Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:34:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818939.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_SRR1818939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818939.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:34:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818939.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,593,067
Mapped reads	5,498,603 / 98.31%
Unmapped reads	94,464 / 1.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,237 / 1.15%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	3,252,206 / 58.15%
Duplication rate	47.25%
Clipped reads	5,530,112 / 98.87%

2.2. ACGT Content

Number/percentage of A's	145,966,878 / 28.63%
Number/percentage of C's	112,059,447 / 21.98%
Number/percentage of T's	146,332,835 / 28.7%
Number/percentage of G's	105,403,270 / 20.68%
Number/percentage of N's	23,525 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.1648

Standard Deviation	1.6879

2.4. Mapping Quality

Mean Mapping Quality	49.44

2.5. Mismatches and indels

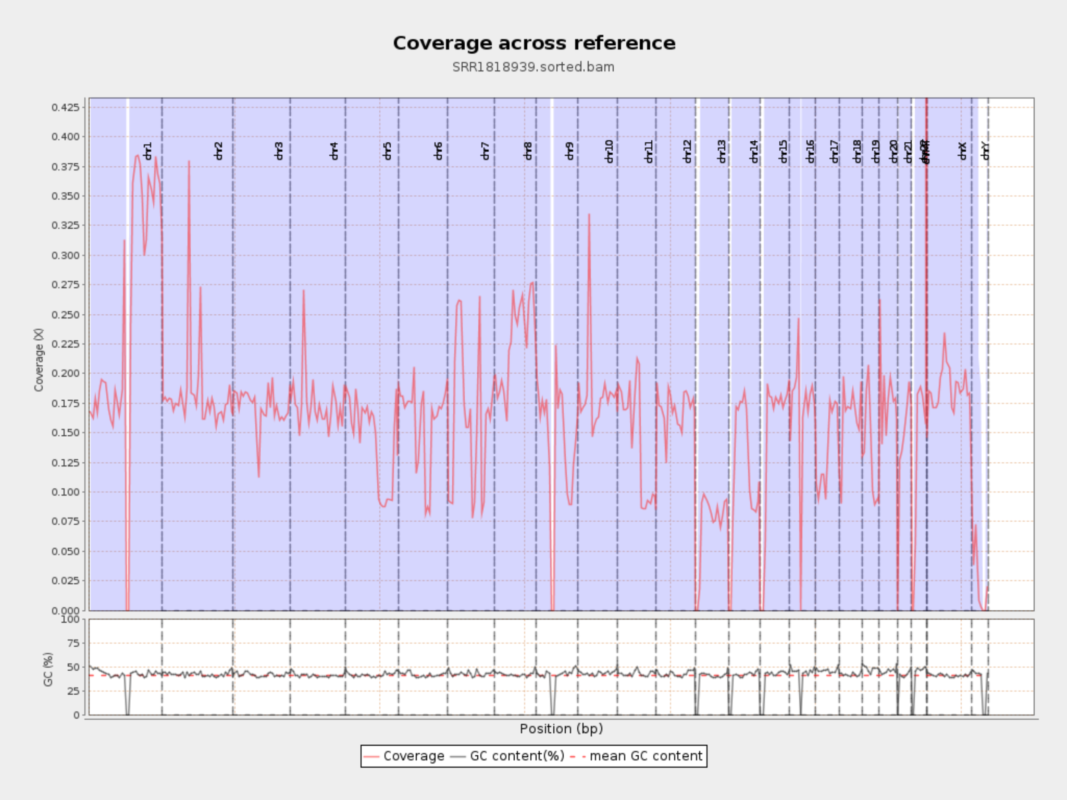
General error rate	0.68%
Mismatches	3,311,204
Insertions	58,935
Mapped reads with at least one insertion	1.05%
Deletions	152,211
Mapped reads with at least one deletion	2.71%
Homopolymer indels	43.78%

2.6. Chromosome stats

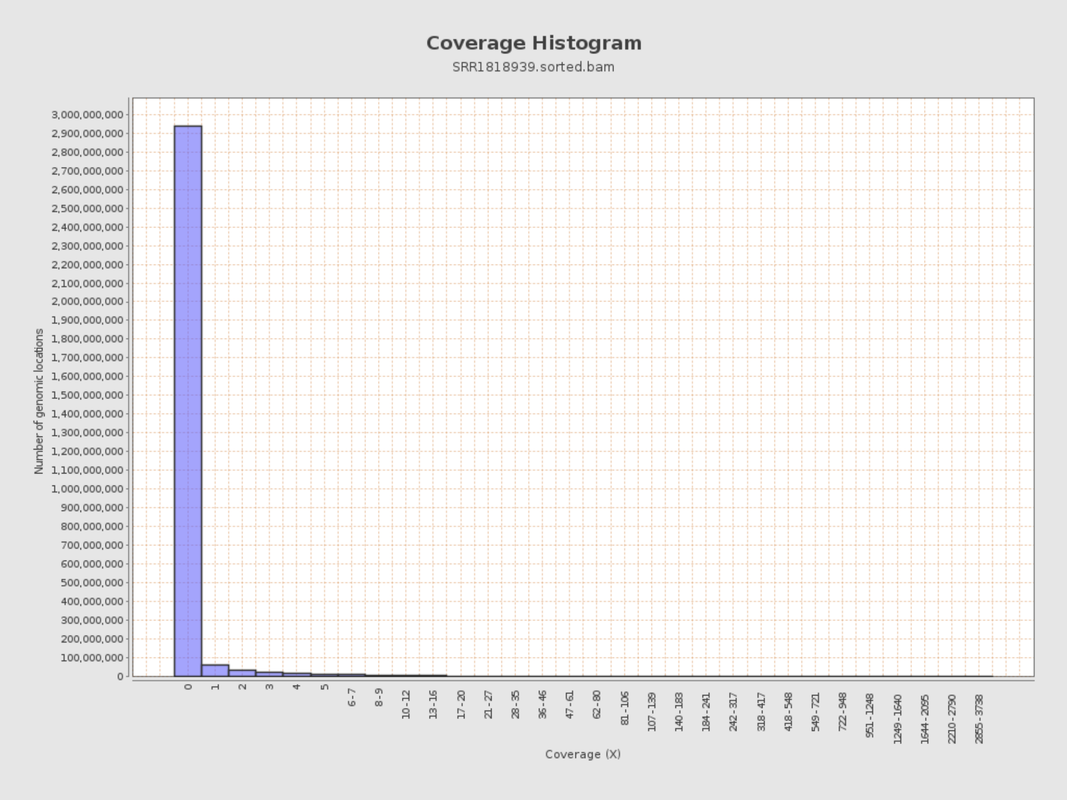
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61242182	0.2457	3.1329
chr2	243199373	44817840	0.1843	2.2027
chr3	198022430	33904066	0.1712	1.0221
chr4	191154276	33305512	0.1742	1.1492
chr5	180915260	26005681	0.1437	0.9544
chr6	171115067	27355740	0.1599	1.1098
chr7	159138663	25678808	0.1614	1.4765

chr8	146364022	33502116	0.2289	1.4924
chr9	141213431	19143197	0.1356	2.0645
chr10	135534747	24910391	0.1838	2.0375
chr11	135006516	19567658	0.1449	1.2323
chr12	133851895	22814454	0.1704	1.0394
chr13	115169878	8255252	0.0717	0.6371
chr14	107349540	12330086	0.1149	0.9709
chr15	102531392	14884480	0.1452	0.9528
chr16	90354753	15333407	0.1697	1.5403
chr17	81195210	11075748	0.1364	1.0728
chr18	78077248	12706468	0.1627	2.7352
chr19	59128983	8067313	0.1364	2.6705
chr20	63025520	11431891	0.1814	1.1385
chr21	48129895	6852889	0.1424	1.0795
chr22	51304566	6305101	0.1229	0.9402
chrMT	16571	32911	1.9861	3.7432
chrX	155270560	29085617	0.1873	1.4995
chrY	59373566	1452119	0.0245	1.1531

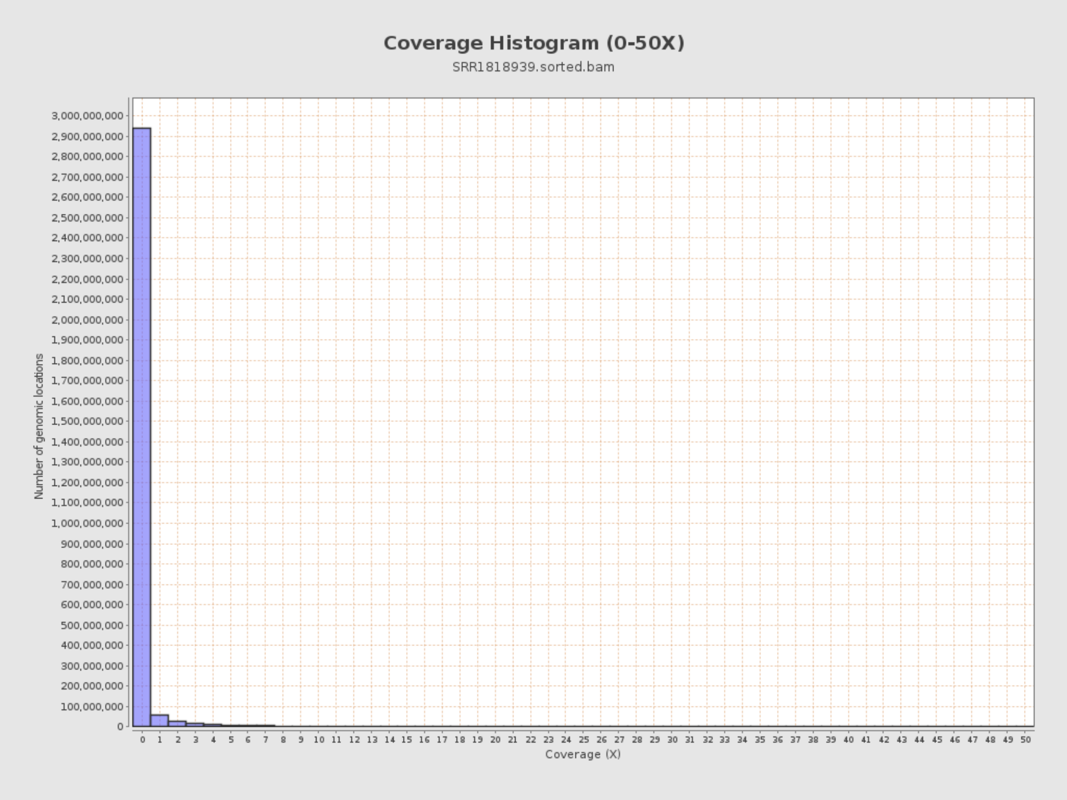
3. Results : Coverage across reference



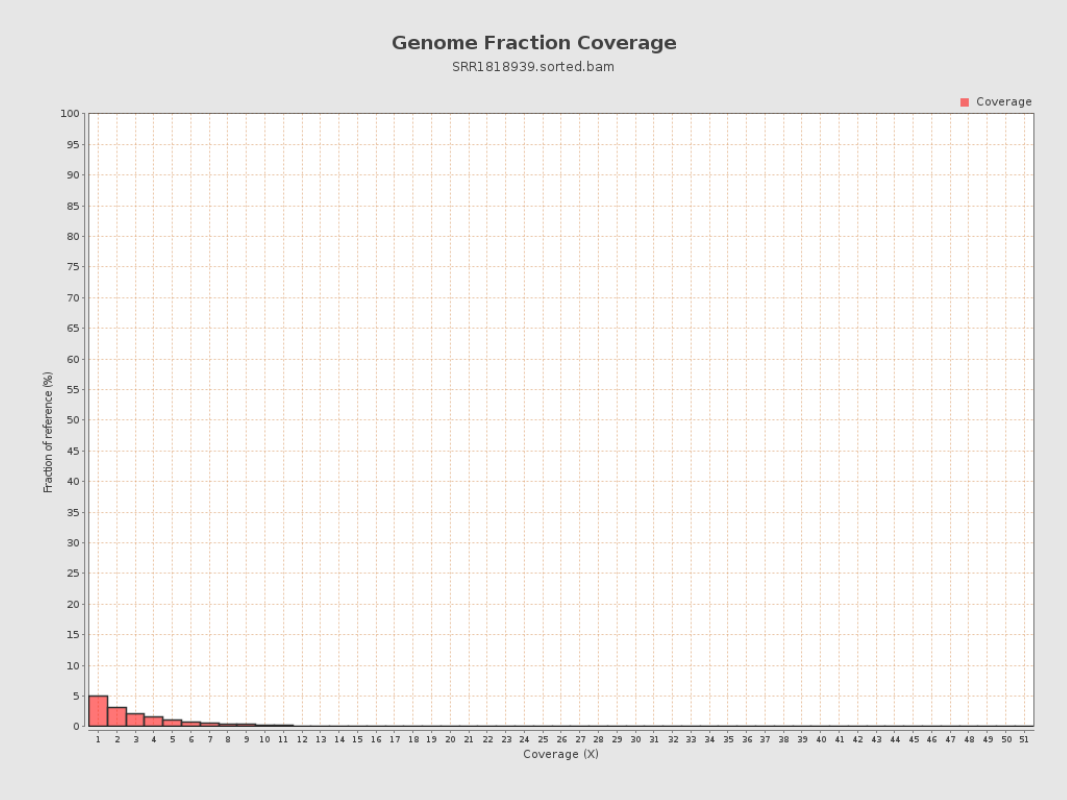
4. Results : Coverage Histogram



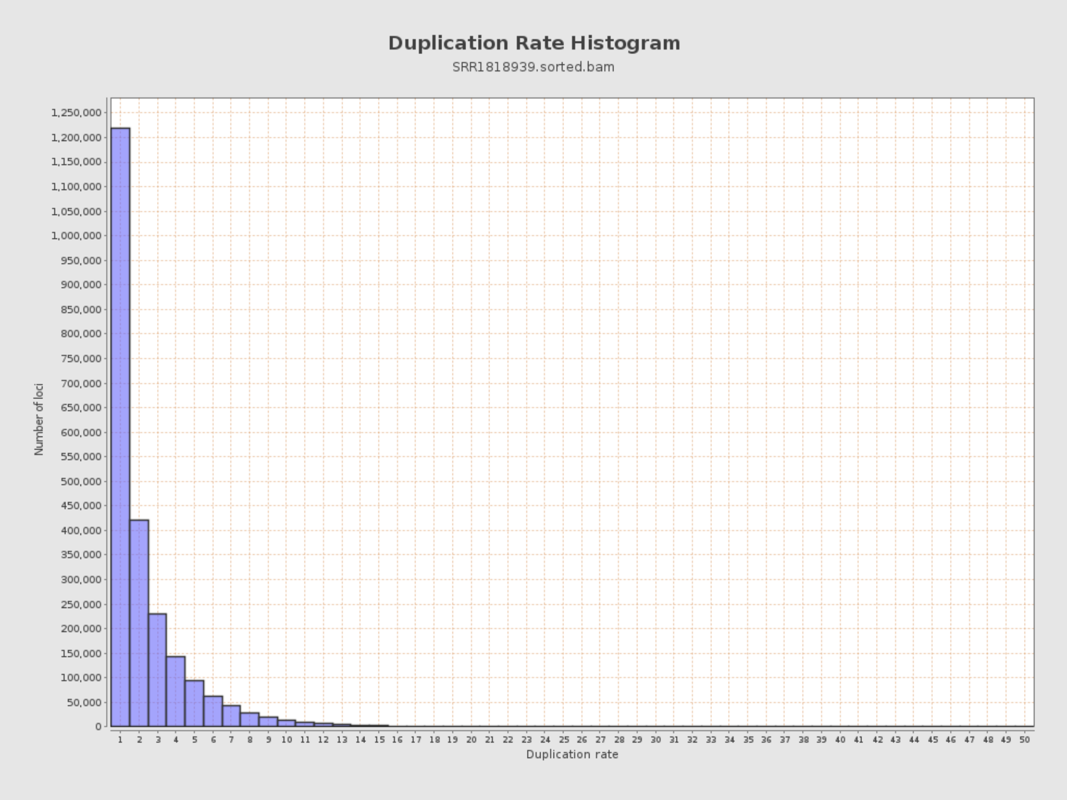
5. Results : Coverage Histogram (0-50X)



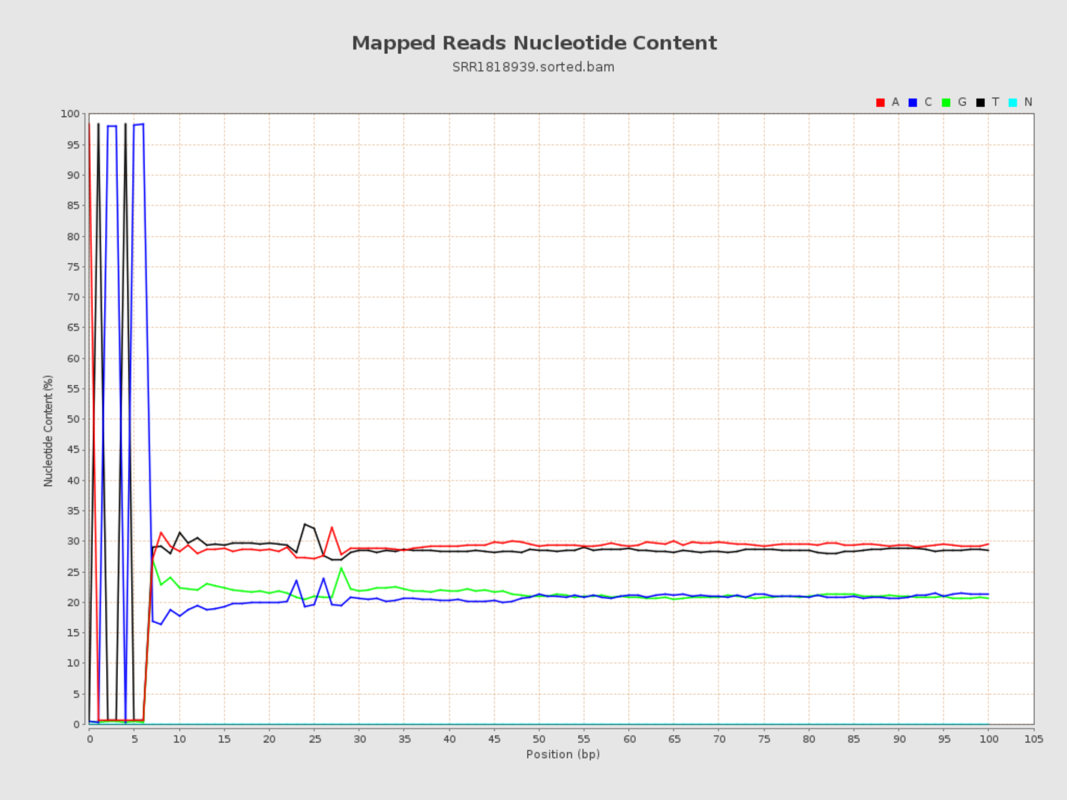
6. Results : Genome Fraction Coverage



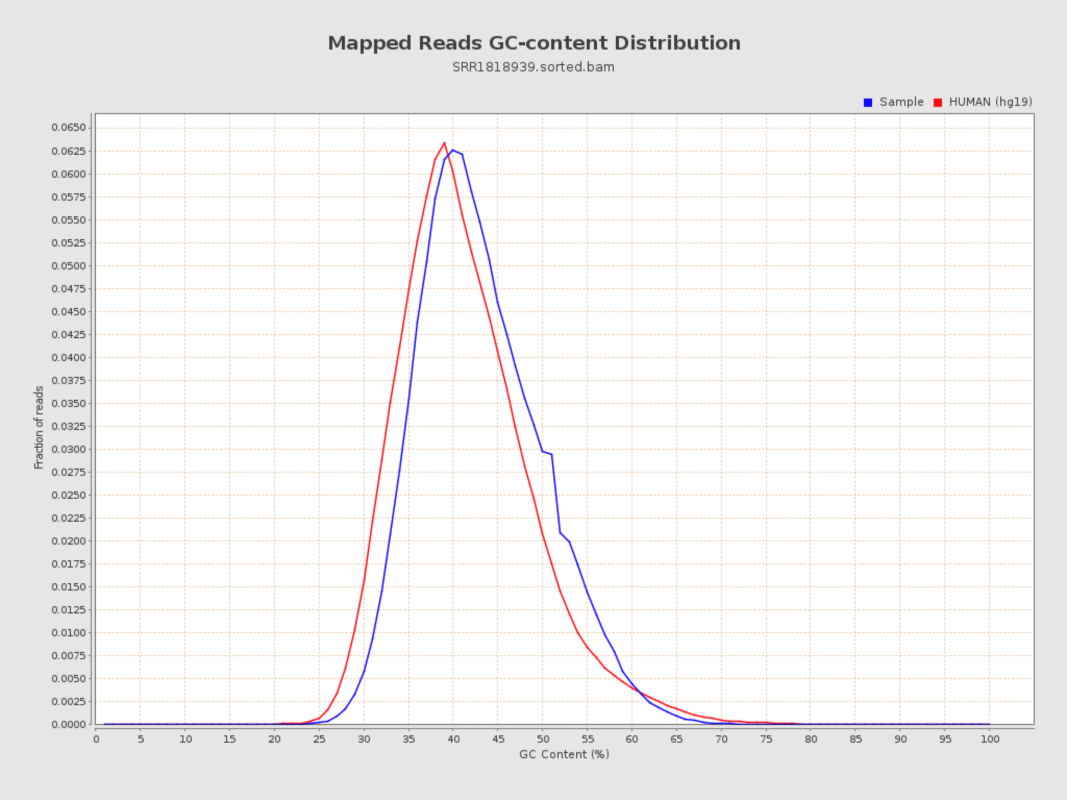
7. Results : Duplication Rate Histogram



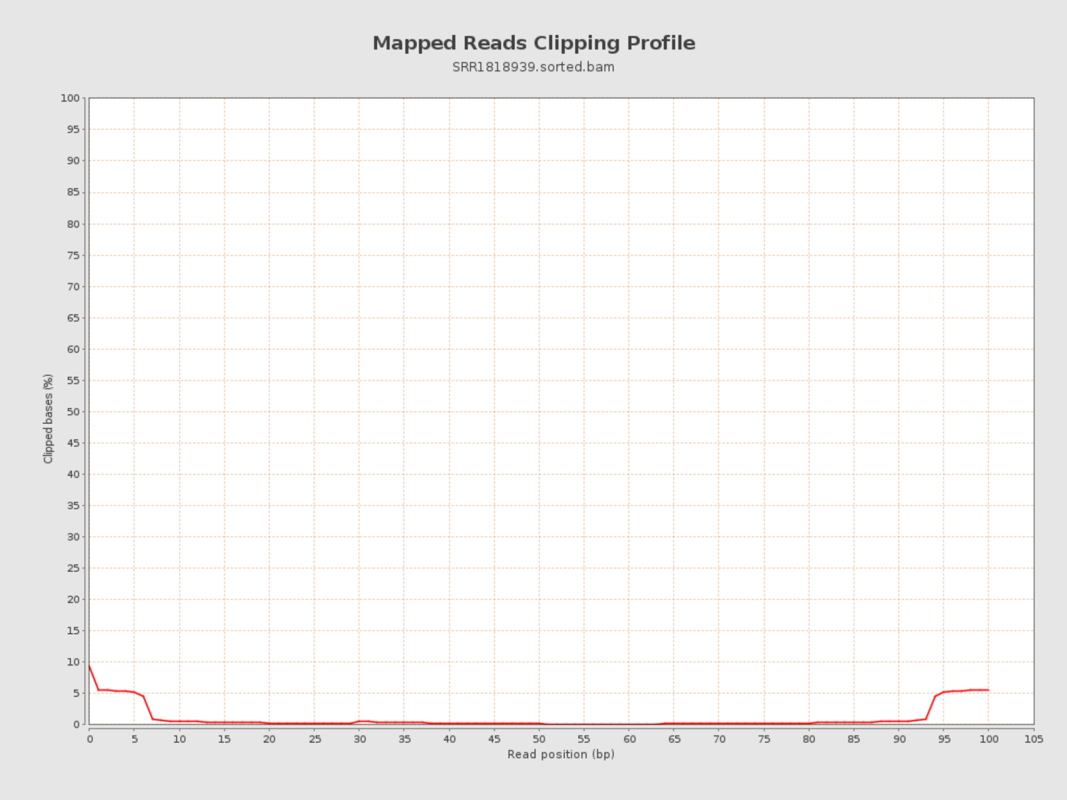
8. Results : Mapped Reads Nucleotide Content



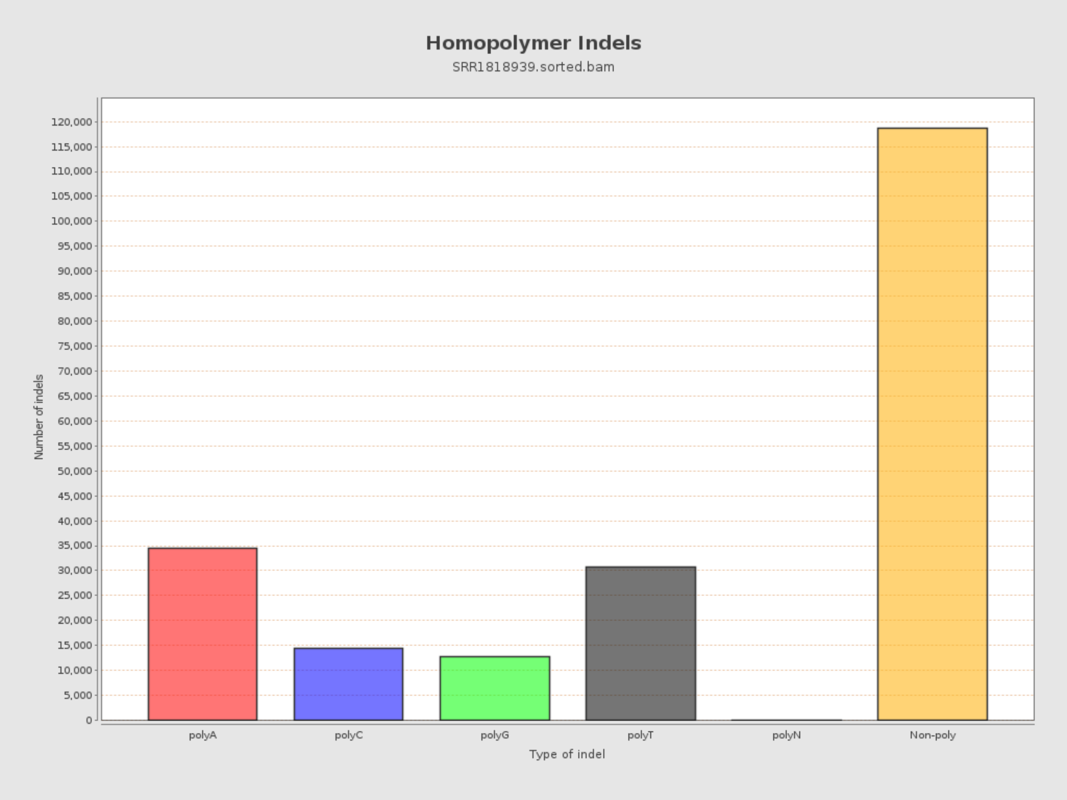
9. Results : Mapped Reads GC-content Distribution



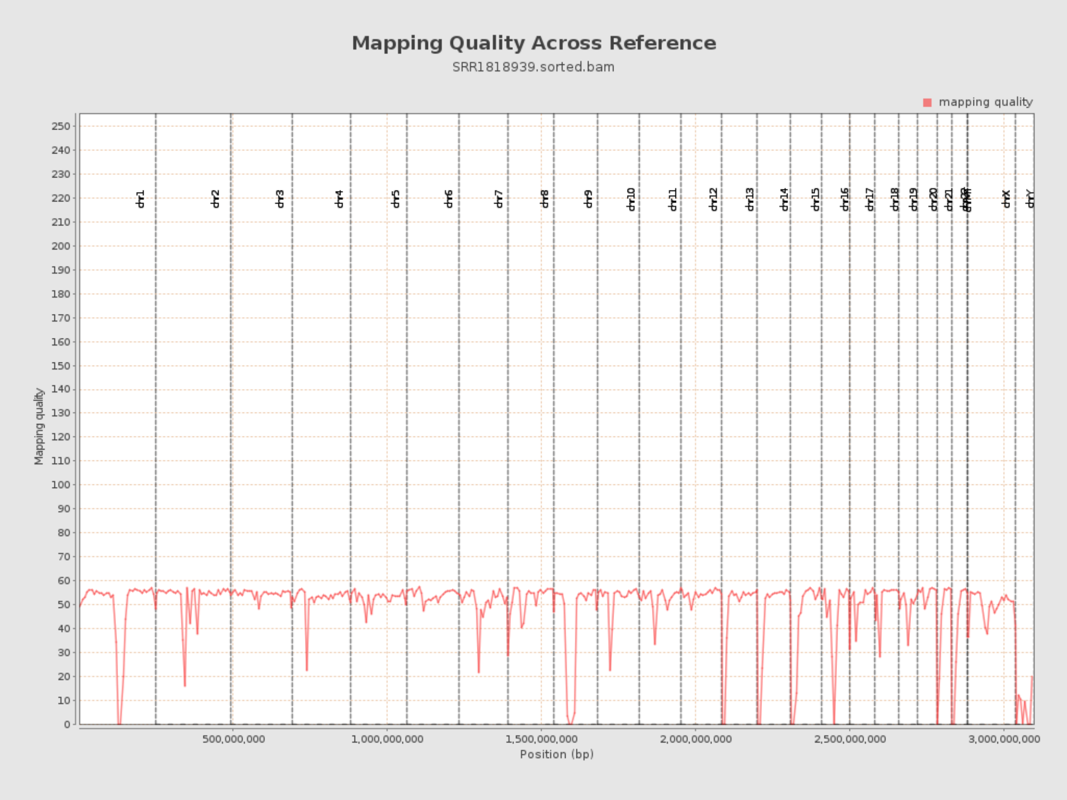
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram