Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:04:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818841.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_SRR1818841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:04:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,495,181
Mapped reads	2,431,855 / 97.46%
Unmapped reads	63,326 / 2.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,723 / 1.43%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	623,494 / 24.99%
Duplication rate	22.05%
Clipped reads	2,443,907 / 97.95%

2.2. ACGT Content

Number/percentage of A's	64,202,658 / 28.49%
Number/percentage of C's	47,067,181 / 20.88%
Number/percentage of T's	65,455,857 / 29.04%
Number/percentage of G's	48,636,033 / 21.58%
Number/percentage of N's	3,116 / 0%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0728

Standard Deviation	0.8077

2.4. Mapping Quality

Mean Mapping Quality	49.35

2.5. Mismatches and indels

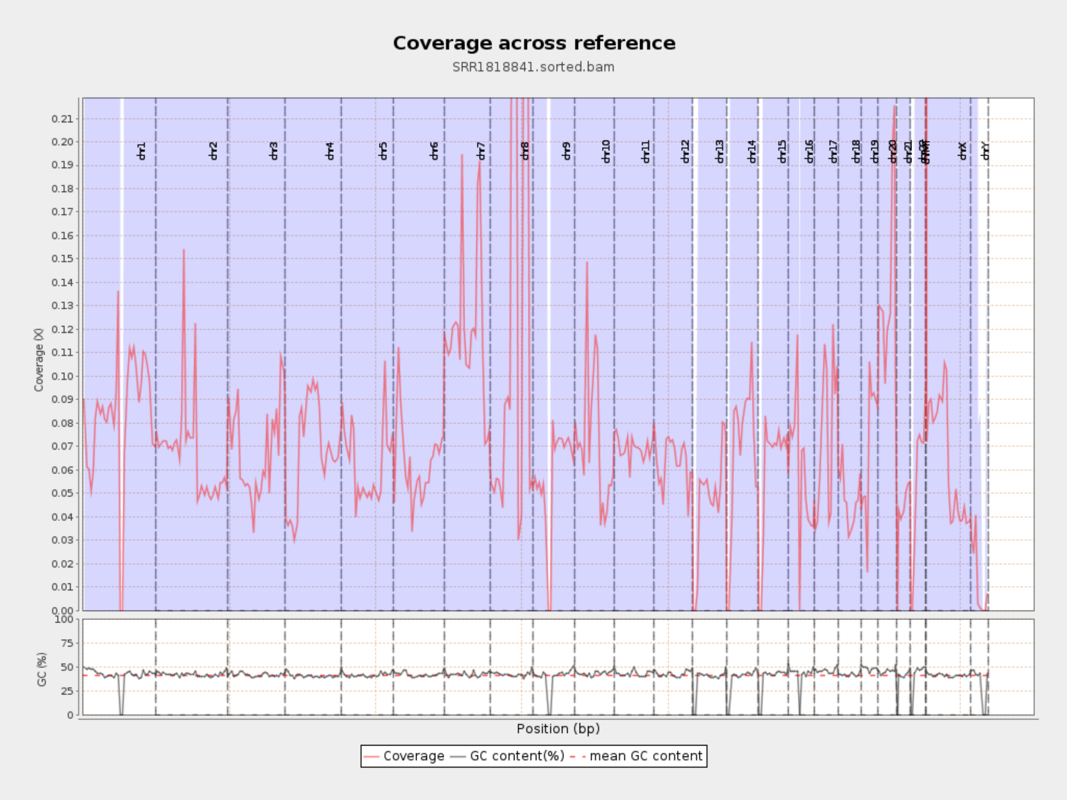
General error rate	0.62%
Mismatches	1,323,063
Insertions	31,319
Mapped reads with at least one insertion	1.24%
Deletions	71,424
Mapped reads with at least one deletion	2.87%
Homopolymer indels	40.96%

2.6. Chromosome stats

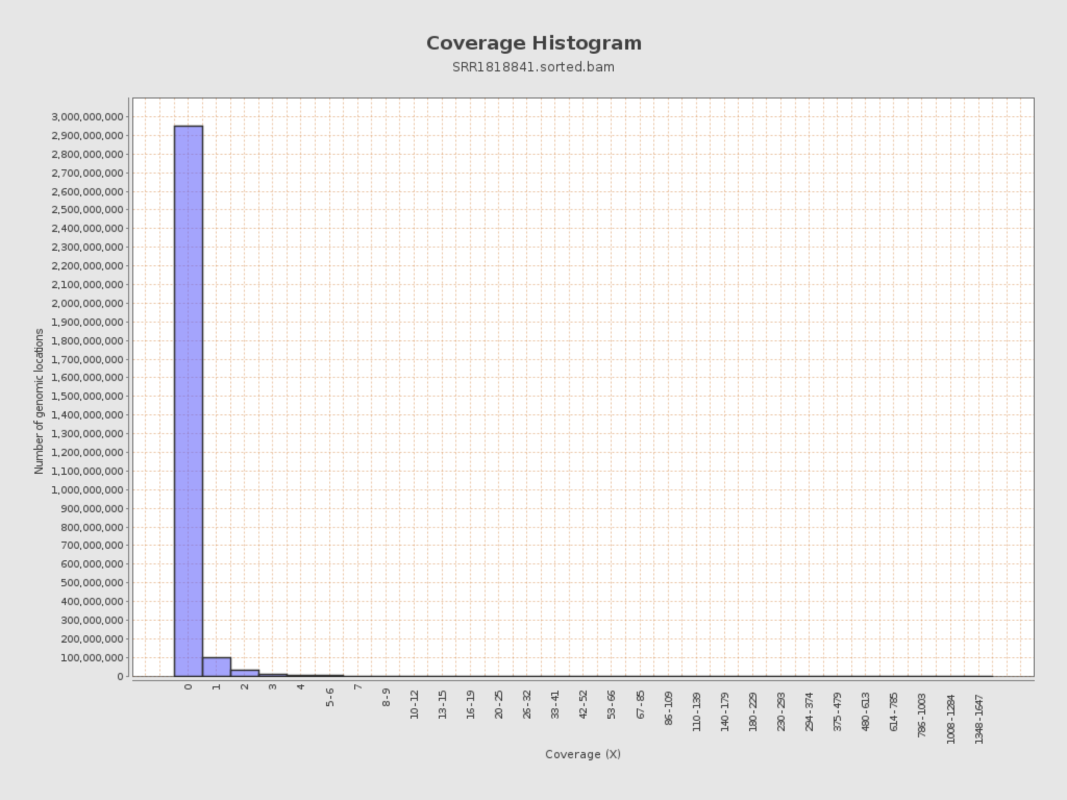
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20723775	0.0831	1.2577
chr2	243199373	16367691	0.0673	1.1463
chr3	198022430	13503873	0.0682	0.3719
chr4	191154276	13118495	0.0686	0.4567
chr5	180915260	11448962	0.0633	0.3836
chr6	171115067	10836758	0.0633	0.4065
chr7	159138663	19014050	0.1195	1.7185

chr8	146364022	21745249	0.1486	0.7243
chr9	141213431	8071220	0.0572	0.6905
chr10	135534747	9830418	0.0725	0.961
chr11	135006516	9340809	0.0692	0.4879
chr12	133851895	8524721	0.0637	0.3641
chr13	115169878	5384110	0.0467	0.3021
chr14	107349540	7423370	0.0692	0.4296
chr15	102531392	6075231	0.0593	0.3626
chr16	90354753	5290501	0.0586	0.8341
chr17	81195210	5958708	0.0734	0.5212
chr18	78077248	3733714	0.0478	0.7617
chr19	59128983	4119783	0.0697	1.1078
chr20	63025520	8892859	0.1411	0.5874
chr21	48129895	2046224	0.0425	0.342
chr22	51304566	2636374	0.0514	0.3714
chrMT	16571	596082	35.9714	21.4311
chrX	155270560	10066483	0.0648	0.4575
chrY	59373566	750680	0.0126	0.9186

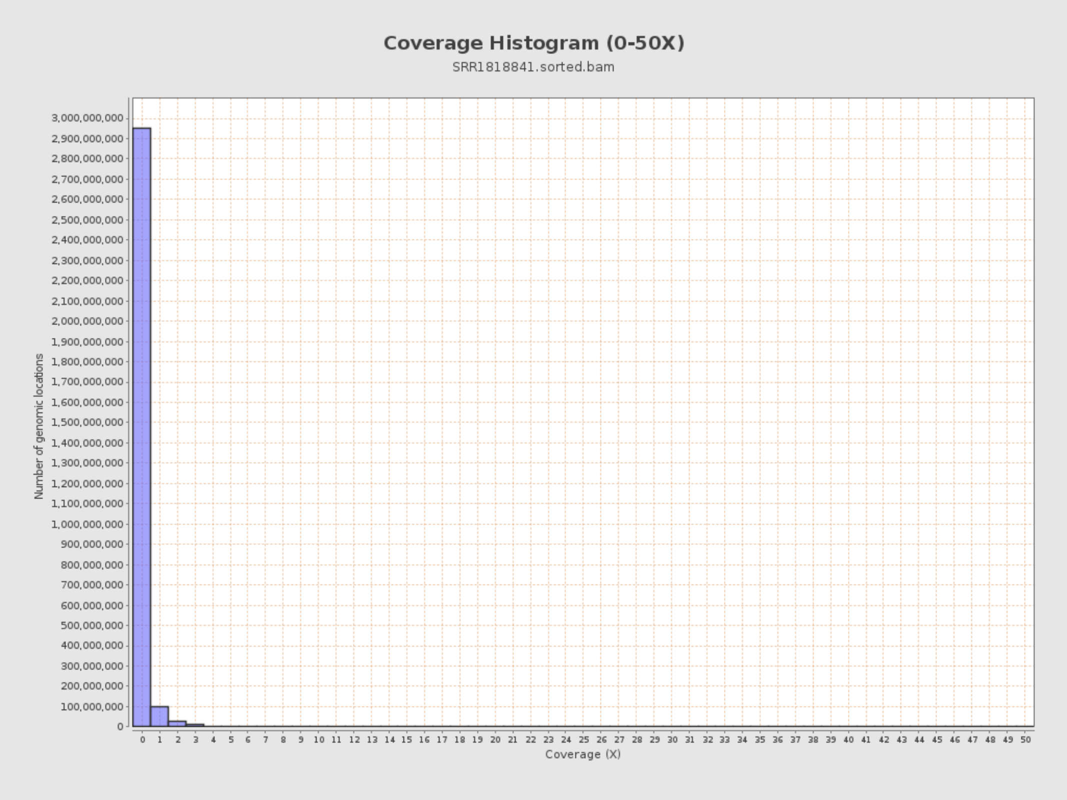
3. Results : Coverage across reference



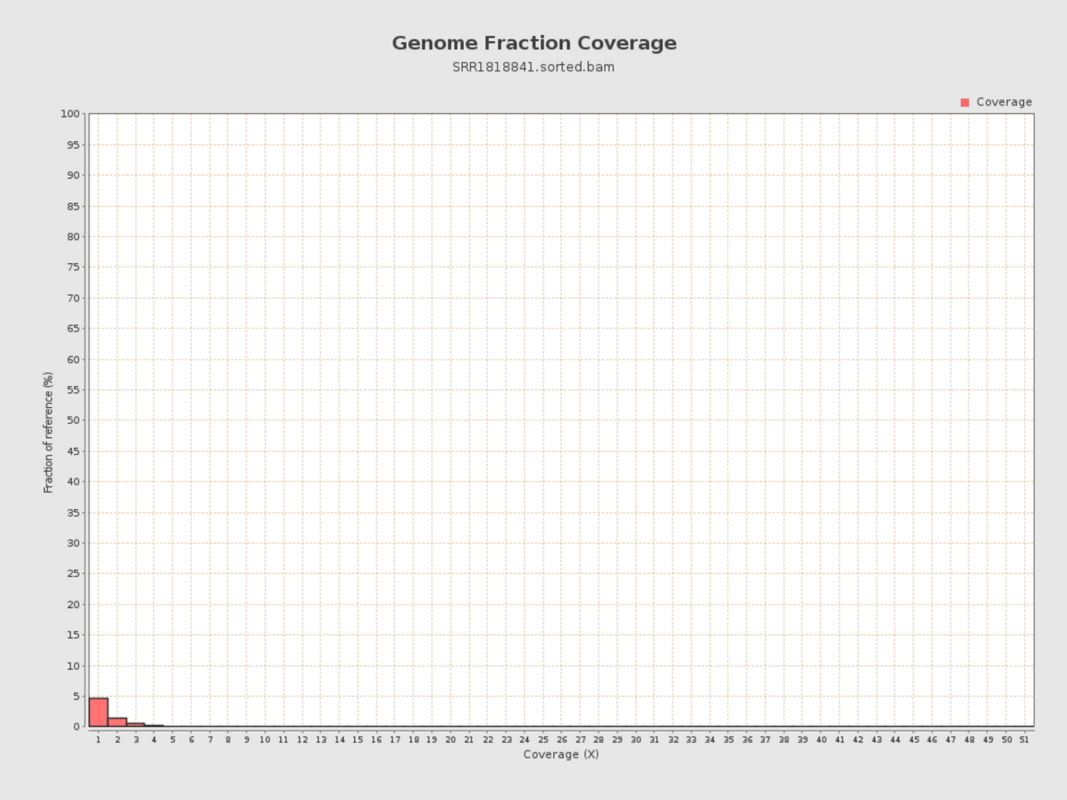
4. Results : Coverage Histogram



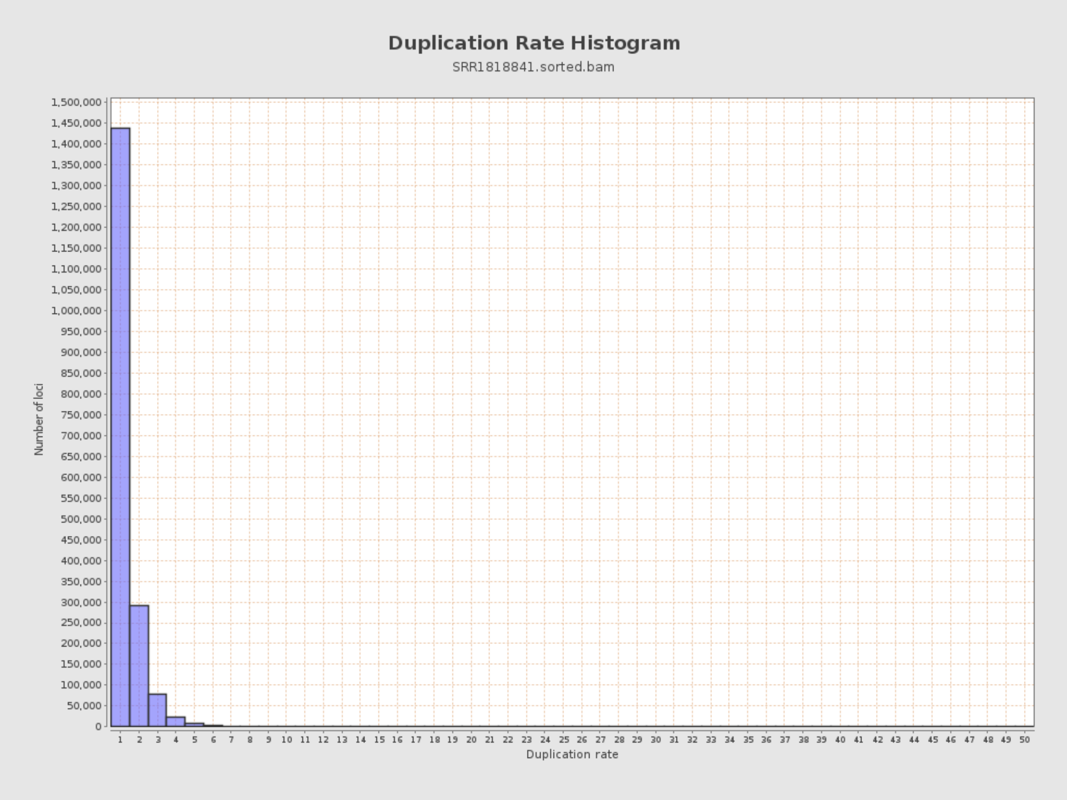
5. Results : Coverage Histogram (0-50X)



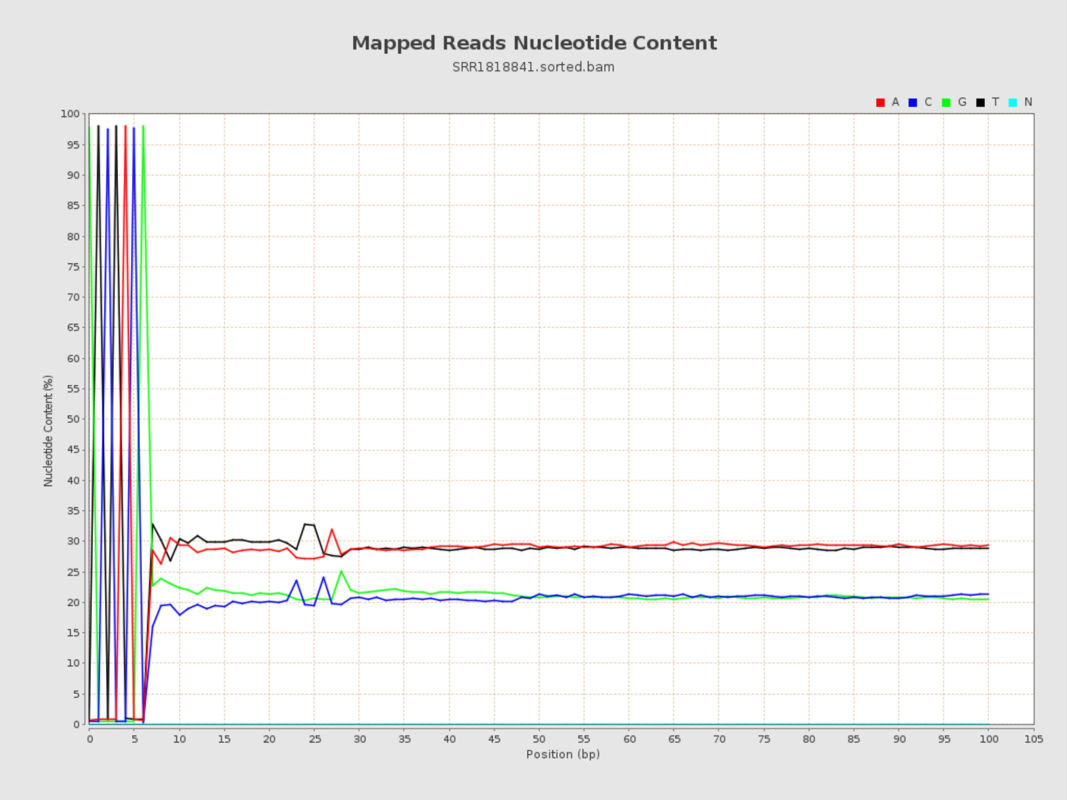
6. Results : Genome Fraction Coverage



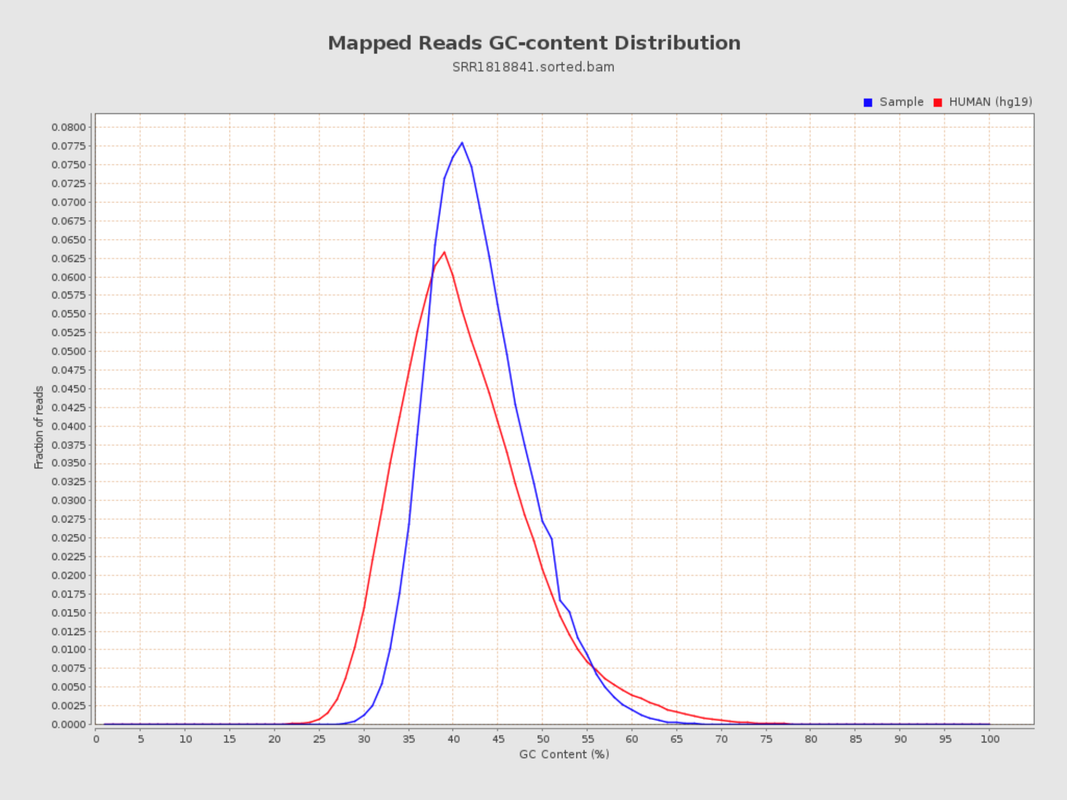
7. Results : Duplication Rate Histogram



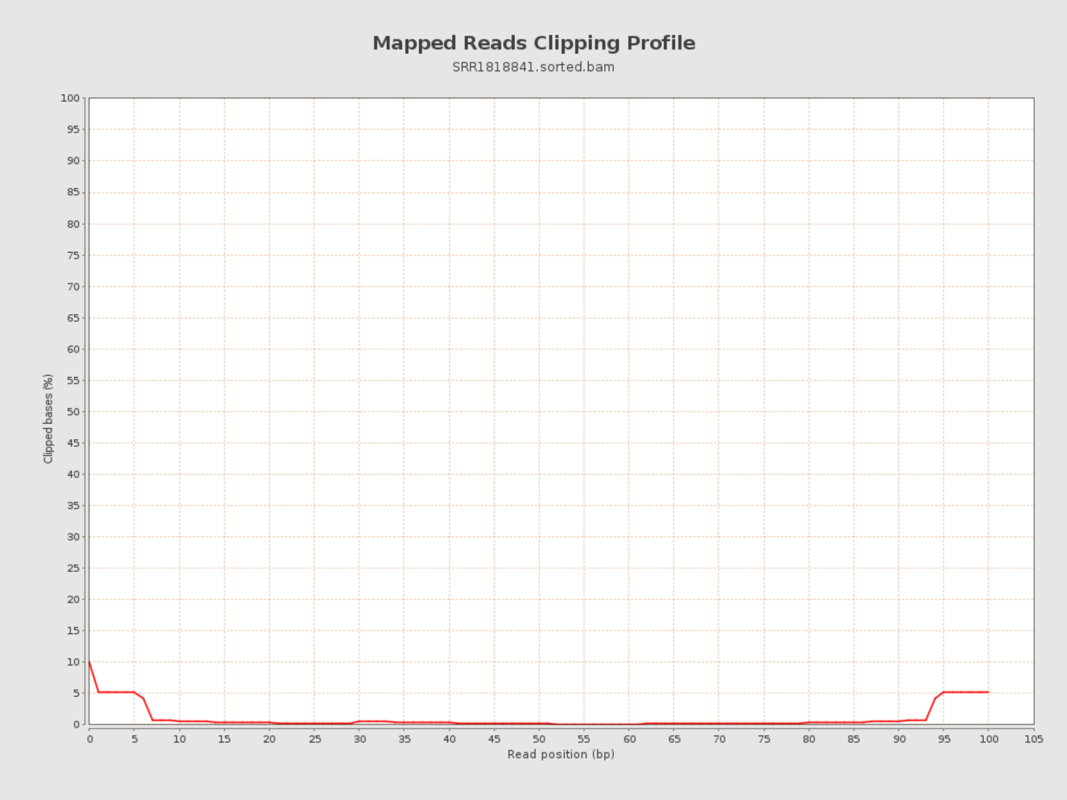
8. Results : Mapped Reads Nucleotide Content



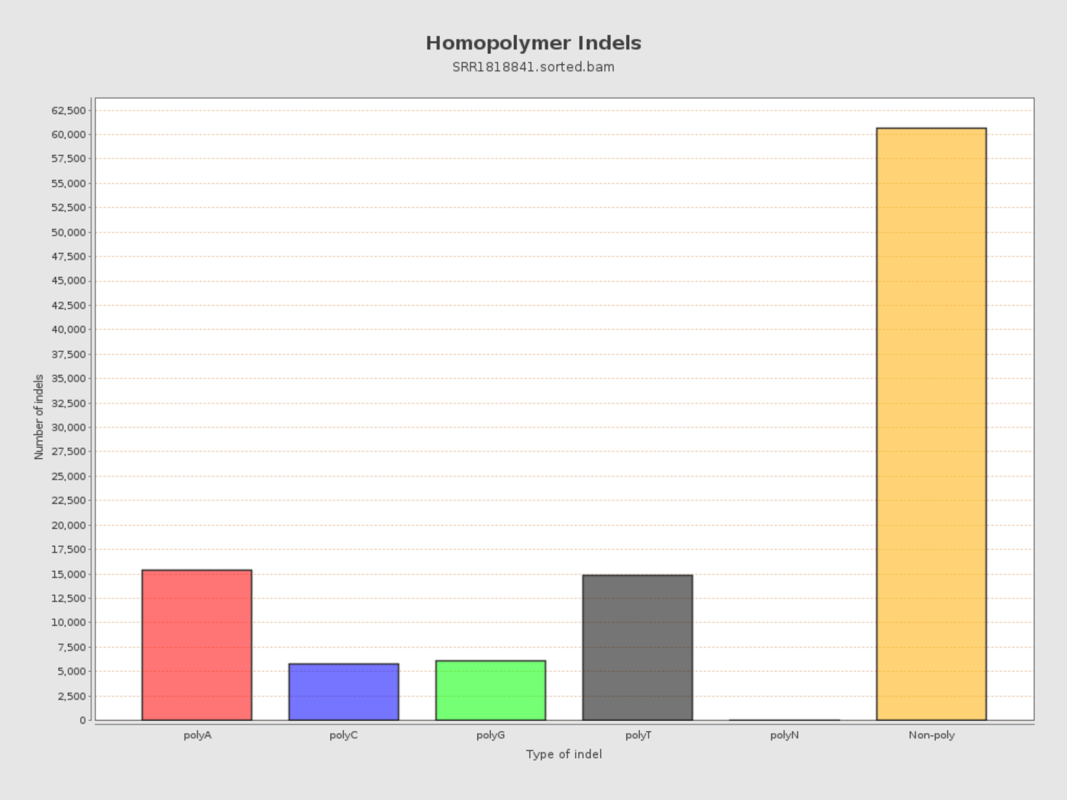
9. Results : Mapped Reads GC-content Distribution



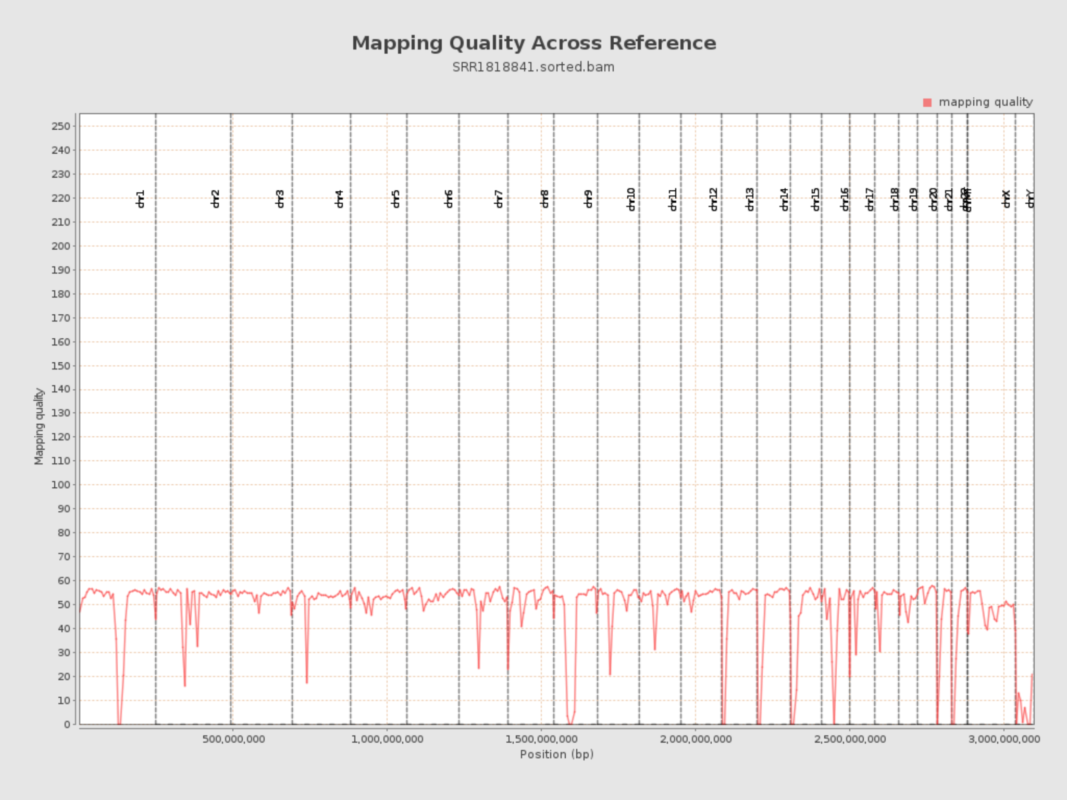
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram