Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818738.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_SRR1818738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:04:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,365,313
Mapped reads	1,307,039 / 95.73%
Unmapped reads	58,274 / 4.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,866 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	577,924 / 42.33%
Duplication rate	38.48%
Clipped reads	1,311,851 / 96.08%

2.2. ACGT Content

Number/percentage of A's	25,030,572 / 28.22%
Number/percentage of C's	18,732,463 / 21.12%
Number/percentage of T's	25,861,190 / 29.15%
Number/percentage of G's	19,077,544 / 21.51%
Number/percentage of N's	5,658 / 0.01%
GC Percentage	42.62%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.3777

2.4. Mapping Quality

Mean Mapping Quality	47.72

2.5. Mismatches and indels

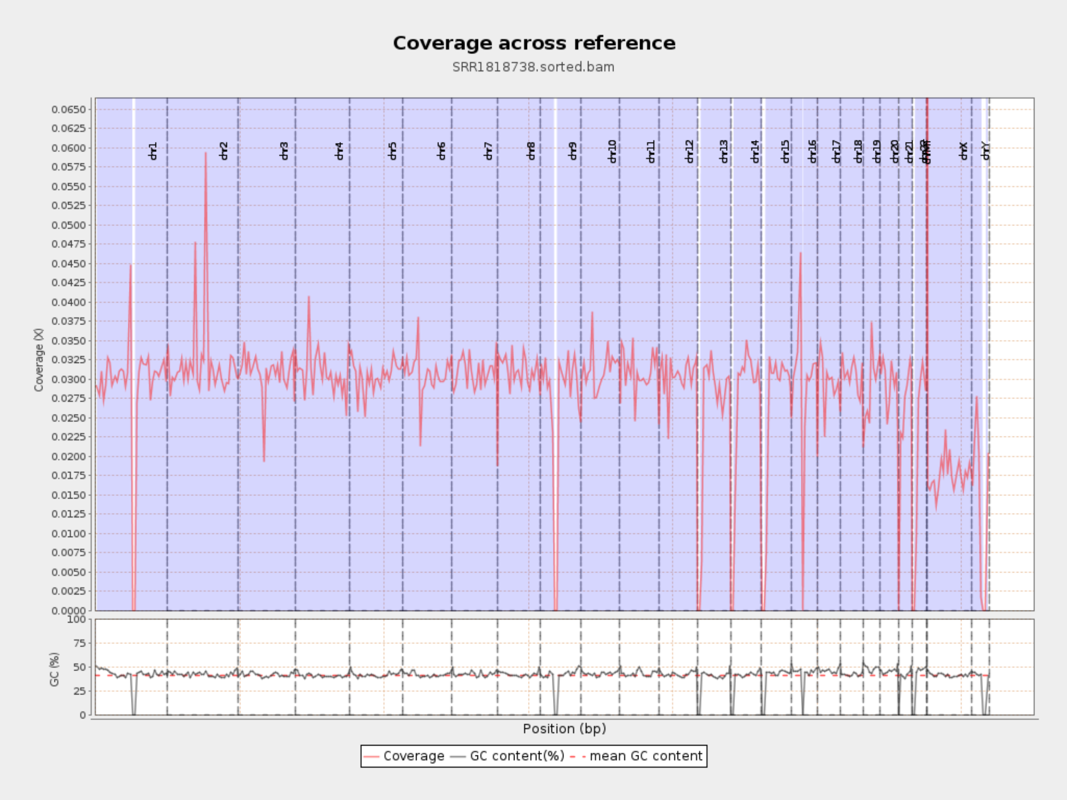
General error rate	0.51%
Mismatches	435,079
Insertions	9,659
Mapped reads with at least one insertion	0.73%
Deletions	22,795
Mapped reads with at least one deletion	1.72%
Homopolymer indels	41.77%

2.6. Chromosome stats

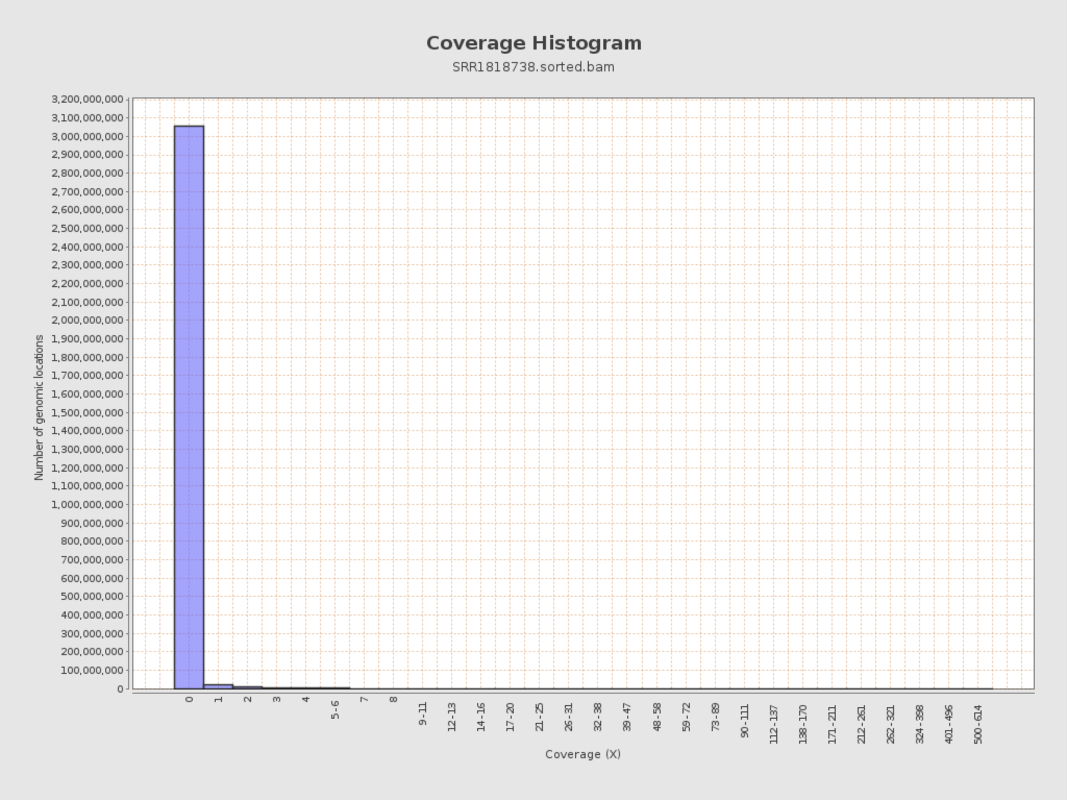
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7231422	0.029	0.4785
chr2	243199373	7843498	0.0323	0.554
chr3	198022430	6116374	0.0309	0.3166
chr4	191154276	5921776	0.031	0.3526
chr5	180915260	5505336	0.0304	0.3173
chr6	171115067	5256935	0.0307	0.3386
chr7	159138663	4925715	0.031	0.3585

chr8	146364022	4571604	0.0312	0.3529
chr9	141213431	3782723	0.0268	0.3343
chr10	135534747	4253243	0.0314	0.3863
chr11	135006516	4196176	0.0311	0.3372
chr12	133851895	4086716	0.0305	0.3258
chr13	115169878	2871451	0.0249	0.2849
chr14	107349540	2782840	0.0259	0.3093
chr15	102531392	2551803	0.0249	0.2852
chr16	90354753	2609230	0.0289	0.415
chr17	81195210	2405719	0.0296	0.3277
chr18	78077248	2394496	0.0307	0.4401
chr19	59128983	1729098	0.0292	0.4353
chr20	63025520	1852923	0.0294	0.3264
chr21	48129895	1198804	0.0249	0.3057
chr22	51304566	1050221	0.0205	0.2869
chrMT	16571	67494	4.073	5.187
chrX	155270560	2736059	0.0176	0.252
chrY	59373566	802448	0.0135	0.5738

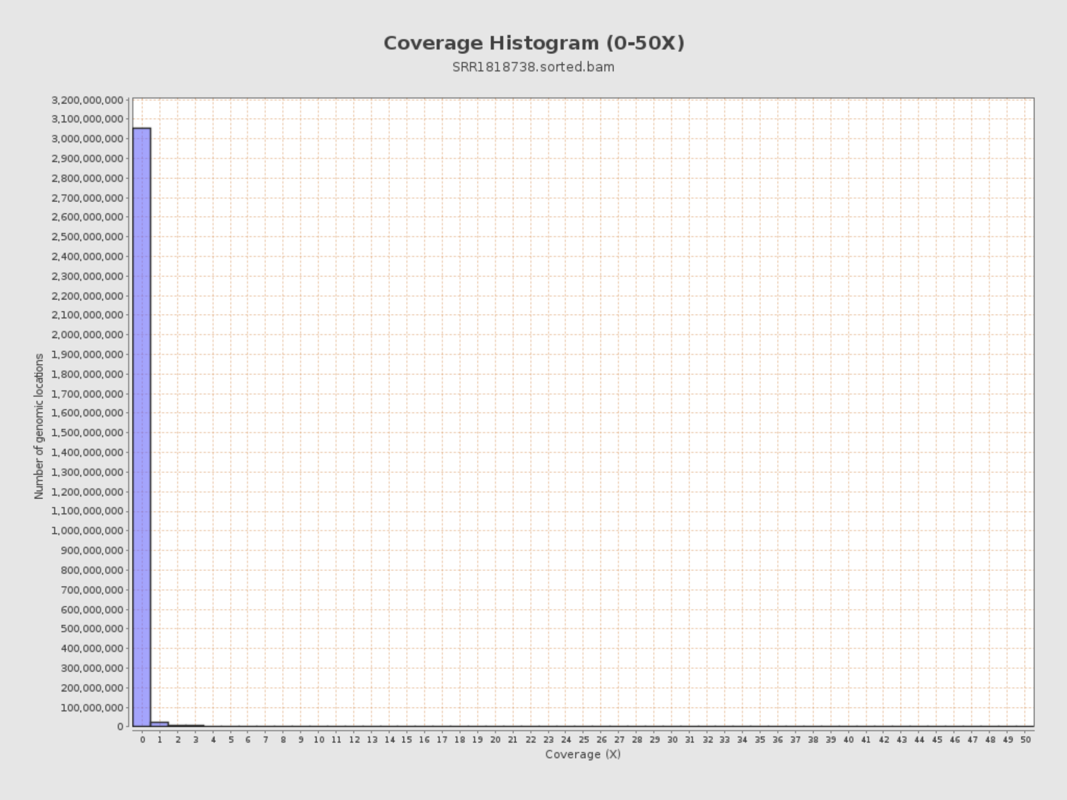
3. Results : Coverage across reference



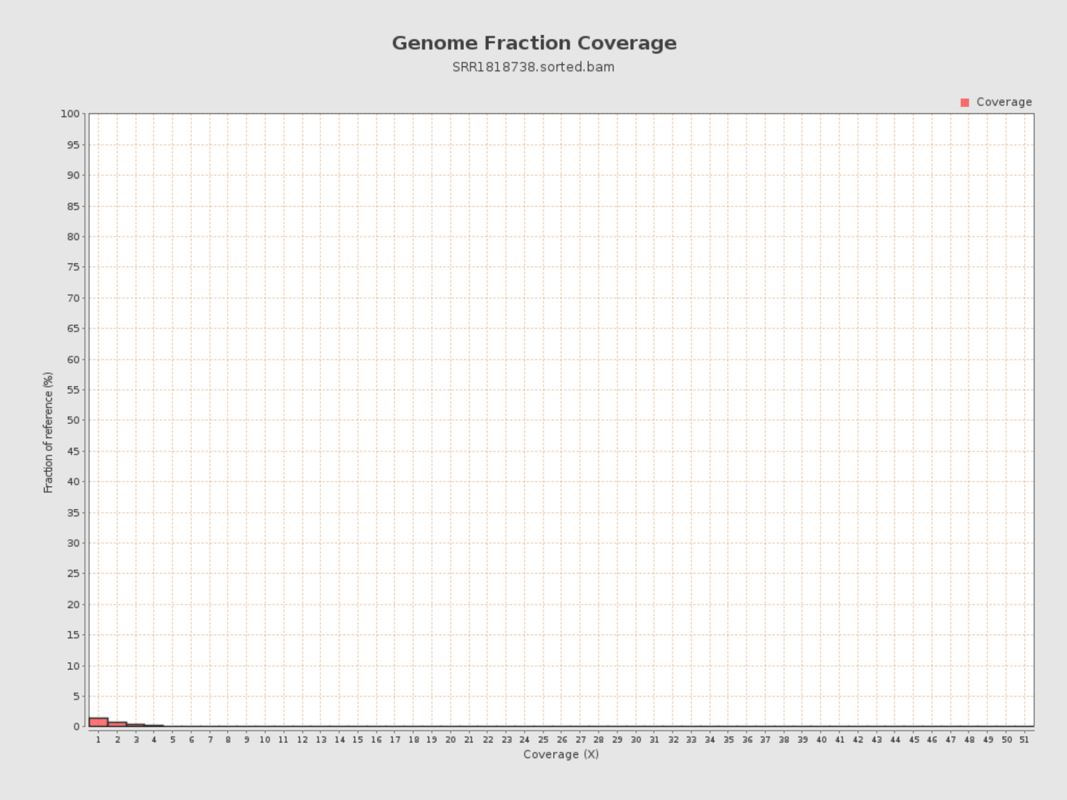
4. Results : Coverage Histogram



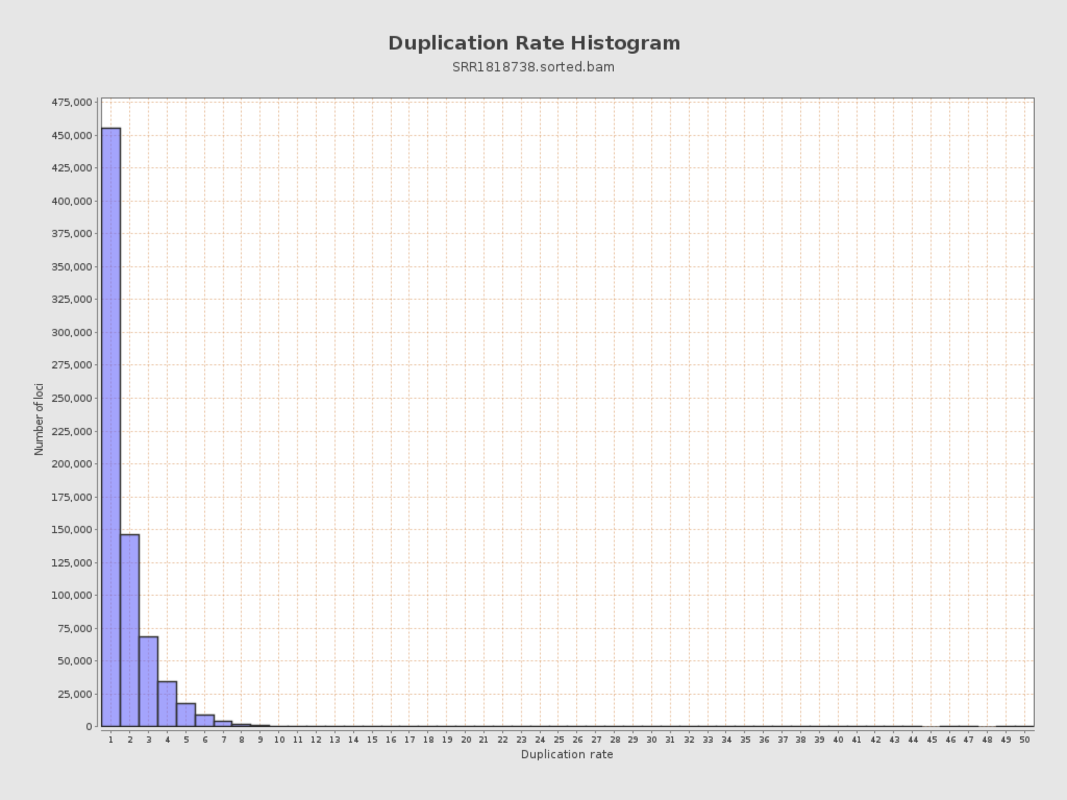
5. Results : Coverage Histogram (0-50X)



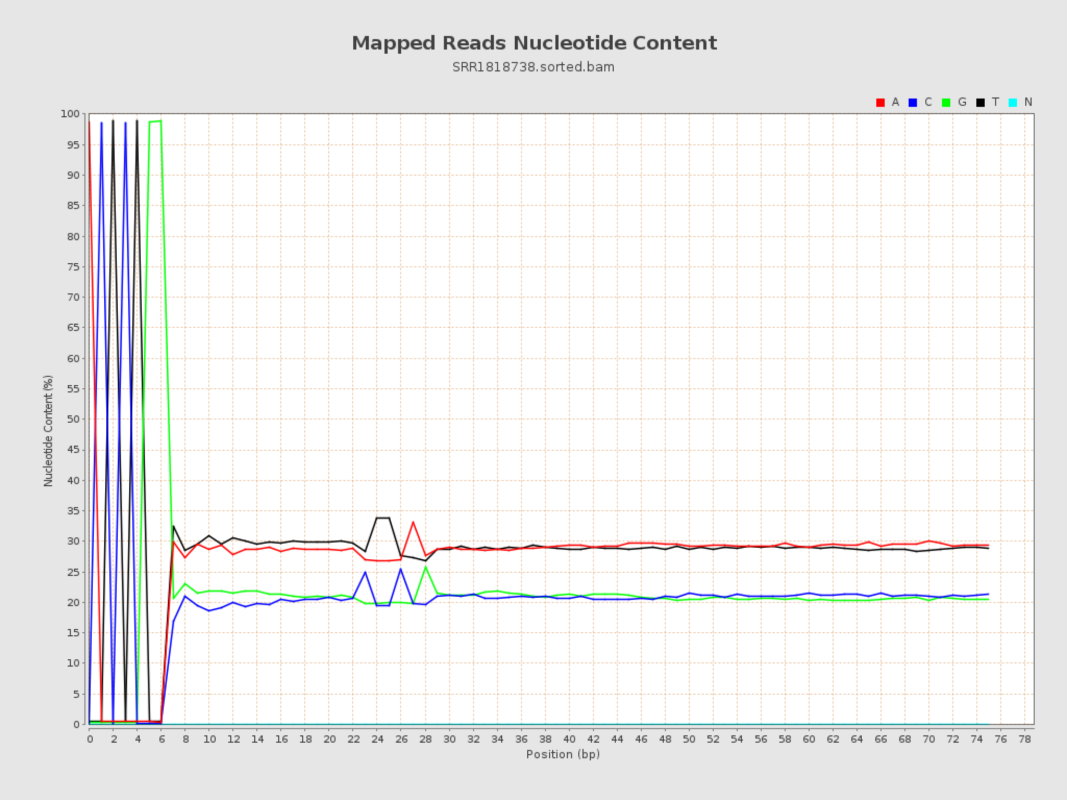
6. Results : Genome Fraction Coverage



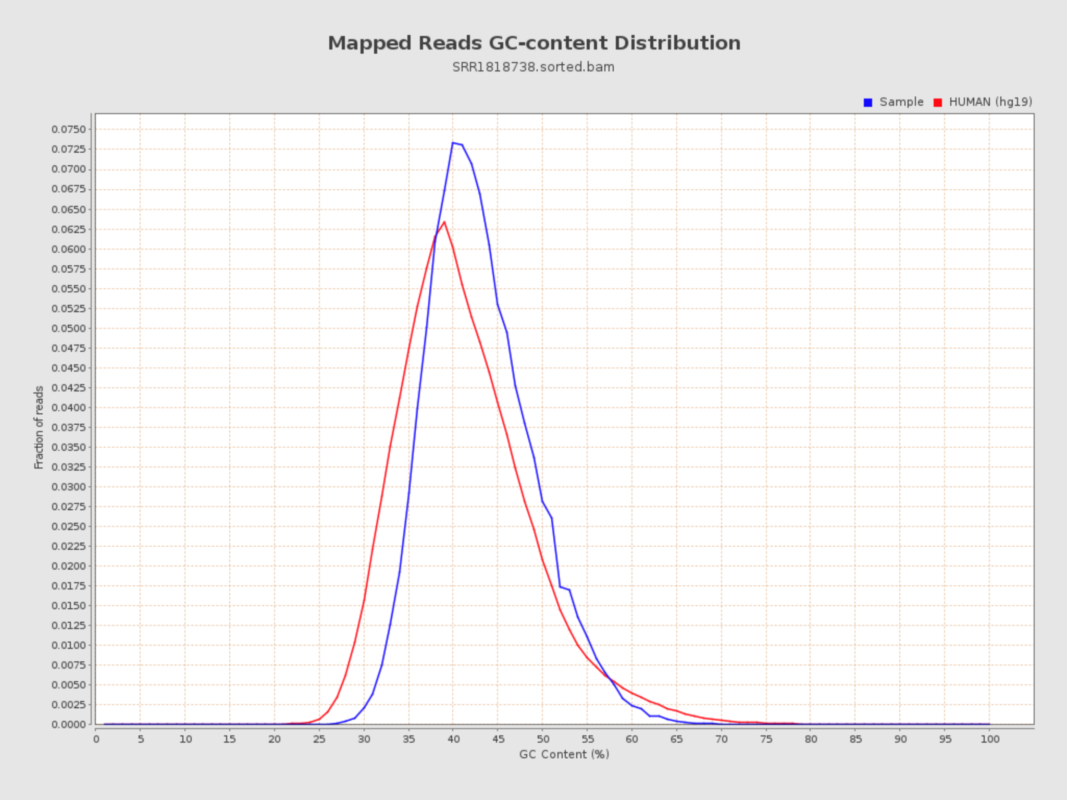
7. Results : Duplication Rate Histogram



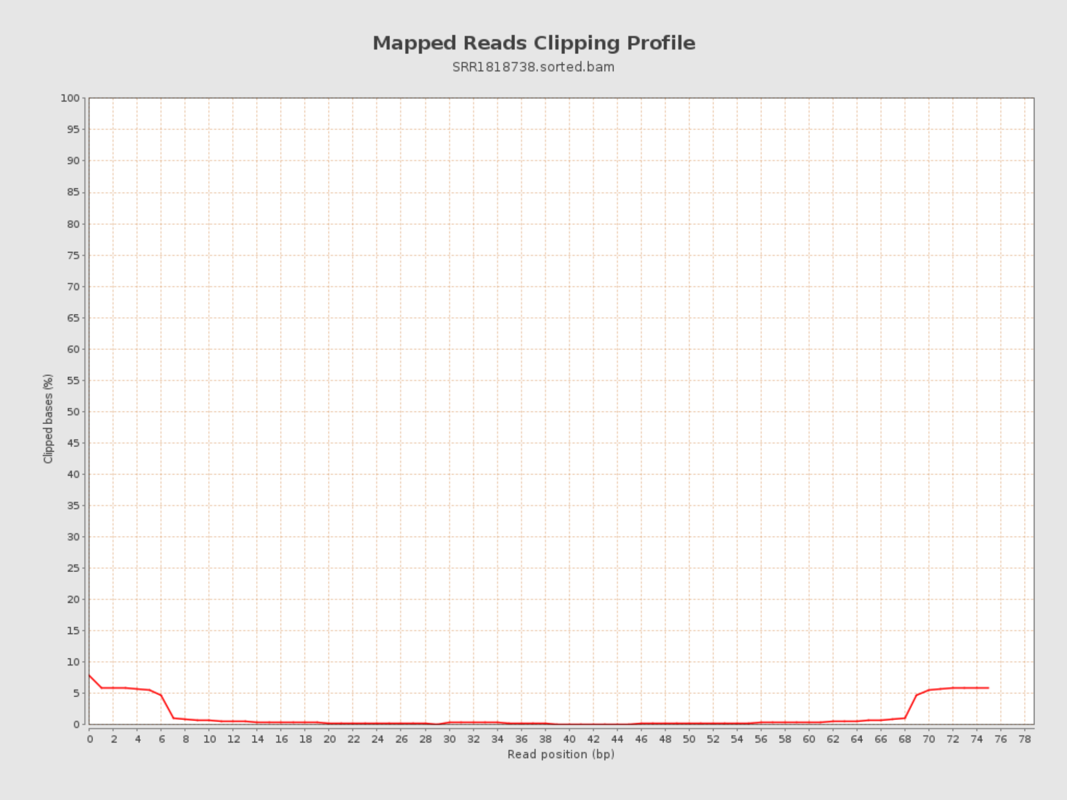
8. Results : Mapped Reads Nucleotide Content



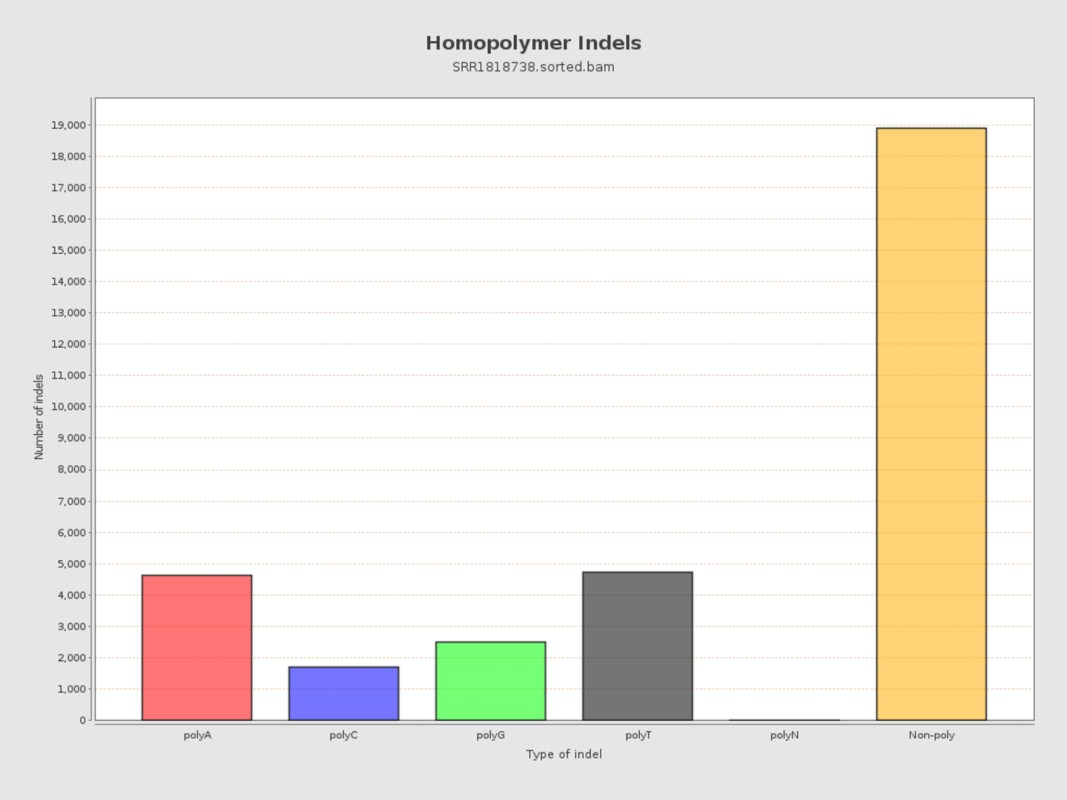
9. Results : Mapped Reads GC-content Distribution



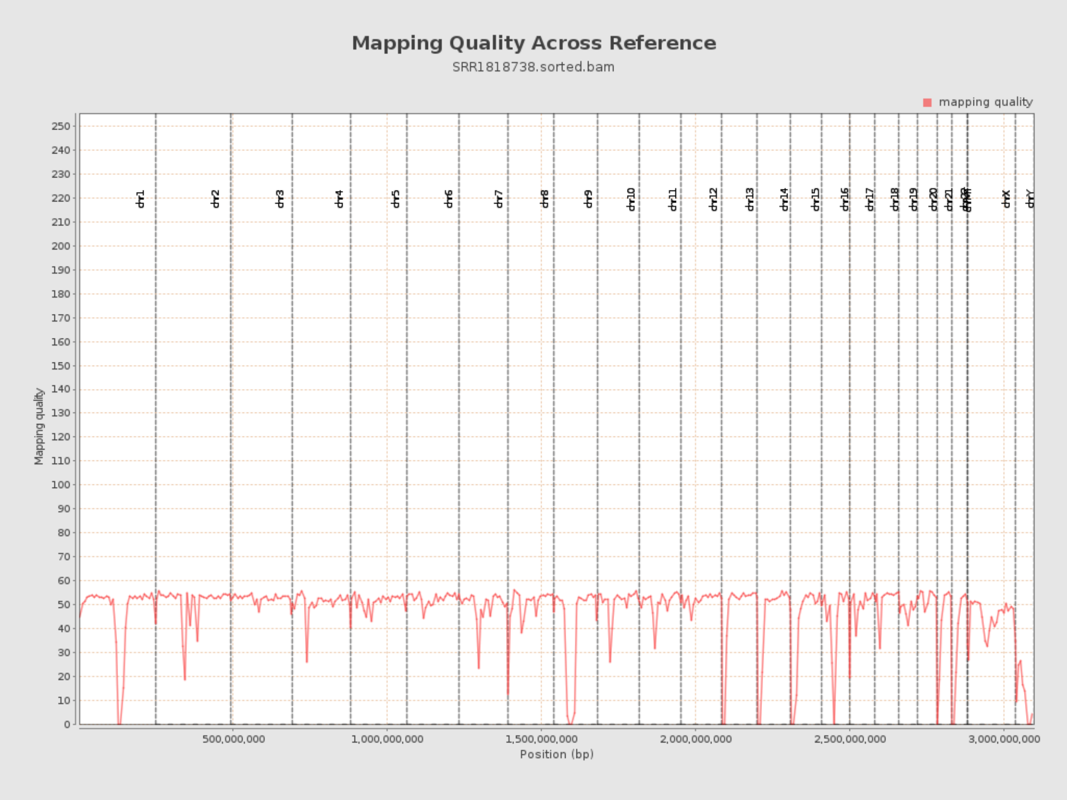
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram