Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:35:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971317.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_SRR2971317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:35:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,024,185
Mapped reads	8,359,680 / 92.64%
Unmapped reads	664,505 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,317 / 0.01%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	758,983 / 8.41%
Duplication rate	7.34%
Clipped reads	1,836,925 / 20.36%

2.2. ACGT Content

Number/percentage of A's	111,158,659 / 27.76%
Number/percentage of C's	86,578,609 / 21.62%
Number/percentage of T's	113,525,672 / 28.35%
Number/percentage of G's	89,187,668 / 22.27%
Number/percentage of N's	22,874 / 0.01%
GC Percentage	43.89%

2.3. Coverage

Mean	0.1294

Standard Deviation	1.077

2.4. Mapping Quality

Mean Mapping Quality	35.36

2.5. Mismatches and indels

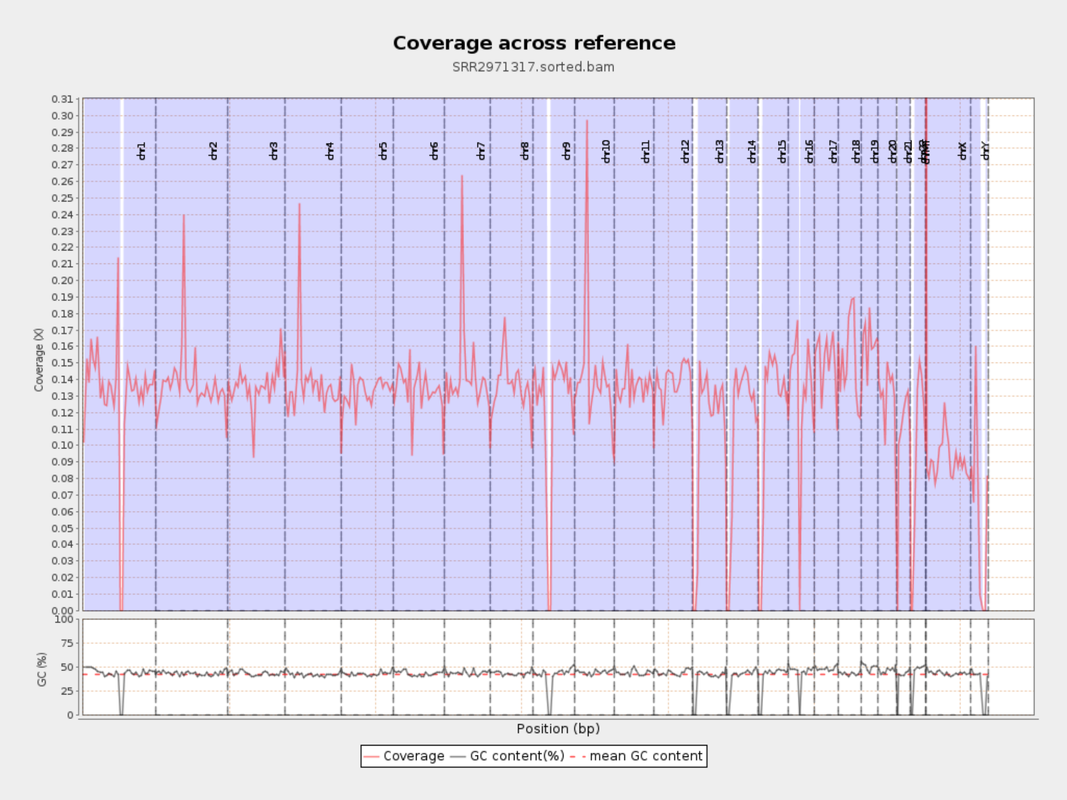
General error rate	0.52%
Mismatches	2,040,343
Insertions	26,896
Mapped reads with at least one insertion	0.32%
Deletions	57,914
Mapped reads with at least one deletion	0.69%
Homopolymer indels	39.82%

2.6. Chromosome stats

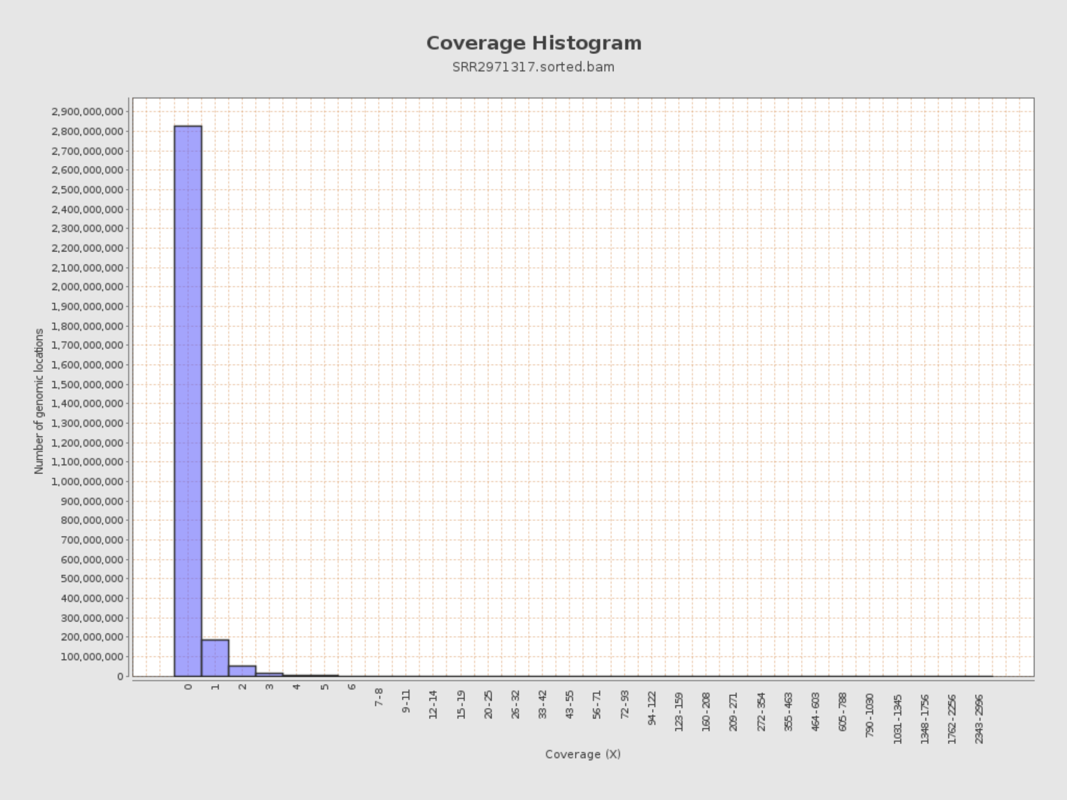
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32581128	0.1307	1.9783
chr2	243199373	33568065	0.138	1.0608
chr3	198022430	26924073	0.136	0.5208
chr4	191154276	26358943	0.1379	0.7684
chr5	180915260	24072889	0.1331	0.5159
chr6	171115067	22926498	0.134	0.5586
chr7	159138663	22886569	0.1438	1.6513

chr8	146364022	19947498	0.1363	1.6458
chr9	141213431	17162868	0.1215	1.0052
chr10	135534747	19461712	0.1436	1.3056
chr11	135006516	18314374	0.1357	0.819
chr12	133851895	18697114	0.1397	0.5529
chr13	115169878	12430296	0.1079	0.4559
chr14	107349540	12075063	0.1125	0.6225
chr15	102531392	11867600	0.1157	0.4818
chr16	90354753	11648746	0.1289	0.6397
chr17	81195210	12371048	0.1524	0.6628
chr18	78077248	11813846	0.1513	1.9088
chr19	59128983	9554394	0.1616	1.6419
chr20	63025520	8198438	0.1301	0.5507
chr21	48129895	5118225	0.1063	0.7378
chr22	51304566	4829973	0.0941	0.5021
chrMT	16571	40184	2.425	2.7708
chrX	155270560	14167411	0.0912	0.5305
chrY	59373566	3541702	0.0597	0.6966

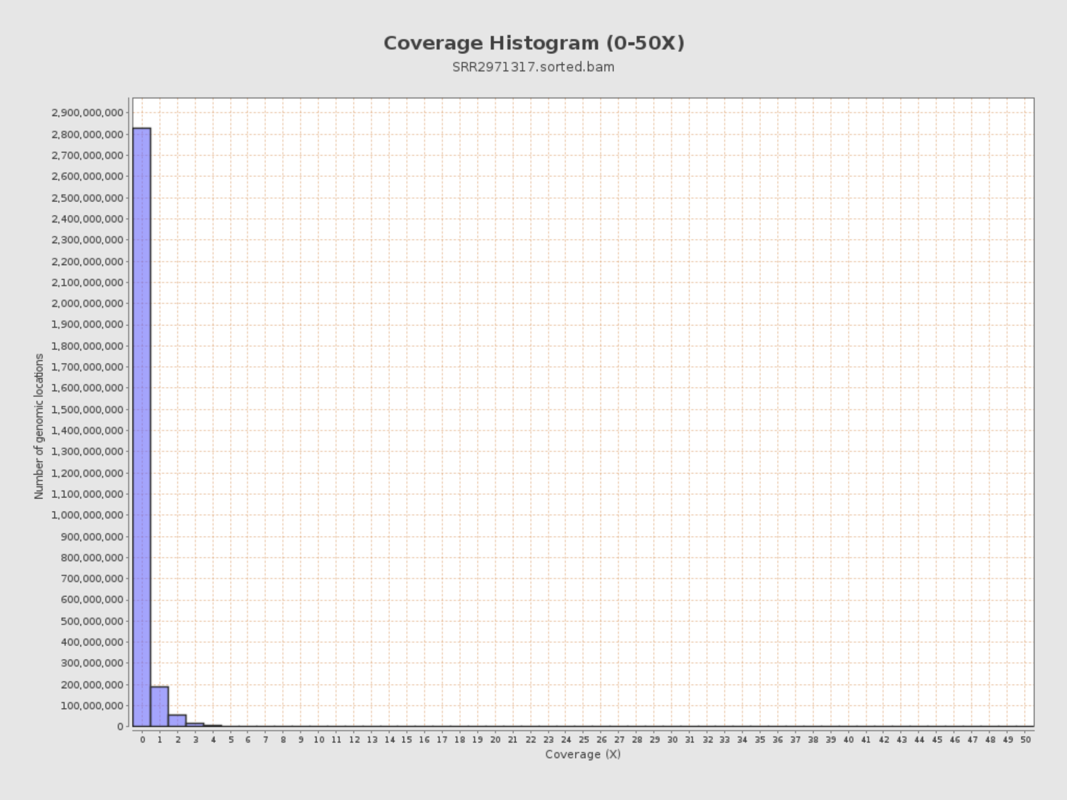
3. Results : Coverage across reference



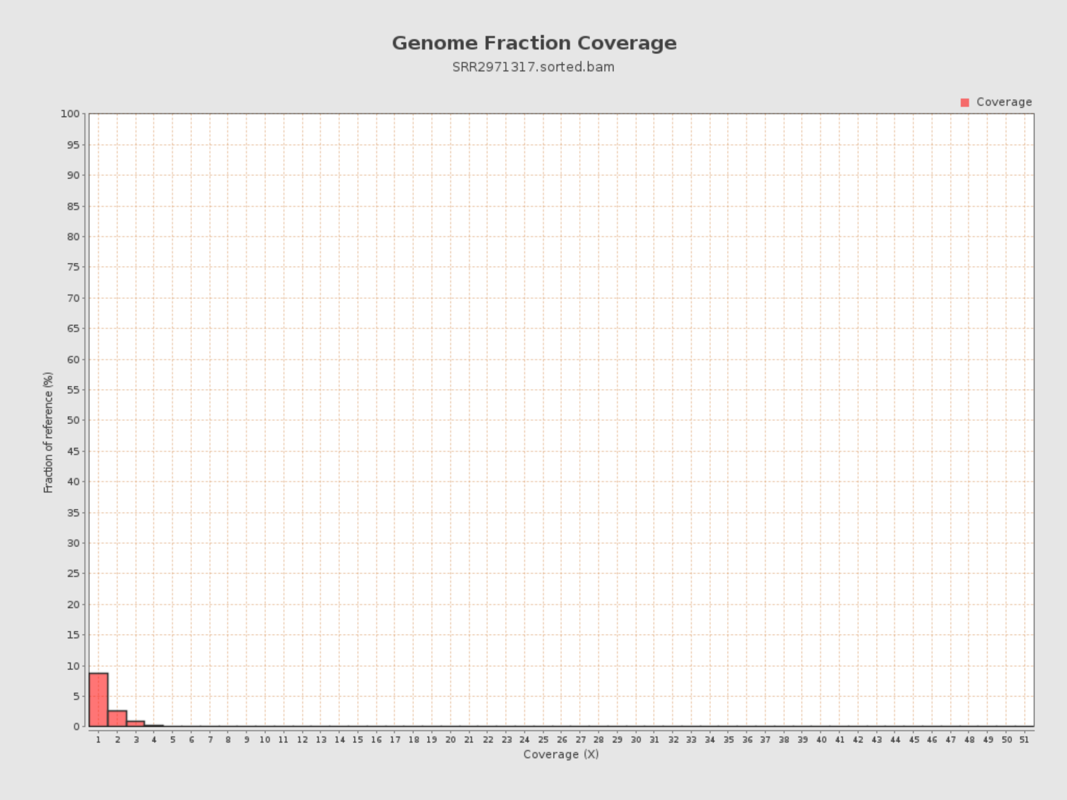
4. Results : Coverage Histogram



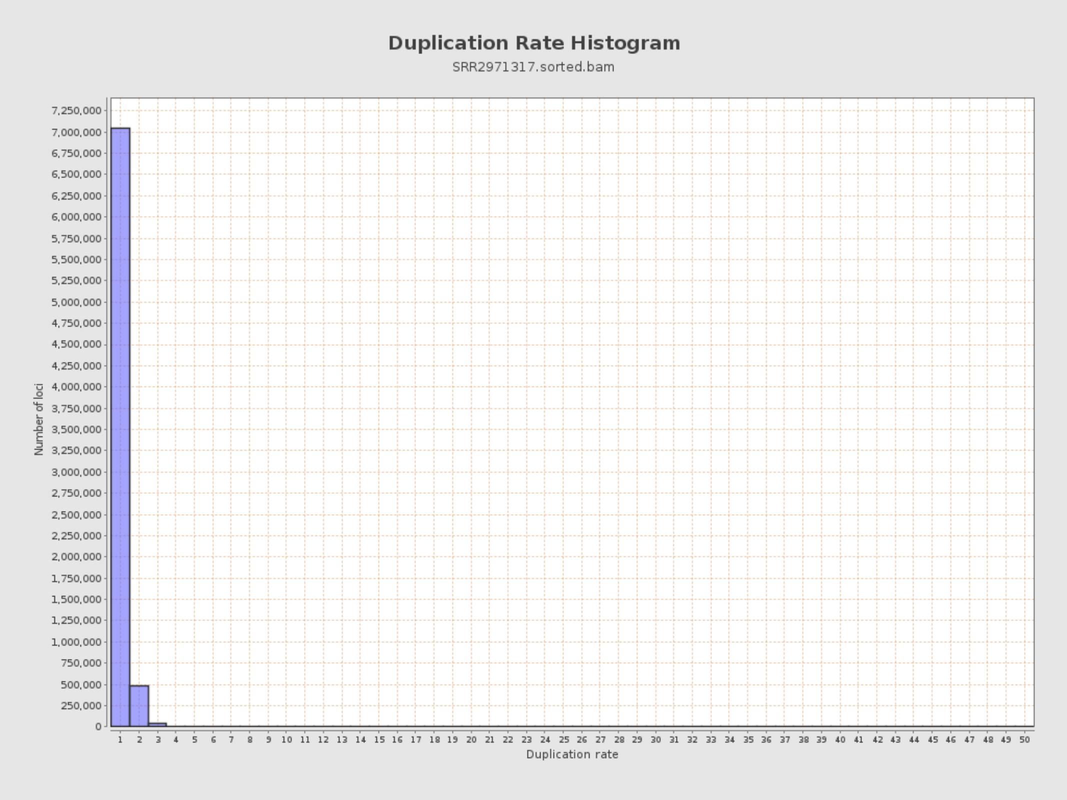
5. Results : Coverage Histogram (0-50X)



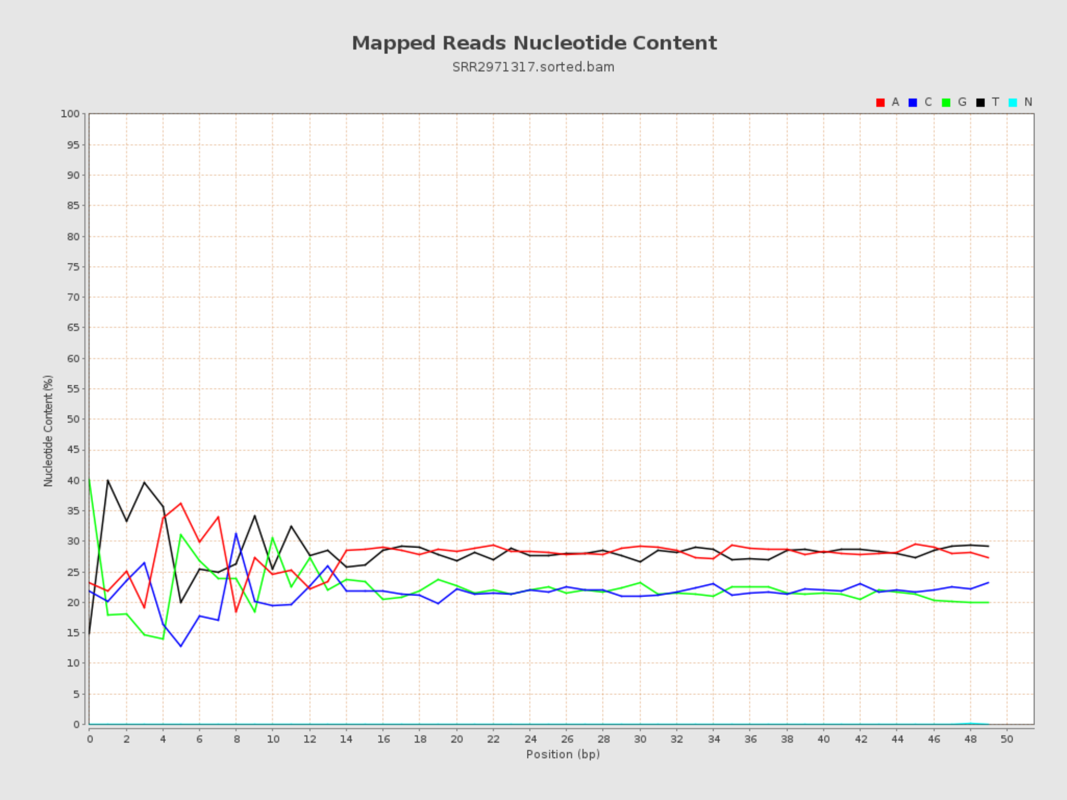
6. Results : Genome Fraction Coverage



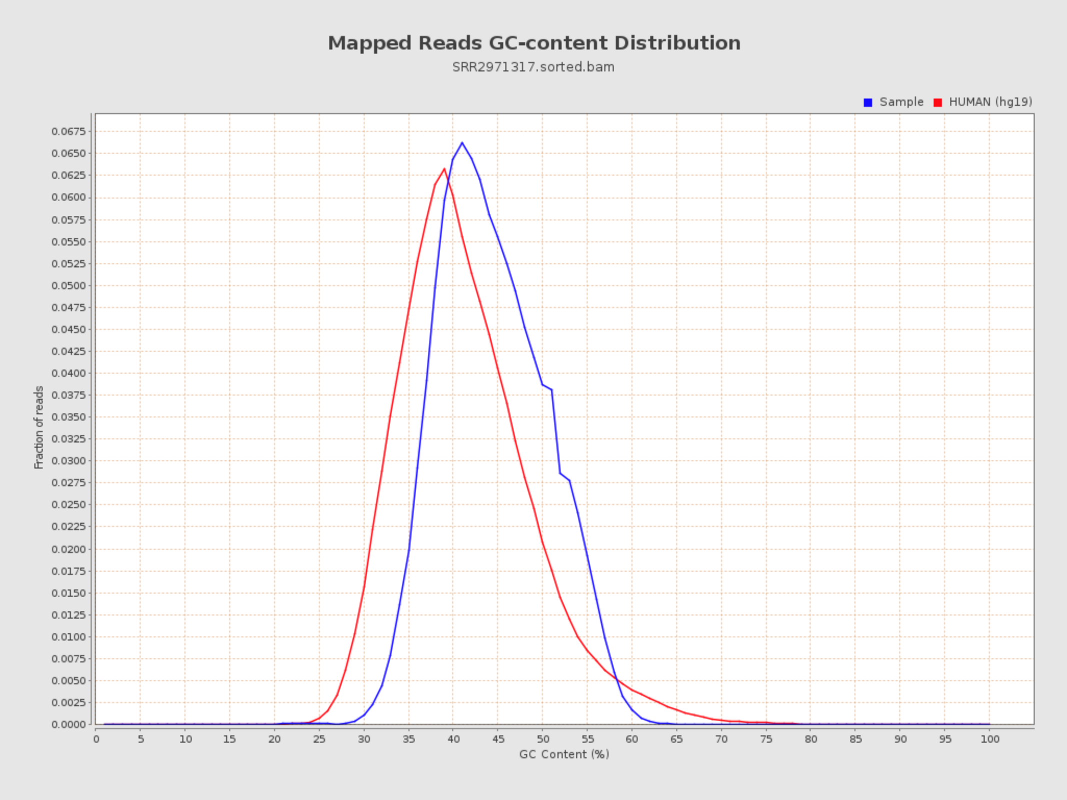
7. Results : Duplication Rate Histogram



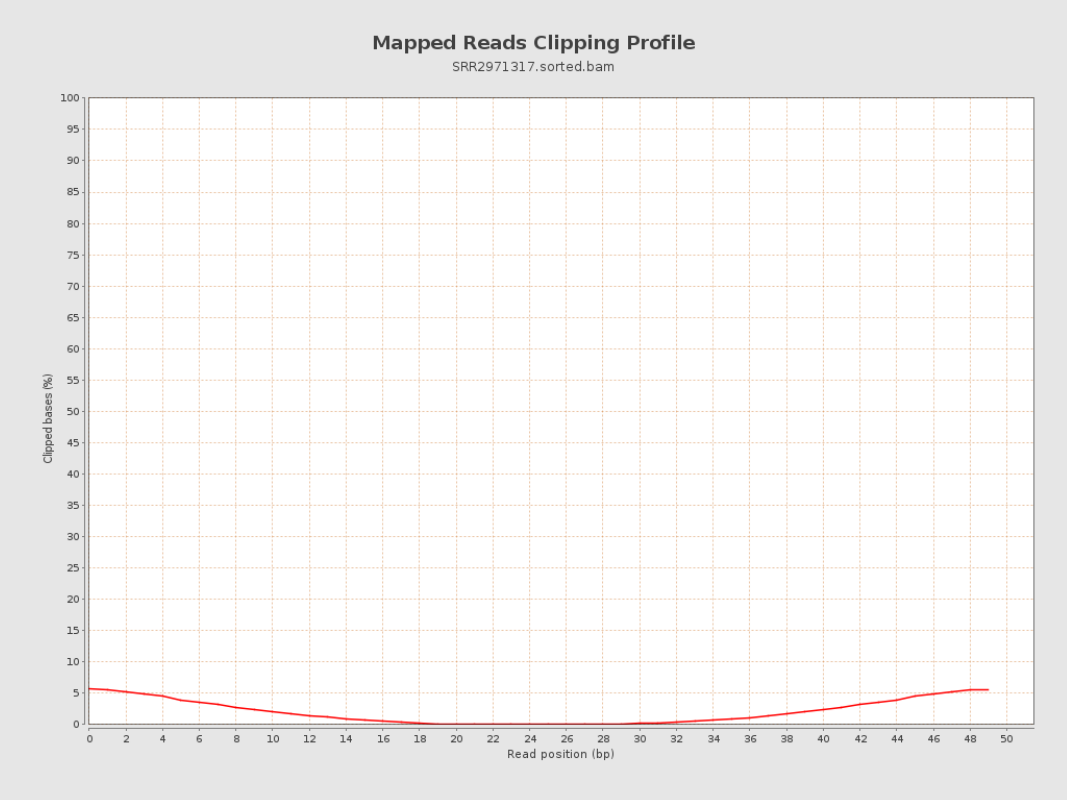
8. Results : Mapped Reads Nucleotide Content



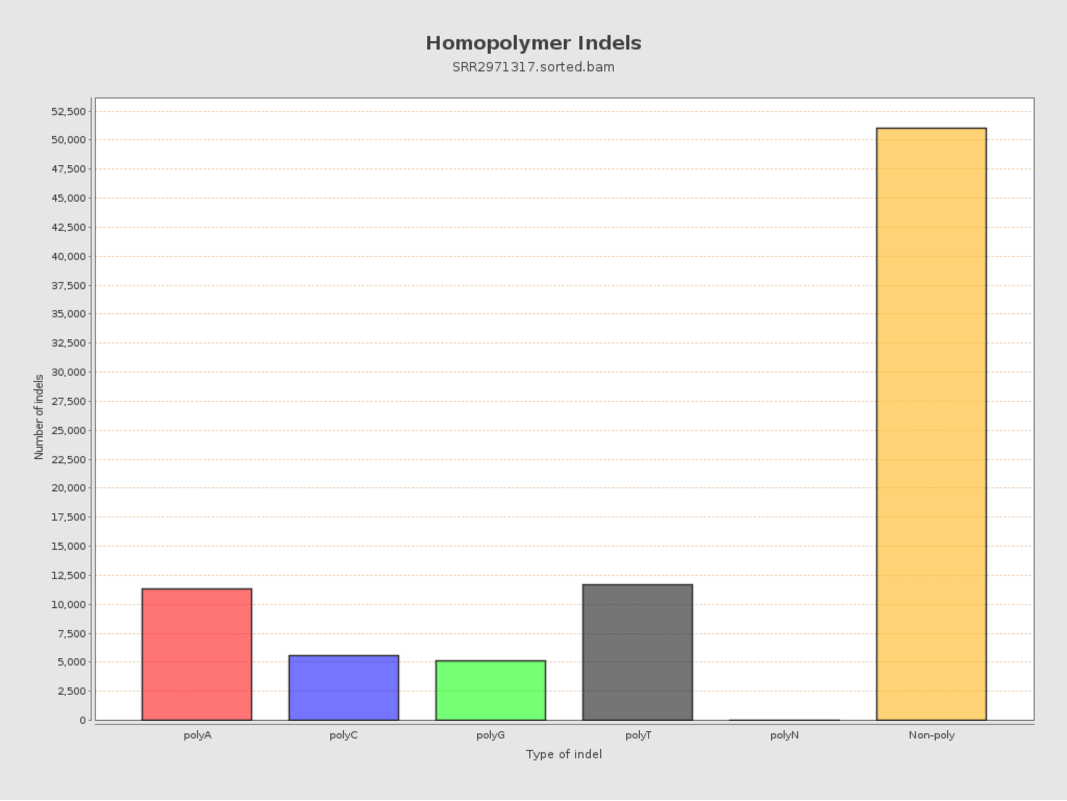
9. Results : Mapped Reads GC-content Distribution



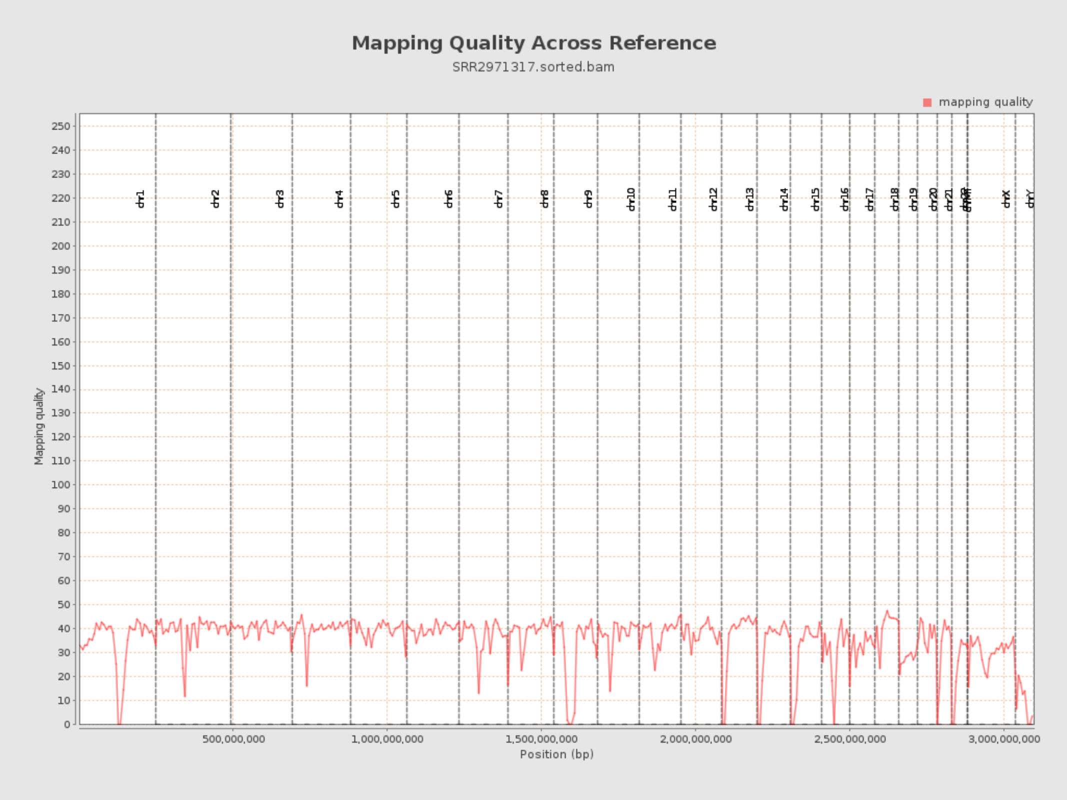
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram