Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 08:22:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090155.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_SRR090155 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 08:22:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,775,453
Mapped reads	15,642,926 / 88%
Unmapped reads	2,132,527 / 12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	110,439 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,957,509 / 11.01%
Duplication rate	9.45%
Clipped reads	8,562,260 / 48.17%

2.2. ACGT Content

Number/percentage of A's	267,126,869 / 26.54%
Number/percentage of C's	180,736,320 / 17.96%
Number/percentage of T's	320,009,146 / 31.79%
Number/percentage of G's	237,898,744 / 23.63%
Number/percentage of N's	832,270 / 0.08%
GC Percentage	41.59%

2.3. Coverage

Mean	0.3253

Standard Deviation	2.11

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

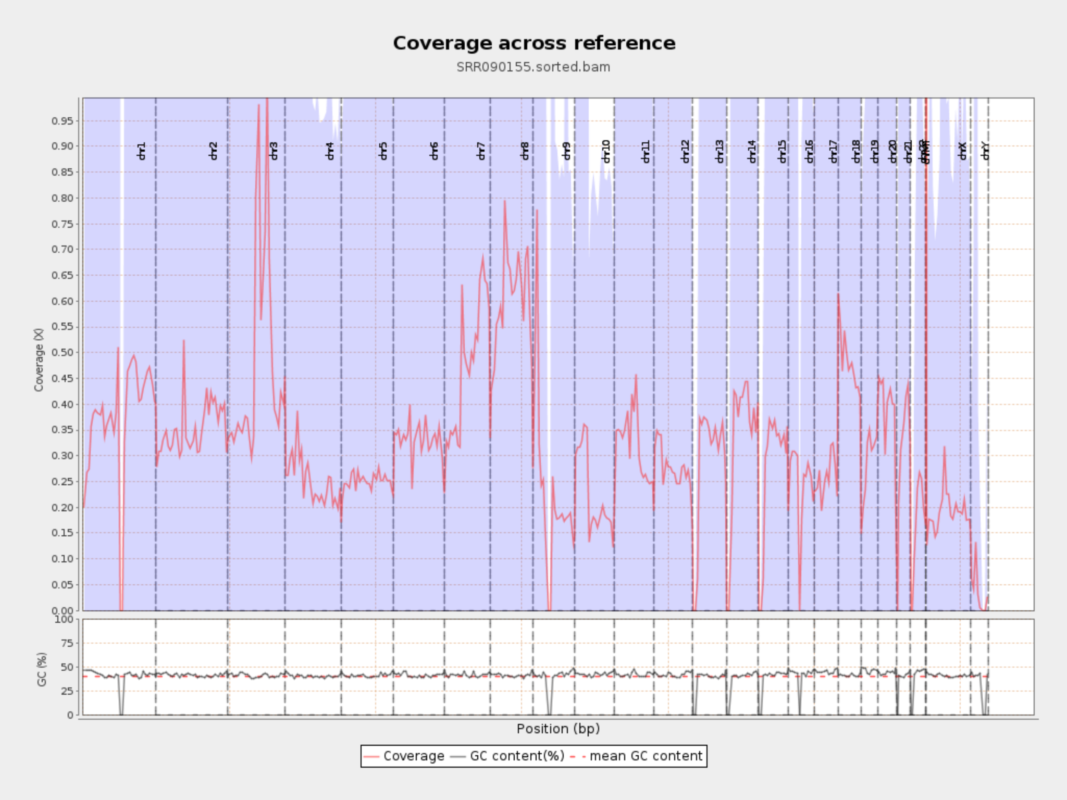
General error rate	0.88%
Mismatches	8,704,732
Insertions	72,071
Mapped reads with at least one insertion	0.46%
Deletions	221,304
Mapped reads with at least one deletion	1.4%
Homopolymer indels	46.88%

2.6. Chromosome stats

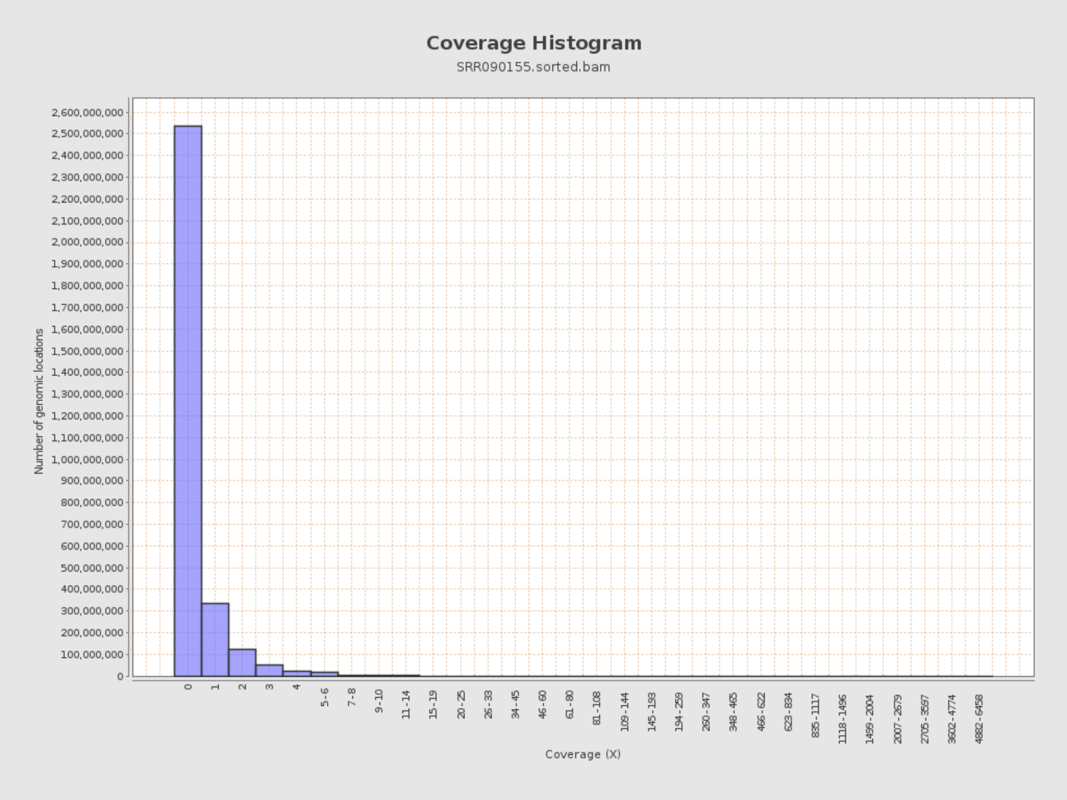
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	92910198	0.3728	4.0156
chr2	243199373	85979546	0.3535	2.5736
chr3	198022430	94338211	0.4764	1.1868
chr4	191154276	48111029	0.2517	0.9423
chr5	180915260	45278203	0.2503	0.8234
chr6	171115067	56857923	0.3323	1.2295
chr7	159138663	75360301	0.4736	3.5162

chr8	146364022	88532183	0.6049	4.0034
chr9	141213431	32056516	0.227	1.5811
chr10	135534747	30497108	0.225	1.5909
chr11	135006516	43288613	0.3206	1.5365
chr12	133851895	37431157	0.2796	0.9138
chr13	115169878	33222951	0.2885	0.855
chr14	107349540	35771379	0.3332	1.0539
chr15	102531392	27514410	0.2684	0.8896
chr16	90354753	21689402	0.24	0.8812
chr17	81195210	21229644	0.2615	1.0629
chr18	78077248	37738088	0.4833	2.9258
chr19	59128983	17394810	0.2942	2.1707
chr20	63025520	25100724	0.3983	1.115
chr21	48129895	15084191	0.3134	1.0473
chr22	51304566	8565748	0.167	0.6325
chrMT	16571	1048614	63.2801	33.1617
chrX	155270560	29802259	0.1919	0.9565
chrY	59373566	2177079	0.0367	1.1149

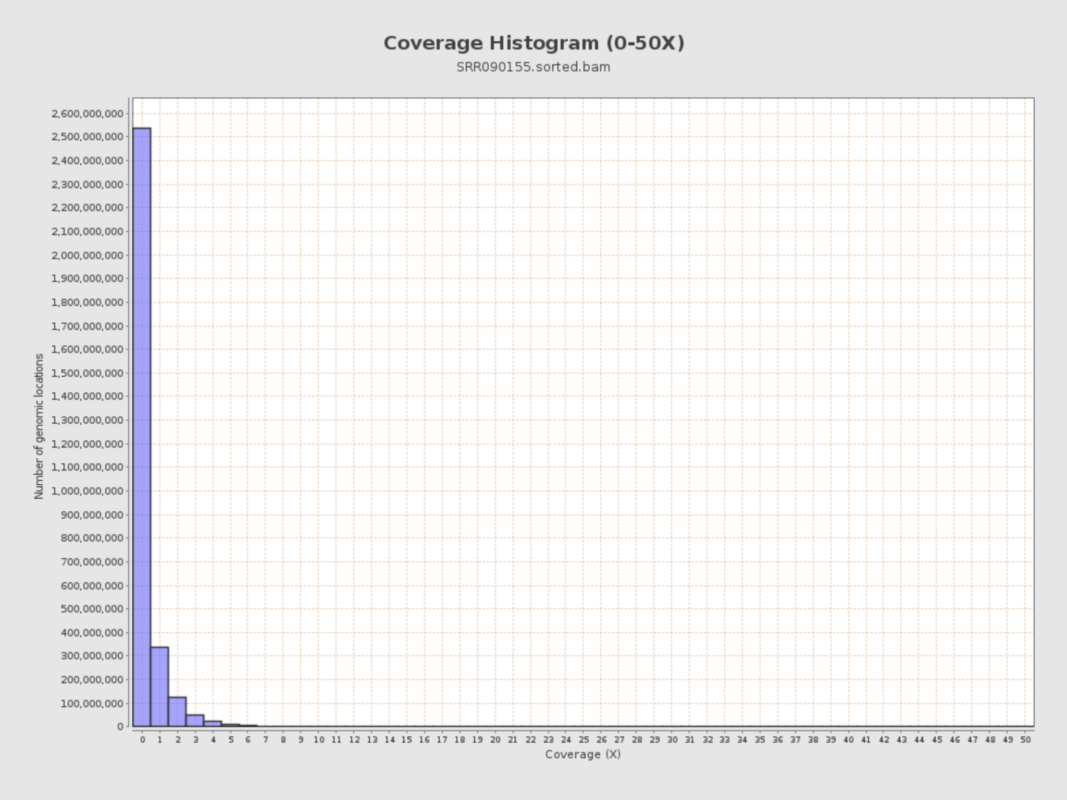
3. Results : Coverage across reference



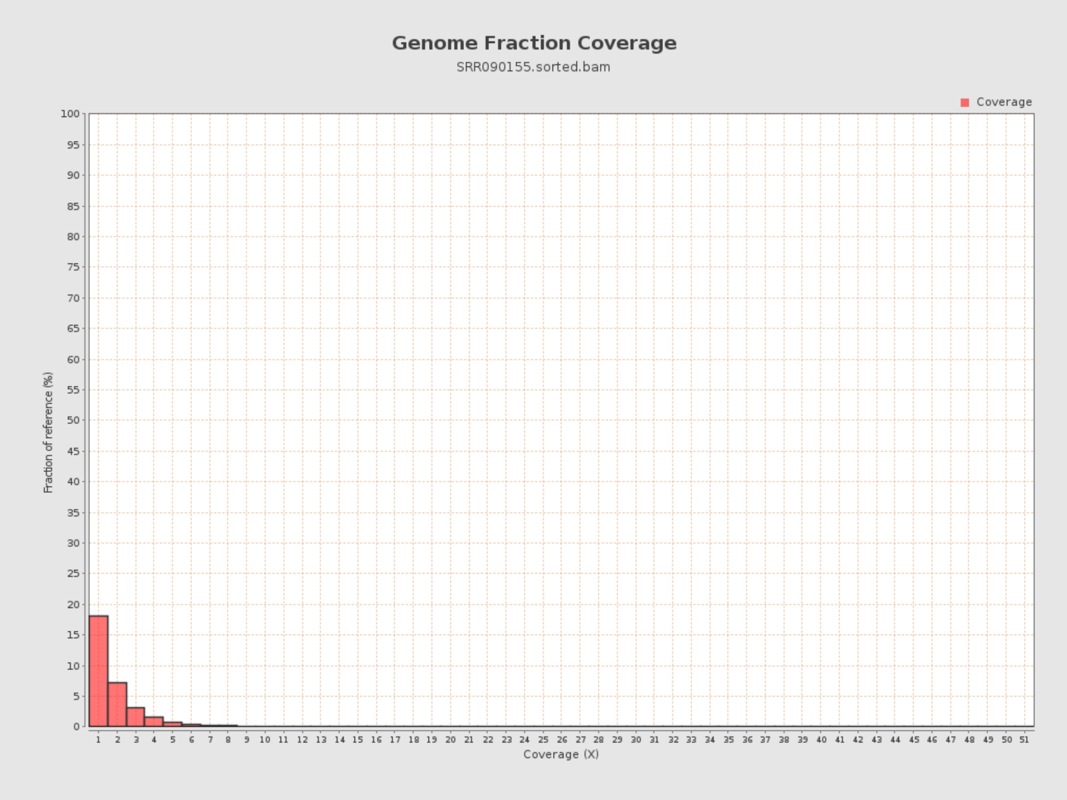
4. Results : Coverage Histogram



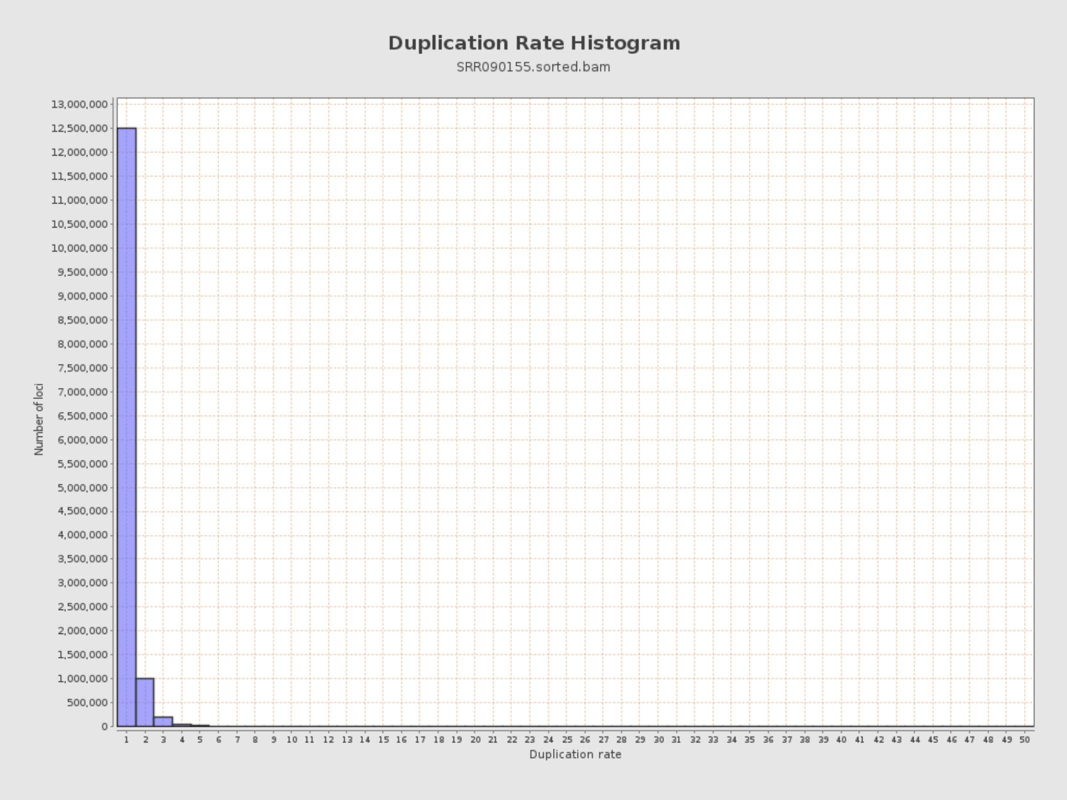
5. Results : Coverage Histogram (0-50X)



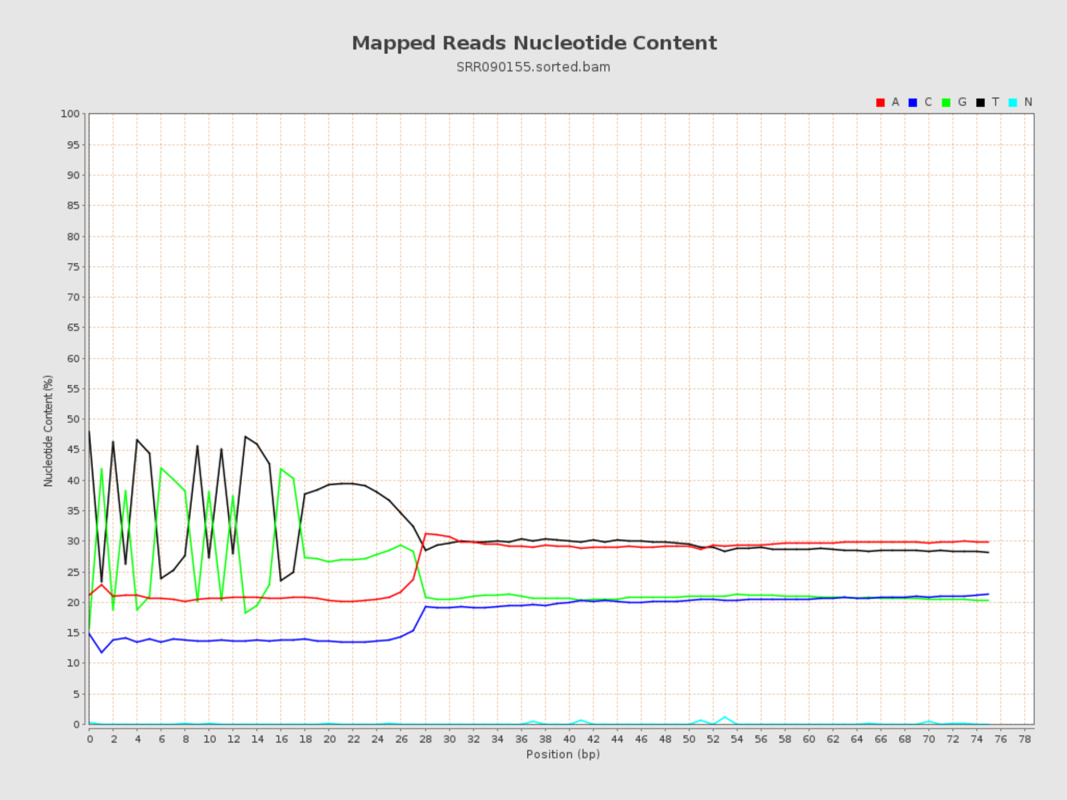
6. Results : Genome Fraction Coverage



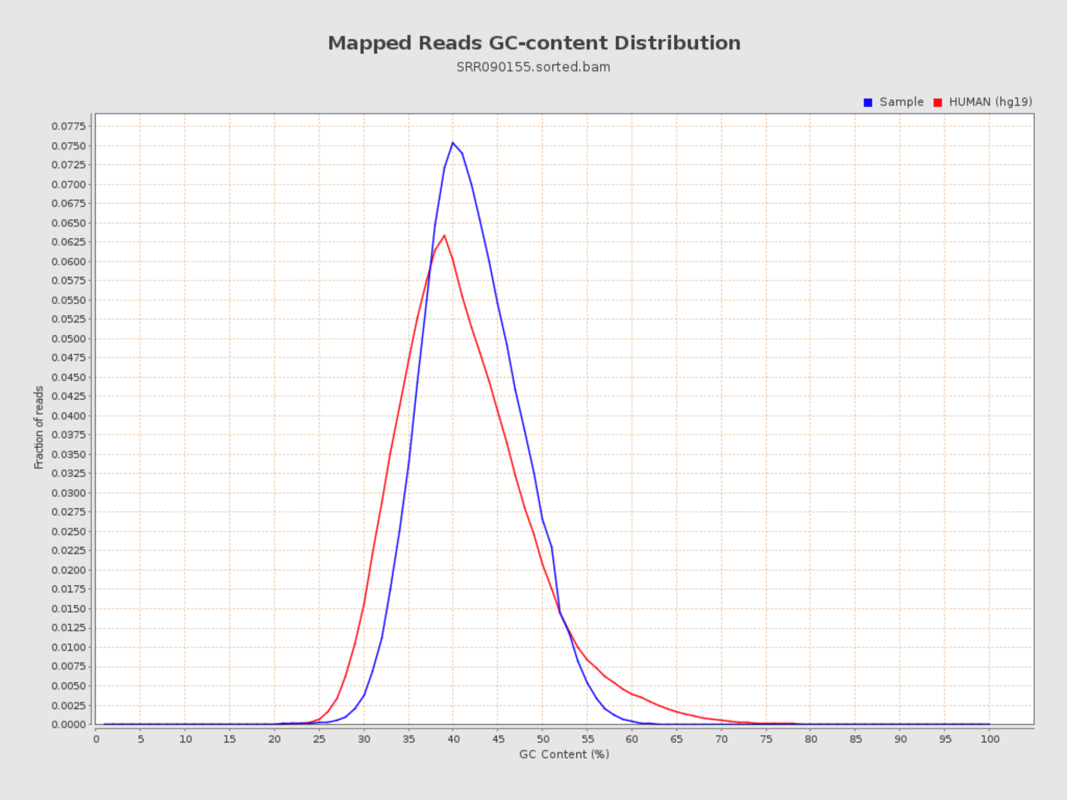
7. Results : Duplication Rate Histogram



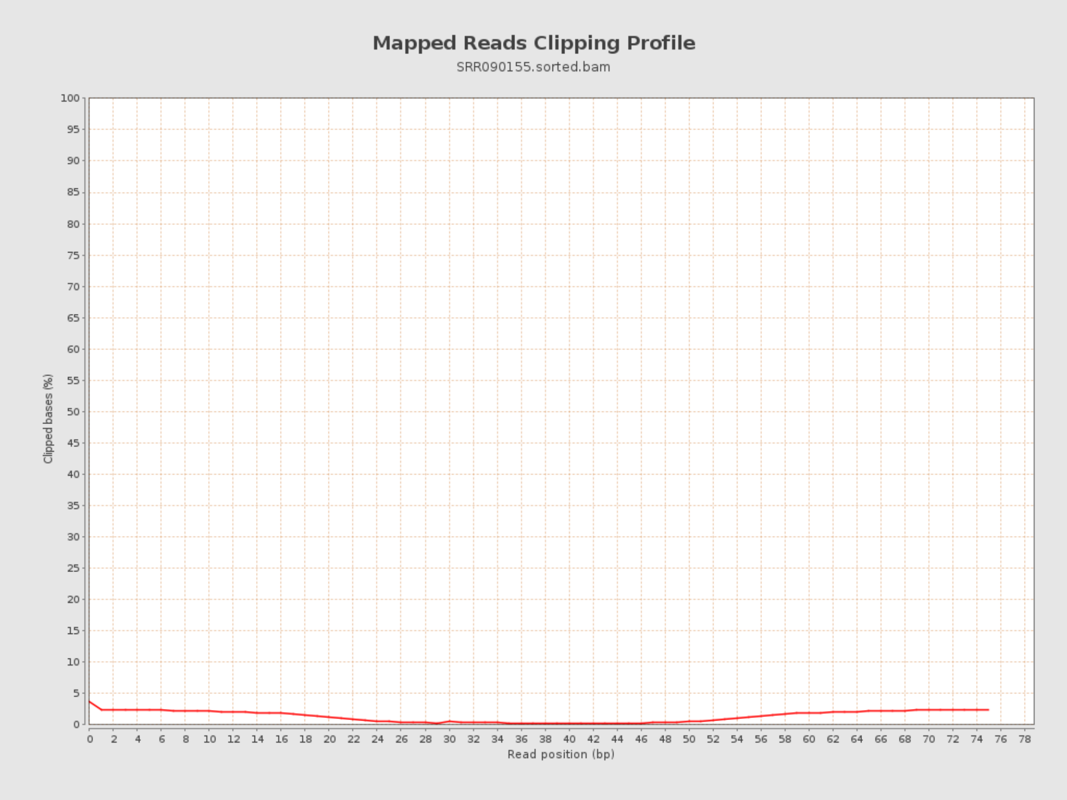
8. Results : Mapped Reads Nucleotide Content



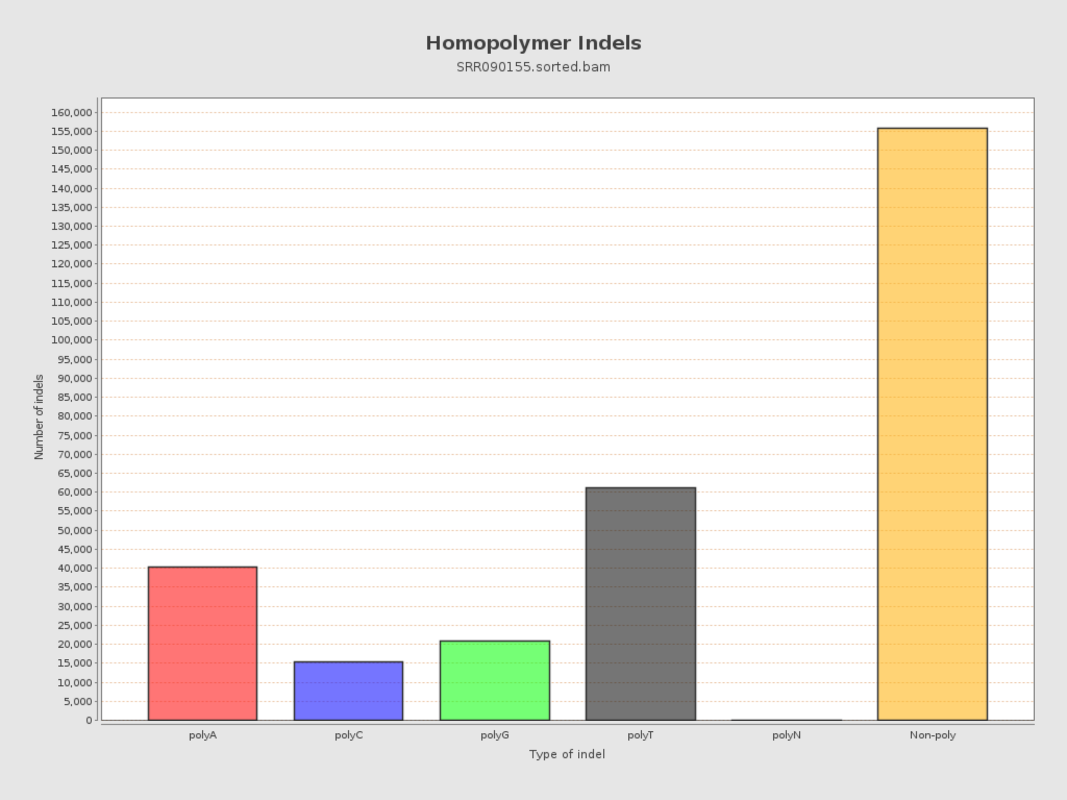
9. Results : Mapped Reads GC-content Distribution



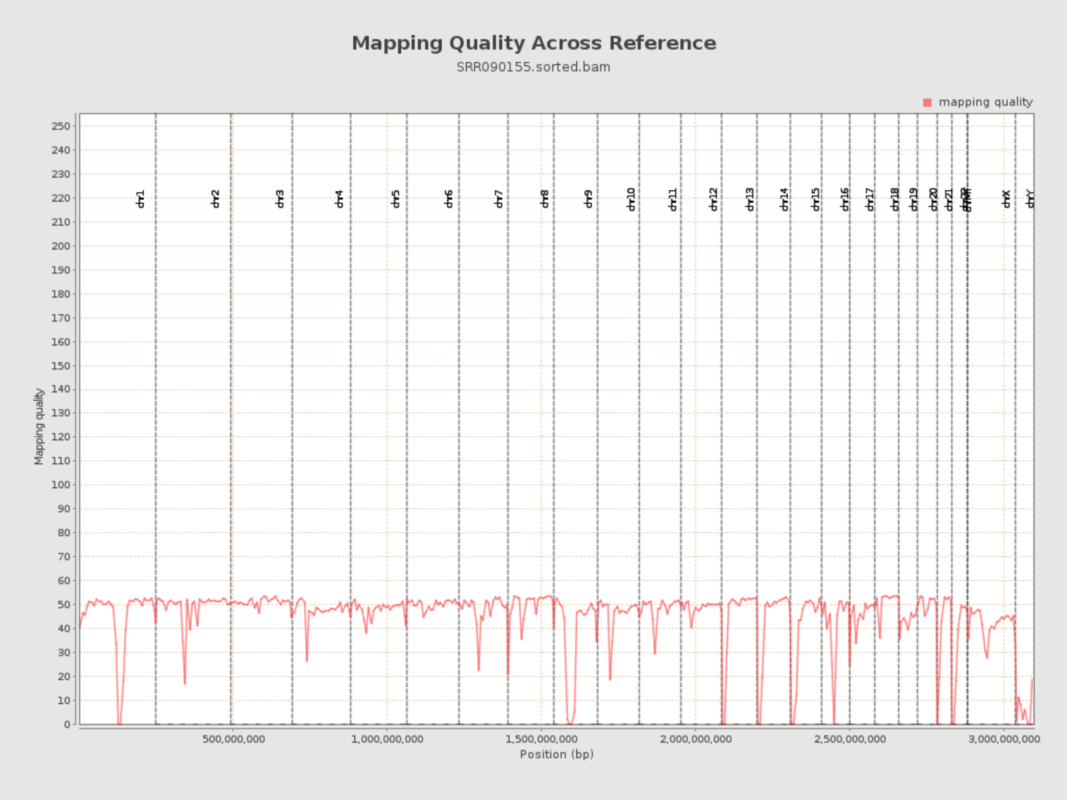
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram