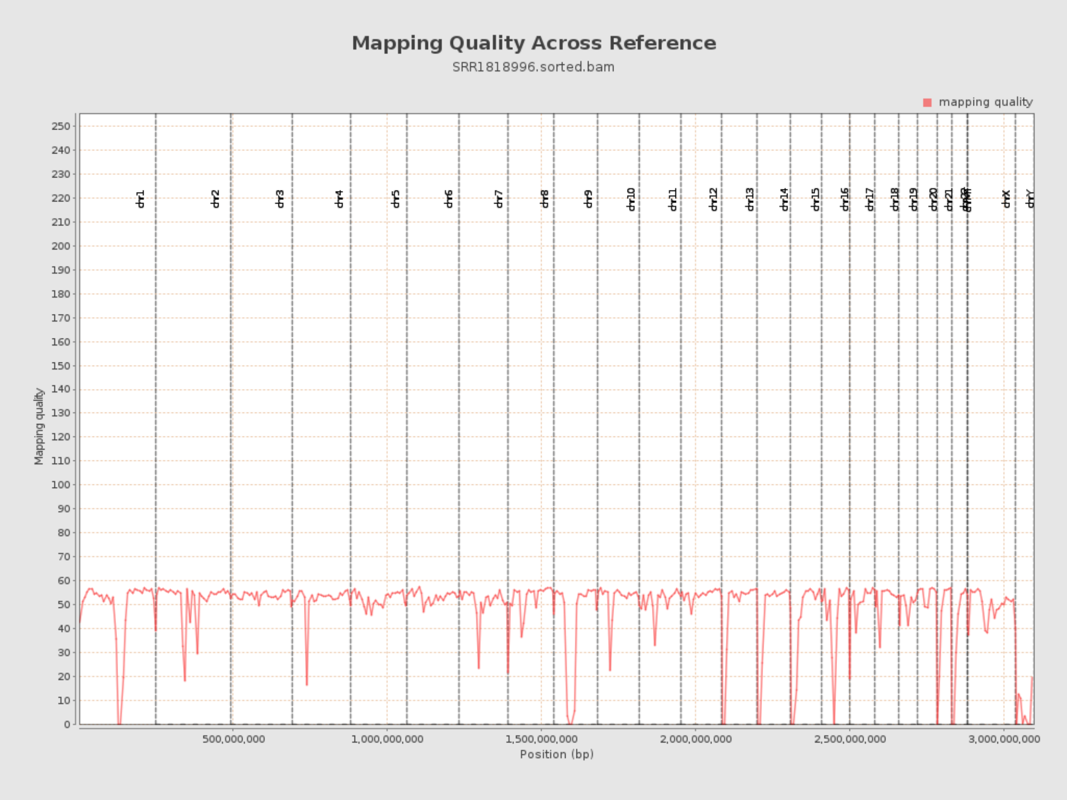
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram