Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:58:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818955.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_SRR1818955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:58:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,307,423
Mapped reads	4,022,563 / 93.39%
Unmapped reads	284,860 / 6.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,873 / 1.37%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	2,251,873 / 52.28%
Duplication rate	45.68%
Clipped reads	4,051,001 / 94.05%

2.2. ACGT Content

Number/percentage of A's	108,978,289 / 29.28%
Number/percentage of C's	77,779,625 / 20.89%
Number/percentage of T's	107,950,088 / 29%
Number/percentage of G's	77,526,570 / 20.83%
Number/percentage of N's	16,589 / 0%
GC Percentage	41.72%

2.3. Coverage

Mean	0.1203

Standard Deviation	1.2625

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

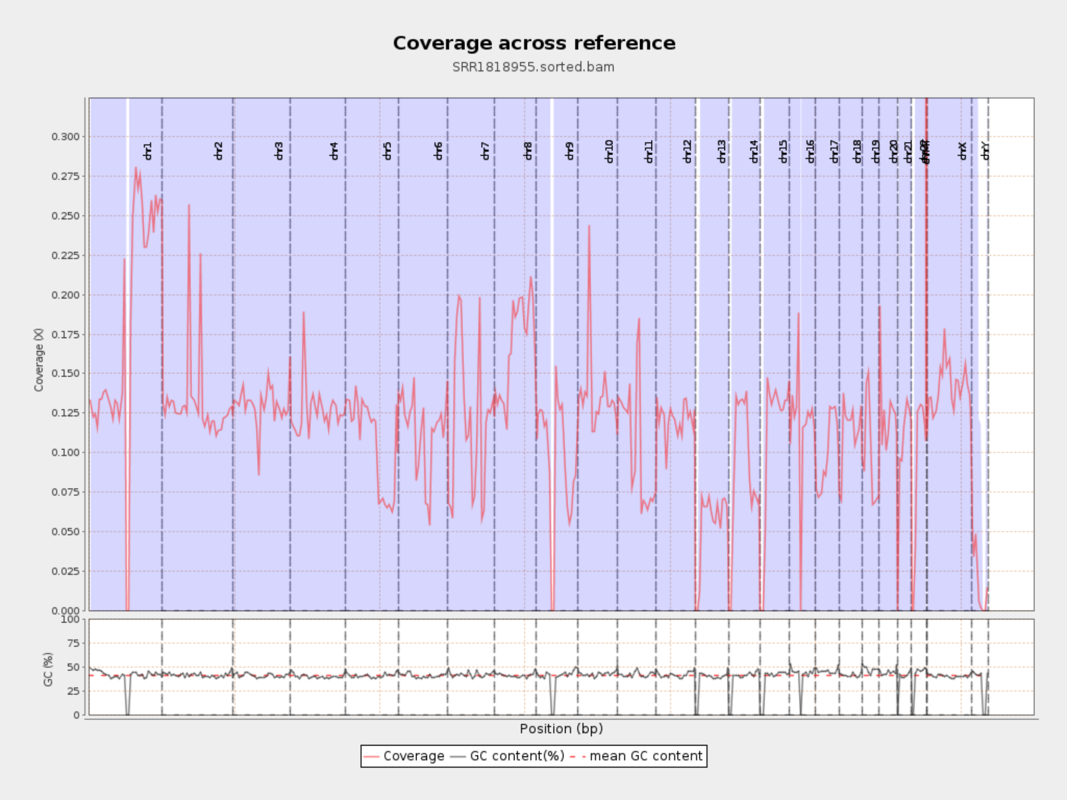
General error rate	0.67%
Mismatches	2,393,405
Insertions	50,897
Mapped reads with at least one insertion	1.23%
Deletions	115,042
Mapped reads with at least one deletion	2.8%
Homopolymer indels	41.54%

2.6. Chromosome stats

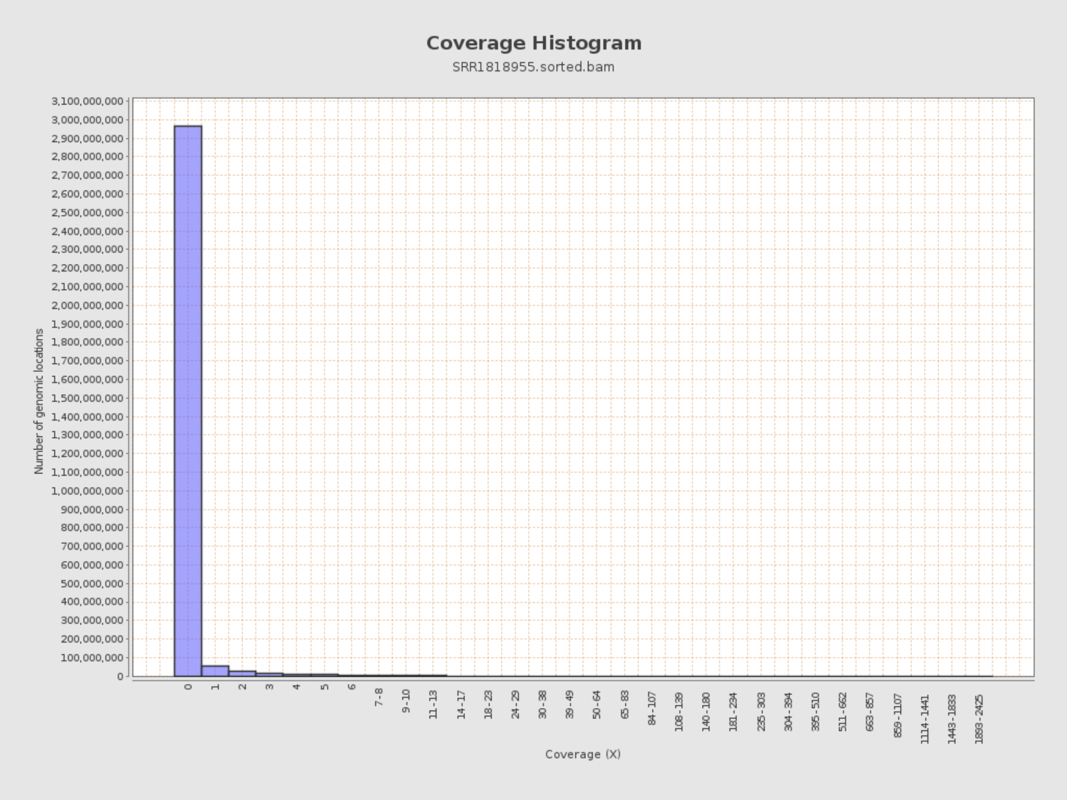
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	44232541	0.1775	2.2224
chr2	243199373	32150859	0.1322	1.8752
chr3	198022430	25697740	0.1298	0.8153
chr4	191154276	24062156	0.1259	0.894
chr5	180915260	19166769	0.1059	0.7574
chr6	171115067	19405298	0.1134	0.8189
chr7	159138663	18954715	0.1191	1.0489

chr8	146364022	24637800	0.1683	1.0998
chr9	141213431	13279911	0.094	1.3726
chr10	135534747	18616535	0.1374	1.5794
chr11	135006516	14210635	0.1053	0.9063
chr12	133851895	16210181	0.1211	0.7927
chr13	115169878	6236581	0.0542	0.518
chr14	107349540	9561931	0.0891	0.7323
chr15	102531392	11197274	0.1092	0.7412
chr16	90354753	10630287	0.1177	1.3573
chr17	81195210	8164627	0.1006	0.7892
chr18	78077248	8864364	0.1135	1.6315
chr19	59128983	5867558	0.0992	1.8708
chr20	63025520	7872680	0.1249	0.8529
chr21	48129895	4995699	0.1038	0.7798
chr22	51304566	4419161	0.0861	0.7144
chrMT	16571	972850	58.708	38.3252
chrX	155270560	21986177	0.1416	1.0254
chrY	59373566	1065593	0.0179	1.0764

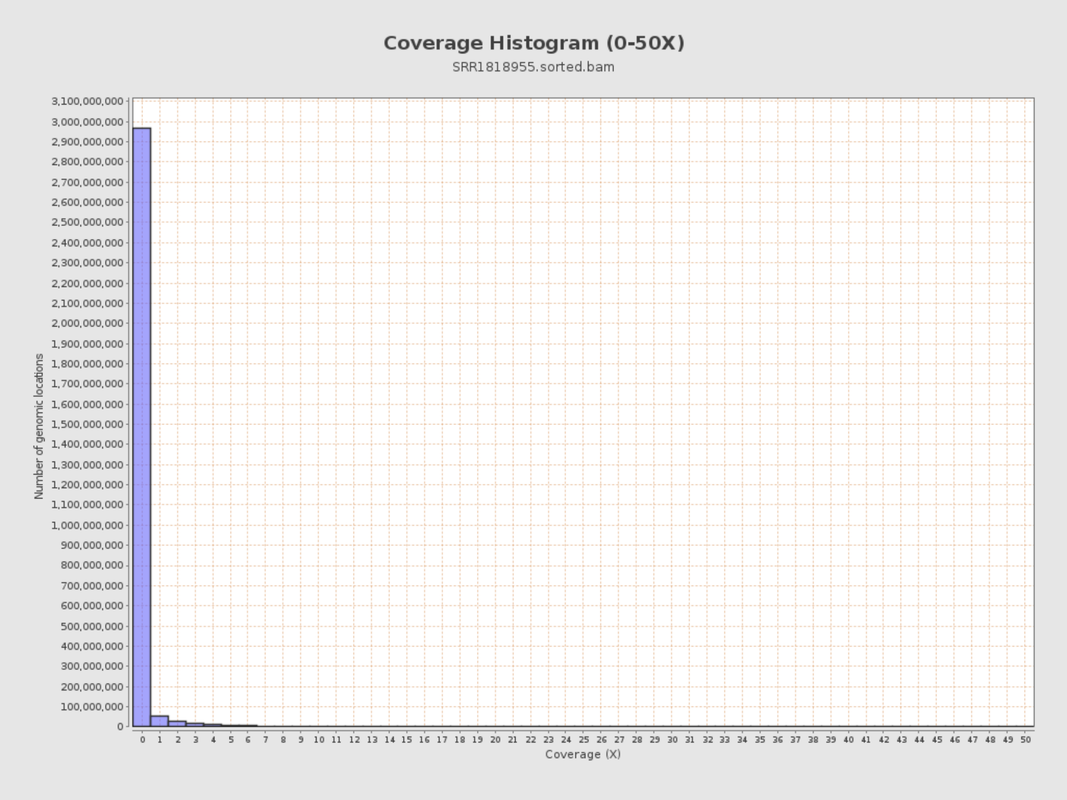
3. Results : Coverage across reference



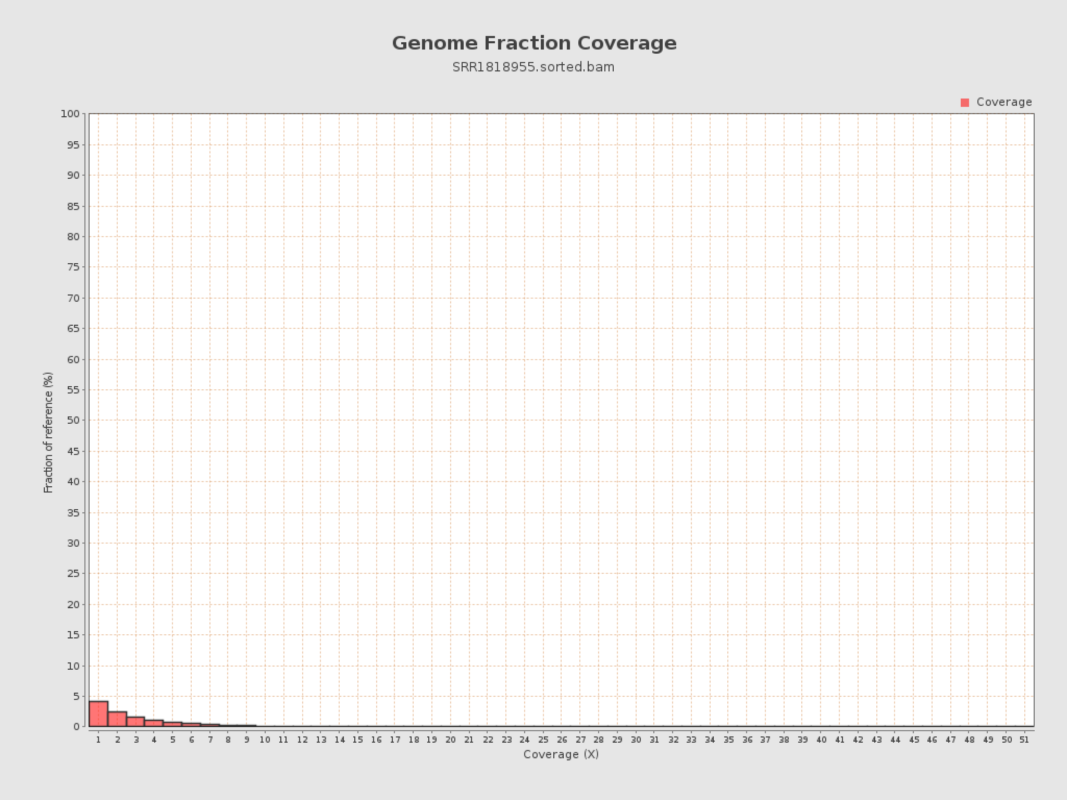
4. Results : Coverage Histogram



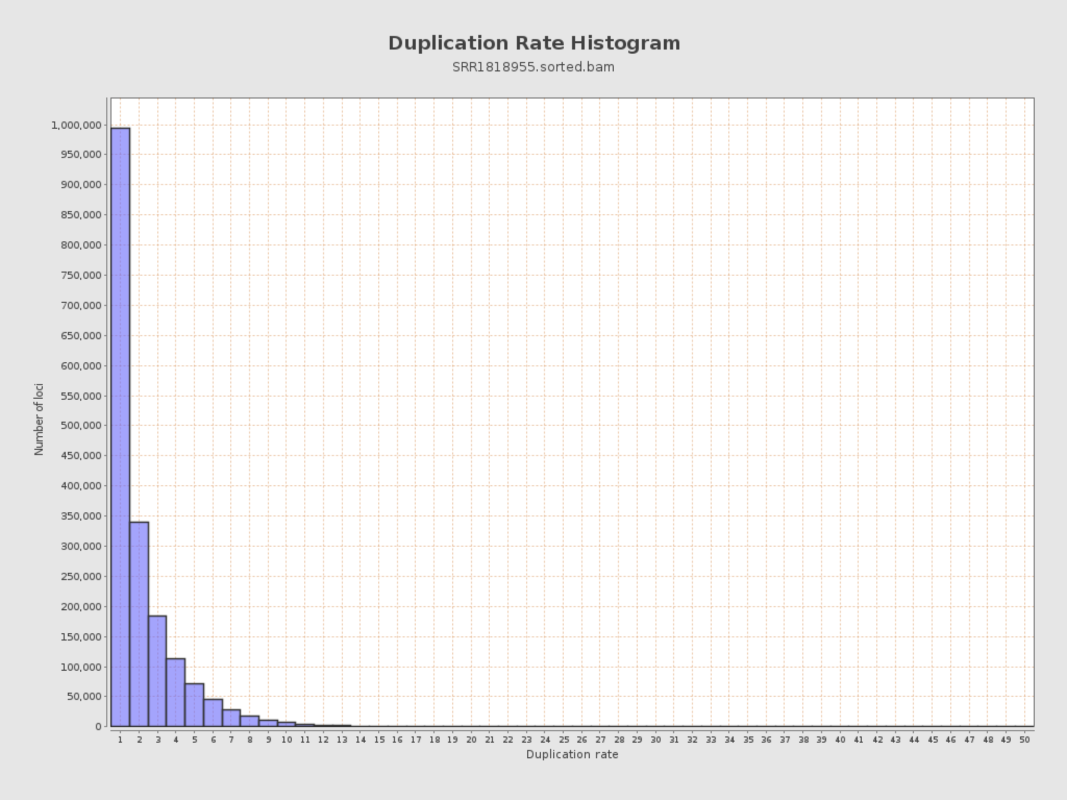
5. Results : Coverage Histogram (0-50X)



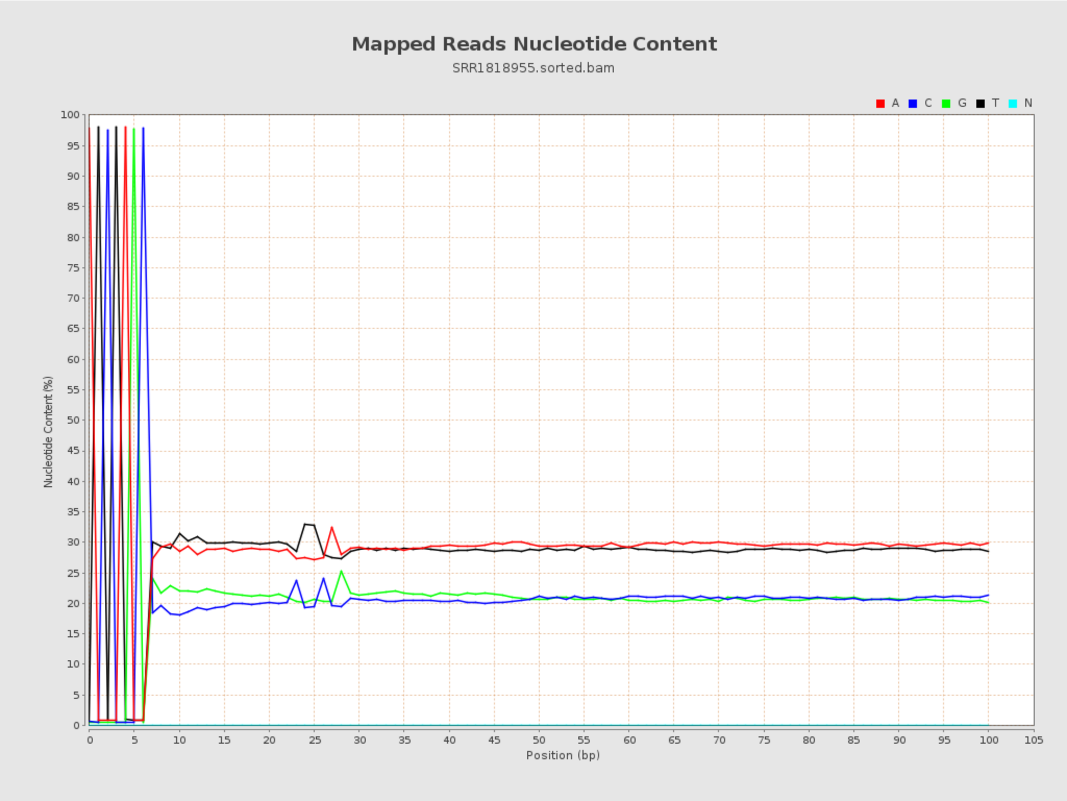
6. Results : Genome Fraction Coverage



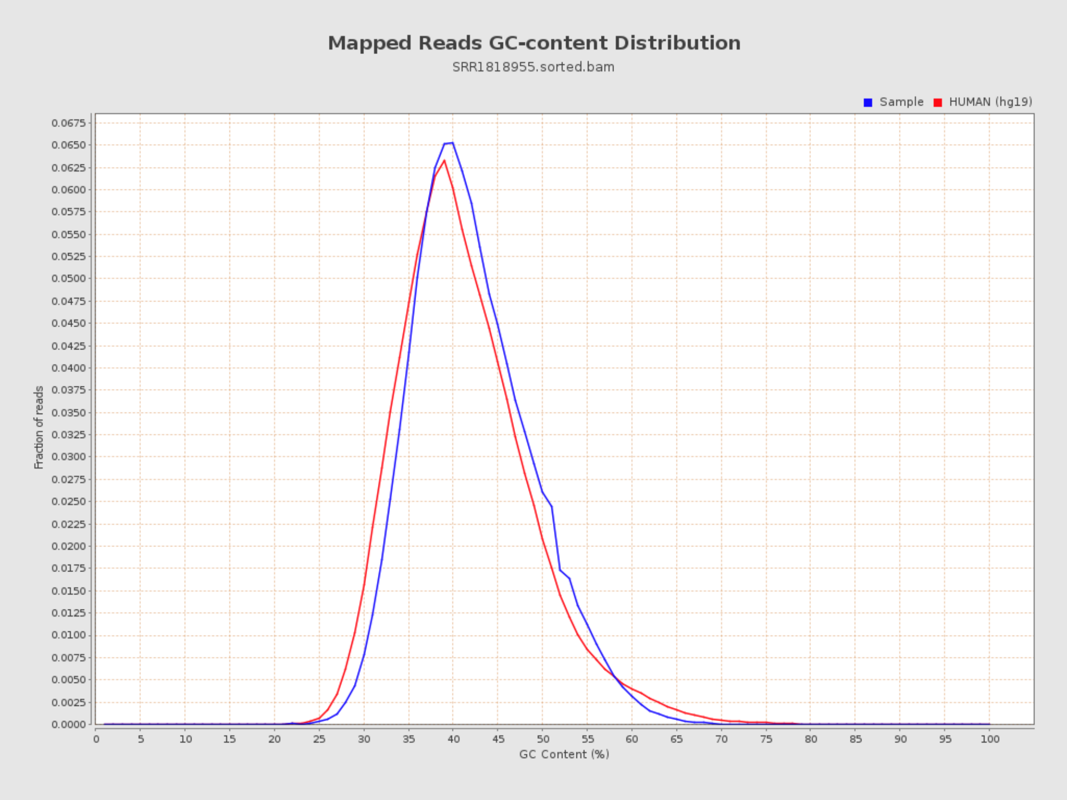
7. Results : Duplication Rate Histogram



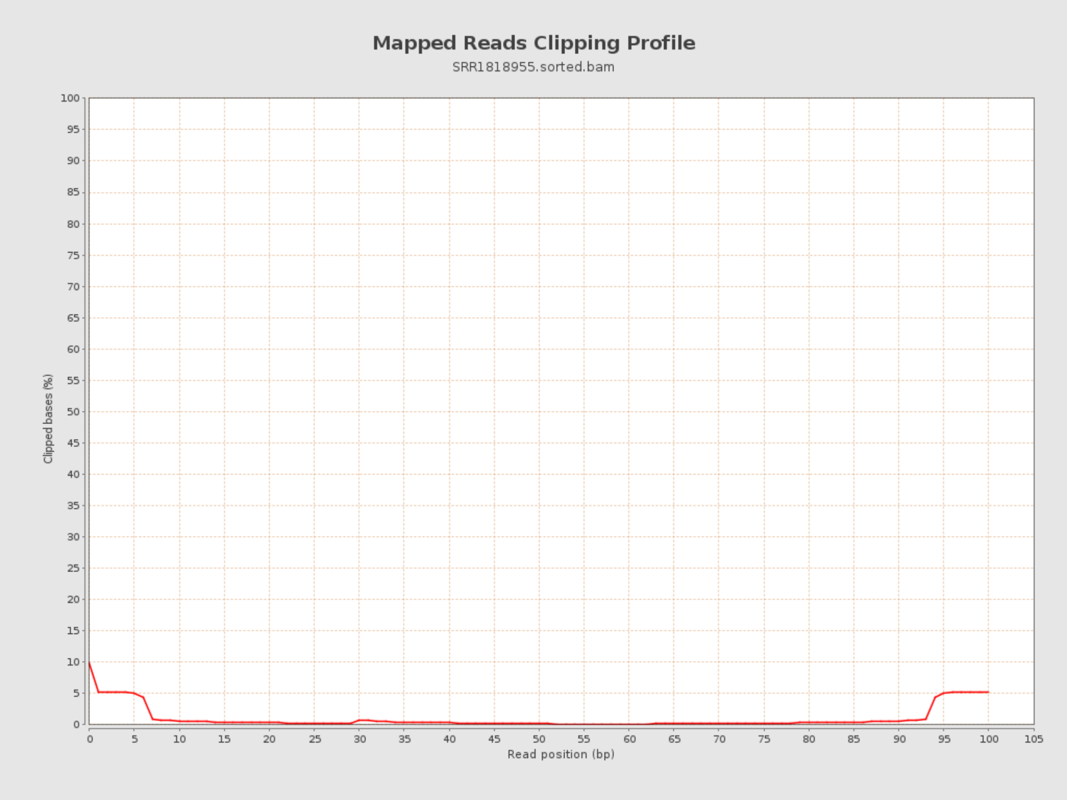
8. Results : Mapped Reads Nucleotide Content



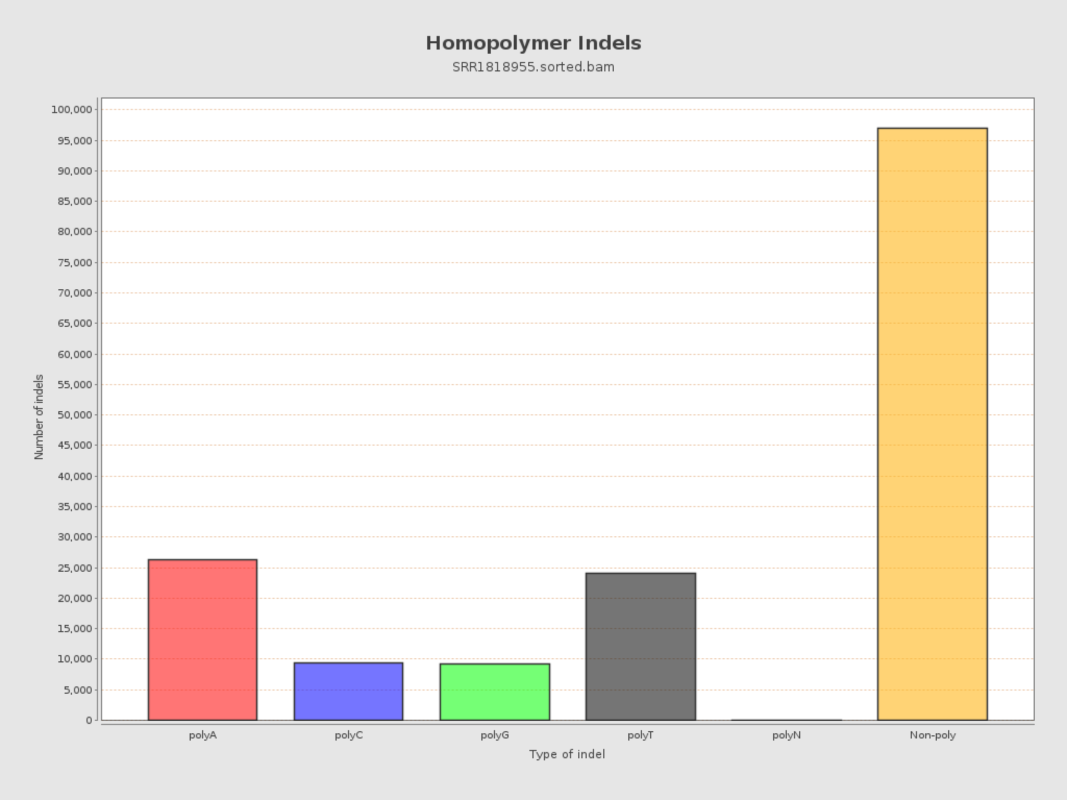
9. Results : Mapped Reads GC-content Distribution



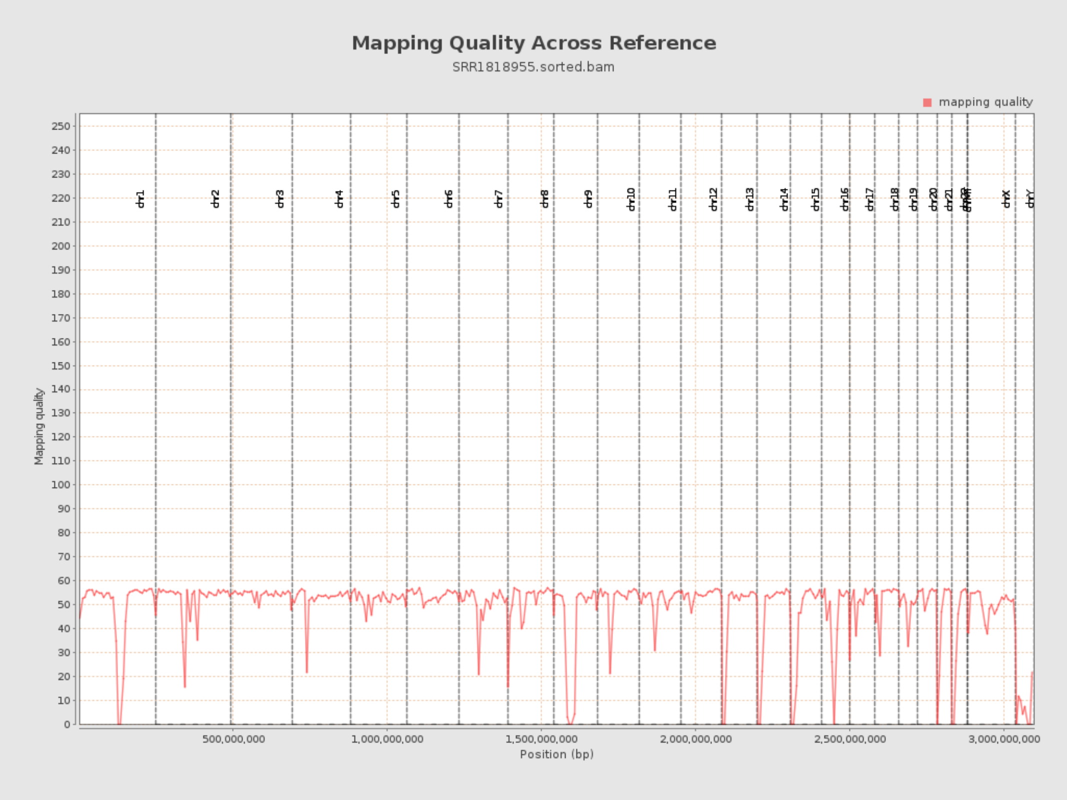
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram