Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:05:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818956.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_SRR1818956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:05:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,445,617
Mapped reads	3,396,450 / 98.57%
Unmapped reads	49,167 / 1.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,946 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	1,749,520 / 50.78%
Duplication rate	42.02%
Clipped reads	3,399,977 / 98.68%

2.2. ACGT Content

Number/percentage of A's	90,016,087 / 28.62%
Number/percentage of C's	68,216,826 / 21.69%
Number/percentage of T's	88,180,126 / 28.03%
Number/percentage of G's	68,135,032 / 21.66%
Number/percentage of N's	14,067 / 0%
GC Percentage	43.35%

2.3. Coverage

Mean	0.1017

Standard Deviation	1.106

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

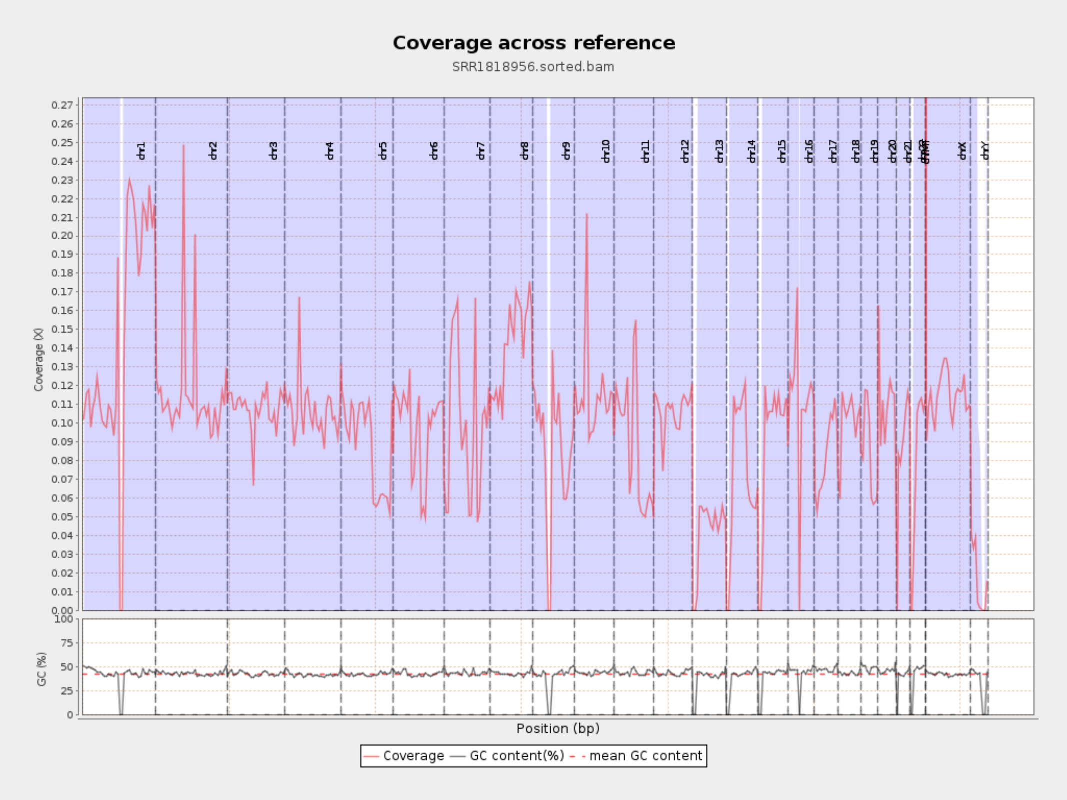
General error rate	0.69%
Mismatches	2,070,190
Insertions	43,748
Mapped reads with at least one insertion	1.25%
Deletions	96,624
Mapped reads with at least one deletion	2.78%
Homopolymer indels	41.66%

2.6. Chromosome stats

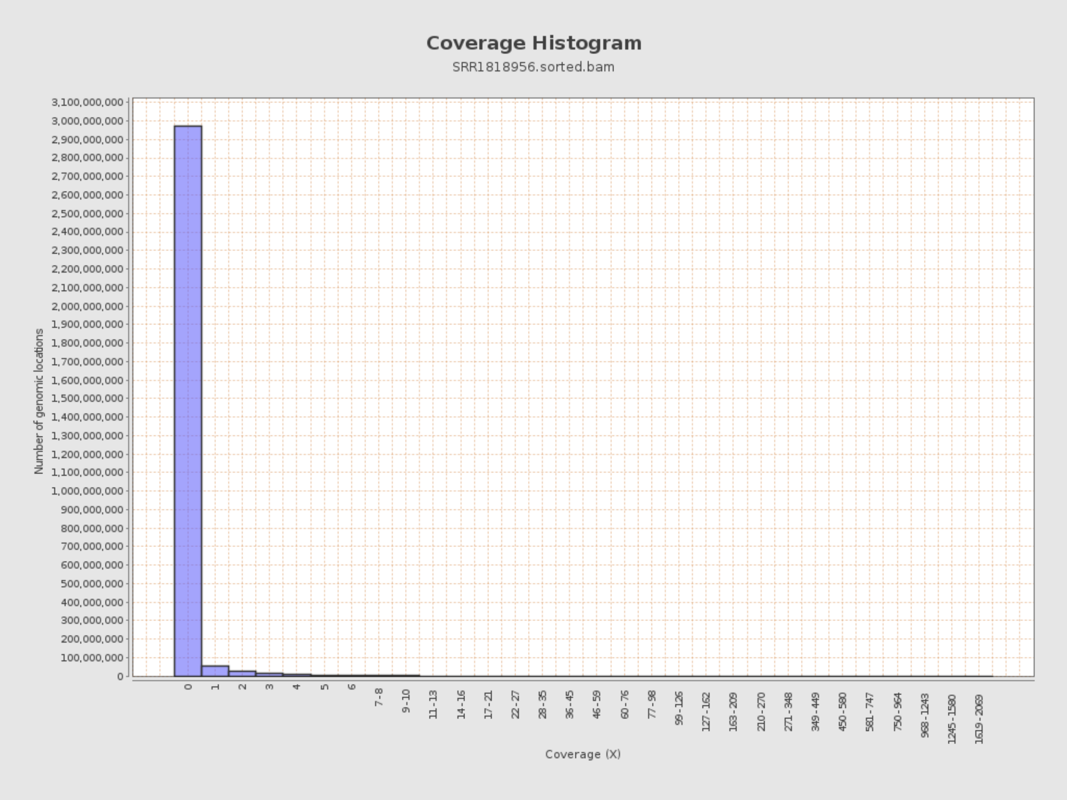
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36610946	0.1469	1.8709
chr2	243199373	28082866	0.1155	1.6999
chr3	198022430	21295371	0.1075	0.6864
chr4	191154276	20444794	0.107	0.7953
chr5	180915260	16059390	0.0888	0.6537
chr6	171115067	16852522	0.0985	0.719
chr7	159138663	15735454	0.0989	0.8567

chr8	146364022	20828208	0.1423	0.9329
chr9	141213431	11911696	0.0844	1.2958
chr10	135534747	15523094	0.1145	1.4236
chr11	135006516	11890090	0.0881	0.7298
chr12	133851895	14311629	0.1069	0.715
chr13	115169878	4842813	0.042	0.4174
chr14	107349540	7885926	0.0735	0.6849
chr15	102531392	9058863	0.0884	0.6299
chr16	90354753	9855166	0.1091	1.2856
chr17	81195210	6738469	0.083	0.6755
chr18	78077248	7840174	0.1004	1.5733
chr19	59128983	4981972	0.0843	1.6947
chr20	63025520	7020663	0.1114	0.7611
chr21	48129895	4238211	0.0881	0.7352
chr22	51304566	3914928	0.0763	0.6446
chrMT	16571	53622	3.2359	4.1425
chrX	155270560	17833312	0.1149	0.8924
chrY	59373566	931055	0.0157	1.046

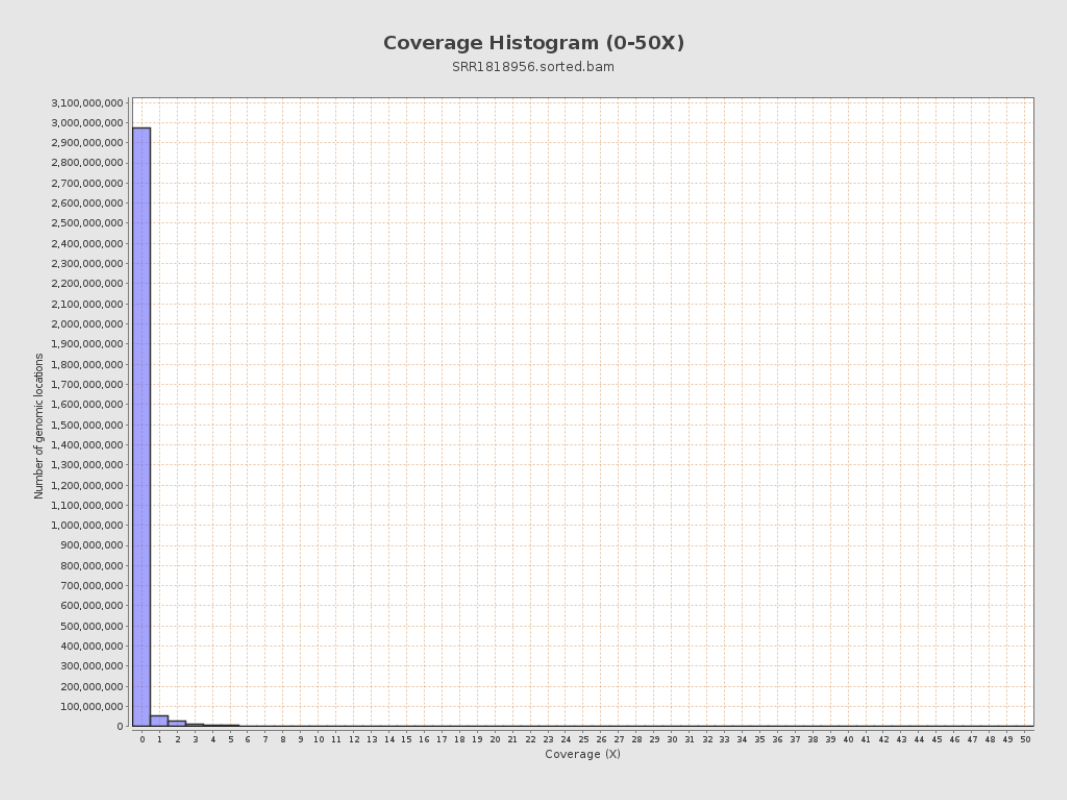
3. Results : Coverage across reference



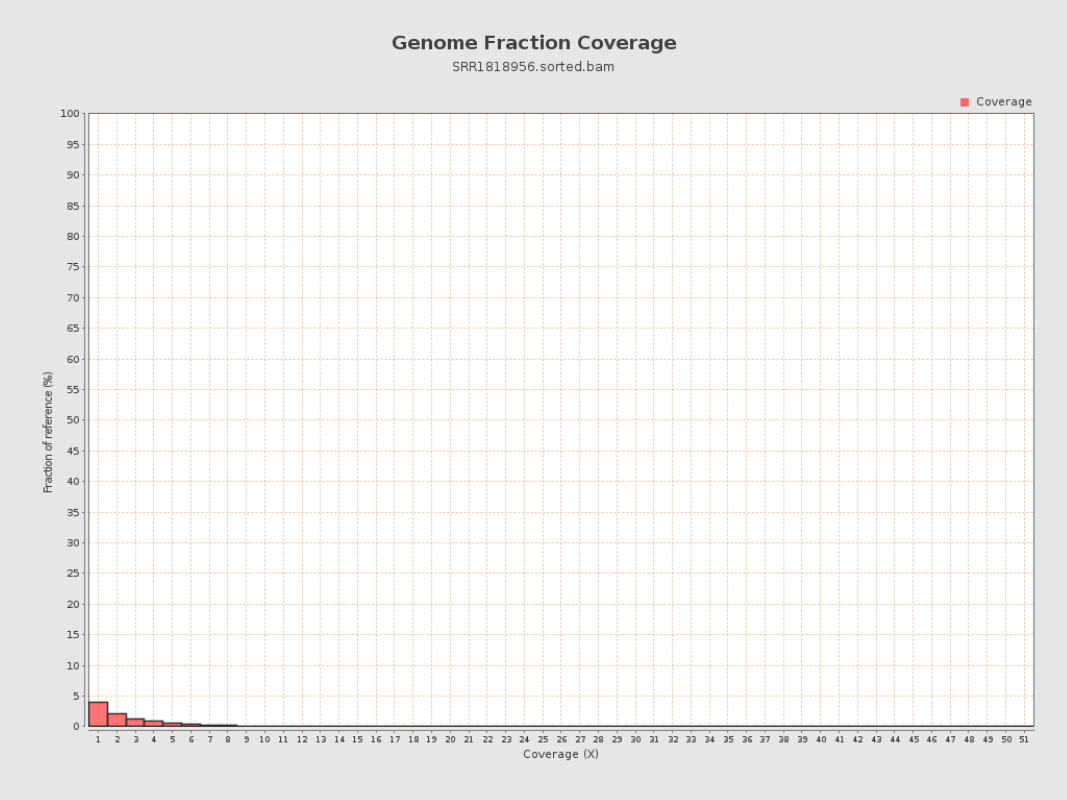
4. Results : Coverage Histogram



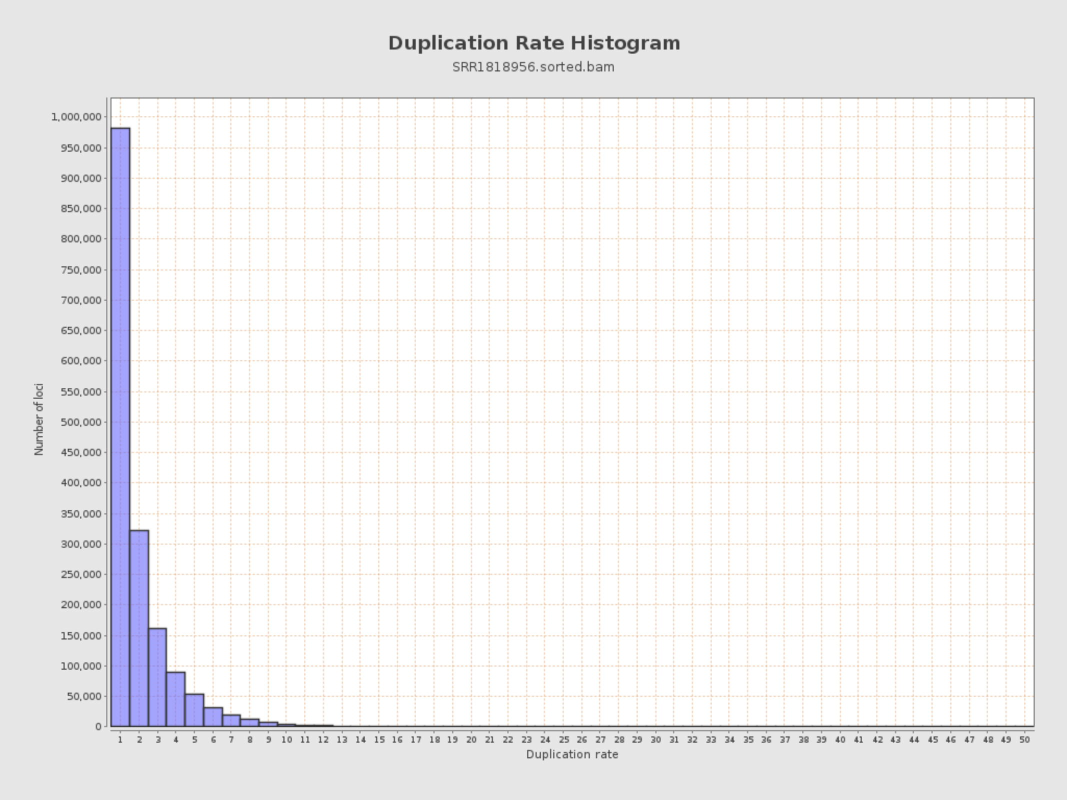
5. Results : Coverage Histogram (0-50X)



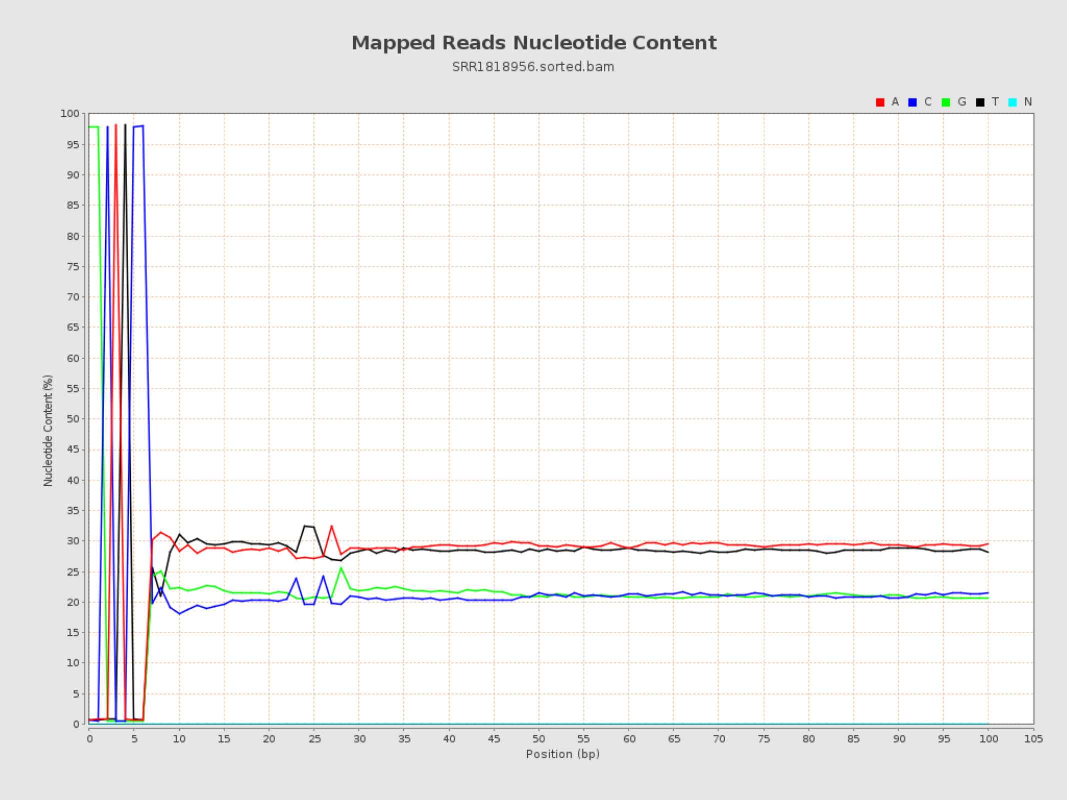
6. Results : Genome Fraction Coverage



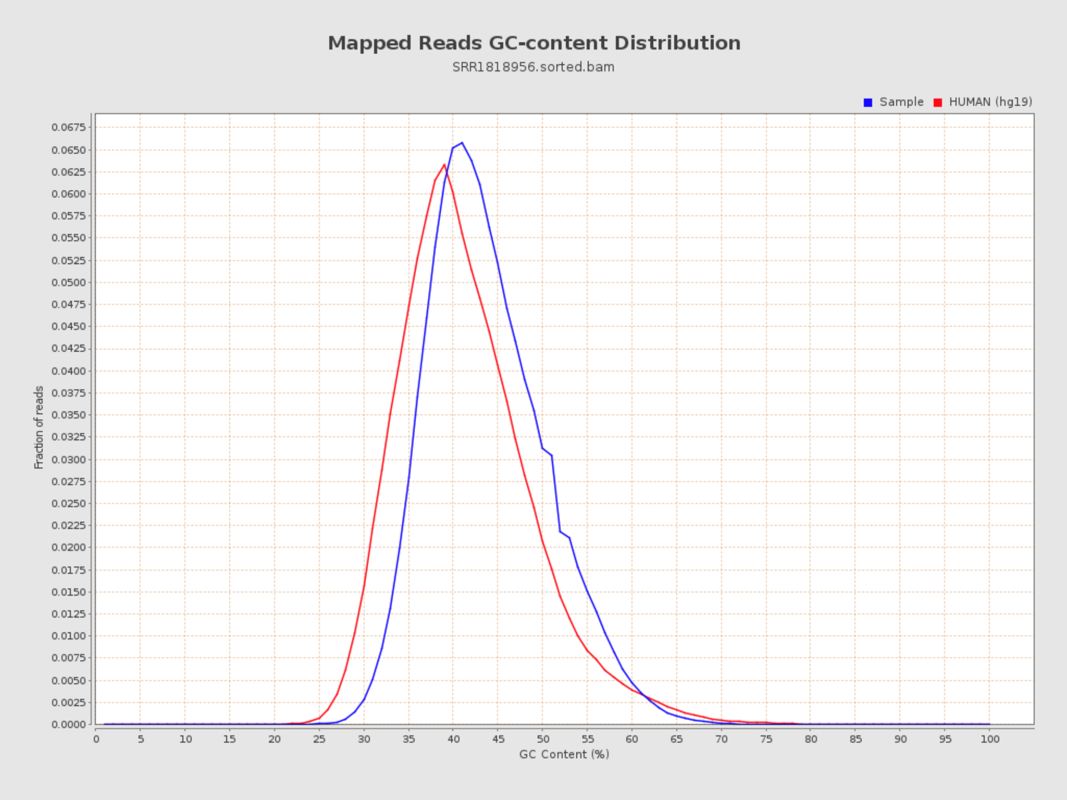
7. Results : Duplication Rate Histogram



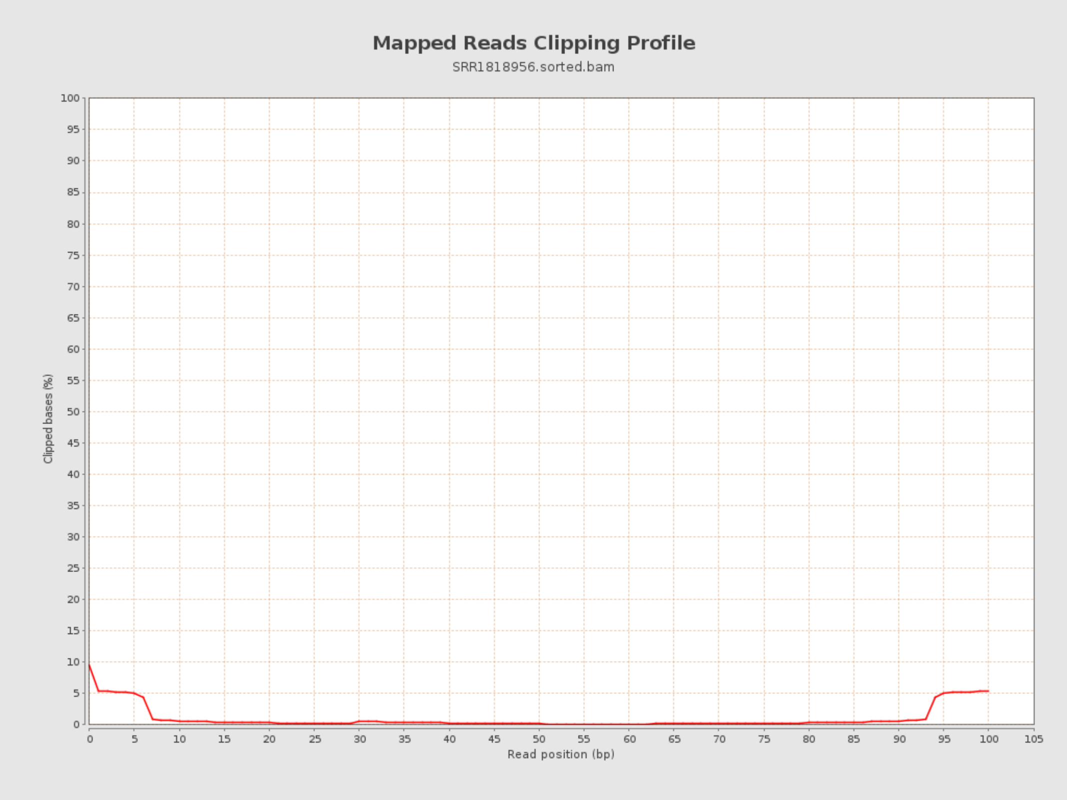
8. Results : Mapped Reads Nucleotide Content



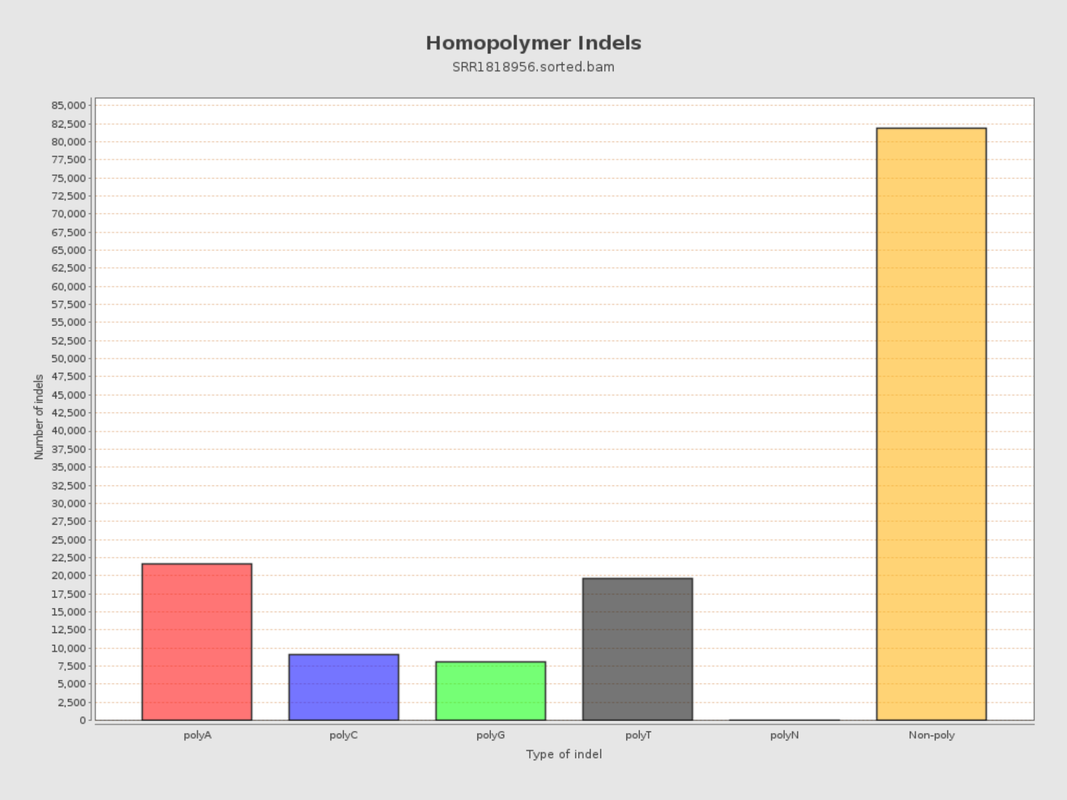
9. Results : Mapped Reads GC-content Distribution



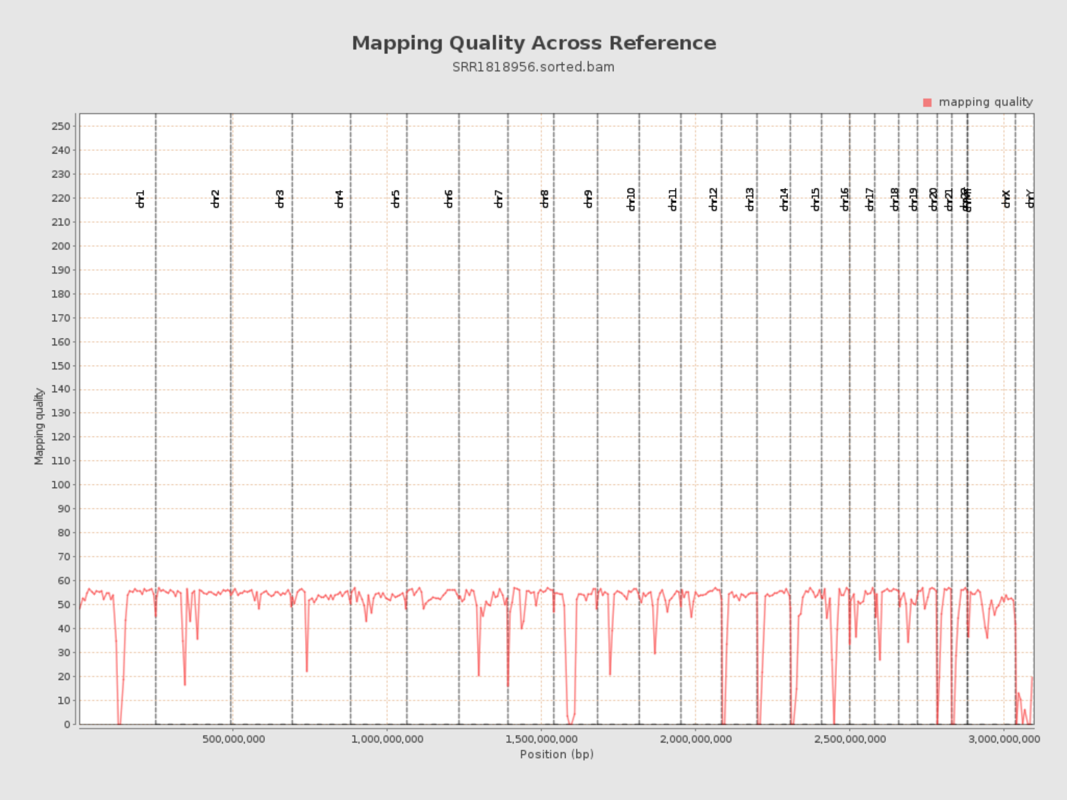
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram