Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 19:47:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089666.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_SRR089666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 19:47:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,931,467
Mapped reads	2,607,955 / 43.97%
Unmapped reads	3,323,512 / 56.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	116 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	62,561 / 1.05%
Duplication rate	1.86%
Clipped reads	571,623 / 9.64%

2.2. ACGT Content

Number/percentage of A's	35,589,431 / 29.66%
Number/percentage of C's	25,434,956 / 21.2%
Number/percentage of T's	34,037,125 / 28.37%
Number/percentage of G's	24,862,938 / 20.72%
Number/percentage of N's	68,222 / 0.06%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.2866

2.4. Mapping Quality

Mean Mapping Quality	39.73

2.5. Mismatches and indels

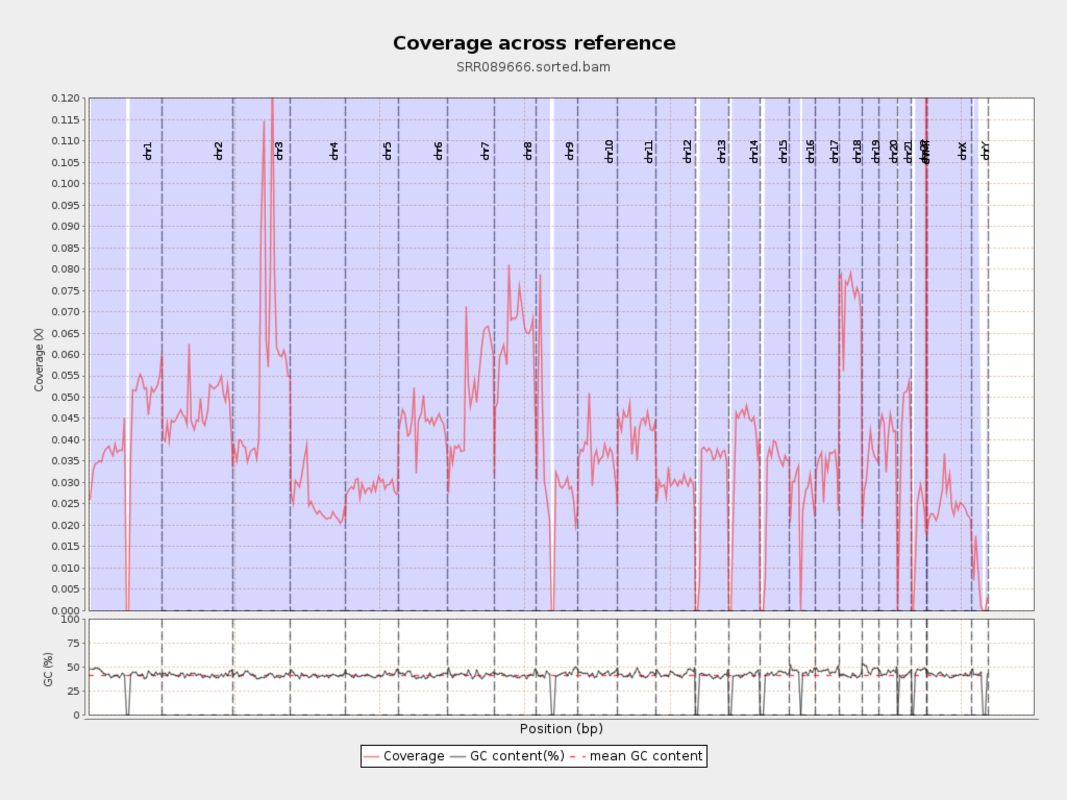
General error rate	1.33%
Mismatches	1,580,700
Insertions	8,499
Mapped reads with at least one insertion	0.33%
Deletions	16,140
Mapped reads with at least one deletion	0.62%
Homopolymer indels	37.77%

2.6. Chromosome stats

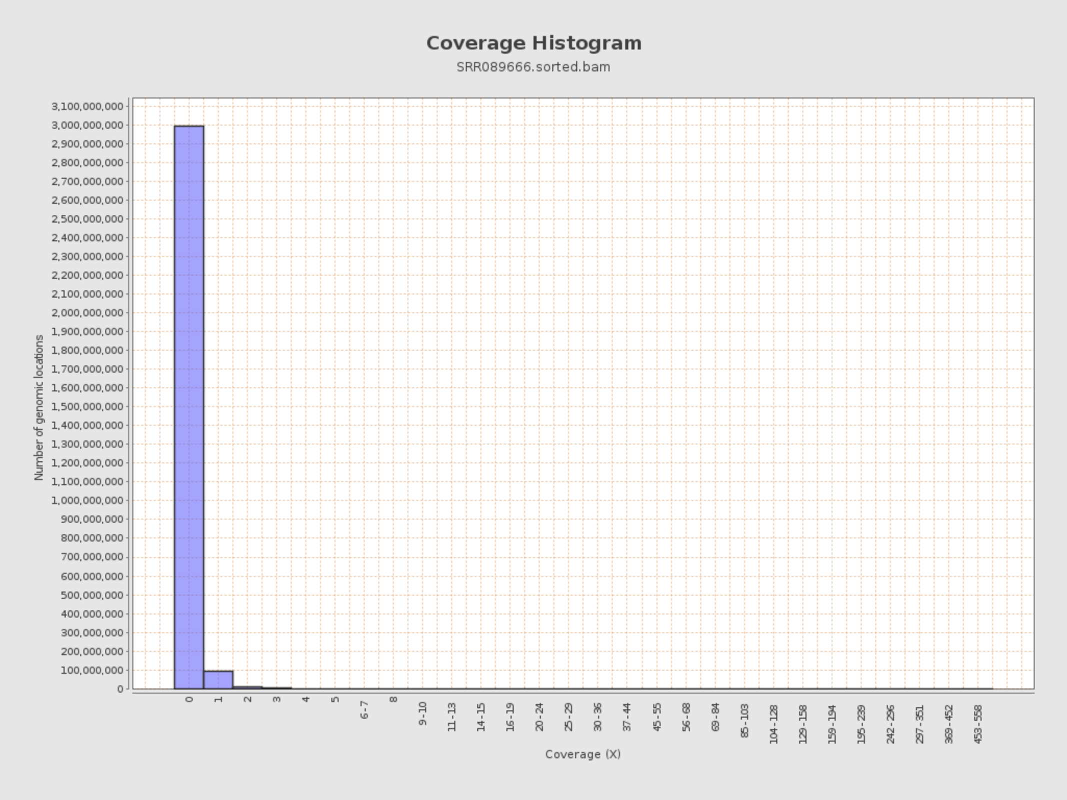
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10132718	0.0407	0.3323
chr2	243199373	11478256	0.0472	0.3976
chr3	198022430	11193785	0.0565	0.2763
chr4	191154276	4824398	0.0252	0.1809
chr5	180915260	5245688	0.029	0.1923
chr6	171115067	7562856	0.0442	0.2634
chr7	159138663	8088206	0.0508	0.4505

chr8	146364022	9376994	0.0641	0.4191
chr9	141213431	4287614	0.0304	0.2541
chr10	135534747	5003495	0.0369	0.269
chr11	135006516	5820143	0.0431	0.2714
chr12	133851895	3963541	0.0296	0.1993
chr13	115169878	3527691	0.0306	0.1967
chr14	107349540	3985776	0.0371	0.2313
chr15	102531392	2990476	0.0292	0.1917
chr16	90354753	2355439	0.0261	0.1958
chr17	81195210	2739535	0.0337	0.2208
chr18	78077248	5768313	0.0739	0.4046
chr19	59128983	2047916	0.0346	0.3181
chr20	63025520	2593432	0.0411	0.2341
chr21	48129895	1904215	0.0396	0.2335
chr22	51304566	932524	0.0182	0.1499
chrMT	16571	36707	2.2151	2.3305
chrX	155270560	3822375	0.0246	0.2179
chrY	59373566	333914	0.0056	0.1031

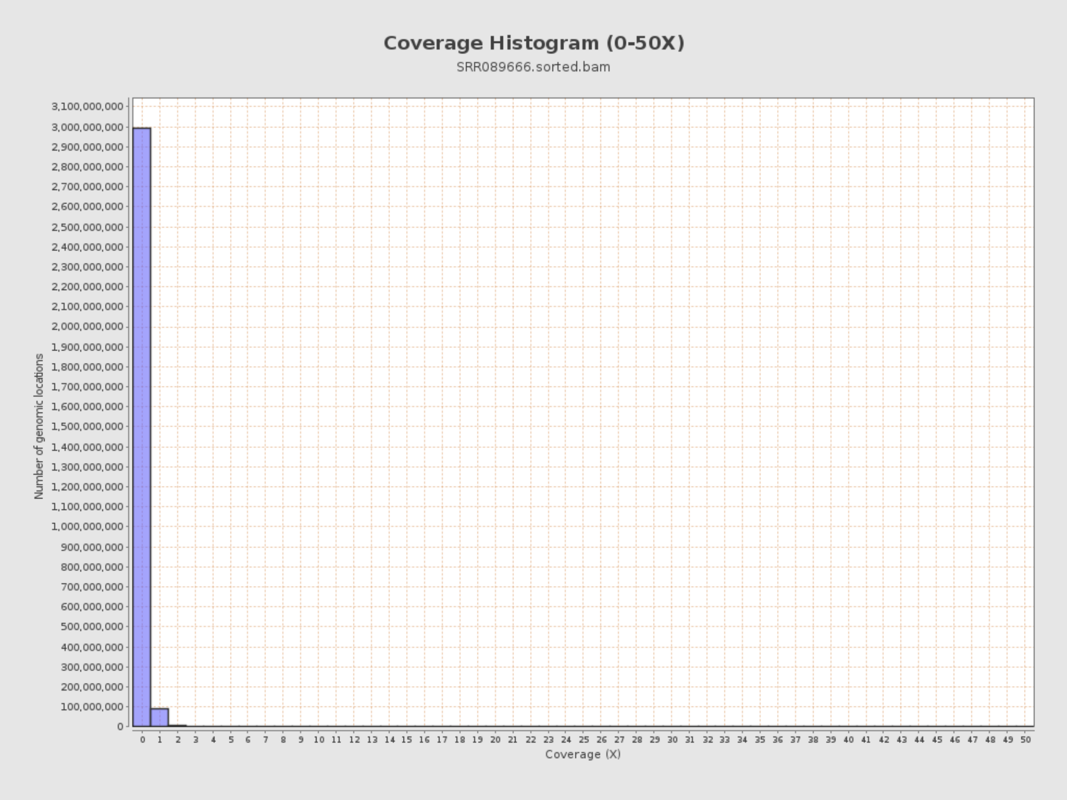
3. Results : Coverage across reference



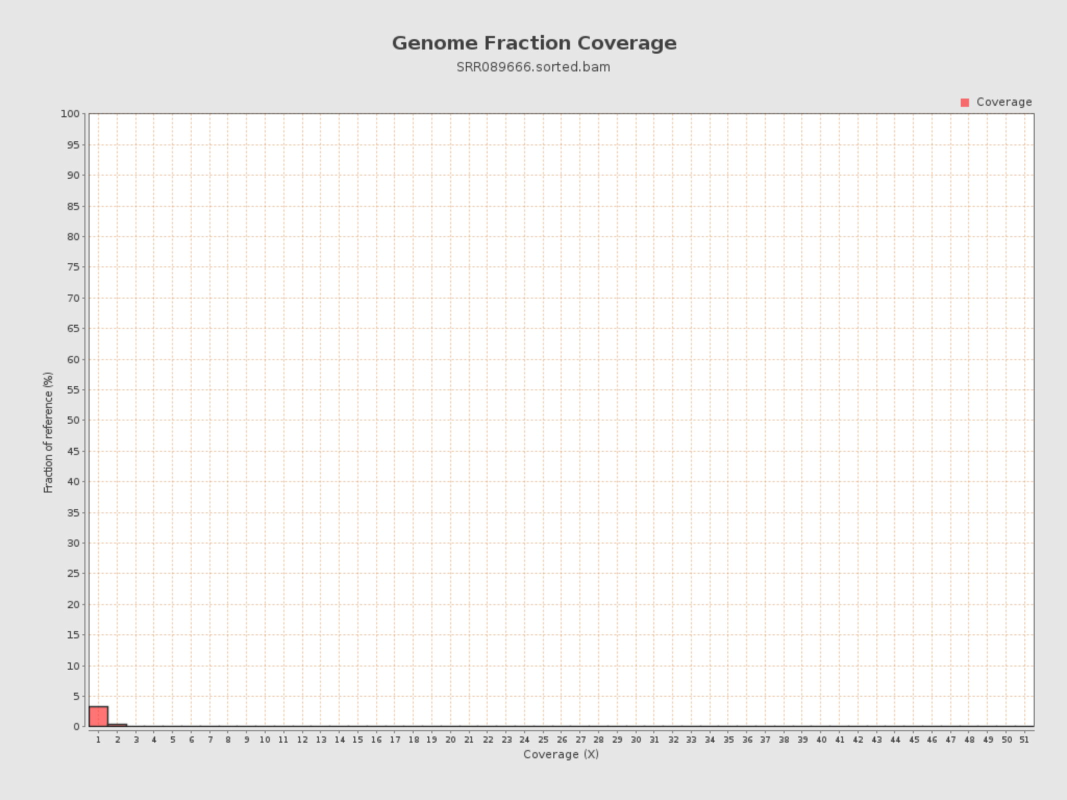
4. Results : Coverage Histogram



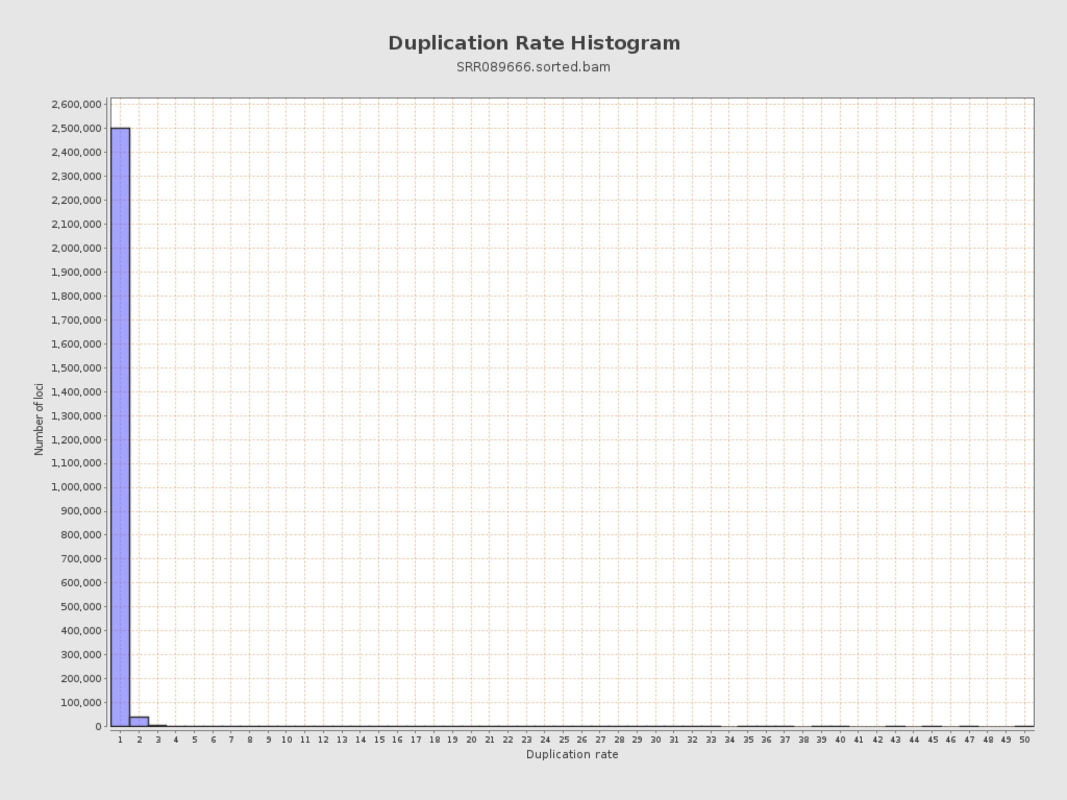
5. Results : Coverage Histogram (0-50X)



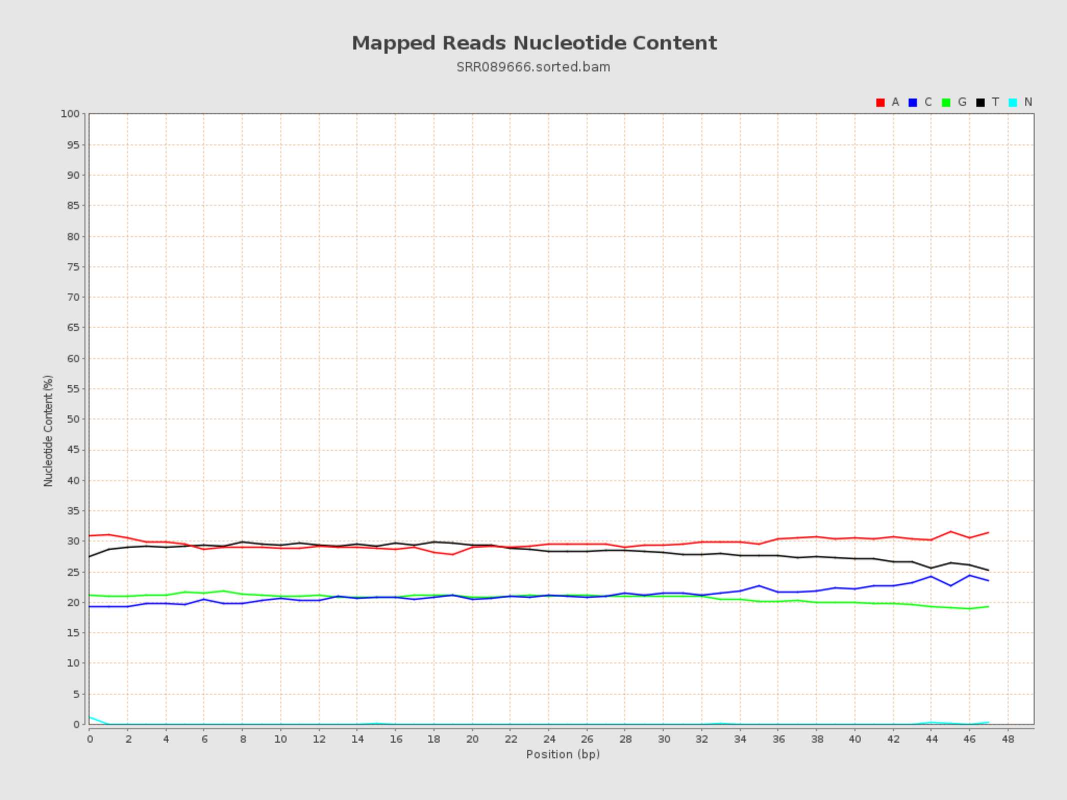
6. Results : Genome Fraction Coverage



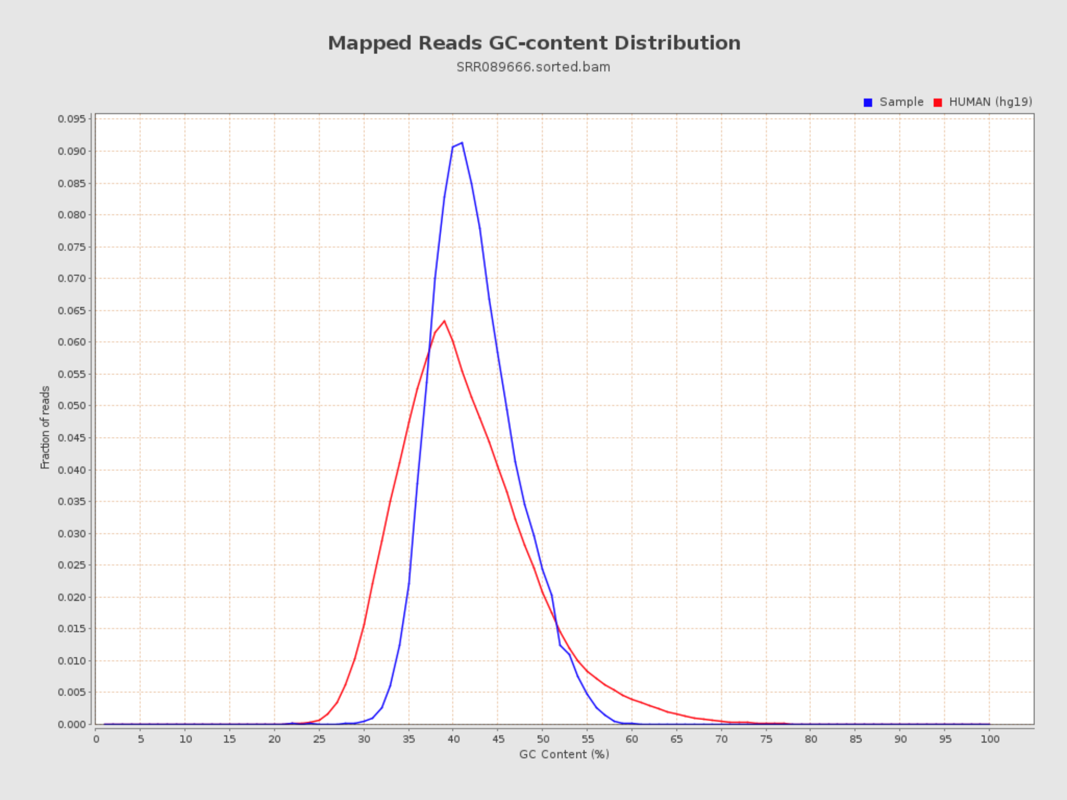
7. Results : Duplication Rate Histogram



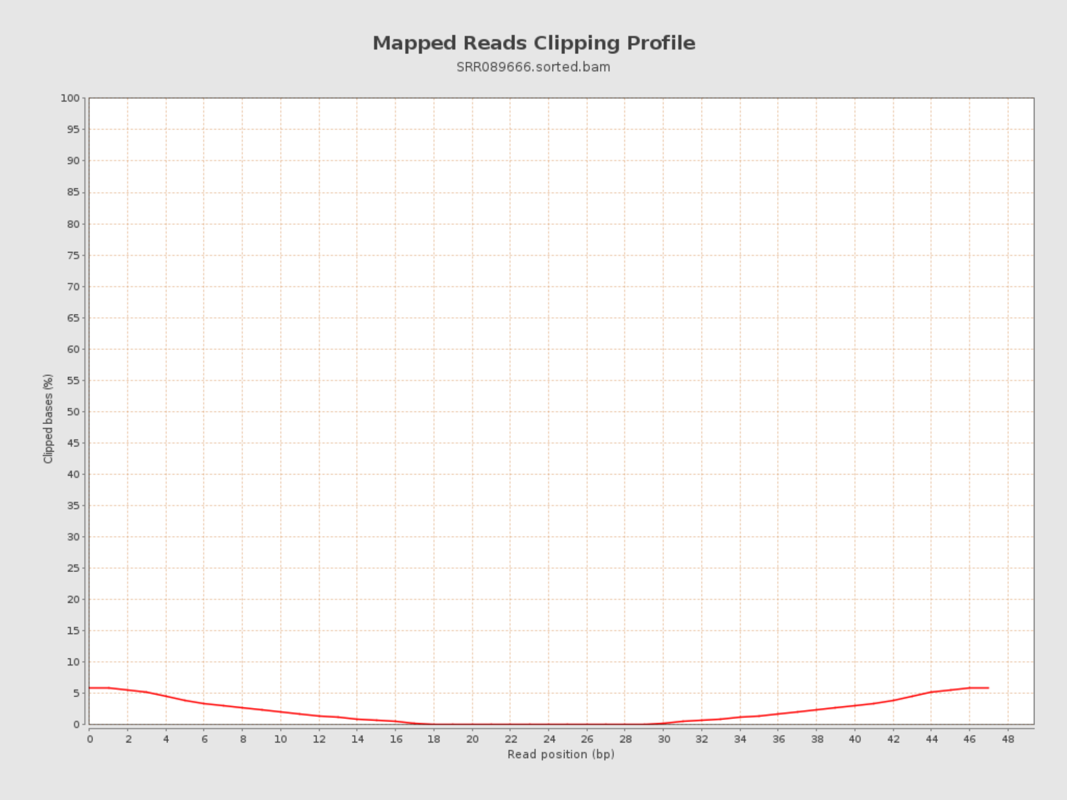
8. Results : Mapped Reads Nucleotide Content



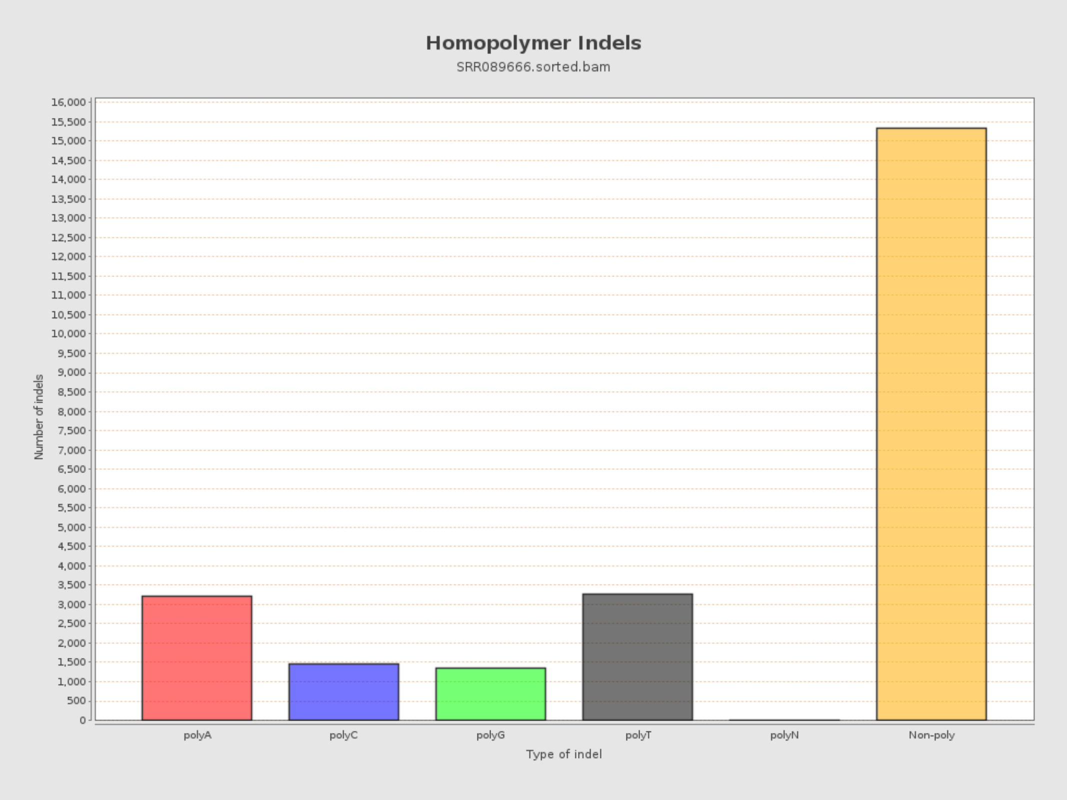
9. Results : Mapped Reads GC-content Distribution



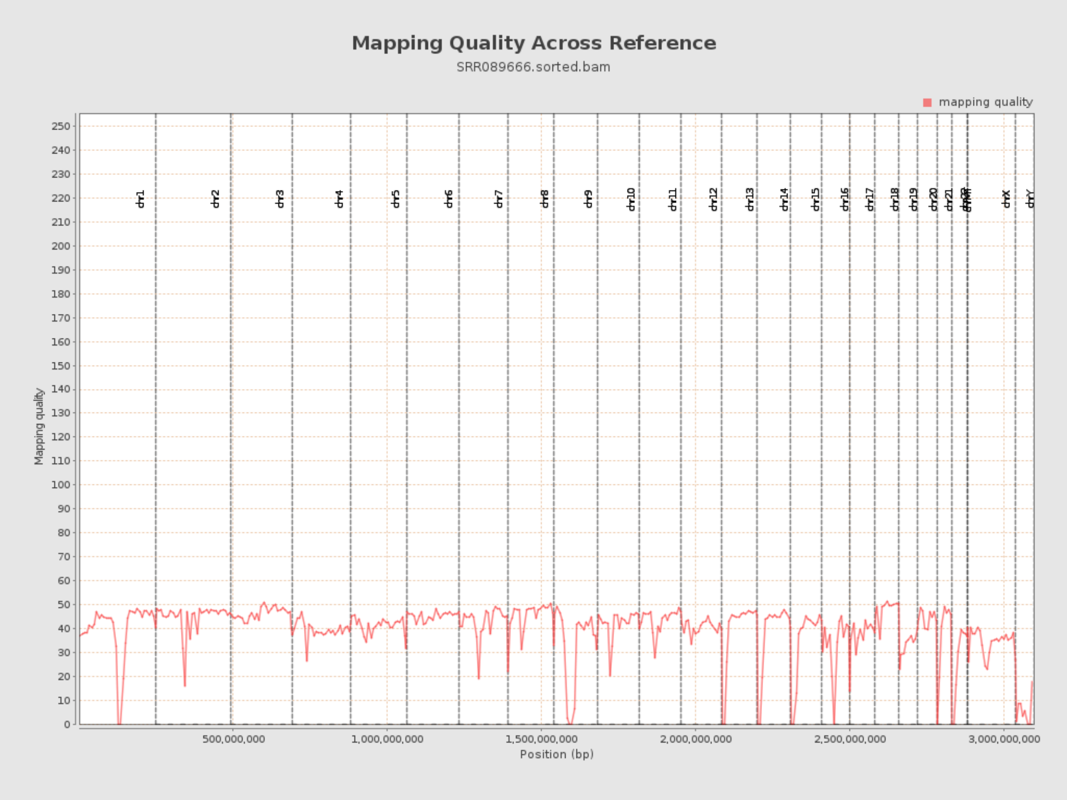
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram