Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:36:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818839.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_SRR1818839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818839.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:36:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,290,976
Mapped reads	1,992,789 / 86.98%
Unmapped reads	298,187 / 13.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,292 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	533,992 / 23.31%
Duplication rate	23.24%
Clipped reads	2,006,523 / 87.58%

2.2. ACGT Content

Number/percentage of A's	52,736,286 / 28.59%
Number/percentage of C's	37,186,689 / 20.16%
Number/percentage of T's	55,096,837 / 29.87%
Number/percentage of G's	39,414,664 / 21.37%
Number/percentage of N's	2,817 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.662

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

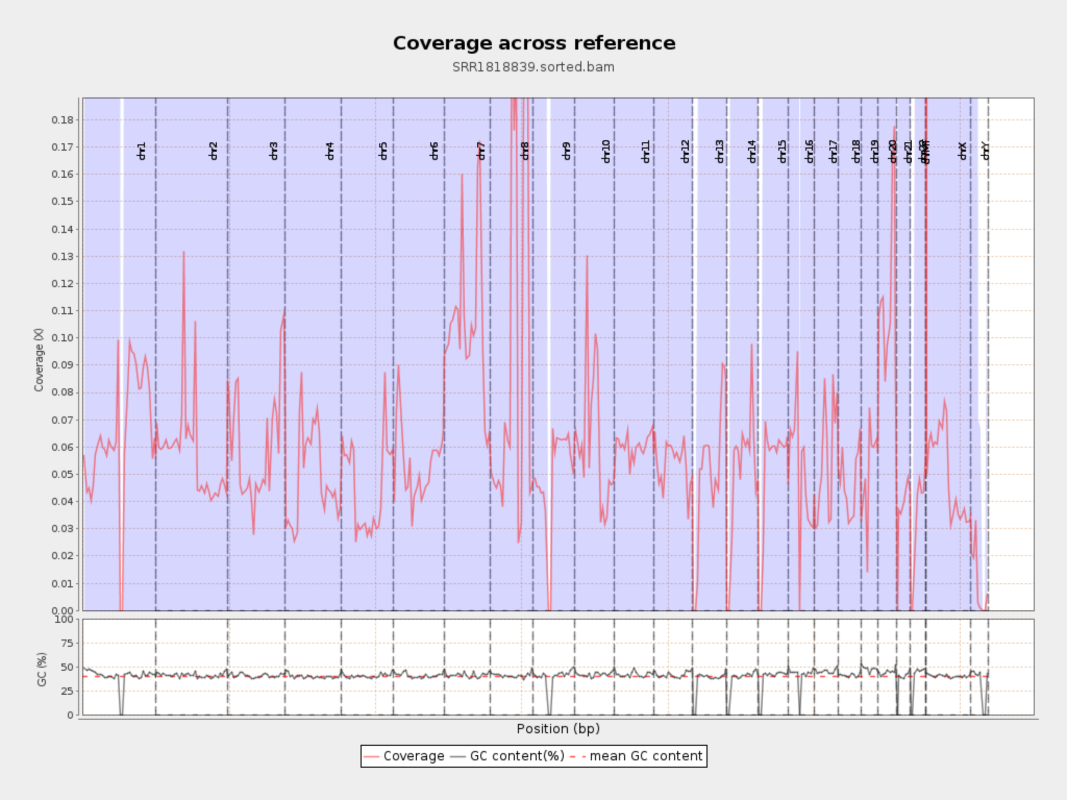
General error rate	0.64%
Mismatches	1,109,086
Insertions	25,718
Mapped reads with at least one insertion	1.25%
Deletions	60,436
Mapped reads with at least one deletion	2.96%
Homopolymer indels	41.58%

2.6. Chromosome stats

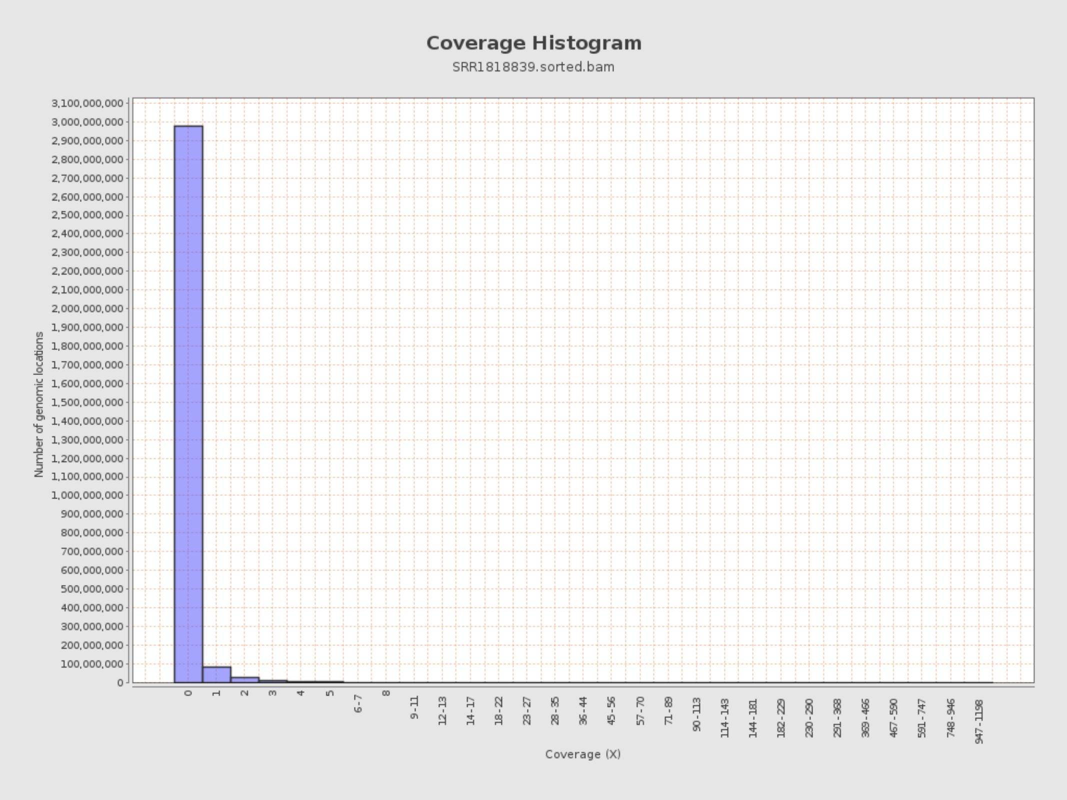
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16219747	0.0651	0.9515
chr2	243199373	14166307	0.0582	1.0169
chr3	198022430	12041396	0.0608	0.3521
chr4	191154276	9413864	0.0492	0.3859
chr5	180915260	8243671	0.0456	0.3193
chr6	171115067	9197723	0.0538	0.3721
chr7	159138663	16725433	0.1051	1.3565

chr8	146364022	16444214	0.1124	0.6155
chr9	141213431	6874575	0.0487	0.5997
chr10	135534747	8408325	0.062	0.8533
chr11	135006516	8141572	0.0603	0.4274
chr12	133851895	7244369	0.0541	0.3414
chr13	115169878	5781871	0.0502	0.3169
chr14	107349540	5492561	0.0512	0.358
chr15	102531392	5107220	0.0498	0.3128
chr16	90354753	4473836	0.0495	0.6662
chr17	81195210	4400928	0.0542	0.423
chr18	78077248	3657102	0.0468	0.6669
chr19	59128983	3015964	0.051	0.7521
chr20	63025520	7520529	0.1193	0.5225
chr21	48129895	1808986	0.0376	0.3039
chr22	51304566	1619069	0.0316	0.2936
chrMT	16571	201697	12.1717	8.7404
chrX	155270560	7756437	0.05	0.3747
chrY	59373566	593297	0.01	0.7694

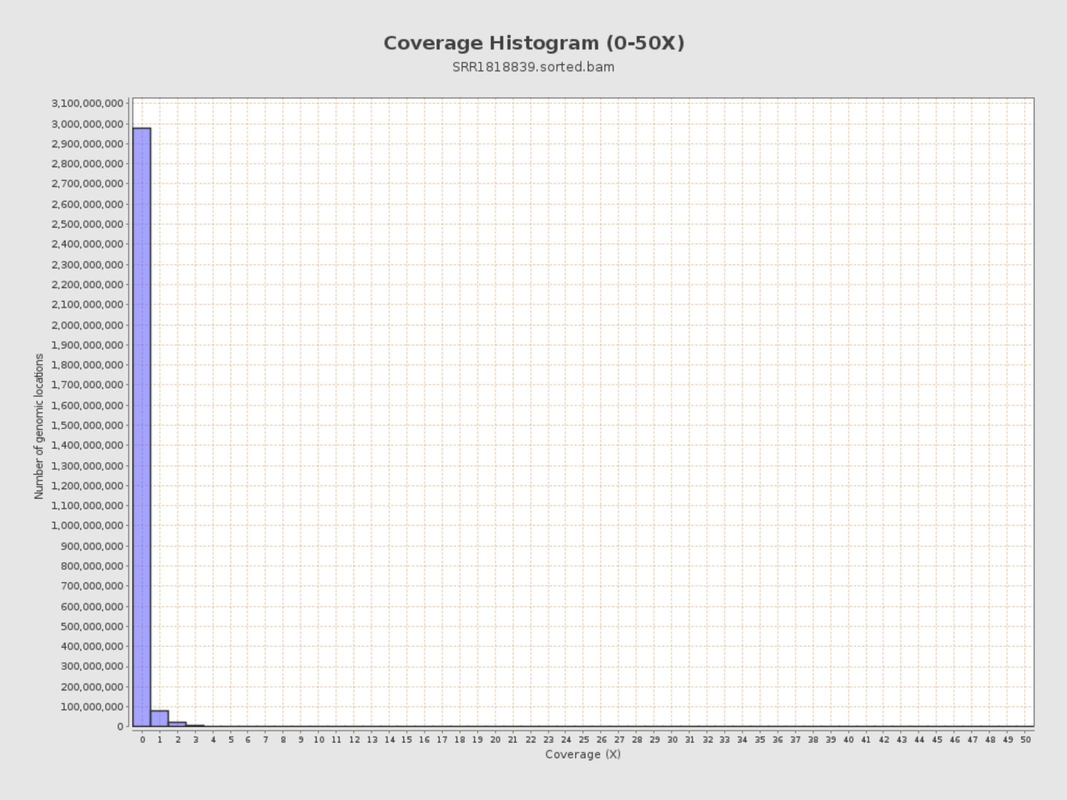
3. Results : Coverage across reference



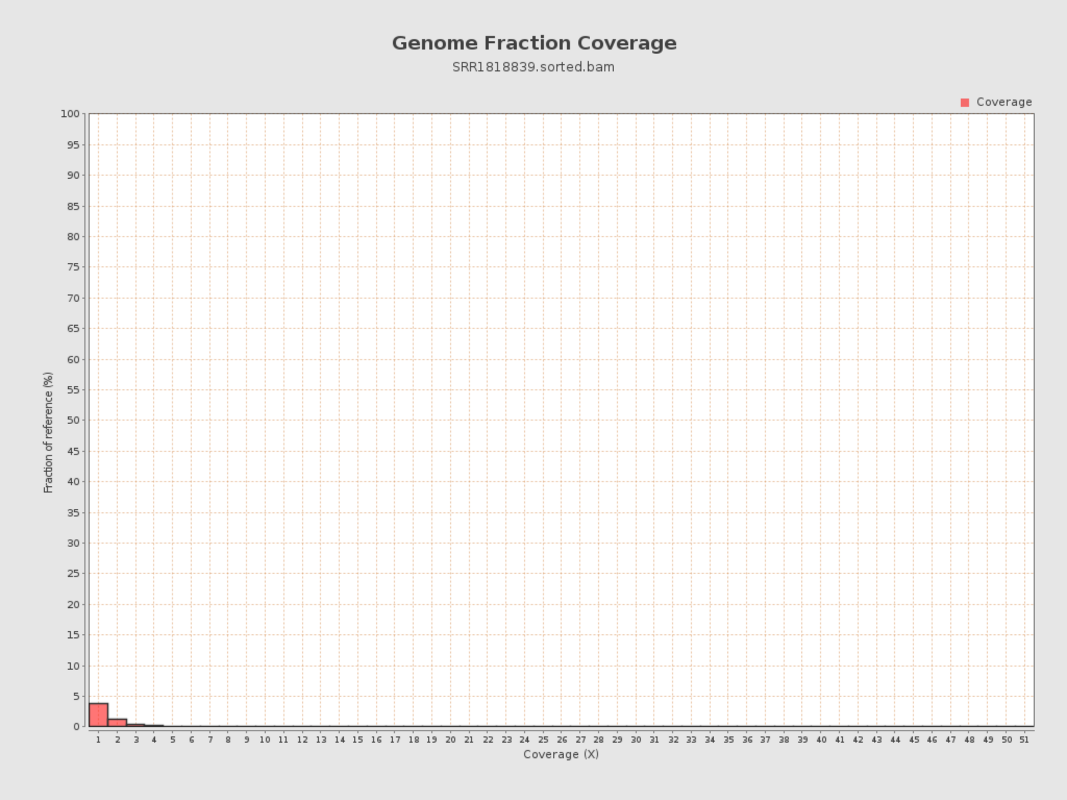
4. Results : Coverage Histogram



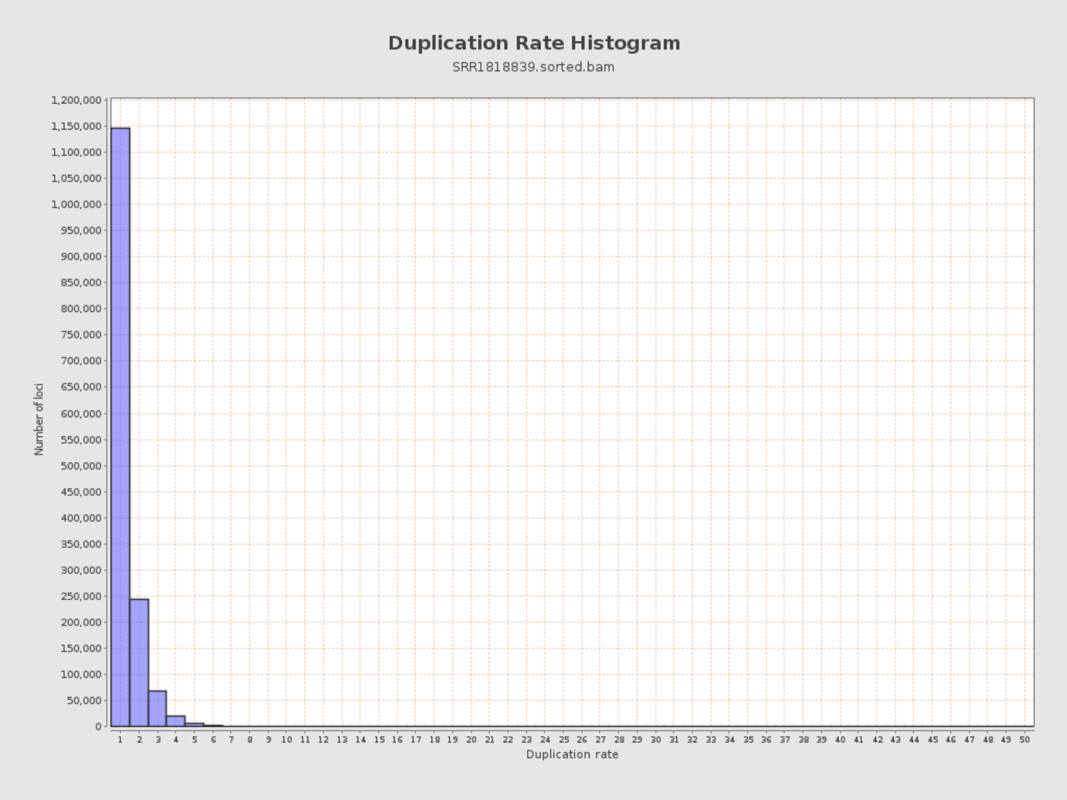
5. Results : Coverage Histogram (0-50X)



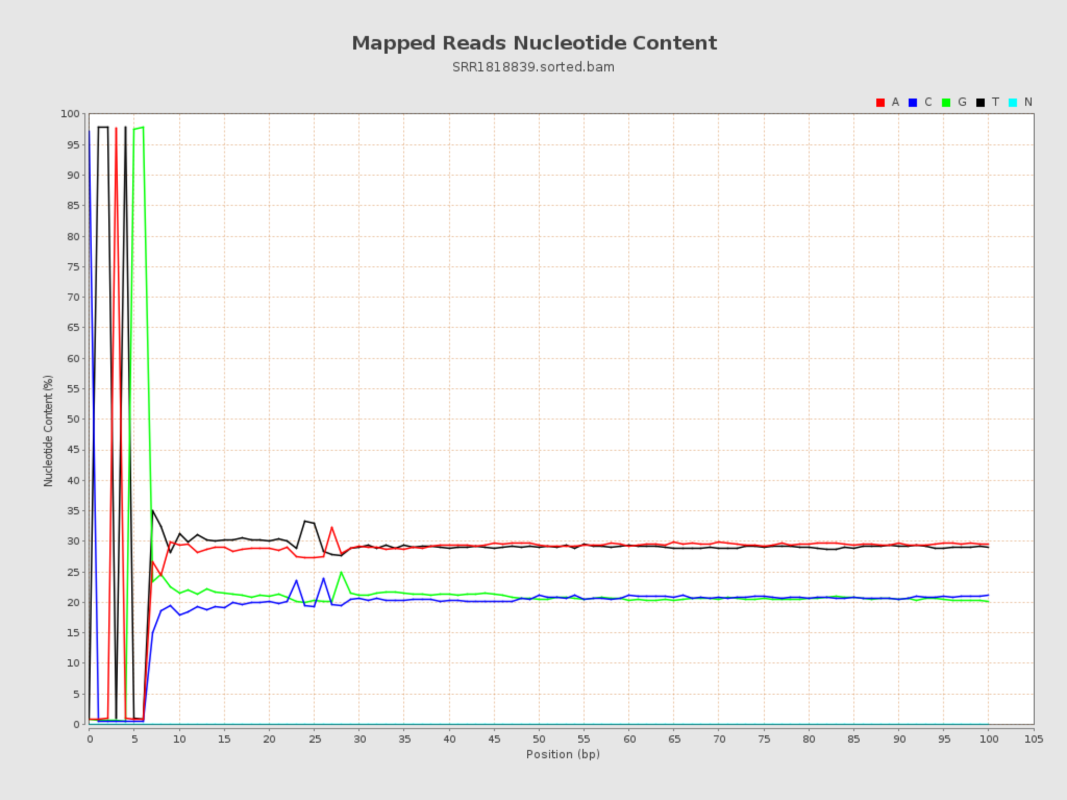
6. Results : Genome Fraction Coverage



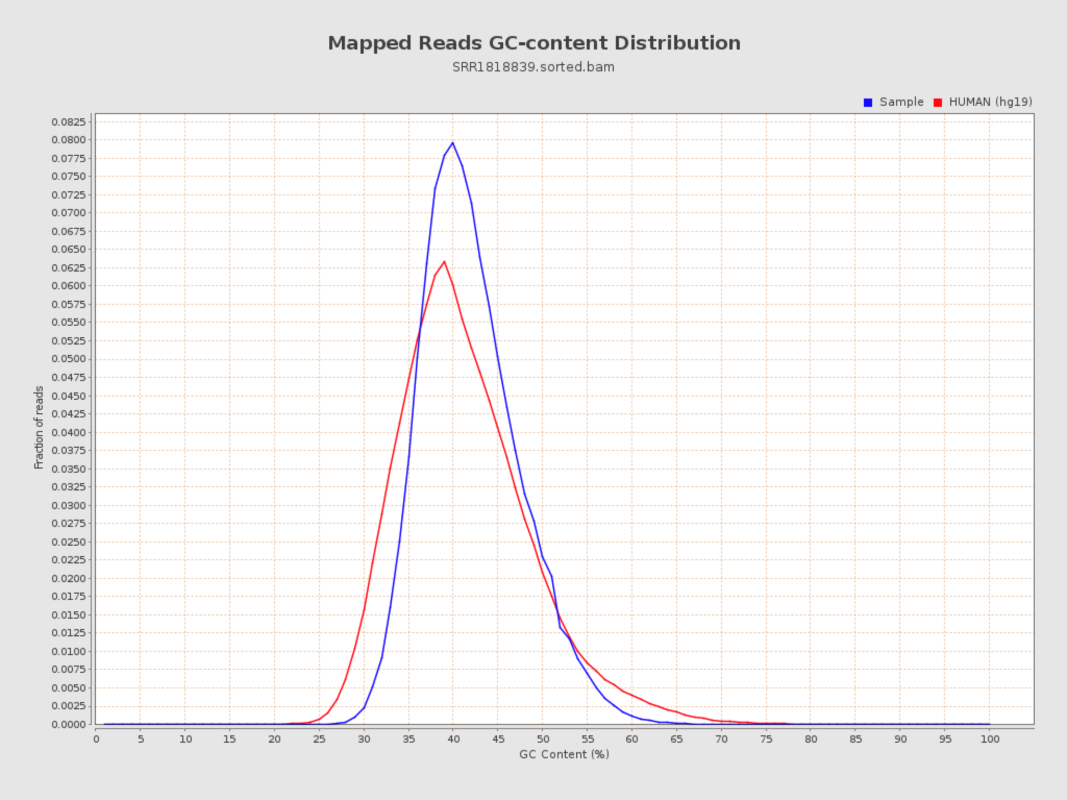
7. Results : Duplication Rate Histogram



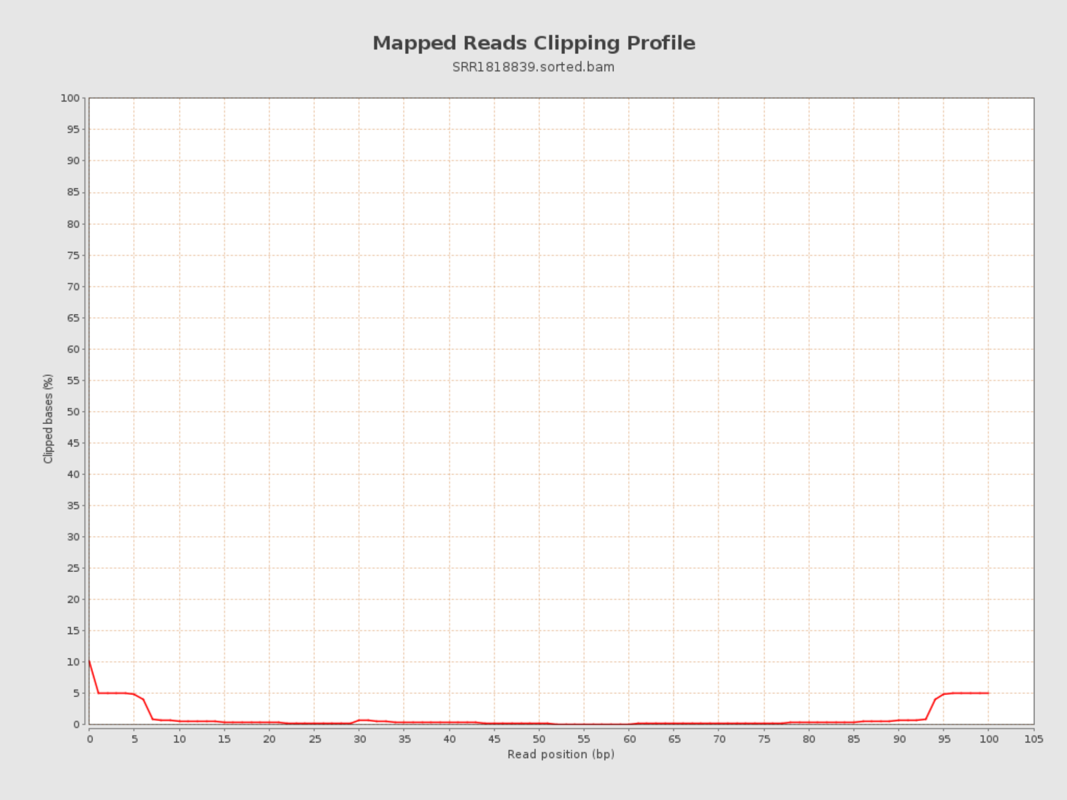
8. Results : Mapped Reads Nucleotide Content



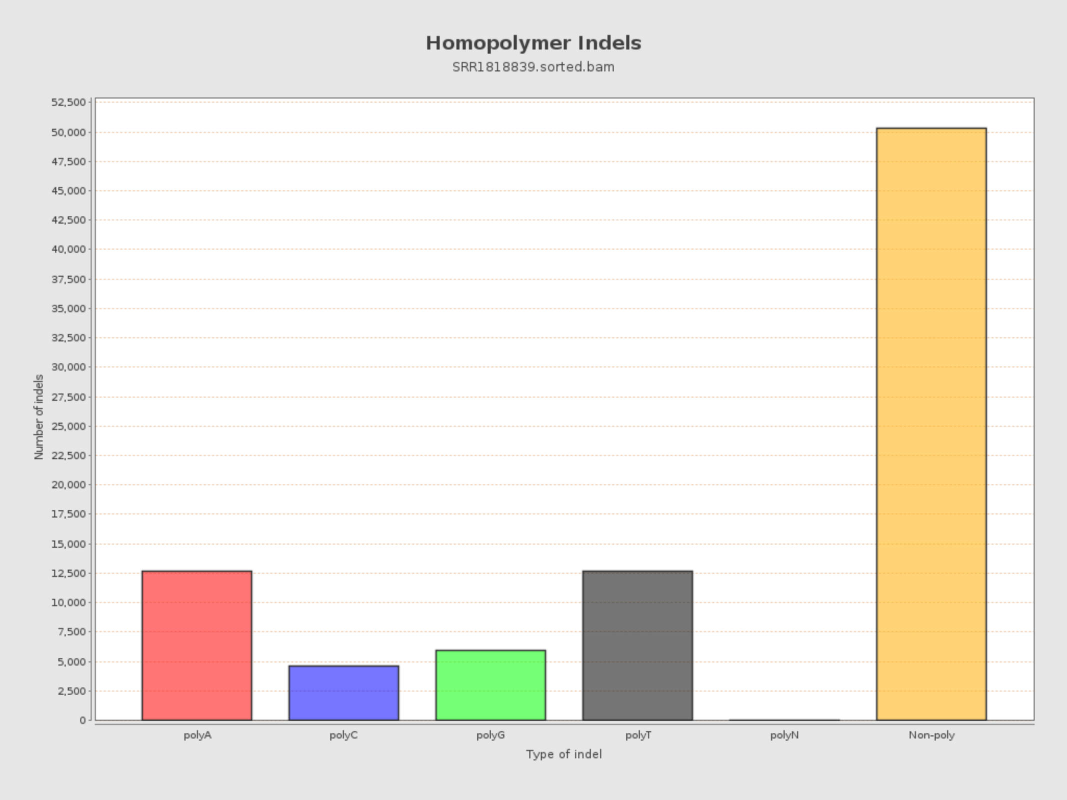
9. Results : Mapped Reads GC-content Distribution



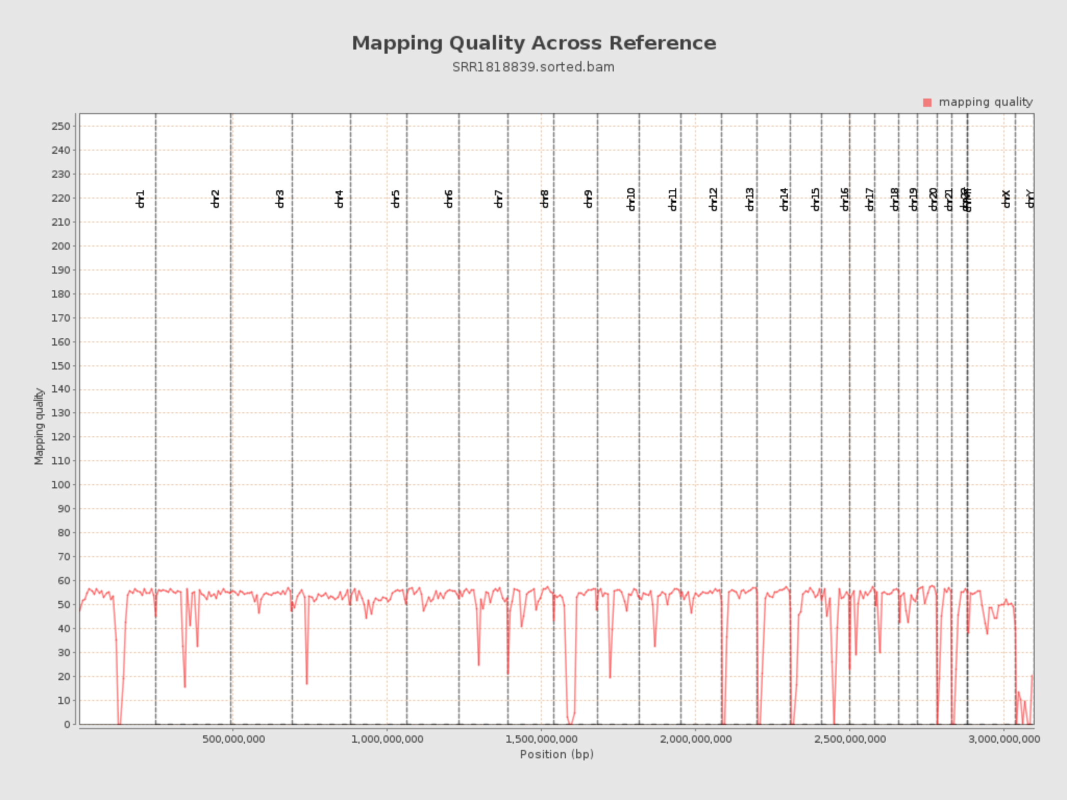
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram