

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:41:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082755.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_SRR3082755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:41:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,068,466
Mapped reads	4,428,631 / 87.38%
Unmapped reads	639,835 / 12.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,415 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	257,675 / 5.08%
Duplication rate	4.66%
Clipped reads	1,668,944 / 32.93%

2.2. ACGT Content

Number/percentage of A's	87,582,136 / 28.88%
Number/percentage of C's	54,687,769 / 18.03%
Number/percentage of T's	98,824,125 / 32.59%
Number/percentage of G's	62,159,331 / 20.5%
Number/percentage of N's	17,275 / 0.01%
GC Percentage	38.53%

2.3. Coverage

Mean	0.098

Standard Deviation	0.7191
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2.4. Mapping Quality

Mean Mapping Quality	47.68
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2.5. Mismatches and indels

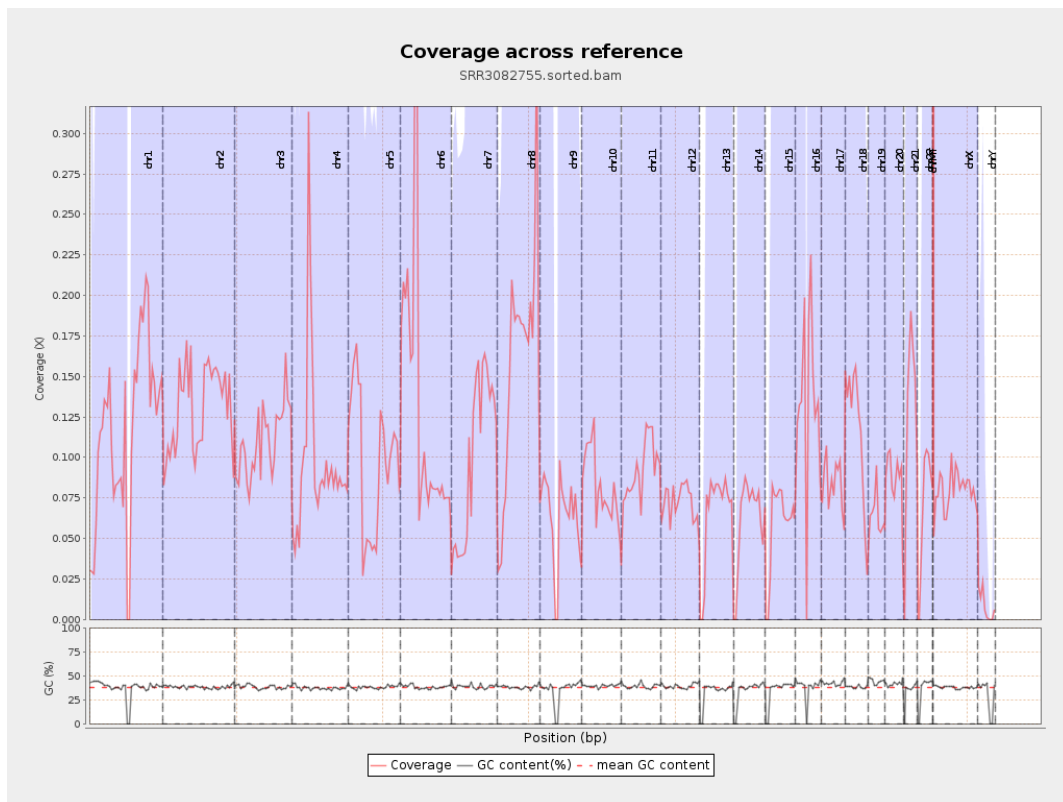
General error rate	0.88%
Mismatches	2,624,024
Insertions	24,109
Mapped reads with at least one insertion	0.54%
Deletions	66,884
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.23%

2.6. Chromosome stats

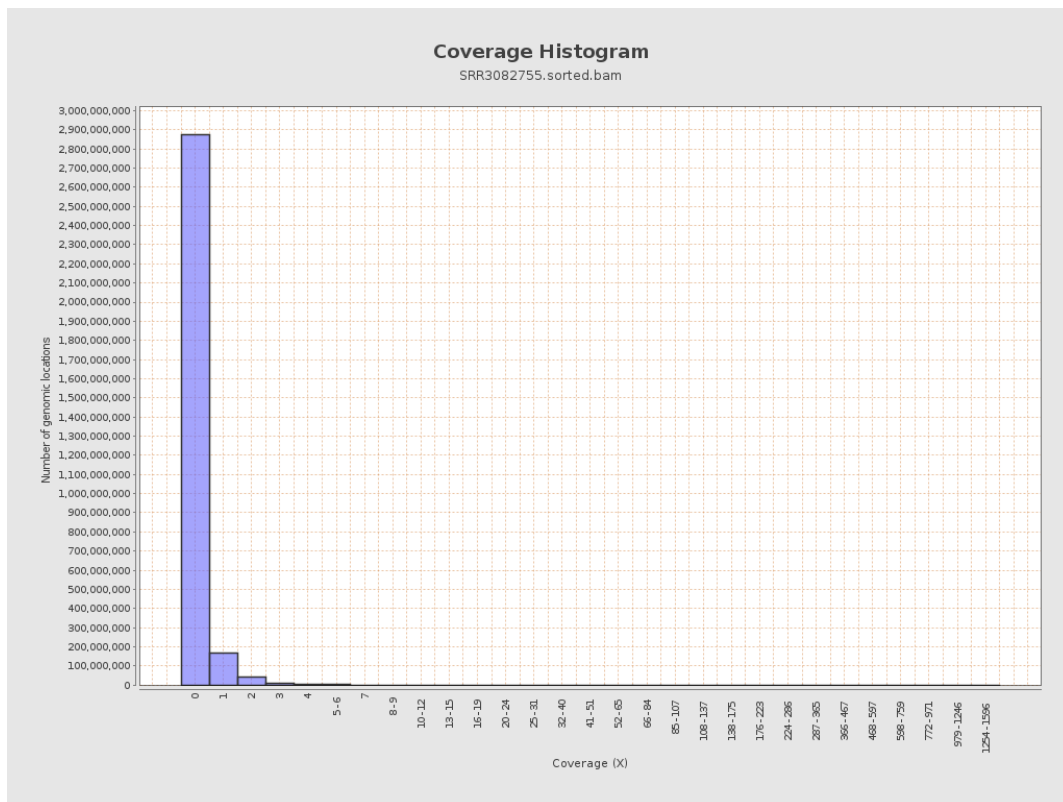
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29202317	0.1172	1.4638
chr2	243199373	31823328	0.1309	0.7831
chr3	198022430	21814412	0.1102	0.4264
chr4	191154276	18732973	0.098	0.4137
chr5	180915260	17240335	0.0953	0.401
chr6	171115067	22582398	0.132	0.719
chr7	159138663	15956436	0.1003	0.7044

chr8	146364022	23516316	0.1607	1.0631
chr9	141213431	9035467	0.064	0.6079
chr10	135534747	11125919	0.0821	0.5534
chr11	135006516	12393262	0.0918	0.5133
chr12	133851895	9679040	0.0723	0.3547
chr13	115169878	7479946	0.0649	0.3276
chr14	107349540	6649117	0.0619	0.3764
chr15	102531392	5918975	0.0577	0.305
chr16	90354753	11939158	0.1321	0.5487
chr17	81195210	6857974	0.0845	0.4654
chr18	78077248	9211851	0.118	1.3457
chr19	59128983	3828361	0.0647	0.8628
chr20	63025520	5602910	0.0889	0.4101
chr21	48129895	5941820	0.1235	0.4628
chr22	51304566	3542727	0.0691	0.3295
chrMT	16571	444831	26.8439	15.6322
chrX	155270560	12383577	0.0798	0.4191
chrY	59373566	481485	0.0081	0.1436

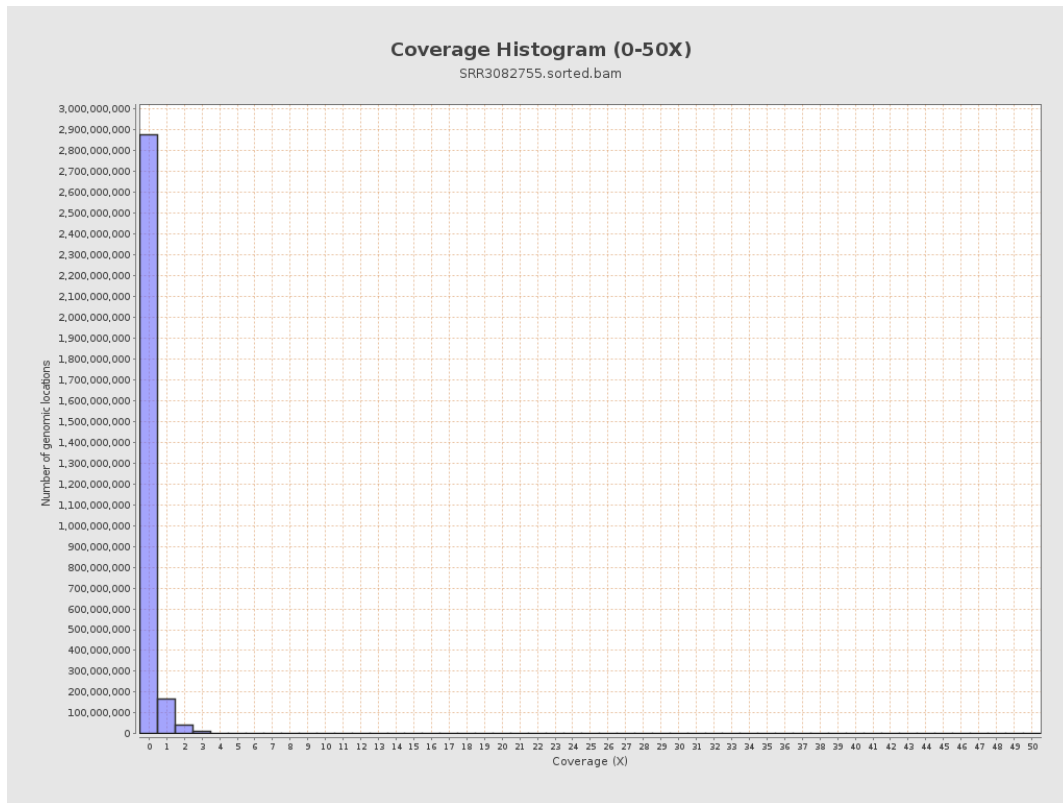
3. Results : Coverage across reference



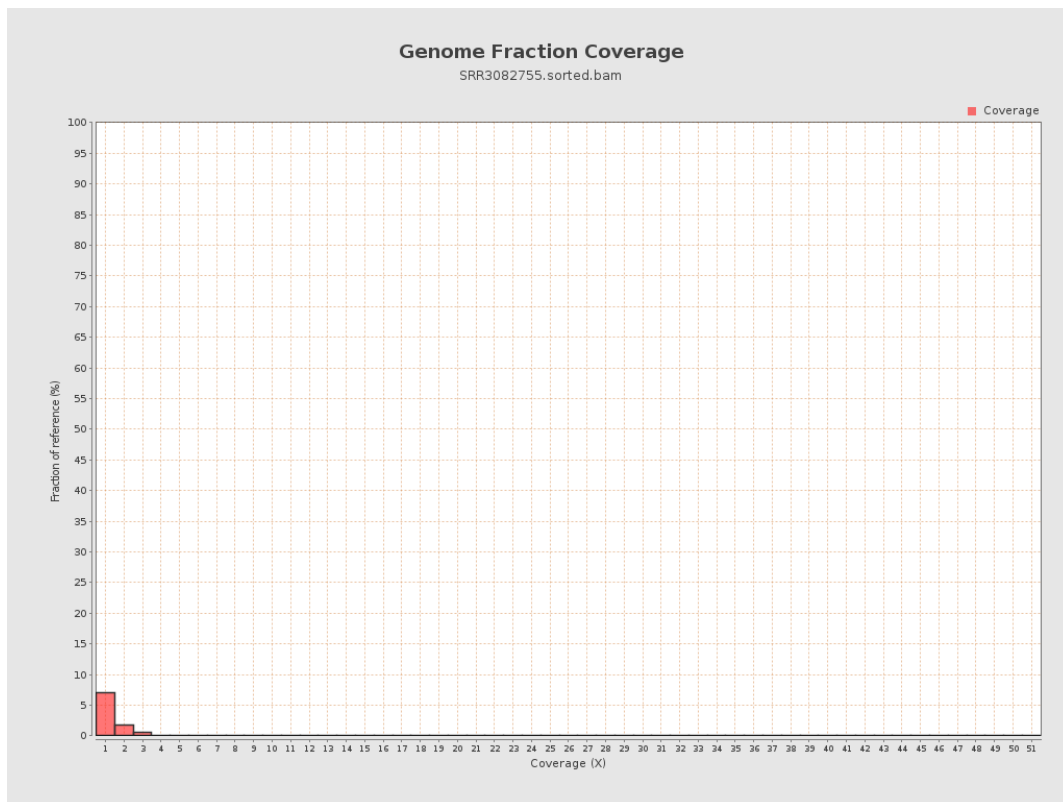
4. Results : Coverage Histogram



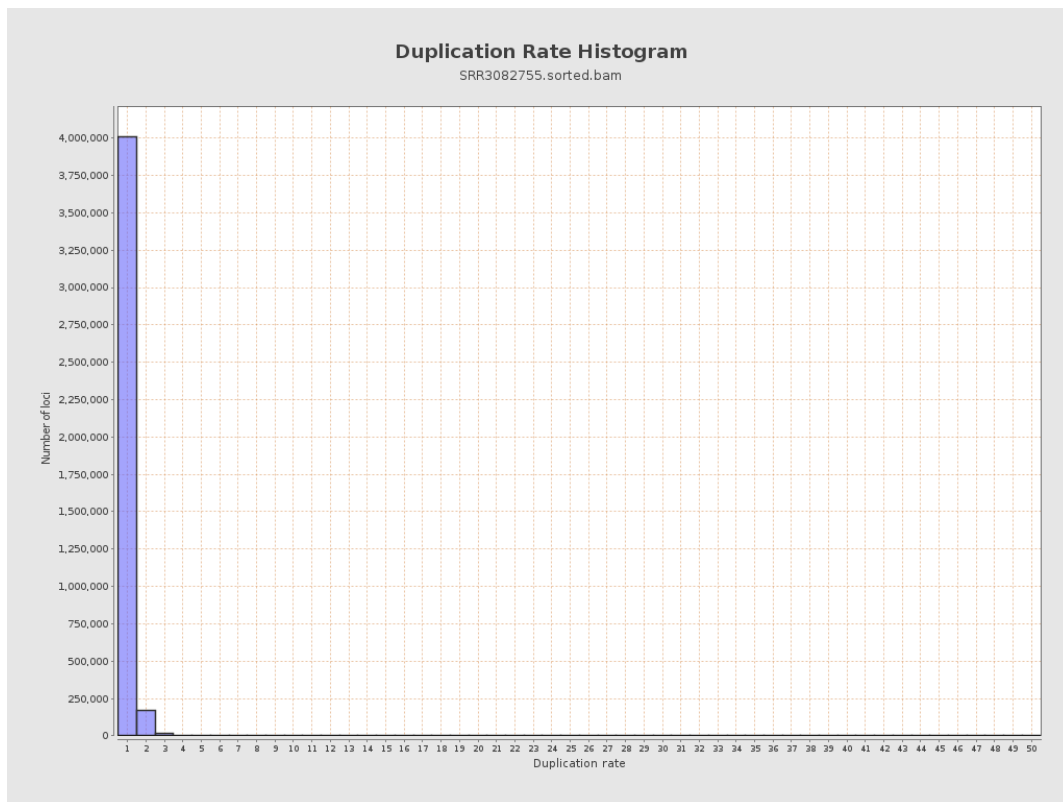
5. Results : Coverage Histogram (0-50X)



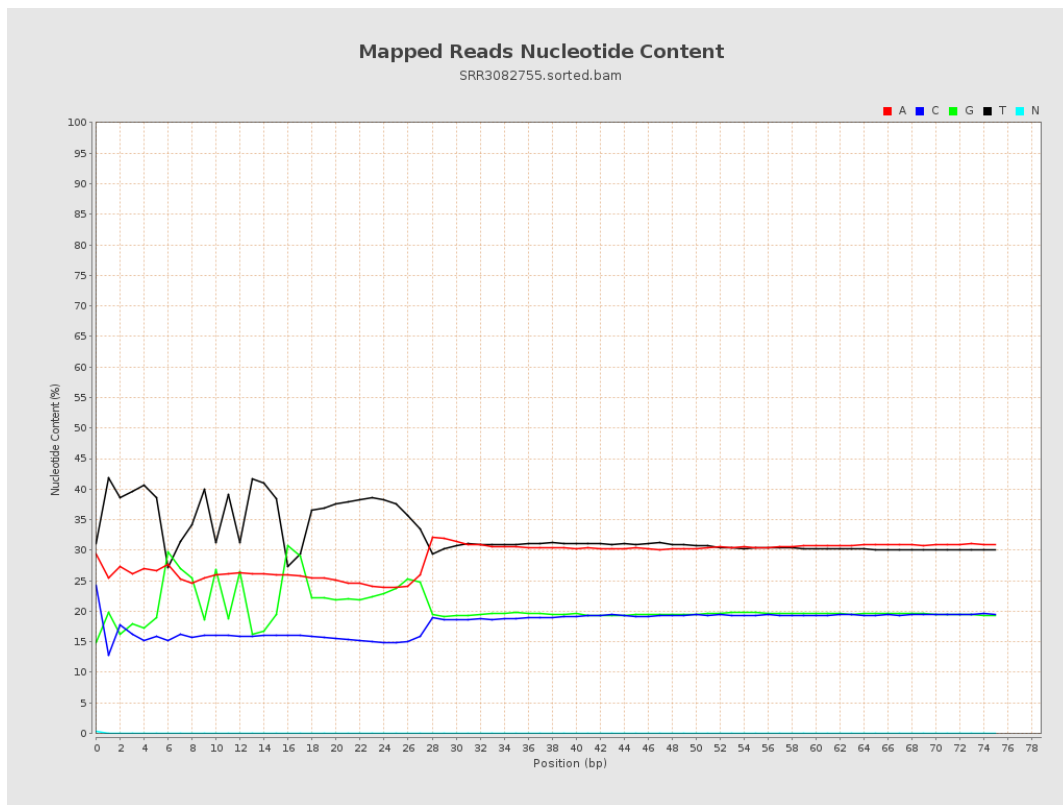
6. Results : Genome Fraction Coverage



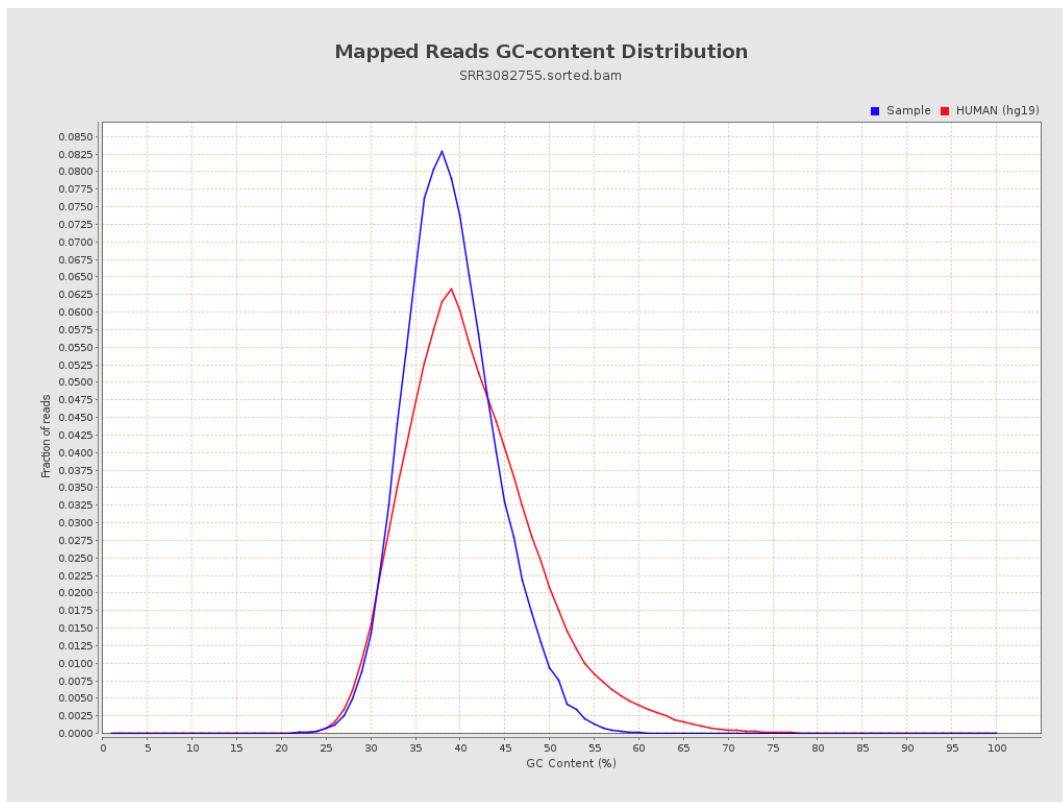
7. Results : Duplication Rate Histogram



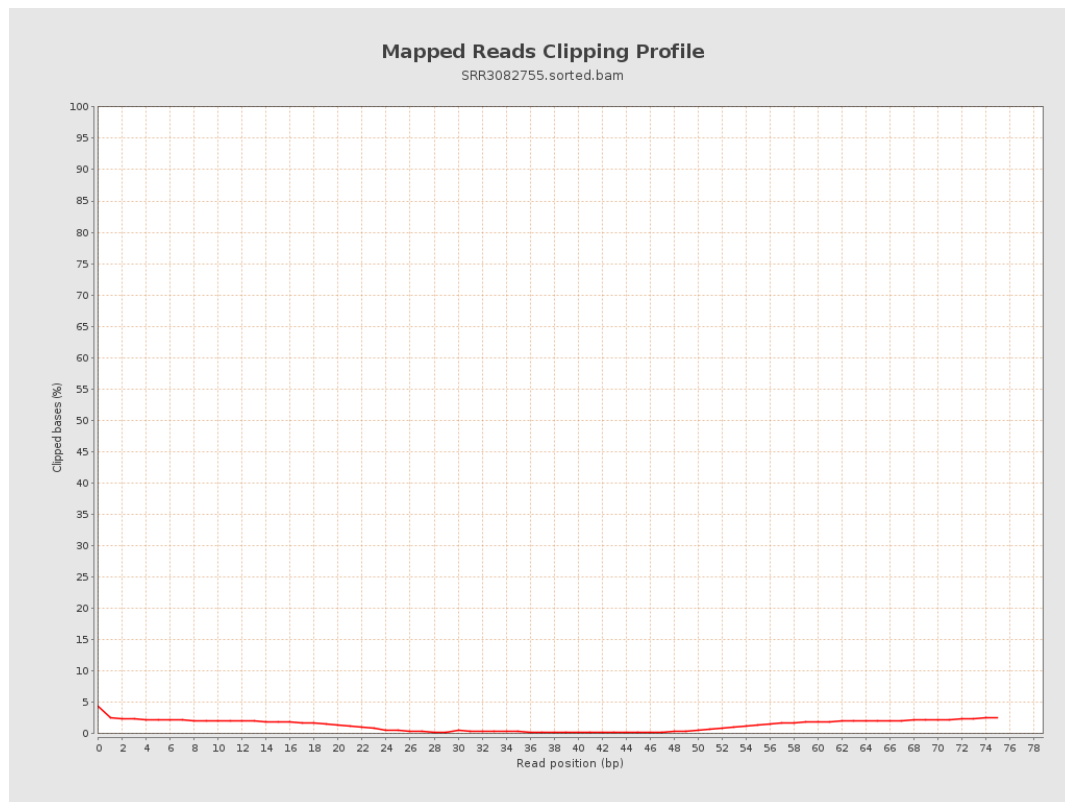
8. Results : Mapped Reads Nucleotide Content



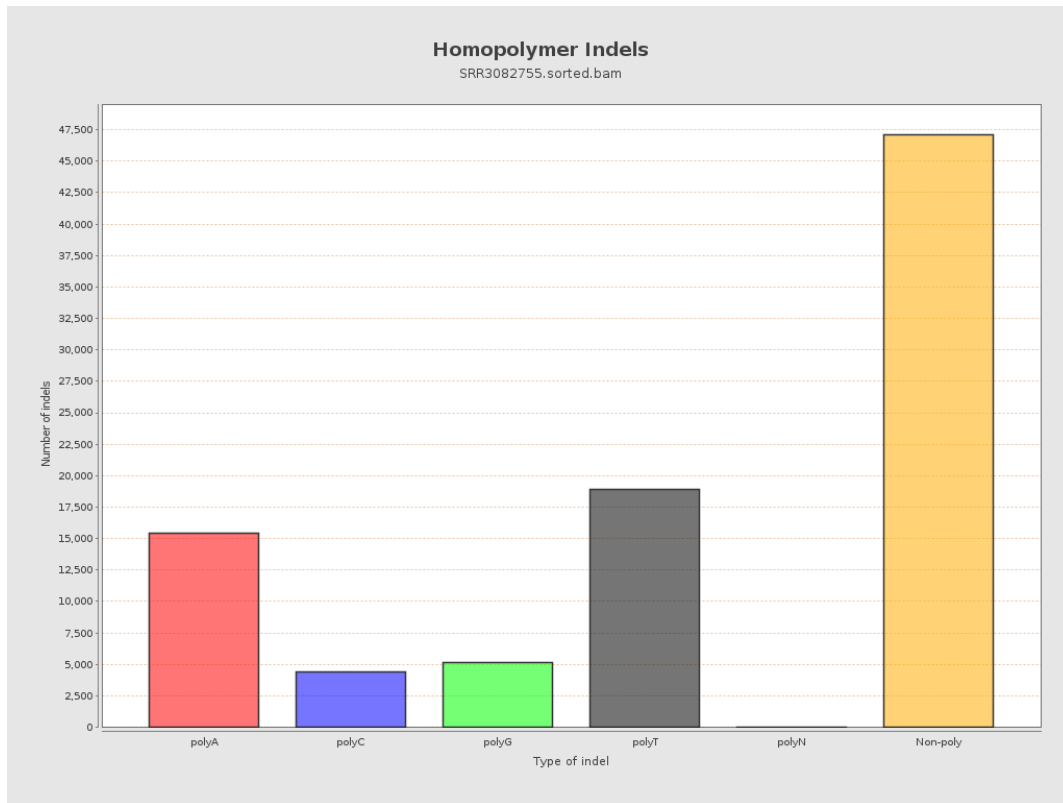
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

