

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:54:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004105.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_SRR6004105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:54:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,986,981
Mapped reads	2,176,553 / 72.87%
Unmapped reads	810,428 / 27.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,355 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	297,374 / 9.96%
Duplication rate	10.33%
Clipped reads	1,153,320 / 38.61%

2.2. ACGT Content

Number/percentage of A's	38,150,651 / 26.99%
Number/percentage of C's	25,380,747 / 17.95%
Number/percentage of T's	46,659,866 / 33.01%
Number/percentage of G's	31,156,207 / 22.04%
Number/percentage of N's	18,528 / 0.01%
GC Percentage	39.99%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.4776
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2.4. Mapping Quality

Mean Mapping Quality	46.16
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2.5. Mismatches and indels

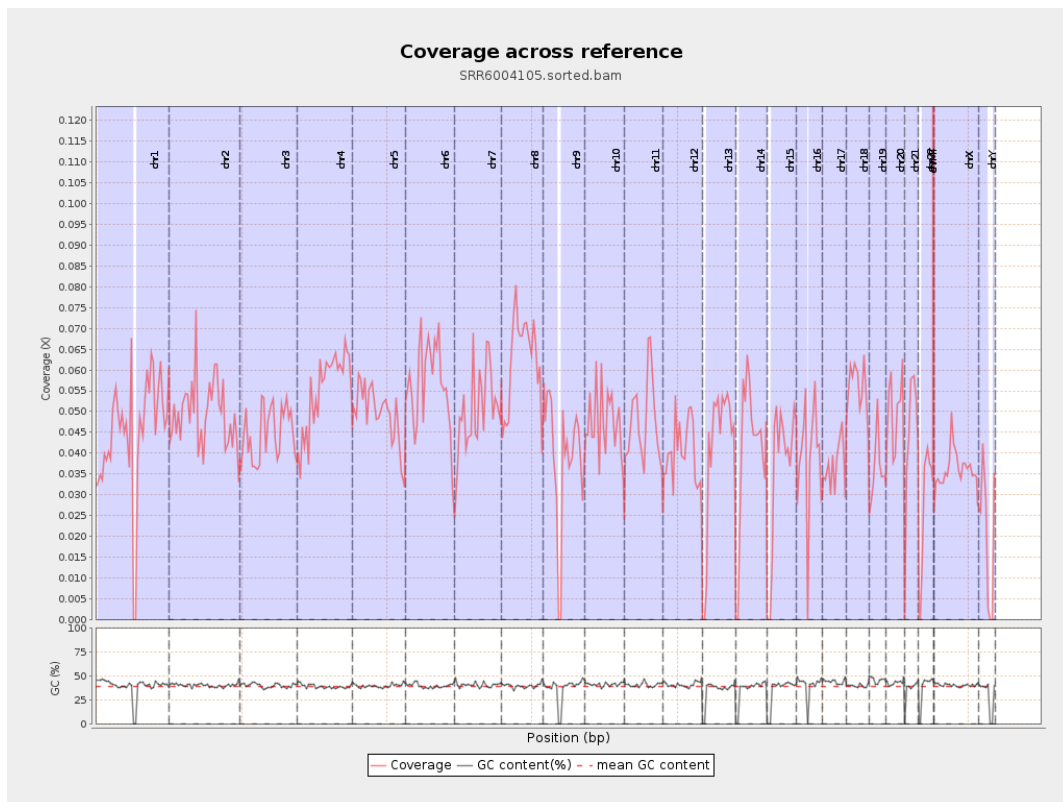
General error rate	1.05%
Mismatches	1,462,788
Insertions	11,810
Mapped reads with at least one insertion	0.54%
Deletions	41,599
Mapped reads with at least one deletion	1.89%
Homopolymer indels	47.51%

2.6. Chromosome stats

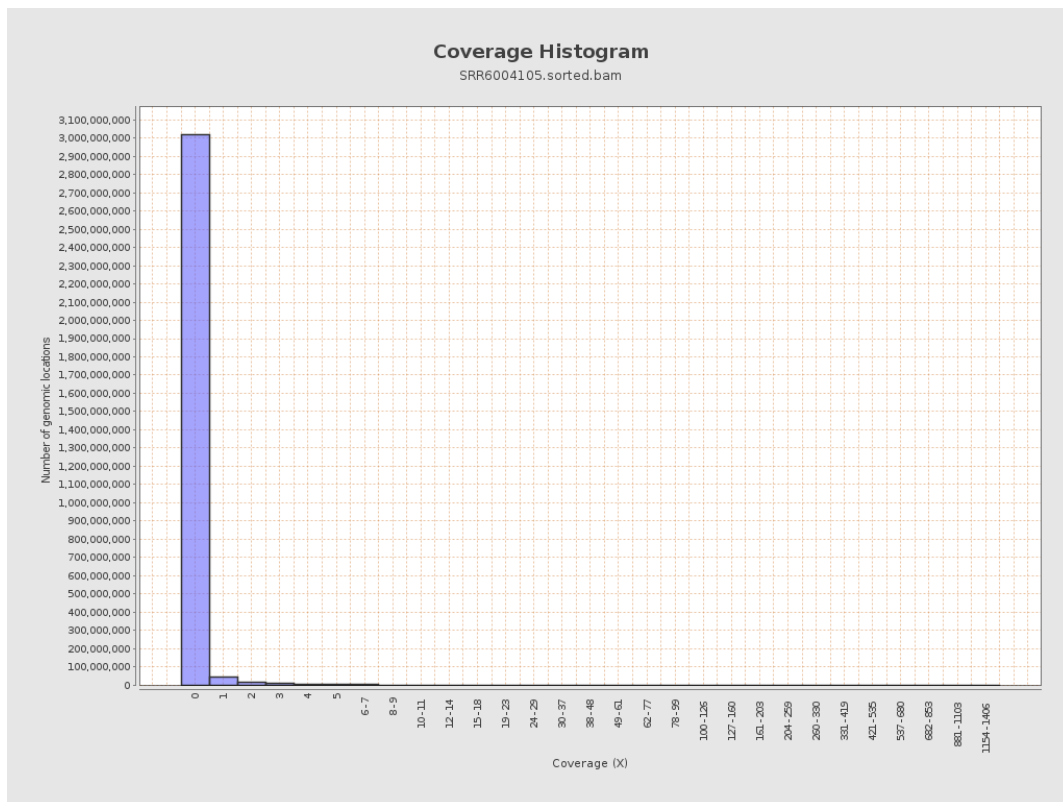
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11241730	0.0451	0.6735
chr2	243199373	12050082	0.0495	0.5183
chr3	198022430	8852429	0.0447	0.352
chr4	191154276	10519011	0.055	0.4072
chr5	180915260	8931064	0.0494	0.3745
chr6	171115067	9624463	0.0562	0.4217
chr7	159138663	8088913	0.0508	0.5296

chr8	146364022	9075757	0.062	0.9479
chr9	141213431	5480303	0.0388	0.4091
chr10	135534747	6444398	0.0475	0.428
chr11	135006516	6402680	0.0474	0.4245
chr12	133851895	5416203	0.0405	0.3412
chr13	115169878	4666104	0.0405	0.3411
chr14	107349540	4361326	0.0406	0.3507
chr15	102531392	3716564	0.0362	0.3206
chr16	90354753	3522288	0.039	0.3419
chr17	81195210	2991461	0.0368	0.3335
chr18	78077248	4385853	0.0562	0.7159
chr19	59128983	2172124	0.0367	0.4716
chr20	63025520	3142120	0.0499	0.3831
chr21	48129895	2130652	0.0443	0.3649
chr22	51304566	1360093	0.0265	0.2732
chrMT	16571	88538	5.3429	5.0288
chrX	155270560	5587868	0.036	0.3225
chrY	59373566	1181749	0.0199	0.276

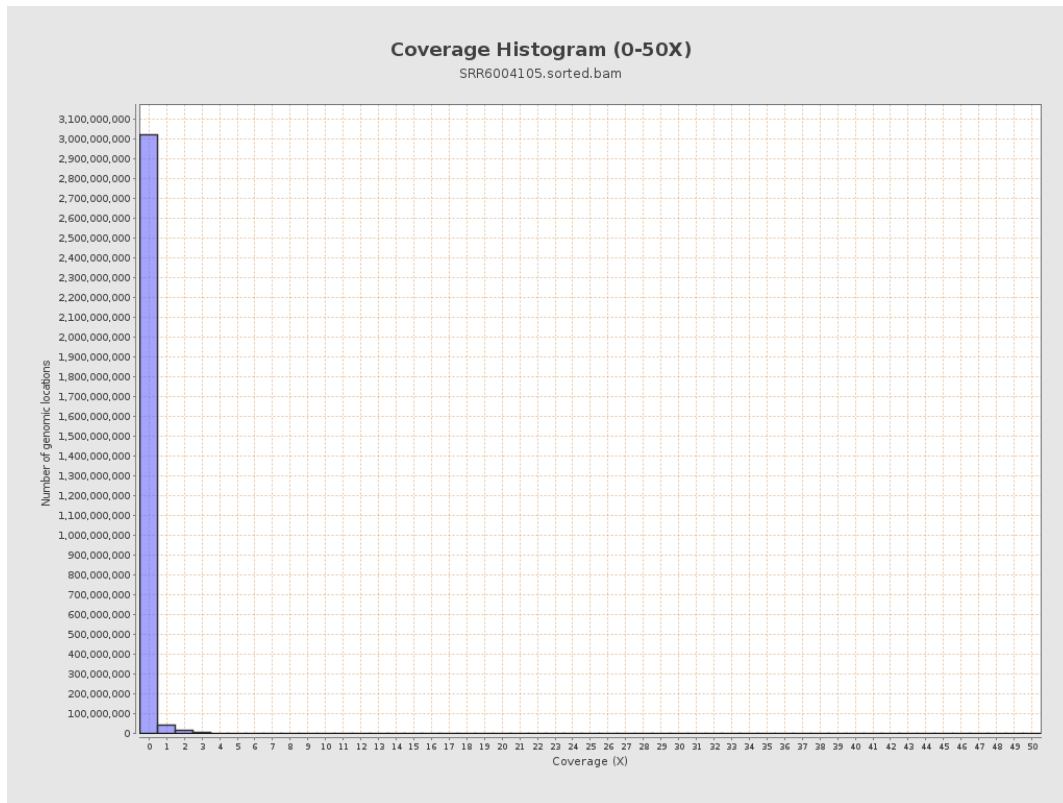
3. Results : Coverage across reference



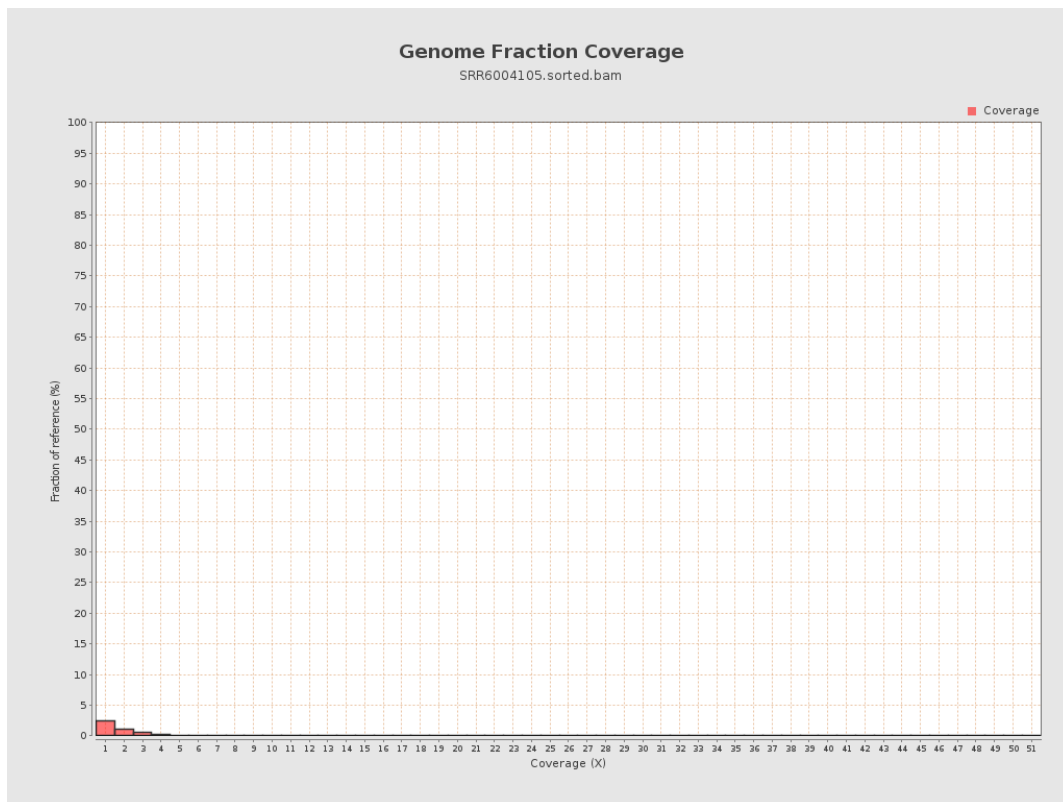
4. Results : Coverage Histogram



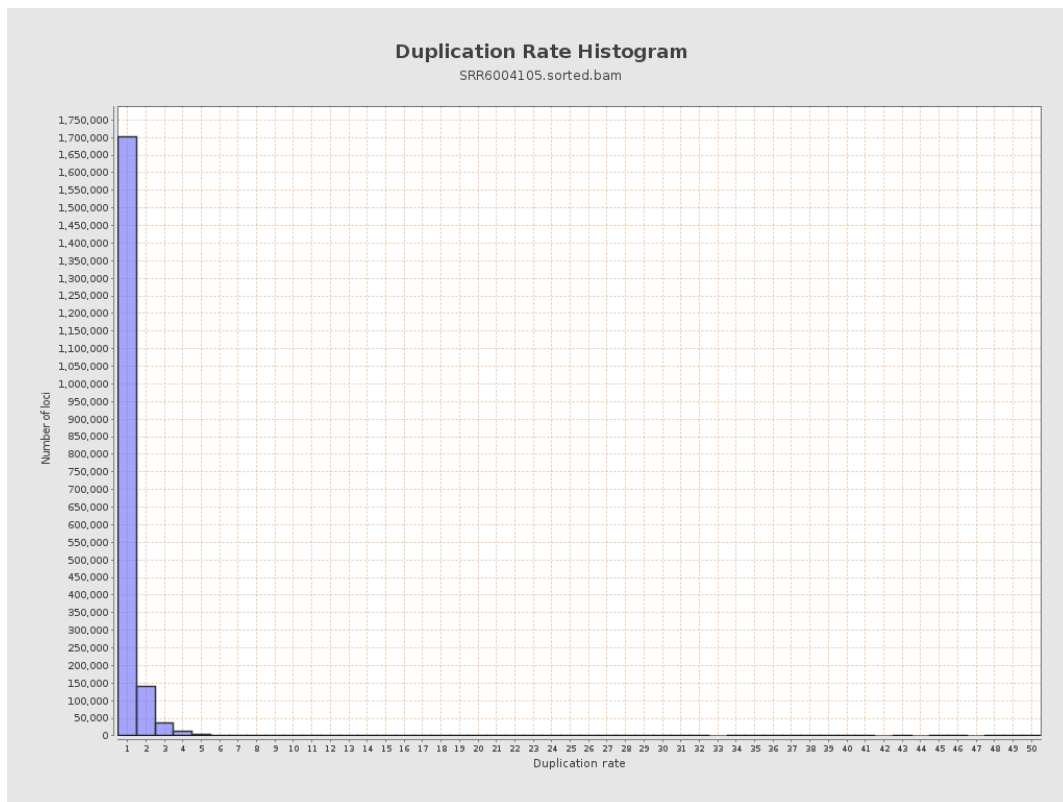
5. Results : Coverage Histogram (0-50X)



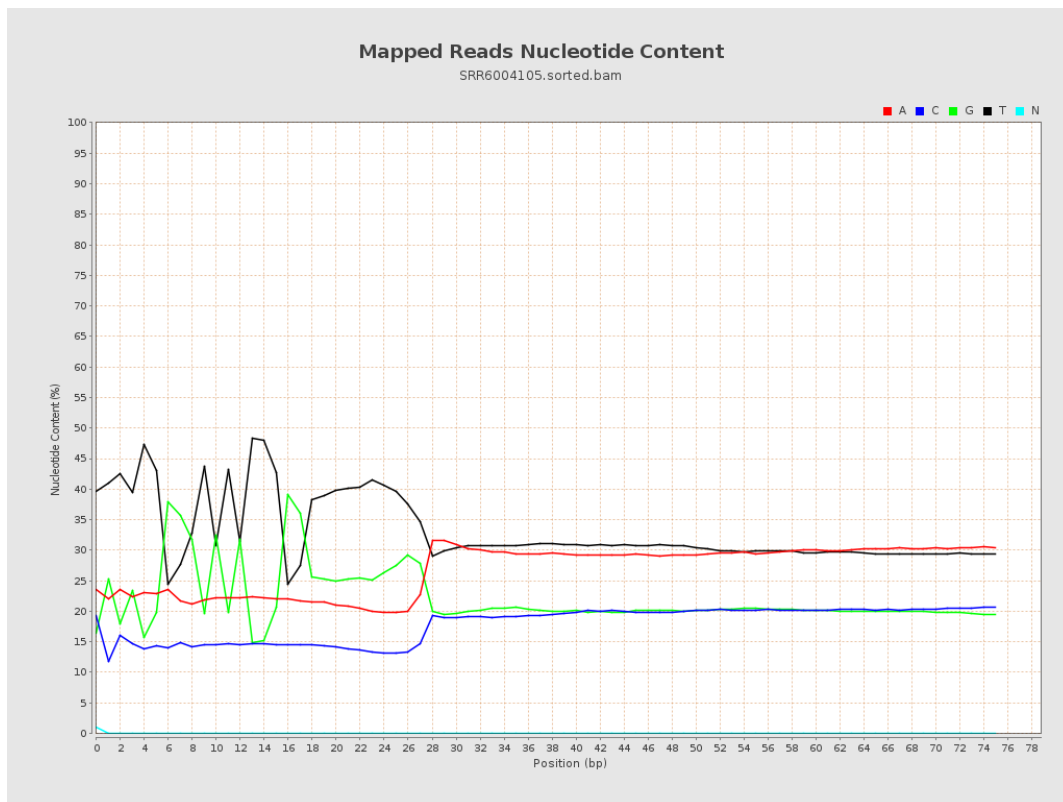
6. Results : Genome Fraction Coverage



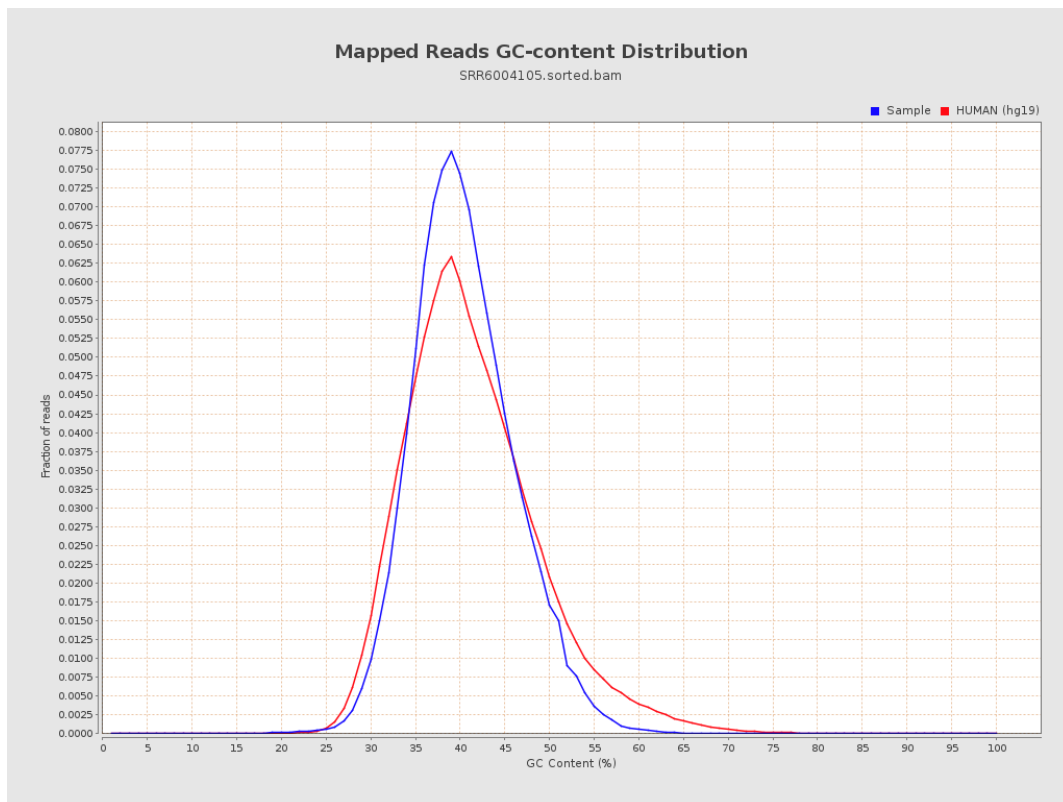
7. Results : Duplication Rate Histogram



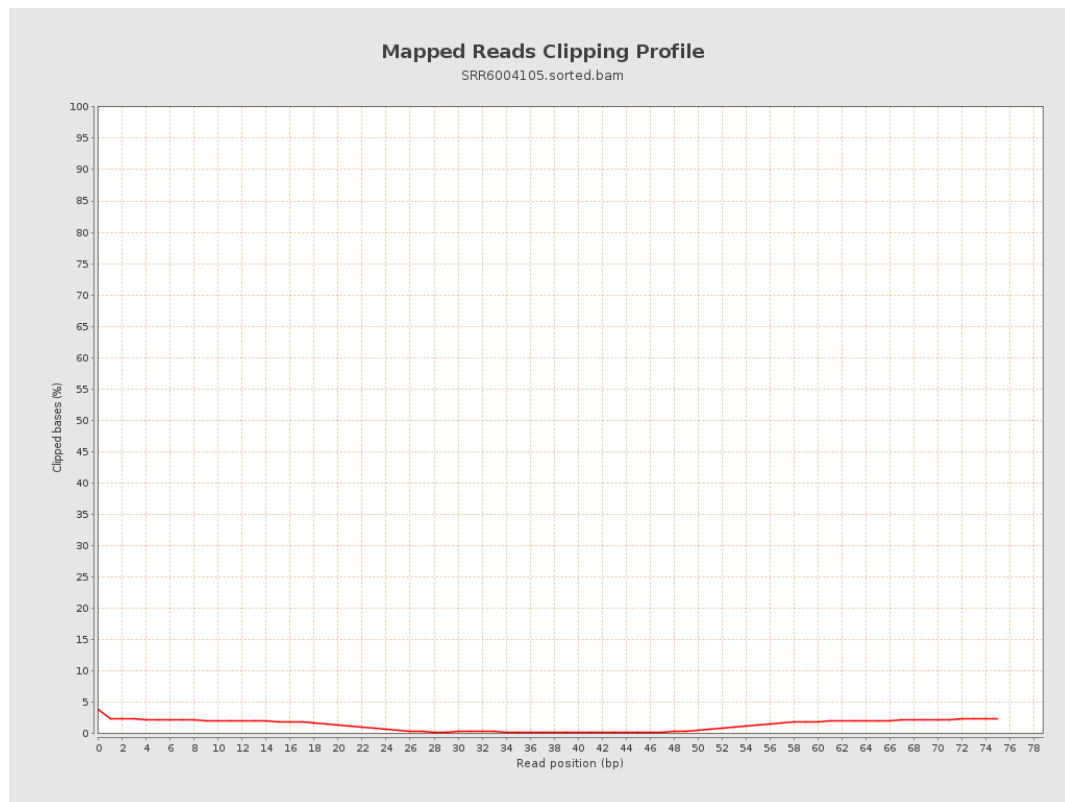
8. Results : Mapped Reads Nucleotide Content



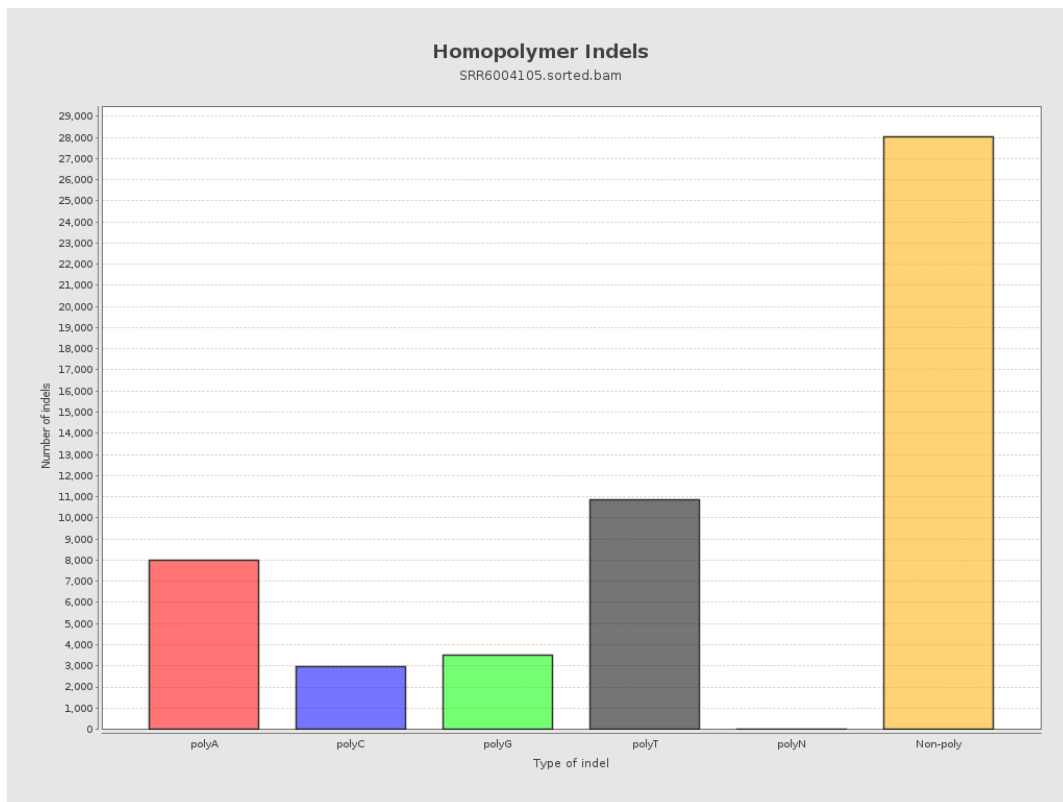
9. Results : Mapped Reads GC-content Distribution



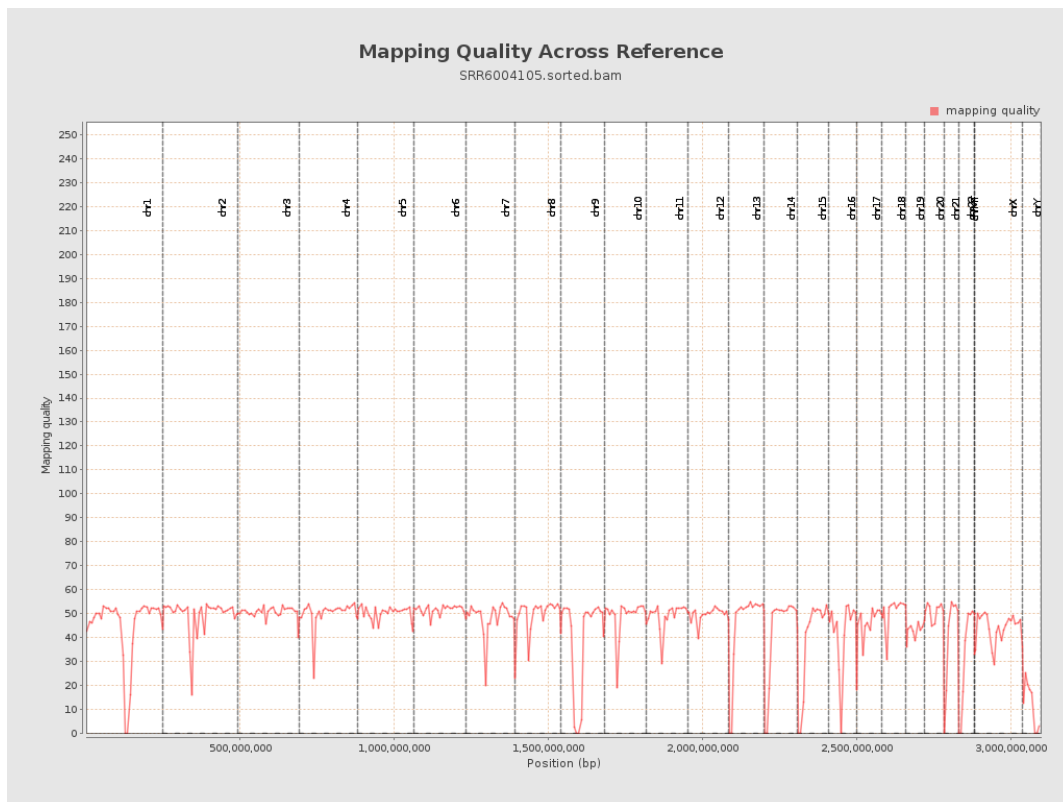
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

