Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:36:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524888.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_SRR10524888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524888.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:36:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,768,006
Mapped reads	1,620,801 / 91.67%
Unmapped reads	147,205 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,228 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	63,059 / 3.57%
Duplication rate	2.84%
Clipped reads	1,622,800 / 91.79%

2.2. ACGT Content

Number/percentage of A's	24,562,314 / 25.95%
Number/percentage of C's	17,438,353 / 18.43%
Number/percentage of T's	30,544,956 / 32.27%
Number/percentage of G's	22,085,009 / 23.33%
Number/percentage of N's	13,098 / 0.01%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.3035

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

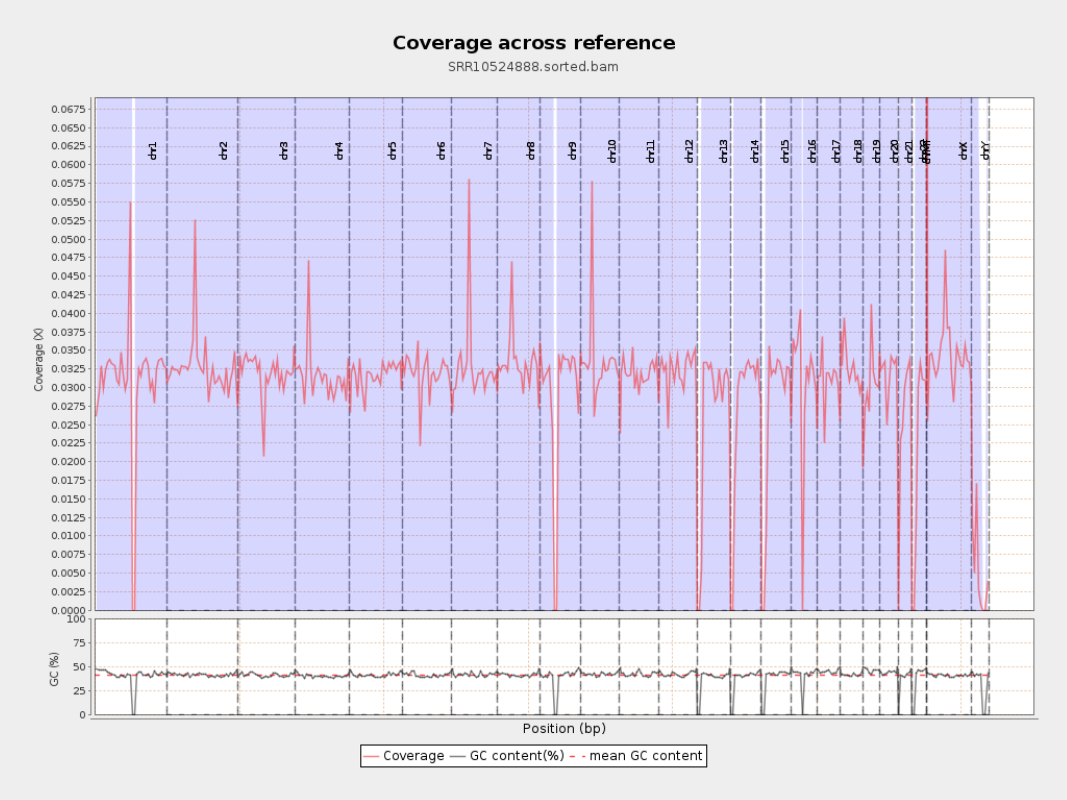
General error rate	0.51%
Mismatches	470,261
Insertions	6,577
Mapped reads with at least one insertion	0.4%
Deletions	17,817
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.63%

2.6. Chromosome stats

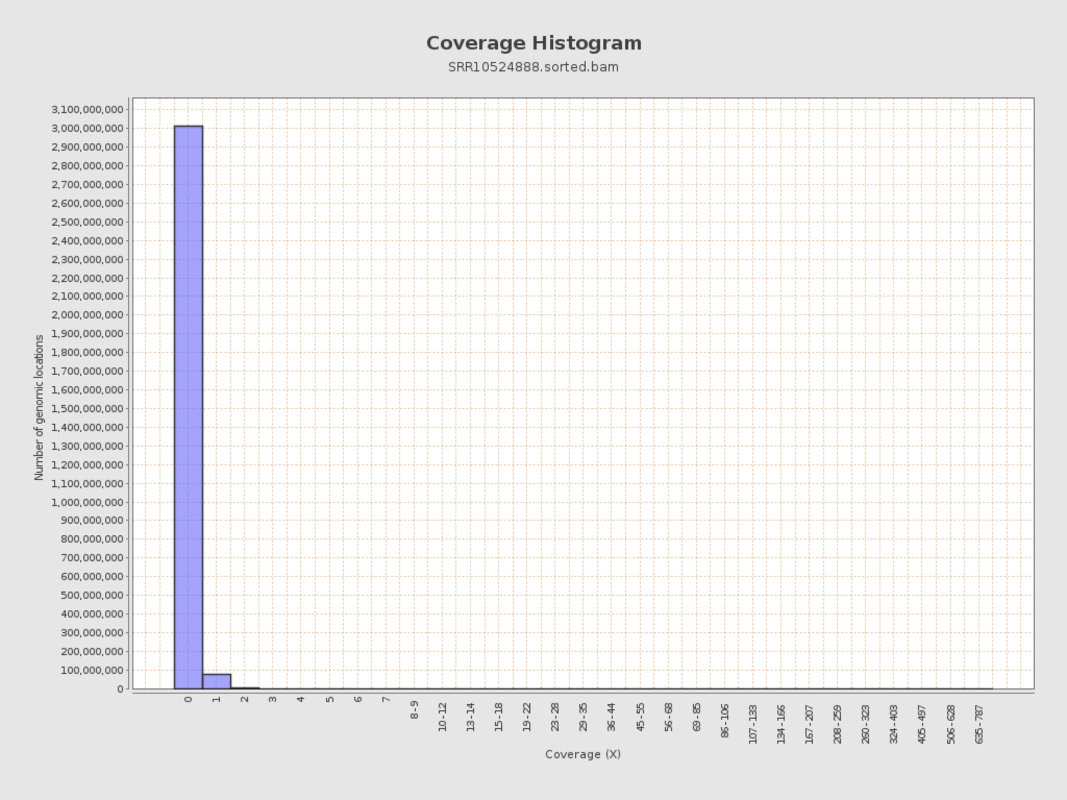
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7587239	0.0304	0.5841
chr2	243199373	7972258	0.0328	0.3287
chr3	198022430	6300215	0.0318	0.192
chr4	191154276	6053206	0.0317	0.214
chr5	180915260	5761118	0.0318	0.1946
chr6	171115067	5453331	0.0319	0.2116
chr7	159138663	5219545	0.0328	0.4398

chr8	146364022	4885112	0.0334	0.2862
chr9	141213431	4038154	0.0286	0.2738
chr10	135534747	4563572	0.0337	0.2818
chr11	135006516	4312637	0.0319	0.2702
chr12	133851895	4327628	0.0323	0.2008
chr13	115169878	3002517	0.0261	0.1743
chr14	107349540	2892112	0.0269	0.1878
chr15	102531392	2691130	0.0262	0.1753
chr16	90354753	2725125	0.0302	0.2102
chr17	81195210	2509724	0.0309	0.2074
chr18	78077248	2553574	0.0327	0.5245
chr19	59128983	1811772	0.0306	0.3992
chr20	63025520	1985045	0.0315	0.1956
chr21	48129895	1251921	0.026	0.1958
chr22	51304566	1117035	0.0218	0.1595
chrMT	16571	16461	0.9934	1.2389
chrX	155270560	5352102	0.0345	0.2319
chrY	59373566	289631	0.0049	0.1302

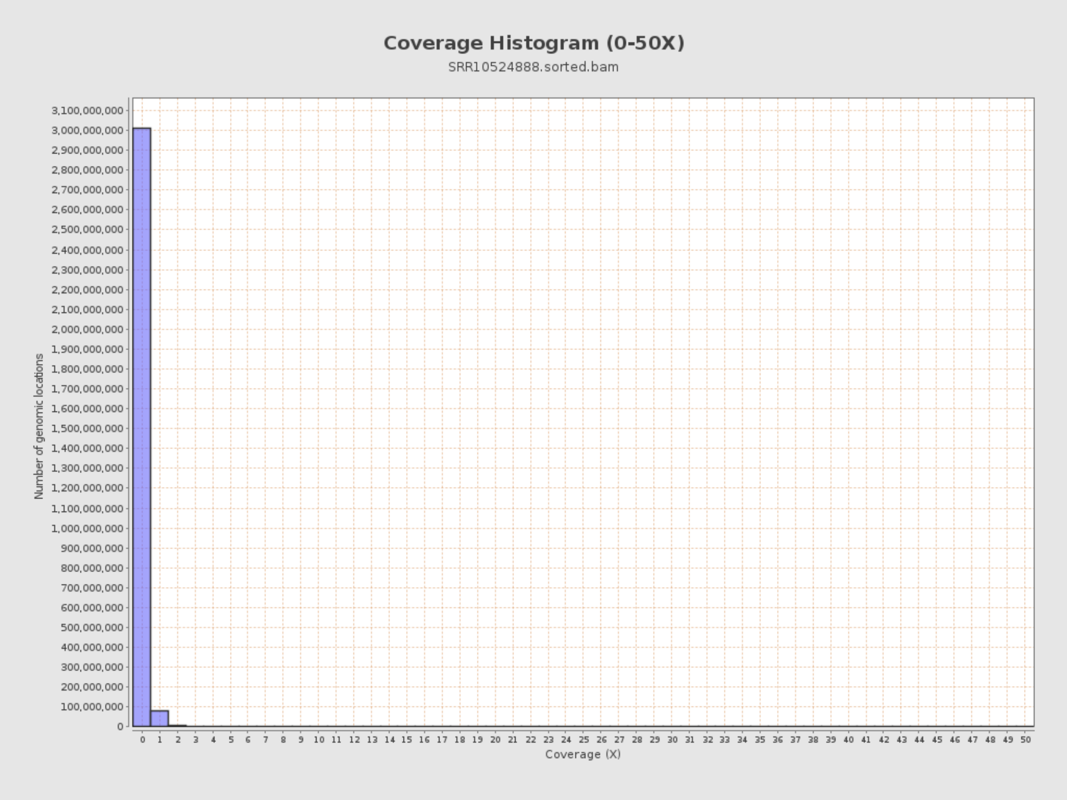
3. Results : Coverage across reference



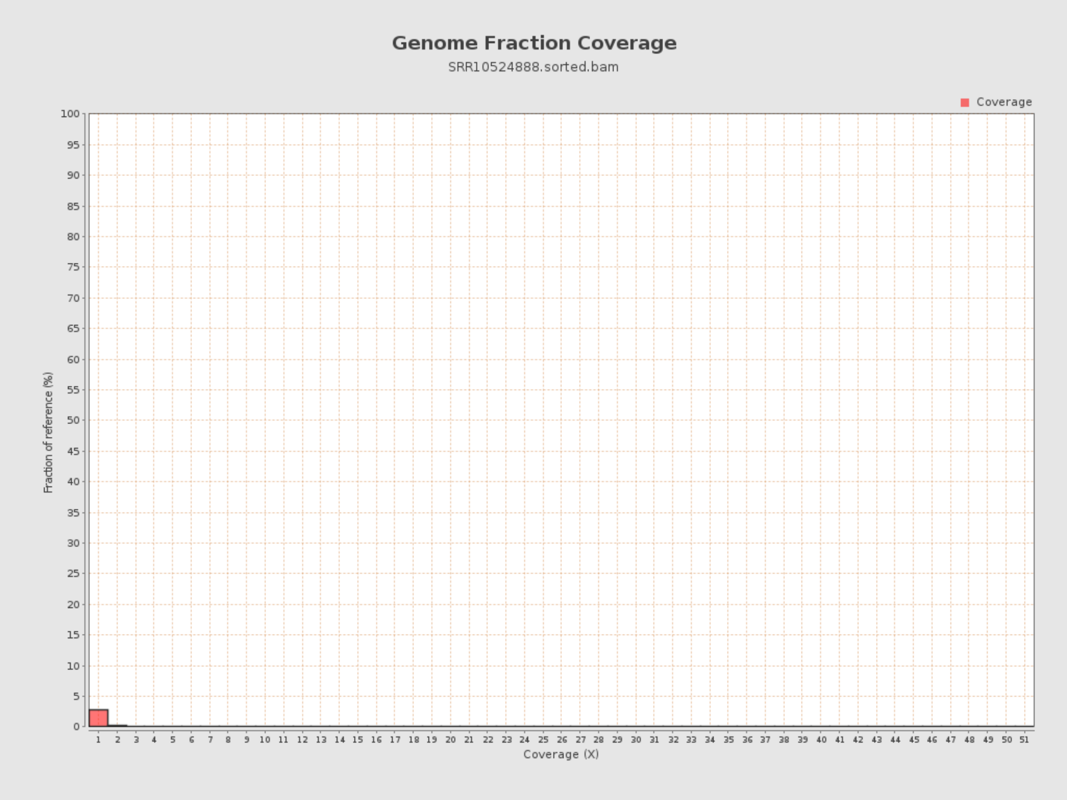
4. Results : Coverage Histogram



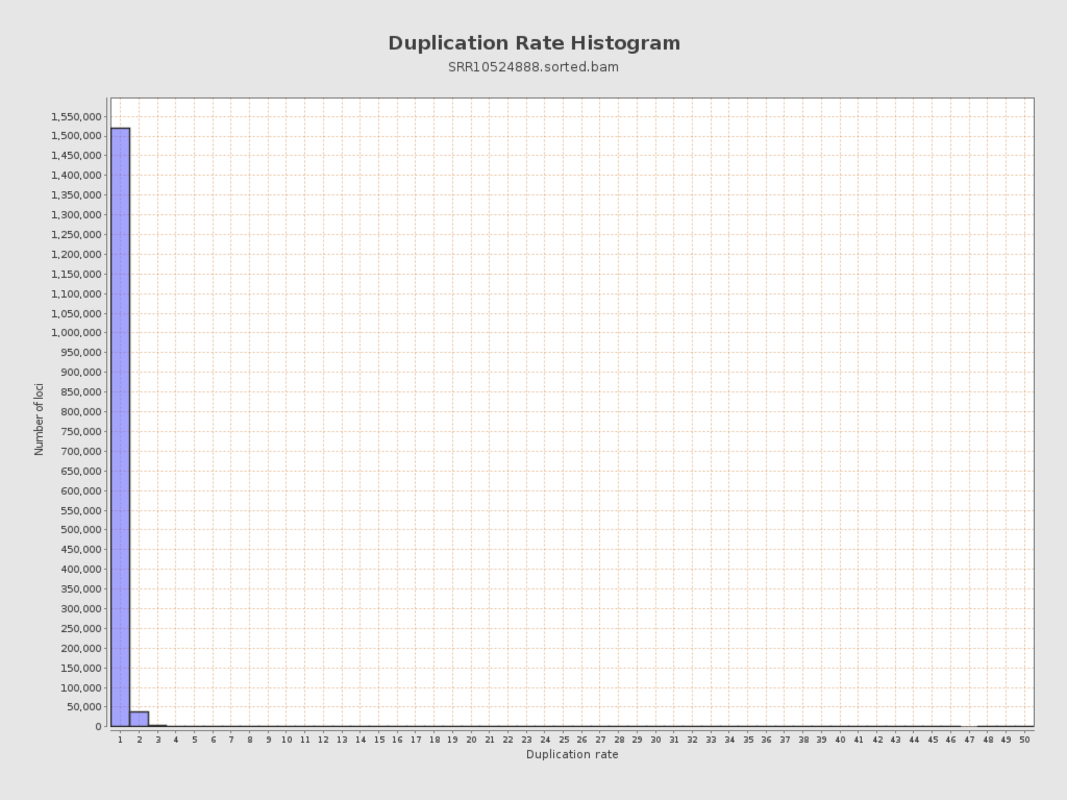
5. Results : Coverage Histogram (0-50X)



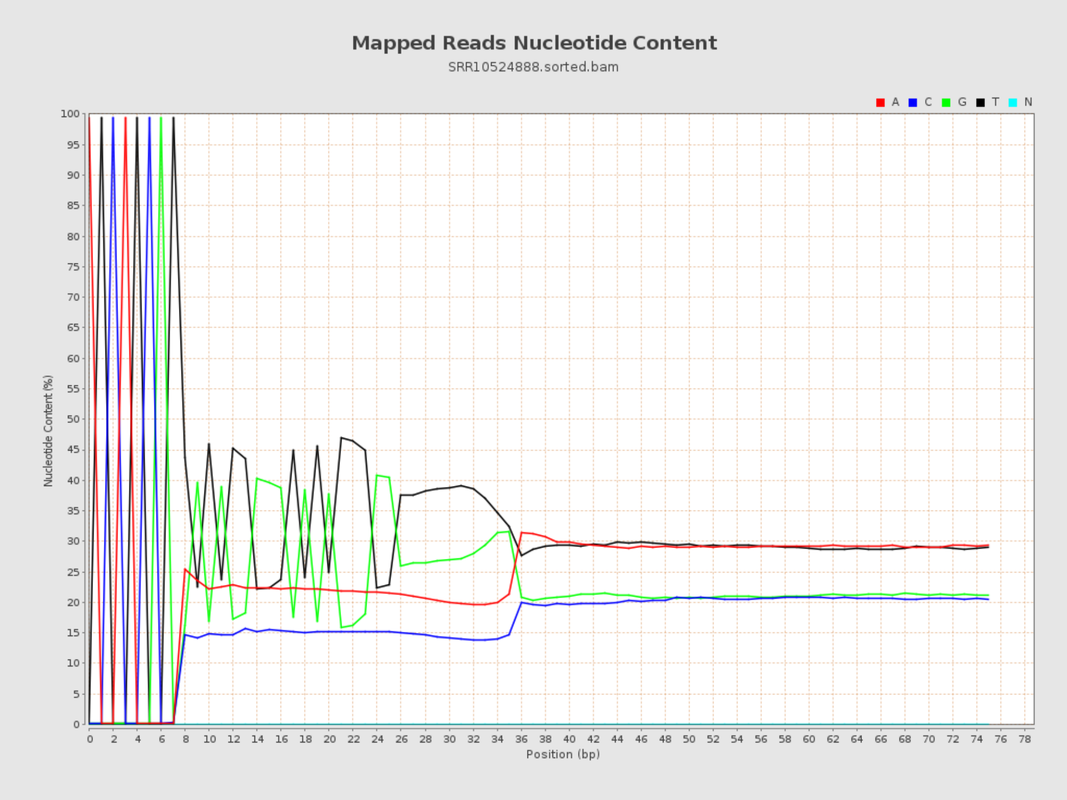
6. Results : Genome Fraction Coverage



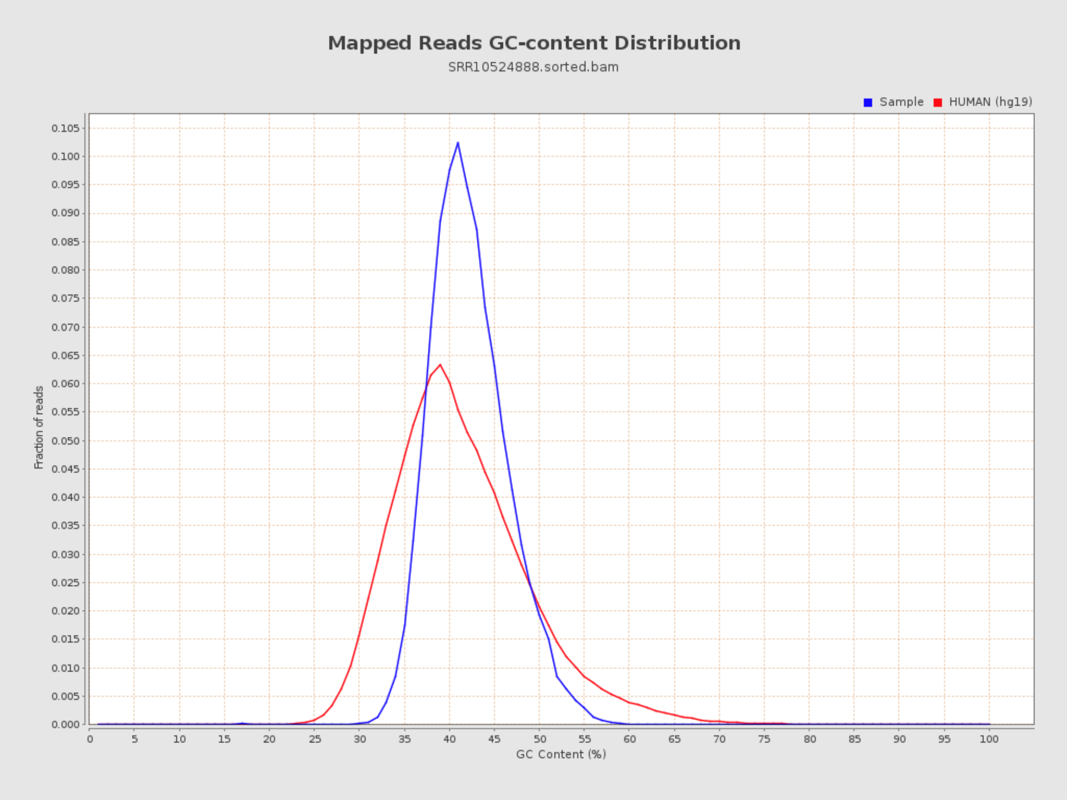
7. Results : Duplication Rate Histogram



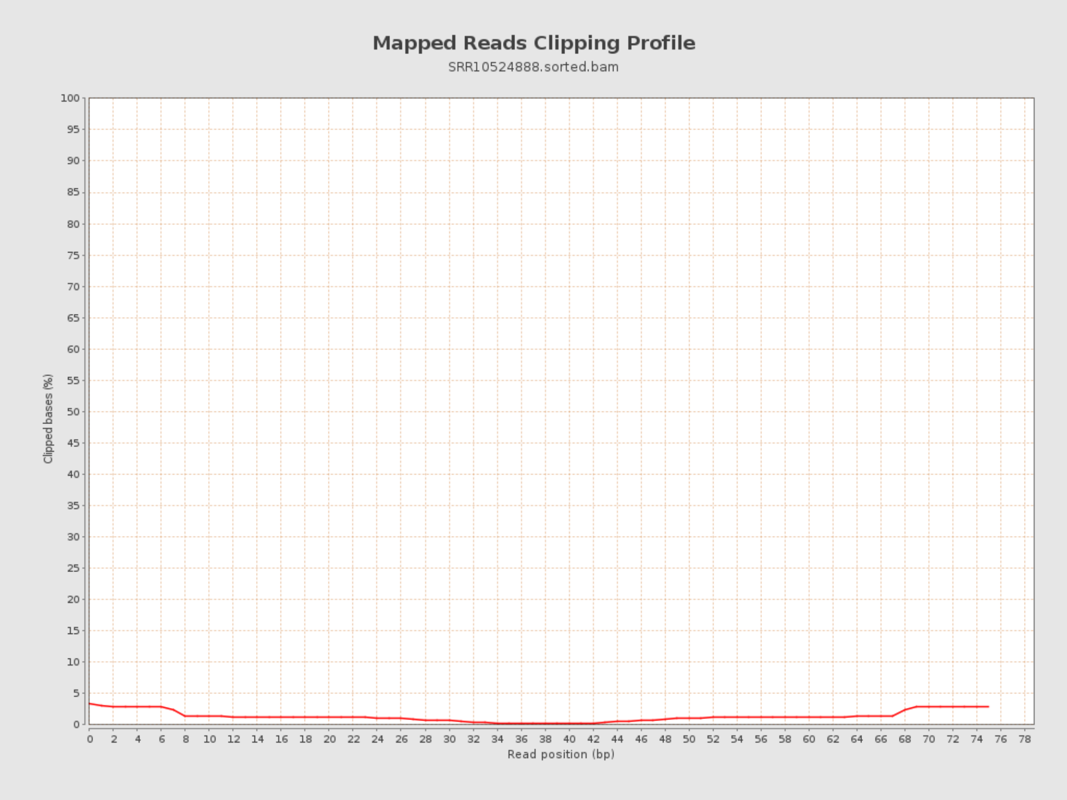
8. Results : Mapped Reads Nucleotide Content



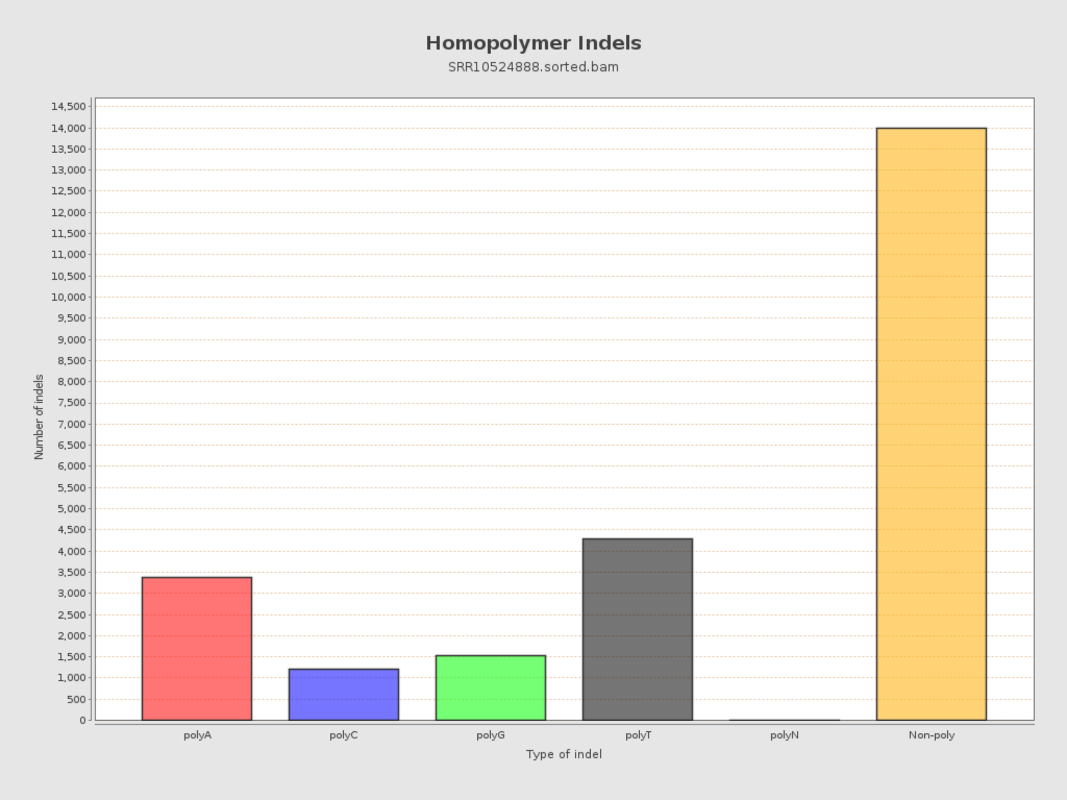
9. Results : Mapped Reads GC-content Distribution



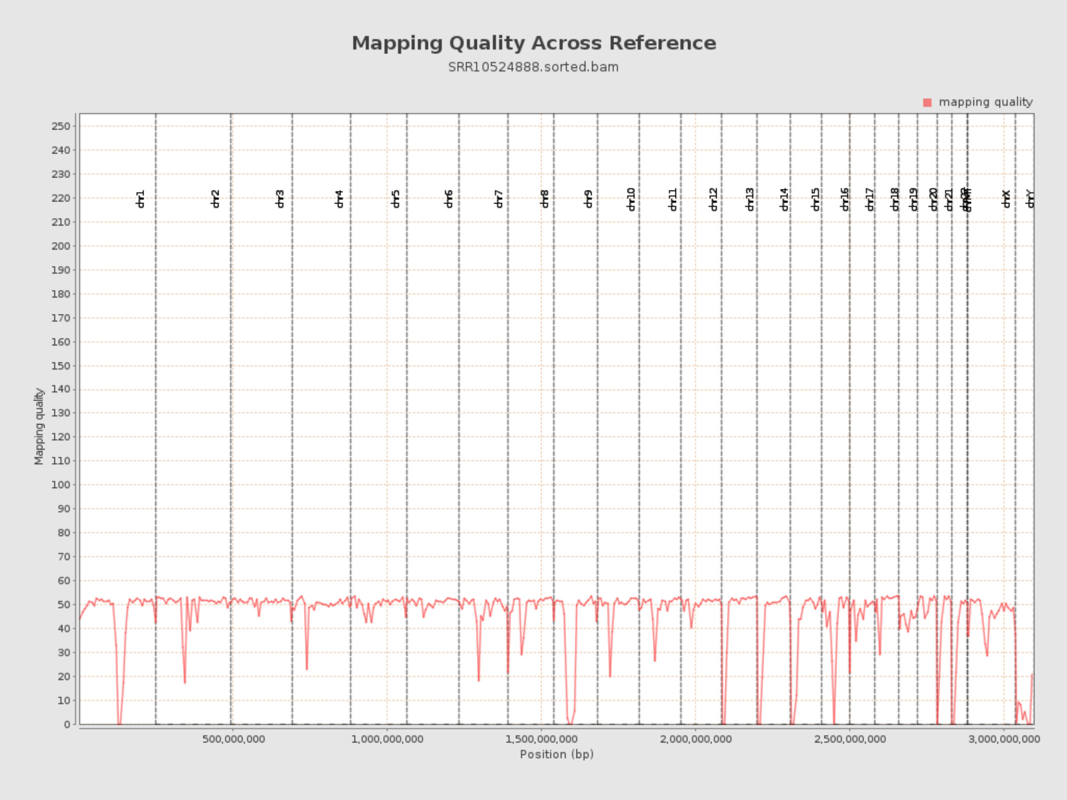
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram