Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 21:36:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089701.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_SRR089701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089701.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 21:36:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,840,551
Mapped reads	17,313,733 / 79.27%
Unmapped reads	4,526,818 / 20.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	735 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,912,115 / 8.75%
Duplication rate	8.54%
Clipped reads	3,410,768 / 15.62%

2.2. ACGT Content

Number/percentage of A's	257,663,395 / 32.27%
Number/percentage of C's	162,179,802 / 20.31%
Number/percentage of T's	209,263,132 / 26.21%
Number/percentage of G's	169,404,353 / 21.21%
Number/percentage of N's	44,119 / 0.01%
GC Percentage	41.52%

2.3. Coverage

Mean	0.258

Standard Deviation	1.3906

2.4. Mapping Quality

Mean Mapping Quality	42.69

2.5. Mismatches and indels

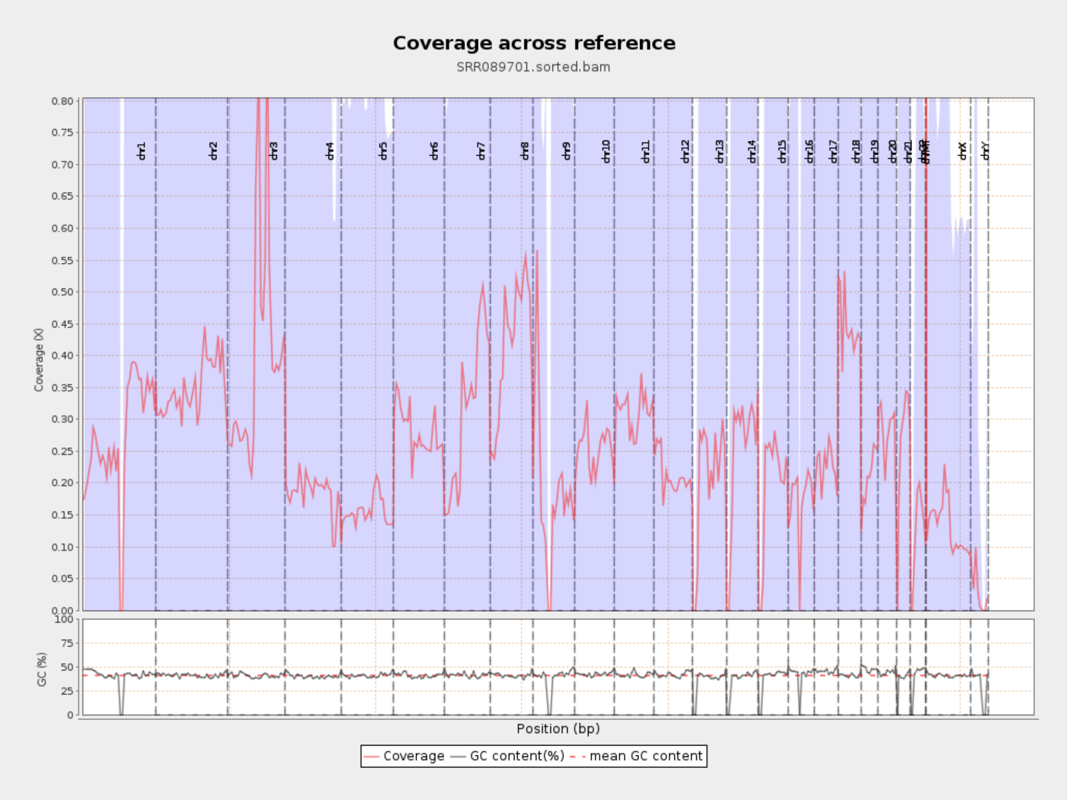
General error rate	0.47%
Mismatches	3,724,551
Insertions	37,358
Mapped reads with at least one insertion	0.22%
Deletions	112,547
Mapped reads with at least one deletion	0.65%
Homopolymer indels	43.03%

2.6. Chromosome stats

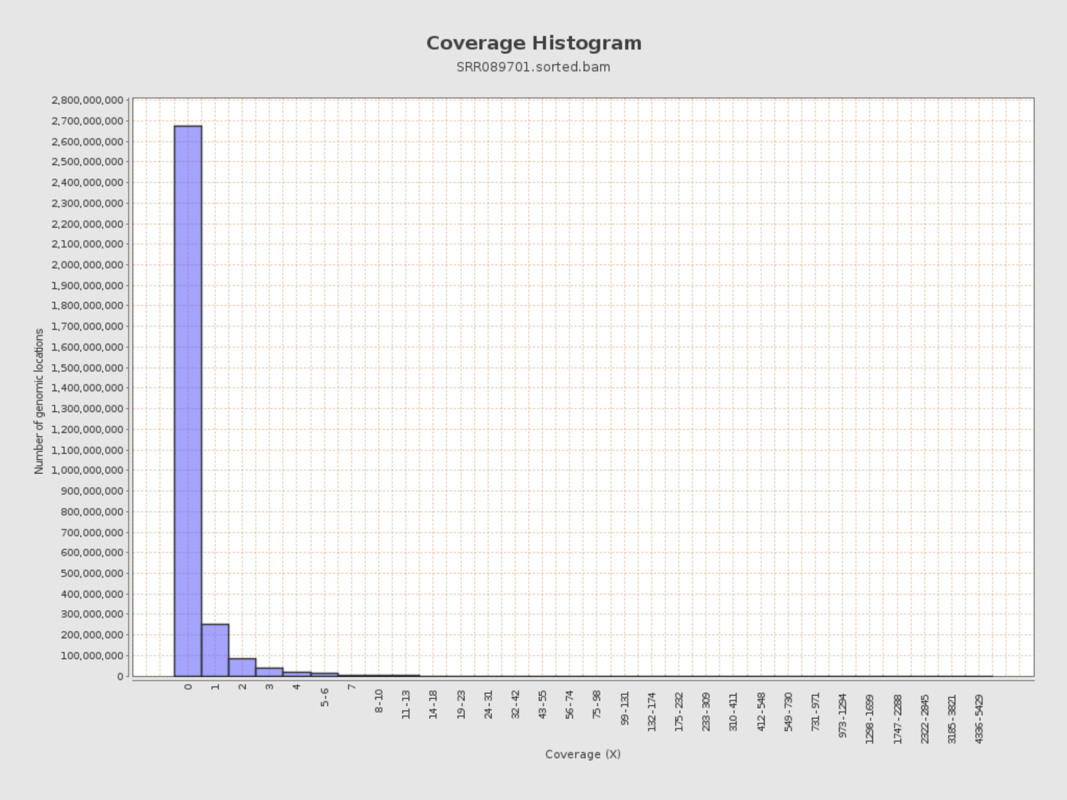
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	67473233	0.2707	1.4338
chr2	243199373	85014072	0.3496	1.8827
chr3	198022430	79215125	0.4	1.1949
chr4	191154276	35452896	0.1855	0.7712
chr5	180915260	28199759	0.1559	0.6785
chr6	171115067	48193541	0.2816	1.0952
chr7	159138663	50430849	0.3169	2.0146

chr8	146364022	61644215	0.4212	3.1551
chr9	141213431	26705864	0.1891	1.1008
chr10	135534747	34468420	0.2543	1.3096
chr11	135006516	42021902	0.3113	1.2635
chr12	133851895	28422370	0.2123	0.814
chr13	115169878	23825367	0.2069	0.795
chr14	107349540	26773864	0.2494	0.9153
chr15	102531392	19856100	0.1937	0.7552
chr16	90354753	15295553	0.1693	0.7968
chr17	81195210	18469182	0.2275	0.9723
chr18	78077248	34841793	0.4462	1.7154
chr19	59128983	12516288	0.2117	1.3995
chr20	63025520	17769264	0.2819	0.9657
chr21	48129895	12424508	0.2581	0.9928
chr22	51304566	6275017	0.1223	0.585
chrMT	16571	1084719	65.4589	48.6255
chrX	155270560	20568847	0.1325	0.9453
chrY	59373566	1779916	0.03	0.5474

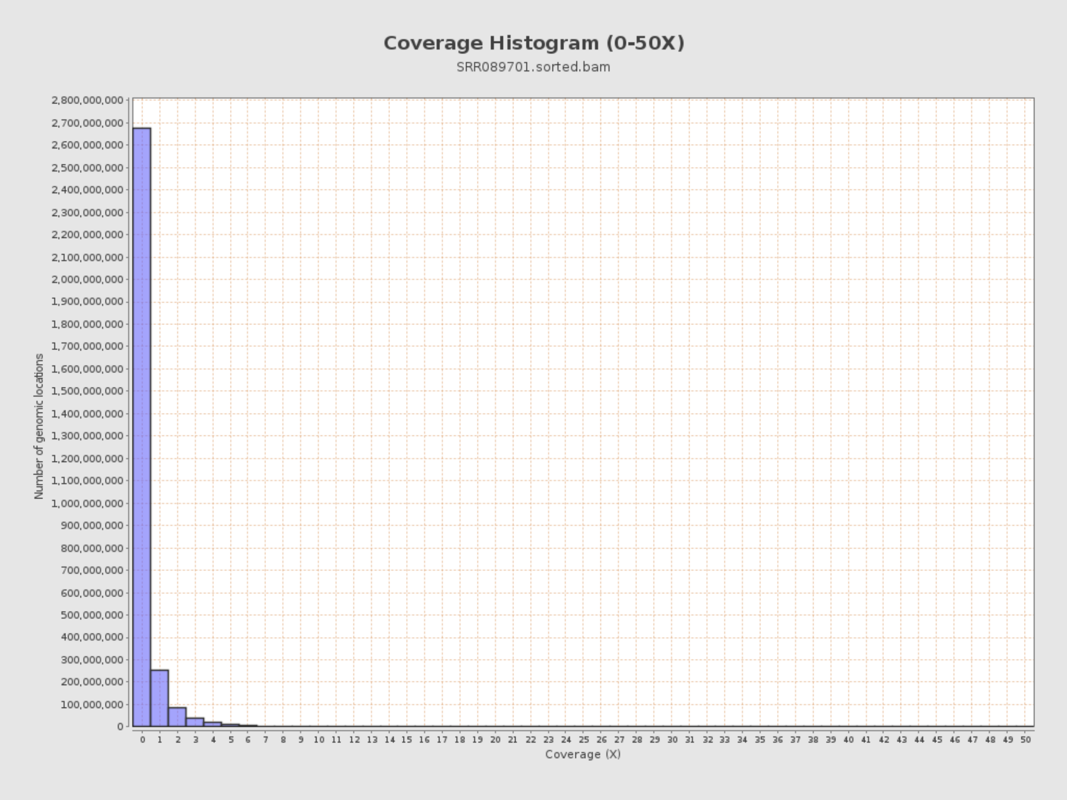
3. Results : Coverage across reference



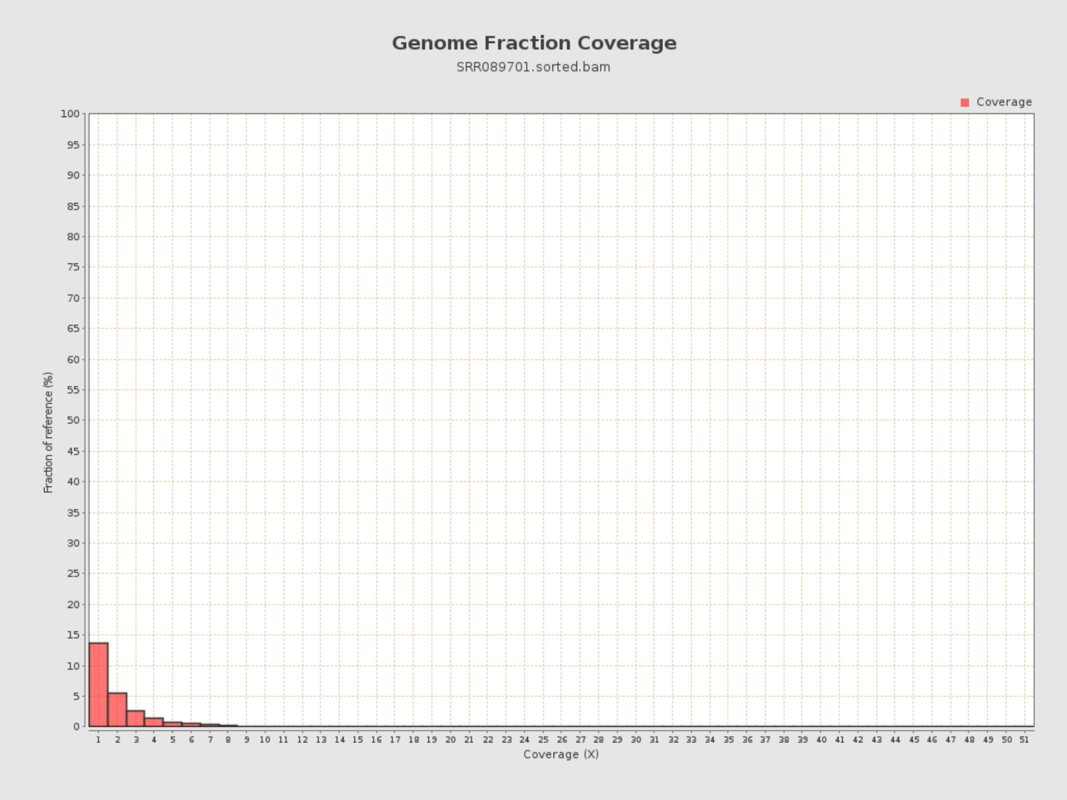
4. Results : Coverage Histogram



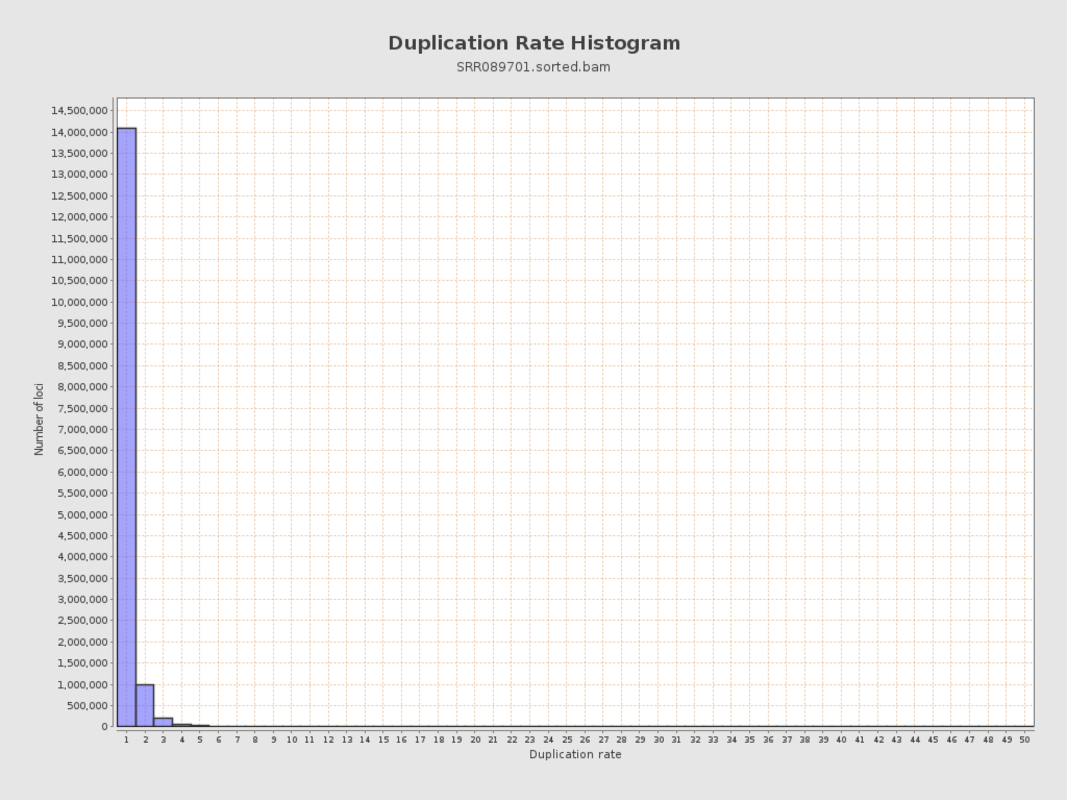
5. Results : Coverage Histogram (0-50X)



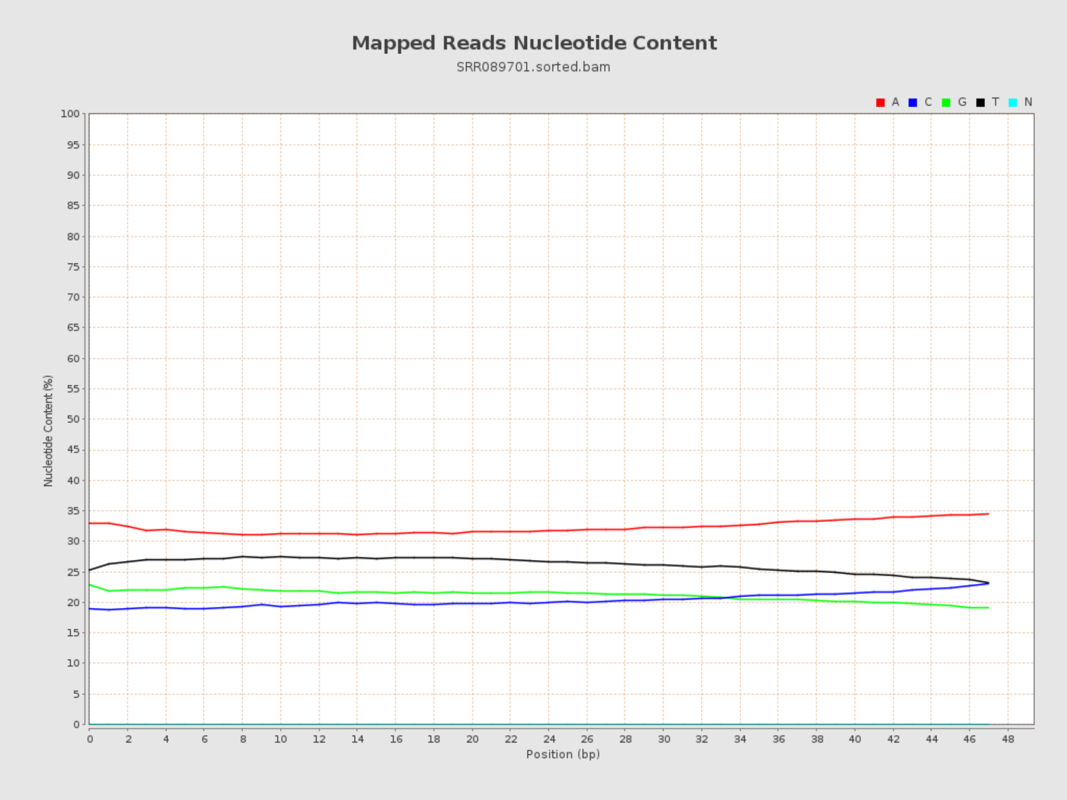
6. Results : Genome Fraction Coverage



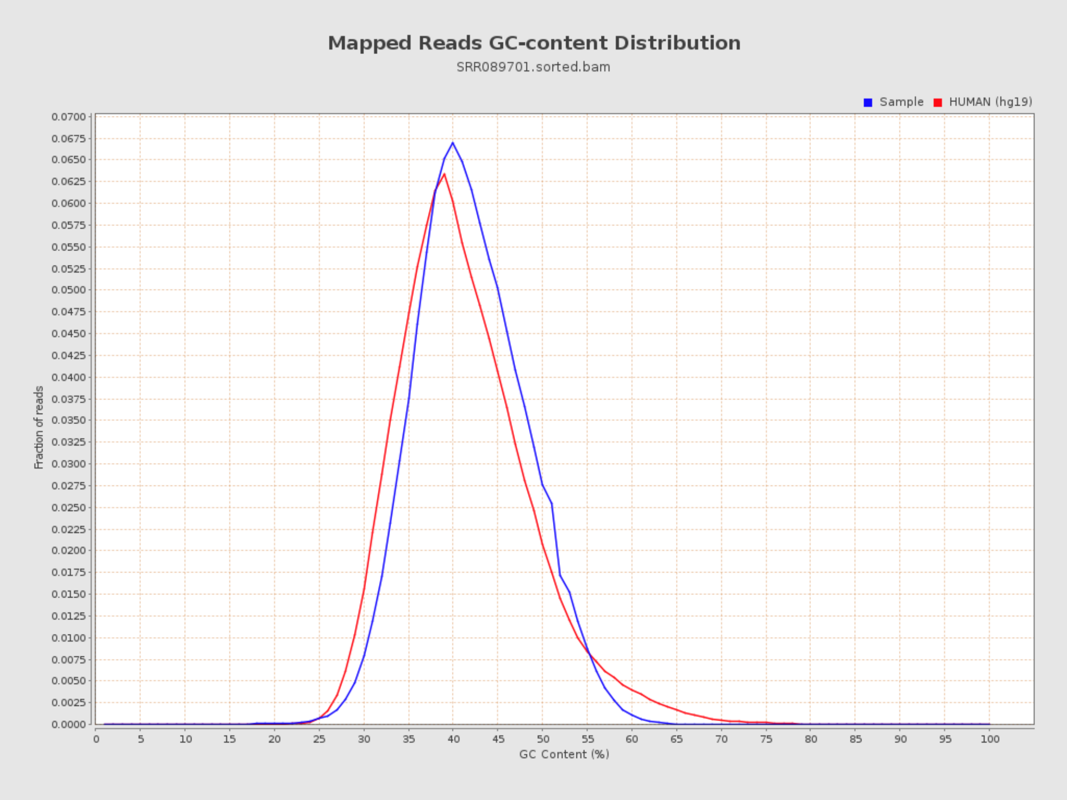
7. Results : Duplication Rate Histogram



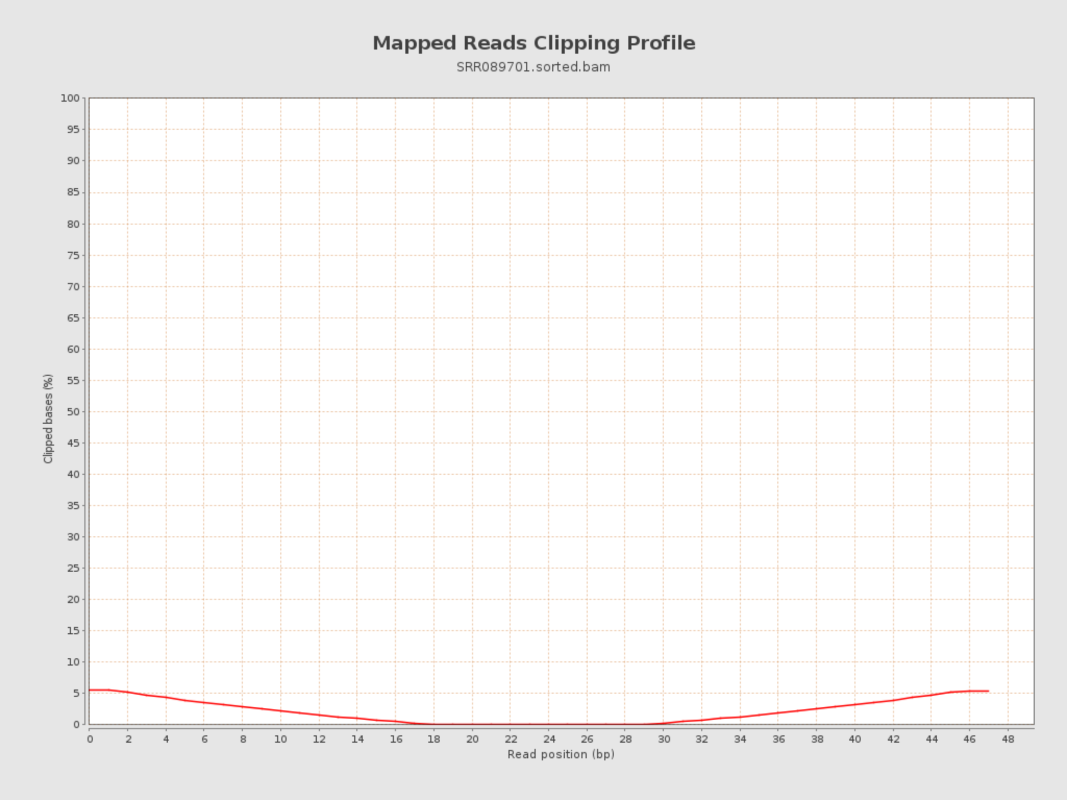
8. Results : Mapped Reads Nucleotide Content



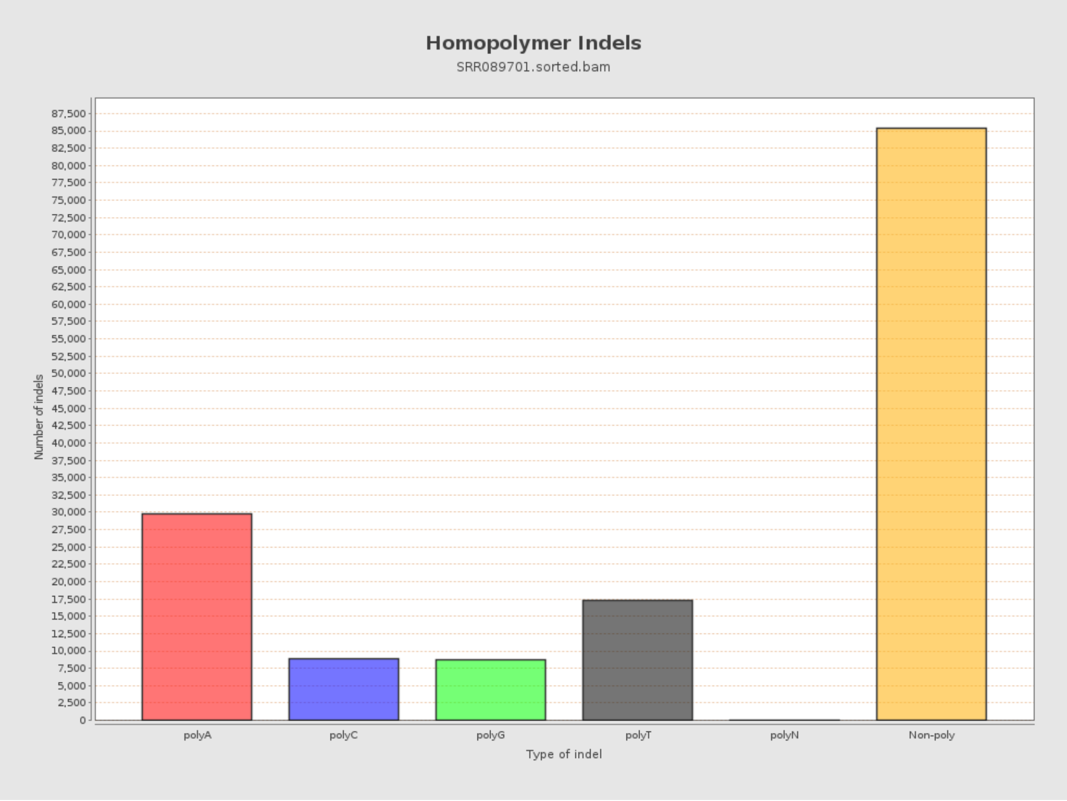
9. Results : Mapped Reads GC-content Distribution



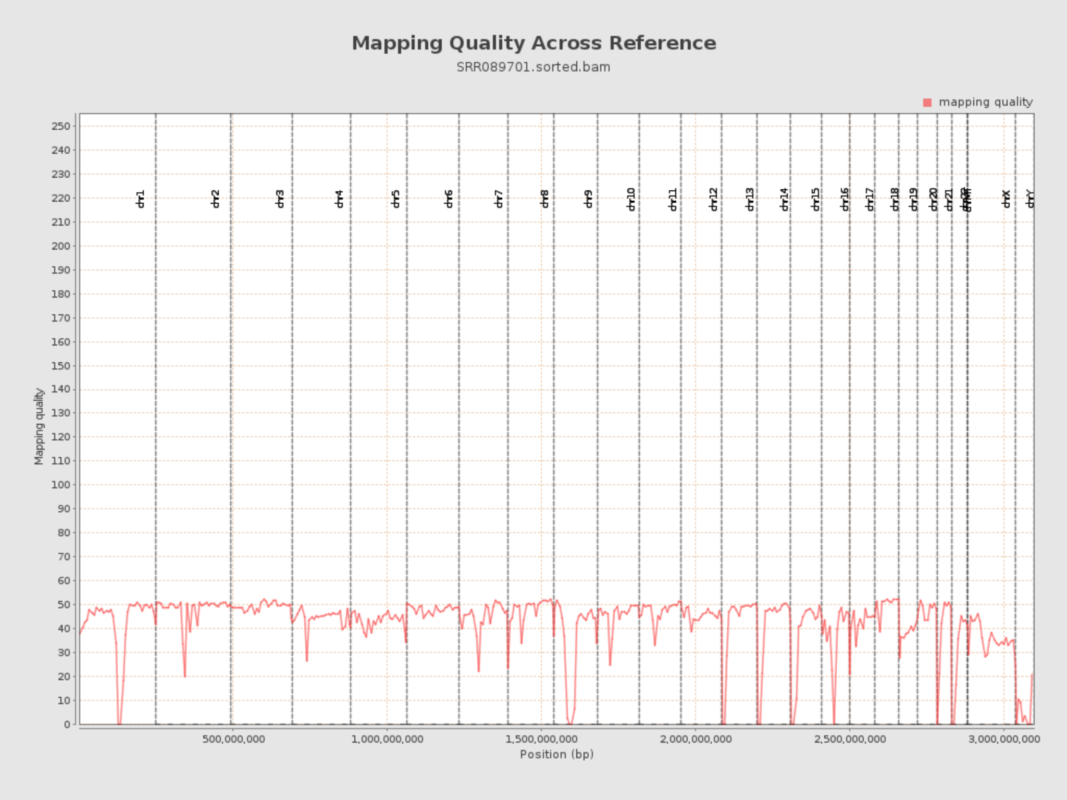
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram