Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:11:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013276.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_SRR6013276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:11:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,705,987
Mapped reads	2,431,456 / 89.85%
Unmapped reads	274,531 / 10.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,357 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	70,186 / 2.59%
Duplication rate	1.91%
Clipped reads	1,300,913 / 48.08%

2.2. ACGT Content

Number/percentage of A's	42,686,403 / 27.23%
Number/percentage of C's	31,057,309 / 19.81%
Number/percentage of T's	46,539,986 / 29.69%
Number/percentage of G's	36,439,503 / 23.25%
Number/percentage of N's	35,221 / 0.02%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.4275

2.4. Mapping Quality

Mean Mapping Quality	43.01

2.5. Mismatches and indels

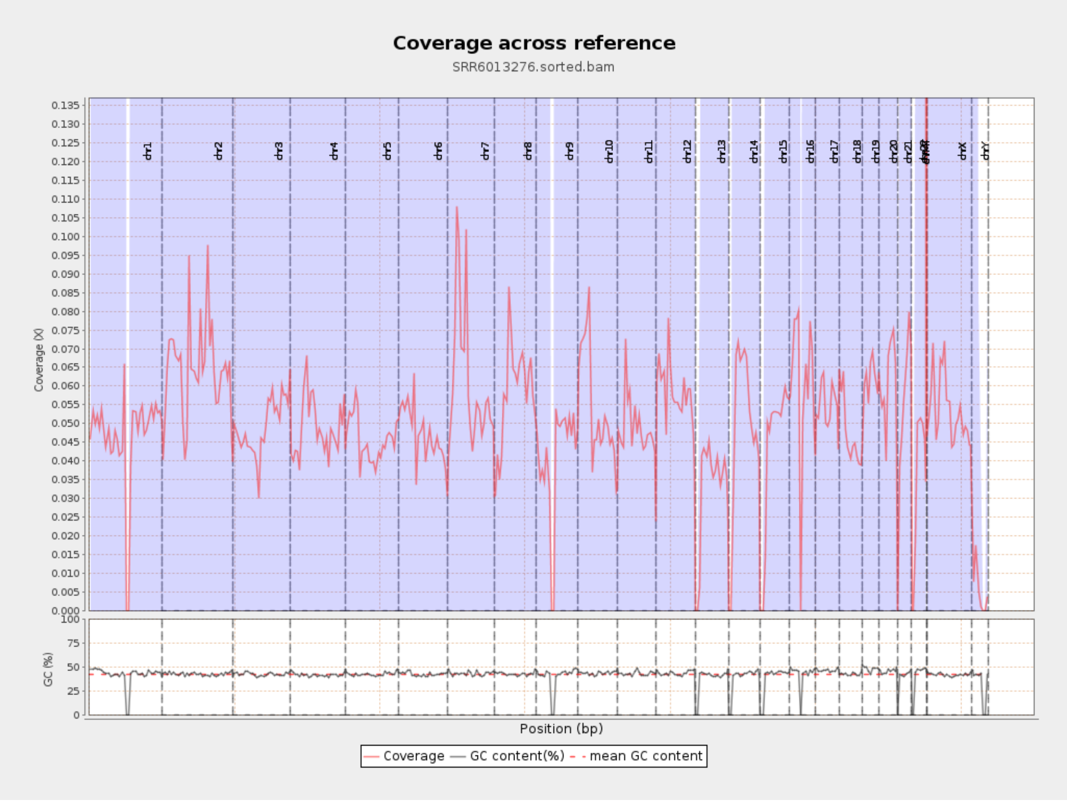
General error rate	0.82%
Mismatches	1,261,420
Insertions	11,049
Mapped reads with at least one insertion	0.45%
Deletions	35,810
Mapped reads with at least one deletion	1.46%
Homopolymer indels	43.53%

2.6. Chromosome stats

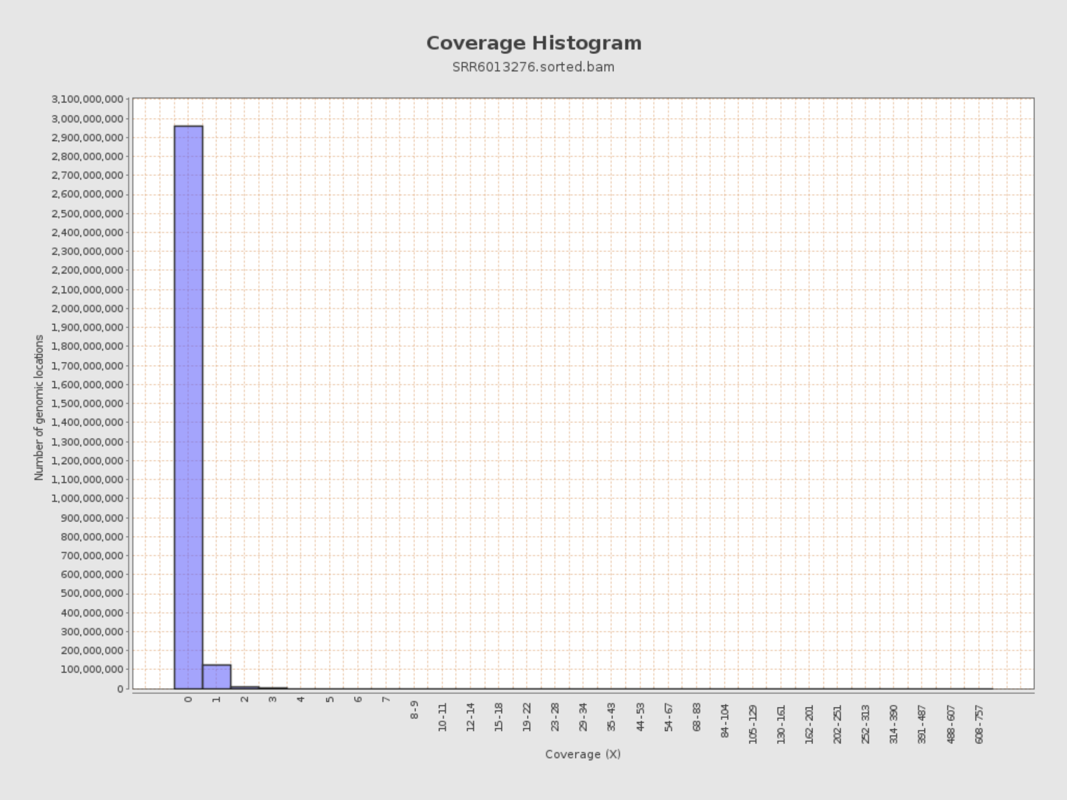
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11603224	0.0466	0.6542
chr2	243199373	15757327	0.0648	0.5543
chr3	198022430	9692897	0.0489	0.241
chr4	191154276	9329227	0.0488	0.2547
chr5	180915260	8248237	0.0456	0.2364
chr6	171115067	8101328	0.0473	0.3054
chr7	159138663	9808578	0.0616	0.8119

chr8	146364022	8549320	0.0584	0.3637
chr9	141213431	5673795	0.0402	0.3633
chr10	135534747	7468556	0.0551	0.4378
chr11	135006516	6599707	0.0489	0.3336
chr12	133851895	7849040	0.0586	0.2685
chr13	115169878	3745533	0.0325	0.2013
chr14	107349540	5277379	0.0492	0.2723
chr15	102531392	4410868	0.043	0.2318
chr16	90354753	5482539	0.0607	0.307
chr17	81195210	4447305	0.0548	0.2924
chr18	78077248	3700752	0.0474	0.6626
chr19	59128983	3637518	0.0615	0.5508
chr20	63025520	3822776	0.0607	0.2773
chr21	48129895	2591754	0.0538	0.2747
chr22	51304566	1738857	0.0339	0.2001
chrMT	16571	580241	35.0154	24.111
chrX	155270560	8324843	0.0536	0.2906
chrY	59373566	379426	0.0064	0.1343

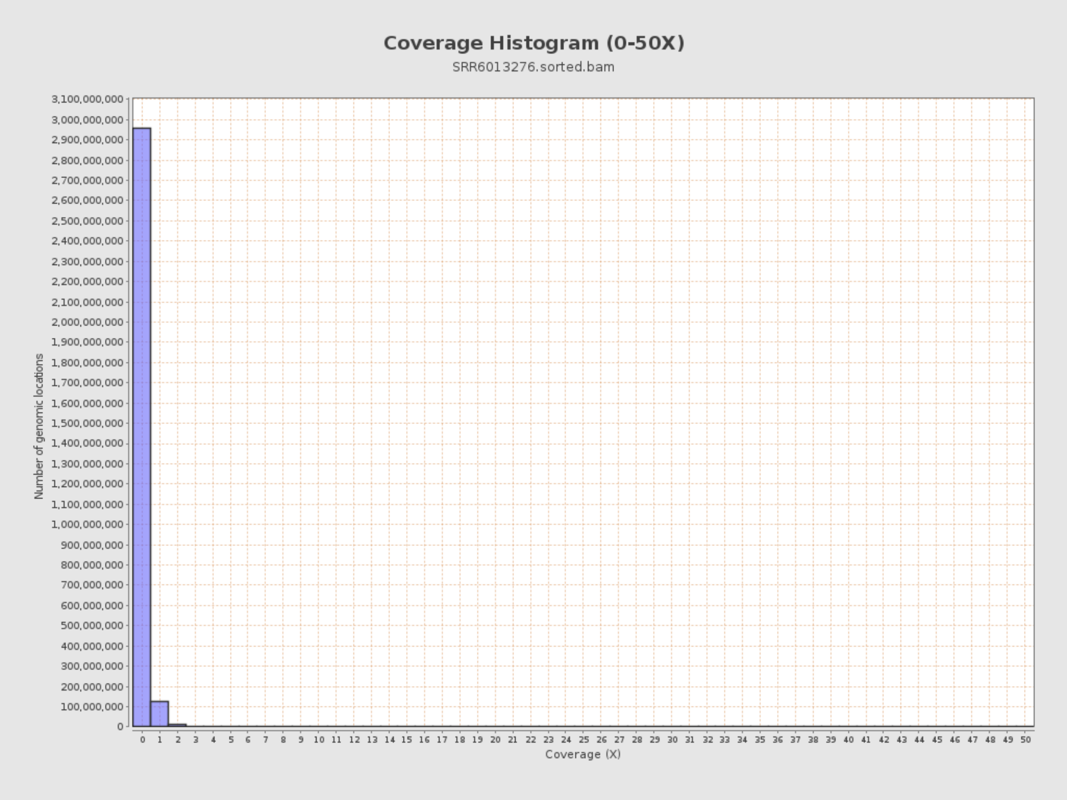
3. Results : Coverage across reference



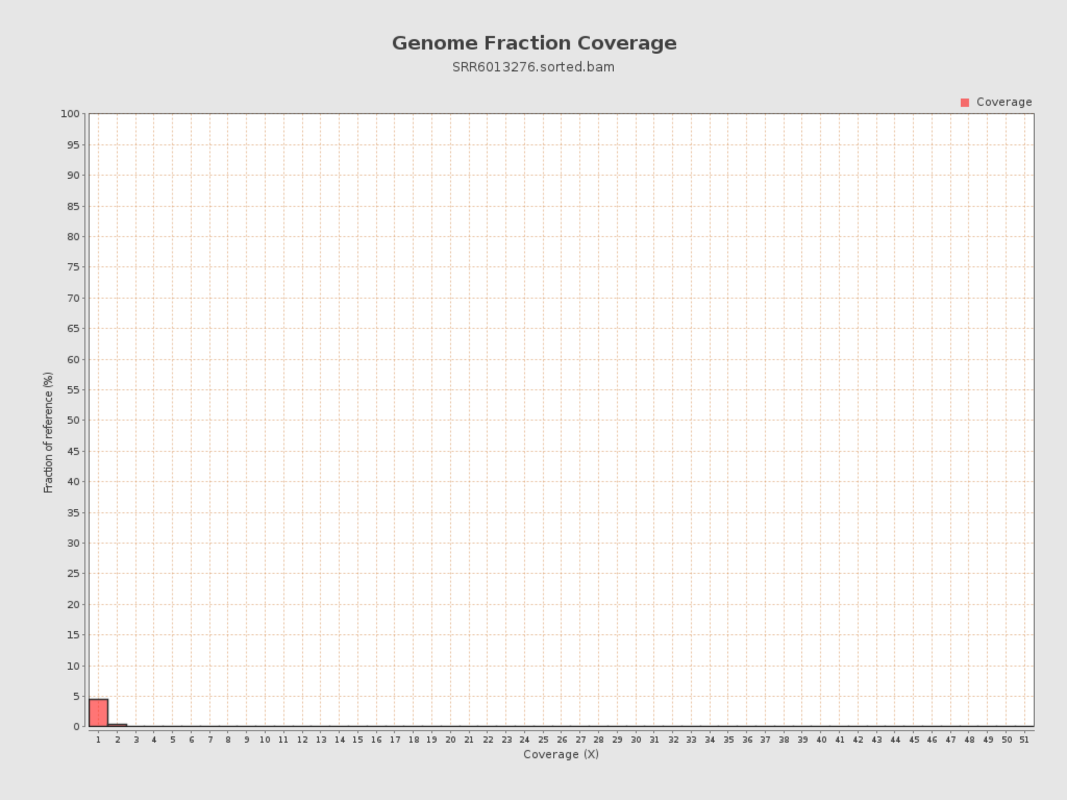
4. Results : Coverage Histogram



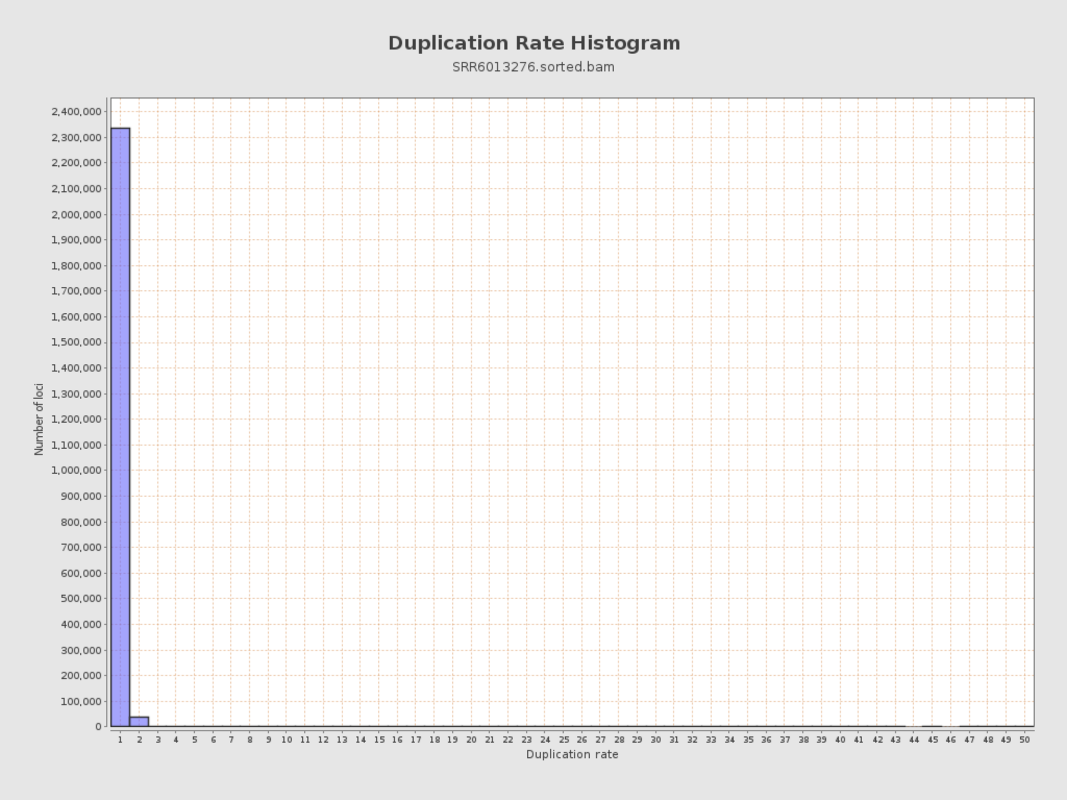
5. Results : Coverage Histogram (0-50X)



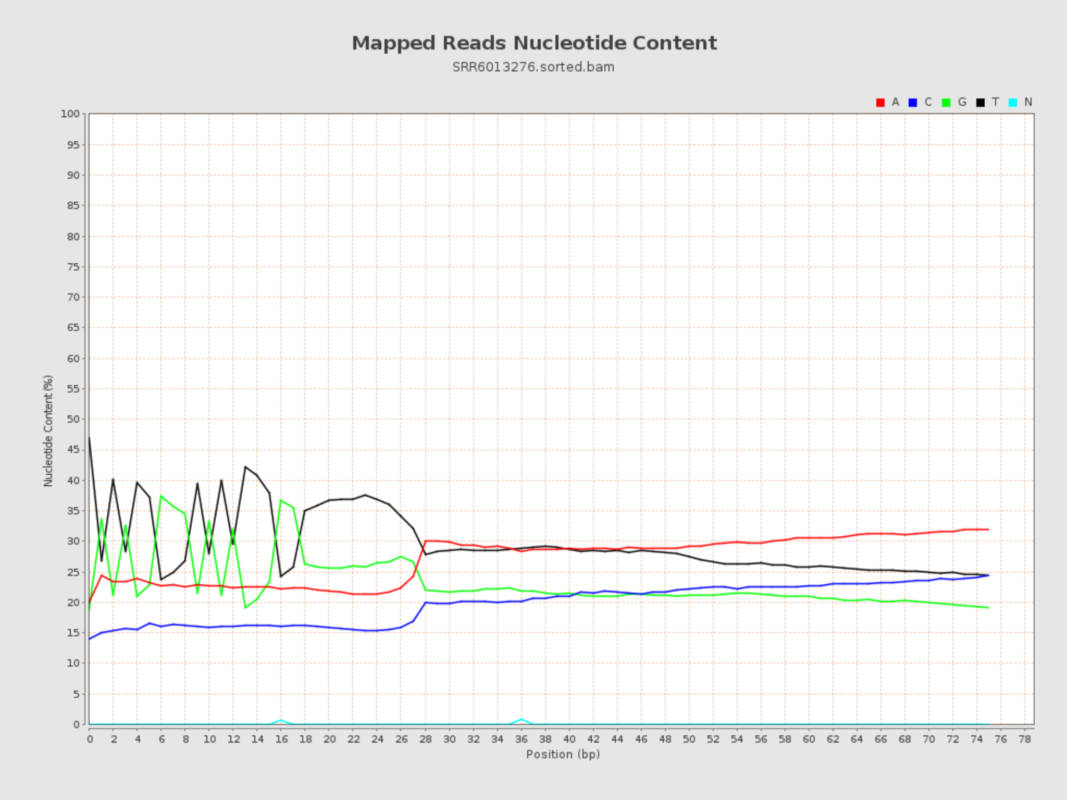
6. Results : Genome Fraction Coverage



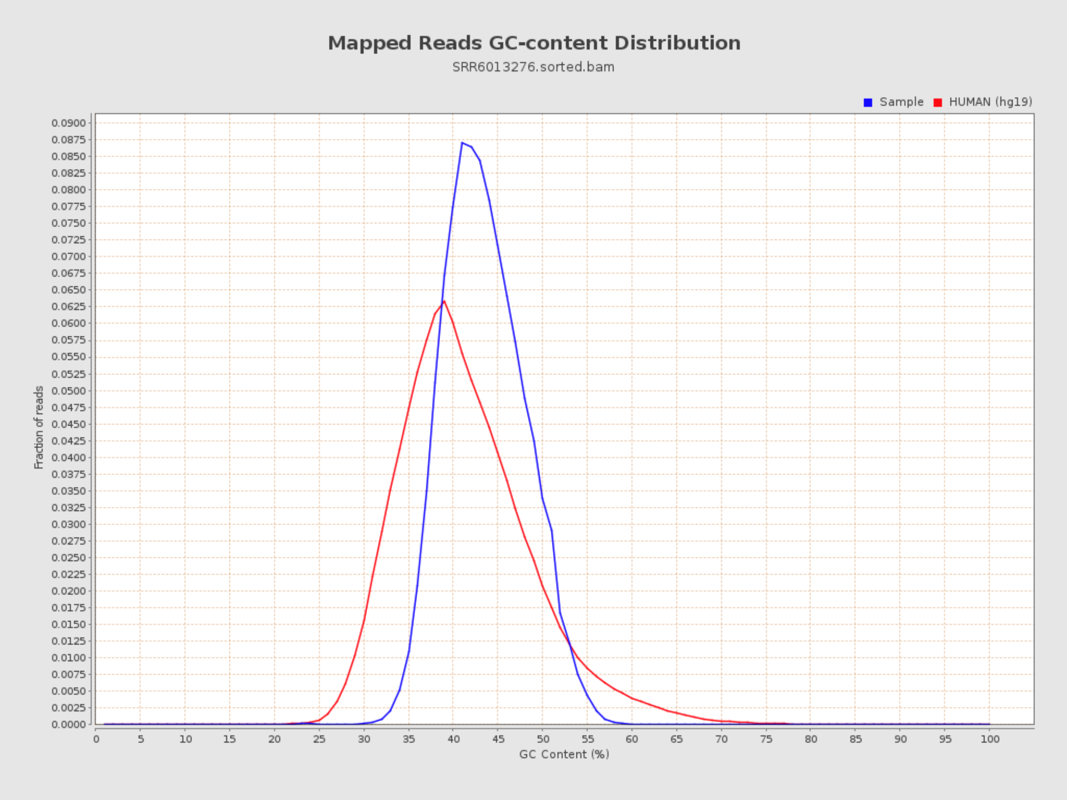
7. Results : Duplication Rate Histogram



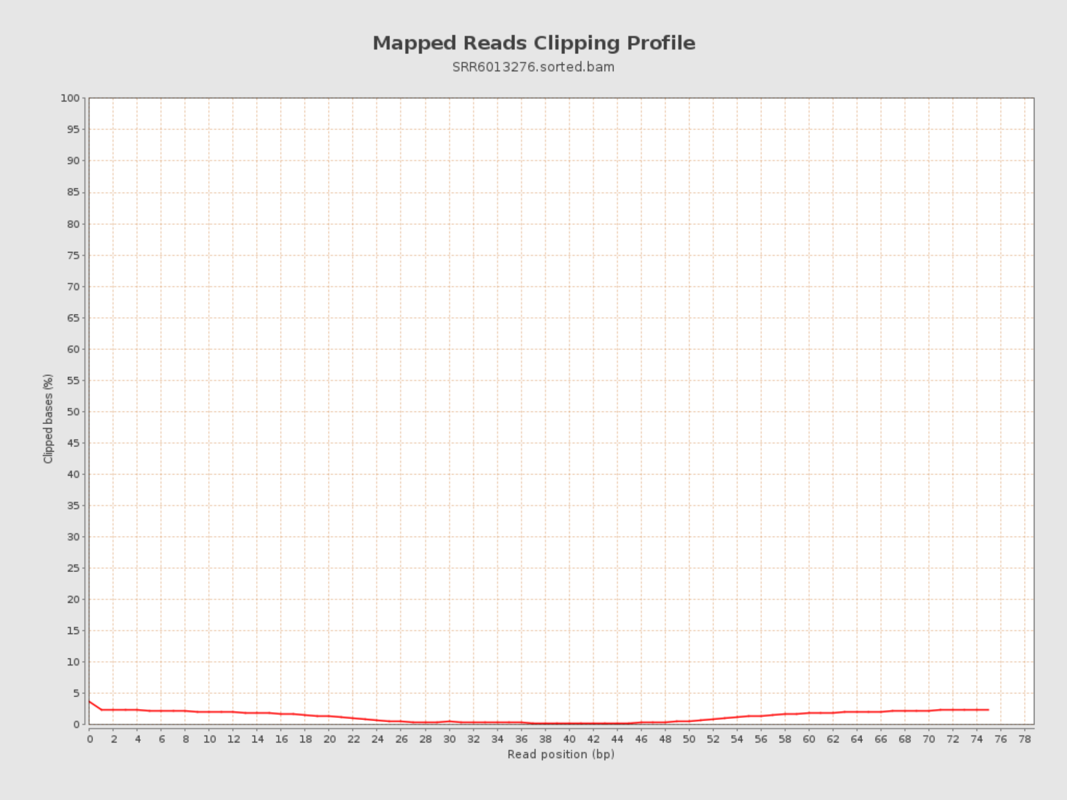
8. Results : Mapped Reads Nucleotide Content



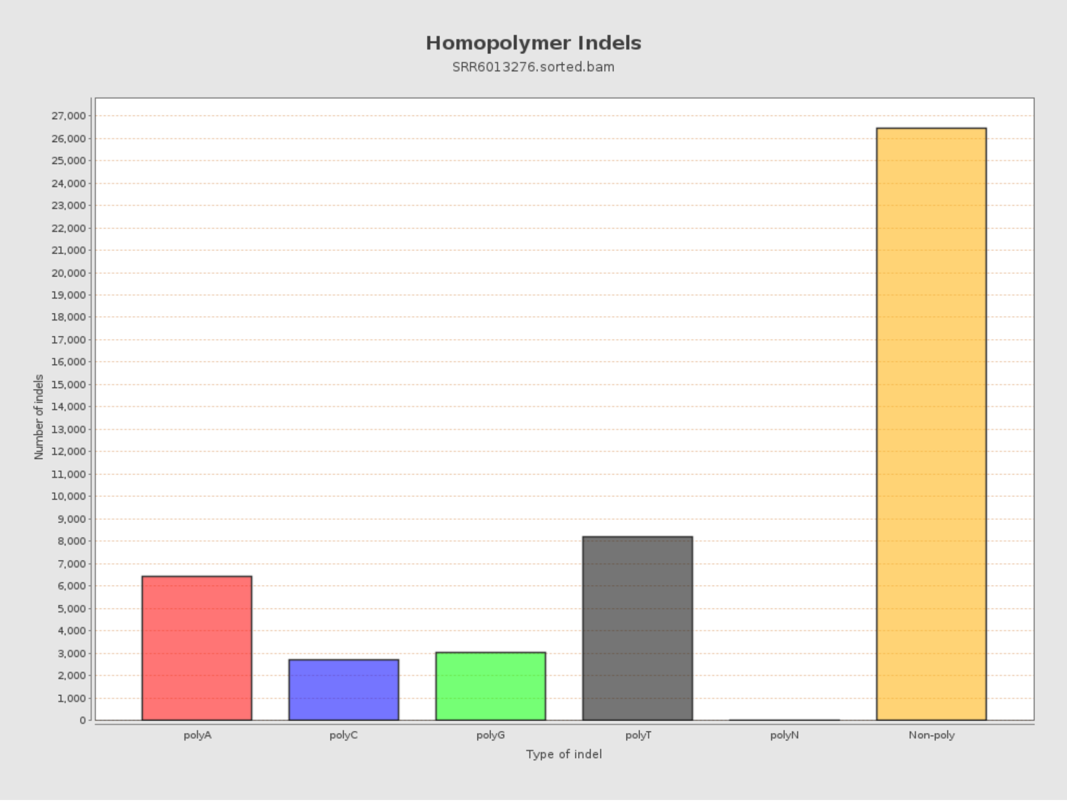
9. Results : Mapped Reads GC-content Distribution



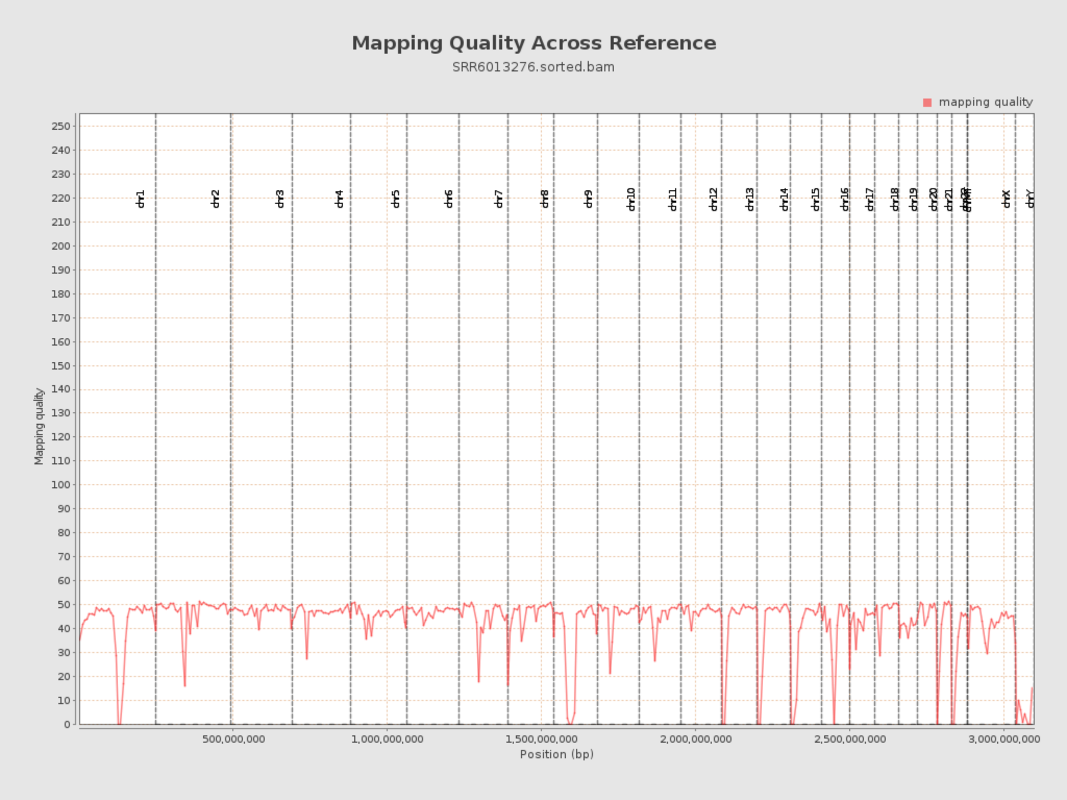
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram