Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:13:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524288.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_SRR10524288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524288.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:13:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,559,092
Mapped reads	1,439,212 / 92.31%
Unmapped reads	119,880 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,126 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	62,715 / 4.02%
Duplication rate	3.29%
Clipped reads	1,440,103 / 92.37%

2.2. ACGT Content

Number/percentage of A's	21,064,531 / 25.09%
Number/percentage of C's	16,096,350 / 19.17%
Number/percentage of T's	26,545,384 / 31.62%
Number/percentage of G's	20,244,790 / 24.11%
Number/percentage of N's	10,208 / 0.01%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2755

2.4. Mapping Quality

Mean Mapping Quality	46.27

2.5. Mismatches and indels

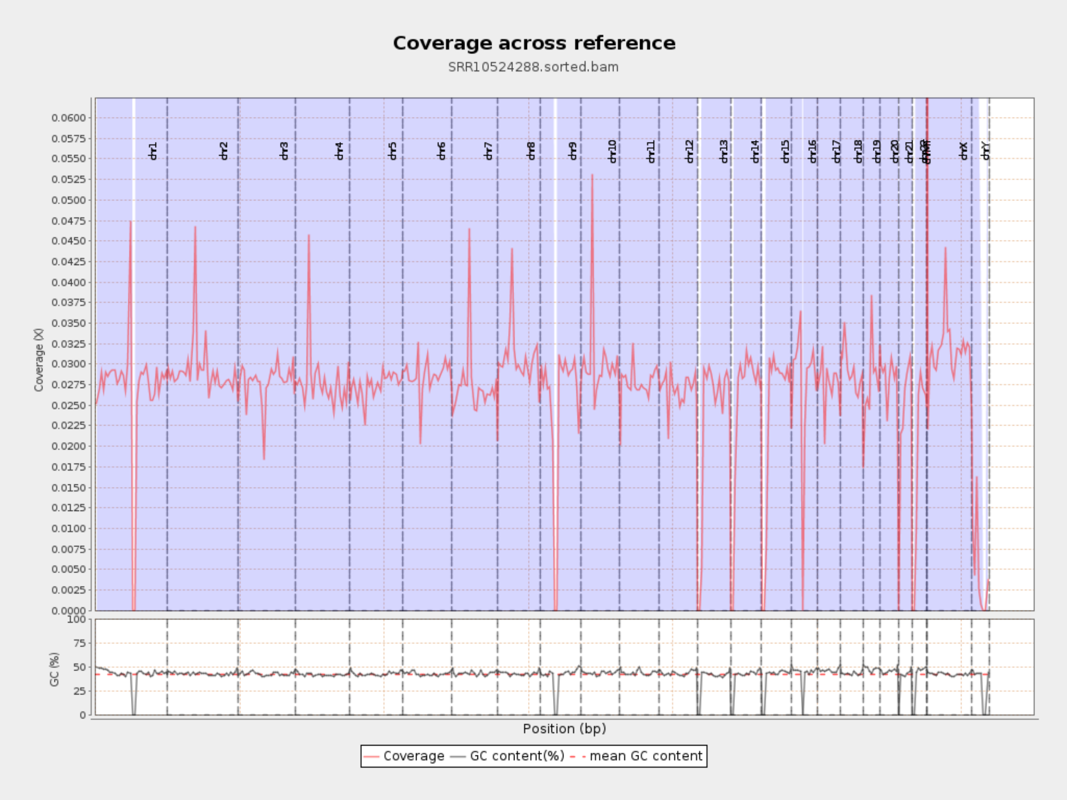
General error rate	0.51%
Mismatches	414,428
Insertions	6,827
Mapped reads with at least one insertion	0.47%
Deletions	15,652
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.24%

2.6. Chromosome stats

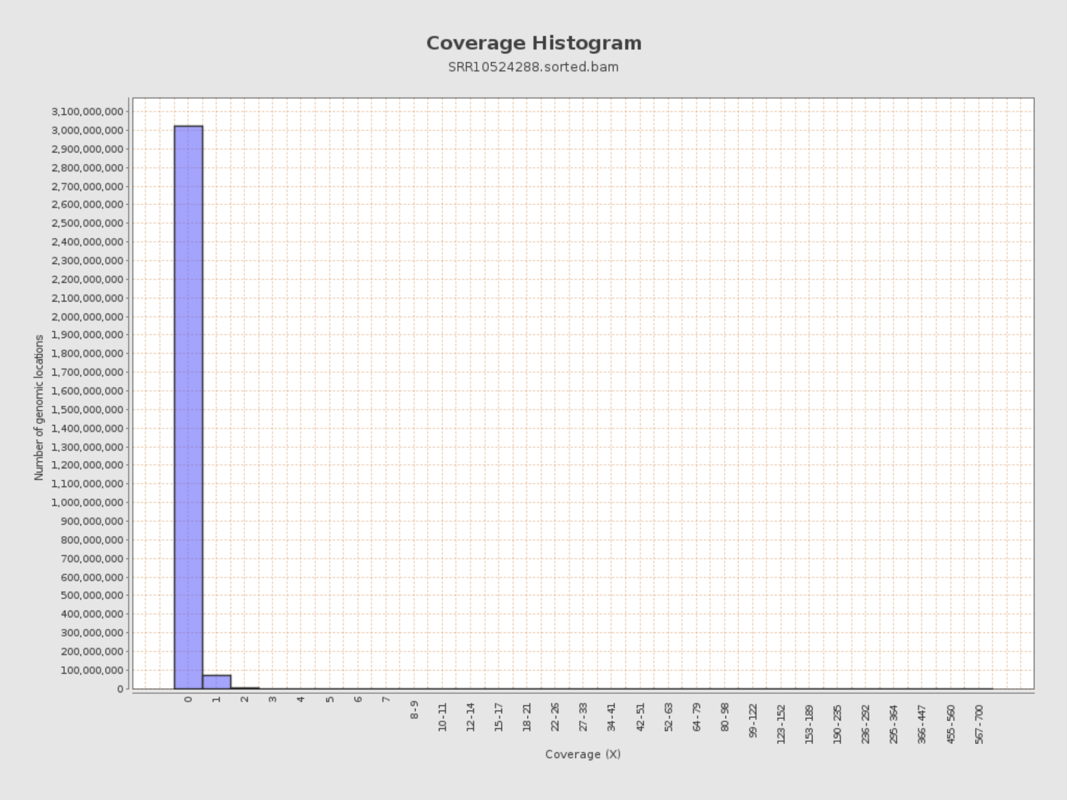
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6700512	0.0269	0.526
chr2	243199373	7138959	0.0294	0.3008
chr3	198022430	5518106	0.0279	0.1813
chr4	191154276	5345417	0.028	0.2032
chr5	180915260	4976192	0.0275	0.1823
chr6	171115067	4895190	0.0286	0.2013
chr7	159138663	4381817	0.0275	0.3439

chr8	146364022	4529747	0.0309	0.2807
chr9	141213431	3532922	0.025	0.2399
chr10	135534747	4118762	0.0304	0.2649
chr11	135006516	3766501	0.0279	0.2532
chr12	133851895	3623922	0.0271	0.183
chr13	115169878	2667138	0.0232	0.1663
chr14	107349540	2636757	0.0246	0.1809
chr15	102531392	2417241	0.0236	0.1693
chr16	90354753	2441705	0.027	0.195
chr17	81195210	2244552	0.0276	0.1952
chr18	78077248	2278416	0.0292	0.4847
chr19	59128983	1656744	0.028	0.3544
chr20	63025520	1776266	0.0282	0.1855
chr21	48129895	1154849	0.024	0.1893
chr22	51304566	969972	0.0189	0.1499
chrMT	16571	11496	0.6937	0.9166
chrX	155270560	4935387	0.0318	0.2199
chrY	59373566	267709	0.0045	0.1324

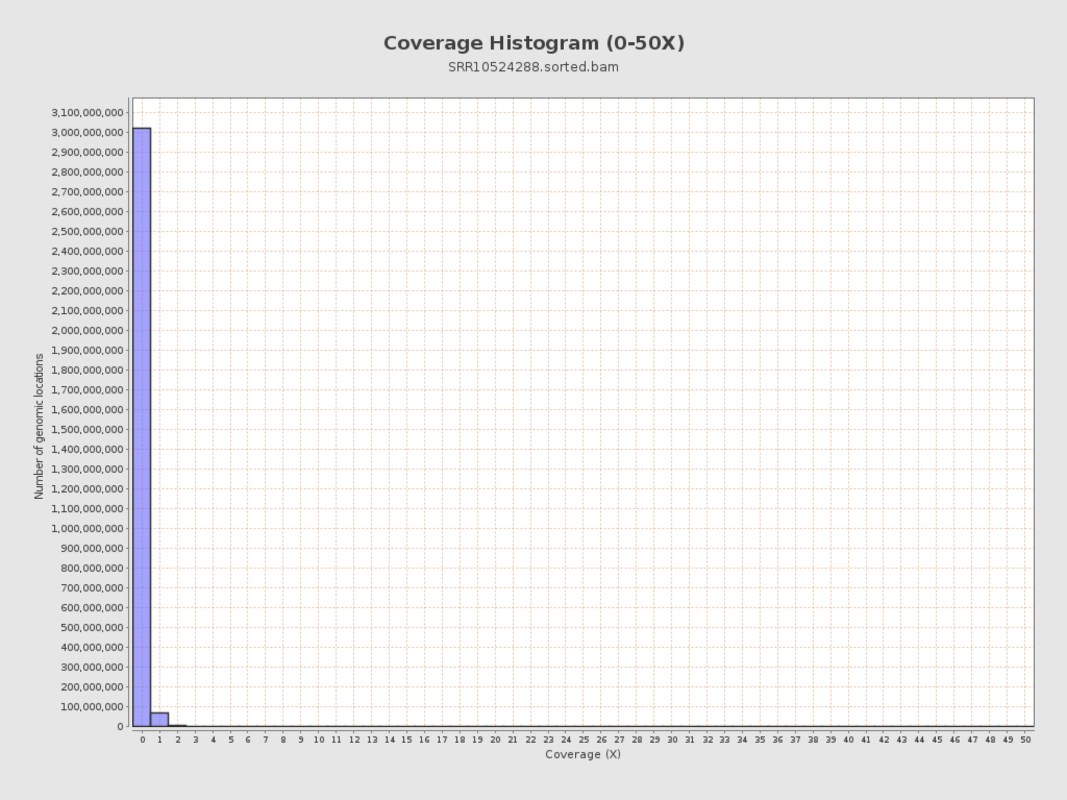
3. Results : Coverage across reference



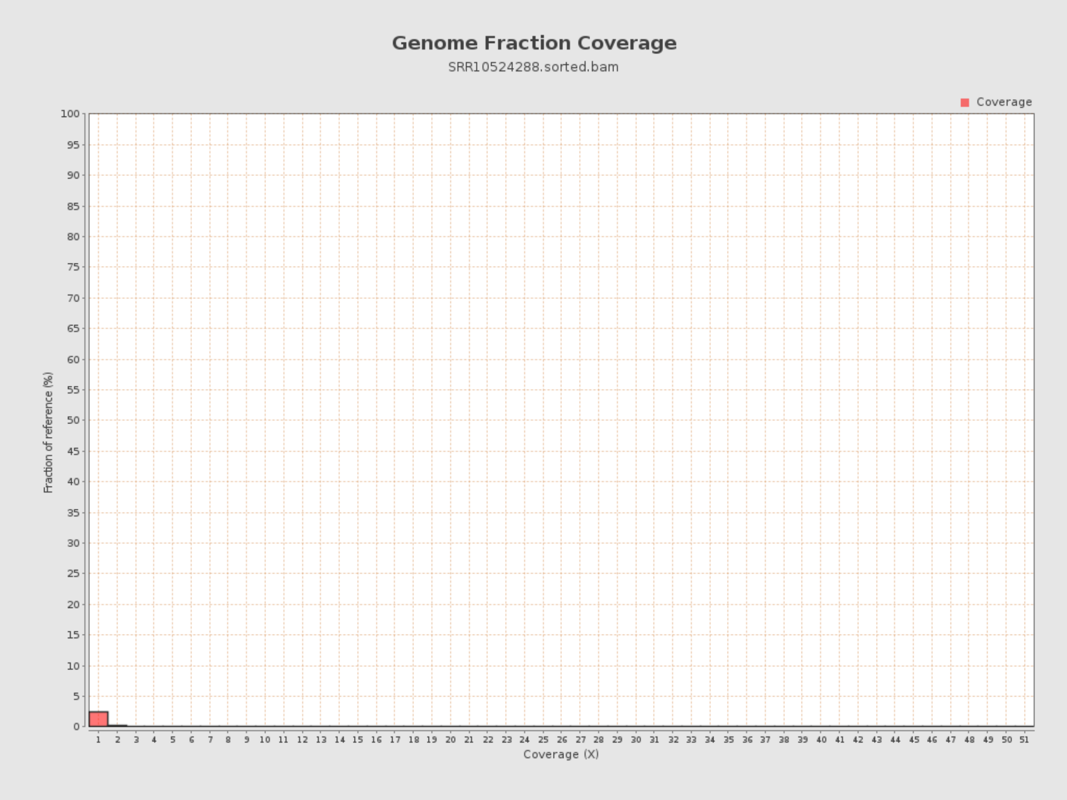
4. Results : Coverage Histogram



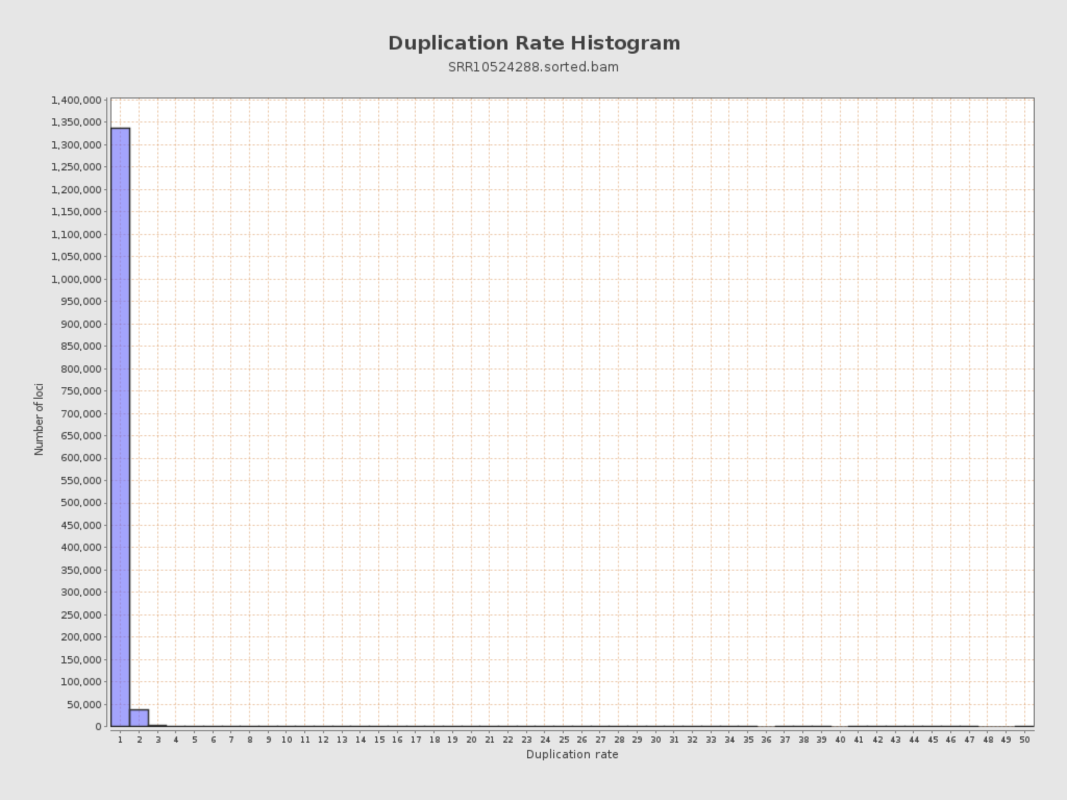
5. Results : Coverage Histogram (0-50X)



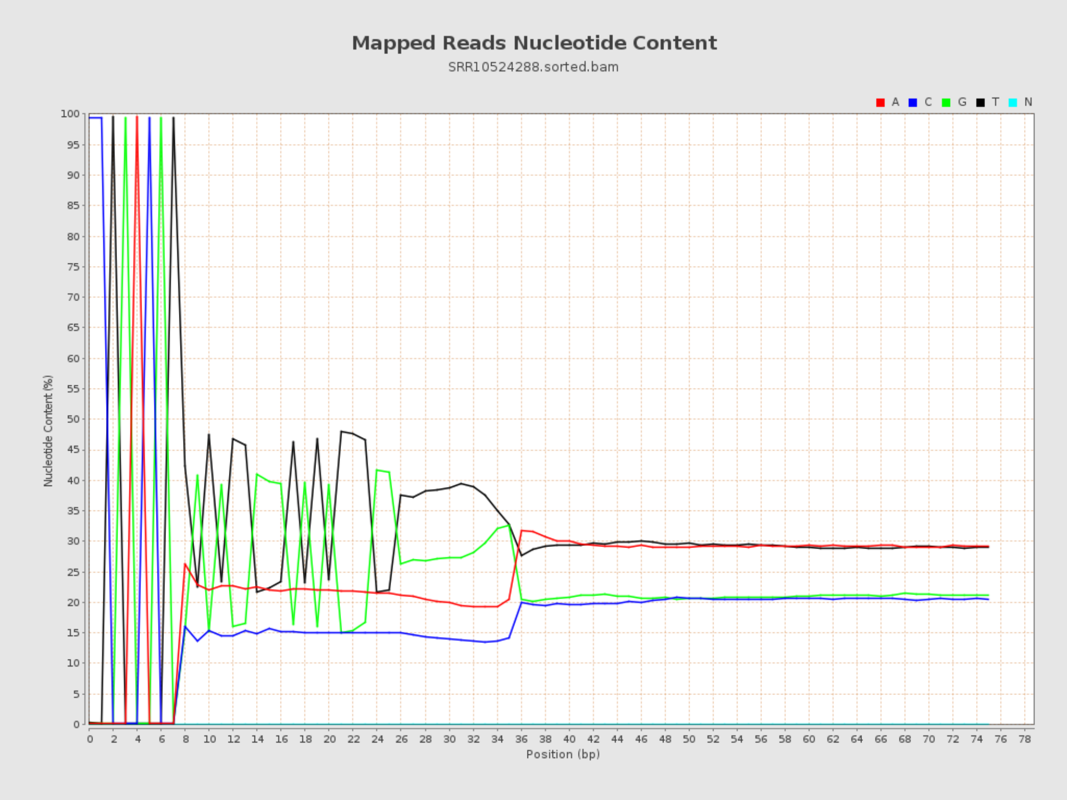
6. Results : Genome Fraction Coverage



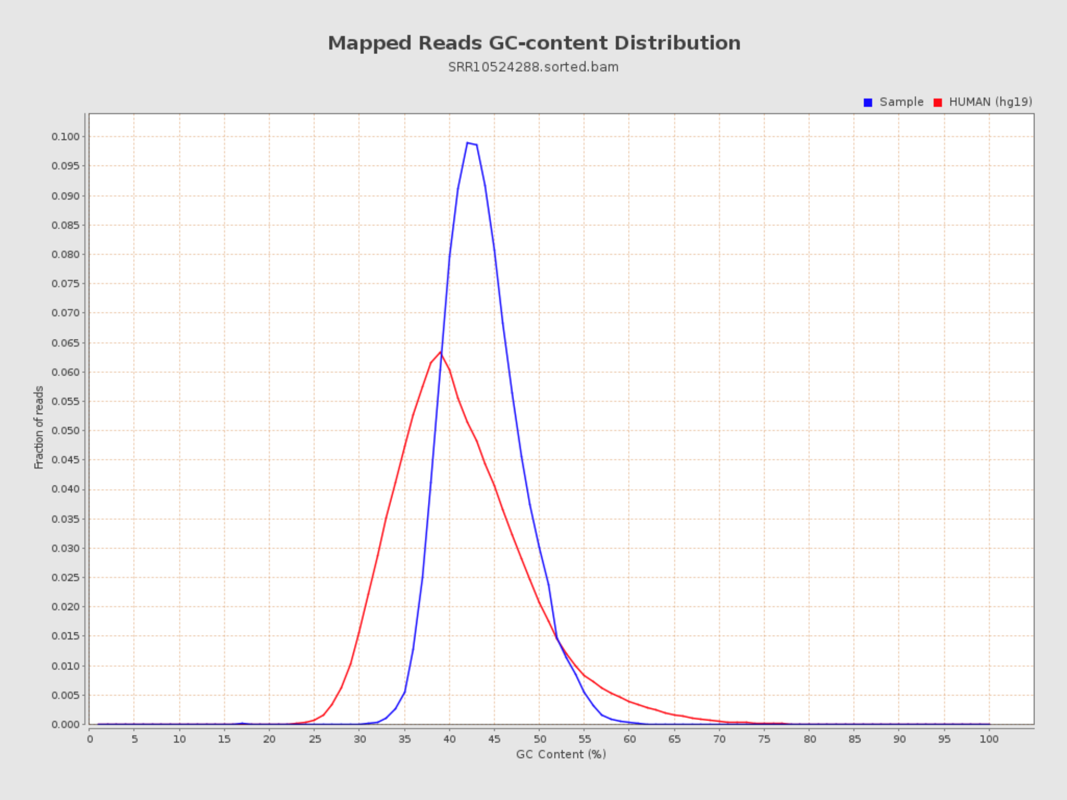
7. Results : Duplication Rate Histogram



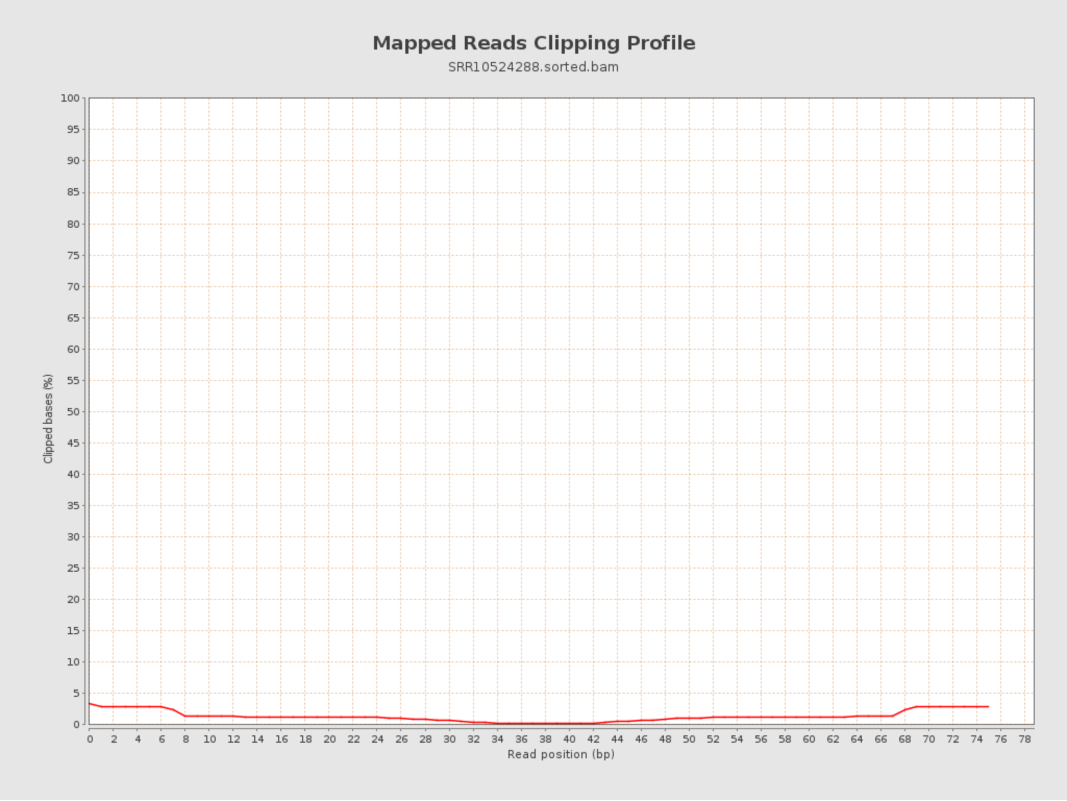
8. Results : Mapped Reads Nucleotide Content



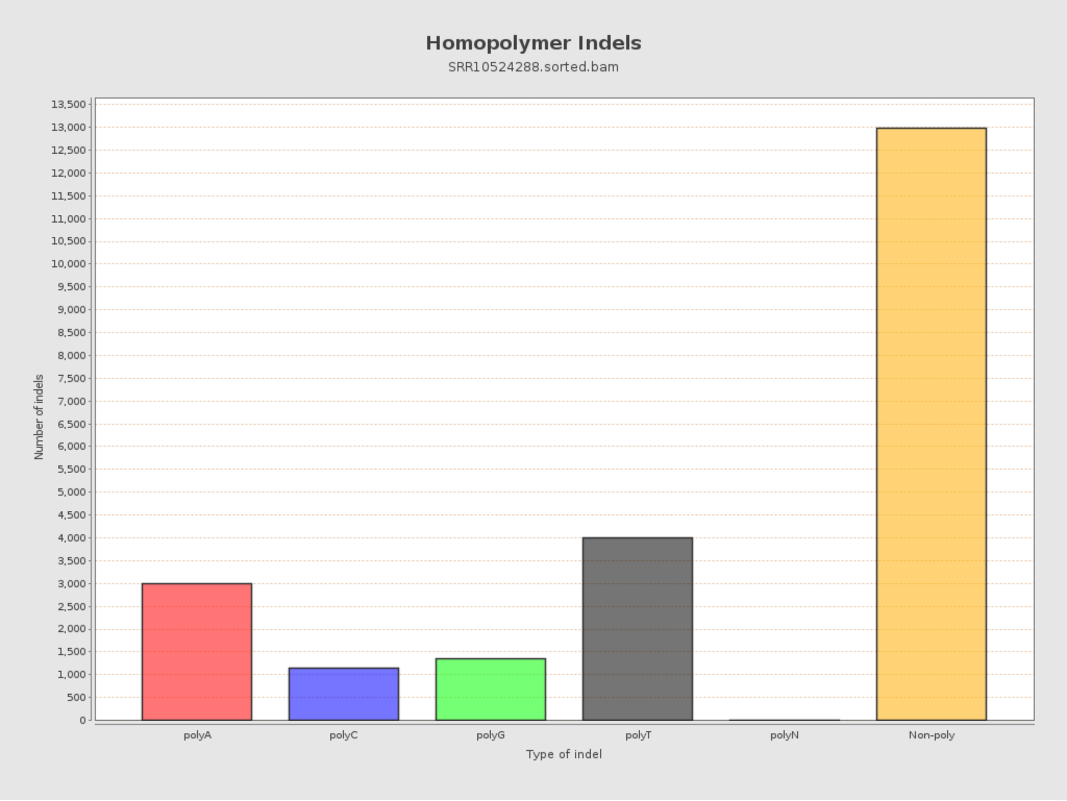
9. Results : Mapped Reads GC-content Distribution



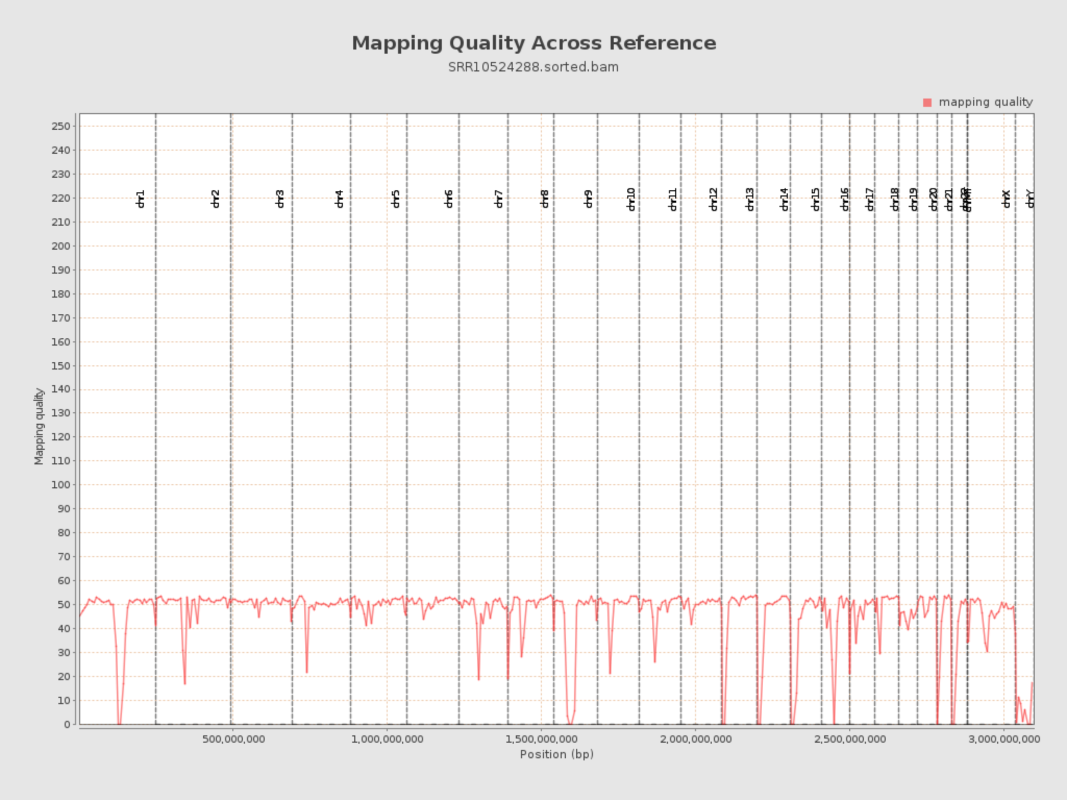
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram