

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:16:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084276.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_SRR3084276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:16:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,348,603
Mapped reads	3,033,604 / 90.59%
Unmapped reads	314,999 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,851 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	105,695 / 3.16%
Duplication rate	2.85%
Clipped reads	1,541,787 / 46.04%

2.2. ACGT Content

Number/percentage of A's	55,523,176 / 27.83%
Number/percentage of C's	38,828,580 / 19.46%
Number/percentage of T's	60,480,907 / 30.31%
Number/percentage of G's	44,424,421 / 22.27%
Number/percentage of N's	262,652 / 0.13%
GC Percentage	41.73%

2.3. Coverage

Mean	0.0645

Standard Deviation	0.4038
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2.4. Mapping Quality

Mean Mapping Quality	45.05
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2.5. Mismatches and indels

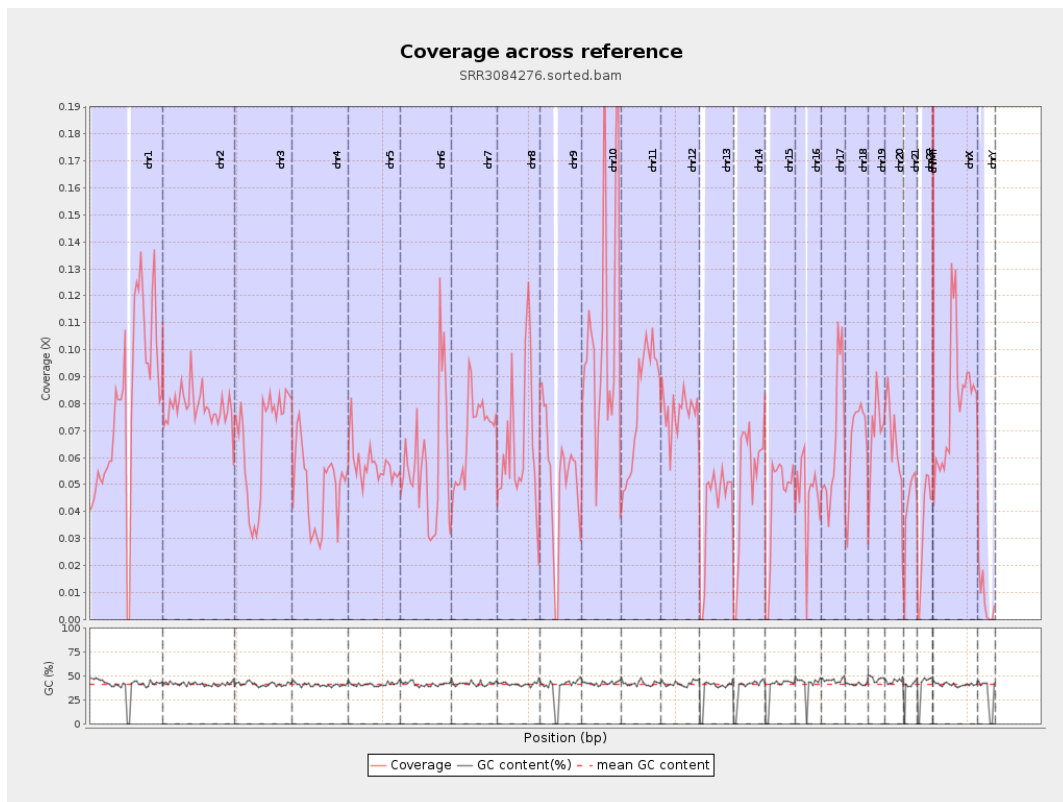
General error rate	1.05%
Mismatches	2,063,266
Insertions	14,963
Mapped reads with at least one insertion	0.49%
Deletions	41,494
Mapped reads with at least one deletion	1.36%
Homopolymer indels	45.57%

2.6. Chromosome stats

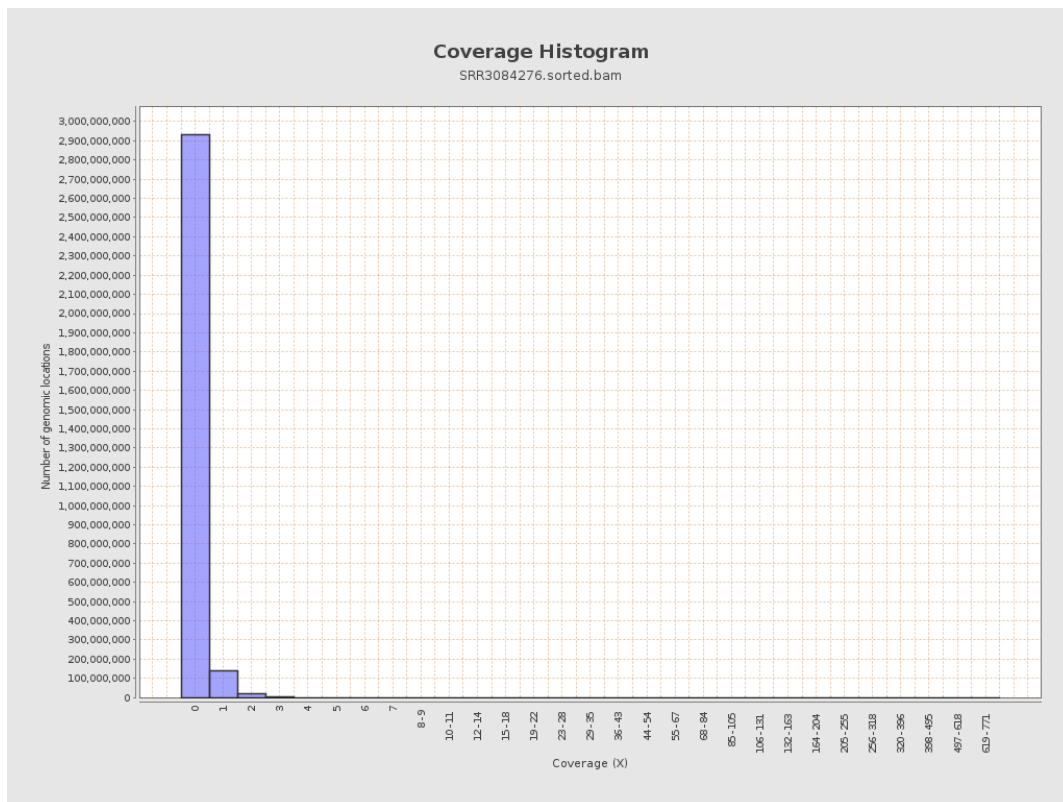
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19811991	0.0795	0.713
chr2	243199373	19198556	0.0789	0.4711
chr3	198022430	13139413	0.0664	0.3031
chr4	191154276	9326809	0.0488	0.2654
chr5	180915260	10415675	0.0576	0.2771
chr6	171115067	9991323	0.0584	0.3312
chr7	159138663	10921259	0.0686	0.5261

chr8	146364022	9307876	0.0636	0.358
chr9	141213431	7394820	0.0524	0.3245
chr10	135534747	14363593	0.106	0.559
chr11	135006516	10755551	0.0797	0.3972
chr12	133851895	10327661	0.0772	0.3236
chr13	115169878	4768959	0.0414	0.2366
chr14	107349540	5604190	0.0522	0.2731
chr15	102531392	4446009	0.0434	0.2532
chr16	90354753	4110227	0.0455	0.272
chr17	81195210	5465309	0.0673	0.3191
chr18	78077248	5130016	0.0657	0.5024
chr19	59128983	4193334	0.0709	0.5076
chr20	63025520	4135935	0.0656	0.3024
chr21	48129895	2057078	0.0427	0.2491
chr22	51304566	1758206	0.0343	0.2119
chrMT	16571	14442	0.8715	1.1503
chrX	155270560	12531212	0.0807	0.3638
chrY	59373566	416773	0.007	0.1309

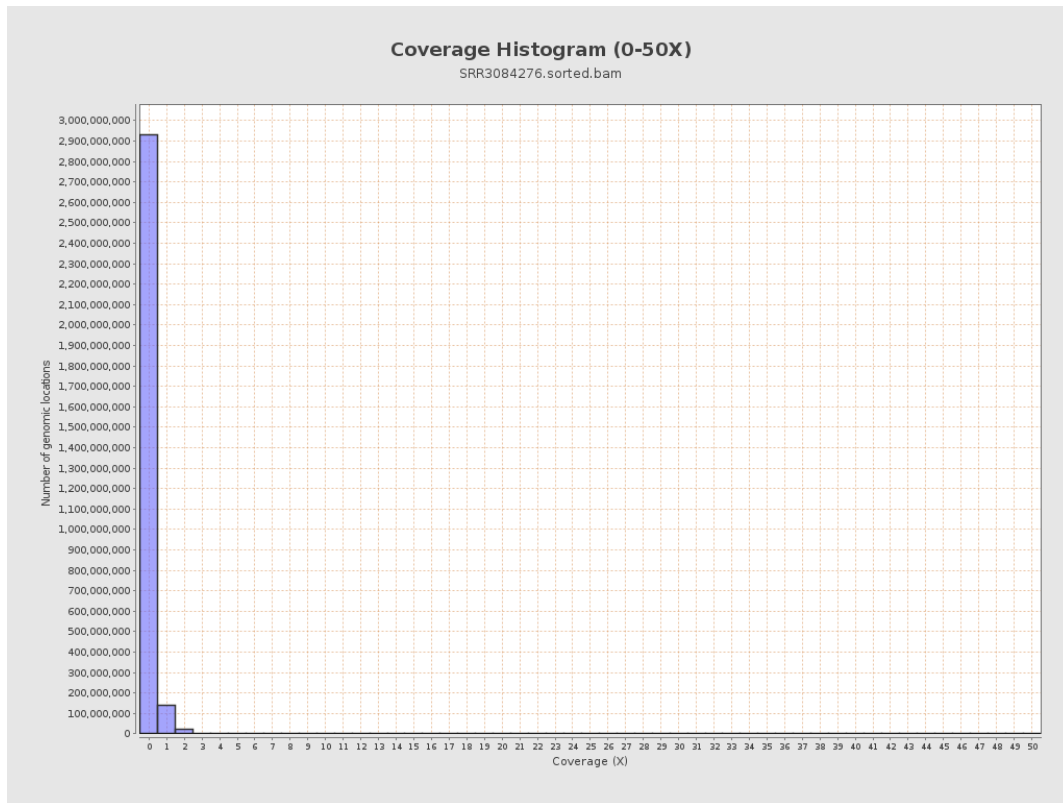
3. Results : Coverage across reference



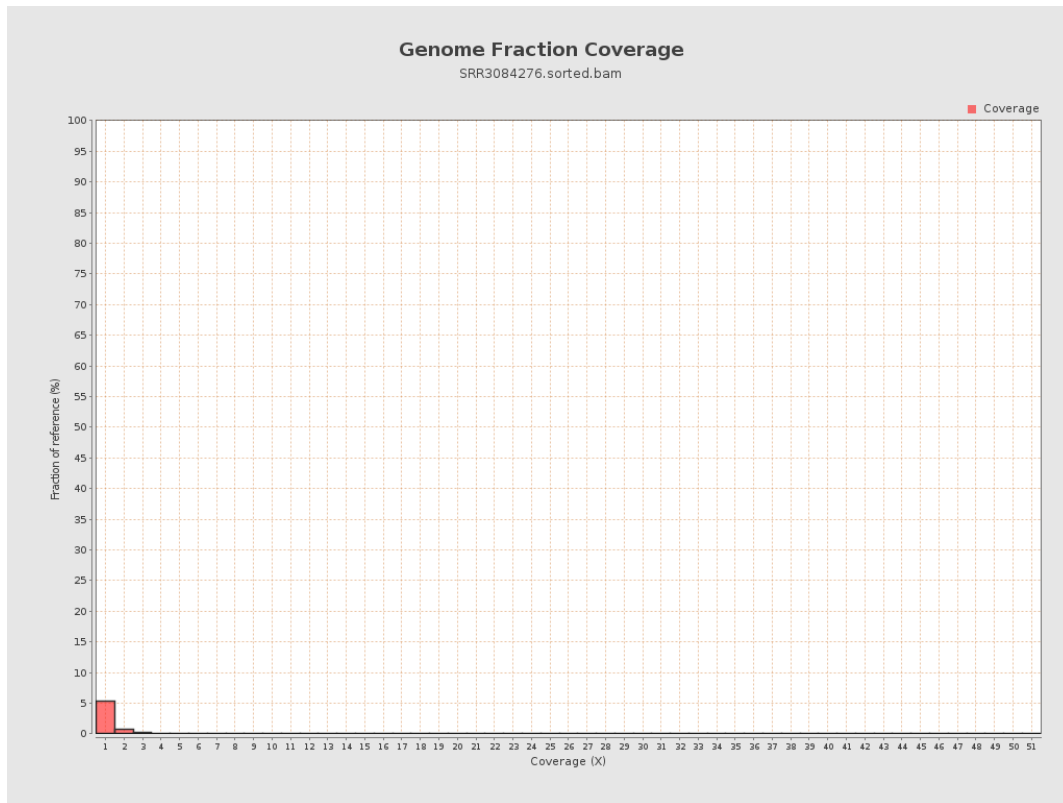
4. Results : Coverage Histogram



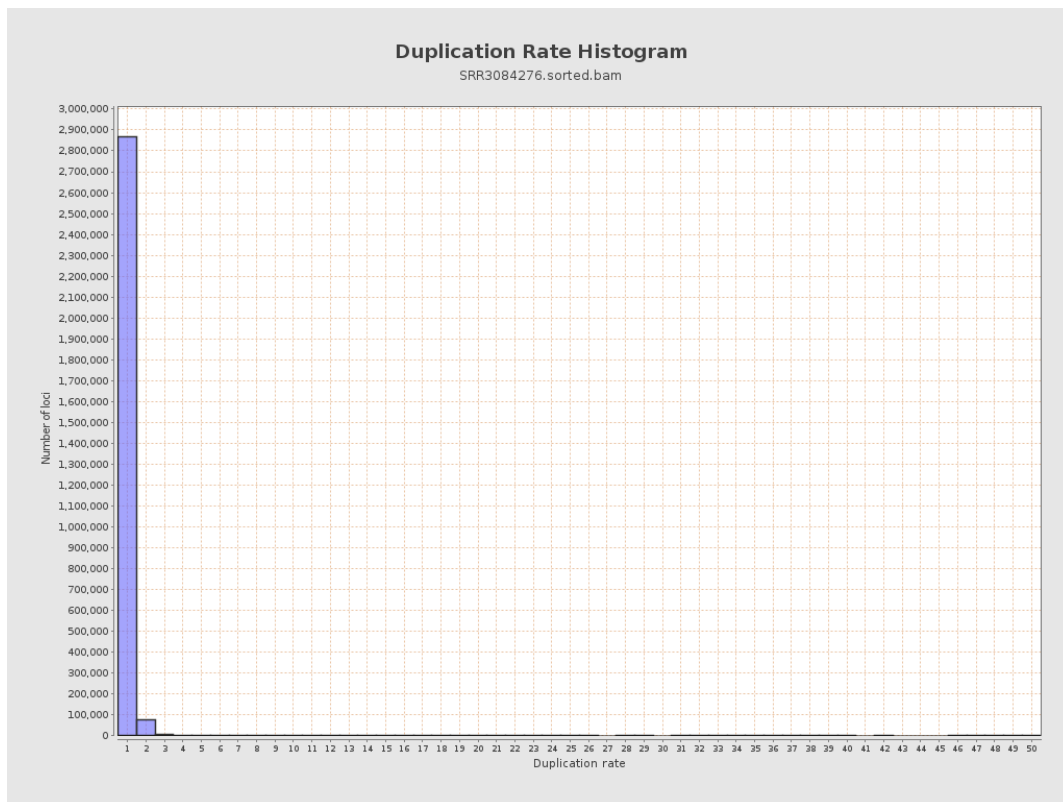
5. Results : Coverage Histogram (0-50X)



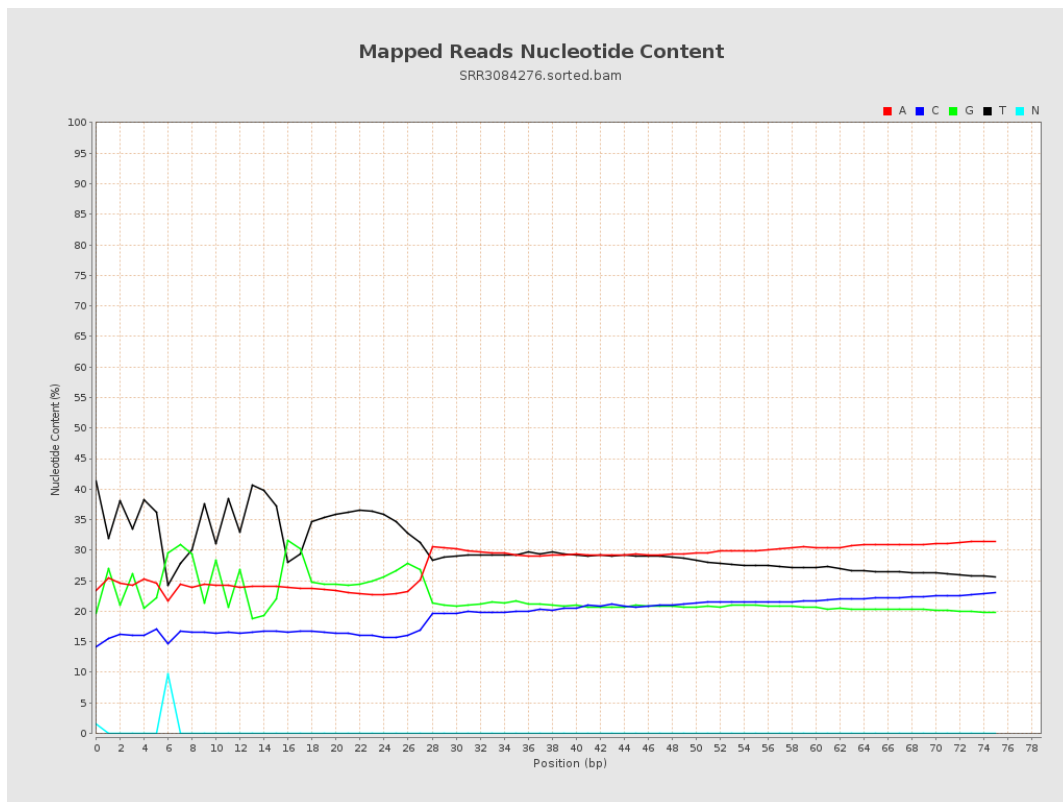
6. Results : Genome Fraction Coverage



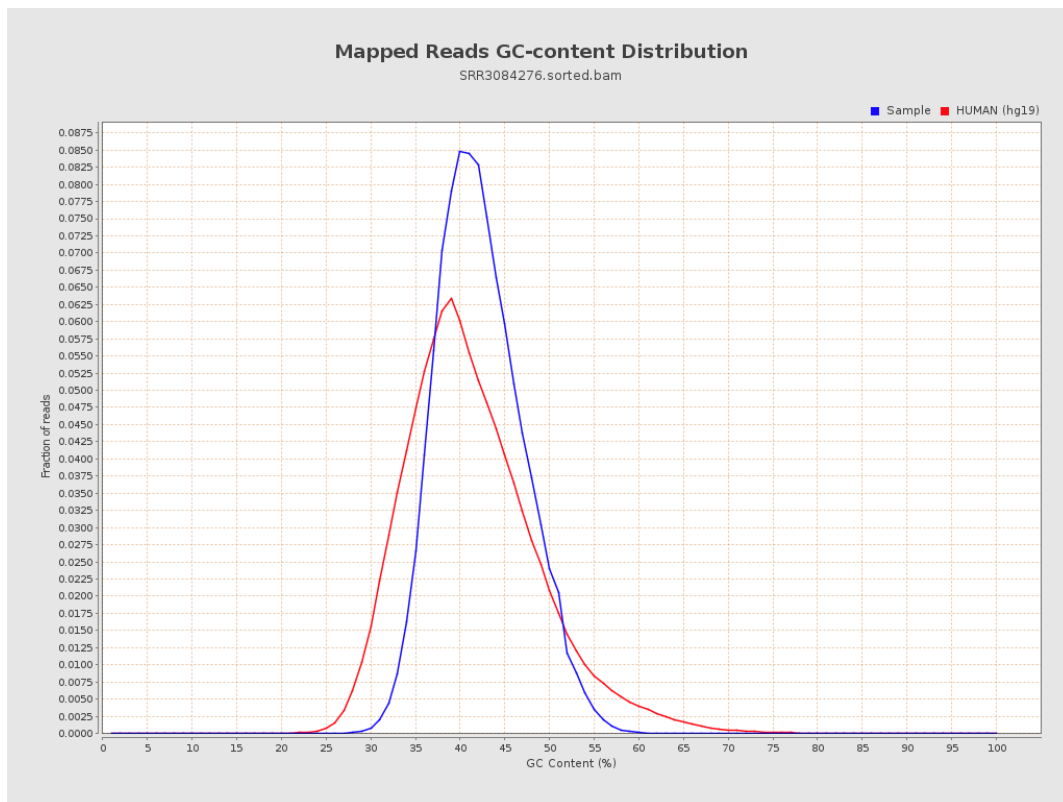
7. Results : Duplication Rate Histogram



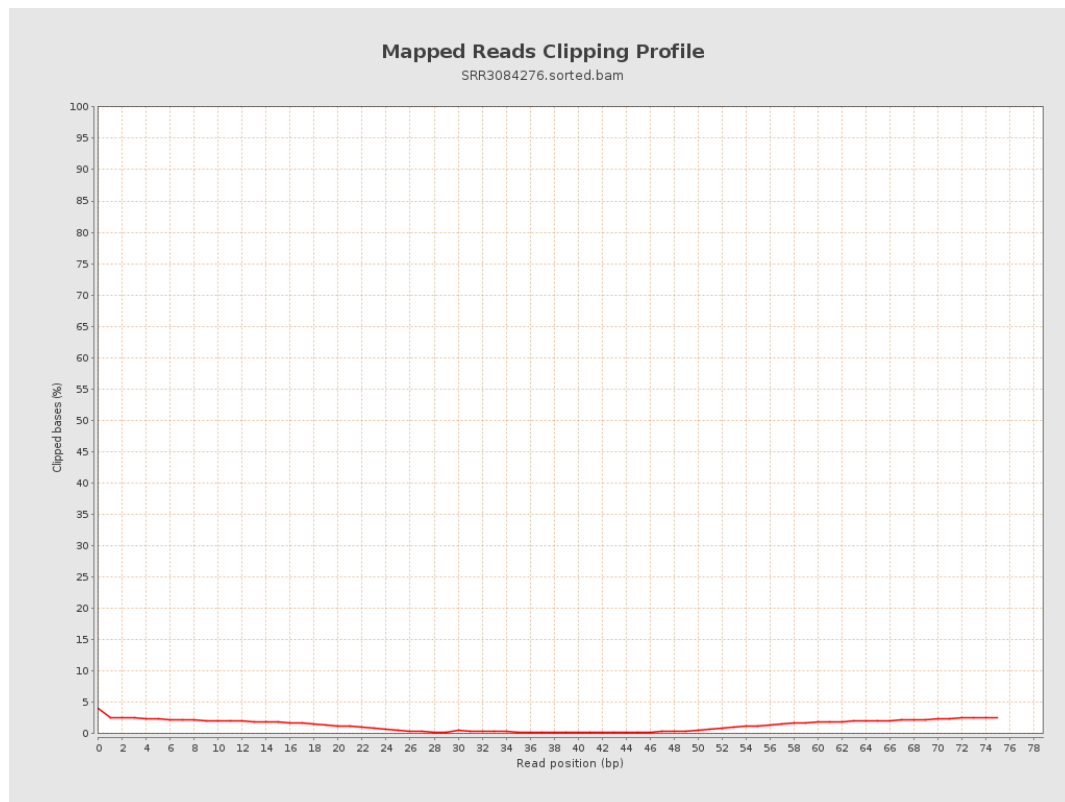
8. Results : Mapped Reads Nucleotide Content



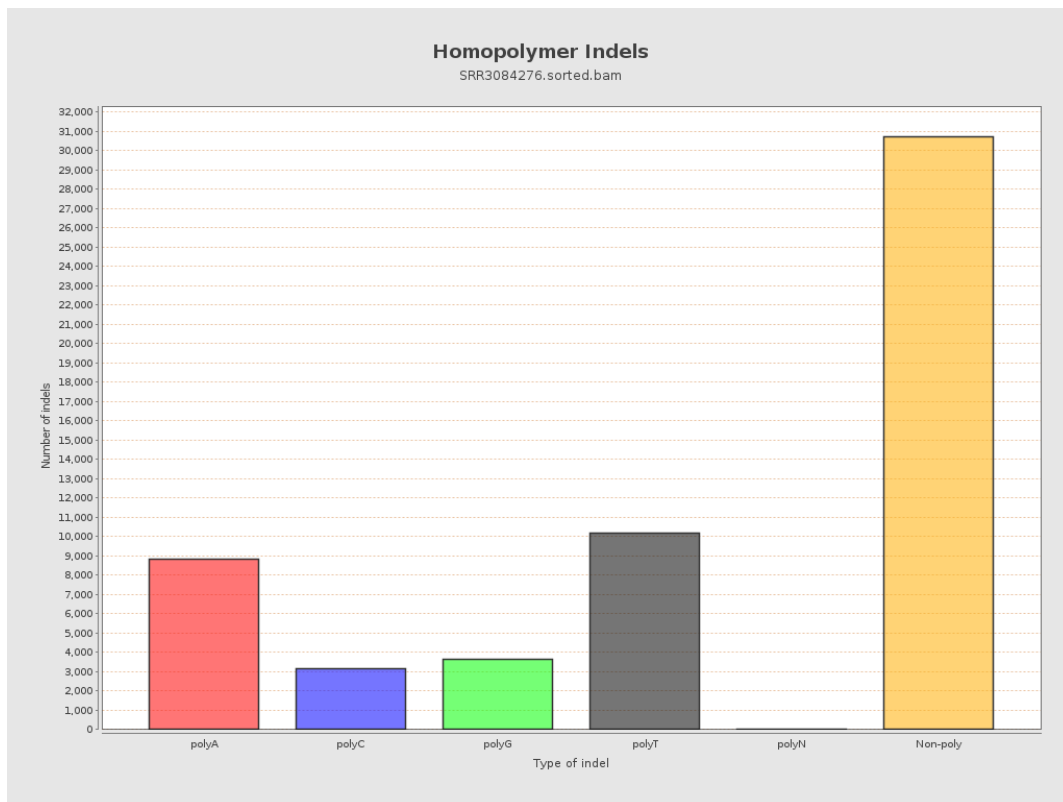
9. Results : Mapped Reads GC-content Distribution



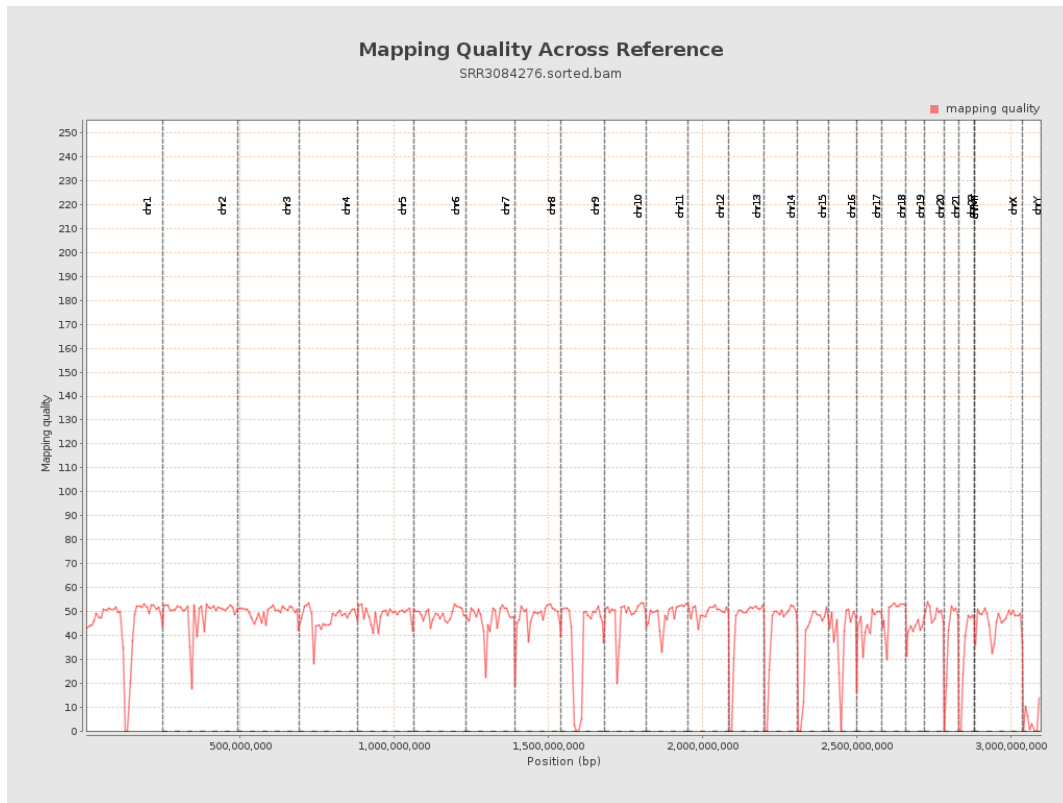
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

