Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:39:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524788.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_SRR10524788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:39:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,068,206
Mapped reads	973,930 / 91.17%
Unmapped reads	94,276 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,437 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	28,071 / 2.63%
Duplication rate	2.22%
Clipped reads	976,073 / 91.37%

2.2. ACGT Content

Number/percentage of A's	13,980,806 / 24.66%
Number/percentage of C's	10,656,762 / 18.8%
Number/percentage of T's	17,202,775 / 30.35%
Number/percentage of G's	14,843,436 / 26.18%
Number/percentage of N's	6,593 / 0.01%
GC Percentage	44.98%

2.3. Coverage

Mean	0.0183

Standard Deviation	0.1789

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

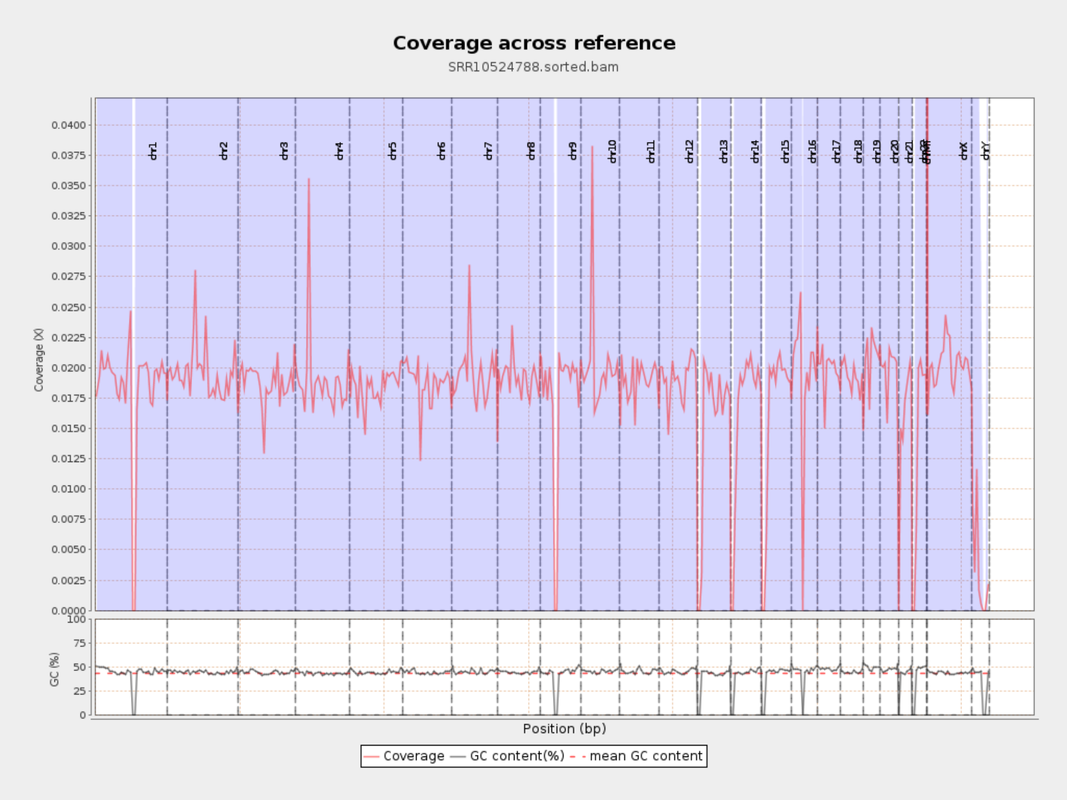
General error rate	0.52%
Mismatches	287,423
Insertions	3,445
Mapped reads with at least one insertion	0.35%
Deletions	11,257
Mapped reads with at least one deletion	1.15%
Homopolymer indels	44.31%

2.6. Chromosome stats

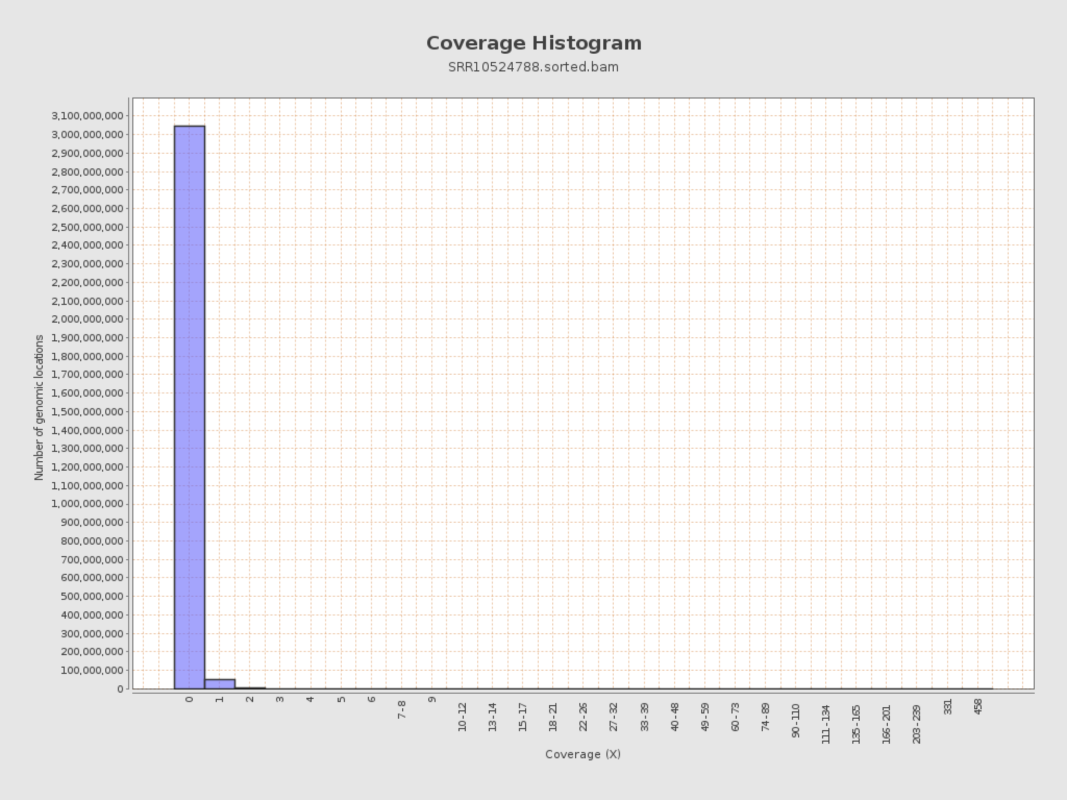
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4543254	0.0182	0.2307
chr2	243199373	4771213	0.0196	0.2515
chr3	198022430	3700778	0.0187	0.1468
chr4	191154276	3647009	0.0191	0.1632
chr5	180915260	3359914	0.0186	0.1452
chr6	171115067	3211926	0.0188	0.1546
chr7	159138663	3130509	0.0197	0.2169

chr8	146364022	2809814	0.0192	0.168
chr9	141213431	2432323	0.0172	0.1632
chr10	135534747	2745068	0.0203	0.2143
chr11	135006516	2579376	0.0191	0.1668
chr12	133851895	2556154	0.0191	0.149
chr13	115169878	1746518	0.0152	0.1316
chr14	107349540	1726675	0.0161	0.1364
chr15	102531392	1629982	0.0159	0.1342
chr16	90354753	1708578	0.0189	0.1591
chr17	81195210	1606130	0.0198	0.1551
chr18	78077248	1505511	0.0193	0.2372
chr19	59128983	1230985	0.0208	0.204
chr20	63025520	1244227	0.0197	0.156
chr21	48129895	756744	0.0157	0.1454
chr22	51304566	701481	0.0137	0.1251
chrMT	16571	18239	1.1007	1.1599
chrX	155270560	3152595	0.0203	0.1593
chrY	59373566	193275	0.0033	0.0964

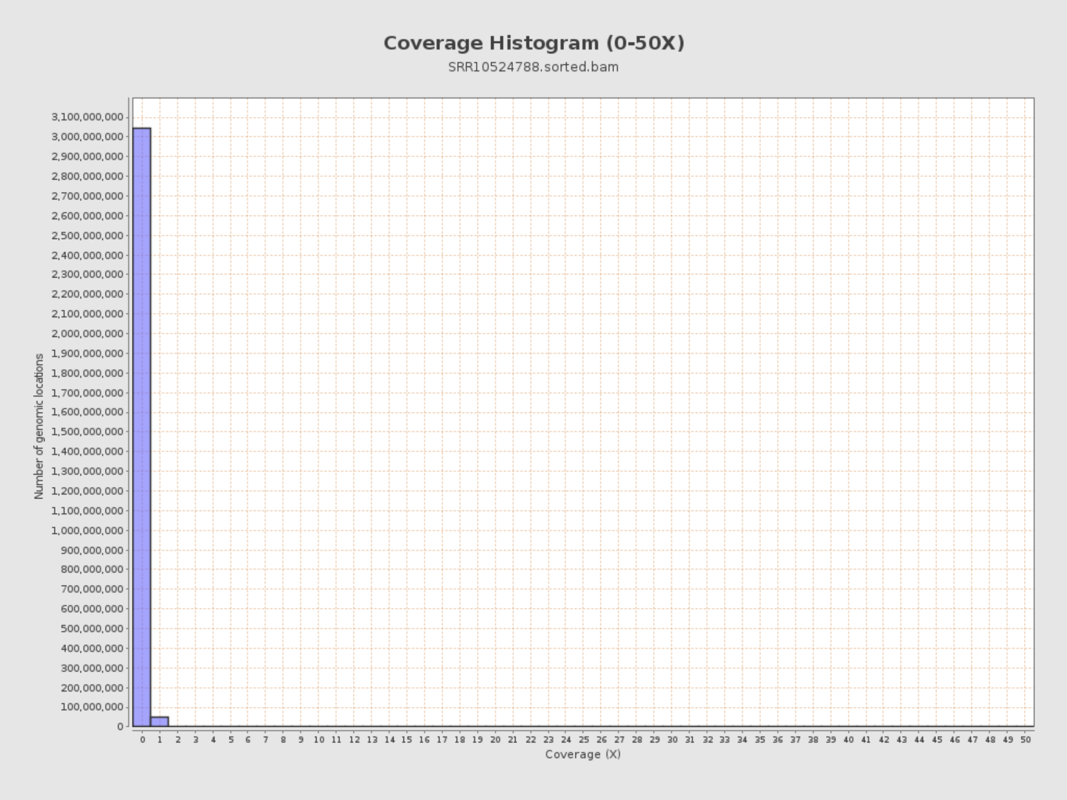
3. Results : Coverage across reference



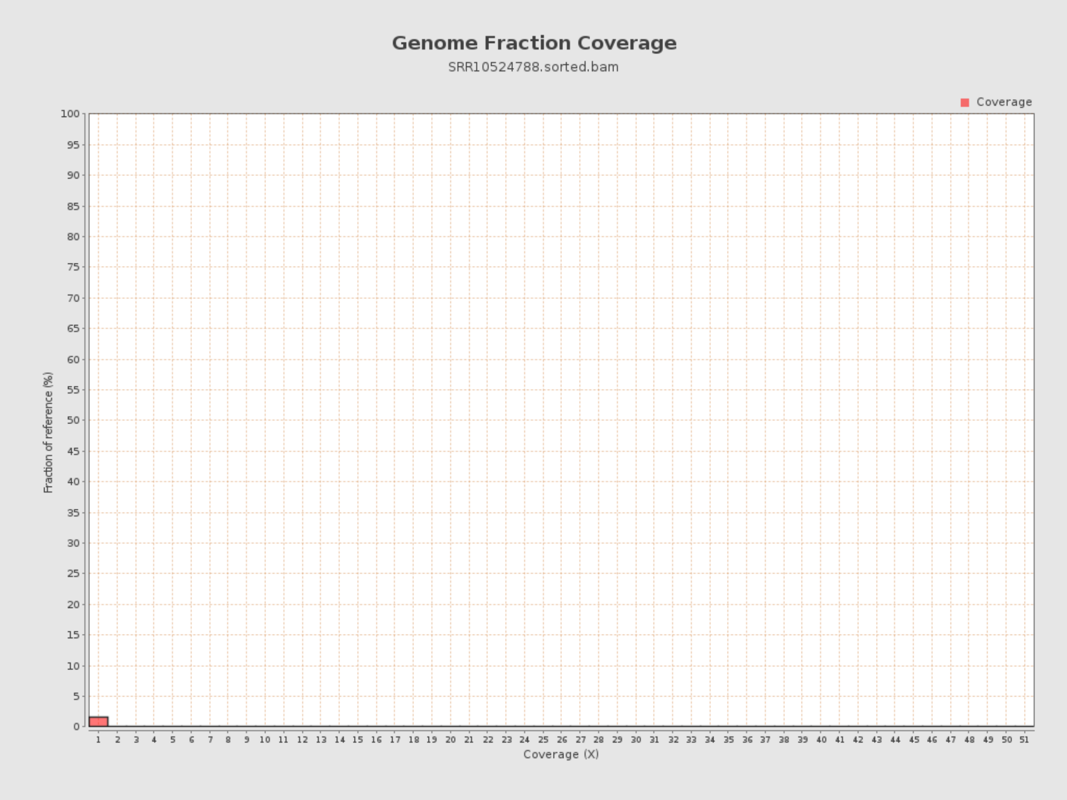
4. Results : Coverage Histogram



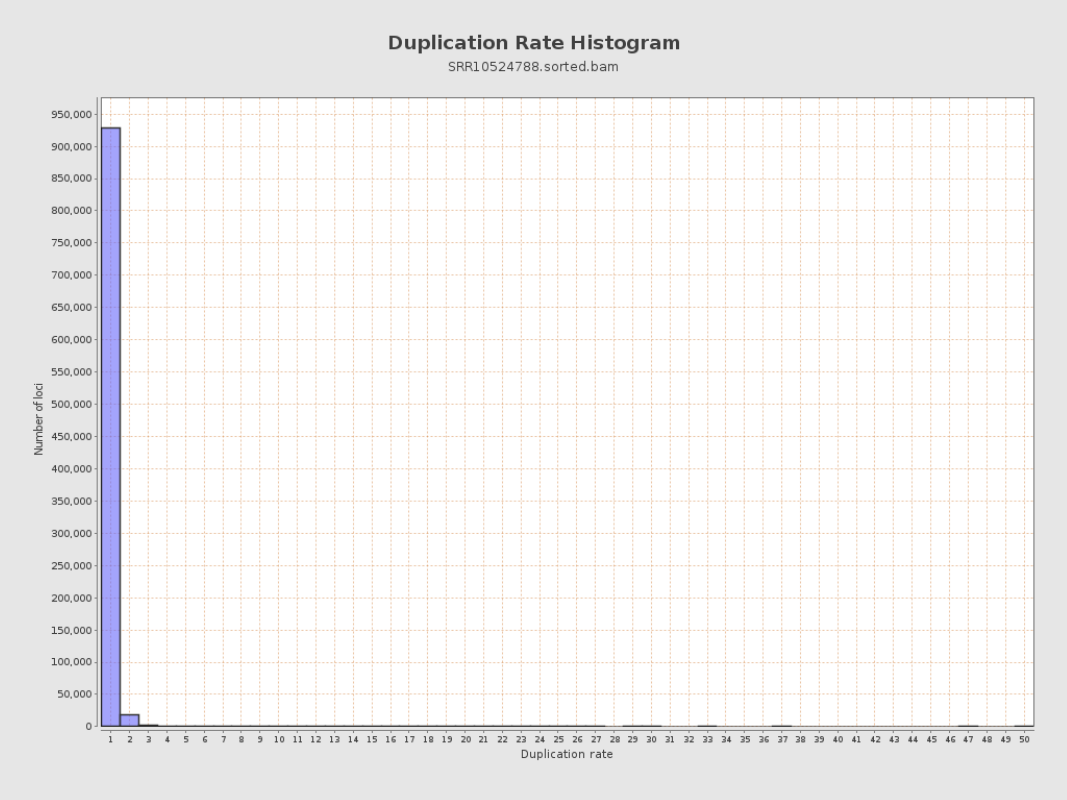
5. Results : Coverage Histogram (0-50X)



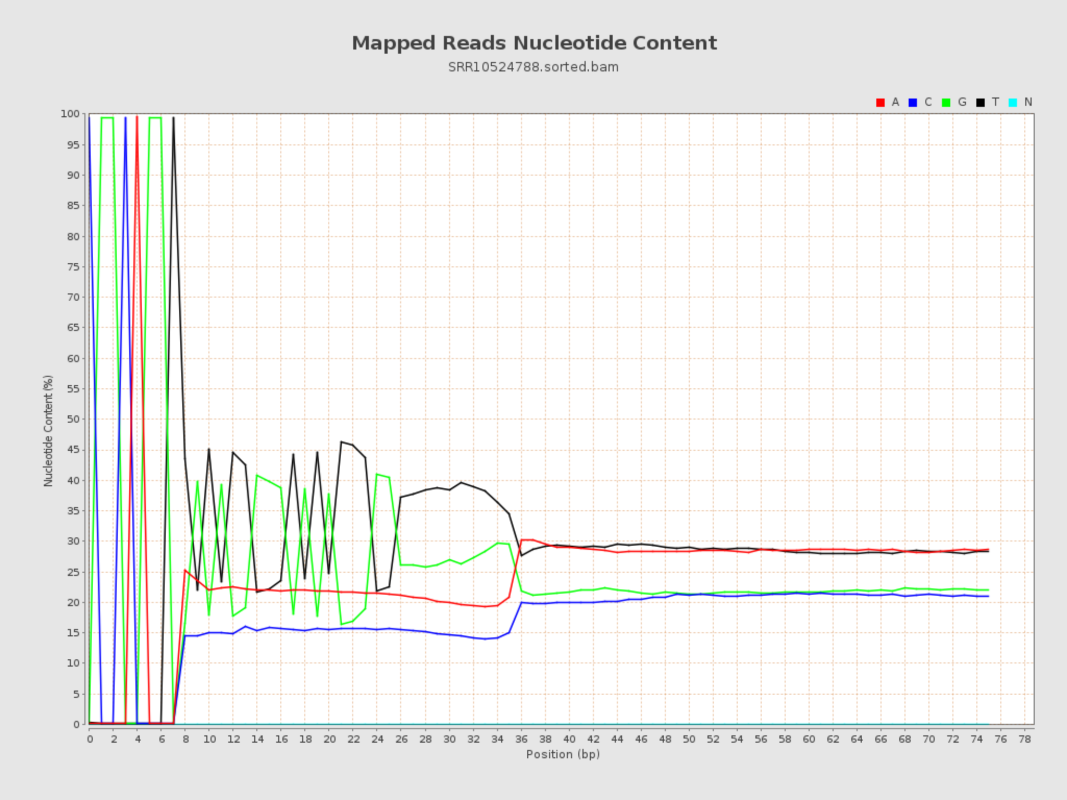
6. Results : Genome Fraction Coverage



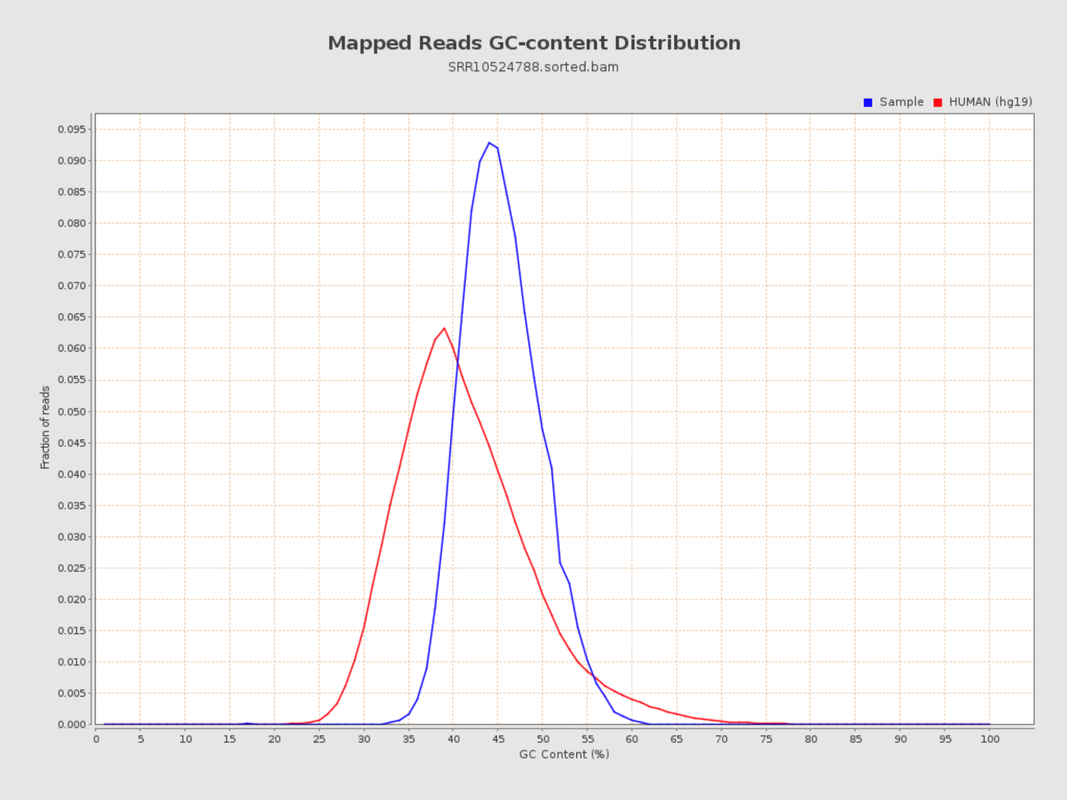
7. Results : Duplication Rate Histogram



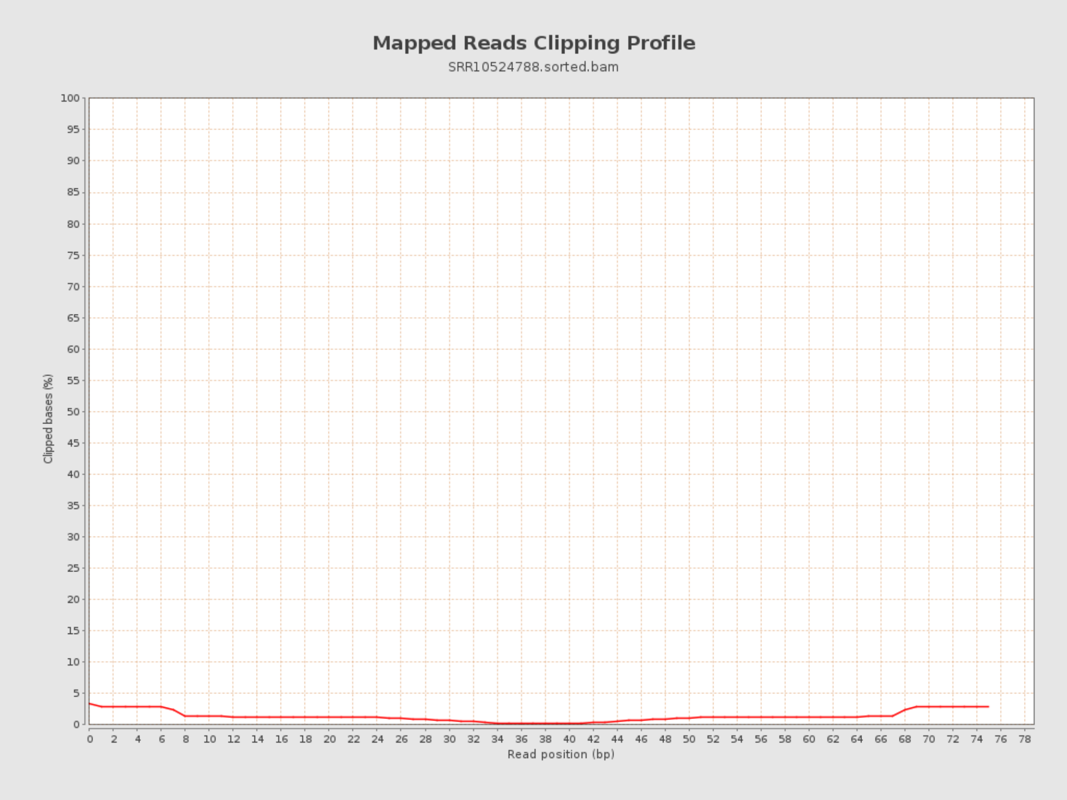
8. Results : Mapped Reads Nucleotide Content



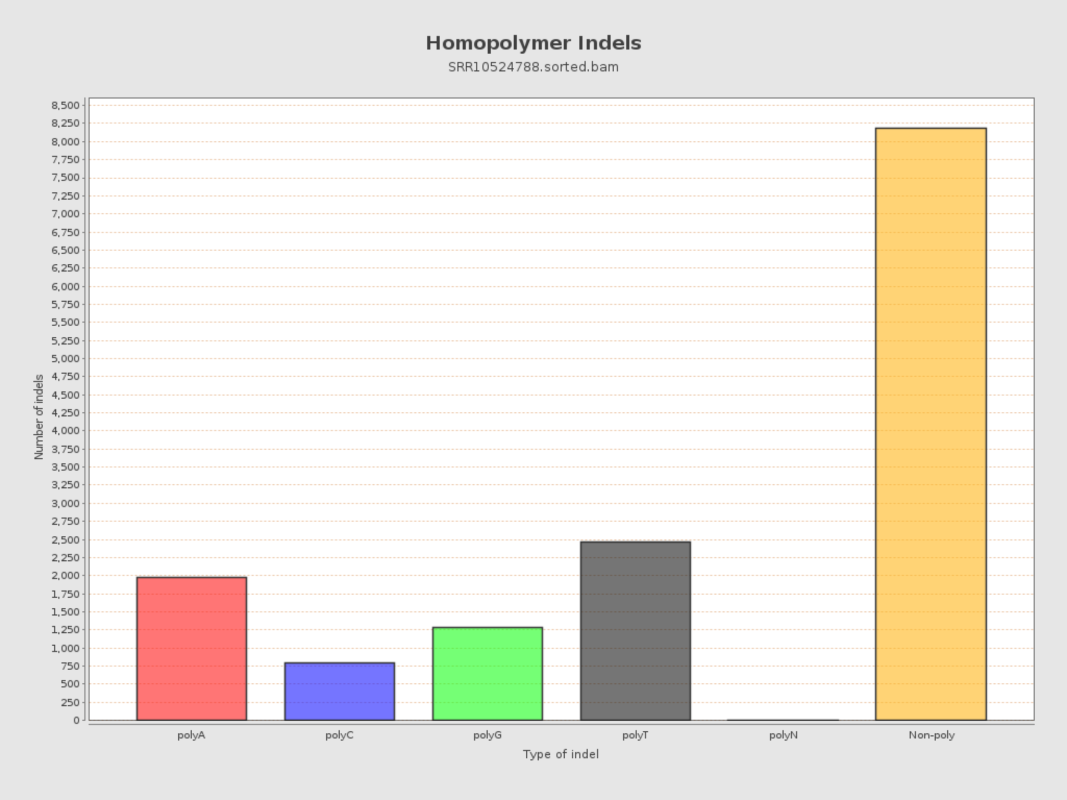
9. Results : Mapped Reads GC-content Distribution



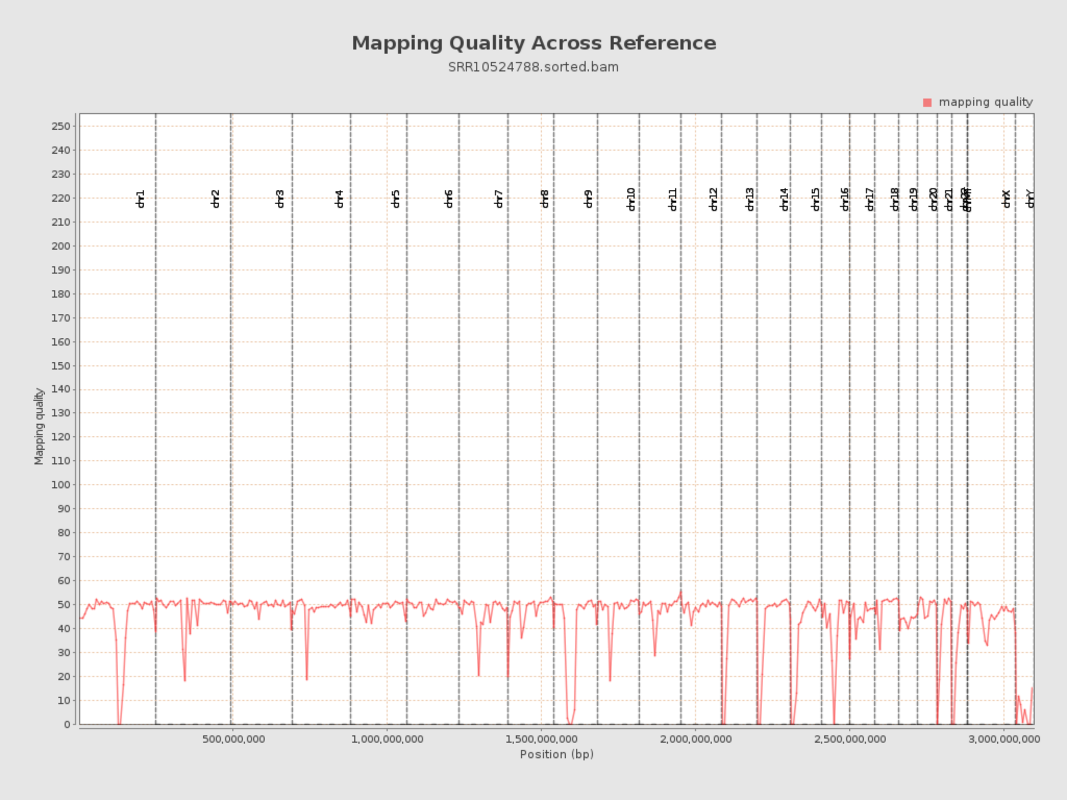
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram