Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472837.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_SRR3472837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:47:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,084,403
Mapped reads	2,469,050 / 80.05%
Unmapped reads	615,353 / 19.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,547 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	78,606 / 2.55%
Duplication rate	2.29%
Clipped reads	1,285,361 / 41.67%

2.2. ACGT Content

Number/percentage of A's	43,339,621 / 27.1%
Number/percentage of C's	31,653,816 / 19.79%
Number/percentage of T's	47,792,250 / 29.88%
Number/percentage of G's	37,157,871 / 23.23%
Number/percentage of N's	2,986 / 0%
GC Percentage	43.02%

2.3. Coverage

Mean	0.0517

Standard Deviation	0.3818

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

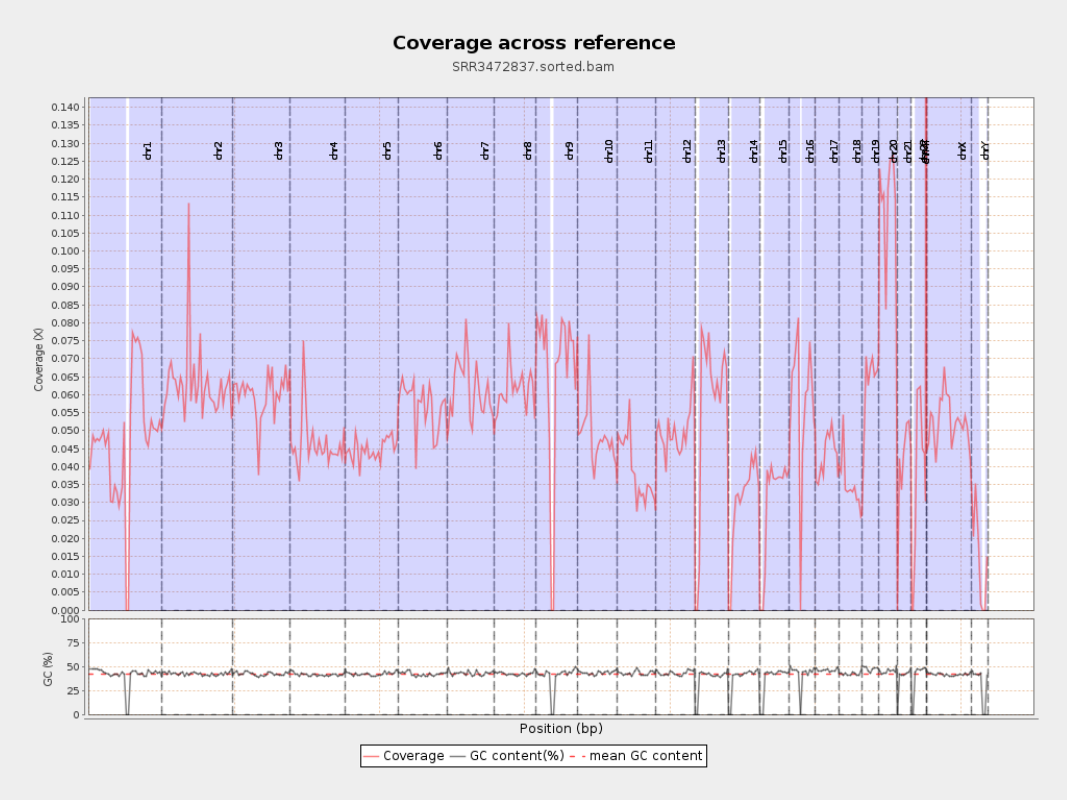
General error rate	0.88%
Mismatches	1,379,268
Insertions	12,688
Mapped reads with at least one insertion	0.51%
Deletions	36,997
Mapped reads with at least one deletion	1.48%
Homopolymer indels	45.27%

2.6. Chromosome stats

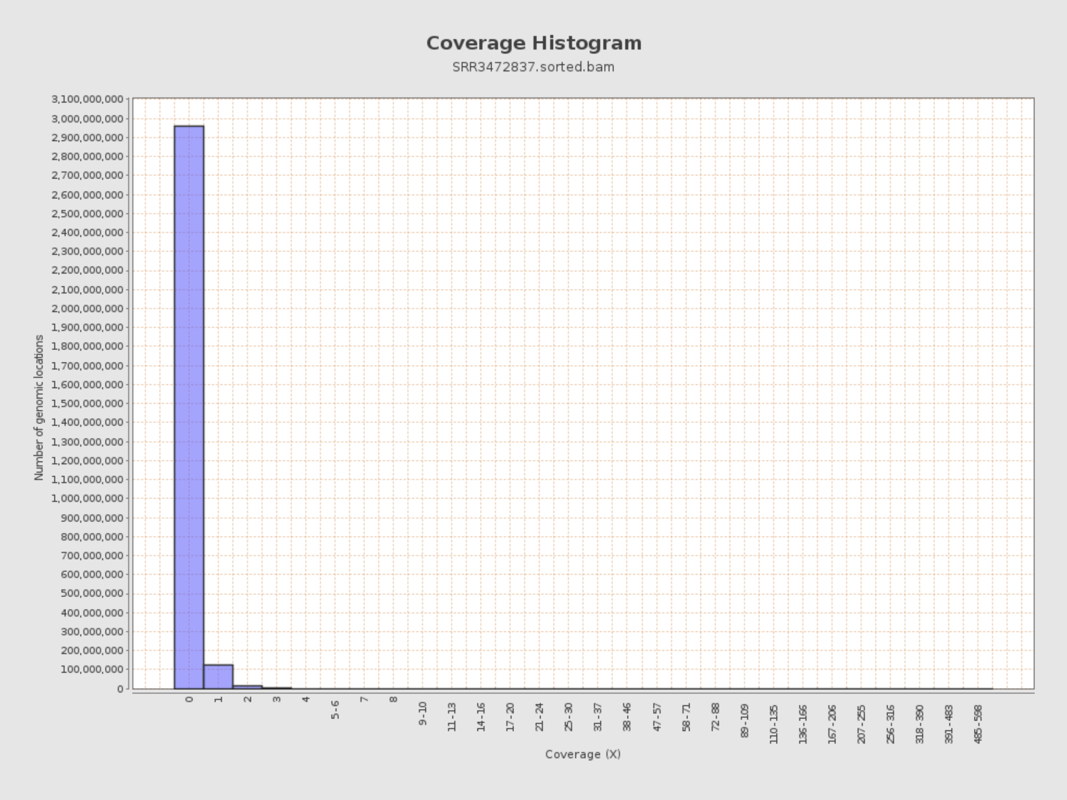
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11670281	0.0468	0.5059
chr2	243199373	15306278	0.0629	0.5899
chr3	198022430	11854593	0.0599	0.2734
chr4	191154276	8834621	0.0462	0.275
chr5	180915260	8089832	0.0447	0.2394
chr6	171115067	9757507	0.057	0.2974
chr7	159138663	9837726	0.0618	0.4974

chr8	146364022	8994680	0.0615	0.385
chr9	141213431	9182324	0.065	0.4485
chr10	135534747	6555136	0.0484	0.3694
chr11	135006516	5229481	0.0387	0.3444
chr12	133851895	6676646	0.0499	0.2587
chr13	115169878	6501874	0.0565	0.2758
chr14	107349540	3252985	0.0303	0.2323
chr15	102531392	3097383	0.0302	0.2166
chr16	90354753	5277140	0.0584	0.3061
chr17	81195210	3506185	0.0432	0.2584
chr18	78077248	2763962	0.0354	0.7088
chr19	59128983	3711693	0.0628	0.4043
chr20	63025520	7115737	0.1129	0.4009
chr21	48129895	1956663	0.0407	0.275
chr22	51304566	1845350	0.036	0.2255
chrMT	16571	16810	1.0144	1.2445
chrX	155270560	8131331	0.0524	0.2982
chrY	59373566	846099	0.0143	0.1932

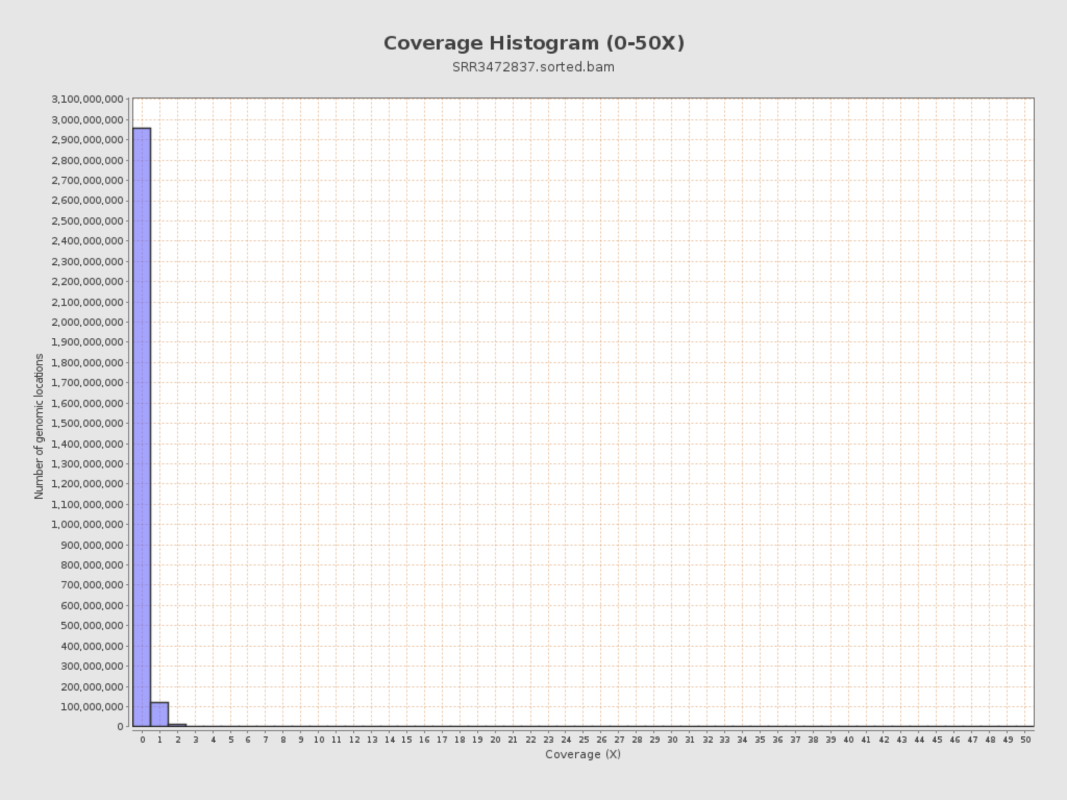
3. Results : Coverage across reference



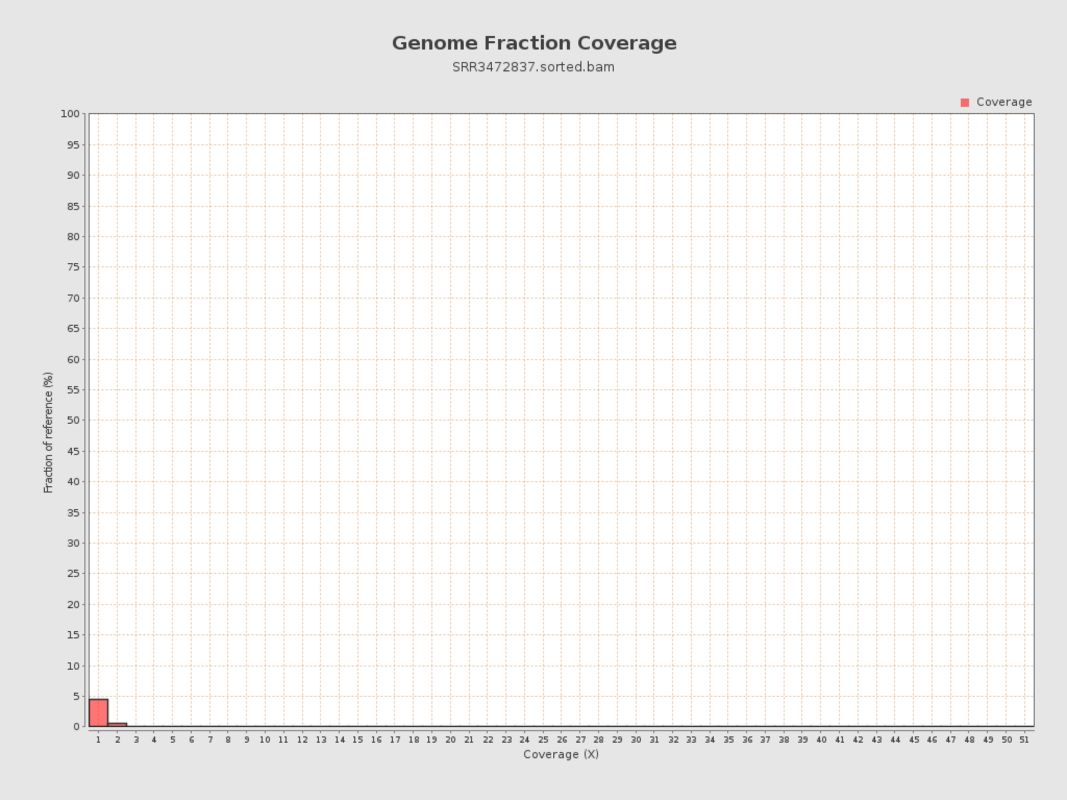
4. Results : Coverage Histogram



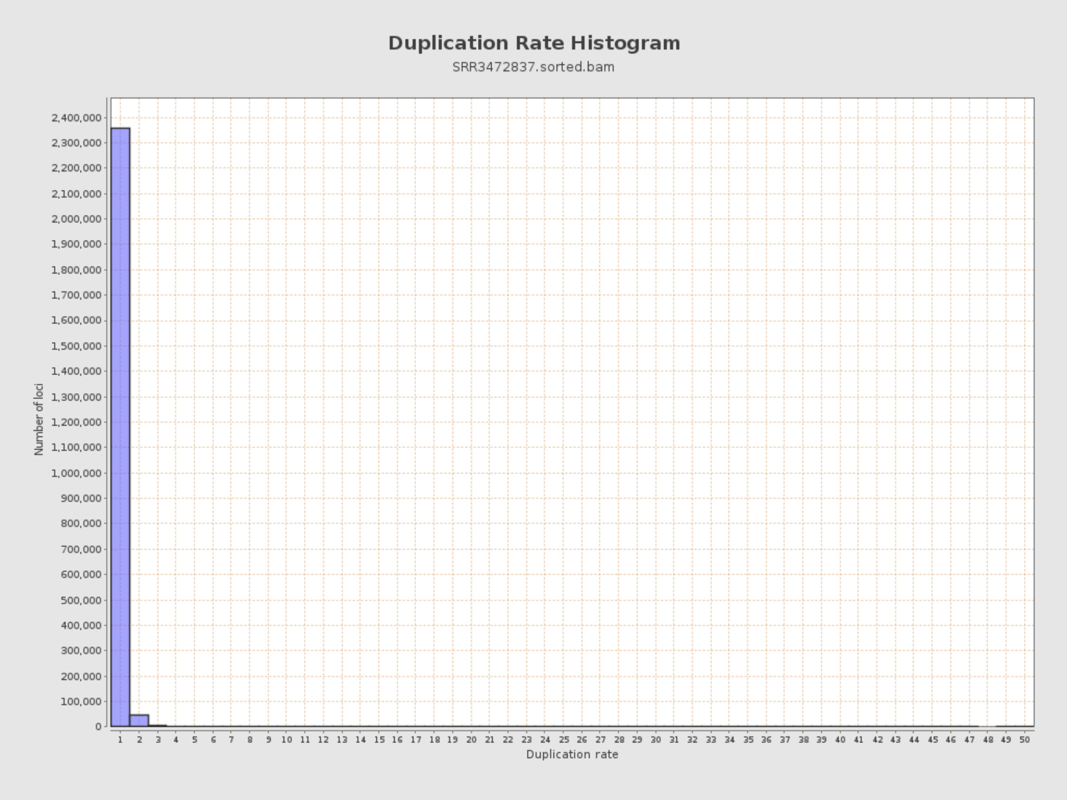
5. Results : Coverage Histogram (0-50X)



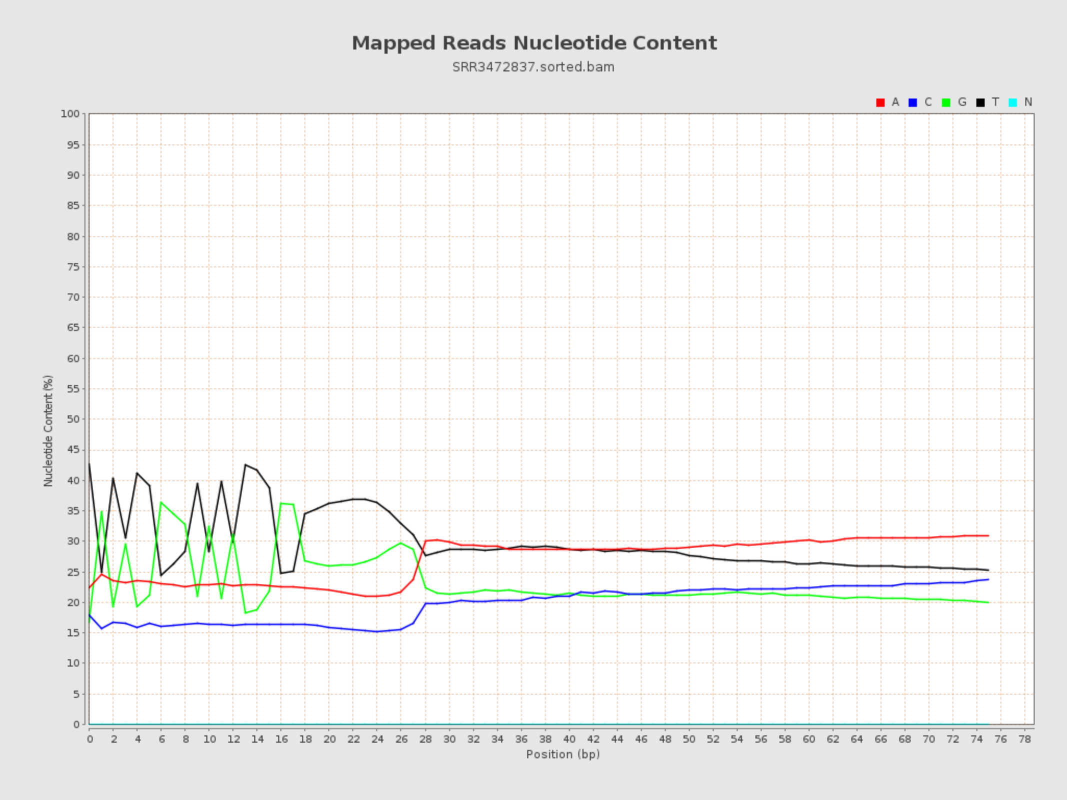
6. Results : Genome Fraction Coverage



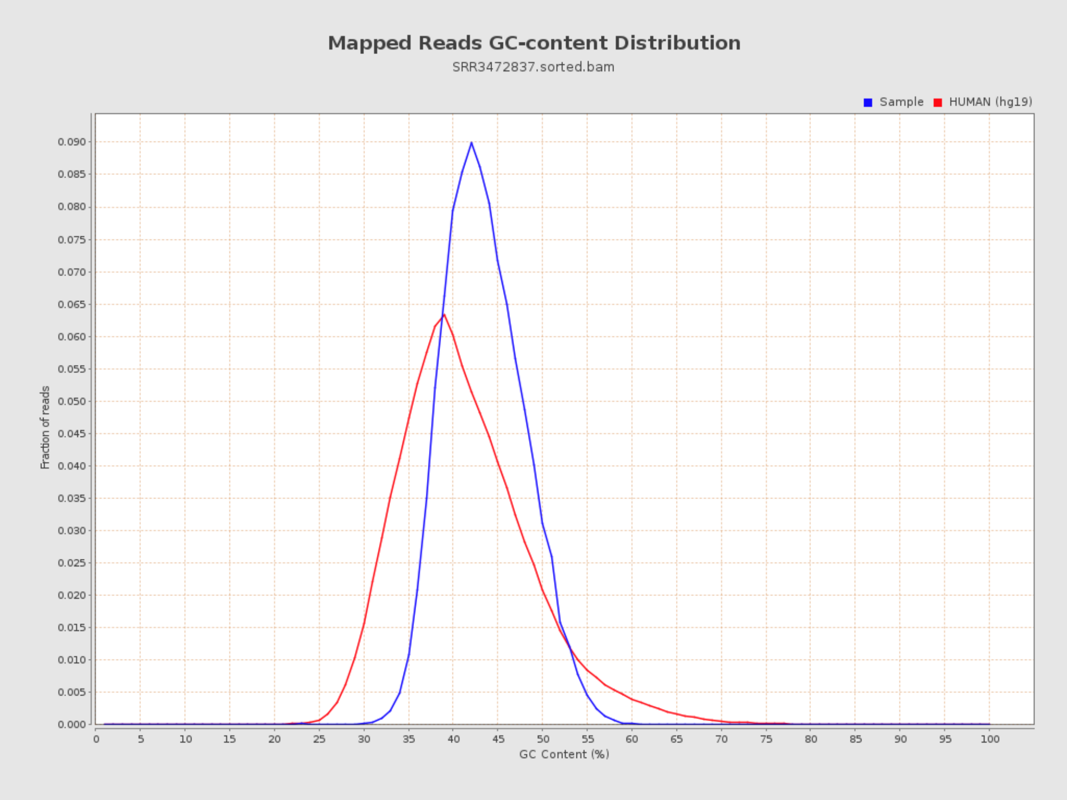
7. Results : Duplication Rate Histogram



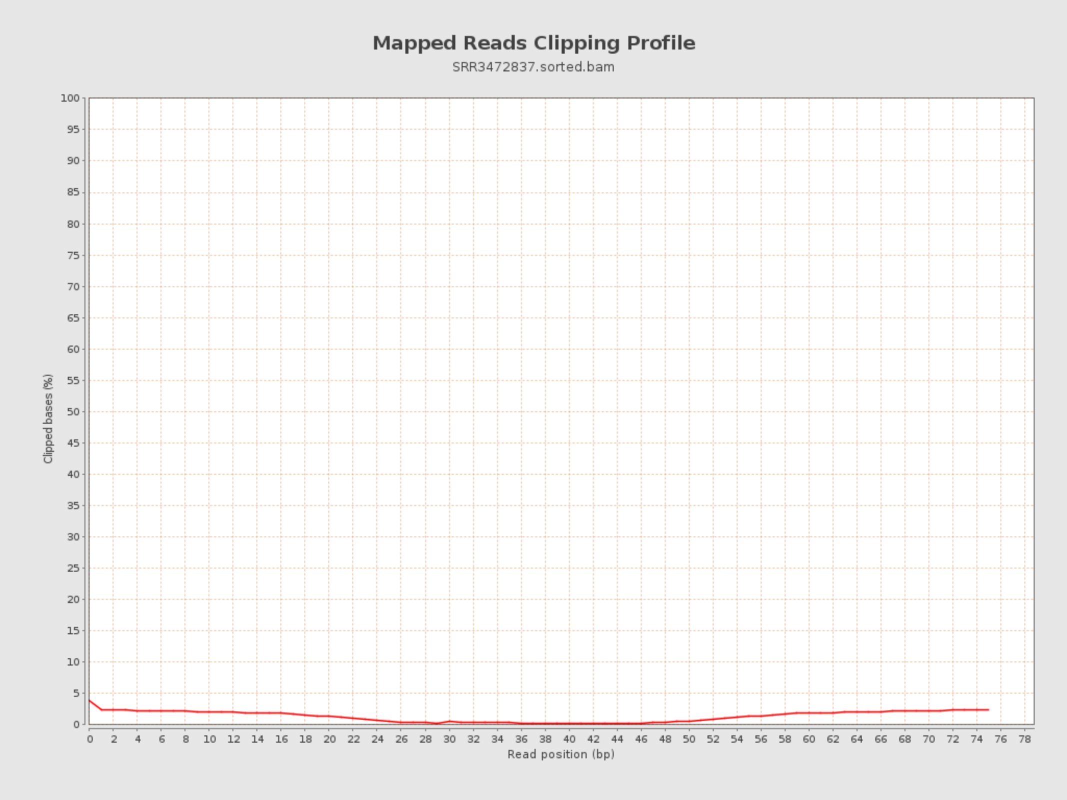
8. Results : Mapped Reads Nucleotide Content



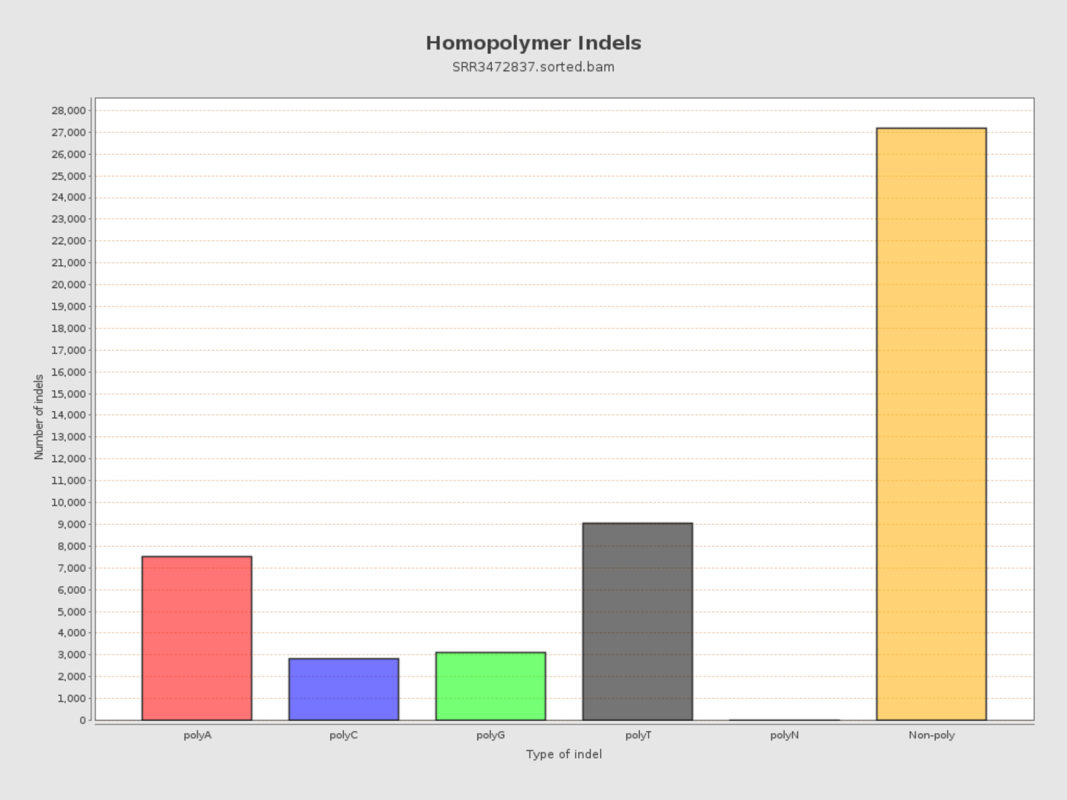
9. Results : Mapped Reads GC-content Distribution



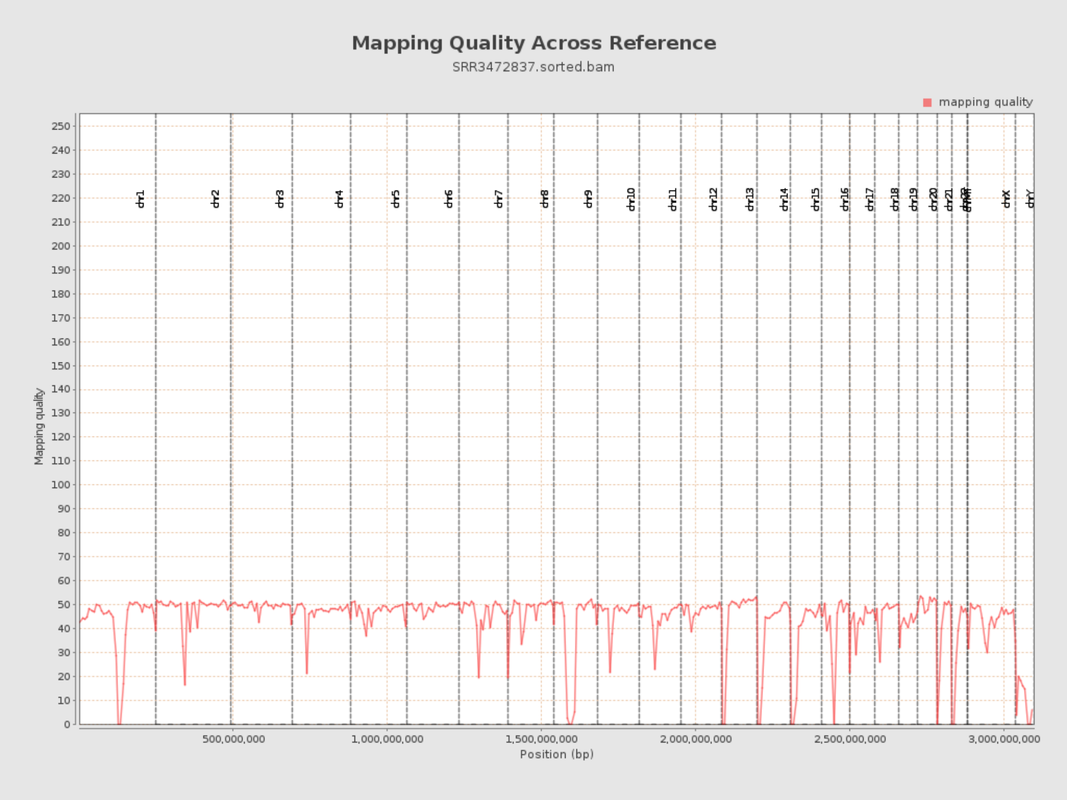
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram