Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:26:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818974.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_SRR1818974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818974.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:26:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,374,901
Mapped reads	3,328,645 / 98.63%
Unmapped reads	46,256 / 1.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,511 / 1.38%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	1,895,576 / 56.17%
Duplication rate	46.86%
Clipped reads	3,365,499 / 99.72%

2.2. ACGT Content

Number/percentage of A's	89,614,711 / 29.1%
Number/percentage of C's	66,066,118 / 21.45%
Number/percentage of T's	87,364,987 / 28.37%
Number/percentage of G's	64,931,187 / 21.08%
Number/percentage of N's	15,187 / 0%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0995

Standard Deviation	1.1958

2.4. Mapping Quality

Mean Mapping Quality	48.98

2.5. Mismatches and indels

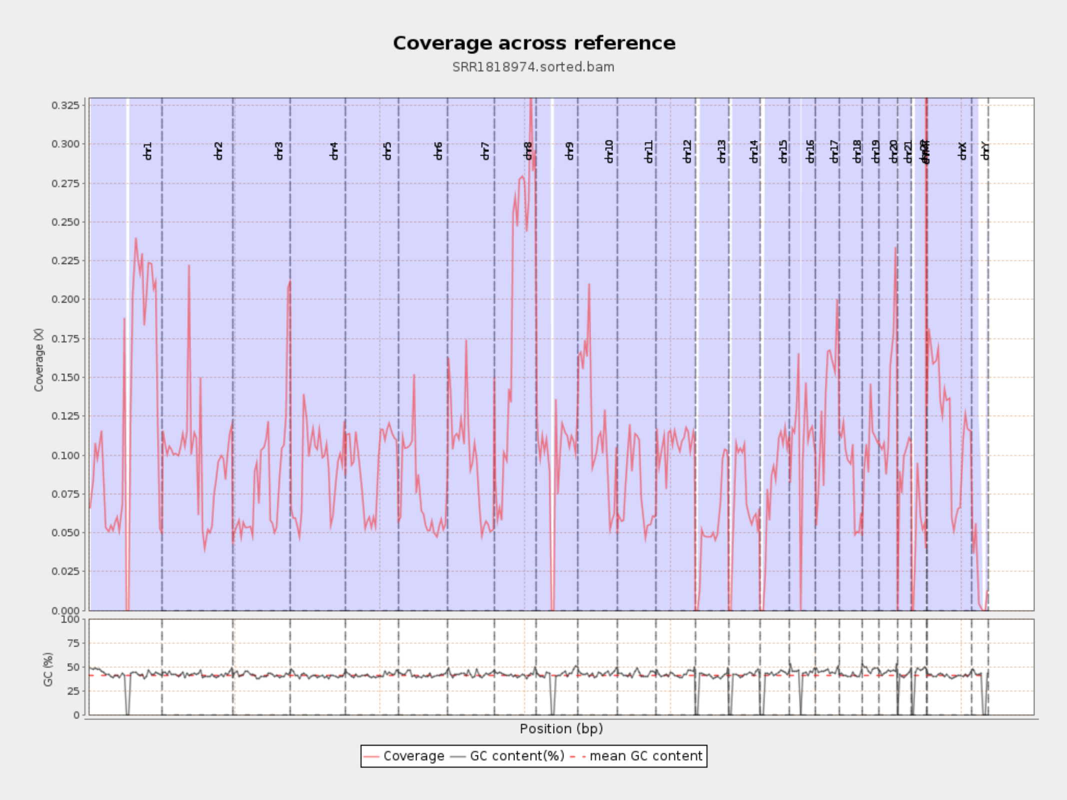
General error rate	0.66%
Mismatches	1,928,289
Insertions	44,221
Mapped reads with at least one insertion	1.29%
Deletions	96,600
Mapped reads with at least one deletion	2.84%
Homopolymer indels	42.15%

2.6. Chromosome stats

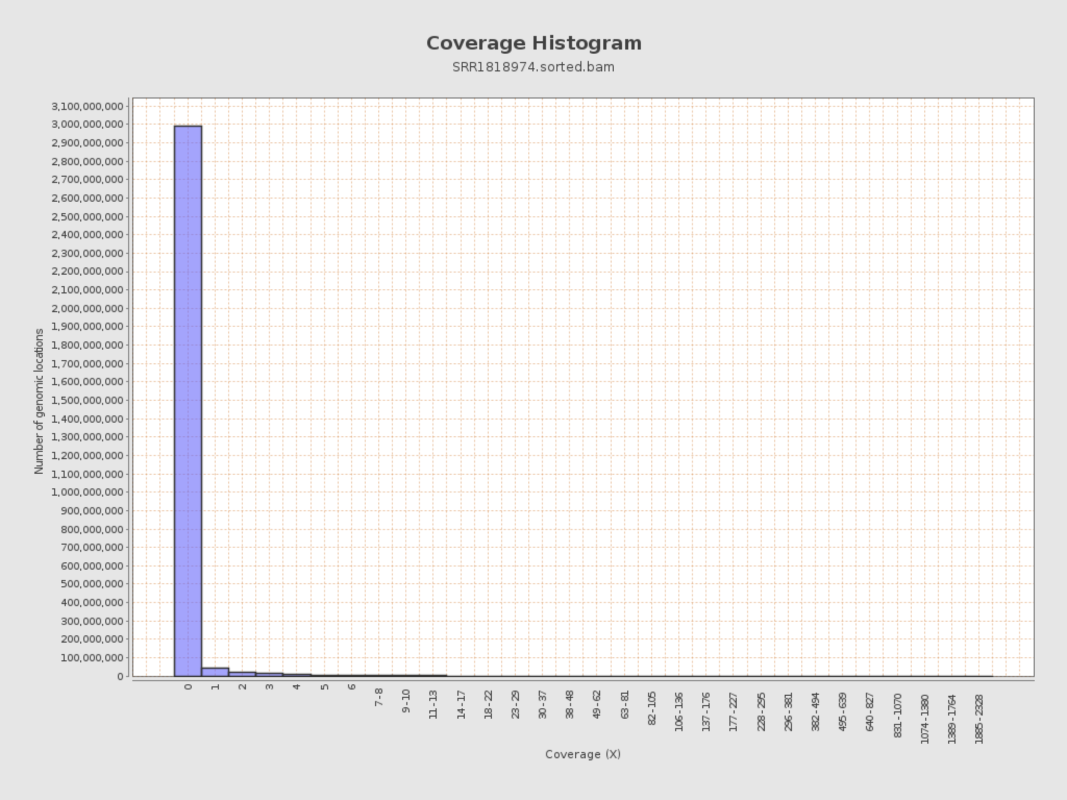
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30770042	0.1235	2.0561
chr2	243199373	23855472	0.0981	1.6833
chr3	198022430	16088384	0.0812	0.6415
chr4	191154276	17400171	0.091	0.7739
chr5	180915260	16953485	0.0937	0.7184
chr6	171115067	12755974	0.0745	0.7975
chr7	159138663	15289351	0.0961	1.4547

chr8	146364022	28942313	0.1977	1.1698
chr9	141213431	13466455	0.0954	1.1534
chr10	135534747	16140076	0.1191	1.4388
chr11	135006516	10361469	0.0767	0.7716
chr12	133851895	14439853	0.1079	0.7667
chr13	115169878	6186729	0.0537	0.5203
chr14	107349540	7238549	0.0674	0.6283
chr15	102531392	7909118	0.0771	0.6402
chr16	90354753	9884186	0.1094	1.3836
chr17	81195210	11013109	0.1356	0.9738
chr18	78077248	6790641	0.087	1.3144
chr19	59128983	6314620	0.1068	1.842
chr20	63025520	8756727	0.1389	0.9109
chr21	48129895	4258204	0.0885	0.7409
chr22	51304566	2406311	0.0469	0.5255
chrMT	16571	1071623	64.6686	41.7361
chrX	155270560	18751404	0.1208	0.942
chrY	59373566	1126787	0.019	1.2184

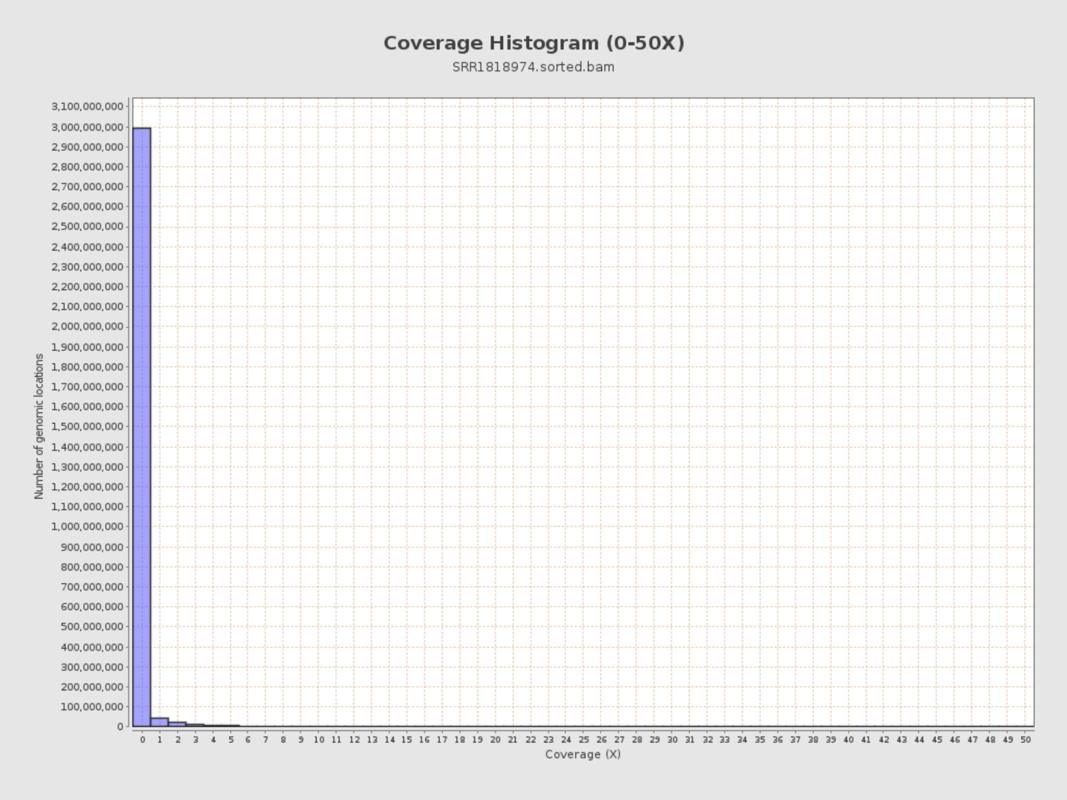
3. Results : Coverage across reference



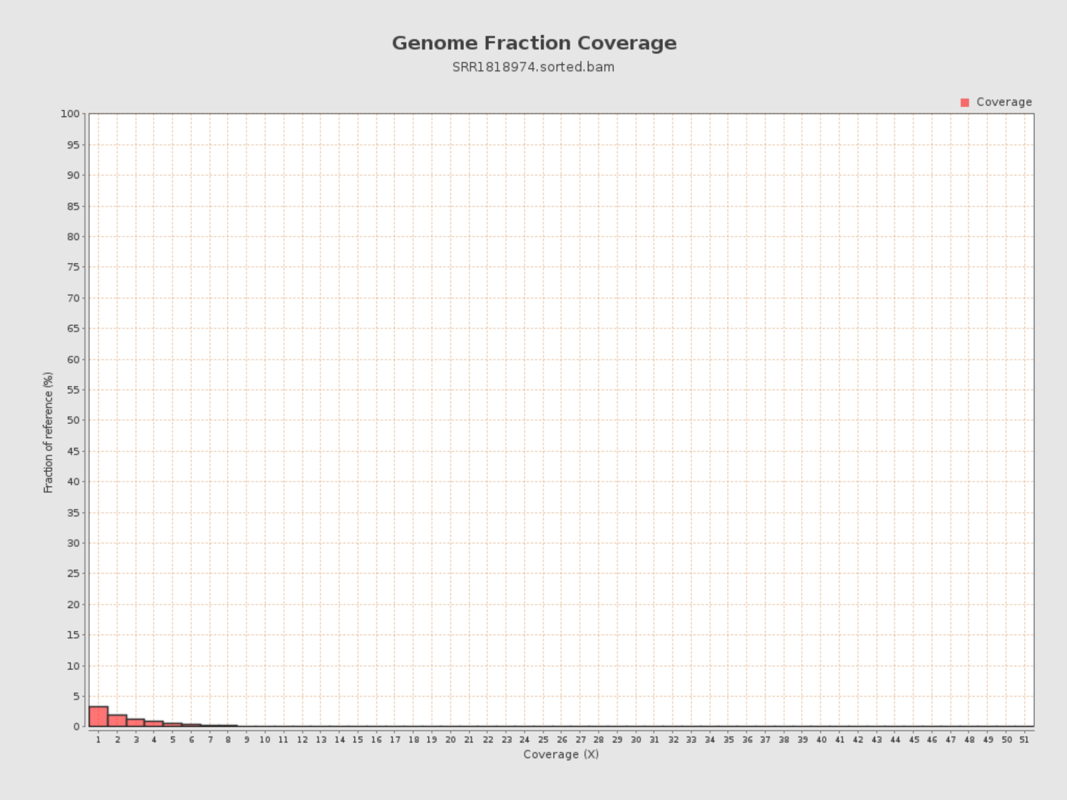
4. Results : Coverage Histogram



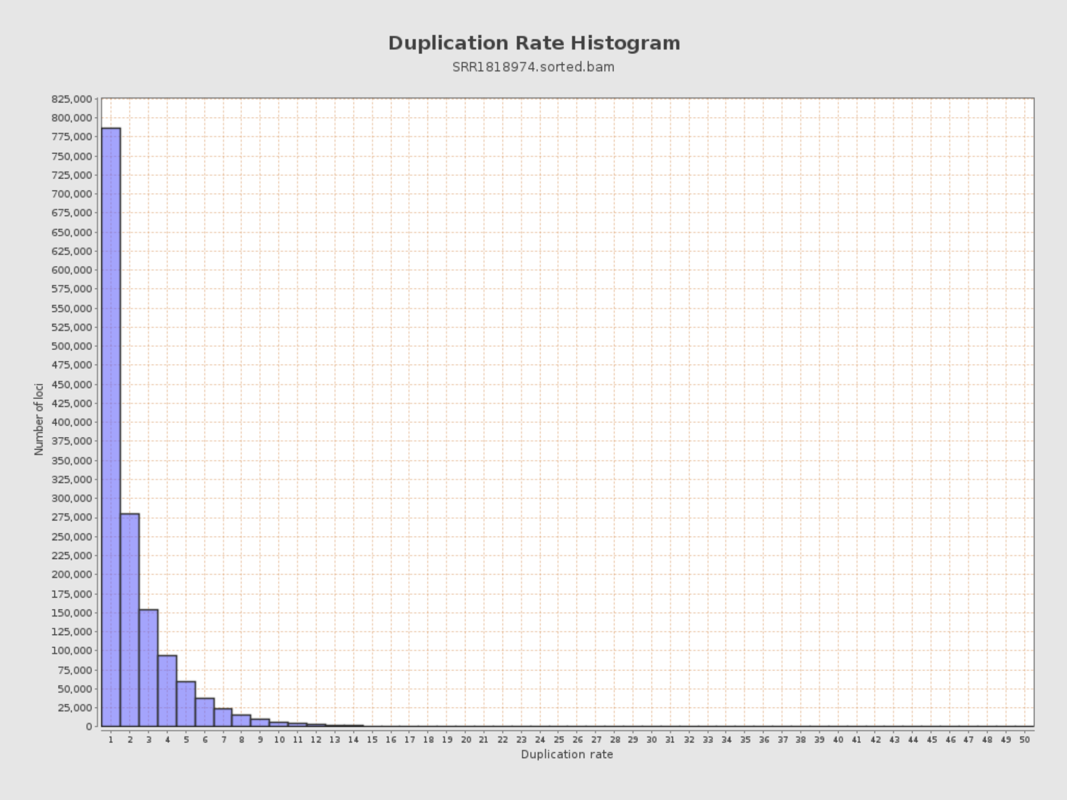
5. Results : Coverage Histogram (0-50X)



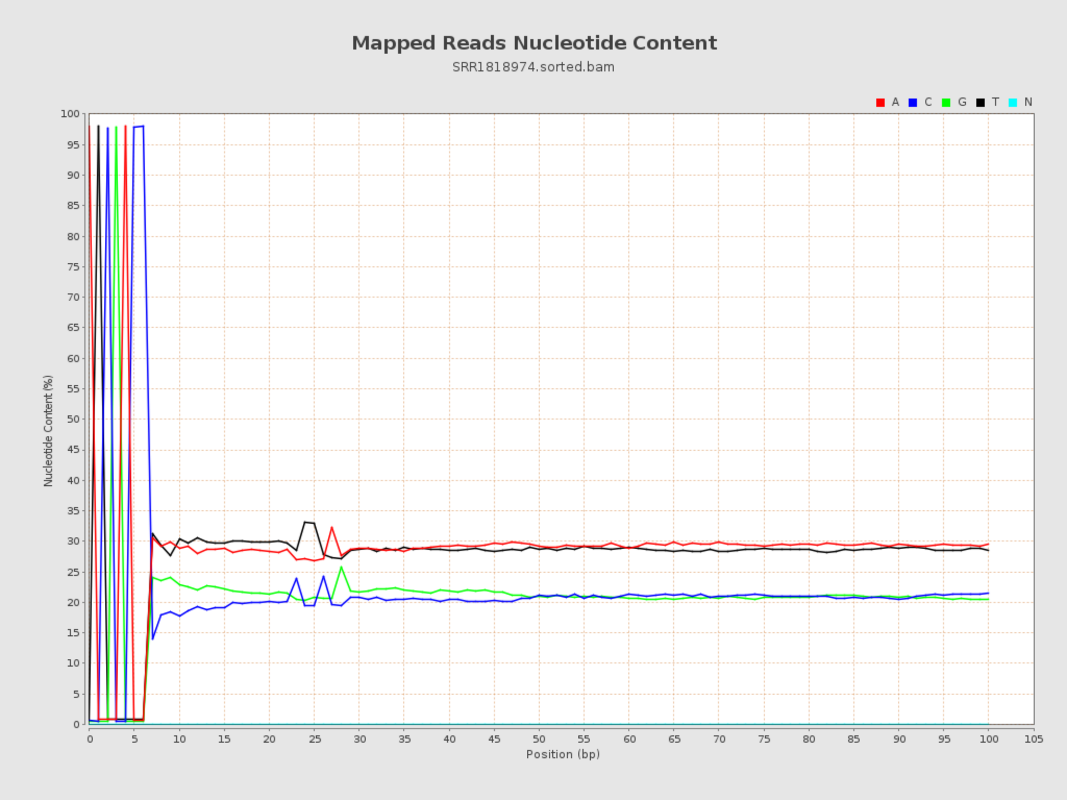
6. Results : Genome Fraction Coverage



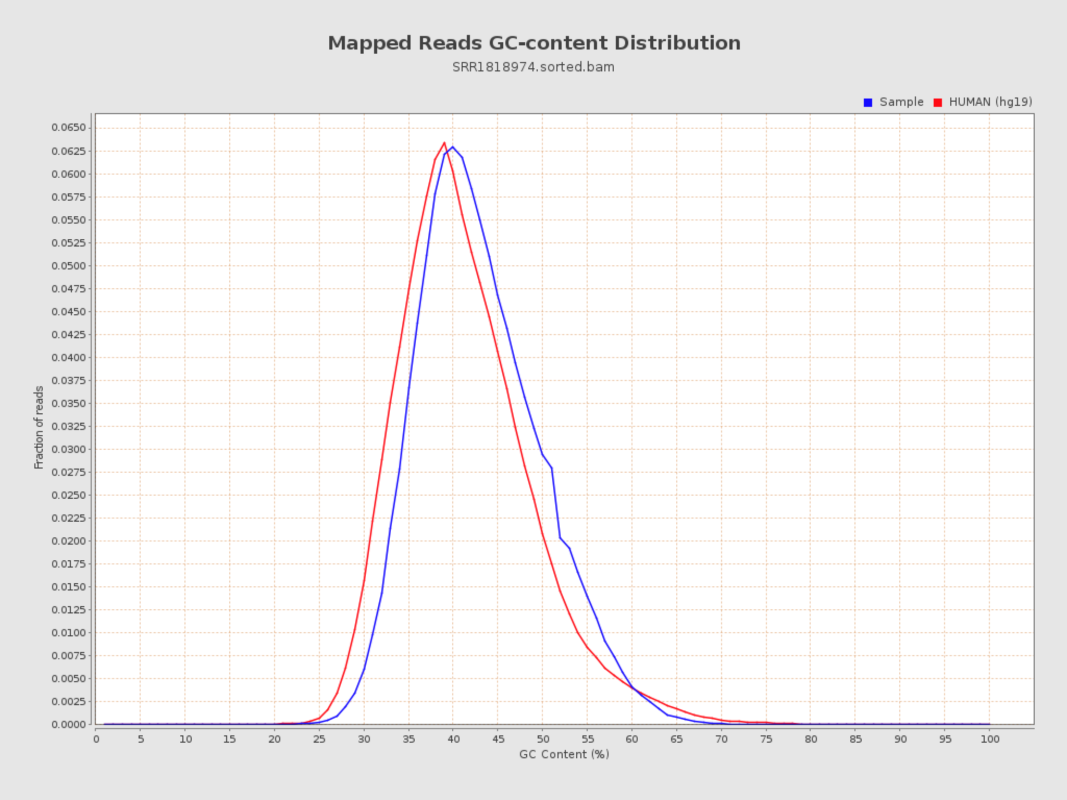
7. Results : Duplication Rate Histogram



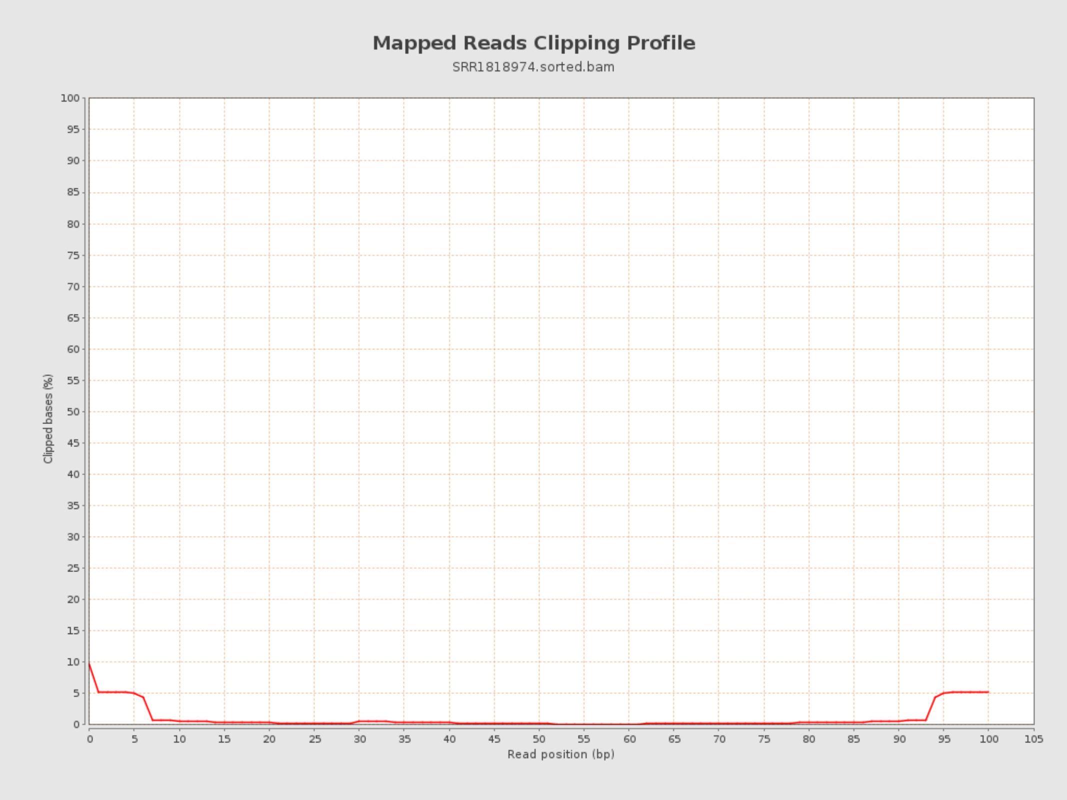
8. Results : Mapped Reads Nucleotide Content



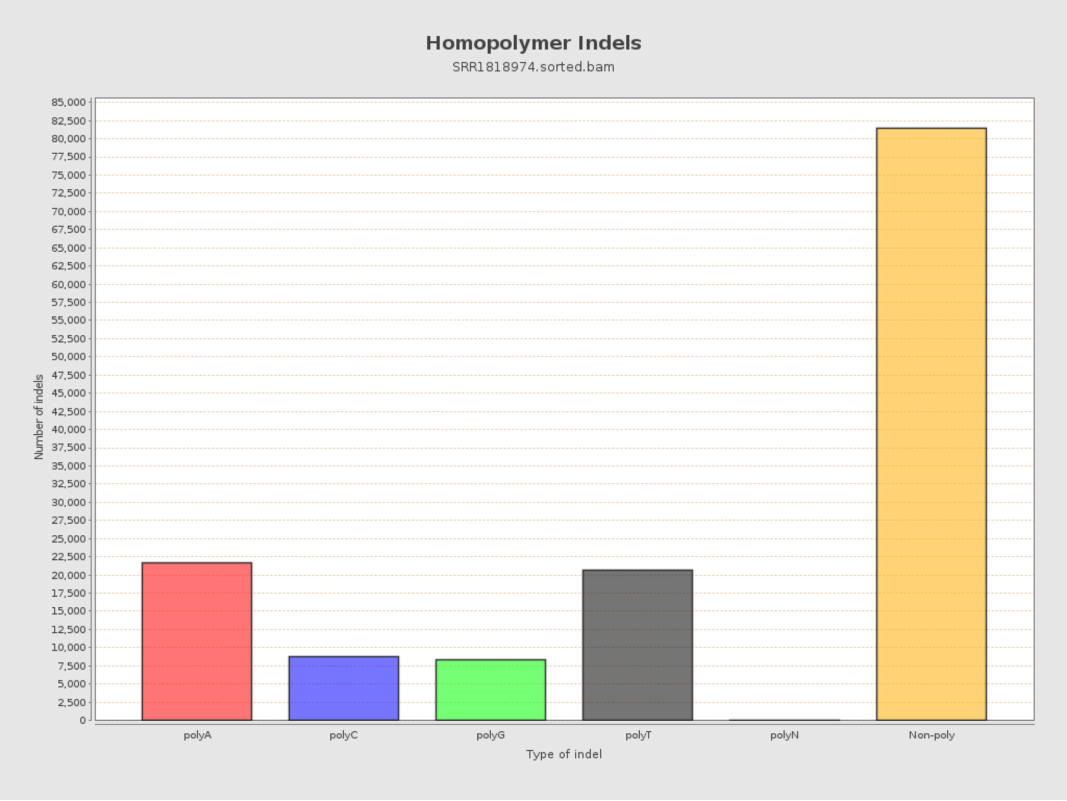
9. Results : Mapped Reads GC-content Distribution



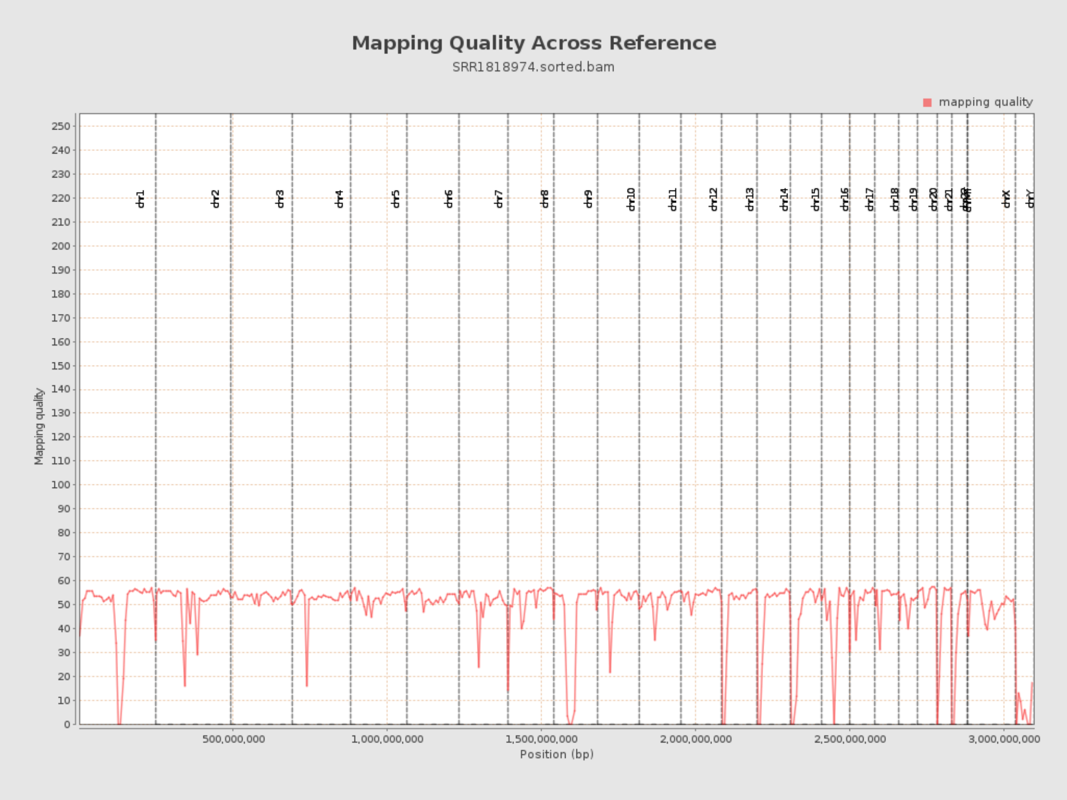
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram