Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:59:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818855.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_SRR1818855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:58:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,673,968
Mapped reads	1,630,498 / 97.4%
Unmapped reads	43,470 / 2.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,333 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	365,416 / 21.83%
Duplication rate	18.94%
Clipped reads	1,636,541 / 97.76%

2.2. ACGT Content

Number/percentage of A's	42,816,544 / 28.39%
Number/percentage of C's	30,959,461 / 20.52%
Number/percentage of T's	44,030,994 / 29.19%
Number/percentage of G's	33,030,739 / 21.9%
Number/percentage of N's	2,336 / 0%
GC Percentage	42.42%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.6004

2.4. Mapping Quality

Mean Mapping Quality	49.34

2.5. Mismatches and indels

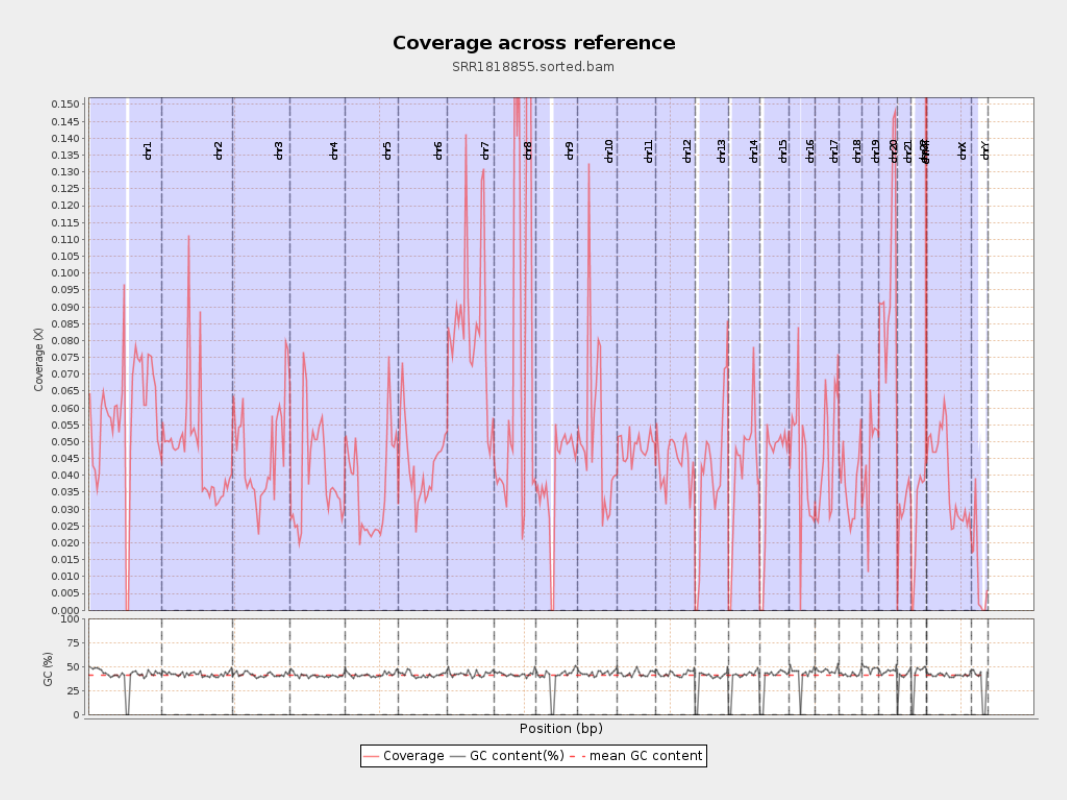
General error rate	0.66%
Mismatches	943,794
Insertions	22,483
Mapped reads with at least one insertion	1.34%
Deletions	48,633
Mapped reads with at least one deletion	2.91%
Homopolymer indels	39.93%

2.6. Chromosome stats

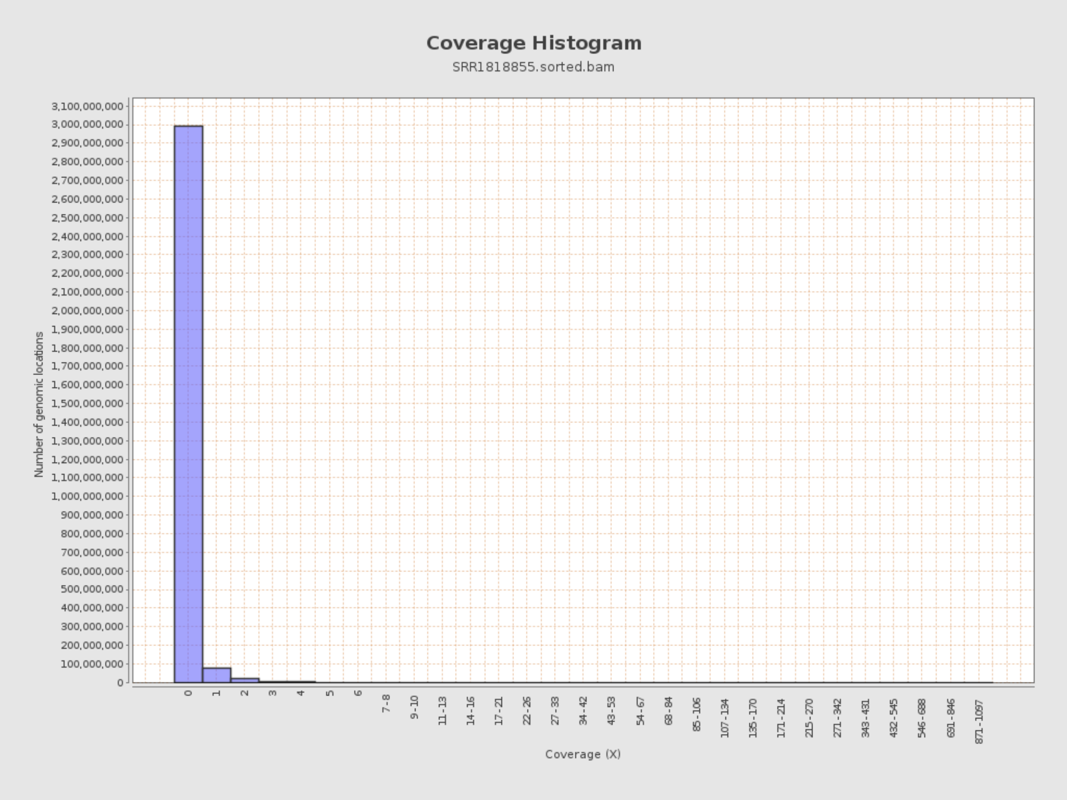
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14310420	0.0574	0.8887
chr2	243199373	11543033	0.0475	0.8423
chr3	198022430	9321676	0.0471	0.2933
chr4	191154276	7573427	0.0396	0.3677
chr5	180915260	6614402	0.0366	0.2743
chr6	171115067	7407772	0.0433	0.3102
chr7	159138663	13497232	0.0848	1.2852

chr8	146364022	13099930	0.0895	0.5045
chr9	141213431	5497379	0.0389	0.4772
chr10	135534747	7041957	0.052	0.8543
chr11	135006516	6534342	0.0484	0.3657
chr12	133851895	5982420	0.0447	0.2916
chr13	115169878	4612198	0.04	0.2689
chr14	107349540	4466292	0.0416	0.2983
chr15	102531392	4182695	0.0408	0.2792
chr16	90354753	3859786	0.0427	0.6108
chr17	81195210	3799531	0.0468	0.3845
chr18	78077248	2906000	0.0372	0.5709
chr19	59128983	2638207	0.0446	0.8038
chr20	63025520	6298185	0.0999	0.4594
chr21	48129895	1423018	0.0296	0.2924
chr22	51304566	1372909	0.0268	0.2384
chrMT	16571	238077	14.3671	9.5692
chrX	155270560	6121814	0.0394	0.3159
chrY	59373566	594600	0.01	0.7803

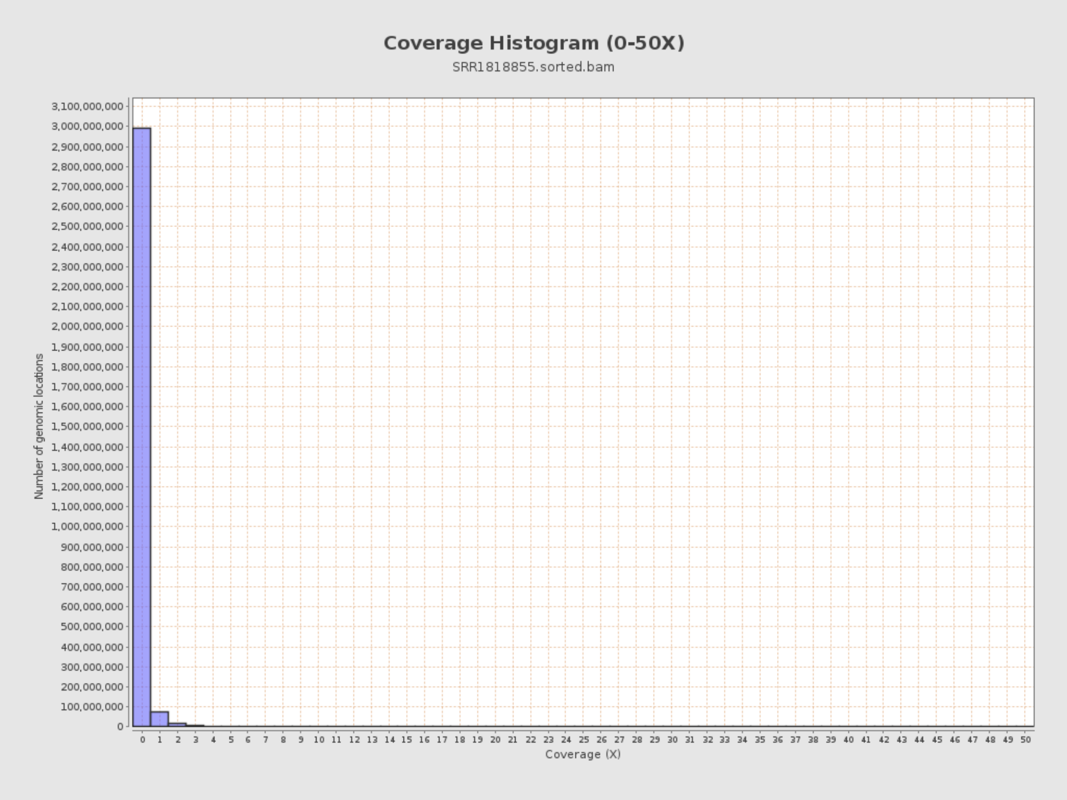
3. Results : Coverage across reference



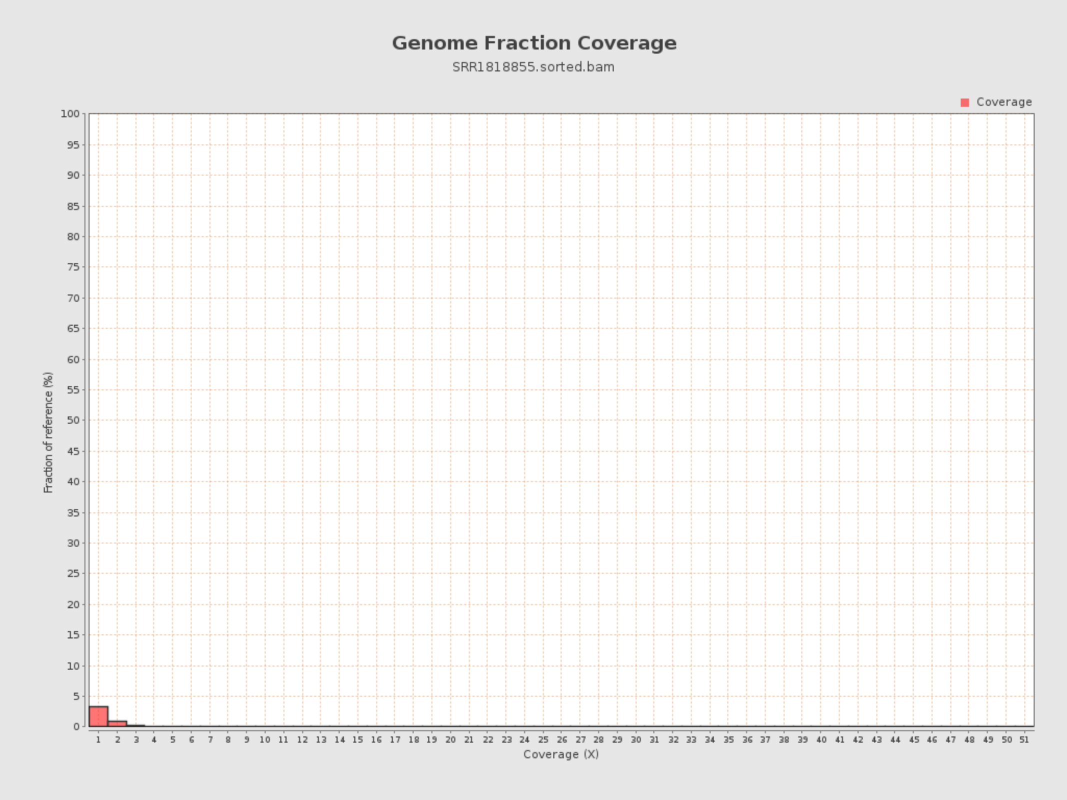
4. Results : Coverage Histogram



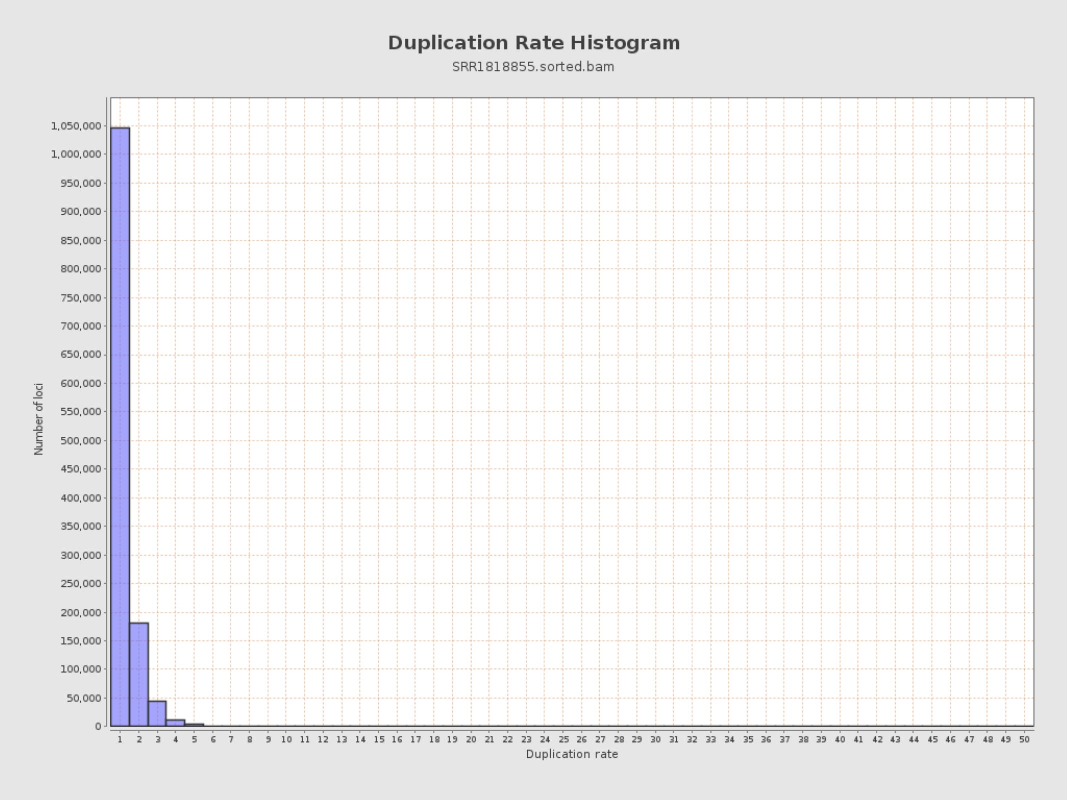
5. Results : Coverage Histogram (0-50X)



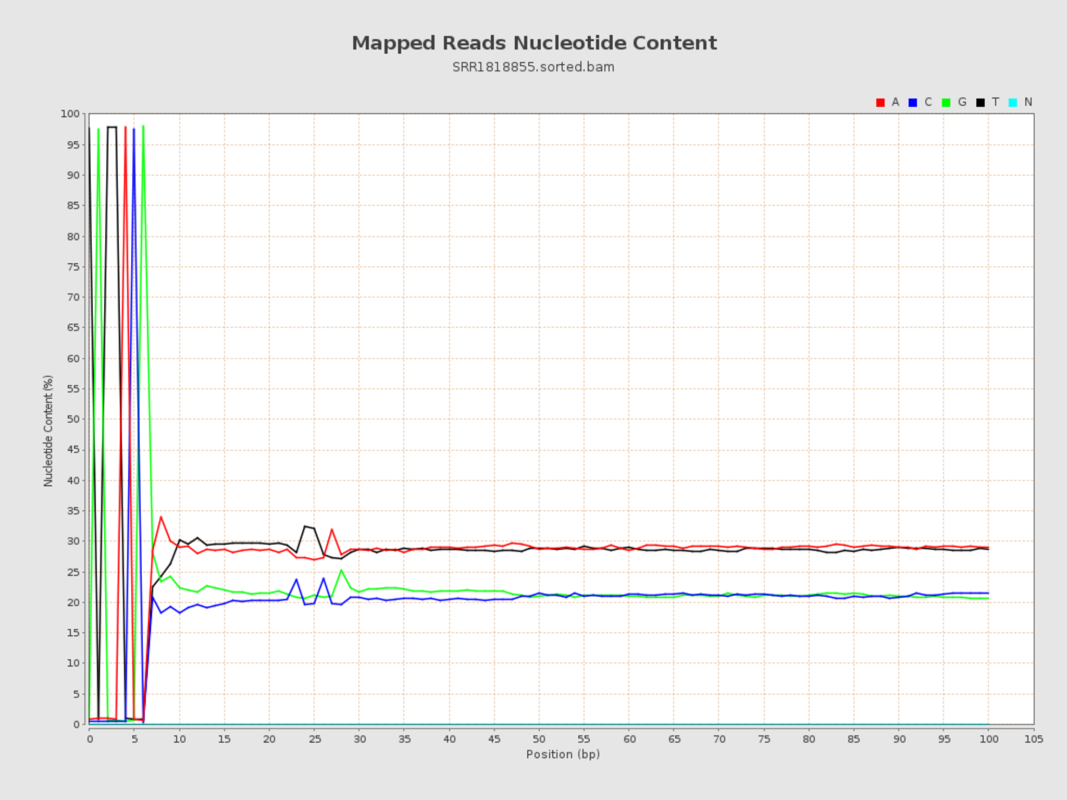
6. Results : Genome Fraction Coverage



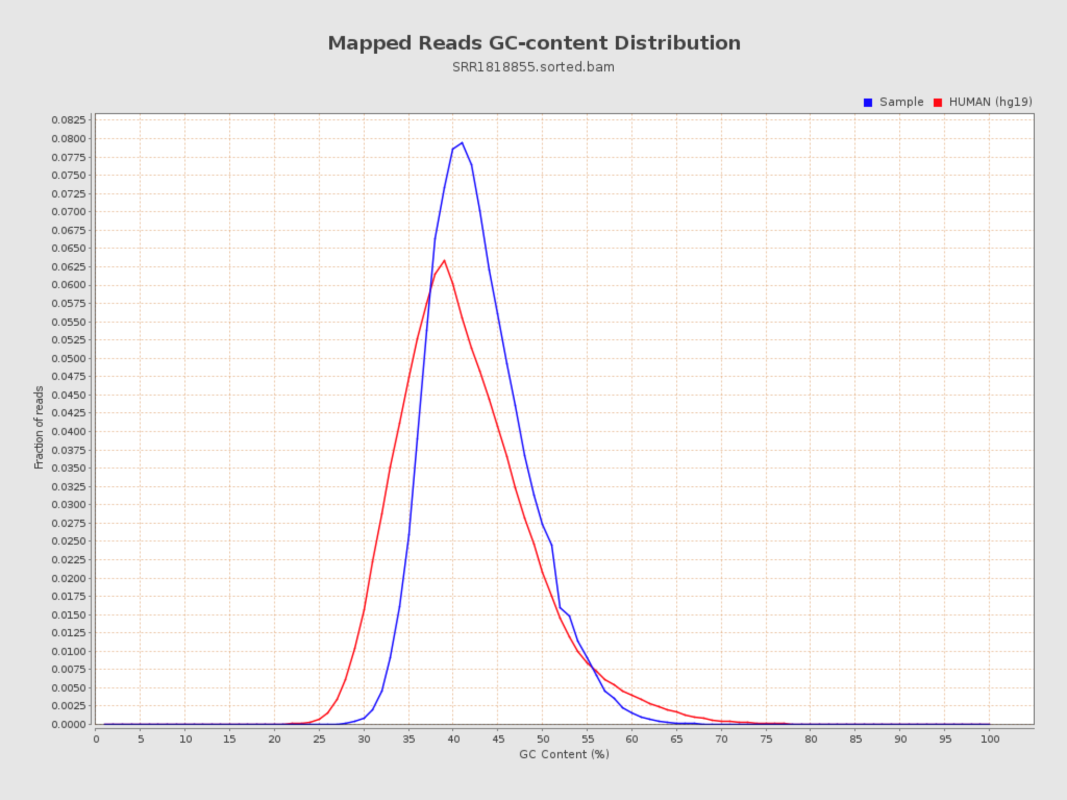
7. Results : Duplication Rate Histogram



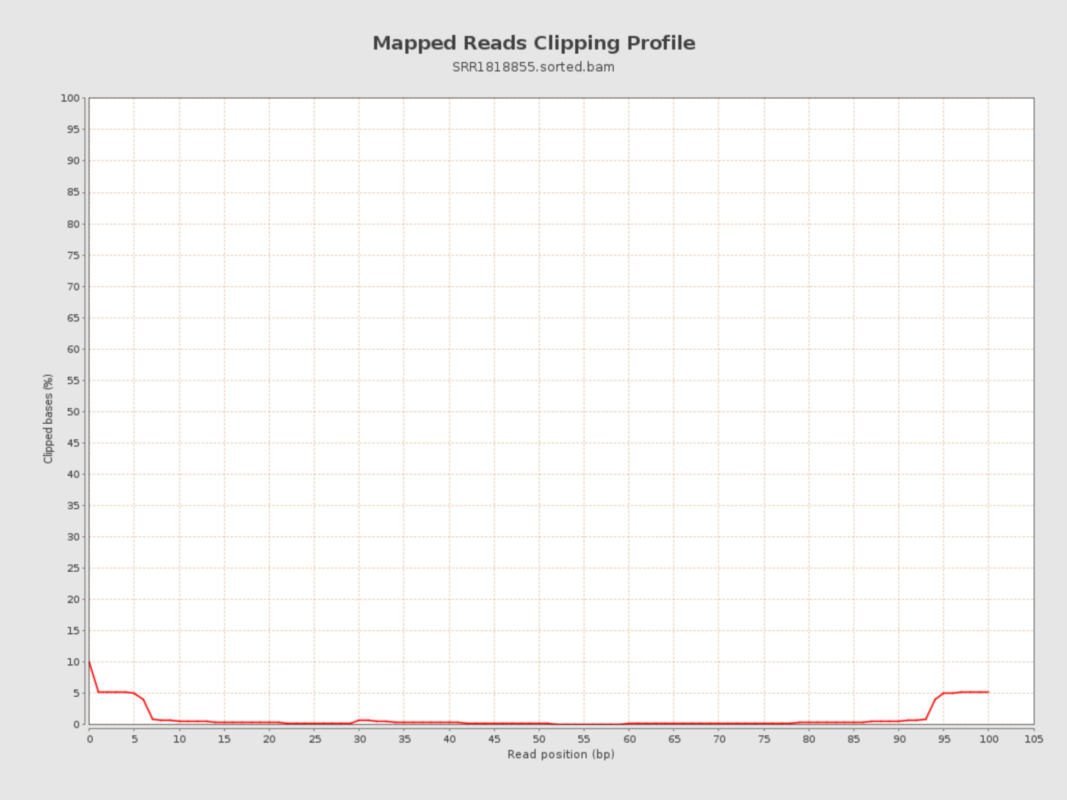
8. Results : Mapped Reads Nucleotide Content



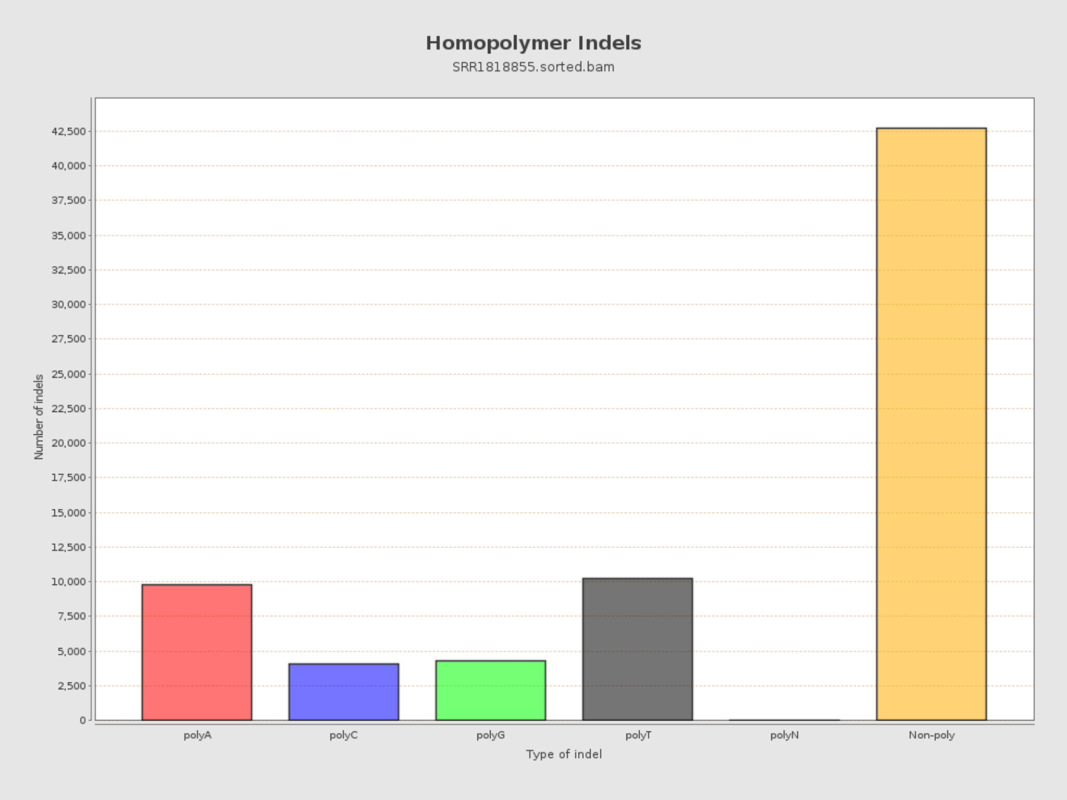
9. Results : Mapped Reads GC-content Distribution



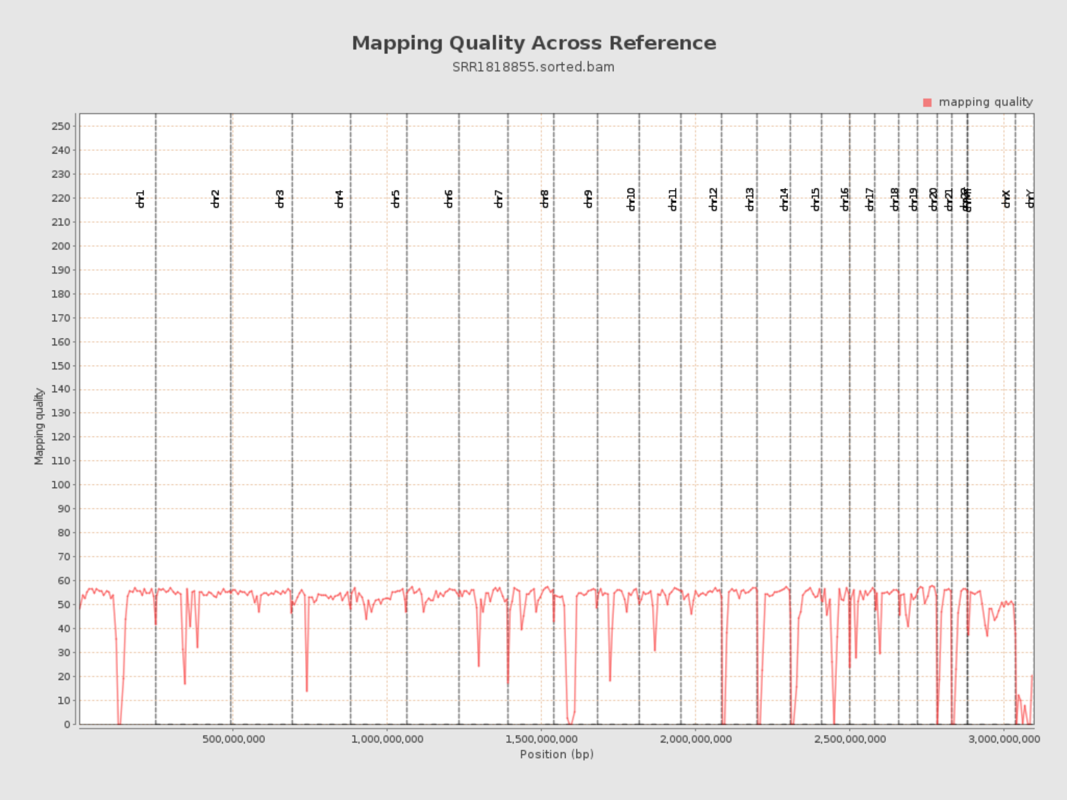
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram