Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 14:17:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777306.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_SRR1777306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 14:17:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,580,297
Mapped reads	2,349,485 / 91.05%
Unmapped reads	230,812 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59 / 0%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	7,764 / 0.3%
Duplication rate	0.31%
Clipped reads	42,647 / 1.65%

2.2. ACGT Content

Number/percentage of A's	33,990,706 / 28.47%
Number/percentage of C's	26,051,807 / 21.82%
Number/percentage of T's	33,288,634 / 27.88%
Number/percentage of G's	26,053,879 / 21.82%
Number/percentage of N's	16,114 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.2147

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

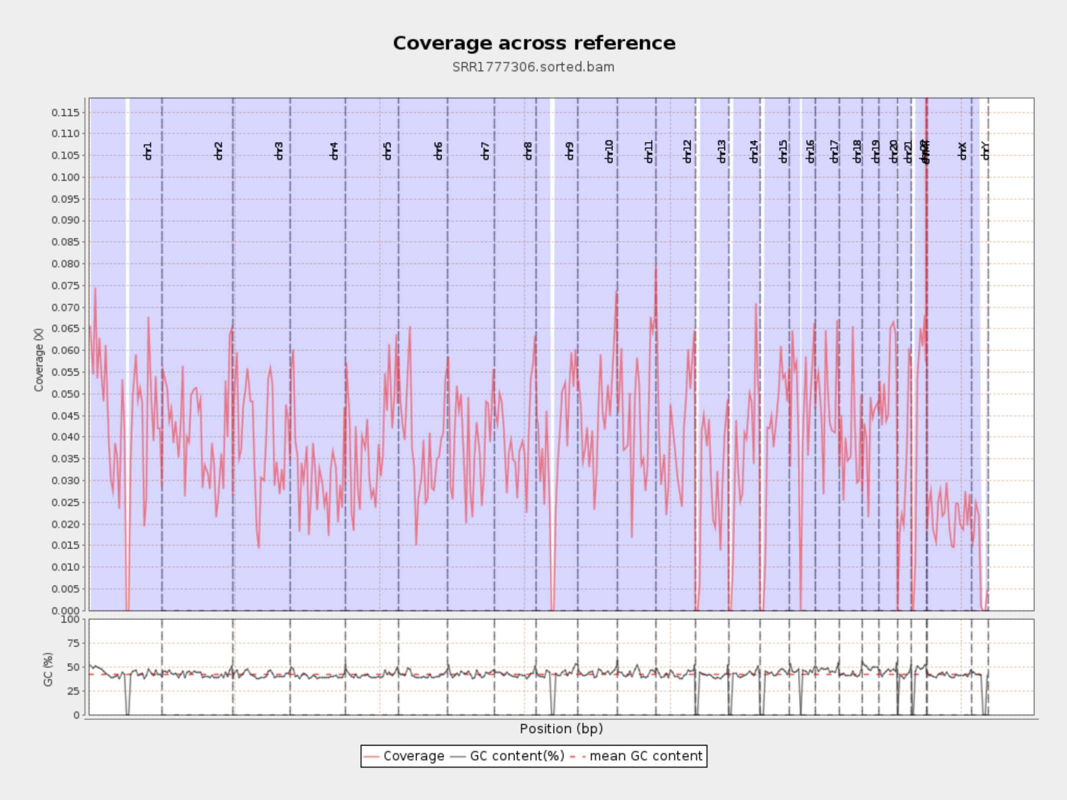
General error rate	0.56%
Mismatches	649,659
Insertions	13,562
Mapped reads with at least one insertion	0.58%
Deletions	42,139
Mapped reads with at least one deletion	1.79%
Homopolymer indels	55.67%

2.6. Chromosome stats

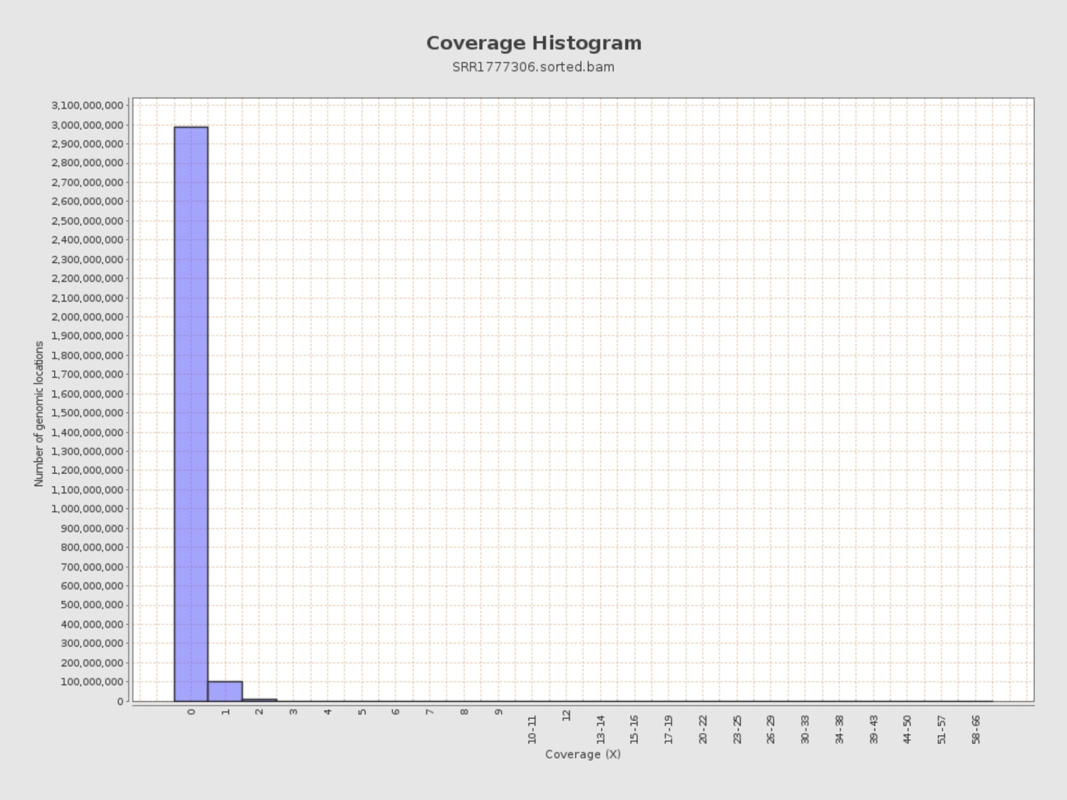
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10834686	0.0435	0.2326
chr2	243199373	10161086	0.0418	0.226
chr3	198022430	7871798	0.0398	0.2141
chr4	191154276	6092666	0.0319	0.1968
chr5	180915260	7010506	0.0388	0.2115
chr6	171115067	6582177	0.0385	0.2109
chr7	159138663	6110906	0.0384	0.2112

chr8	146364022	5957676	0.0407	0.2192
chr9	141213431	5280414	0.0374	0.2124
chr10	135534747	6114535	0.0451	0.2316
chr11	135006516	6192096	0.0459	0.2346
chr12	133851895	5547816	0.0414	0.2198
chr13	115169878	3252063	0.0282	0.1801
chr14	107349540	3721037	0.0347	0.2021
chr15	102531392	3944029	0.0385	0.2128
chr16	90354753	4193599	0.0464	0.2378
chr17	81195210	3978231	0.049	0.2438
chr18	78077248	3056768	0.0392	0.2194
chr19	59128983	2440435	0.0413	0.2239
chr20	63025520	3406483	0.054	0.2543
chr21	48129895	1507252	0.0313	0.204
chr22	51304566	2118965	0.0413	0.2255
chrMT	16571	26540	1.6016	1.7564
chrX	155270560	3432284	0.0221	0.1562
chrY	59373566	617408	0.0104	0.1143

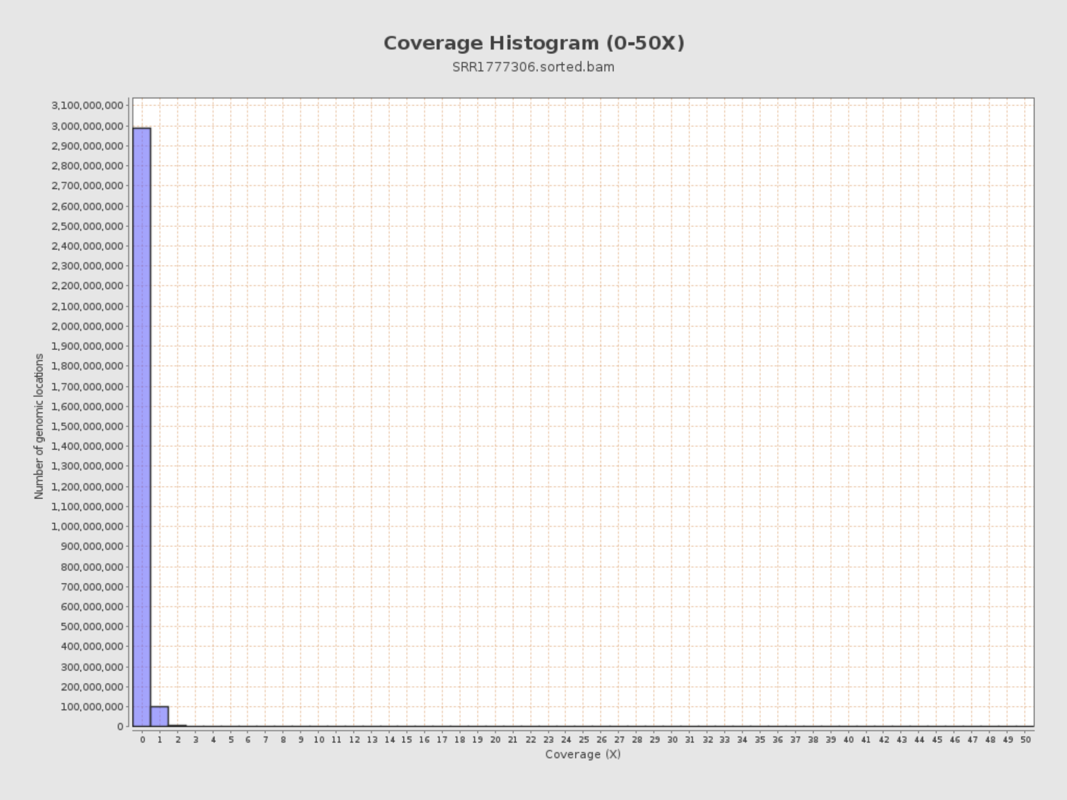
3. Results : Coverage across reference



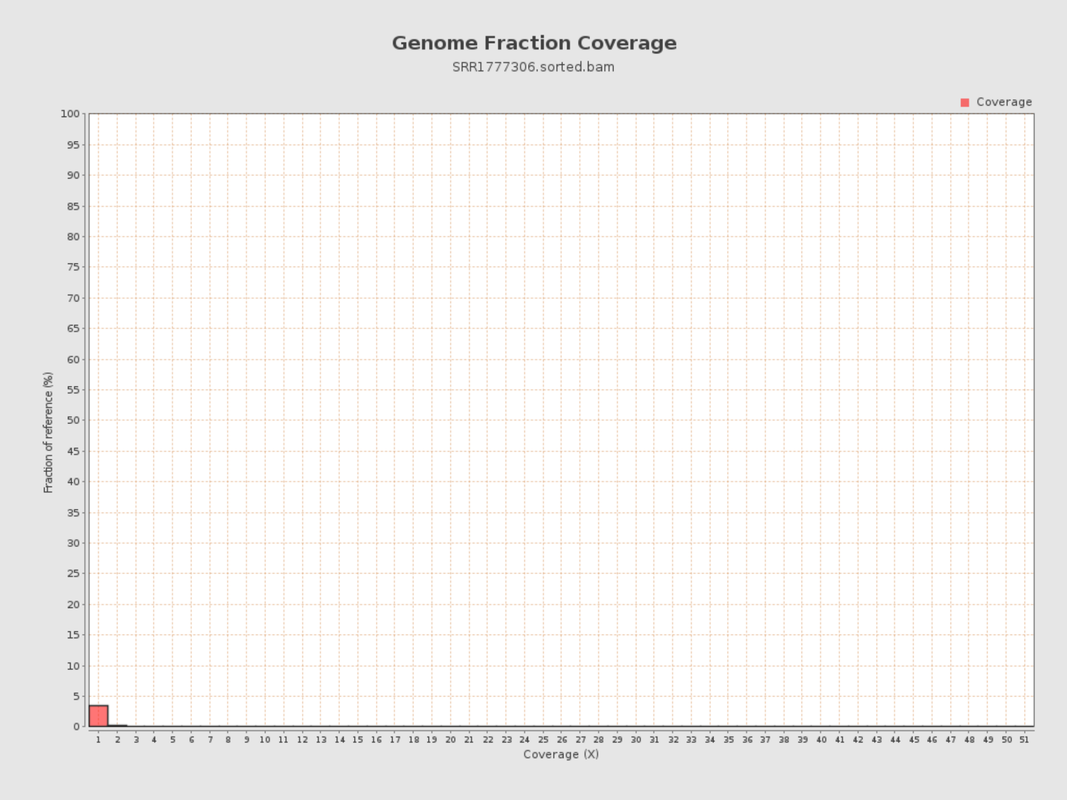
4. Results : Coverage Histogram



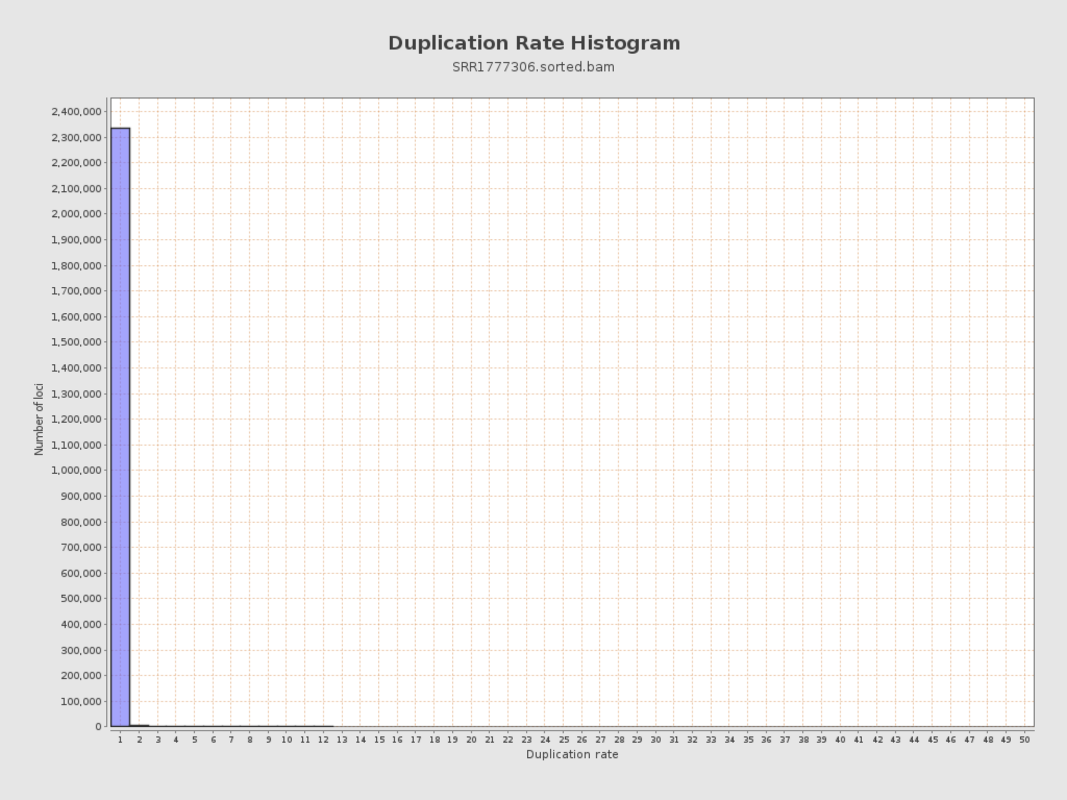
5. Results : Coverage Histogram (0-50X)



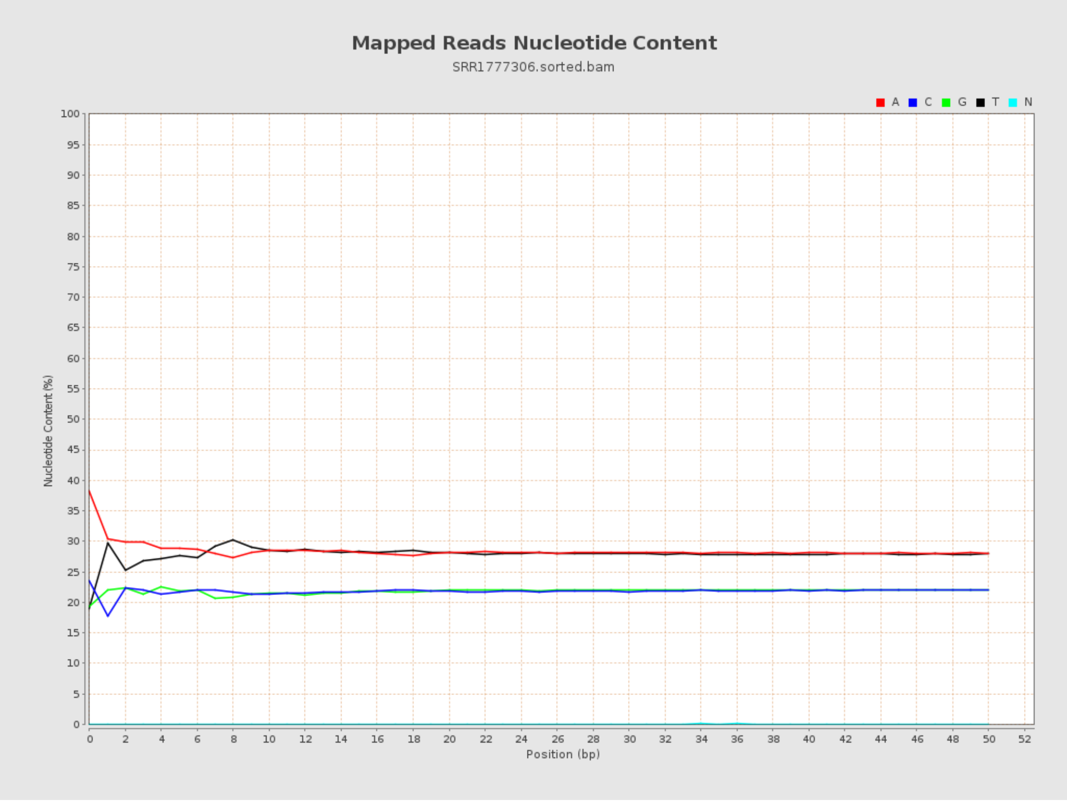
6. Results : Genome Fraction Coverage



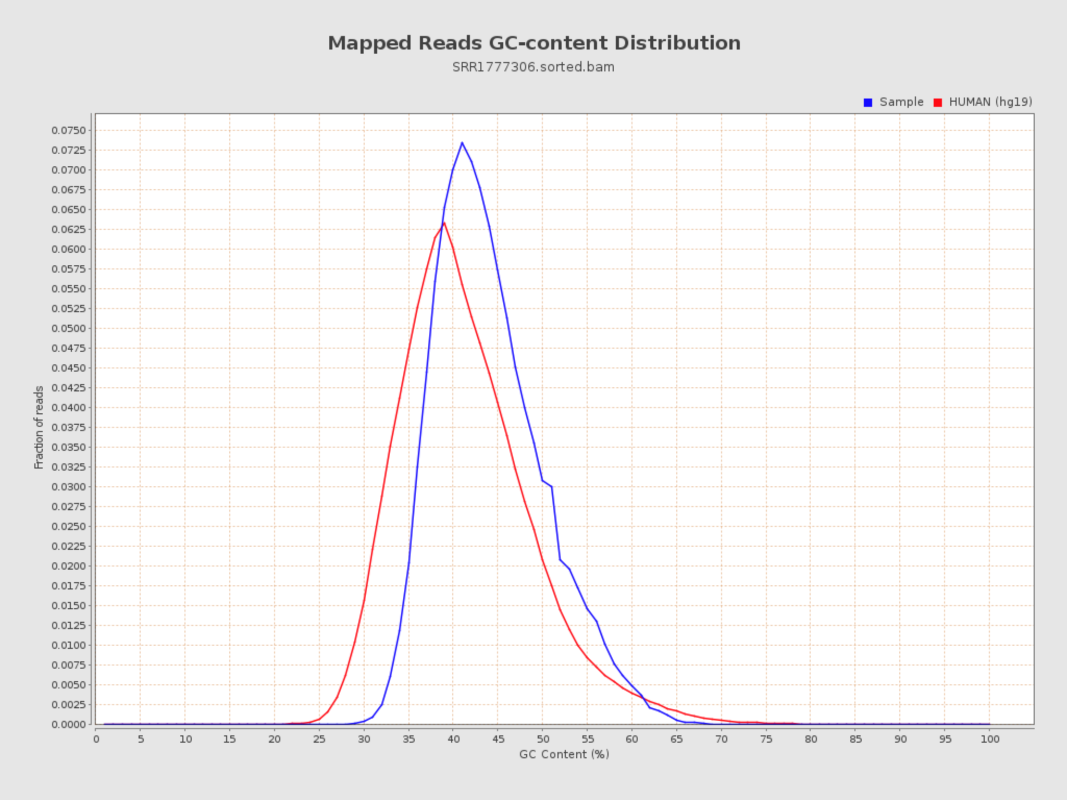
7. Results : Duplication Rate Histogram



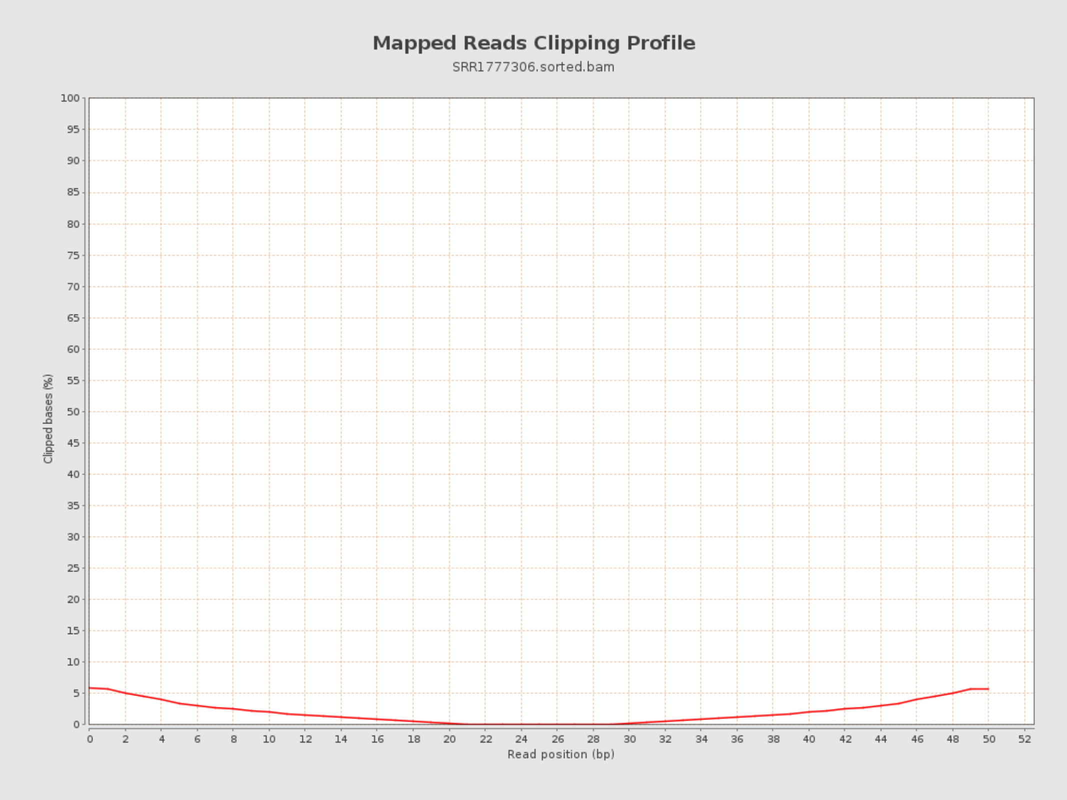
8. Results : Mapped Reads Nucleotide Content



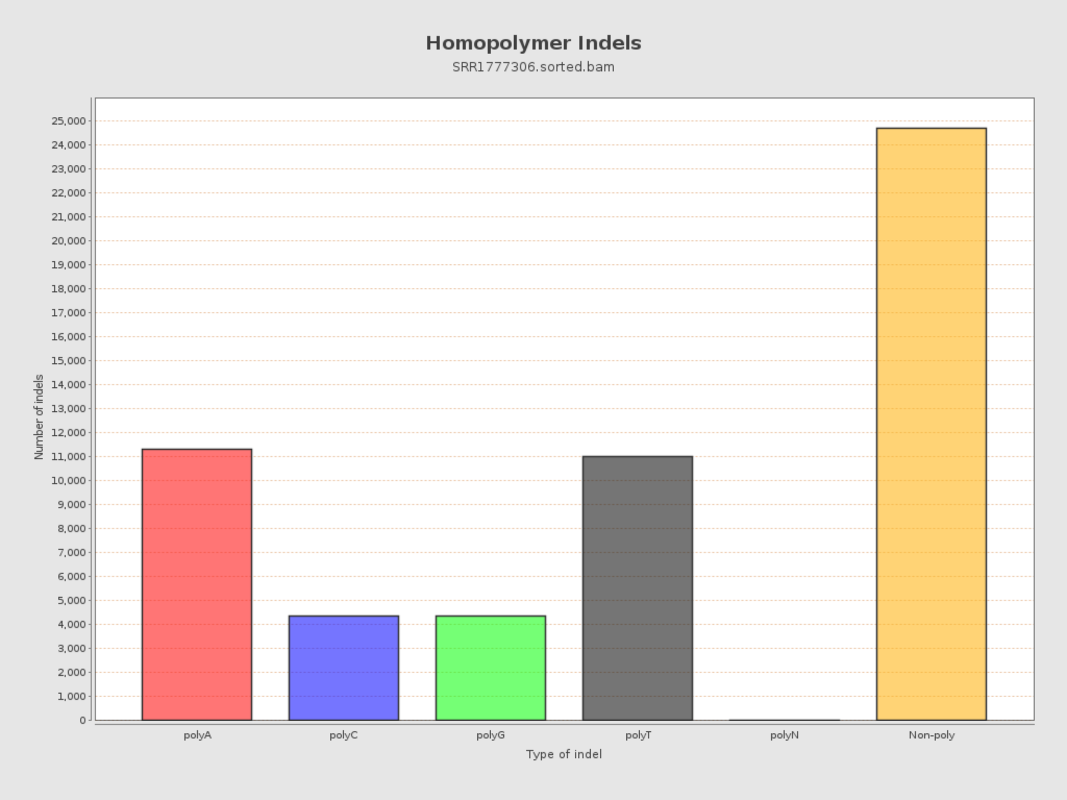
9. Results : Mapped Reads GC-content Distribution



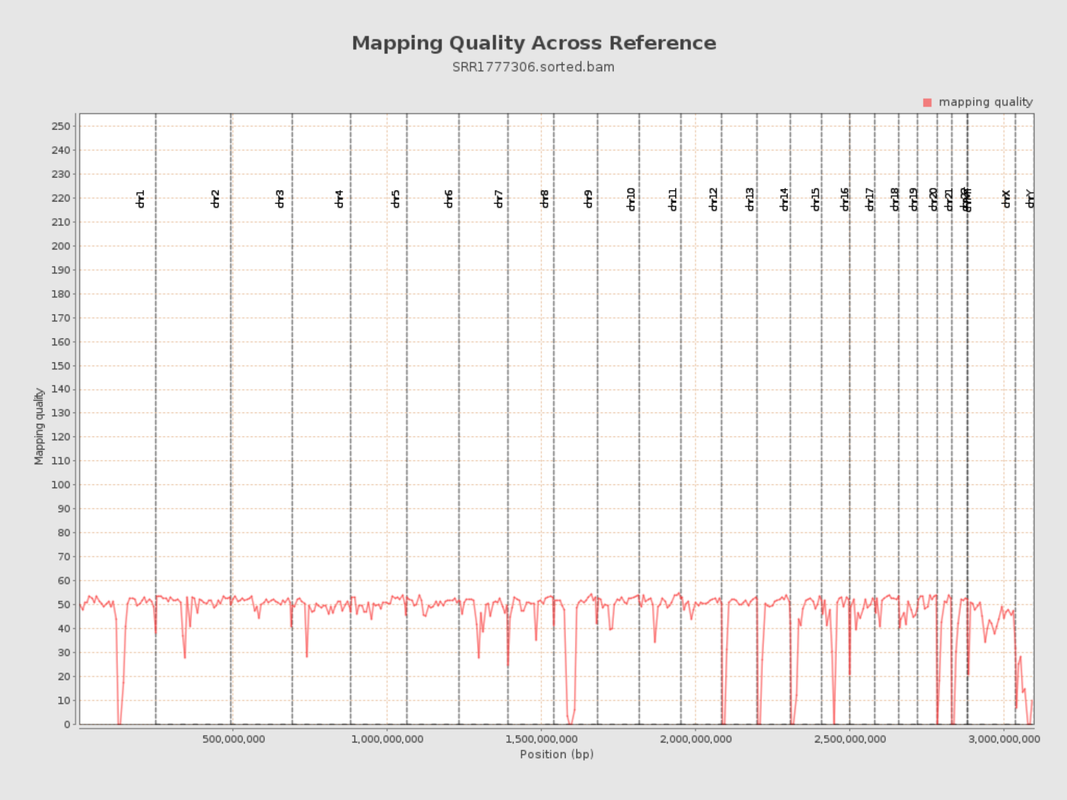
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram