Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:43:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818879.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_SRR1818879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818879.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:43:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,876,299
Mapped reads	1,735,885 / 92.52%
Unmapped reads	140,414 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,480 / 1.25%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	298,176 / 15.89%
Duplication rate	14.1%
Clipped reads	1,752,947 / 93.43%

2.2. ACGT Content

Number/percentage of A's	46,558,811 / 28.96%
Number/percentage of C's	33,576,133 / 20.89%
Number/percentage of T's	46,293,570 / 28.8%
Number/percentage of G's	34,312,798 / 21.35%
Number/percentage of N's	2,299 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.052

Standard Deviation	0.6685

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

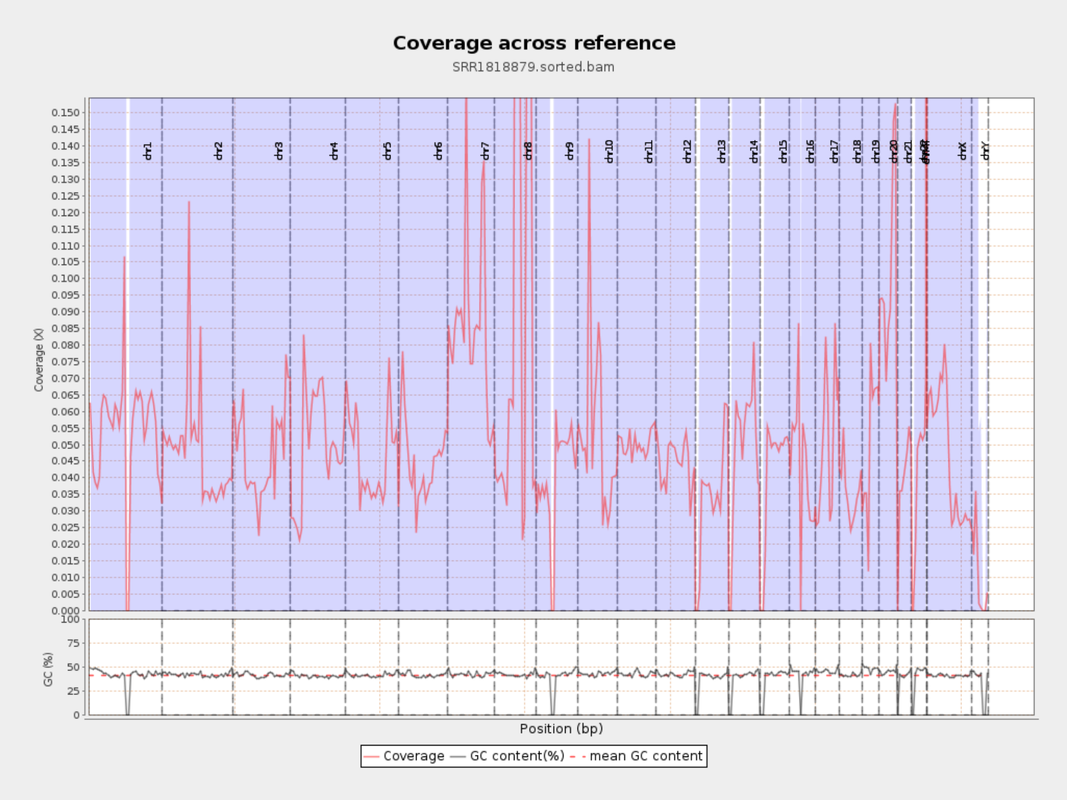
General error rate	0.64%
Mismatches	964,620
Insertions	22,229
Mapped reads with at least one insertion	1.24%
Deletions	50,008
Mapped reads with at least one deletion	2.82%
Homopolymer indels	40.36%

2.6. Chromosome stats

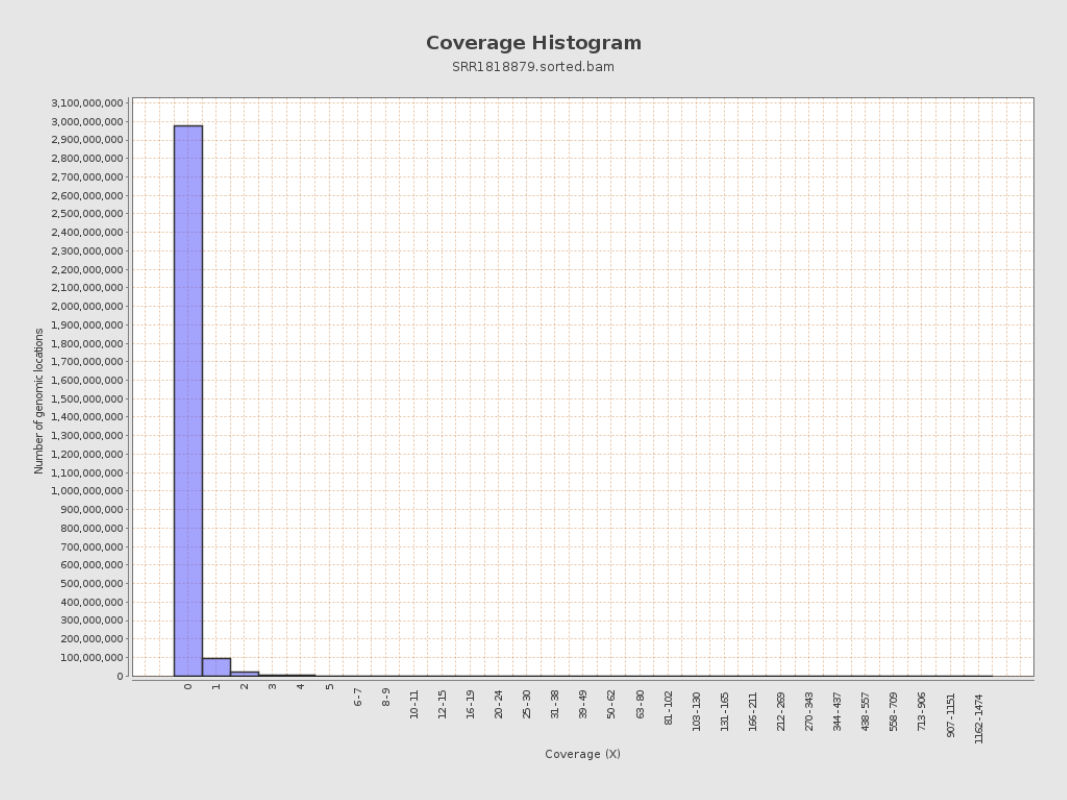
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13410122	0.0538	1.0742
chr2	243199373	11742816	0.0483	0.8387
chr3	198022430	9460129	0.0478	0.2785
chr4	191154276	9400094	0.0492	0.383
chr5	180915260	8409583	0.0465	0.2885
chr6	171115067	7652841	0.0447	0.3051
chr7	159138663	13901124	0.0874	1.5683

chr8	146364022	15464092	0.1057	0.5575
chr9	141213431	5675958	0.0402	0.5648
chr10	135534747	7295011	0.0538	0.8895
chr11	135006516	6787680	0.0503	0.3744
chr12	133851895	6017196	0.045	0.2726
chr13	115169878	3915612	0.034	0.2311
chr14	107349540	5220969	0.0486	0.3081
chr15	102531392	4231855	0.0413	0.2569
chr16	90354753	3871579	0.0428	0.5744
chr17	81195210	4206532	0.0518	0.4111
chr18	78077248	2809318	0.036	0.6525
chr19	59128983	3015758	0.051	0.9923
chr20	63025520	6404069	0.1016	0.4396
chr21	48129895	1913006	0.0397	0.3202
chr22	51304566	1882051	0.0367	0.2649
chrMT	16571	242235	14.618	9.3574
chrX	155270560	7317036	0.0471	0.3665
chrY	59373566	596087	0.01	0.6676

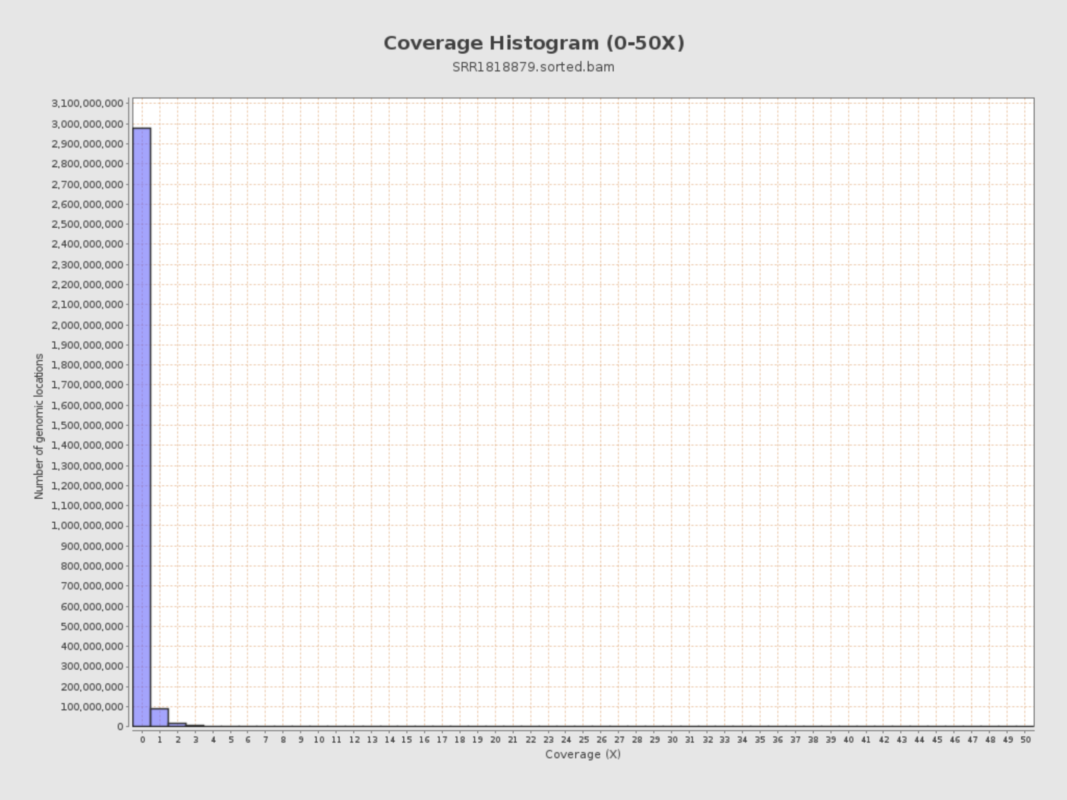
3. Results : Coverage across reference



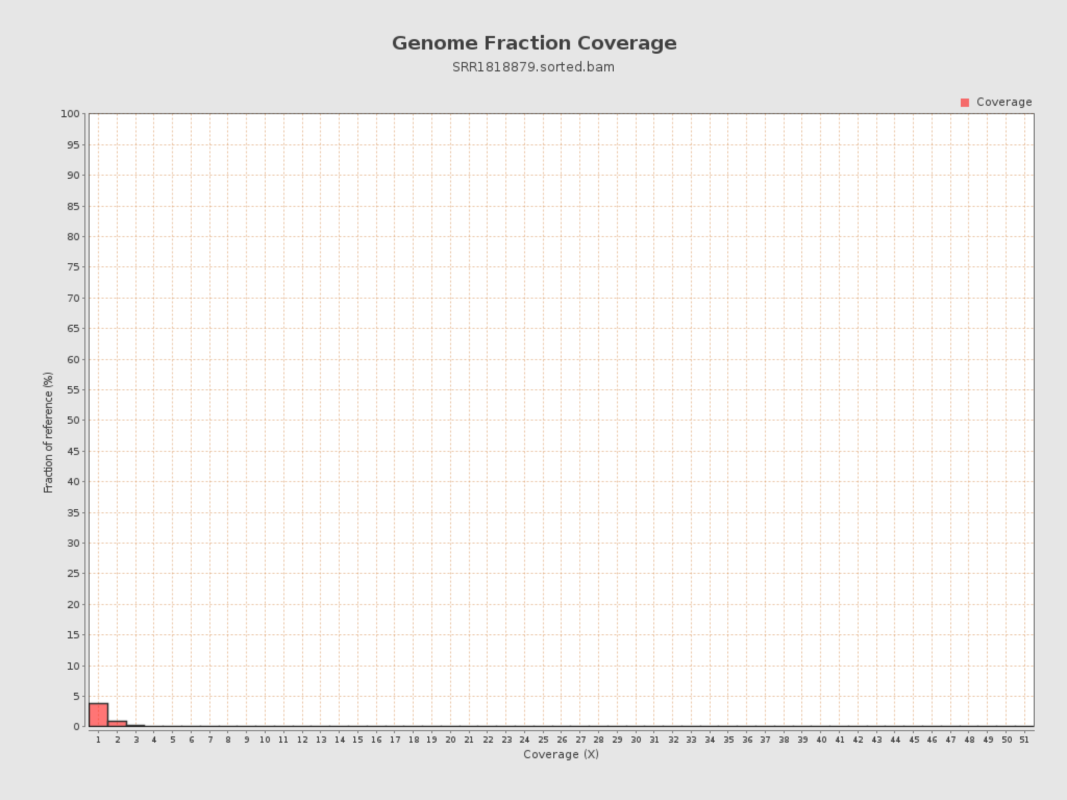
4. Results : Coverage Histogram



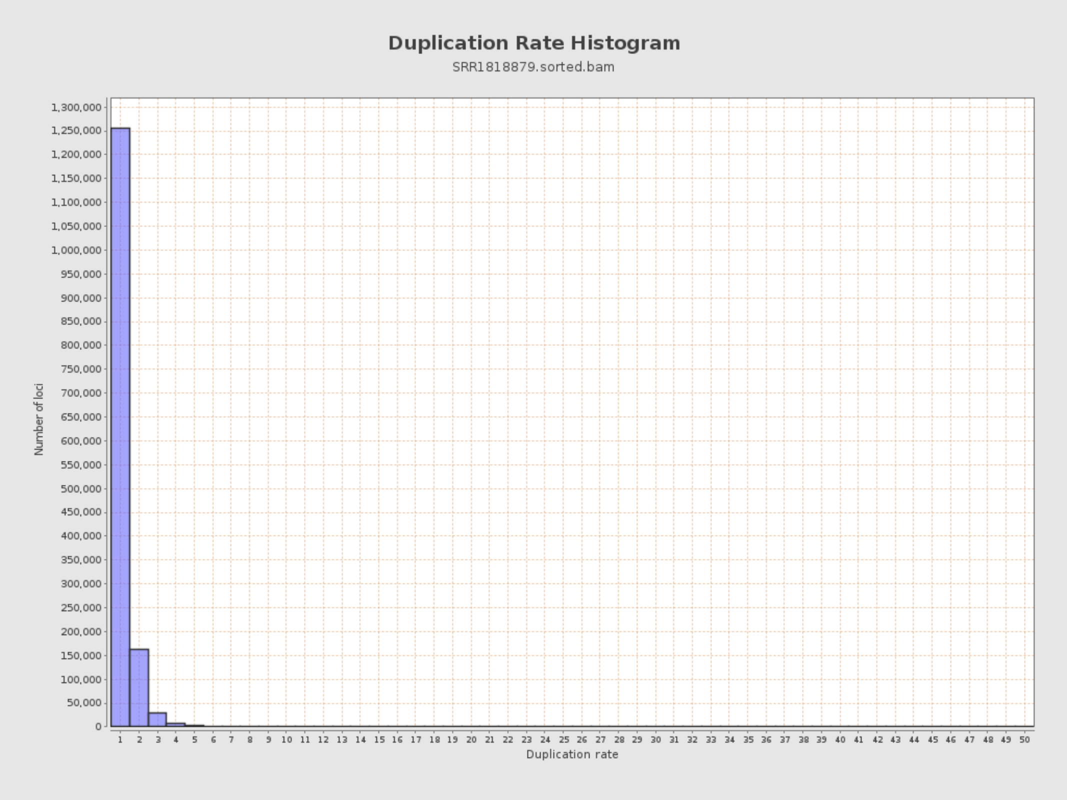
5. Results : Coverage Histogram (0-50X)



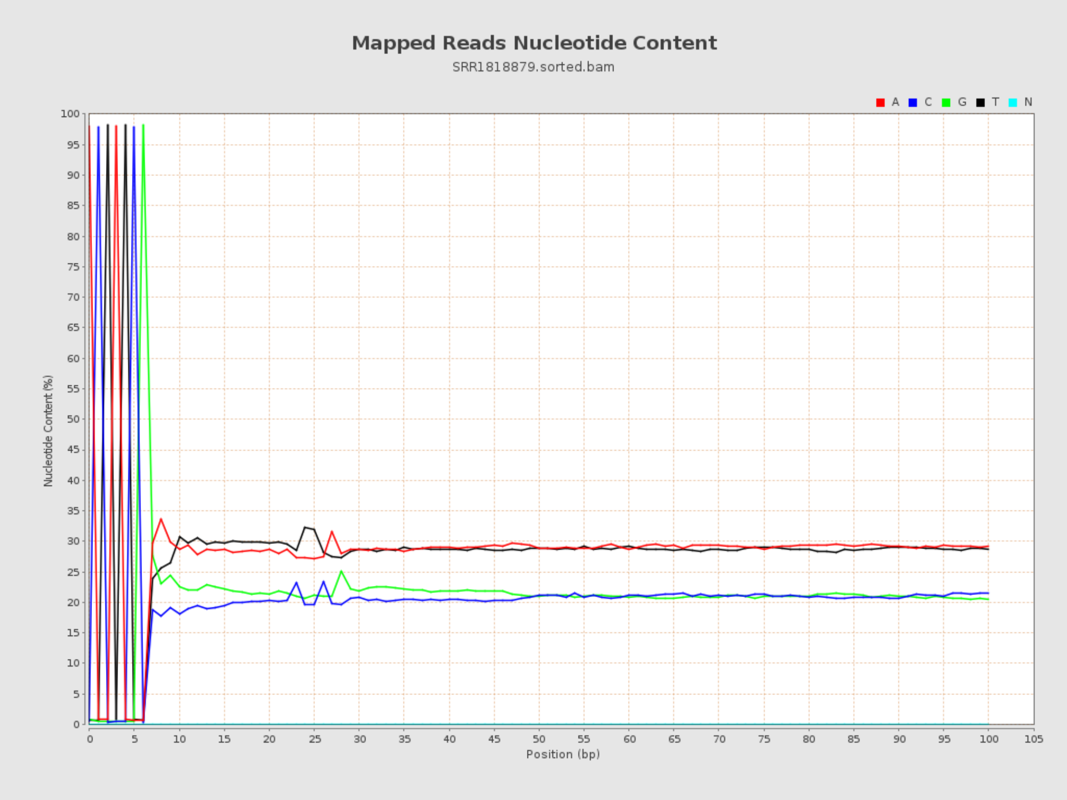
6. Results : Genome Fraction Coverage



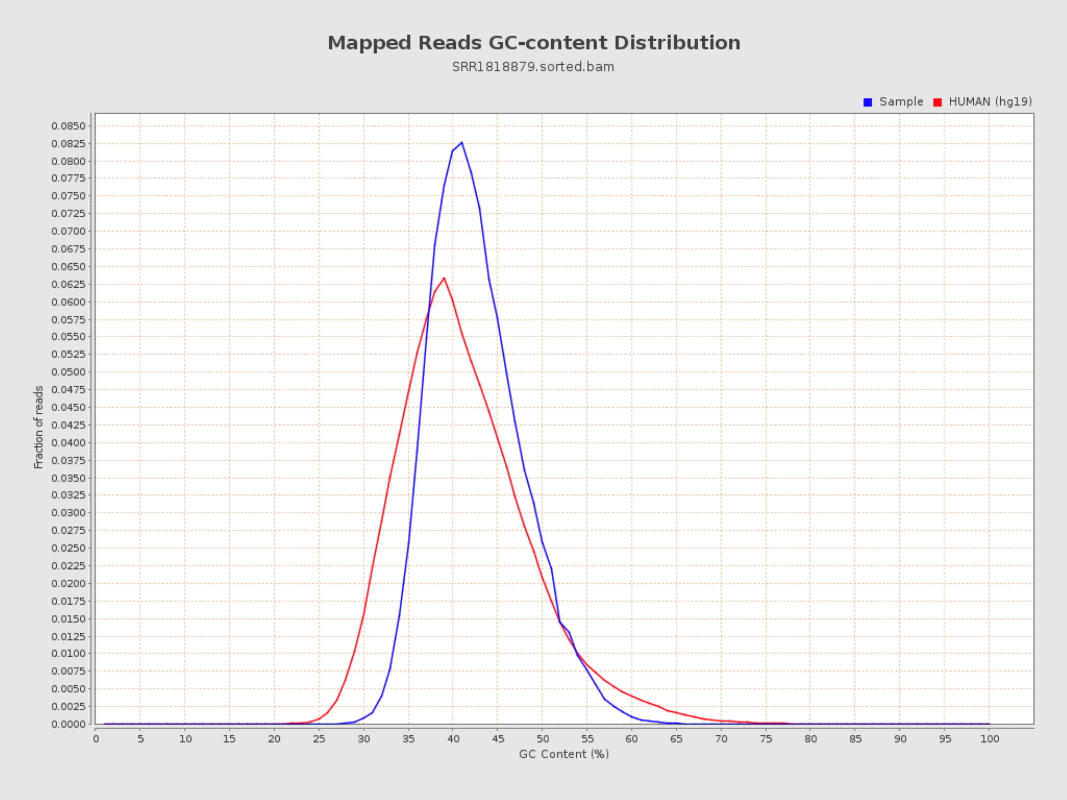
7. Results : Duplication Rate Histogram



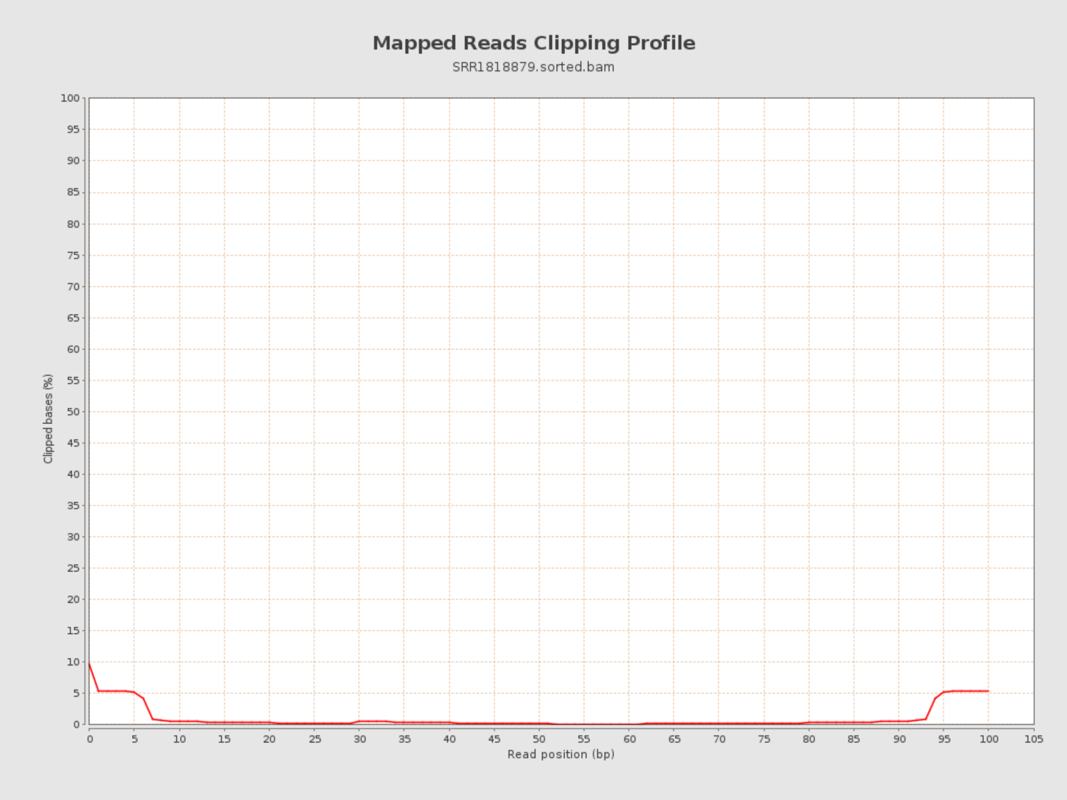
8. Results : Mapped Reads Nucleotide Content



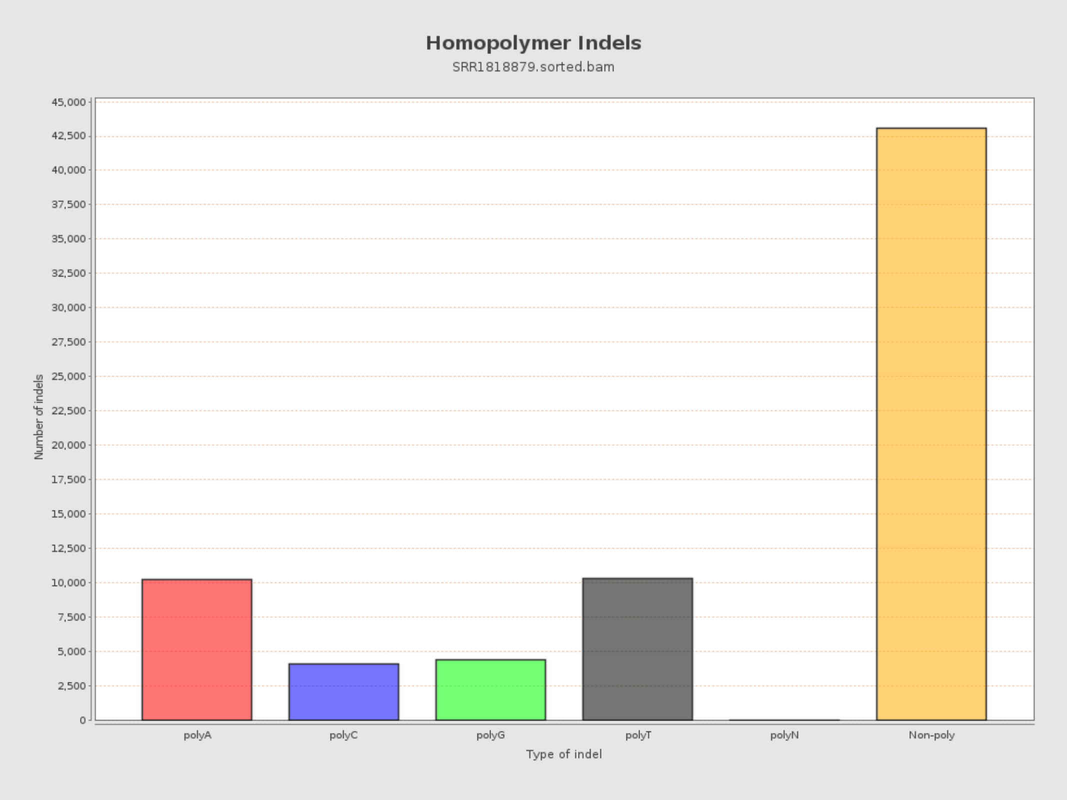
9. Results : Mapped Reads GC-content Distribution



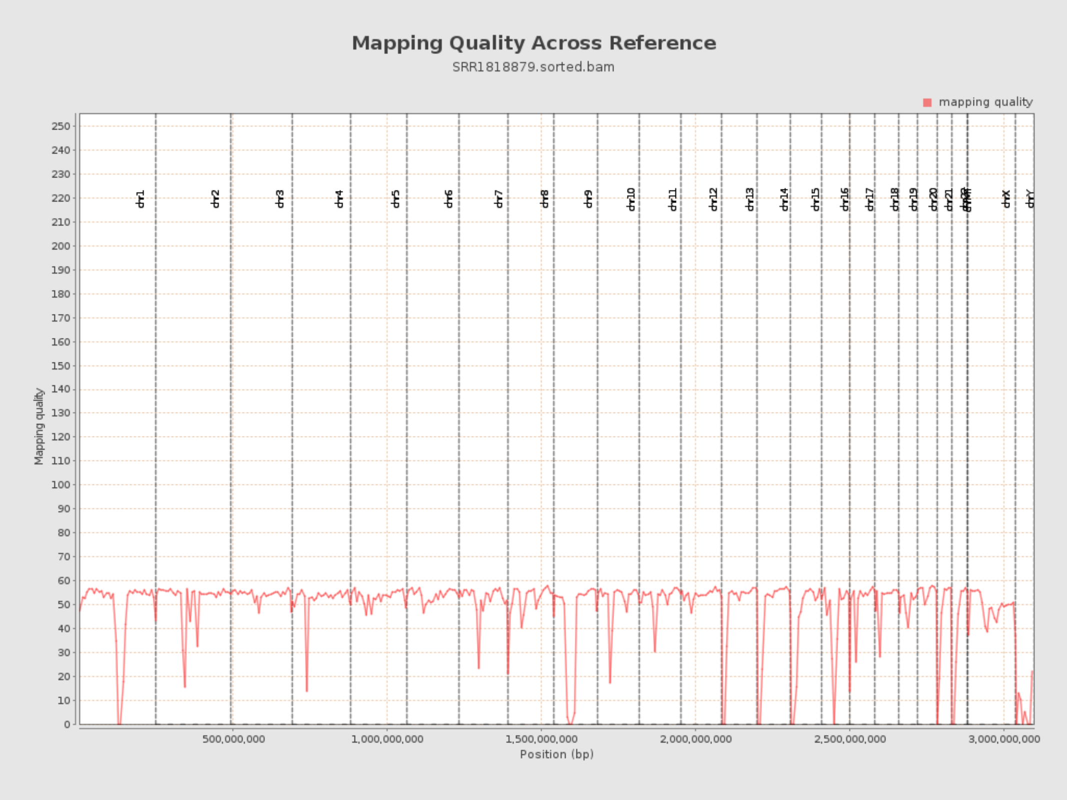
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram