Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:40:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524813.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_SRR10524813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524813.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:40:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,284,541
Mapped reads	1,171,528 / 91.2%
Unmapped reads	113,013 / 8.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,495 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	35,725 / 2.78%
Duplication rate	2.38%
Clipped reads	1,172,099 / 91.25%

2.2. ACGT Content

Number/percentage of A's	17,169,322 / 25.61%
Number/percentage of C's	12,506,645 / 18.66%
Number/percentage of T's	20,466,127 / 30.53%
Number/percentage of G's	16,890,934 / 25.19%
Number/percentage of N's	8,296 / 0.01%
GC Percentage	43.85%

2.3. Coverage

Mean	0.0217

Standard Deviation	0.1941

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

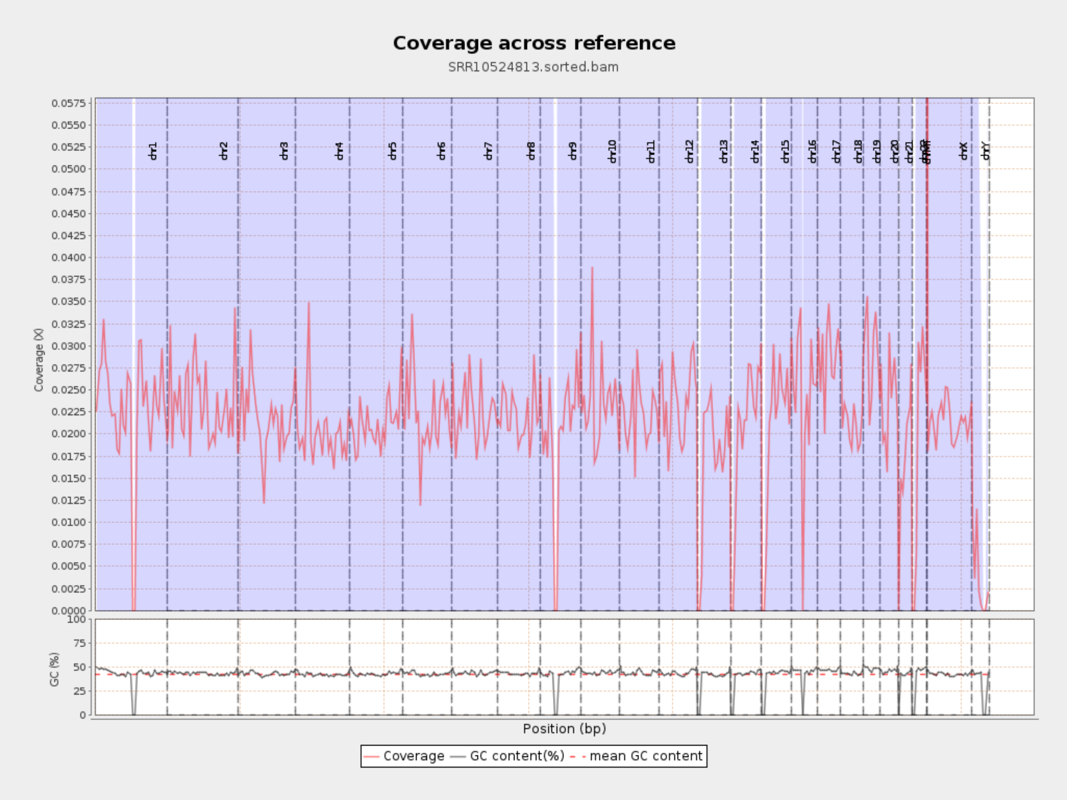
General error rate	0.52%
Mismatches	335,056
Insertions	5,500
Mapped reads with at least one insertion	0.47%
Deletions	13,356
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.29%

2.6. Chromosome stats

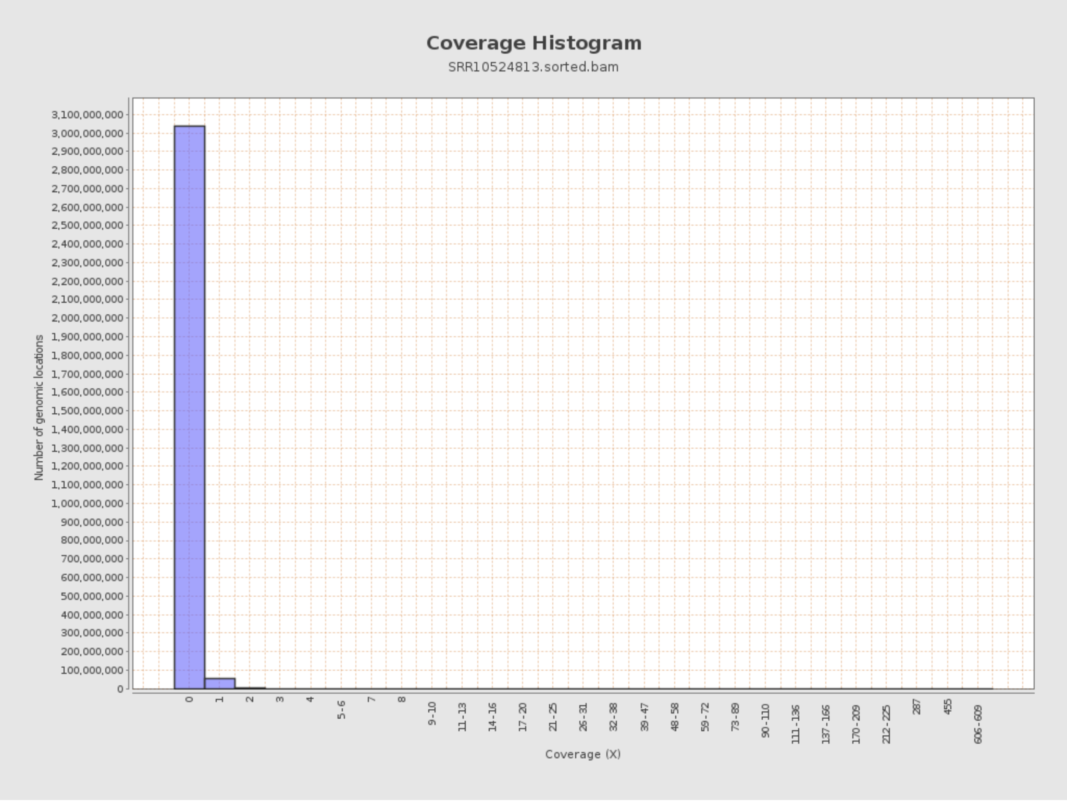
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5667504	0.0227	0.2307
chr2	243199373	5724358	0.0235	0.302
chr3	198022430	4298656	0.0217	0.1611
chr4	191154276	3901770	0.0204	0.1697
chr5	180915260	3837410	0.0212	0.1576
chr6	171115067	3795022	0.0222	0.1734
chr7	159138663	3597669	0.0226	0.2188

chr8	146364022	3220828	0.022	0.18
chr9	141213431	2795158	0.0198	0.1729
chr10	135534747	3186568	0.0235	0.2274
chr11	135006516	3037925	0.0225	0.1806
chr12	133851895	3175674	0.0237	0.1673
chr13	115169878	1949093	0.0169	0.1408
chr14	107349540	2112887	0.0197	0.1549
chr15	102531392	2026072	0.0198	0.1533
chr16	90354753	2160592	0.0239	0.1791
chr17	81195210	2345505	0.0289	0.1869
chr18	78077248	1649945	0.0211	0.2305
chr19	59128983	1723236	0.0291	0.2229
chr20	63025520	1489912	0.0236	0.1718
chr21	48129895	832291	0.0173	0.1523
chr22	51304566	989978	0.0193	0.1517
chrMT	16571	22776	1.3744	1.3831
chrX	155270560	3313133	0.0213	0.1652
chrY	59373566	209205	0.0035	0.1025

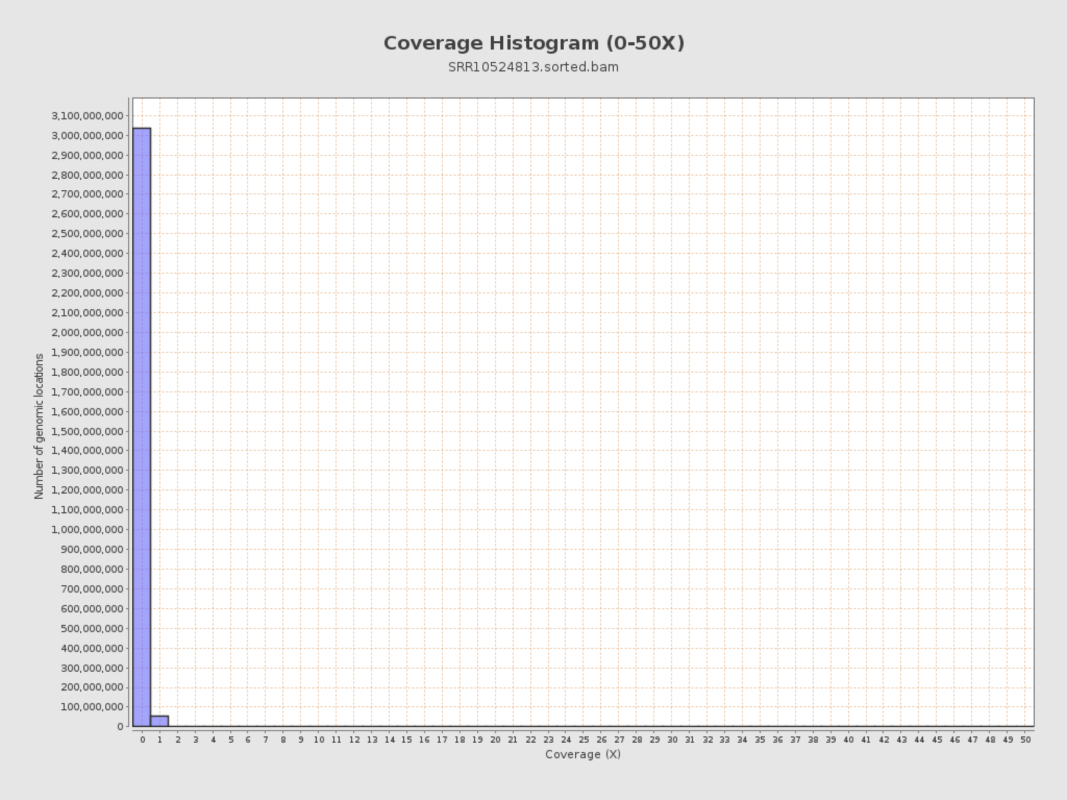
3. Results : Coverage across reference



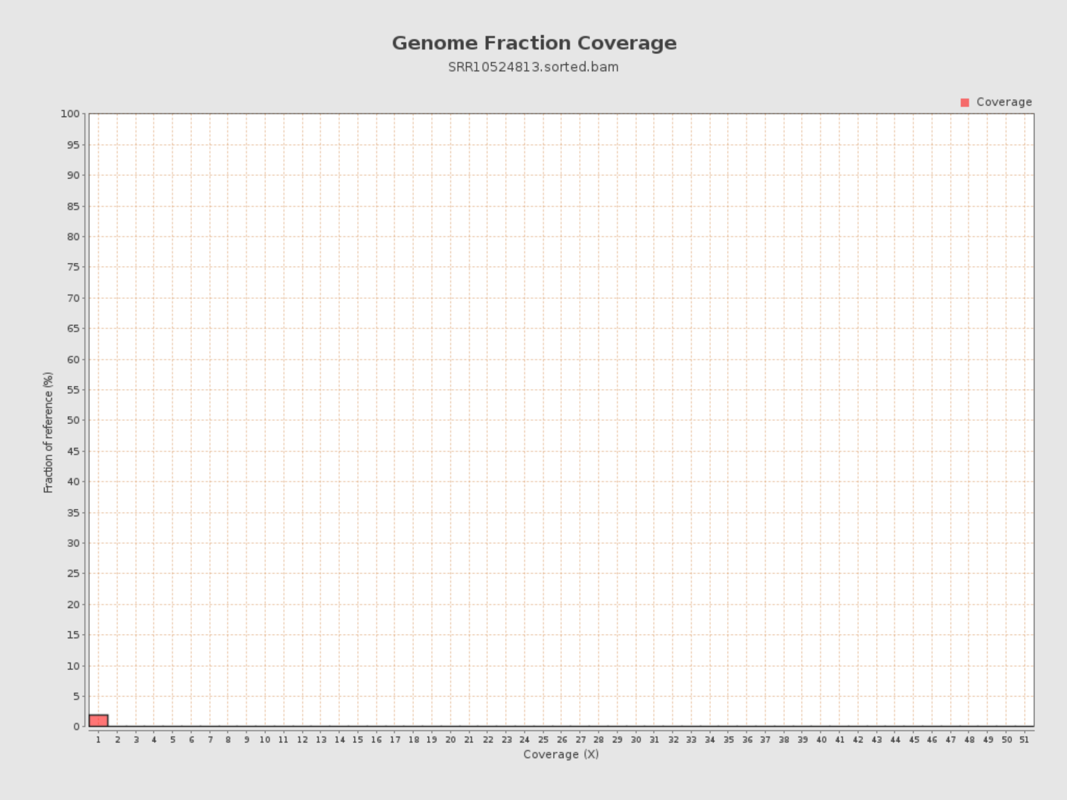
4. Results : Coverage Histogram



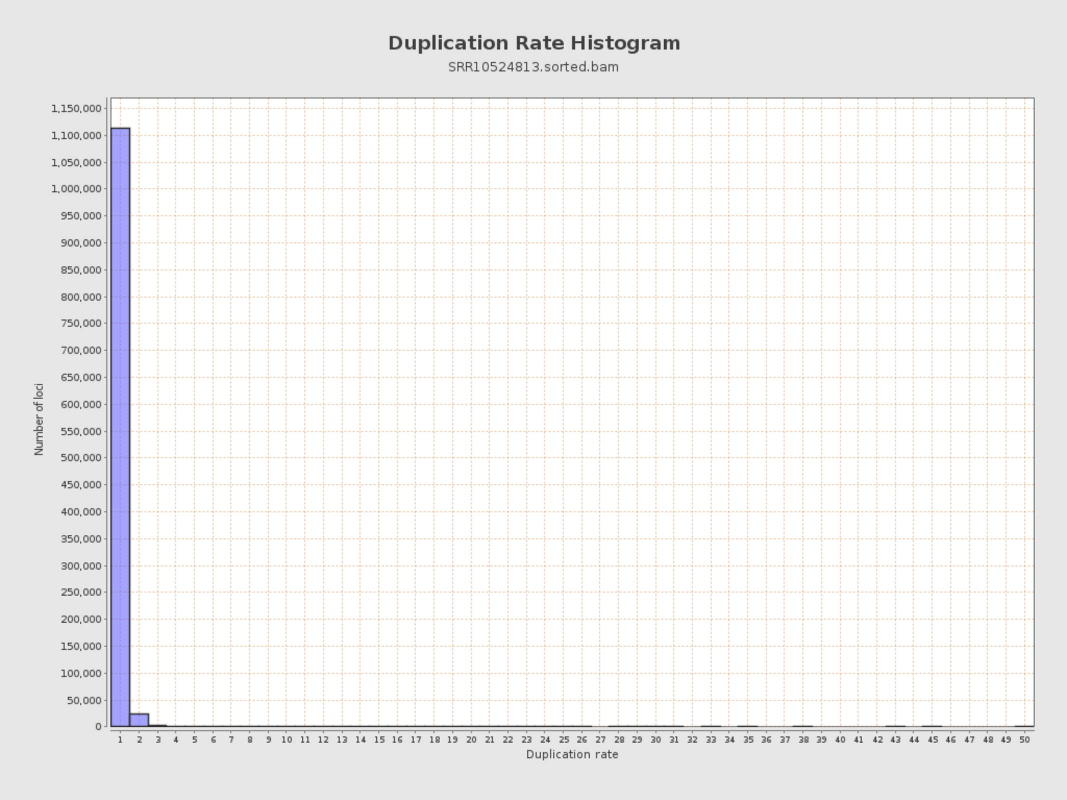
5. Results : Coverage Histogram (0-50X)



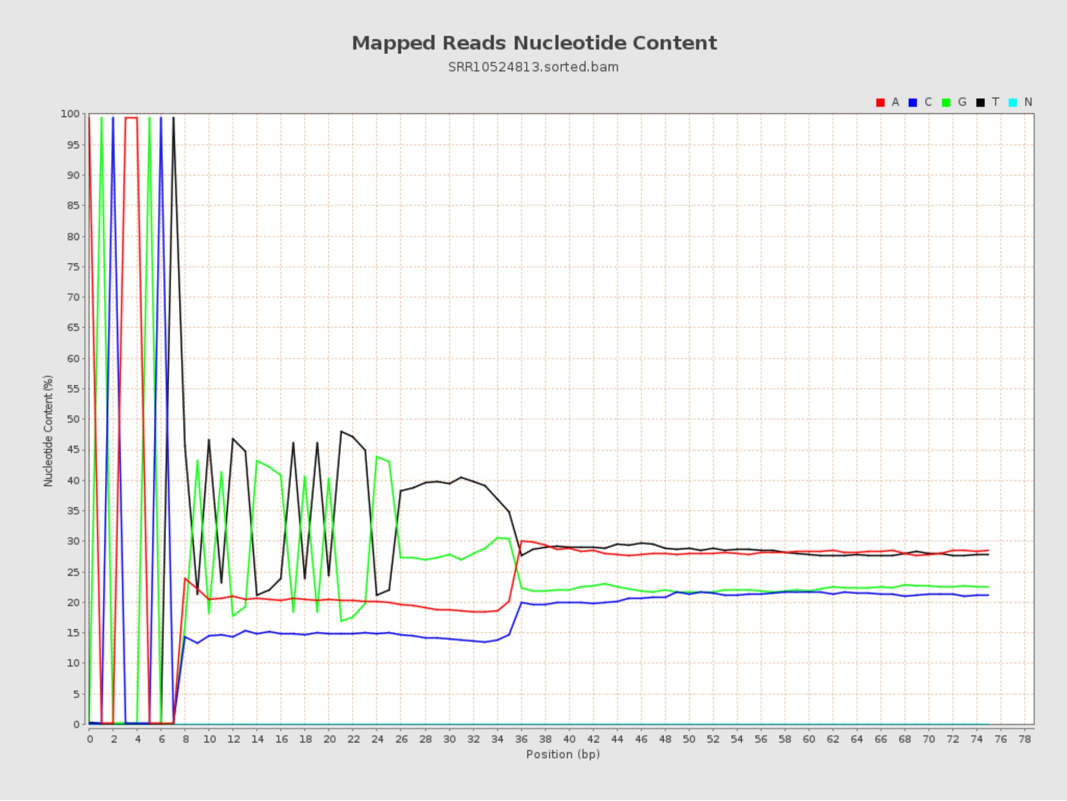
6. Results : Genome Fraction Coverage



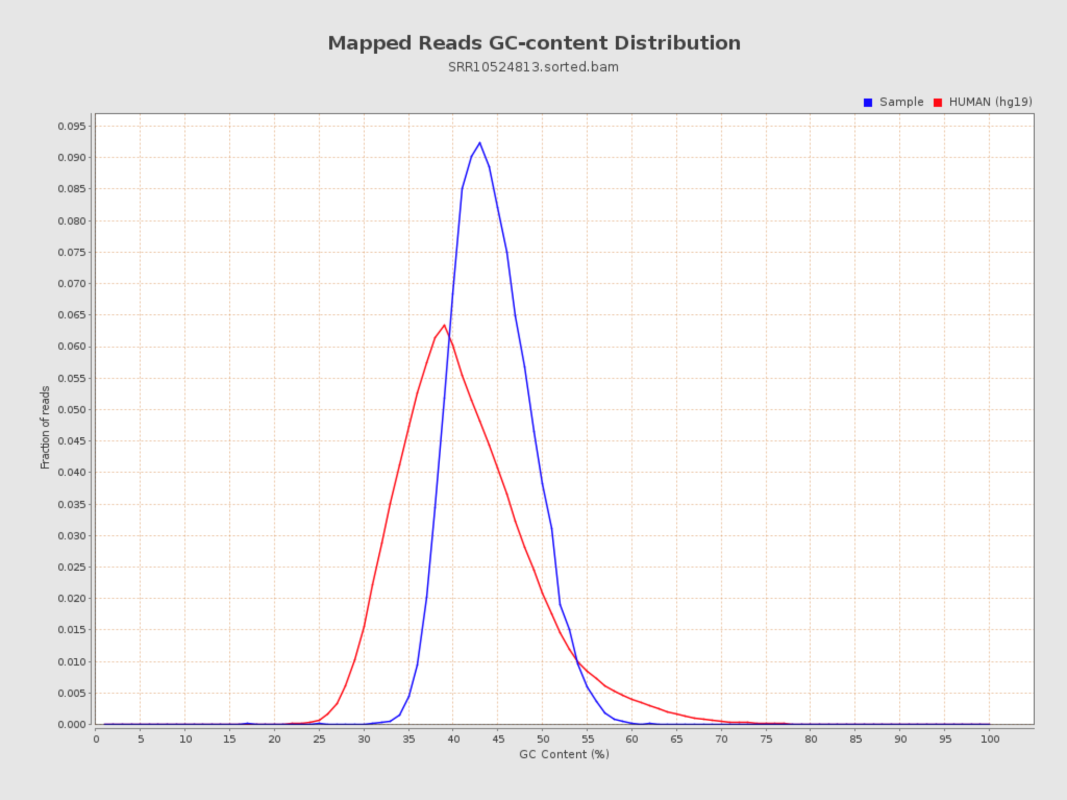
7. Results : Duplication Rate Histogram



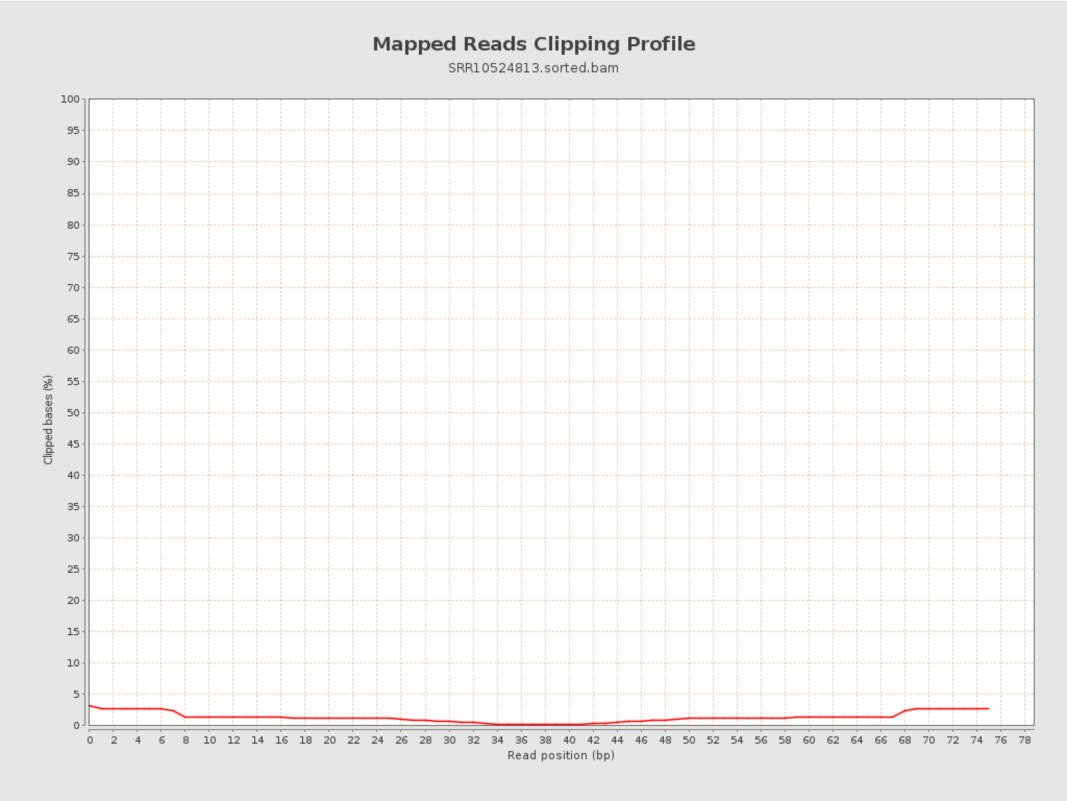
8. Results : Mapped Reads Nucleotide Content



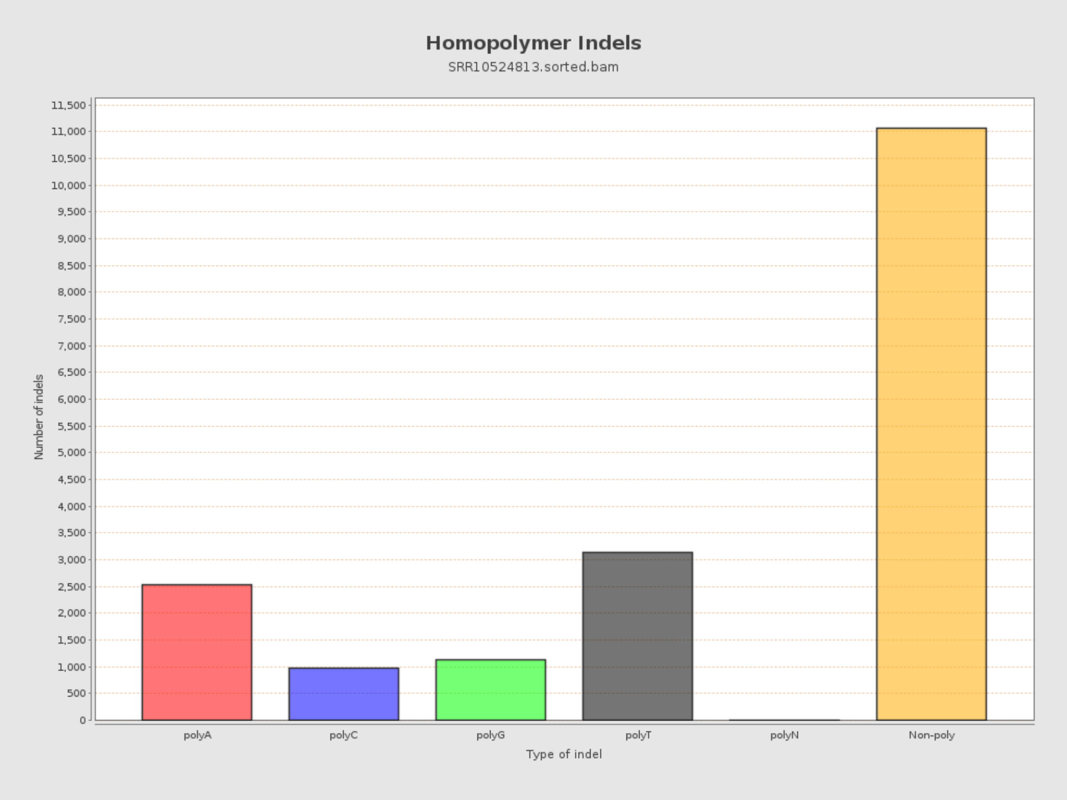
9. Results : Mapped Reads GC-content Distribution



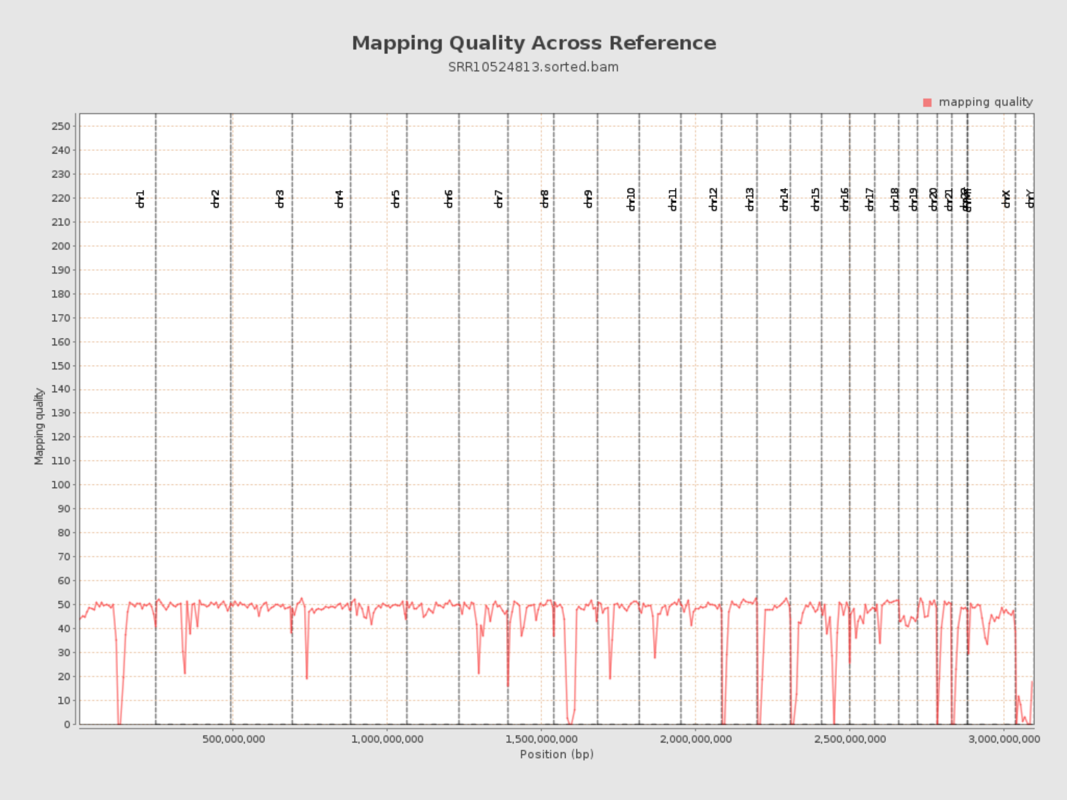
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram