Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 05:17:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089755.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_SRR089755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 05:17:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,899,906
Mapped reads	21,763,273 / 80.9%
Unmapped reads	5,136,633 / 19.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,093 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,393,125 / 16.33%
Duplication rate	12.59%
Clipped reads	1,921,702 / 7.14%

2.2. ACGT Content

Number/percentage of A's	305,992,608 / 29.82%
Number/percentage of C's	211,680,380 / 20.63%
Number/percentage of T's	287,588,302 / 28.03%
Number/percentage of G's	220,728,738 / 21.51%
Number/percentage of N's	123,930 / 0.01%
GC Percentage	42.14%

2.3. Coverage

Mean	0.3315

Standard Deviation	2.2325

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

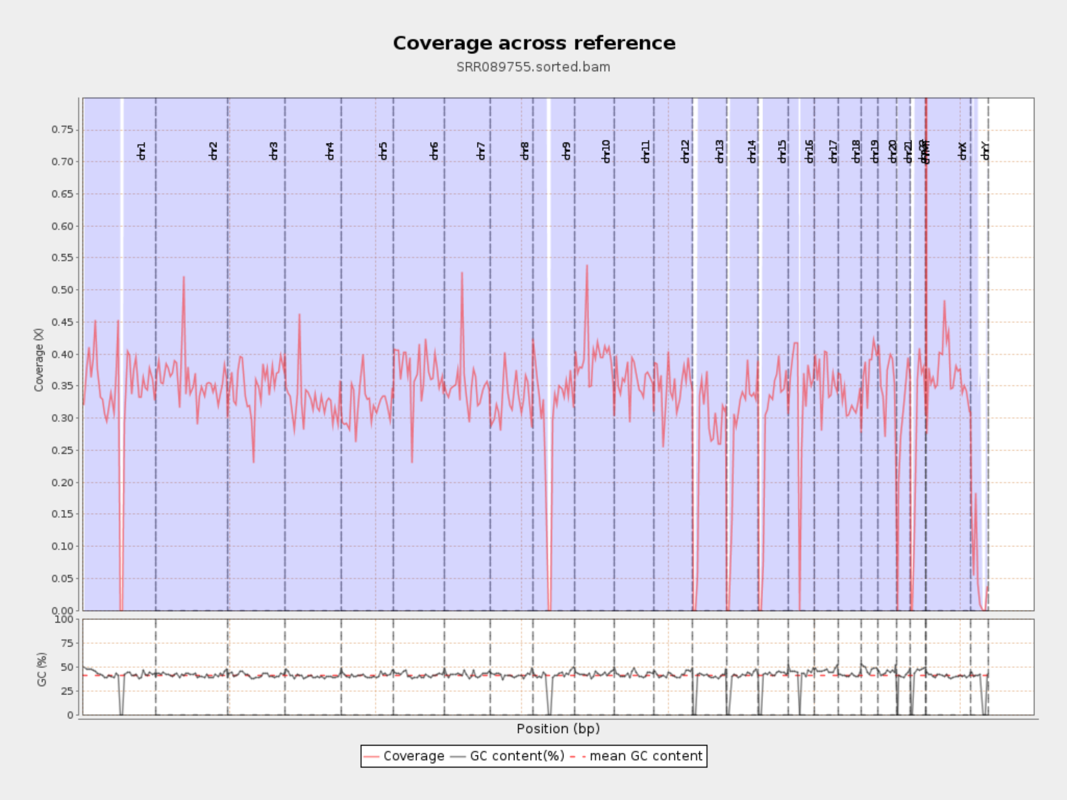
General error rate	0.43%
Mismatches	4,356,165
Insertions	40,314
Mapped reads with at least one insertion	0.19%
Deletions	124,870
Mapped reads with at least one deletion	0.57%
Homopolymer indels	46.2%

2.6. Chromosome stats

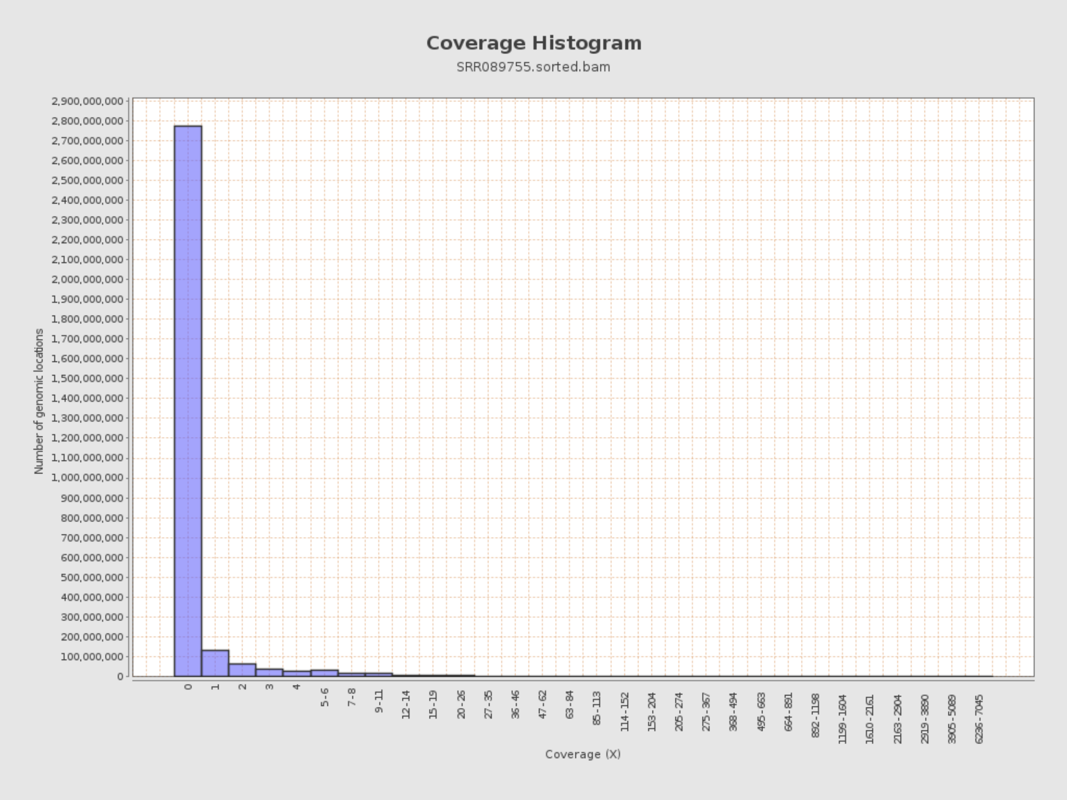
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	83725797	0.3359	3.299
chr2	243199373	88117818	0.3623	2.3599
chr3	198022430	69334127	0.3501	1.4921
chr4	191154276	62637814	0.3277	1.6868
chr5	180915260	58176858	0.3216	1.4396
chr6	171115067	63646664	0.372	1.6875
chr7	159138663	56336948	0.354	3.1484

chr8	146364022	48085918	0.3285	4.0599
chr9	141213431	41817078	0.2961	1.9227
chr10	135534747	53899958	0.3977	2.3449
chr11	135006516	48380632	0.3584	2.1653
chr12	133851895	47217127	0.3528	1.5758
chr13	115169878	29434193	0.2556	1.2893
chr14	107349540	29575334	0.2755	1.4744
chr15	102531392	28443833	0.2774	1.3408
chr16	90354753	29726952	0.329	1.5523
chr17	81195210	29382178	0.3619	1.7421
chr18	78077248	25610698	0.328	3.1586
chr19	59128983	22297944	0.3771	2.7194
chr20	63025520	22327304	0.3543	1.6104
chr21	48129895	13749395	0.2857	1.6749
chr22	51304566	13221432	0.2577	1.2882
chrMT	16571	492191	29.7019	20.6709
chrX	155270560	57349361	0.3694	1.7376
chrY	59373566	3317878	0.0559	1.4305

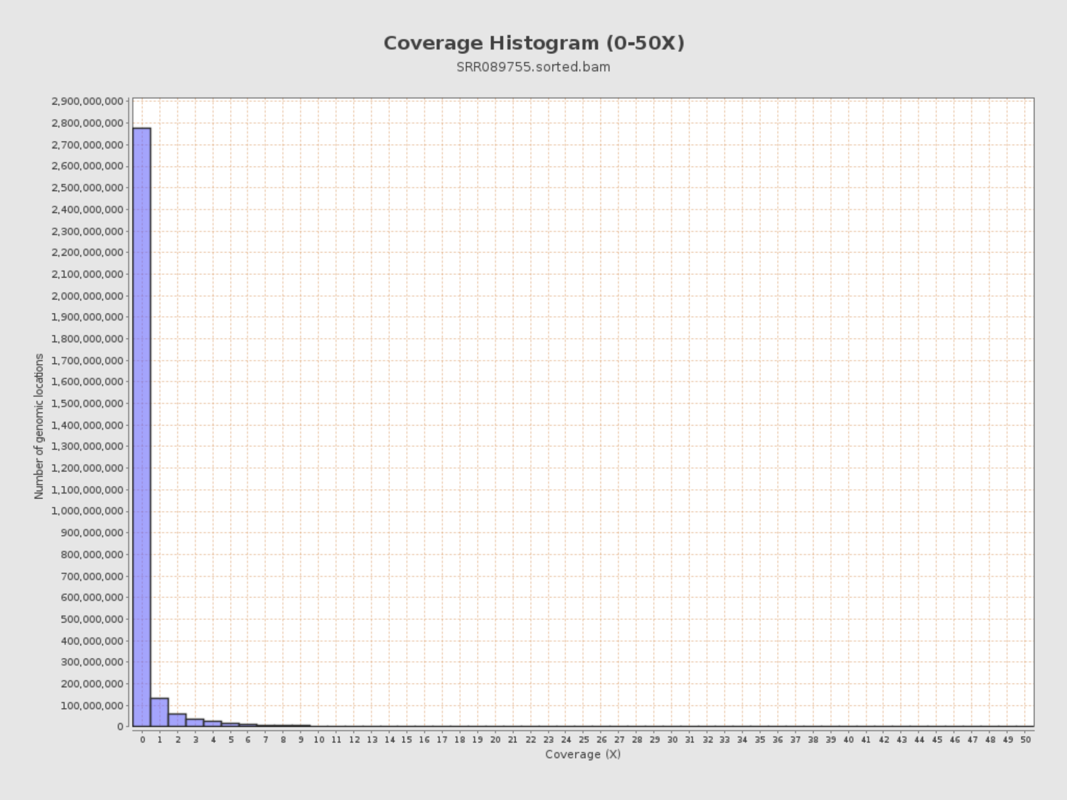
3. Results : Coverage across reference



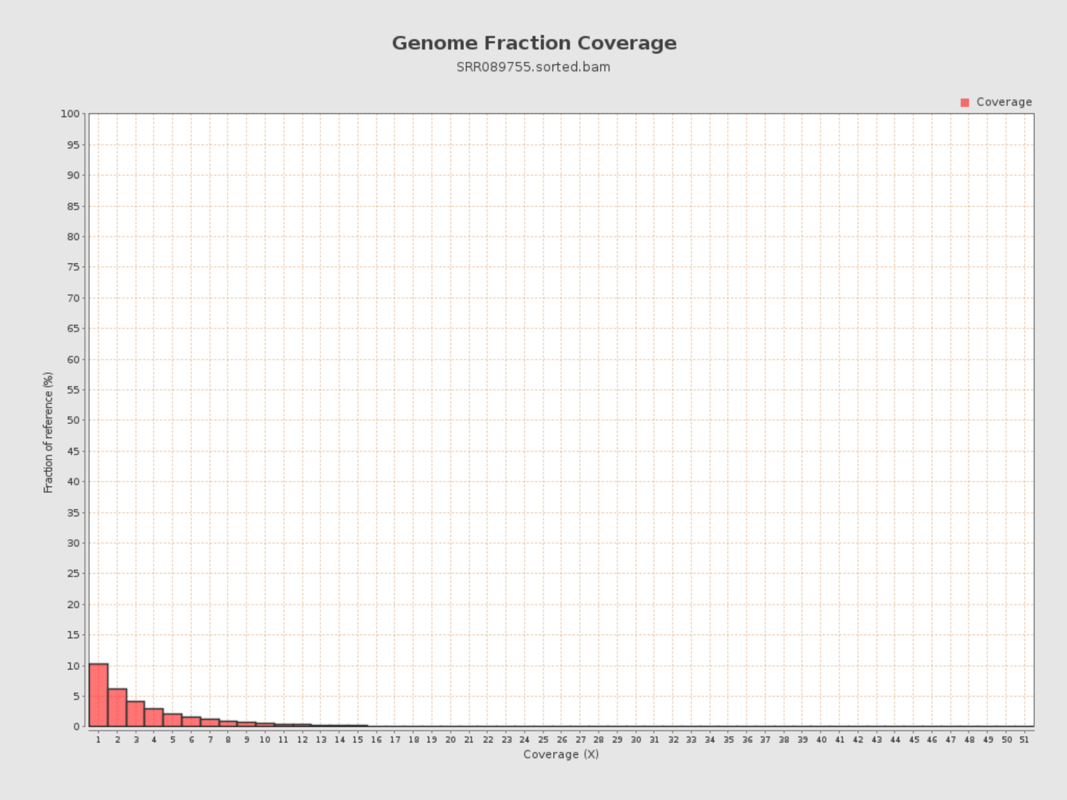
4. Results : Coverage Histogram



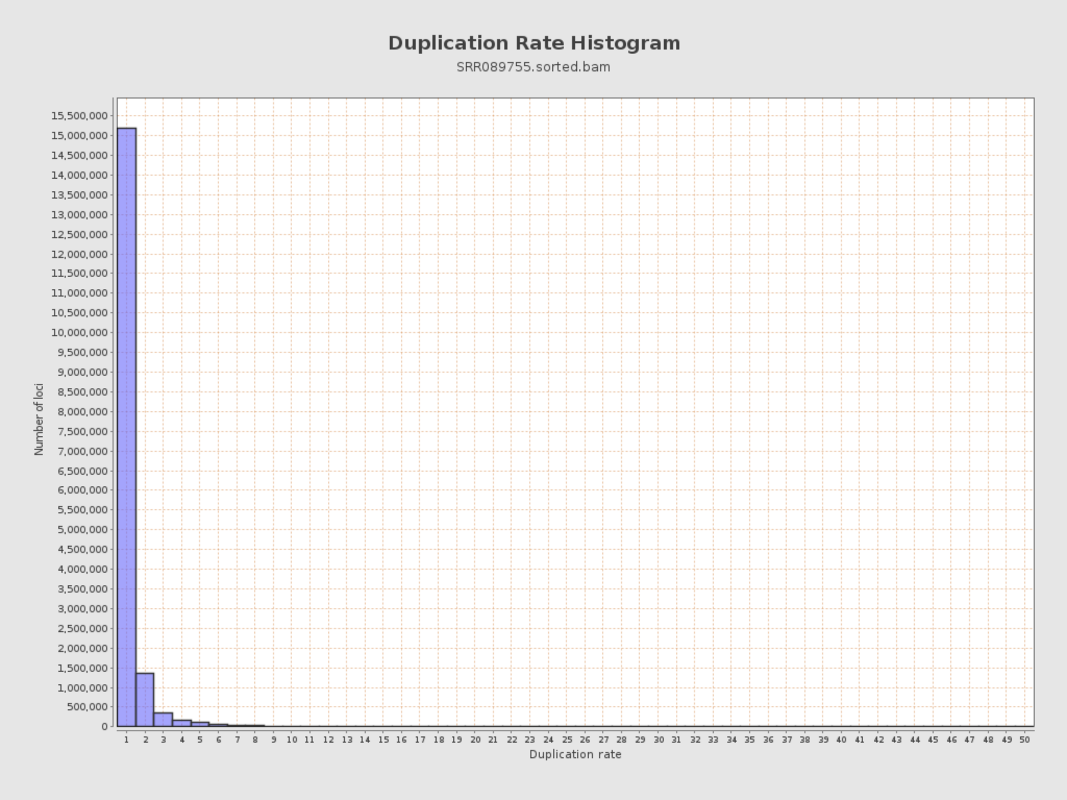
5. Results : Coverage Histogram (0-50X)



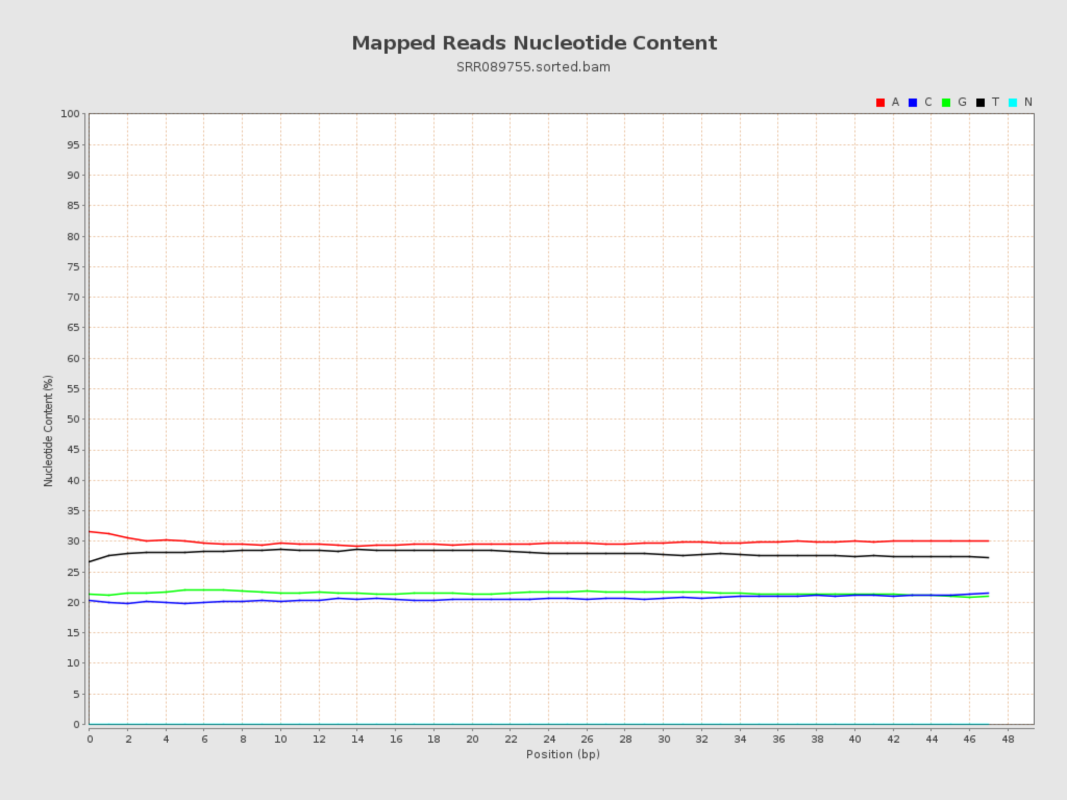
6. Results : Genome Fraction Coverage



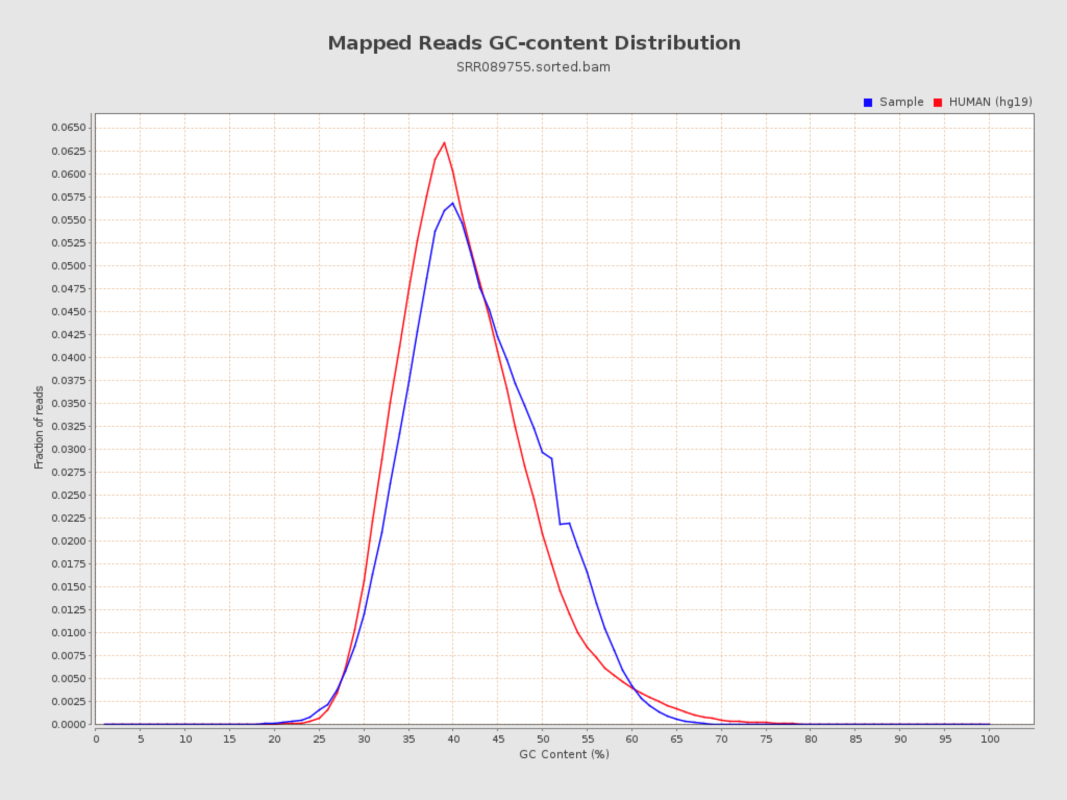
7. Results : Duplication Rate Histogram



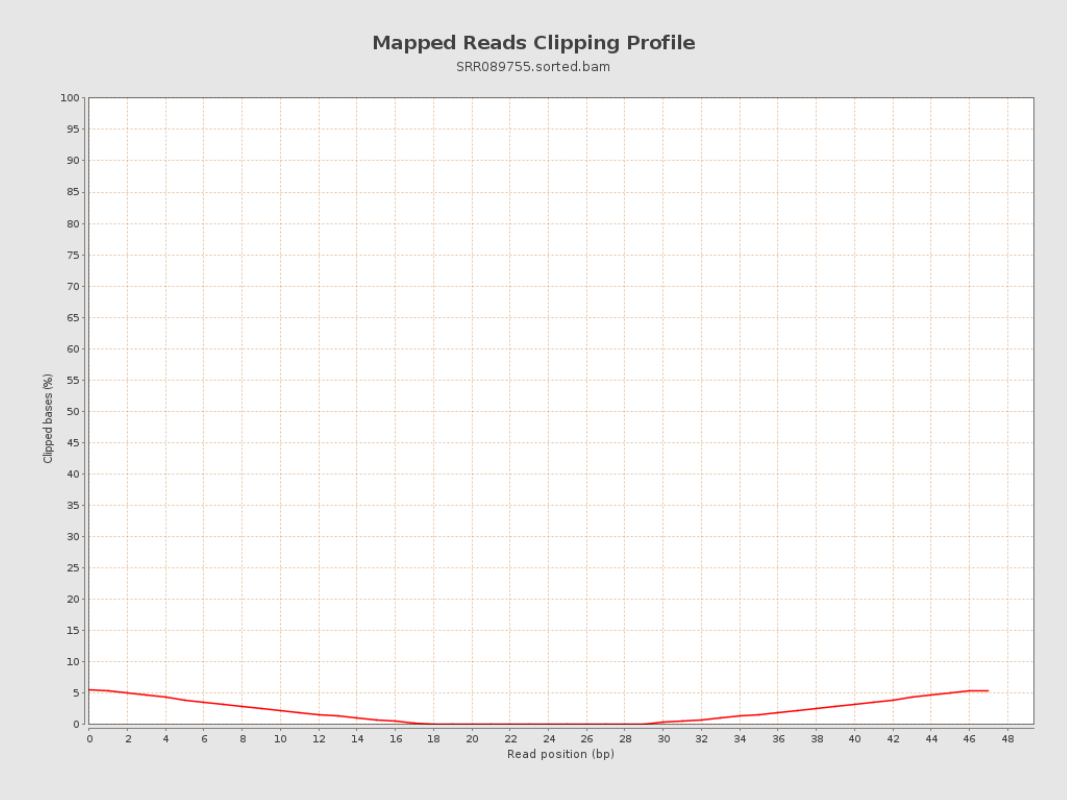
8. Results : Mapped Reads Nucleotide Content



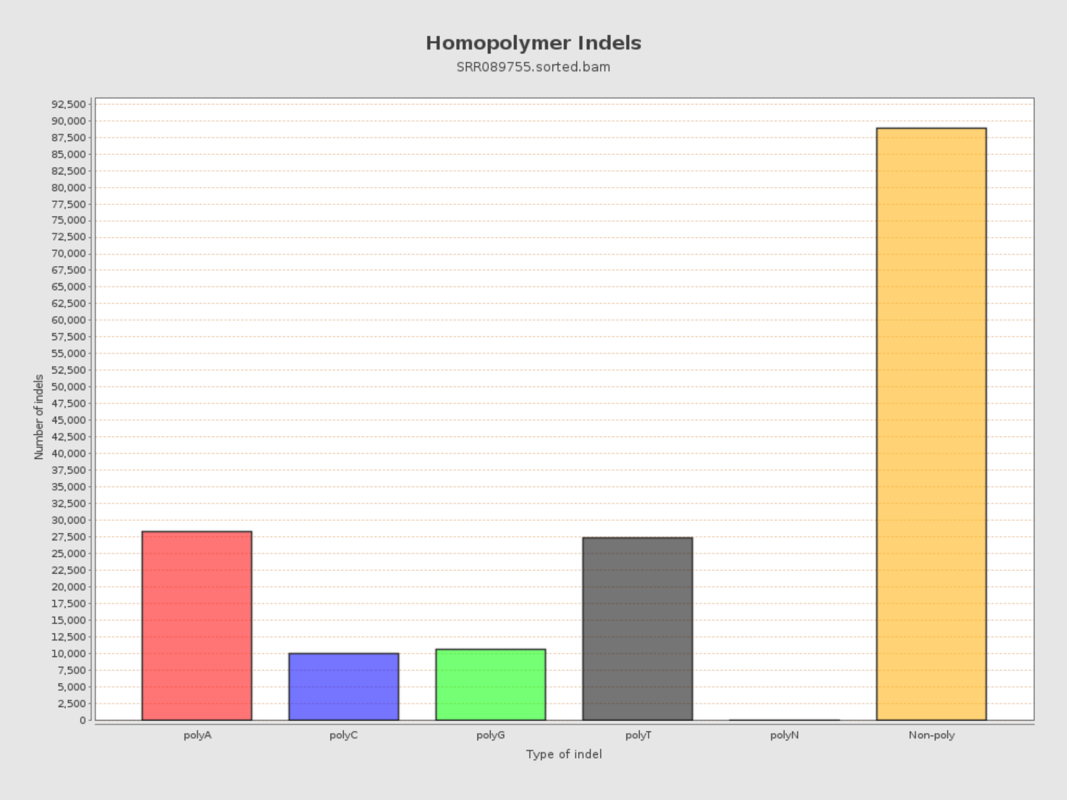
9. Results : Mapped Reads GC-content Distribution



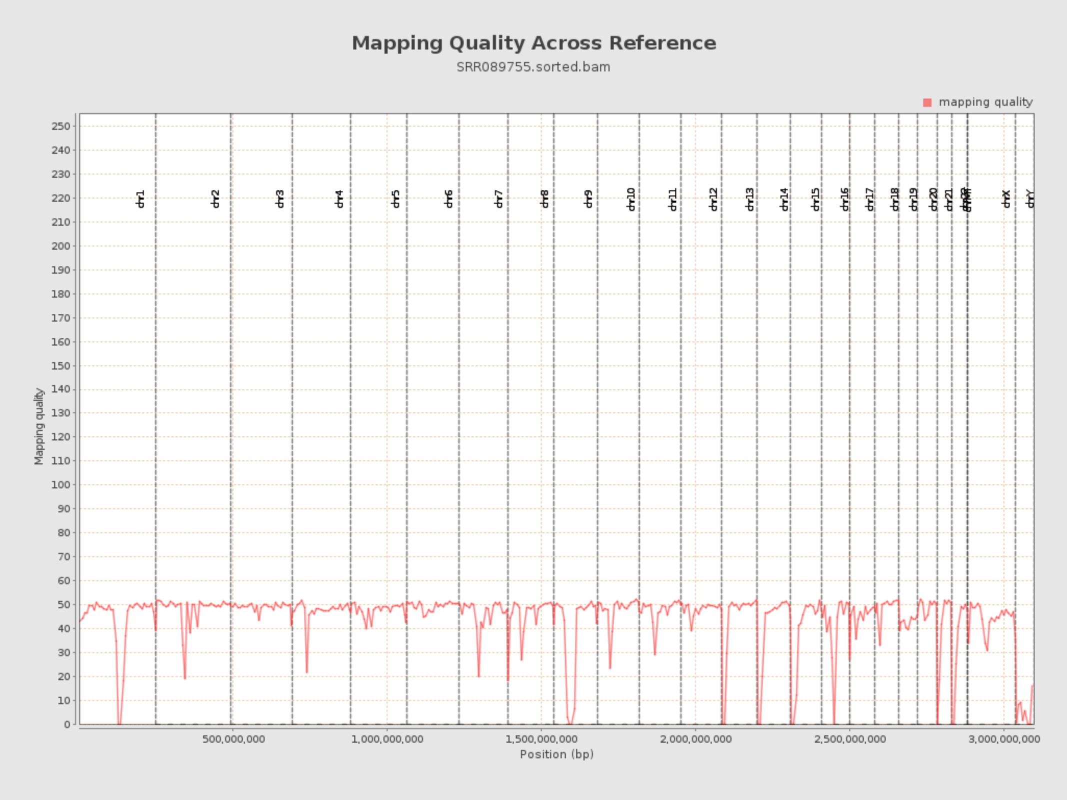
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram