Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 06:59:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212675.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_SRR3212675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212675.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 06:59:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212675.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,167,871
Mapped reads	1,984,407 / 91.54%
Unmapped reads	183,464 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,438 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	83,983 / 3.87%
Duplication rate	3.48%
Clipped reads	809,210 / 37.33%

2.2. ACGT Content

Number/percentage of A's	36,847,941 / 27.45%
Number/percentage of C's	25,934,866 / 19.32%
Number/percentage of T's	41,232,787 / 30.71%
Number/percentage of G's	30,232,629 / 22.52%
Number/percentage of N's	1,490 / 0%
GC Percentage	41.84%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.3352

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

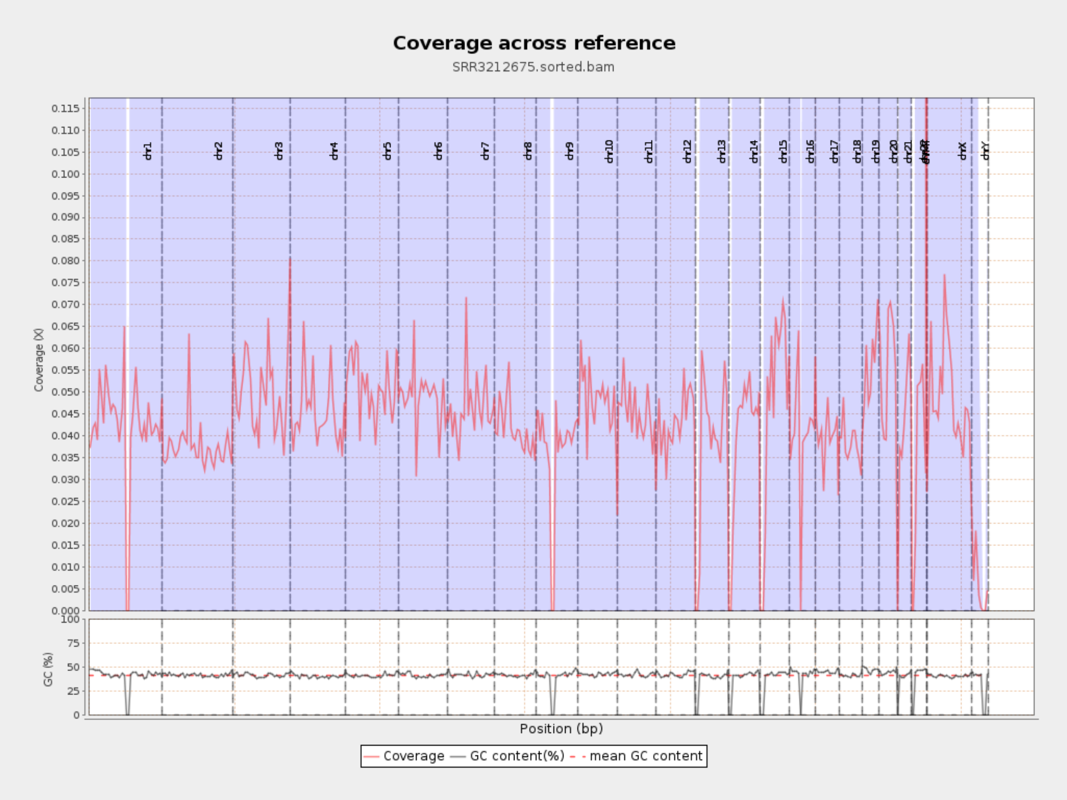
General error rate	0.84%
Mismatches	1,111,805
Insertions	9,847
Mapped reads with at least one insertion	0.49%
Deletions	27,793
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.7%

2.6. Chromosome stats

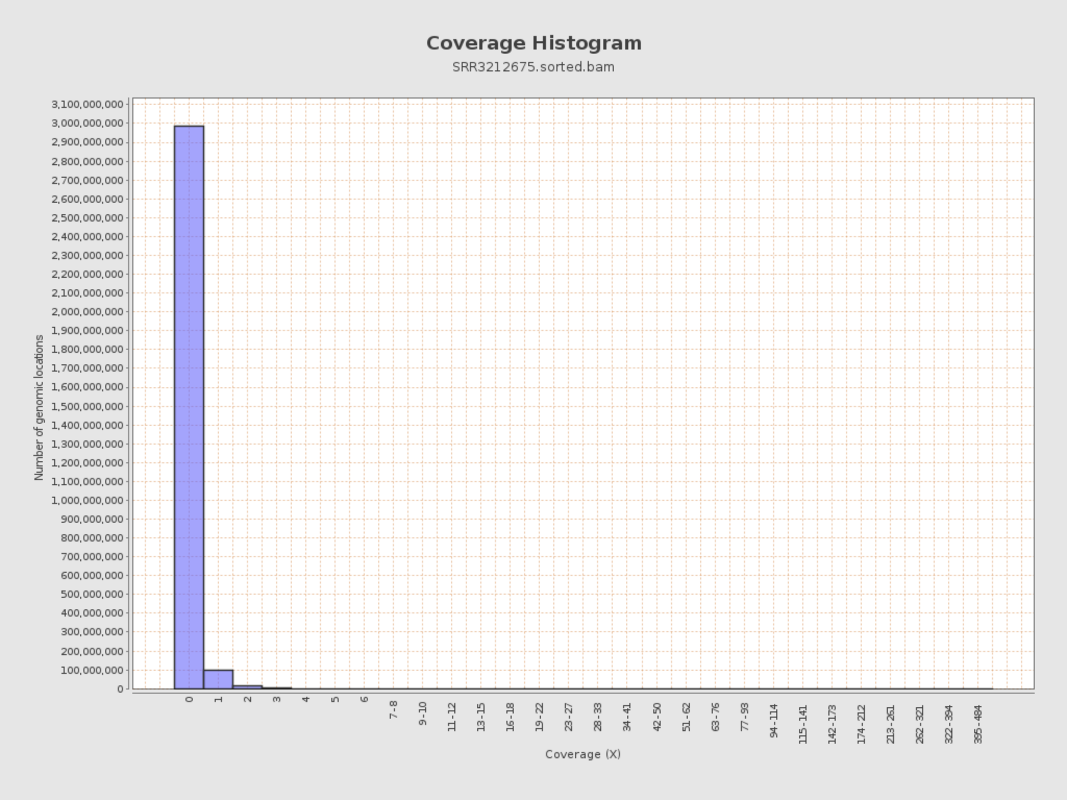
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10499598	0.0421	0.4863
chr2	243199373	9133553	0.0376	0.355
chr3	198022430	9847037	0.0497	0.2586
chr4	191154276	8659062	0.0453	0.2624
chr5	180915260	9298060	0.0514	0.2639
chr6	171115067	8316759	0.0486	0.3219
chr7	159138663	7401434	0.0465	0.49

chr8	146364022	6083144	0.0416	0.3349
chr9	141213431	5072369	0.0359	0.3153
chr10	135534747	6549137	0.0483	0.3266
chr11	135006516	6030632	0.0447	0.3365
chr12	133851895	5780274	0.0432	0.245
chr13	115169878	4367373	0.0379	0.2261
chr14	107349540	4181343	0.039	0.2443
chr15	102531392	4811397	0.0469	0.2553
chr16	90354753	3645203	0.0403	0.2575
chr17	81195210	3221334	0.0397	0.2592
chr18	78077248	3008364	0.0385	0.6116
chr19	59128983	3311970	0.056	0.4191
chr20	63025520	3399956	0.0539	0.2798
chr21	48129895	2035605	0.0423	0.2588
chr22	51304566	1723650	0.0336	0.214
chrMT	16571	25133	1.5167	1.7303
chrX	155270560	7558061	0.0487	0.2902
chrY	59373566	339044	0.0057	0.1402

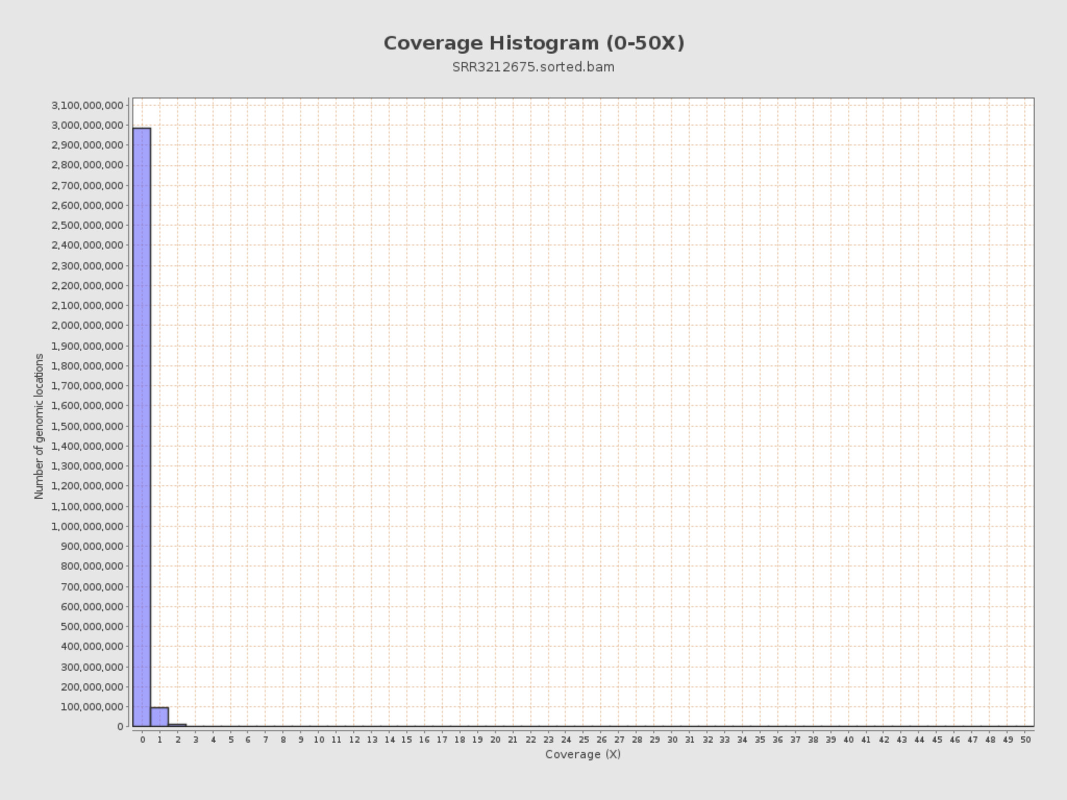
3. Results : Coverage across reference



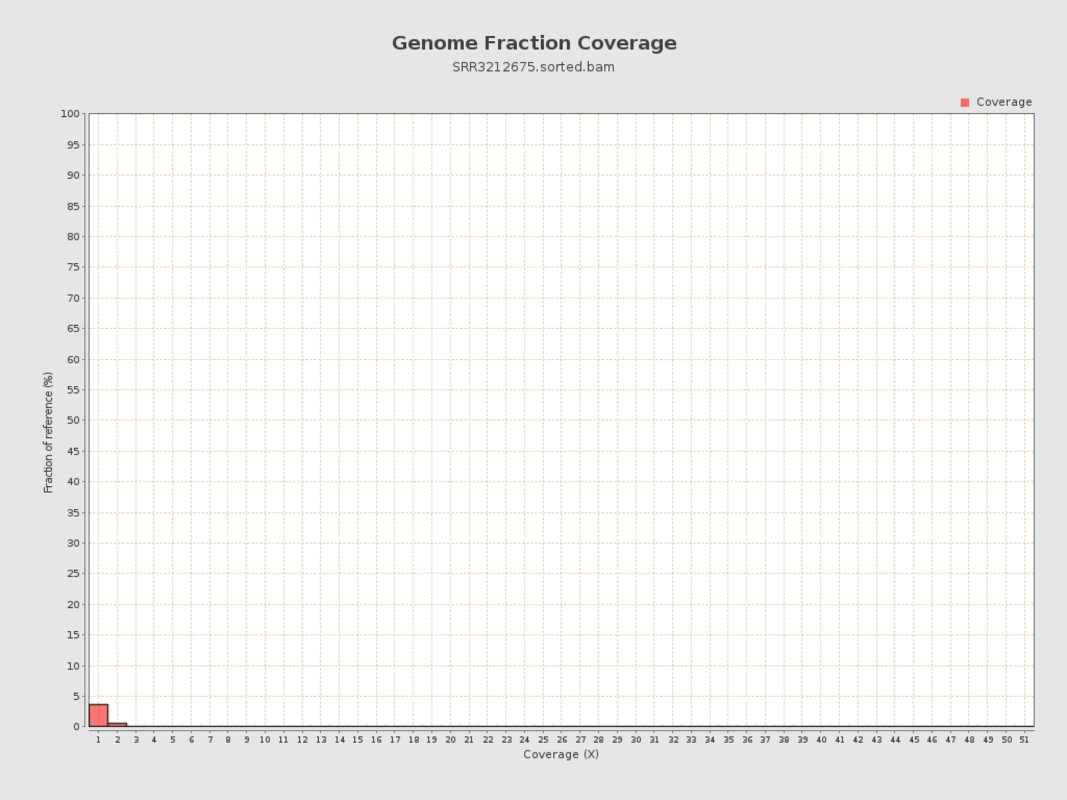
4. Results : Coverage Histogram



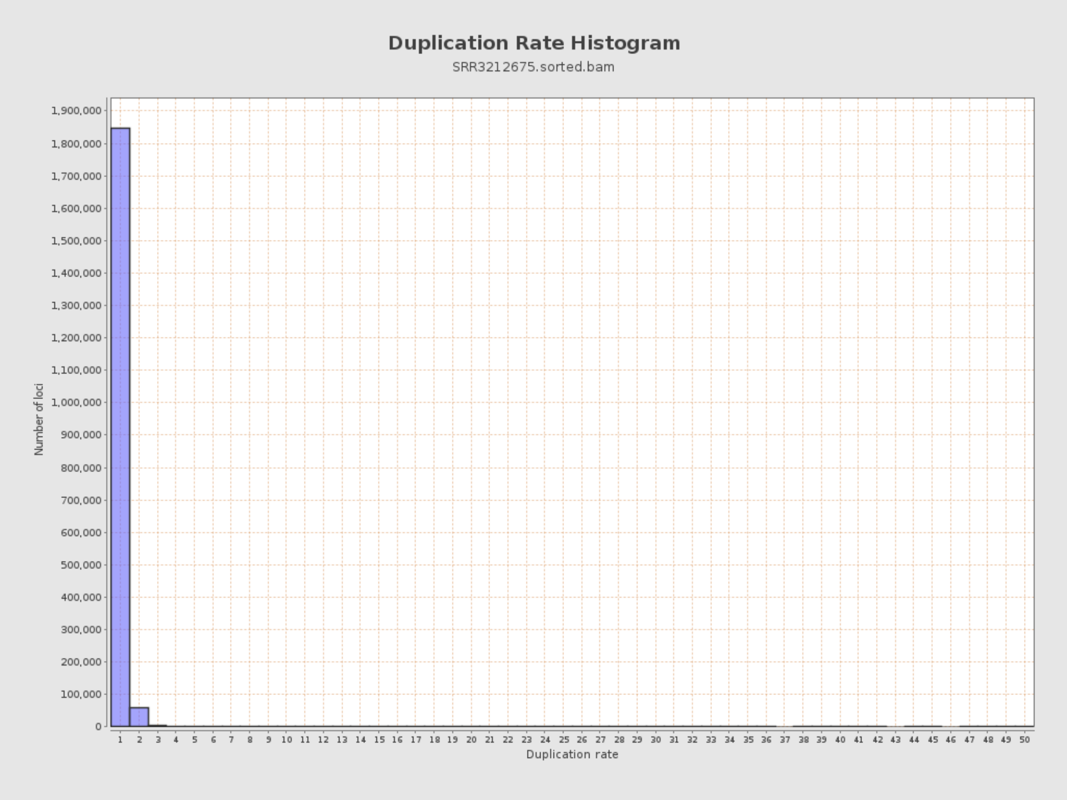
5. Results : Coverage Histogram (0-50X)



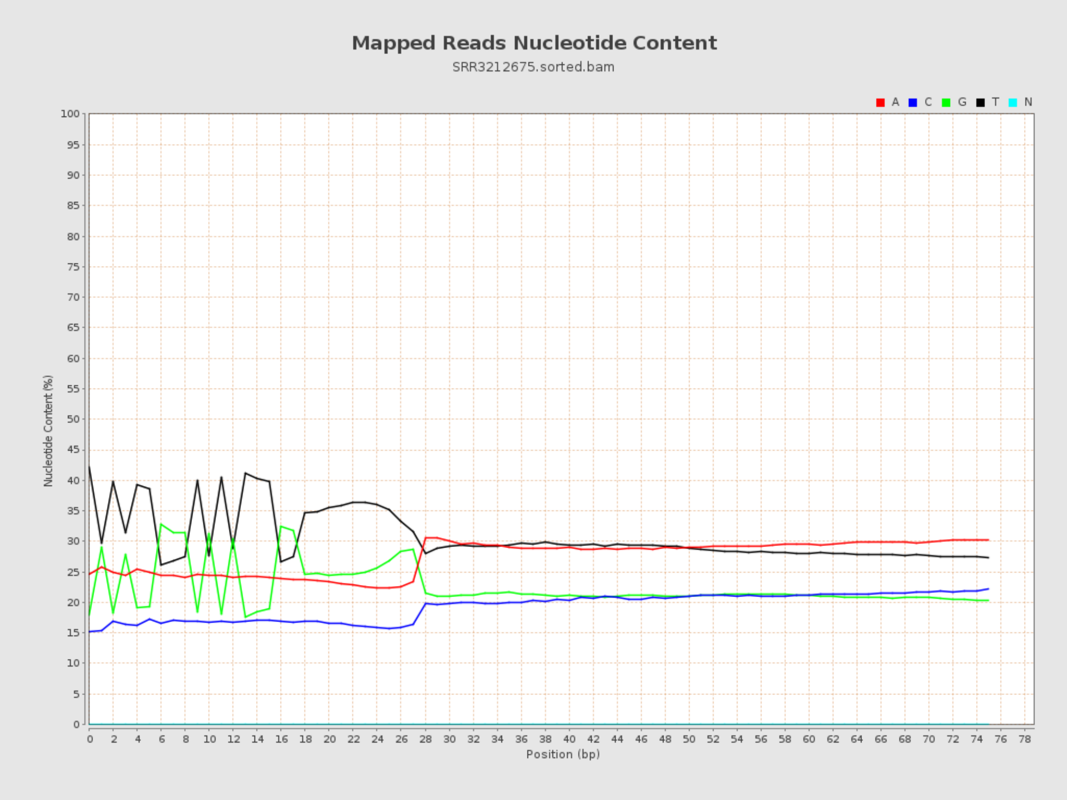
6. Results : Genome Fraction Coverage



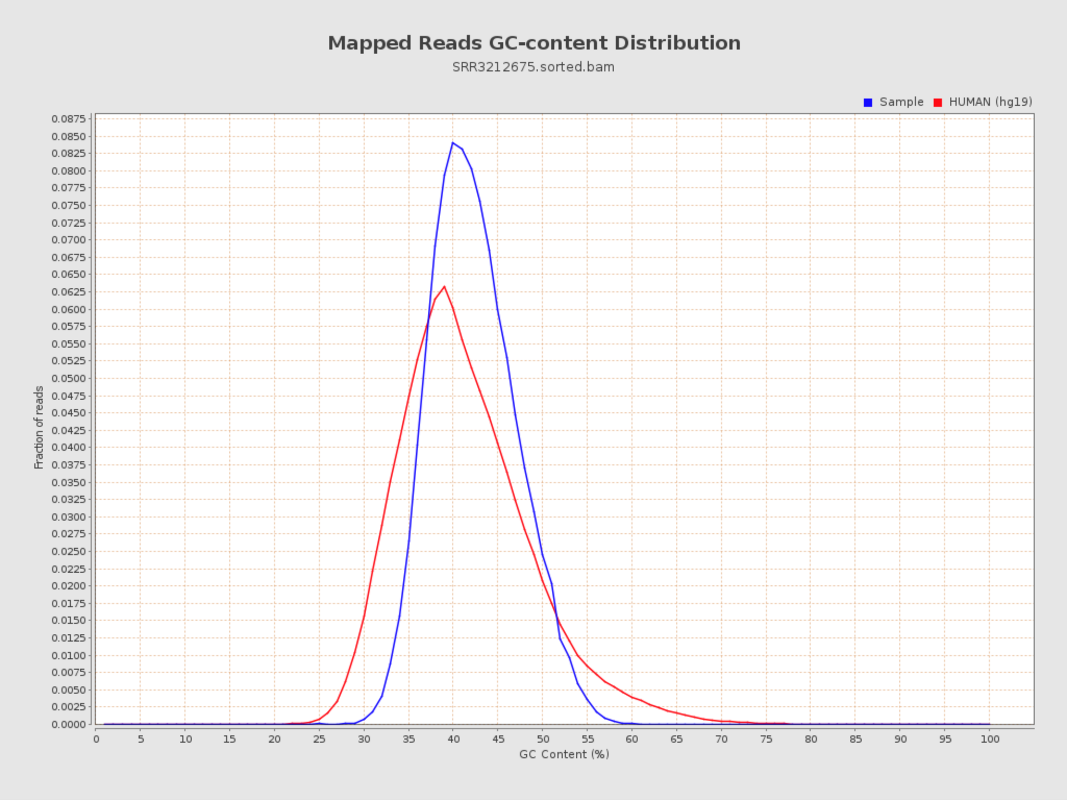
7. Results : Duplication Rate Histogram



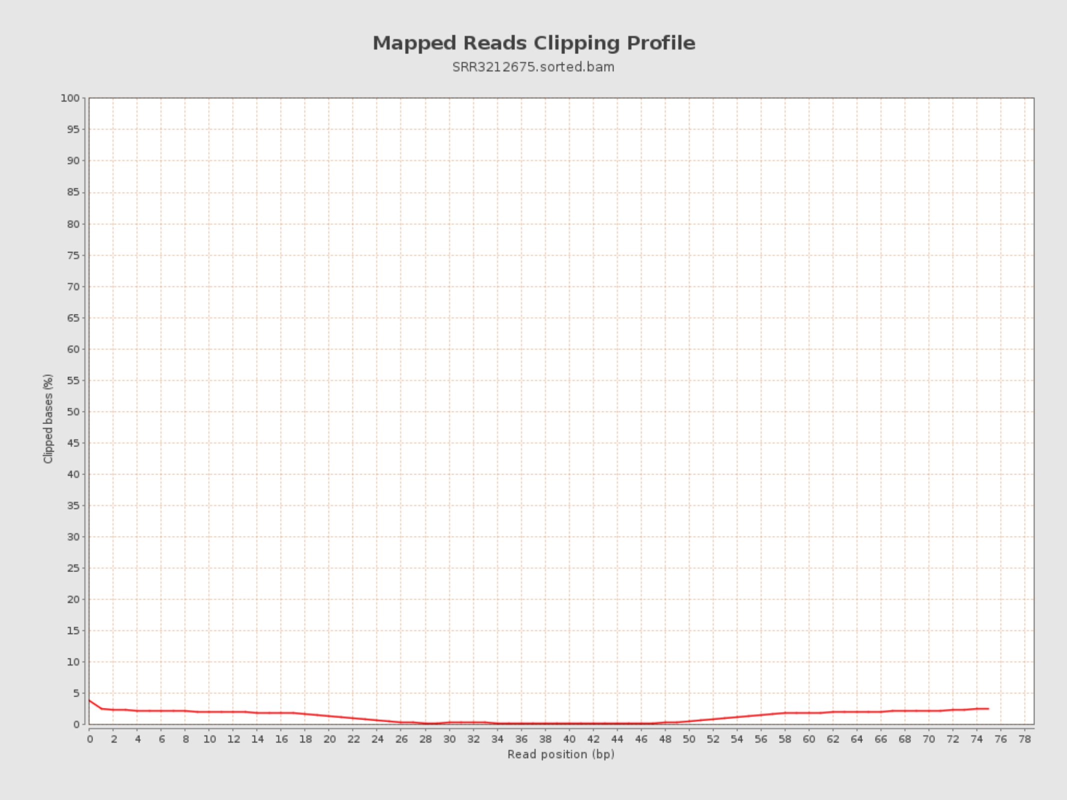
8. Results : Mapped Reads Nucleotide Content



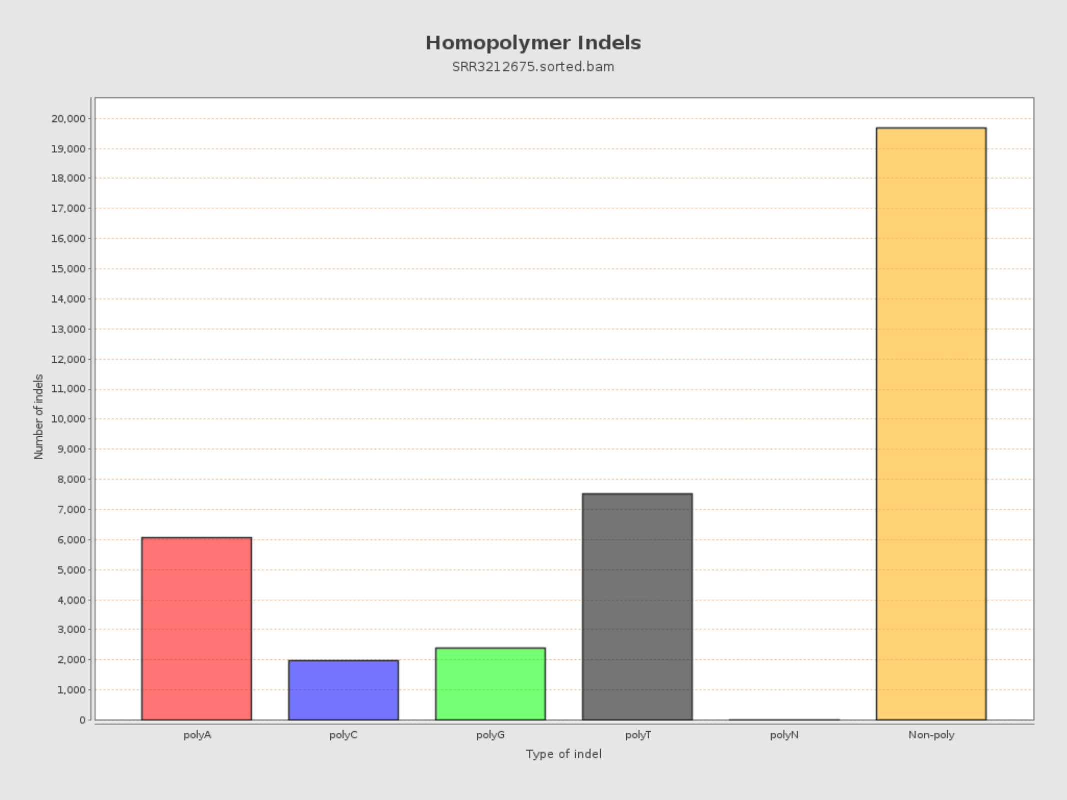
9. Results : Mapped Reads GC-content Distribution



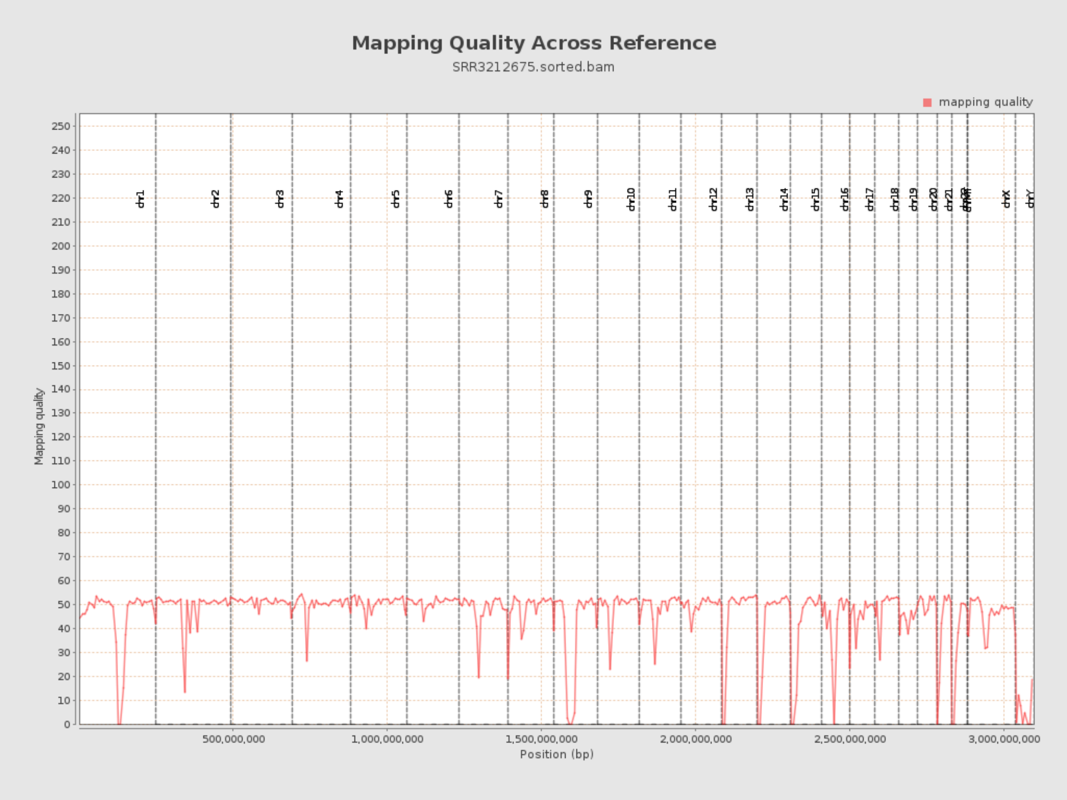
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram