Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:23:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818838.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_SRR1818838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818838.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:23:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,843,625
Mapped reads	1,819,344 / 98.68%
Unmapped reads	24,281 / 1.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,063 / 1.68%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	526,655 / 28.57%
Duplication rate	25.06%
Clipped reads	1,844,278 / 100.04%

2.2. ACGT Content

Number/percentage of A's	48,279,255 / 28.71%
Number/percentage of C's	36,226,223 / 21.54%
Number/percentage of T's	47,452,784 / 28.22%
Number/percentage of G's	36,209,869 / 21.53%
Number/percentage of N's	2,349 / 0%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.6207

2.4. Mapping Quality

Mean Mapping Quality	49.57

2.5. Mismatches and indels

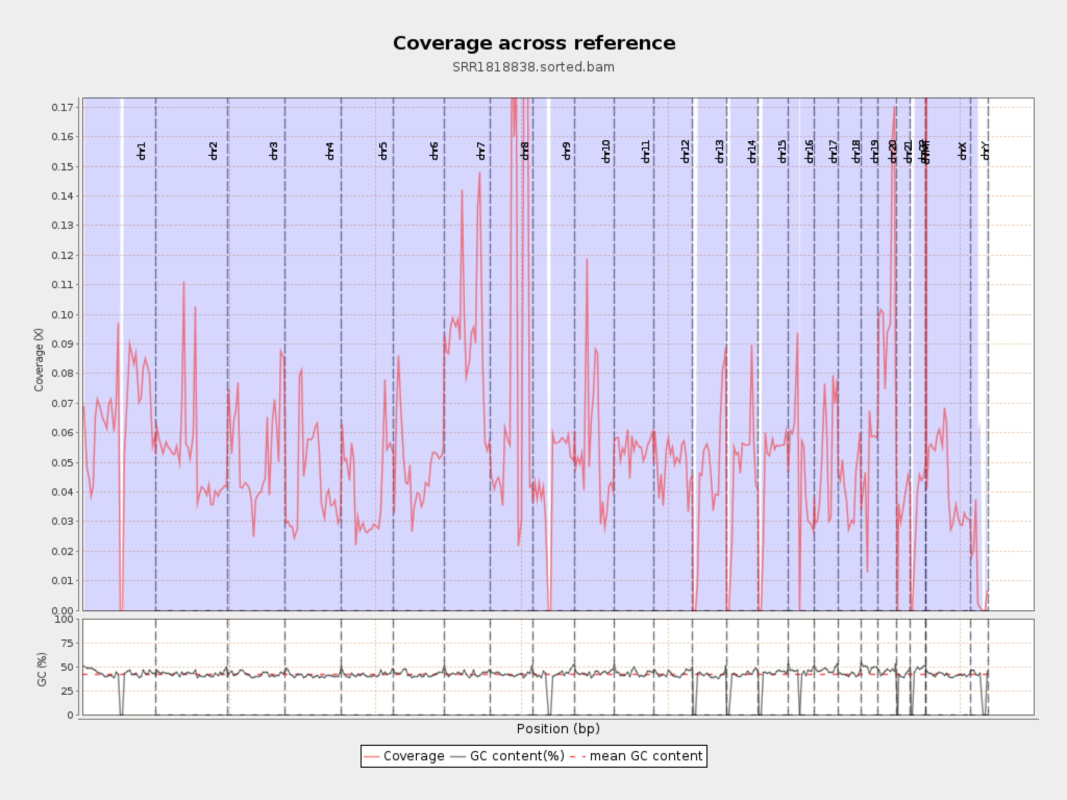
General error rate	0.63%
Mismatches	1,005,400
Insertions	20,928
Mapped reads with at least one insertion	1.11%
Deletions	55,631
Mapped reads with at least one deletion	2.99%
Homopolymer indels	41.71%

2.6. Chromosome stats

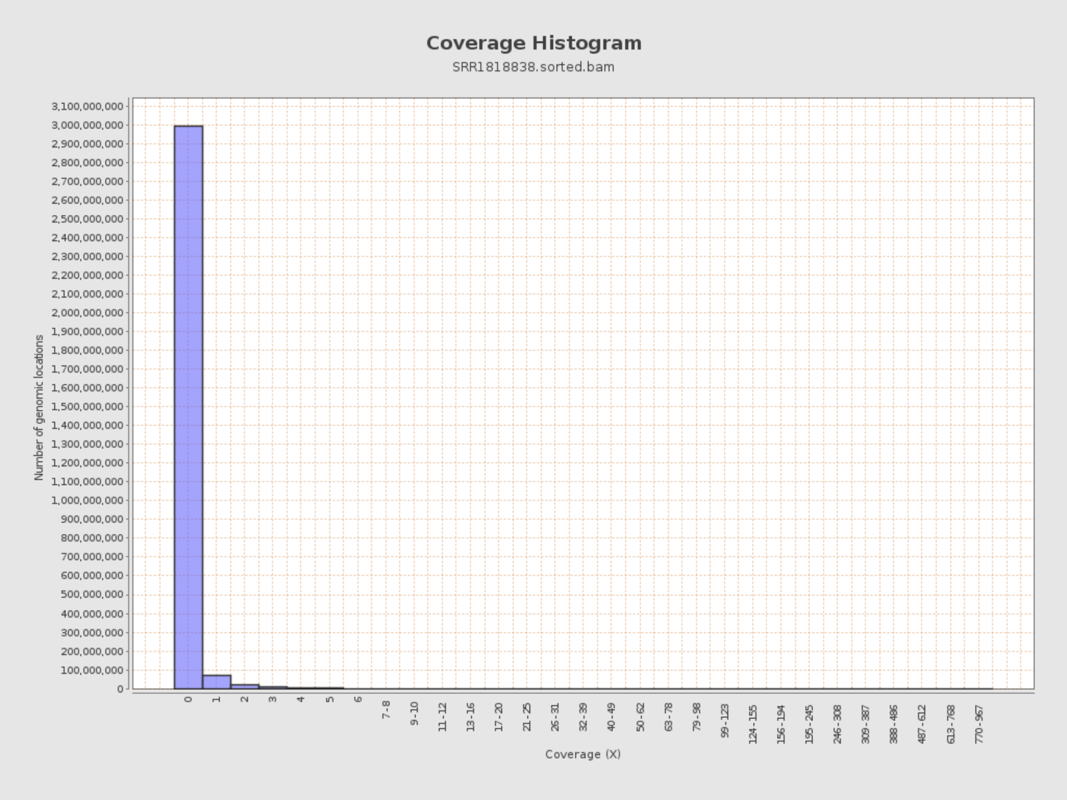
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16085037	0.0645	0.8764
chr2	243199373	12688378	0.0522	0.964
chr3	198022430	10660525	0.0538	0.3378
chr4	191154276	8401206	0.0439	0.4017
chr5	180915260	7500474	0.0415	0.3155
chr6	171115067	8247468	0.0482	0.3516
chr7	159138663	14918667	0.0937	1.2418

chr8	146364022	14802006	0.1011	0.5585
chr9	141213431	6279006	0.0445	0.5352
chr10	135534747	7383985	0.0545	0.7798
chr11	135006516	7449575	0.0552	0.4068
chr12	133851895	6647374	0.0497	0.3268
chr13	115169878	5243884	0.0455	0.3125
chr14	107349540	5025966	0.0468	0.3387
chr15	102531392	4683347	0.0457	0.3127
chr16	90354753	4223589	0.0467	0.6896
chr17	81195210	4125035	0.0508	0.3953
chr18	78077248	3252376	0.0417	0.5565
chr19	59128983	2895157	0.049	0.7028
chr20	63025520	6996923	0.111	0.5245
chr21	48129895	1668016	0.0347	0.3264
chr22	51304566	1578556	0.0308	0.2996
chrMT	16571	78053	4.7102	4.114
chrX	155270560	6826622	0.044	0.3508
chrY	59373566	618707	0.0104	0.837

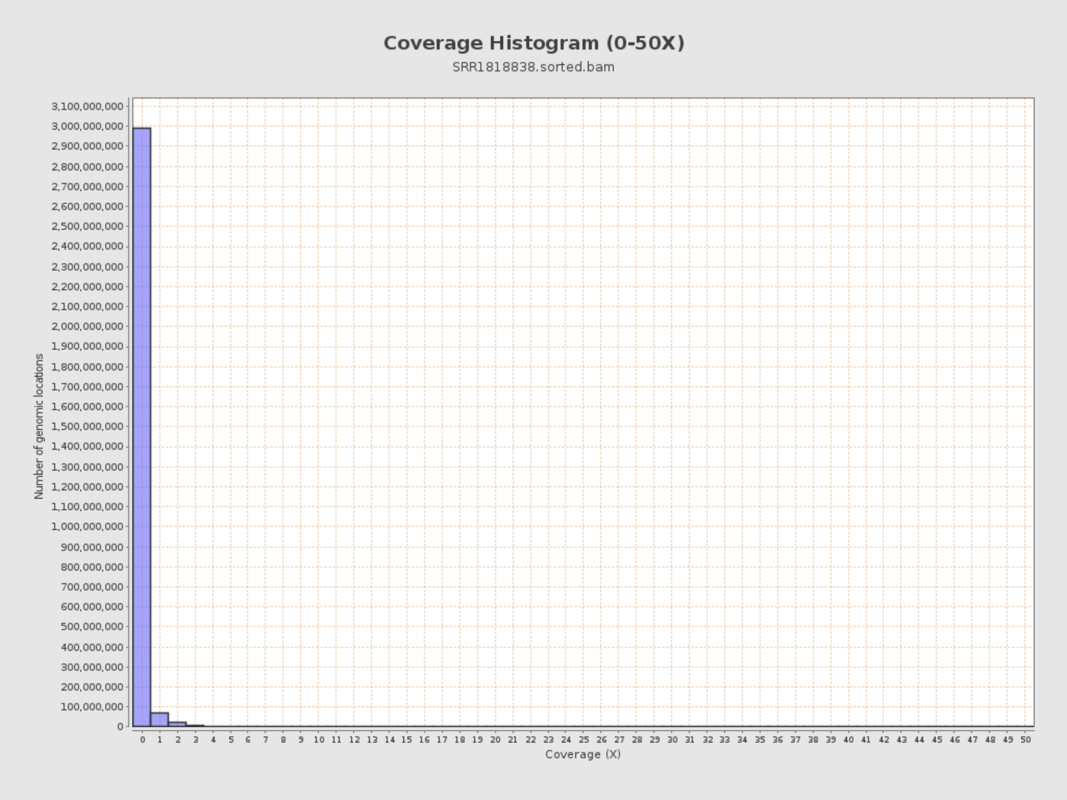
3. Results : Coverage across reference



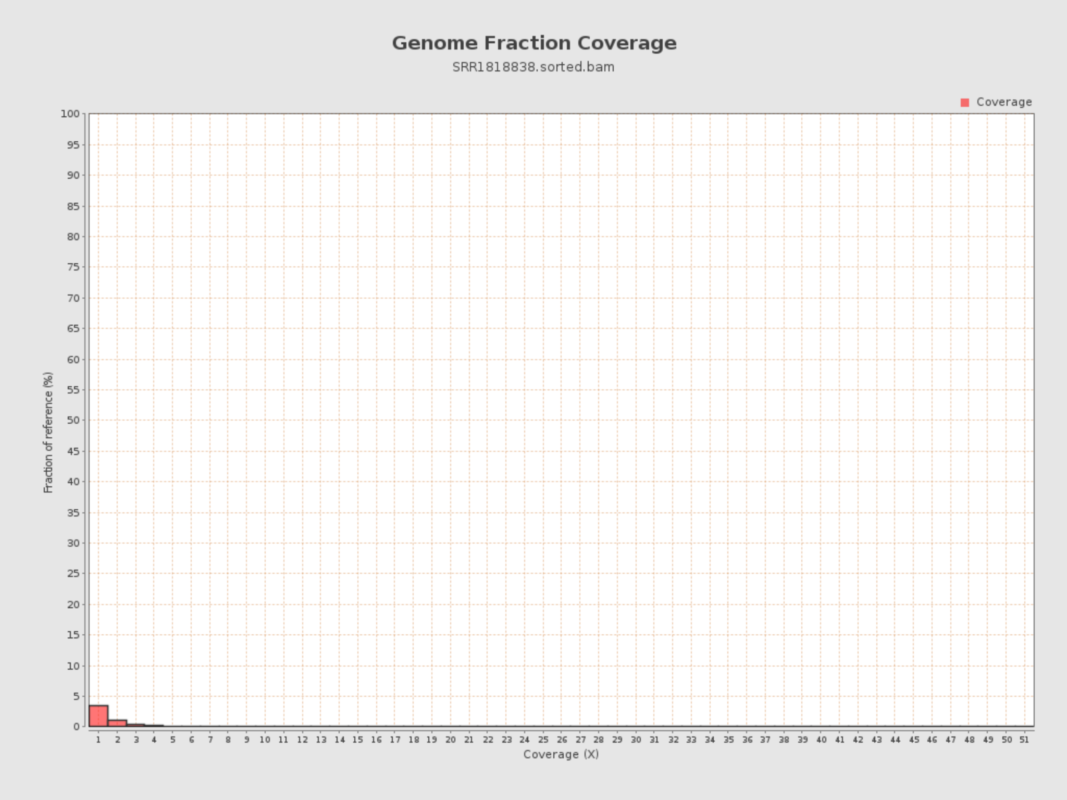
4. Results : Coverage Histogram



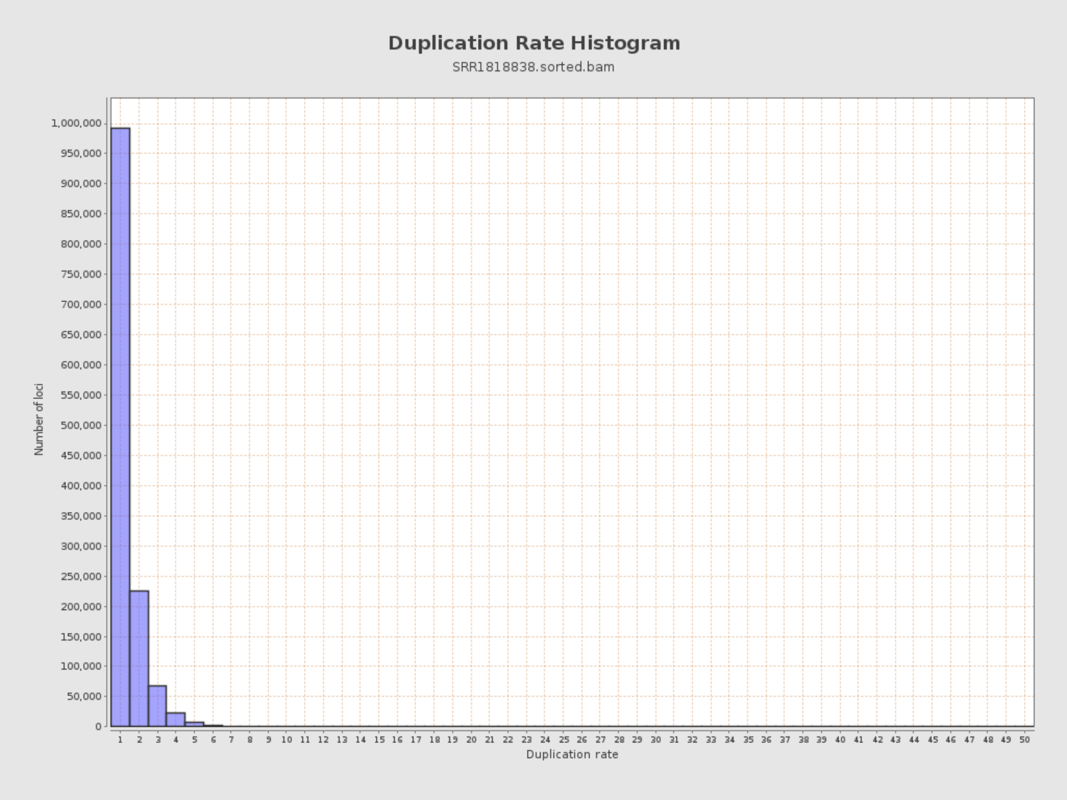
5. Results : Coverage Histogram (0-50X)



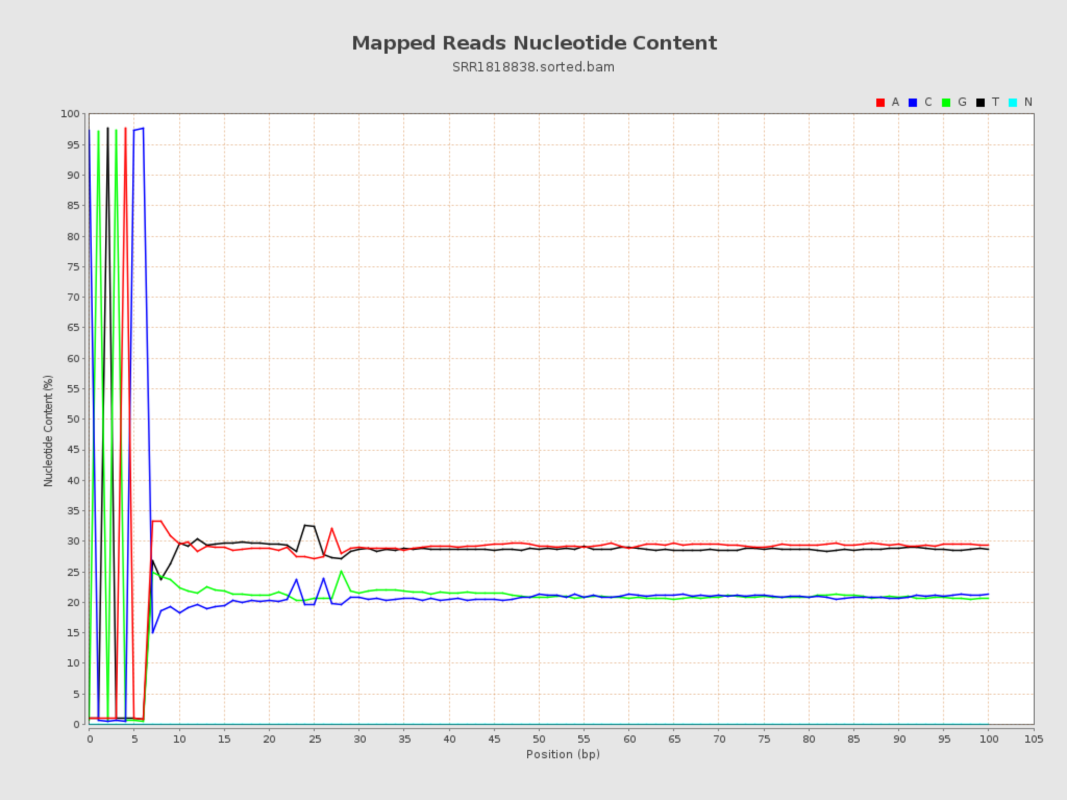
6. Results : Genome Fraction Coverage



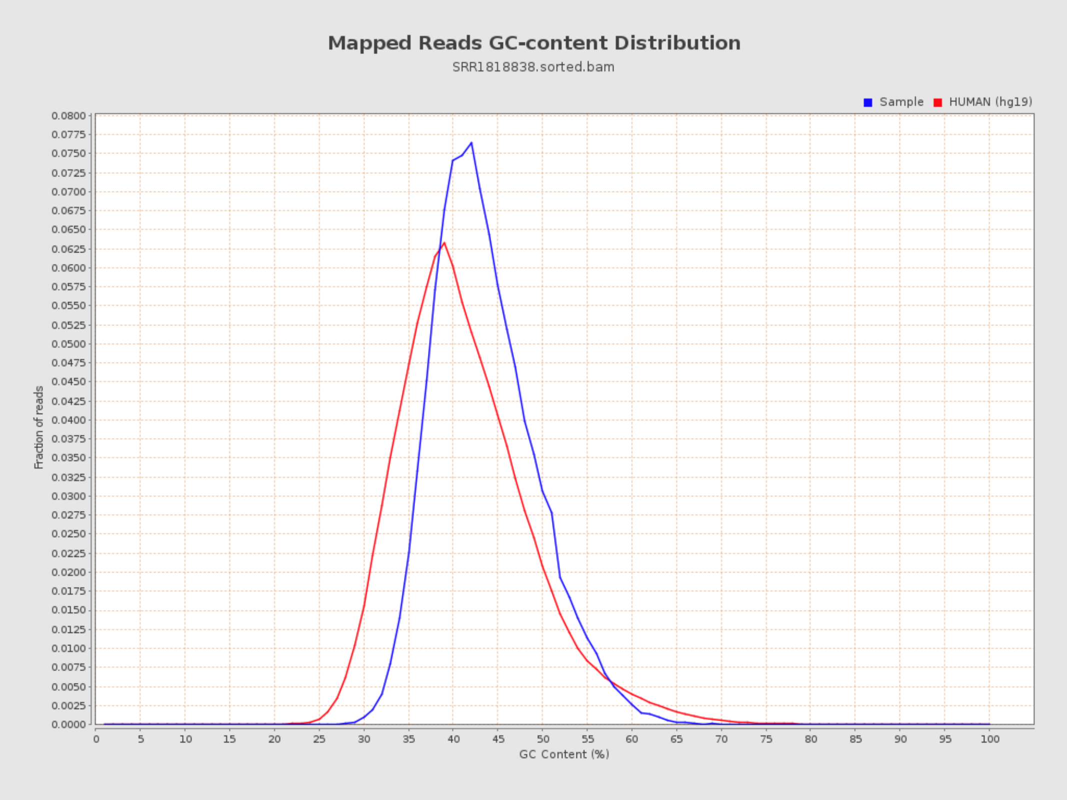
7. Results : Duplication Rate Histogram



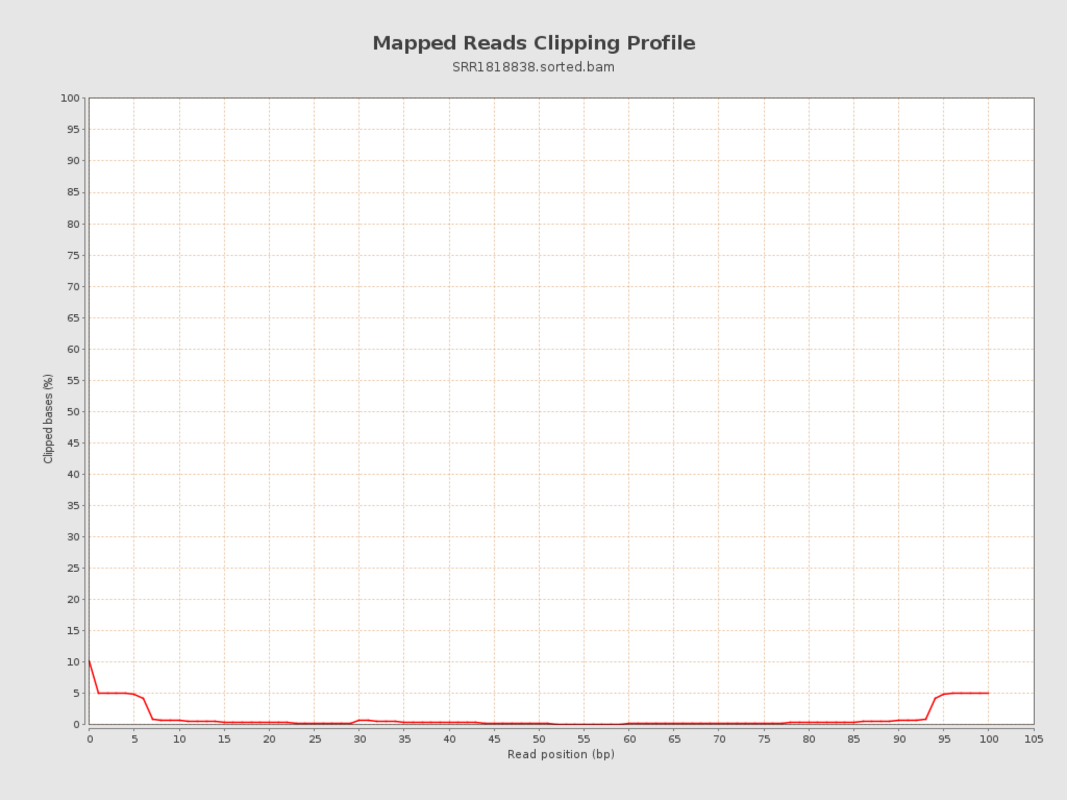
8. Results : Mapped Reads Nucleotide Content



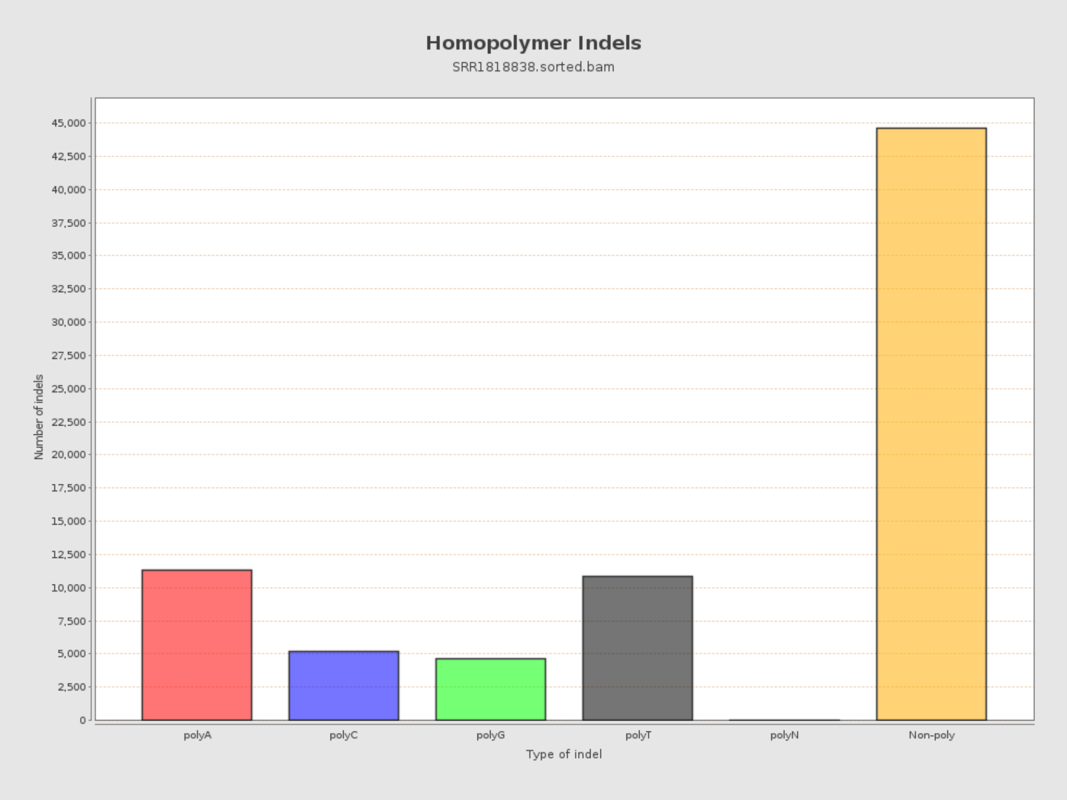
9. Results : Mapped Reads GC-content Distribution



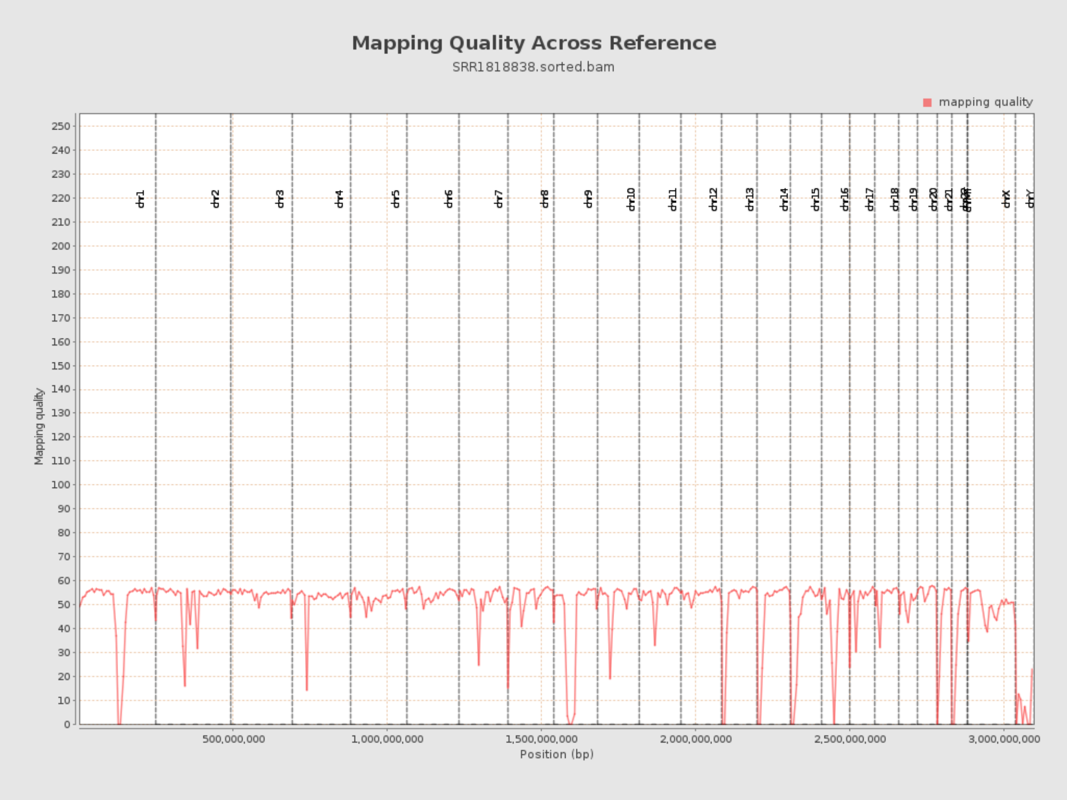
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram