Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:36:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524977.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_SRR10524977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524977.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:36:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,567,377
Mapped reads	2,378,238 / 92.63%
Unmapped reads	189,139 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,659 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	135,848 / 5.29%
Duplication rate	4.38%
Clipped reads	2,377,296 / 92.6%

2.2. ACGT Content

Number/percentage of A's	35,764,677 / 25.84%
Number/percentage of C's	25,443,318 / 18.38%
Number/percentage of T's	44,575,486 / 32.21%
Number/percentage of G's	32,626,227 / 23.57%
Number/percentage of N's	1,553 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.3628

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

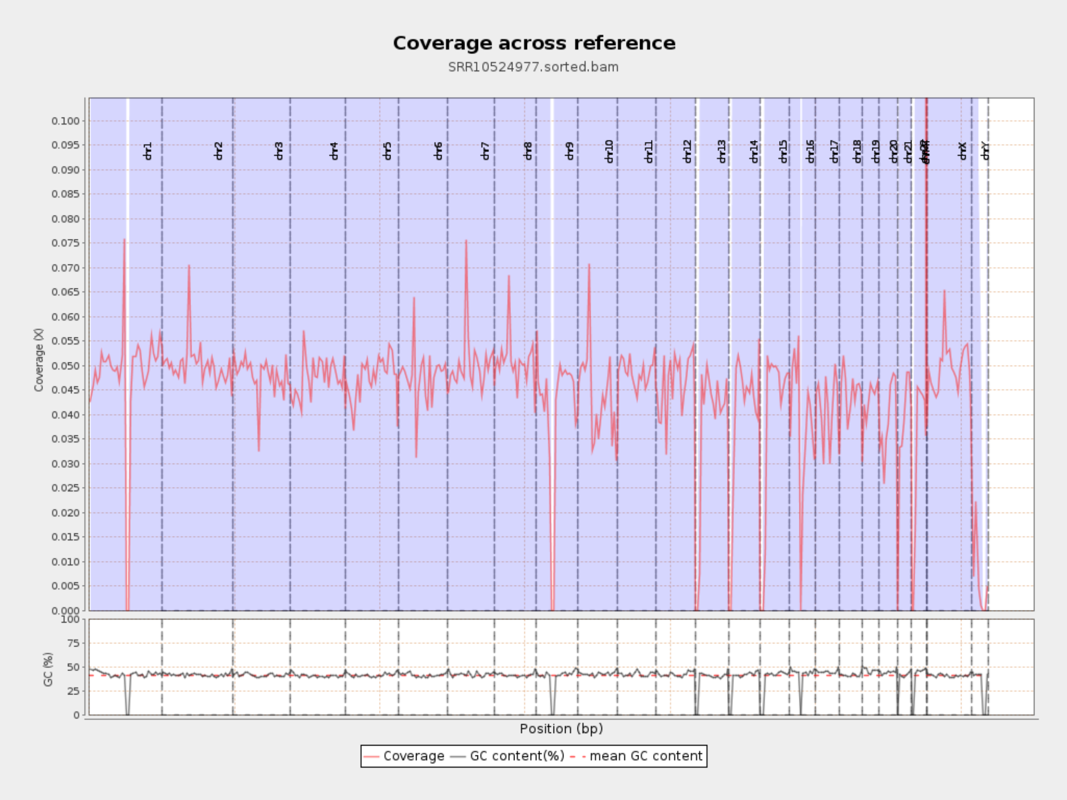
General error rate	0.49%
Mismatches	661,272
Insertions	9,750
Mapped reads with at least one insertion	0.41%
Deletions	24,998
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.46%

2.6. Chromosome stats

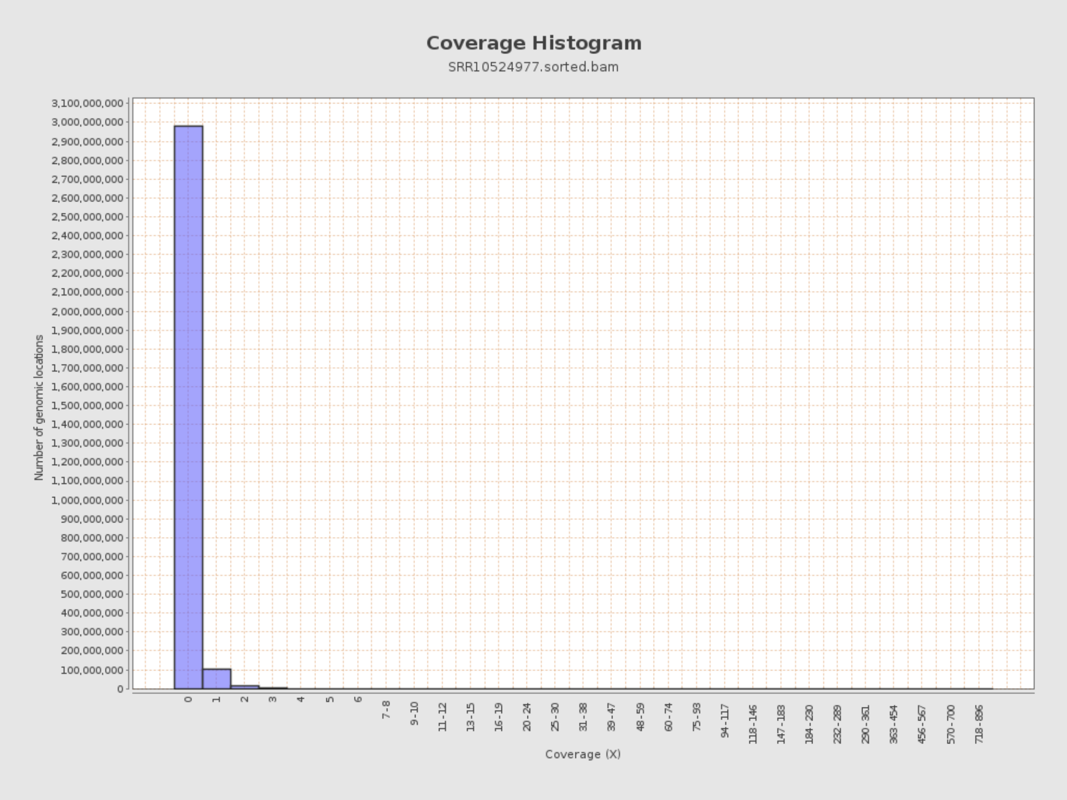
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11880599	0.0477	0.6543
chr2	243199373	12228795	0.0503	0.4249
chr3	198022430	9501703	0.048	0.2542
chr4	191154276	9086348	0.0475	0.2922
chr5	180915260	8606644	0.0476	0.2529
chr6	171115067	8168236	0.0477	0.3338
chr7	159138663	8043135	0.0505	0.4819

chr8	146364022	7455736	0.0509	0.3617
chr9	141213431	5675162	0.0402	0.2988
chr10	135534747	5976022	0.0441	0.3658
chr11	135006516	6540798	0.0484	0.3667
chr12	133851895	6207544	0.0464	0.2518
chr13	115169878	4253323	0.0369	0.2242
chr14	107349540	4118650	0.0384	0.234
chr15	102531392	3973351	0.0388	0.2401
chr16	90354753	3434460	0.038	0.2454
chr17	81195210	3359440	0.0414	0.2566
chr18	78077248	3486472	0.0447	0.515
chr19	59128983	2536013	0.0429	0.4316
chr20	63025520	2439941	0.0387	0.2344
chr21	48129895	1772949	0.0368	0.2494
chr22	51304566	1578613	0.0308	0.2015
chrMT	16571	33123	1.9989	1.8978
chrX	155270560	7699142	0.0496	0.287
chrY	59373566	397298	0.0067	0.1807

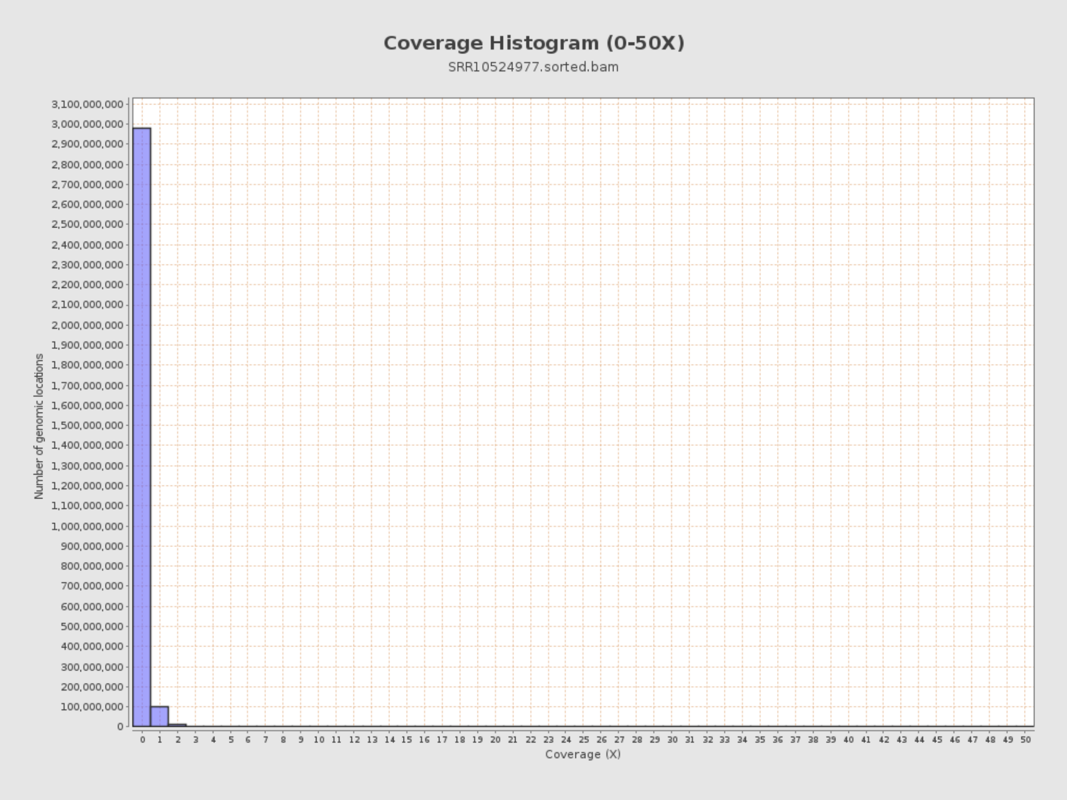
3. Results : Coverage across reference



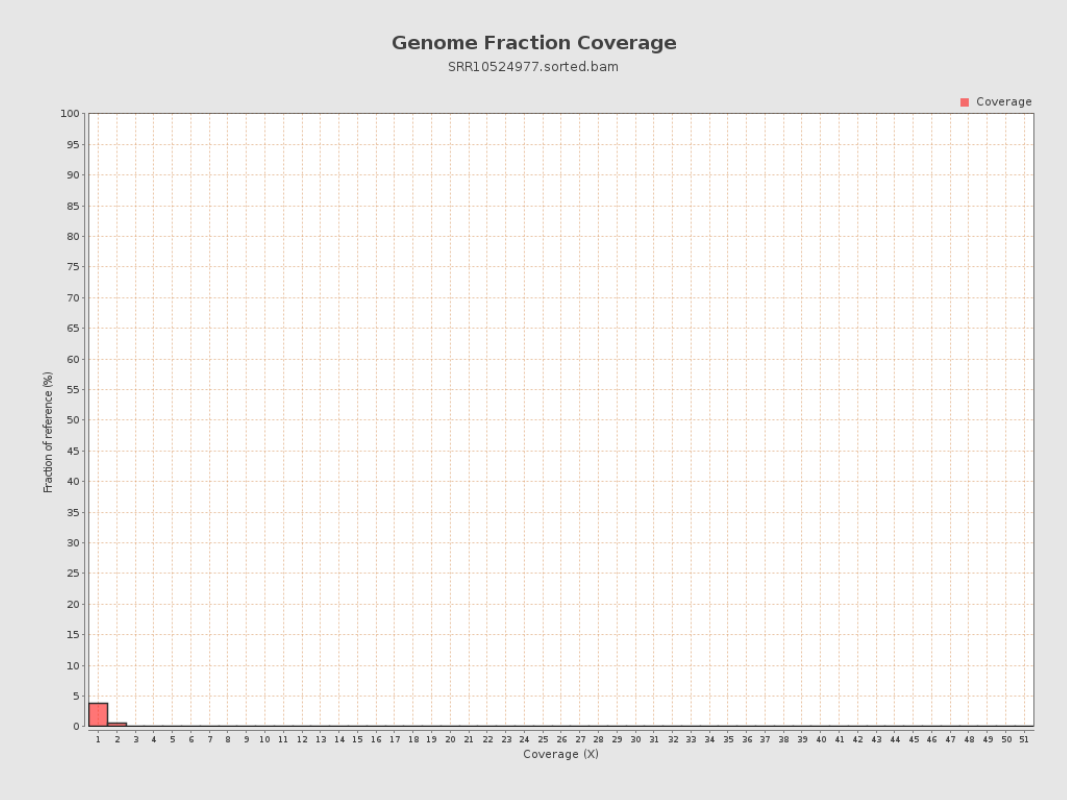
4. Results : Coverage Histogram



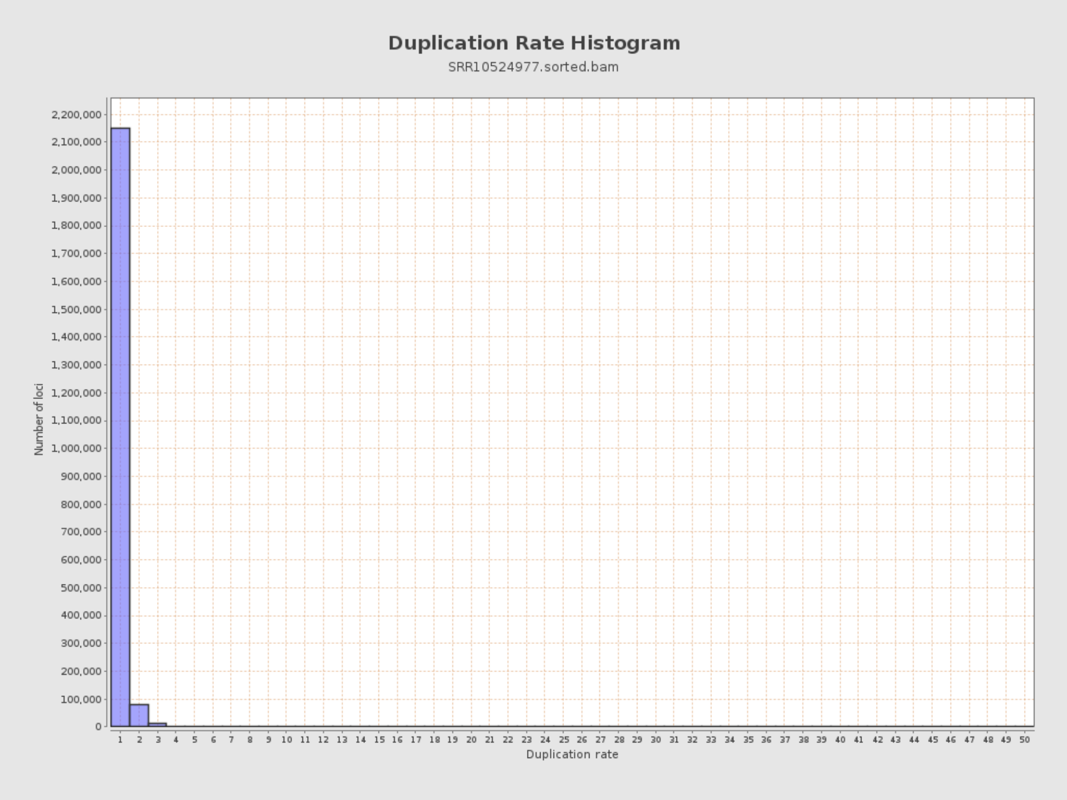
5. Results : Coverage Histogram (0-50X)



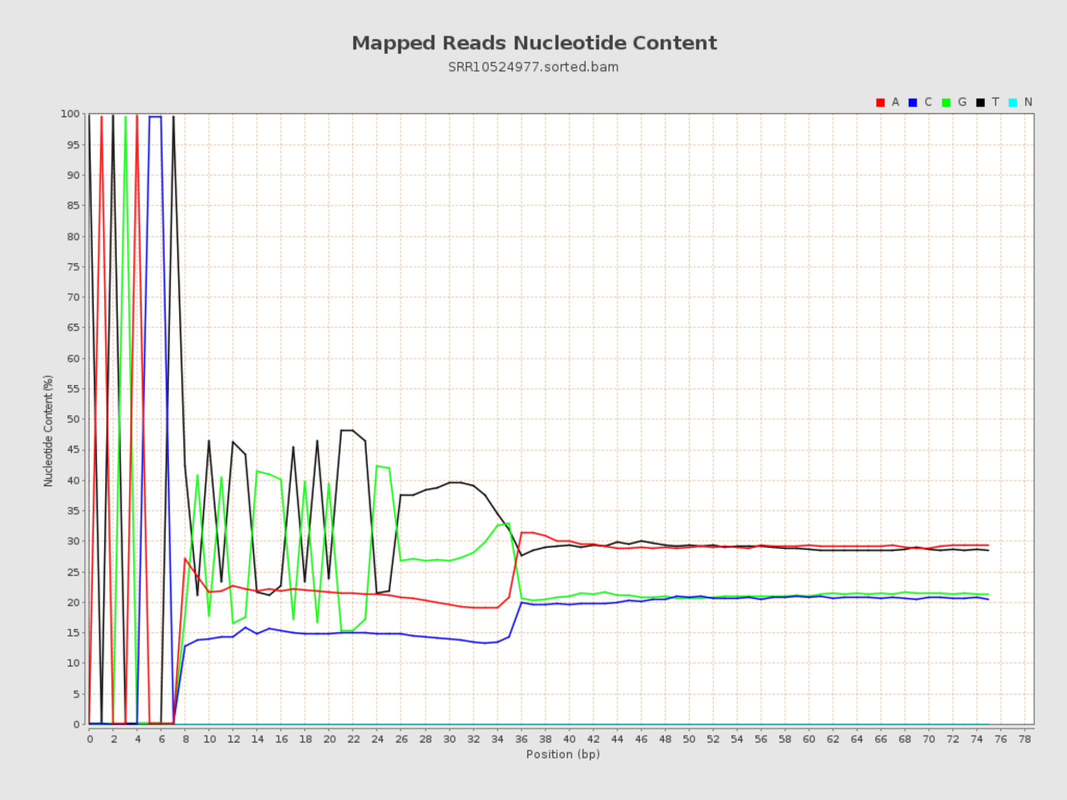
6. Results : Genome Fraction Coverage



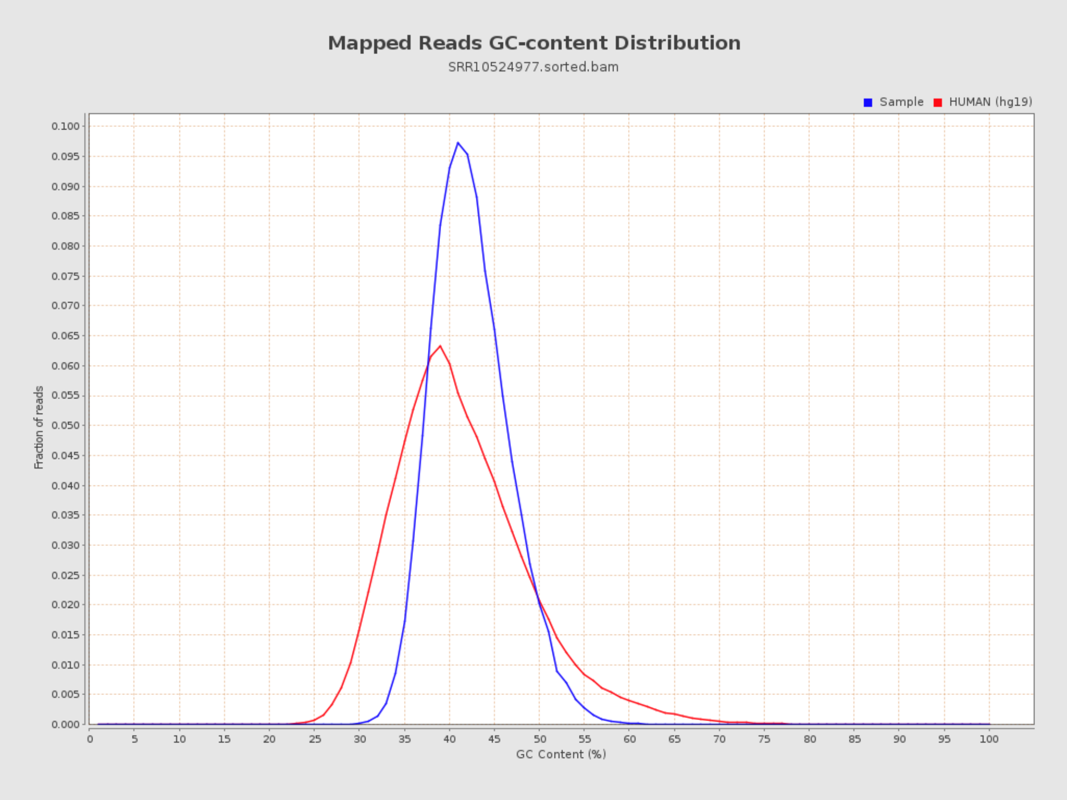
7. Results : Duplication Rate Histogram



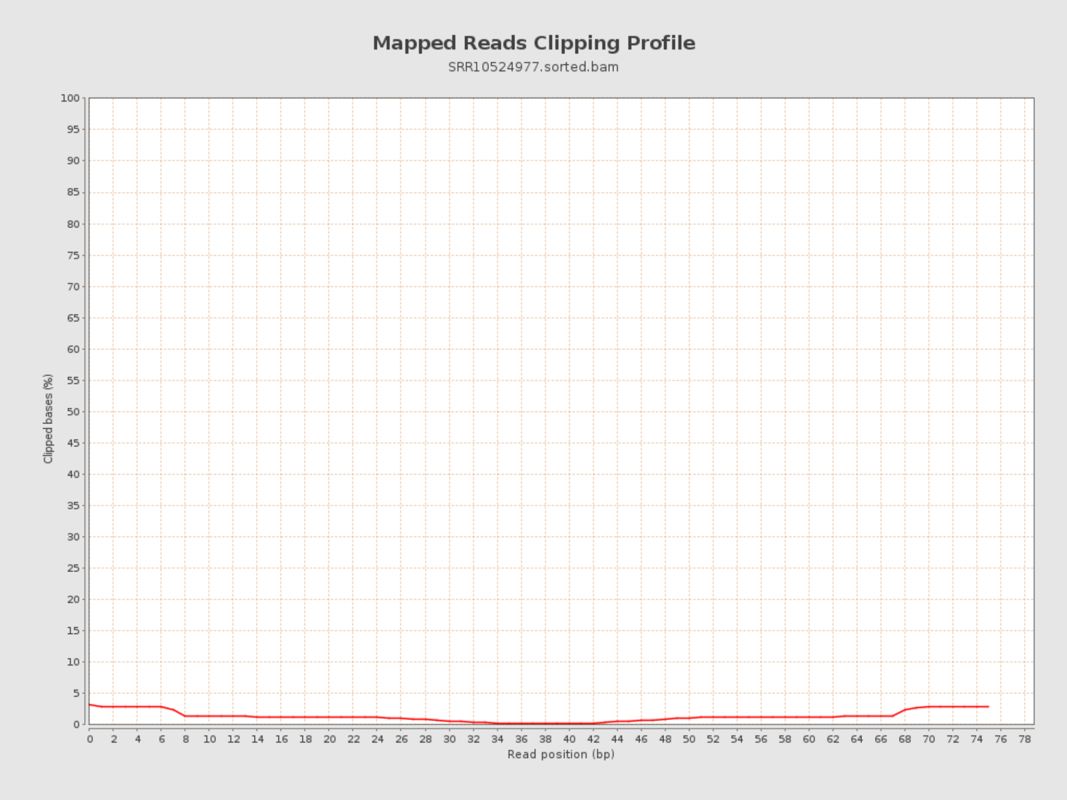
8. Results : Mapped Reads Nucleotide Content



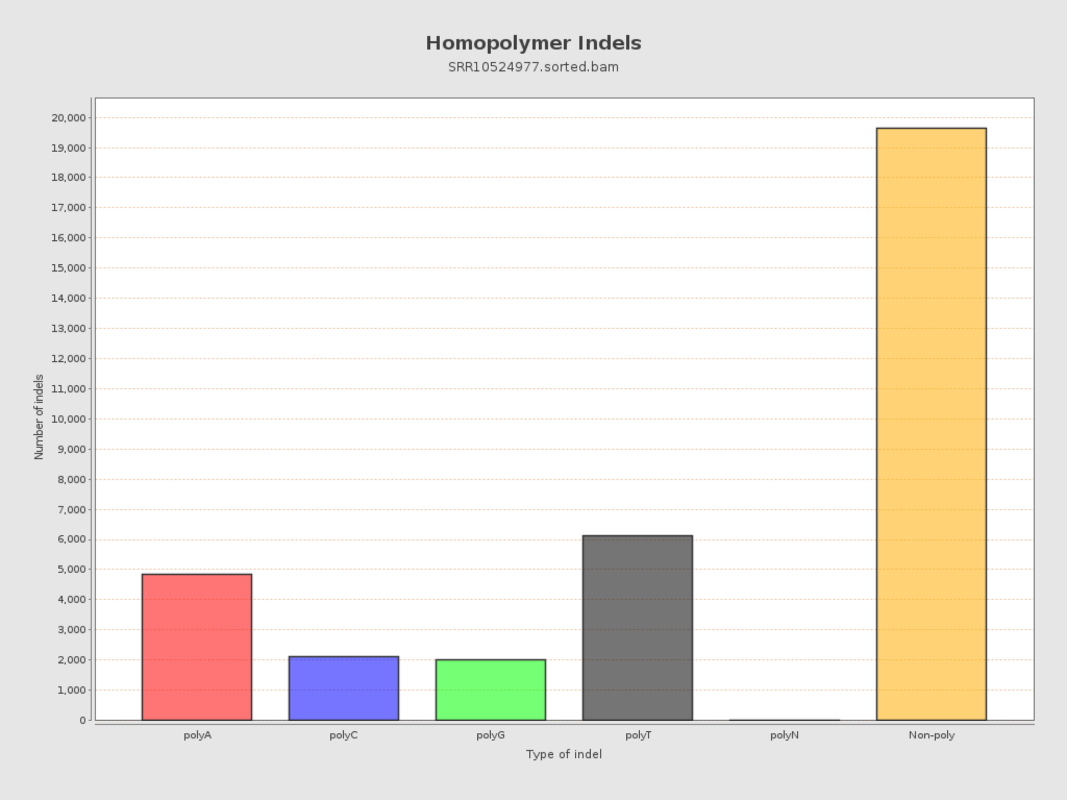
9. Results : Mapped Reads GC-content Distribution



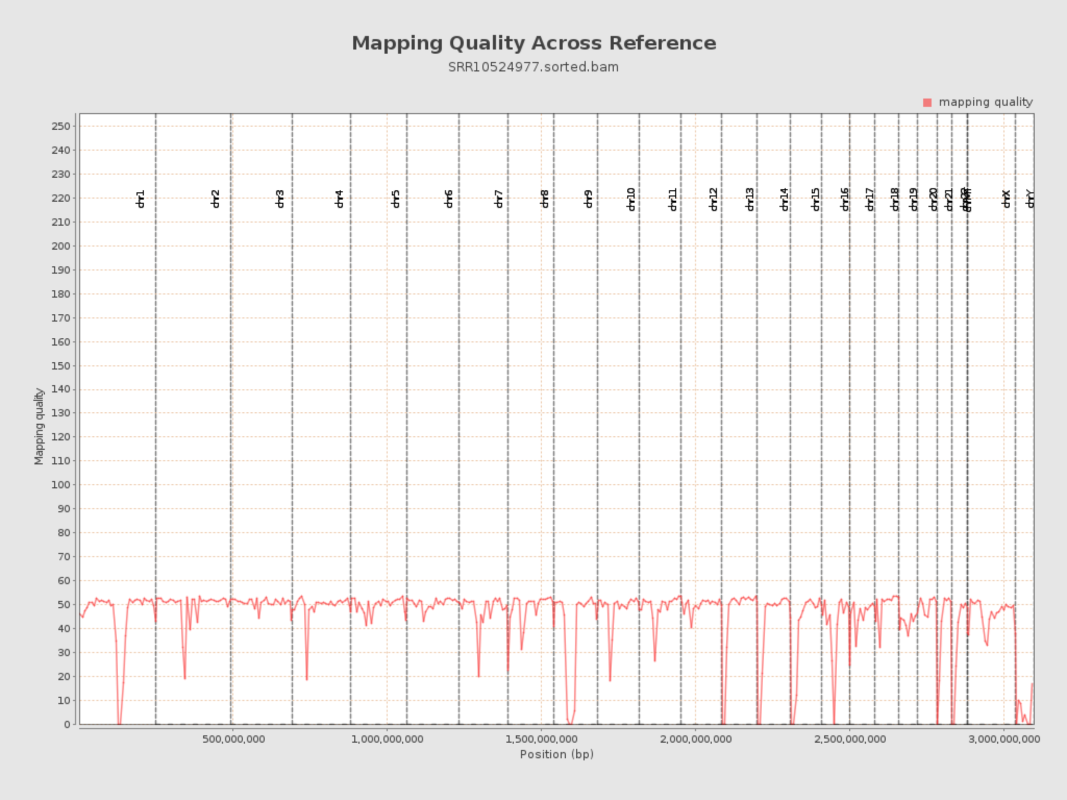
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram