Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:02:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524877.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_SRR10524877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524877.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:02:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,254,555
Mapped reads	2,064,300 / 91.56%
Unmapped reads	190,255 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,956 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	87,283 / 3.87%
Duplication rate	3.02%
Clipped reads	2,073,254 / 91.96%

2.2. ACGT Content

Number/percentage of A's	29,859,860 / 24.98%
Number/percentage of C's	22,729,407 / 19.02%
Number/percentage of T's	37,956,328 / 31.76%
Number/percentage of G's	28,975,904 / 24.24%
Number/percentage of N's	2,455 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3758

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

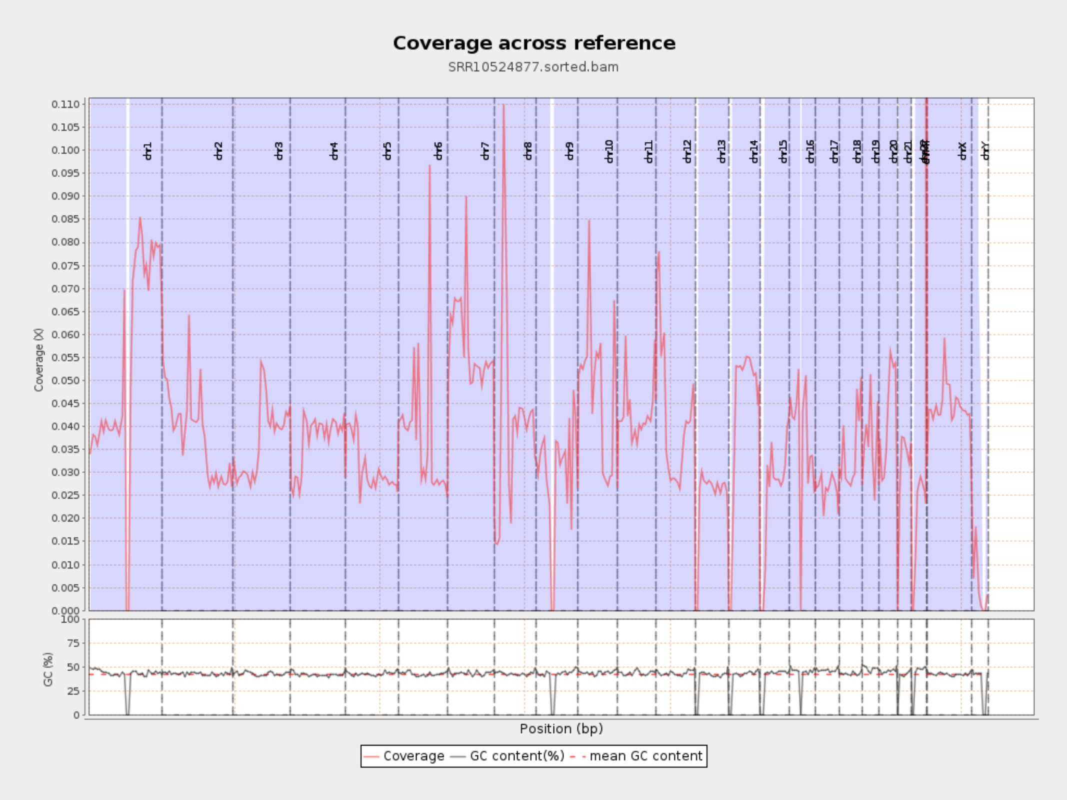
General error rate	0.51%
Mismatches	599,927
Insertions	6,929
Mapped reads with at least one insertion	0.33%
Deletions	24,008
Mapped reads with at least one deletion	1.15%
Homopolymer indels	44%

2.6. Chromosome stats

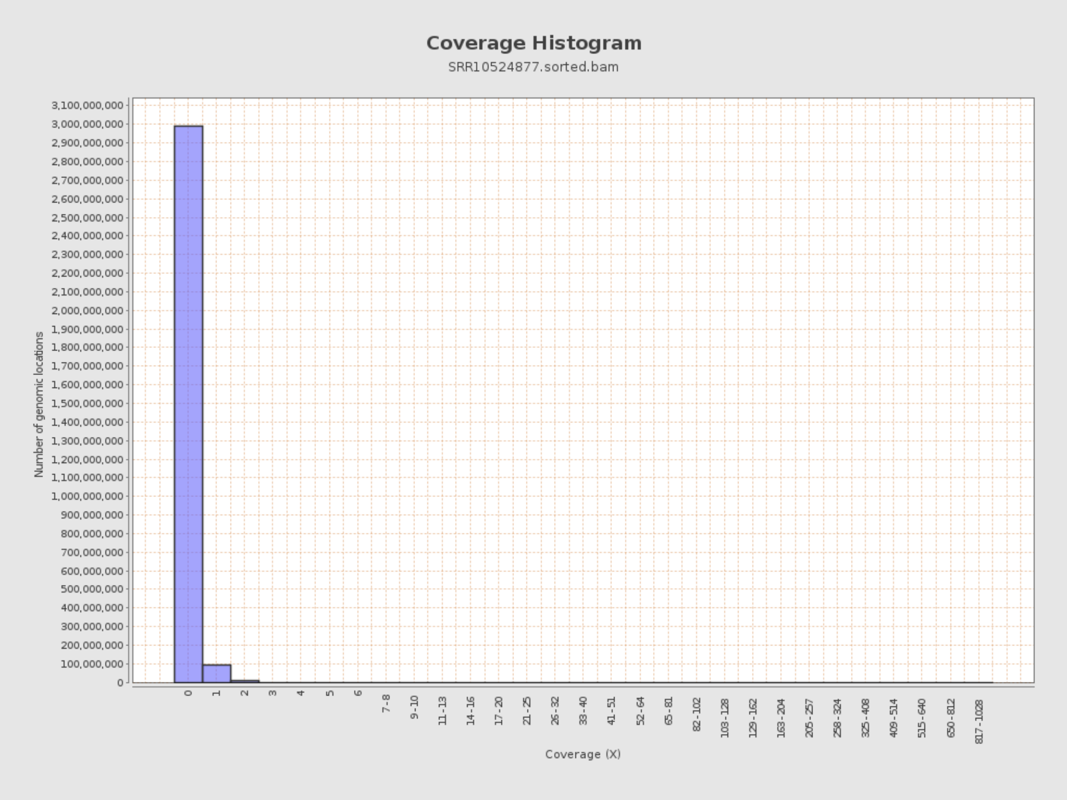
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13366498	0.0536	0.7147
chr2	243199373	9326511	0.0383	0.4894
chr3	198022430	7287104	0.0368	0.2182
chr4	191154276	7078270	0.037	0.2268
chr5	180915260	5653443	0.0312	0.1963
chr6	171115067	6575050	0.0384	0.2617
chr7	159138663	9294679	0.0584	0.6759

chr8	146364022	6016421	0.0411	0.3449
chr9	141213431	4187388	0.0297	0.259
chr10	135534747	6585162	0.0486	0.3914
chr11	135006516	5770178	0.0427	0.2947
chr12	133851895	5611255	0.0419	0.2322
chr13	115169878	2793260	0.0243	0.1738
chr14	107349540	4657070	0.0434	0.237
chr15	102531392	2576983	0.0251	0.1803
chr16	90354753	3302744	0.0366	0.24
chr17	81195210	2143832	0.0264	0.1891
chr18	78077248	2688928	0.0344	0.4985
chr19	59128983	2192687	0.0371	0.4783
chr20	63025520	2649133	0.042	0.2295
chr21	48129895	1474816	0.0306	0.2065
chr22	51304566	966190	0.0188	0.1497
chrMT	16571	135253	8.162	5.1265
chrX	155270560	6887493	0.0444	0.2594
chrY	59373566	341881	0.0058	0.1686

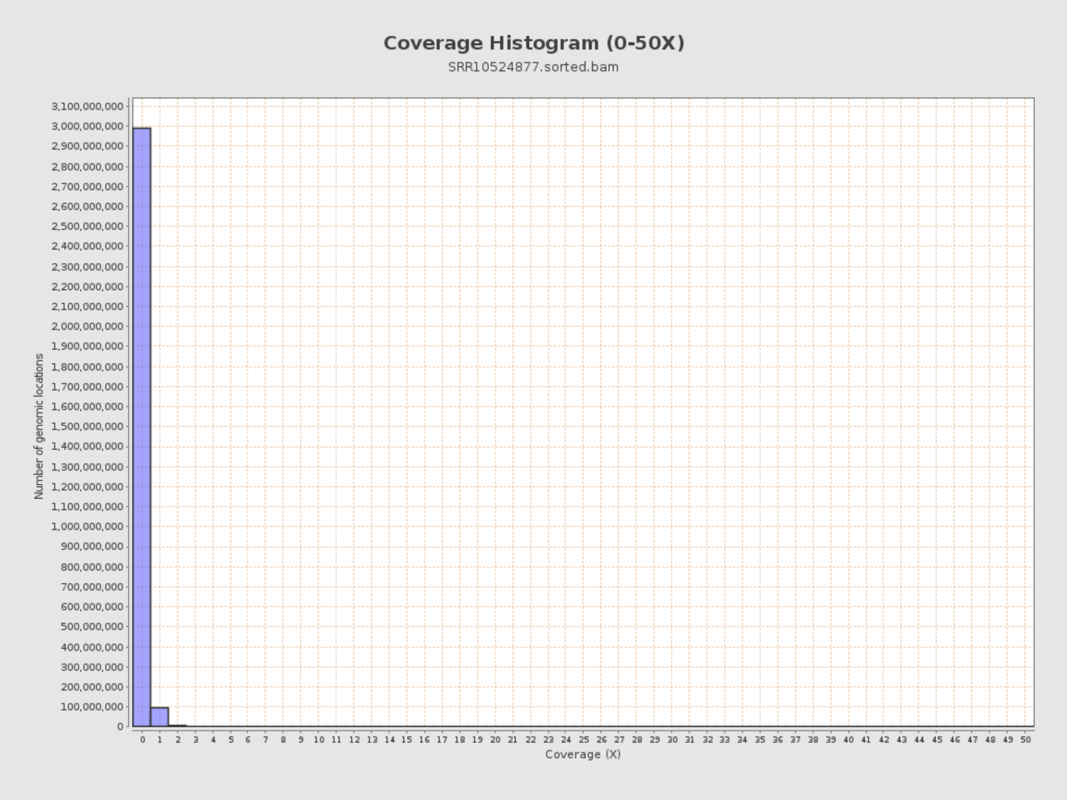
3. Results : Coverage across reference



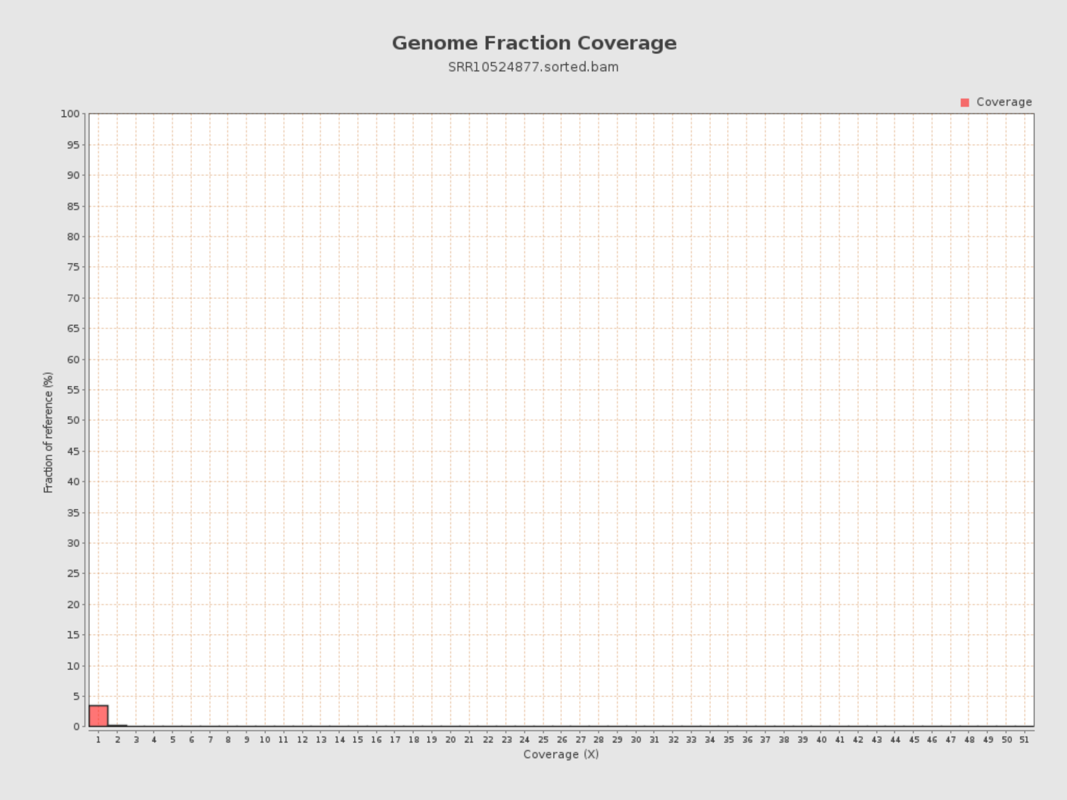
4. Results : Coverage Histogram



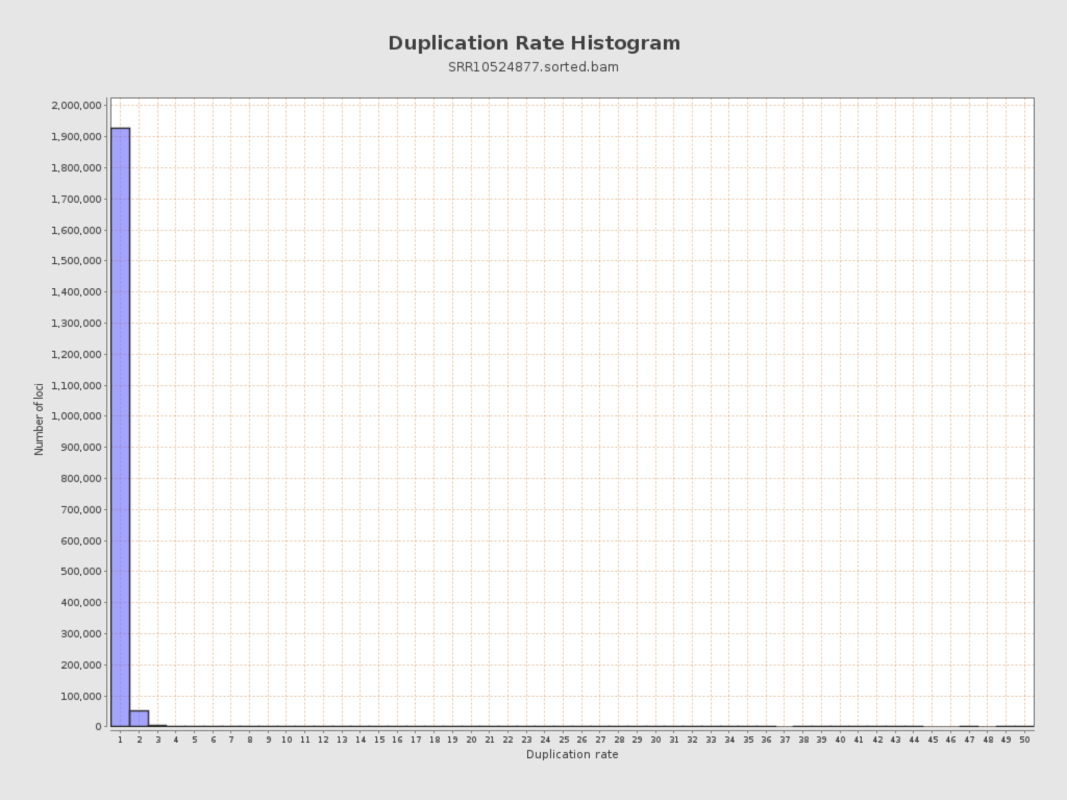
5. Results : Coverage Histogram (0-50X)



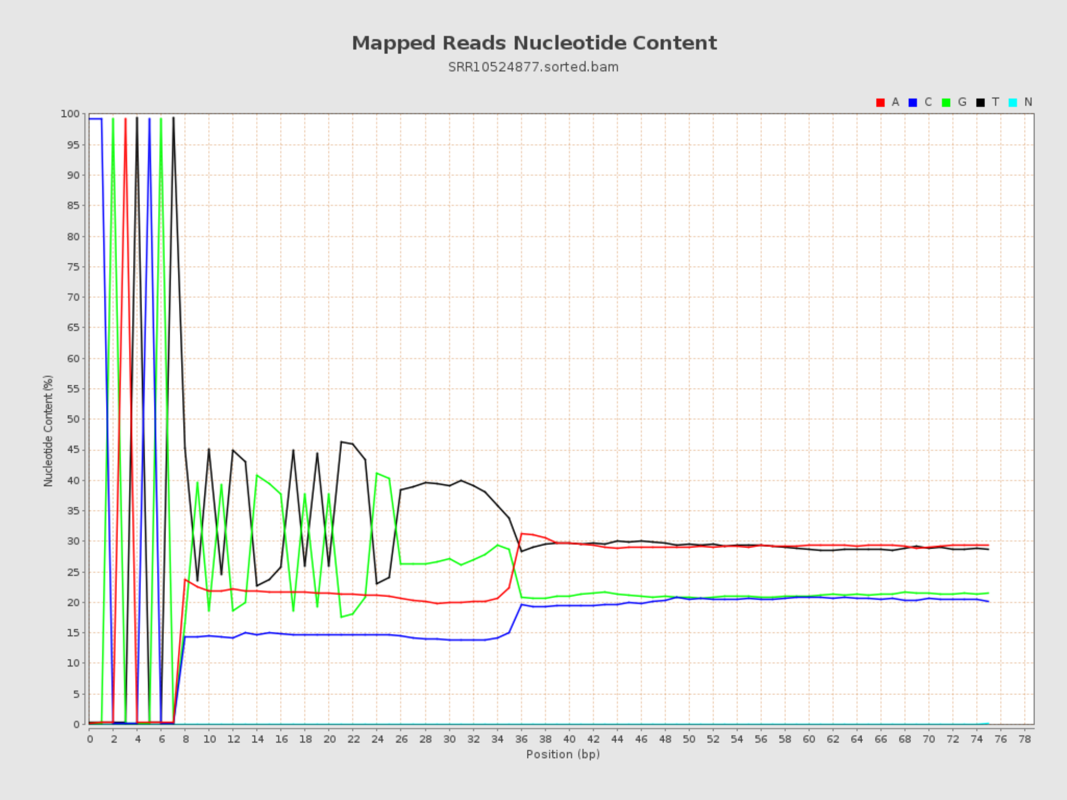
6. Results : Genome Fraction Coverage



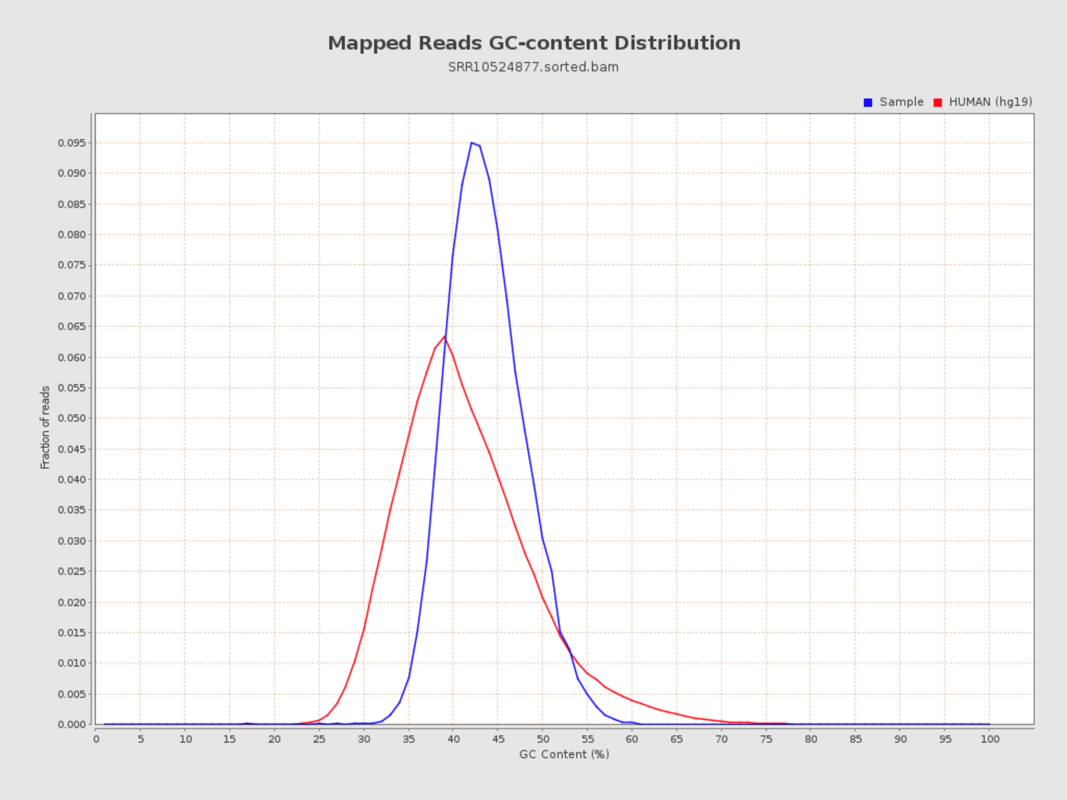
7. Results : Duplication Rate Histogram



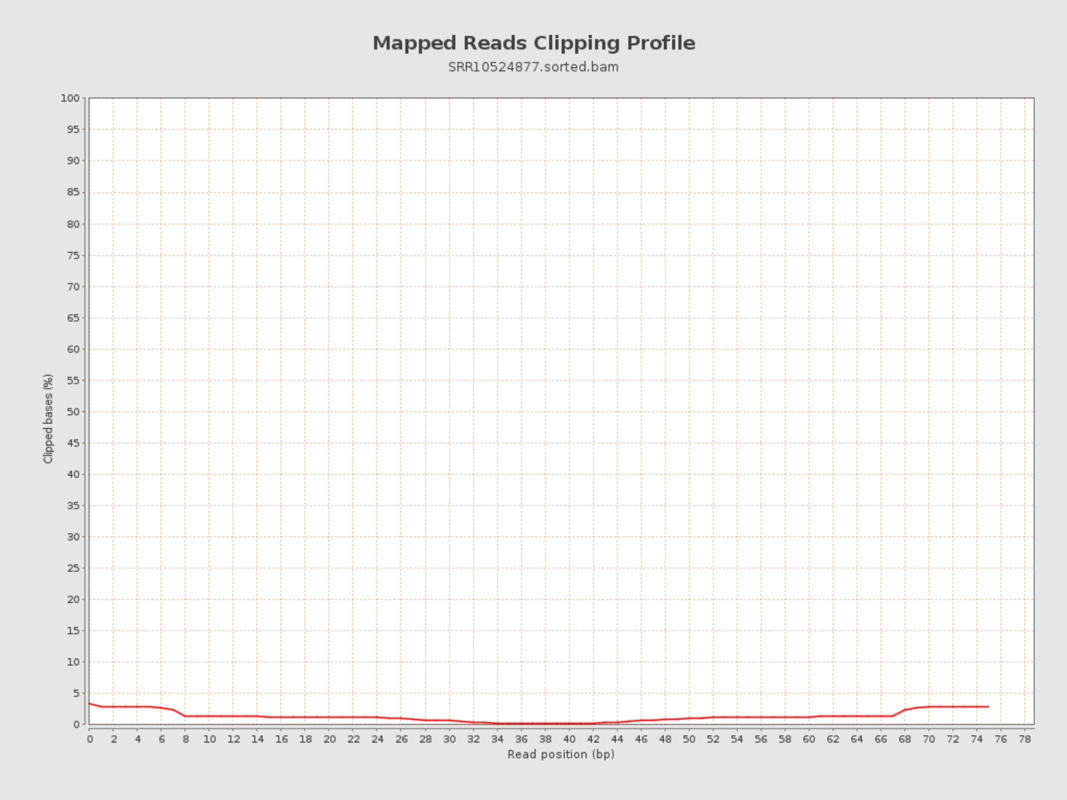
8. Results : Mapped Reads Nucleotide Content



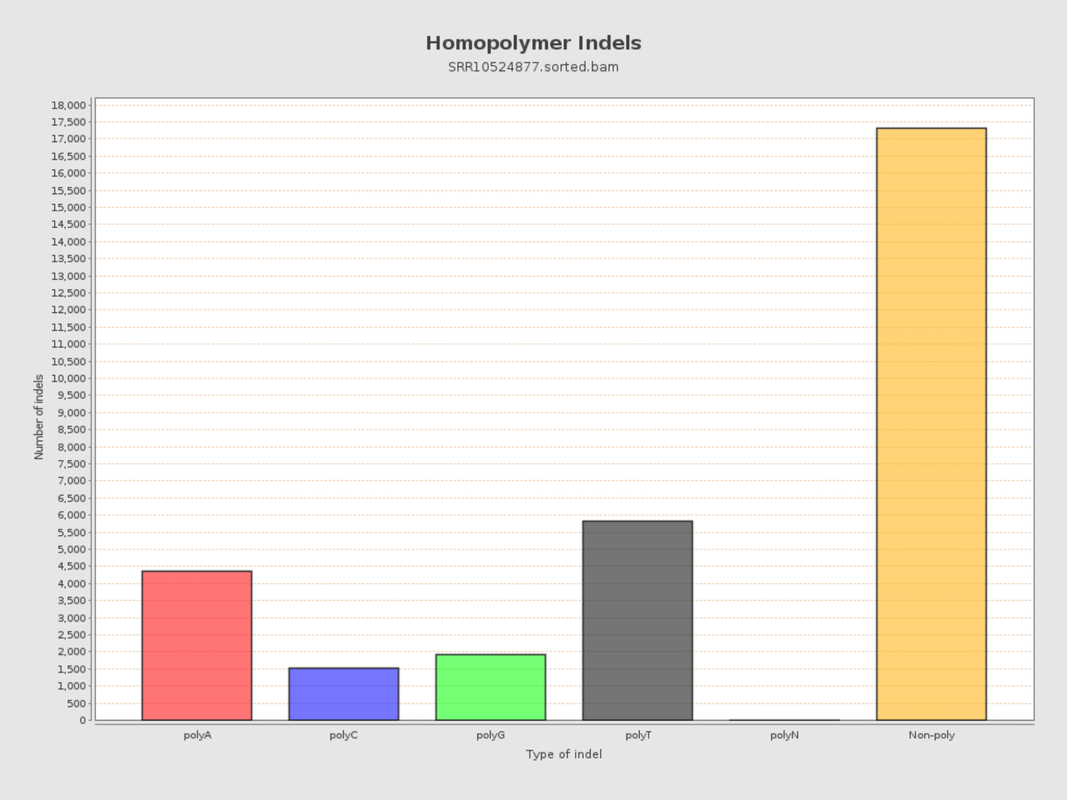
9. Results : Mapped Reads GC-content Distribution



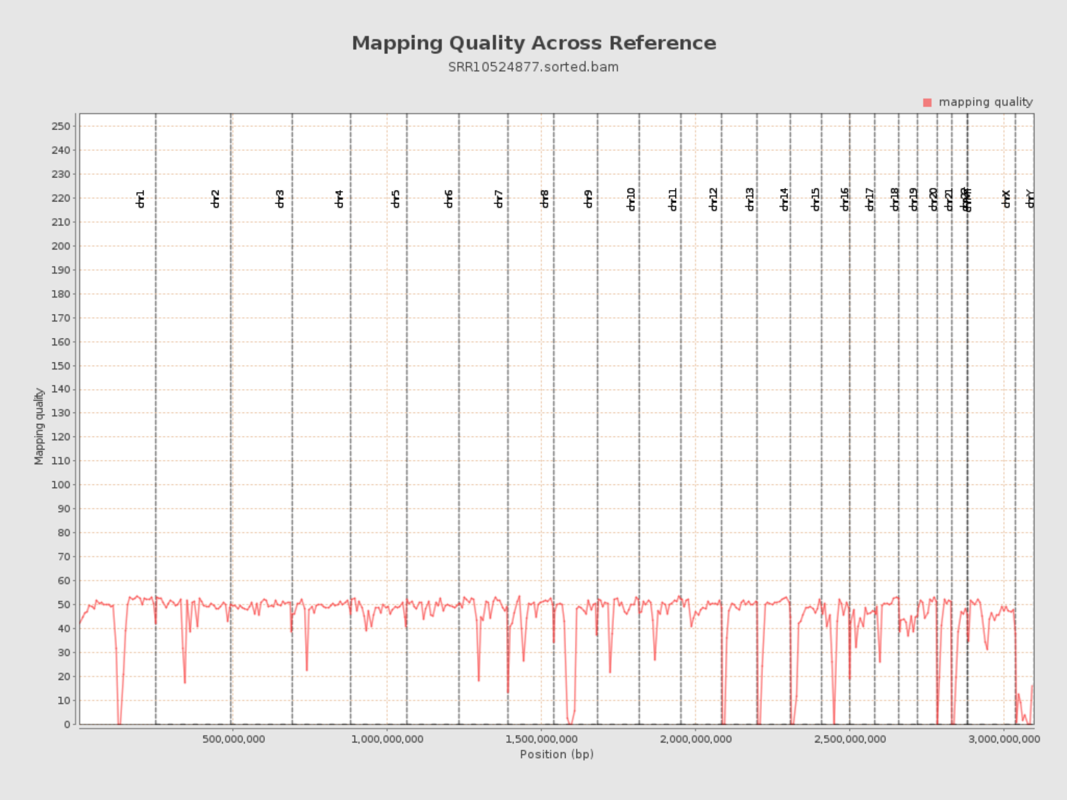
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram