Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 22:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089705.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_SRR089705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089705.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 22:14:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,893,657
Mapped reads	25,331,493 / 94.19%
Unmapped reads	1,562,164 / 5.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	201,941 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	6,159,888 / 22.9%
Duplication rate	15.17%
Clipped reads	11,772,318 / 43.77%

2.2. ACGT Content

Number/percentage of A's	433,556,401 / 26.02%
Number/percentage of C's	320,979,146 / 19.26%
Number/percentage of T's	509,730,049 / 30.59%
Number/percentage of G's	401,960,384 / 24.12%
Number/percentage of N's	107,909 / 0.01%
GC Percentage	43.39%

2.3. Coverage

Mean	0.5385

Standard Deviation	2.9845

2.4. Mapping Quality

Mean Mapping Quality	46.55

2.5. Mismatches and indels

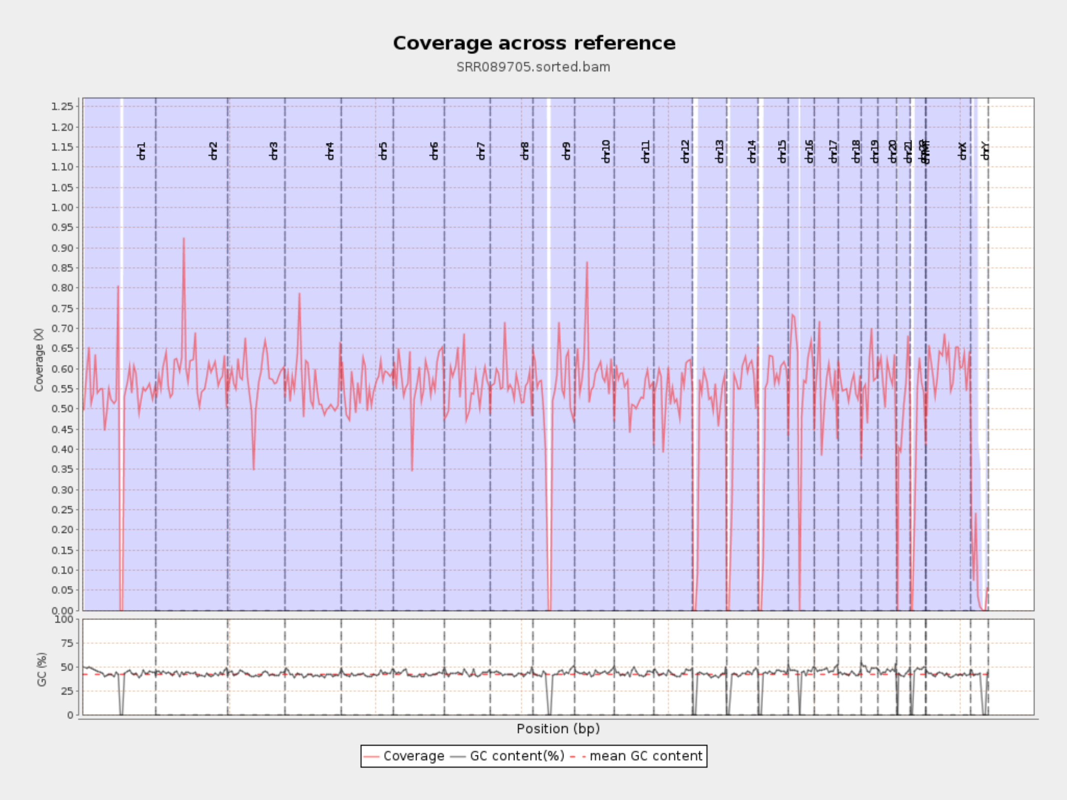
General error rate	0.63%
Mismatches	10,253,583
Insertions	102,650
Mapped reads with at least one insertion	0.4%
Deletions	326,179
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.9%

2.6. Chromosome stats

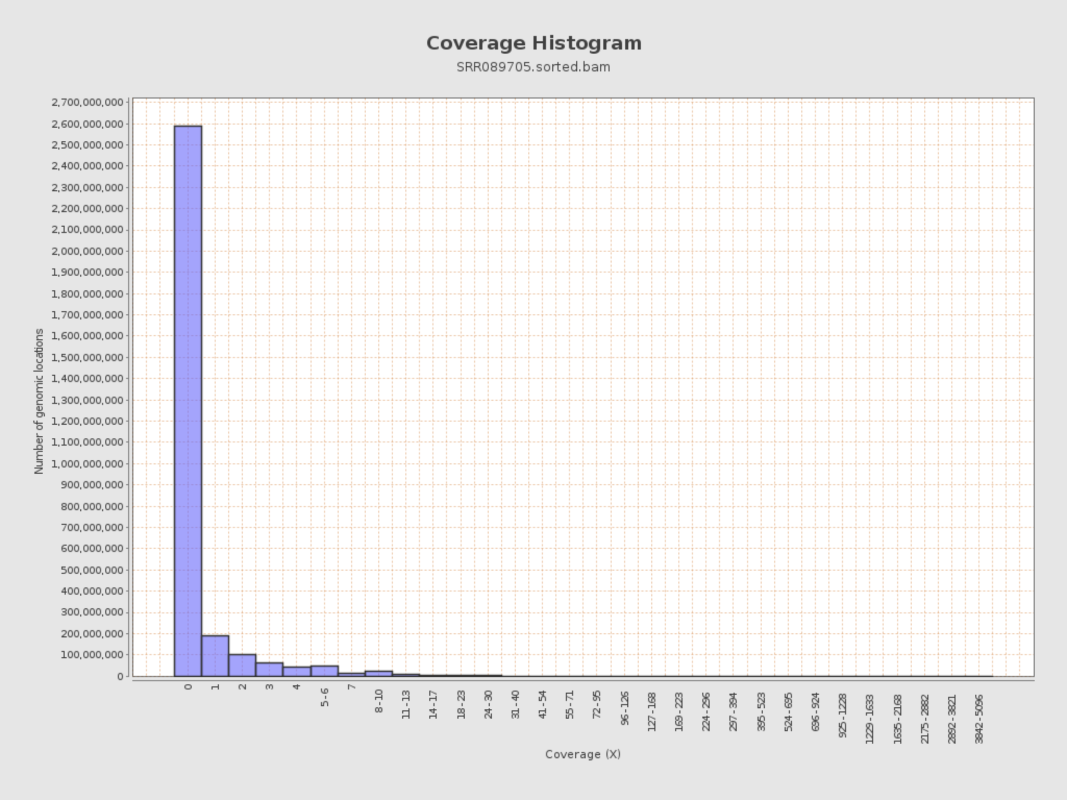
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	129887665	0.5211	4.954
chr2	243199373	144861022	0.5956	3.6776
chr3	198022430	113578569	0.5736	1.9378
chr4	191154276	106188263	0.5555	2.2785
chr5	180915260	101110595	0.5589	1.8952
chr6	171115067	97953937	0.5724	2.4076
chr7	159138663	89018225	0.5594	3.1956

chr8	146364022	82360632	0.5627	3.4206
chr9	141213431	69999197	0.4957	3.1383
chr10	135534747	80891647	0.5968	3.6149
chr11	135006516	73616219	0.5453	2.9793
chr12	133851895	74091545	0.5535	2.0298
chr13	115169878	51996746	0.4515	1.7338
chr14	107349540	52231634	0.4866	1.9225
chr15	102531392	48453405	0.4726	1.8729
chr16	90354753	50789977	0.5621	2.2401
chr17	81195210	45251825	0.5573	2.6349
chr18	78077248	43382107	0.5556	4.9149
chr19	59128983	33768958	0.5711	3.8636
chr20	63025520	36515876	0.5794	2.1979
chr21	48129895	22323653	0.4638	2.2675
chr22	51304566	20051757	0.3908	1.6929
chrMT	16571	8967	0.5411	1.3114
chrX	155270560	94241486	0.607	2.2455
chrY	59373566	4342293	0.0731	1.5993

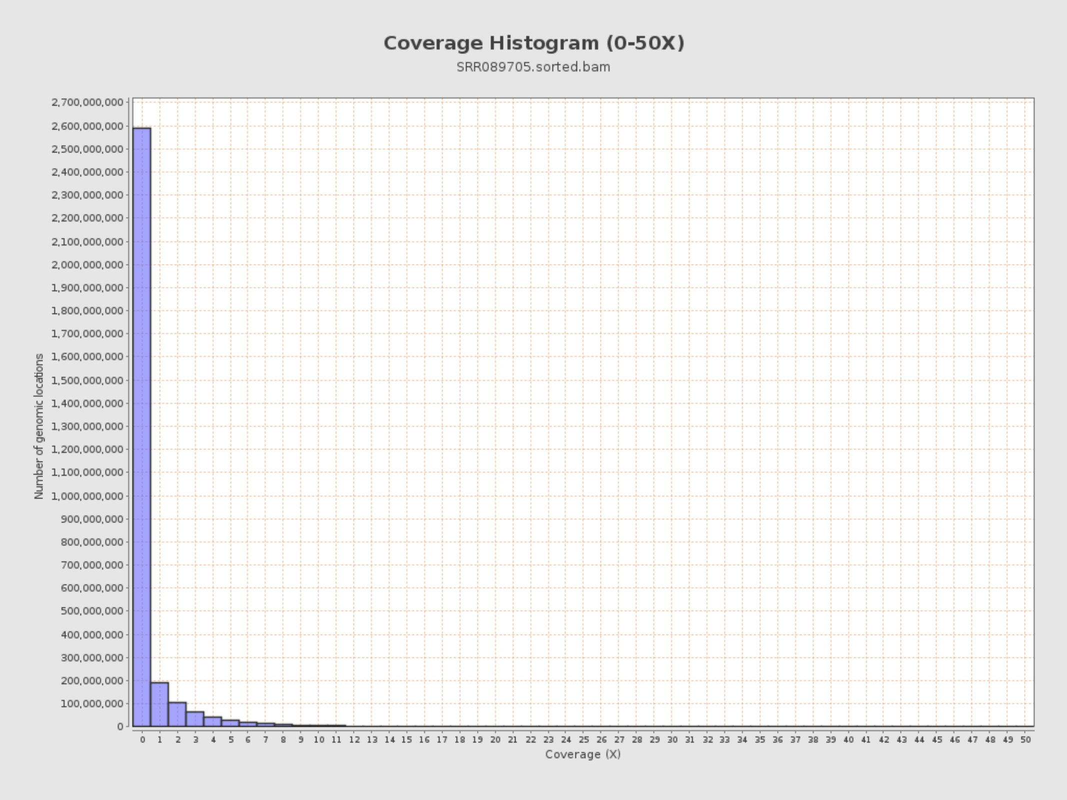
3. Results : Coverage across reference



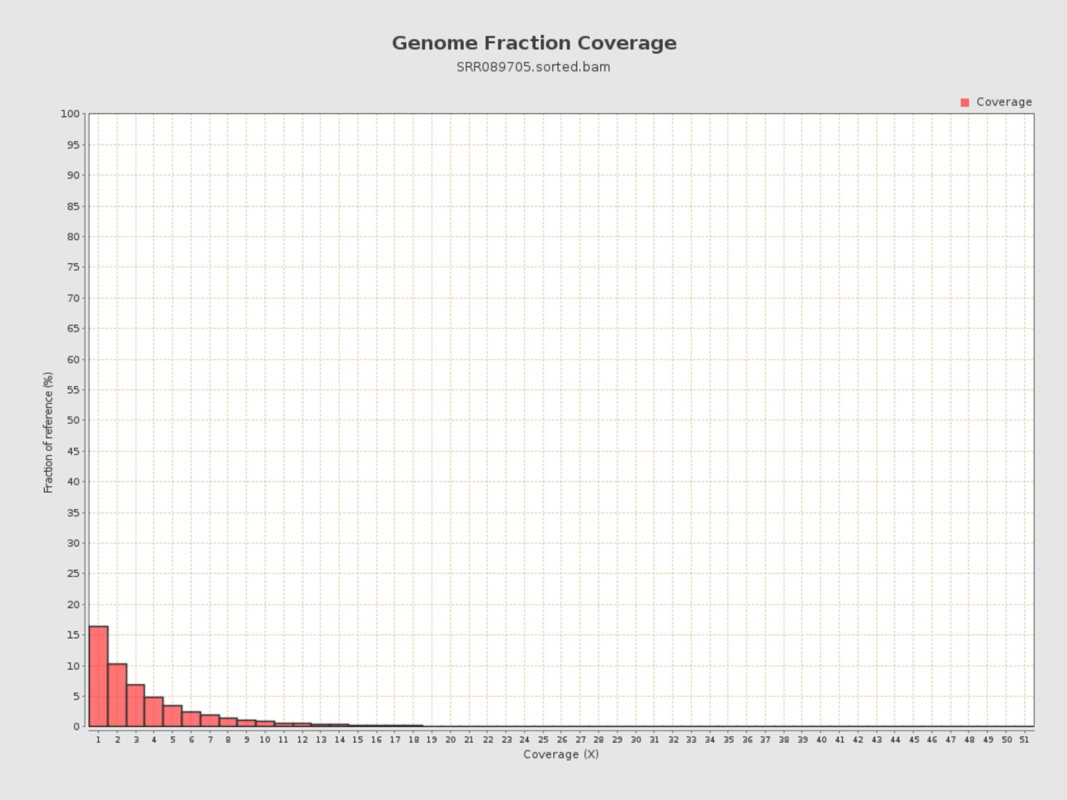
4. Results : Coverage Histogram



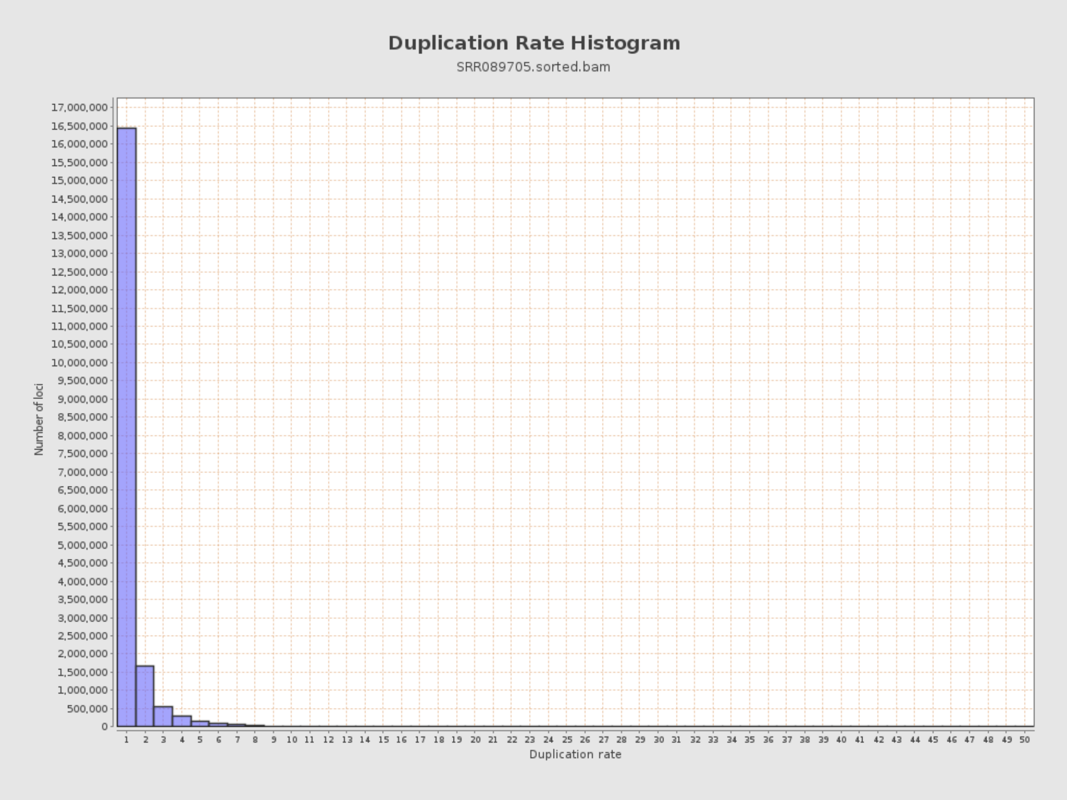
5. Results : Coverage Histogram (0-50X)



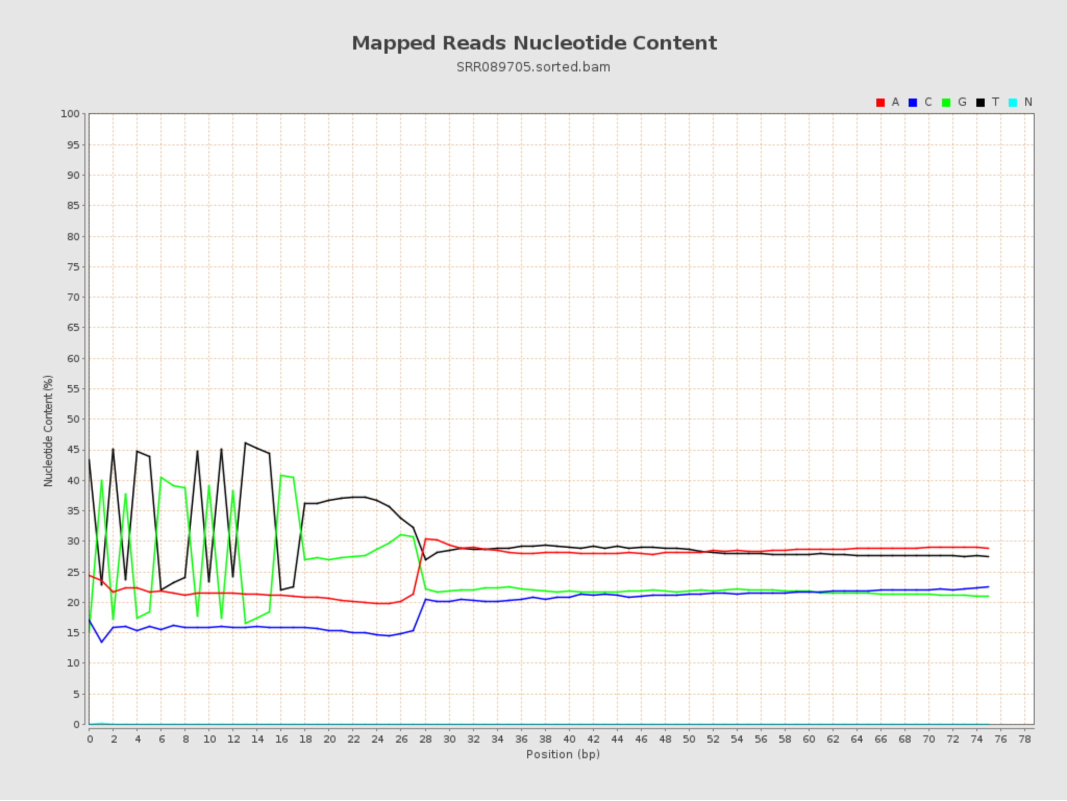
6. Results : Genome Fraction Coverage



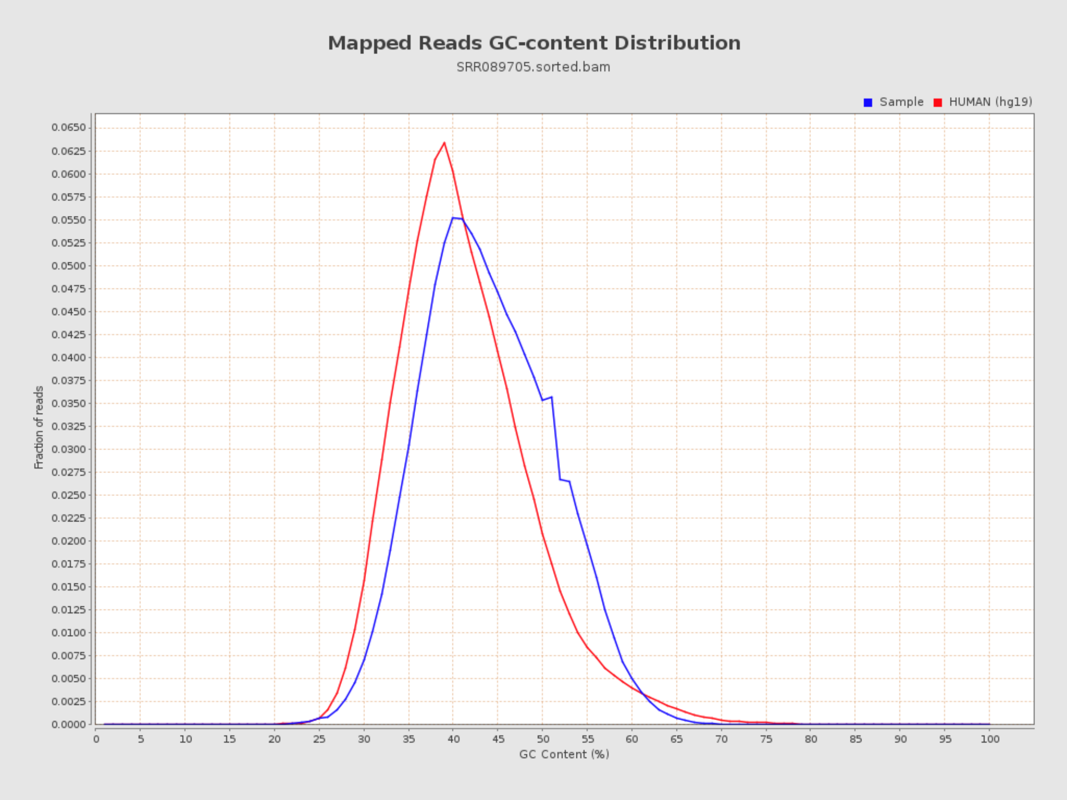
7. Results : Duplication Rate Histogram



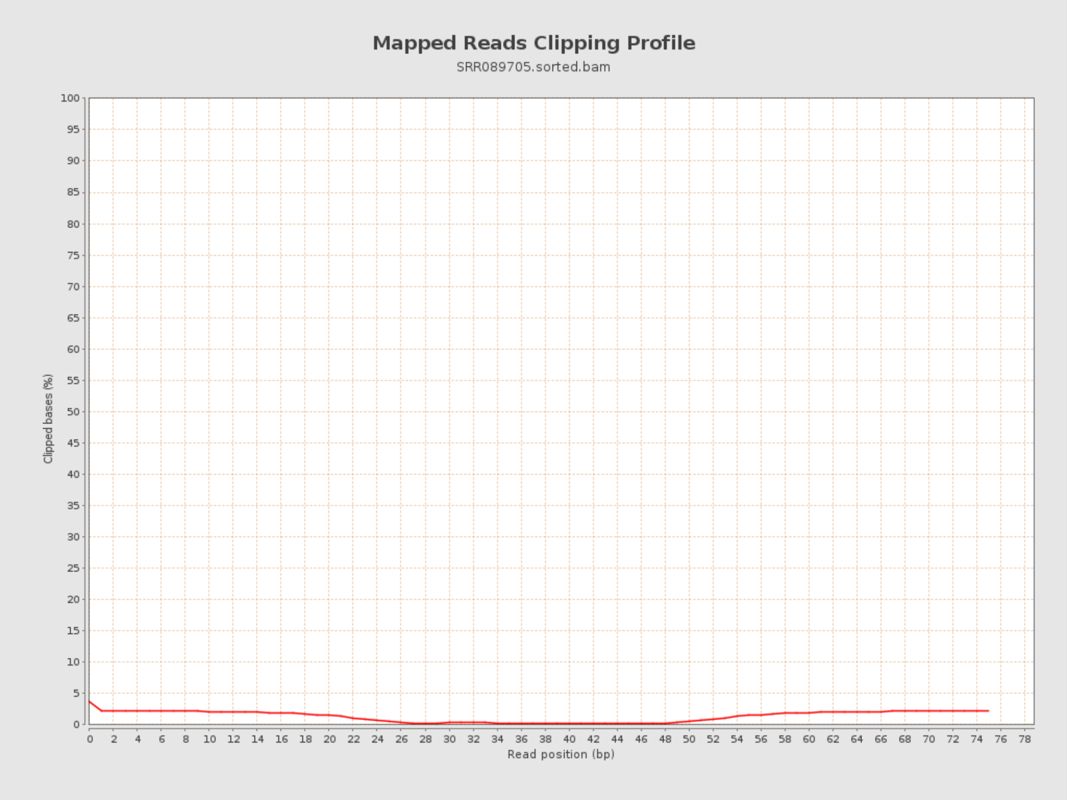
8. Results : Mapped Reads Nucleotide Content



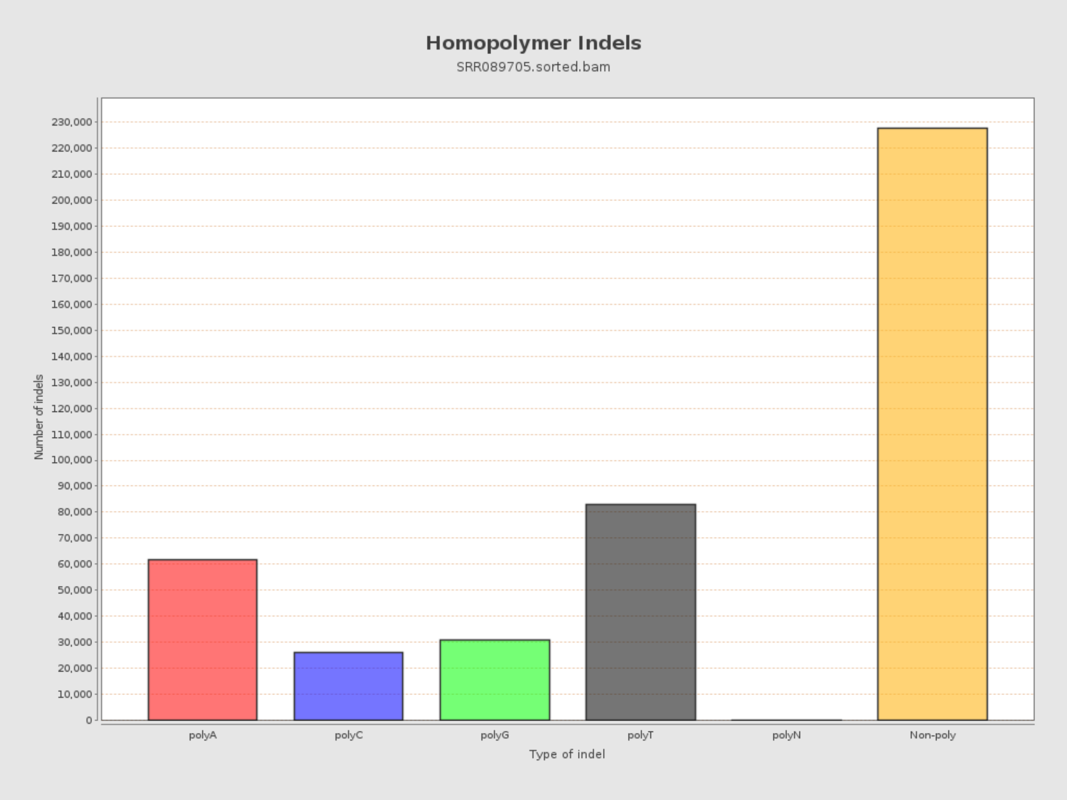
9. Results : Mapped Reads GC-content Distribution



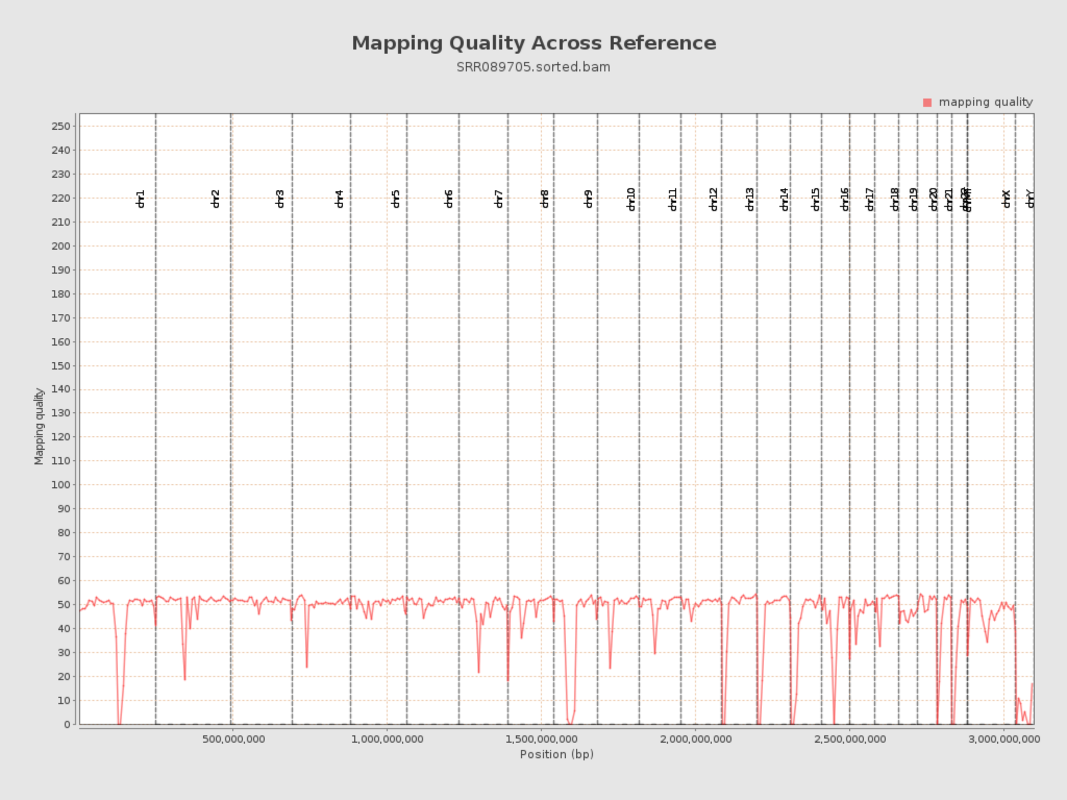
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram