Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 16:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089598.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_SRR089598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 16:27:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,998,489
Mapped reads	6,584,472 / 73.17%
Unmapped reads	2,414,017 / 26.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	216 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,873,424 / 20.82%
Duplication rate	21.97%
Clipped reads	1,075,076 / 11.95%

2.2. ACGT Content

Number/percentage of A's	98,405,013 / 32.14%
Number/percentage of C's	60,288,515 / 19.69%
Number/percentage of T's	77,131,629 / 25.19%
Number/percentage of G's	70,333,279 / 22.97%
Number/percentage of N's	40,210 / 0.01%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0989

Standard Deviation	0.8504

2.4. Mapping Quality

Mean Mapping Quality	41.66

2.5. Mismatches and indels

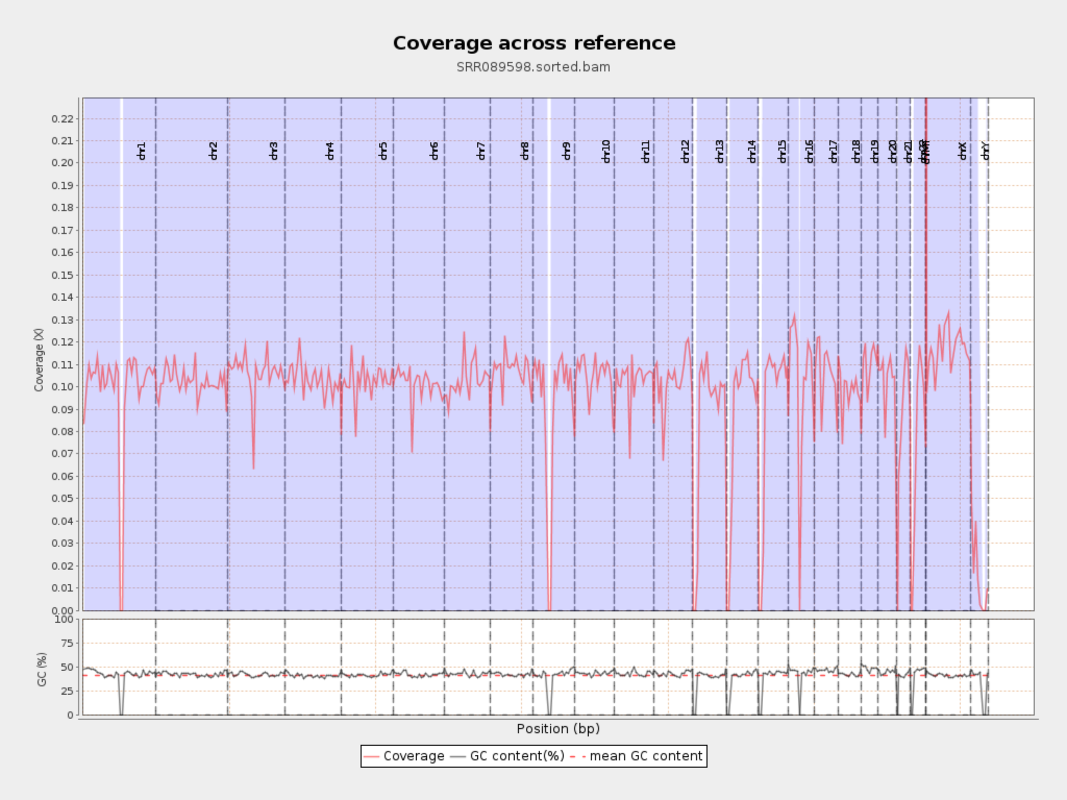
General error rate	0.89%
Mismatches	2,704,252
Insertions	17,040
Mapped reads with at least one insertion	0.26%
Deletions	40,346
Mapped reads with at least one deletion	0.61%
Homopolymer indels	41.03%

2.6. Chromosome stats

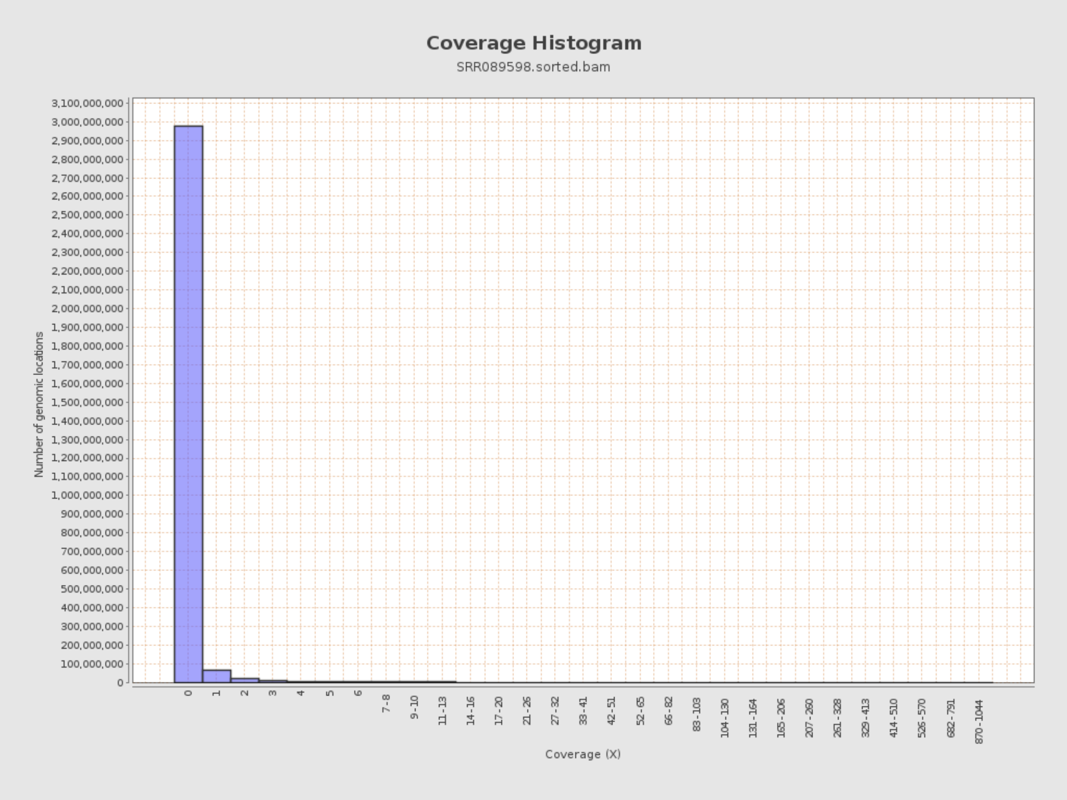
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24478740	0.0982	0.9006
chr2	243199373	24863942	0.1022	0.9276
chr3	198022430	20983767	0.106	0.8353
chr4	191154276	19803019	0.1036	0.8612
chr5	180915260	18568240	0.1026	0.8196
chr6	171115067	17281260	0.101	0.8615
chr7	159138663	16458768	0.1034	0.8746

chr8	146364022	15692215	0.1072	1.0116
chr9	141213431	12772367	0.0904	0.7878
chr10	135534747	14309251	0.1056	0.87
chr11	135006516	13864286	0.1027	0.8928
chr12	133851895	13921300	0.104	0.83
chr13	115169878	9734873	0.0845	0.7458
chr14	107349540	9431464	0.0879	0.7915
chr15	102531392	8910234	0.0869	0.7384
chr16	90354753	9045463	0.1001	0.8209
chr17	81195210	8701471	0.1072	0.829
chr18	78077248	7656817	0.0981	0.8359
chr19	59128983	6473150	0.1095	0.8768
chr20	63025520	6438416	0.1022	0.8252
chr21	48129895	4048866	0.0841	0.7893
chr22	51304566	3754216	0.0732	0.7122
chrMT	16571	65321	3.9419	7.042
chrX	155270560	18109495	0.1166	0.9075
chrY	59373566	891167	0.015	0.2916

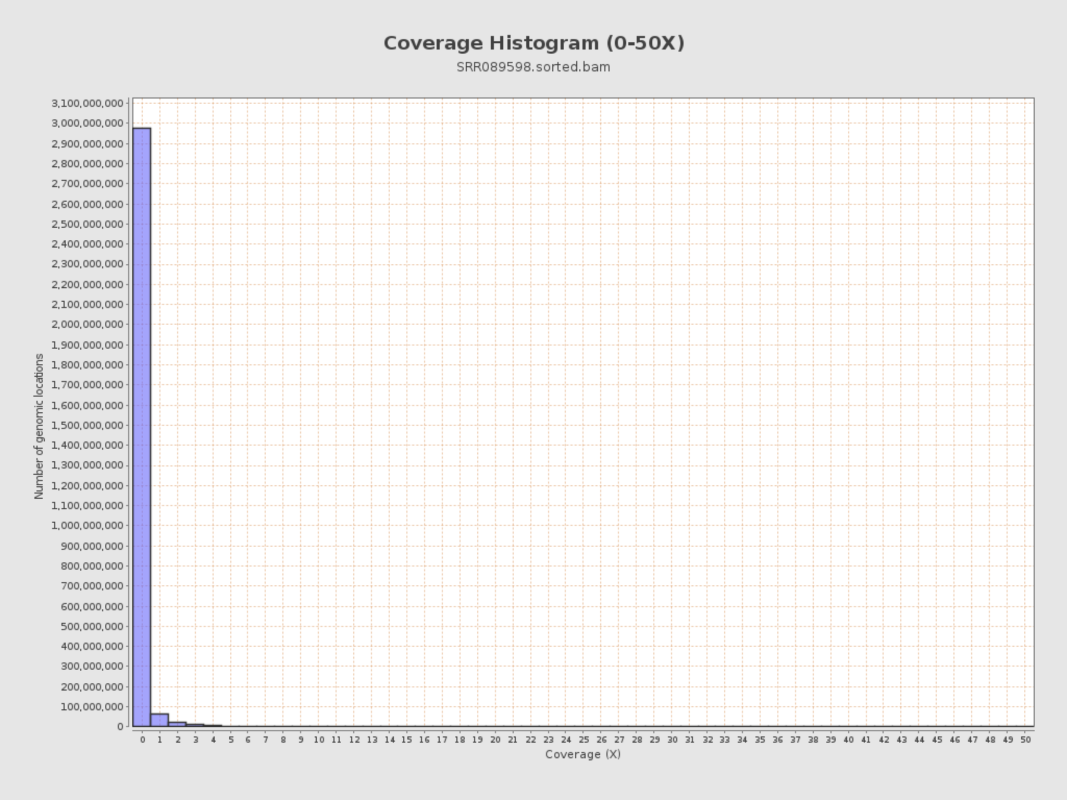
3. Results : Coverage across reference



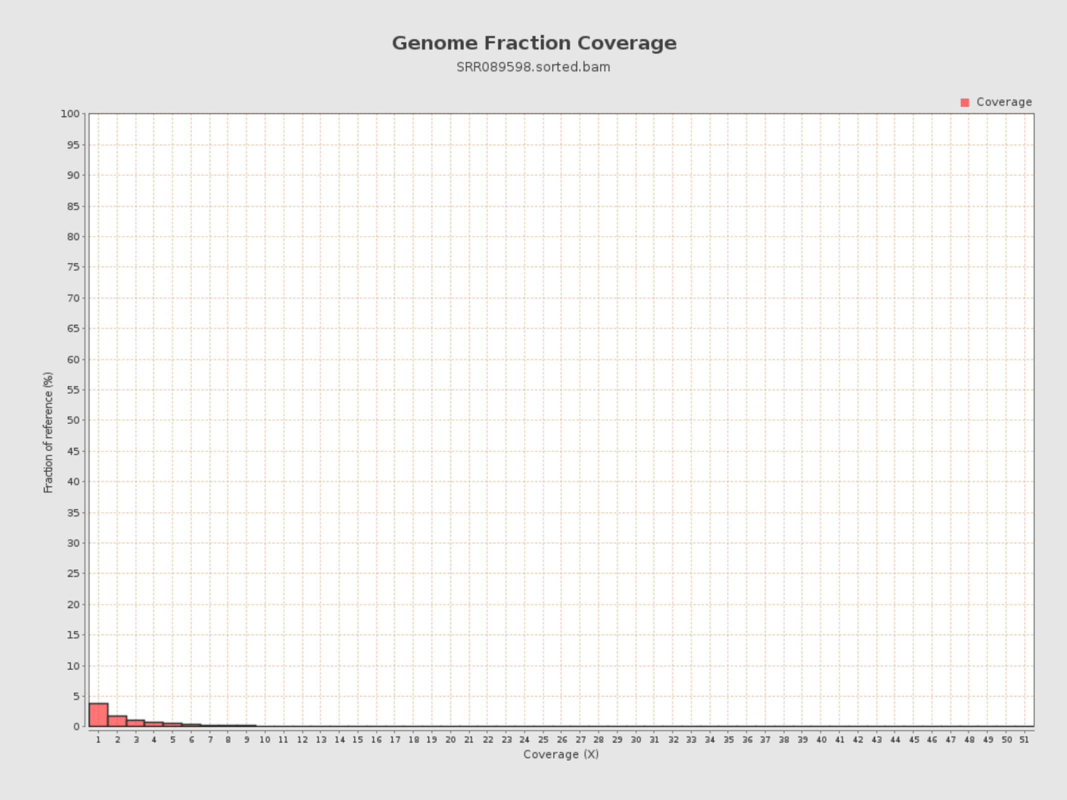
4. Results : Coverage Histogram



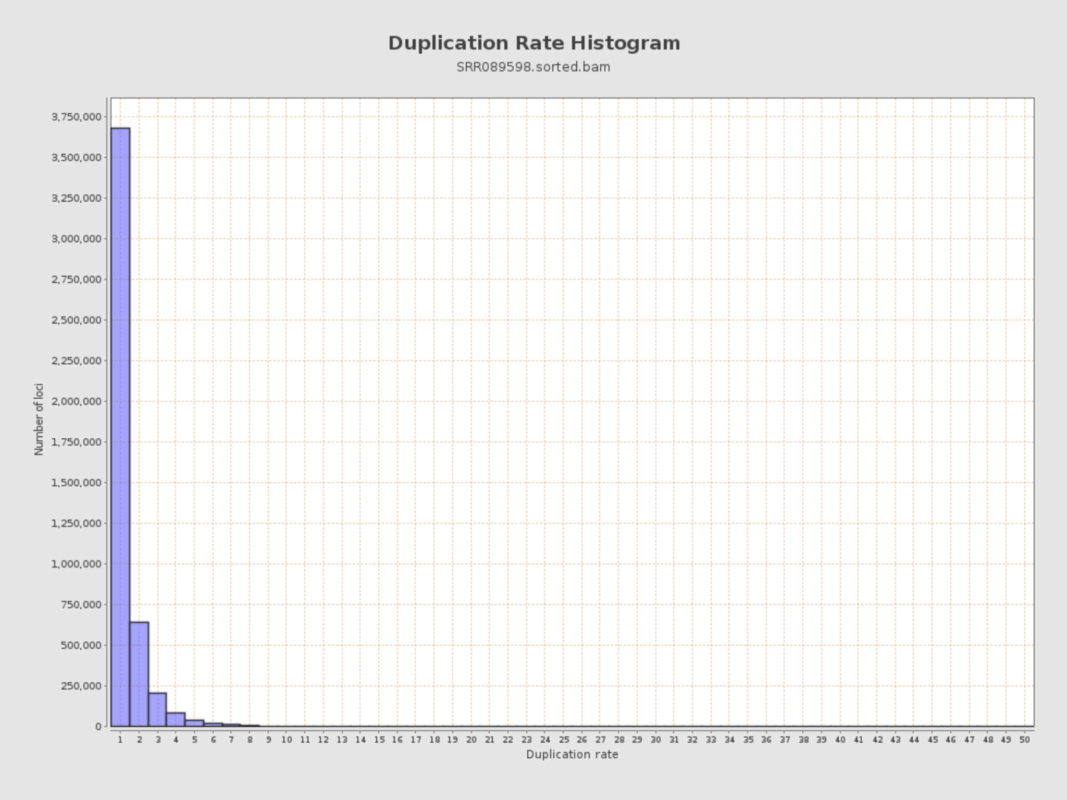
5. Results : Coverage Histogram (0-50X)



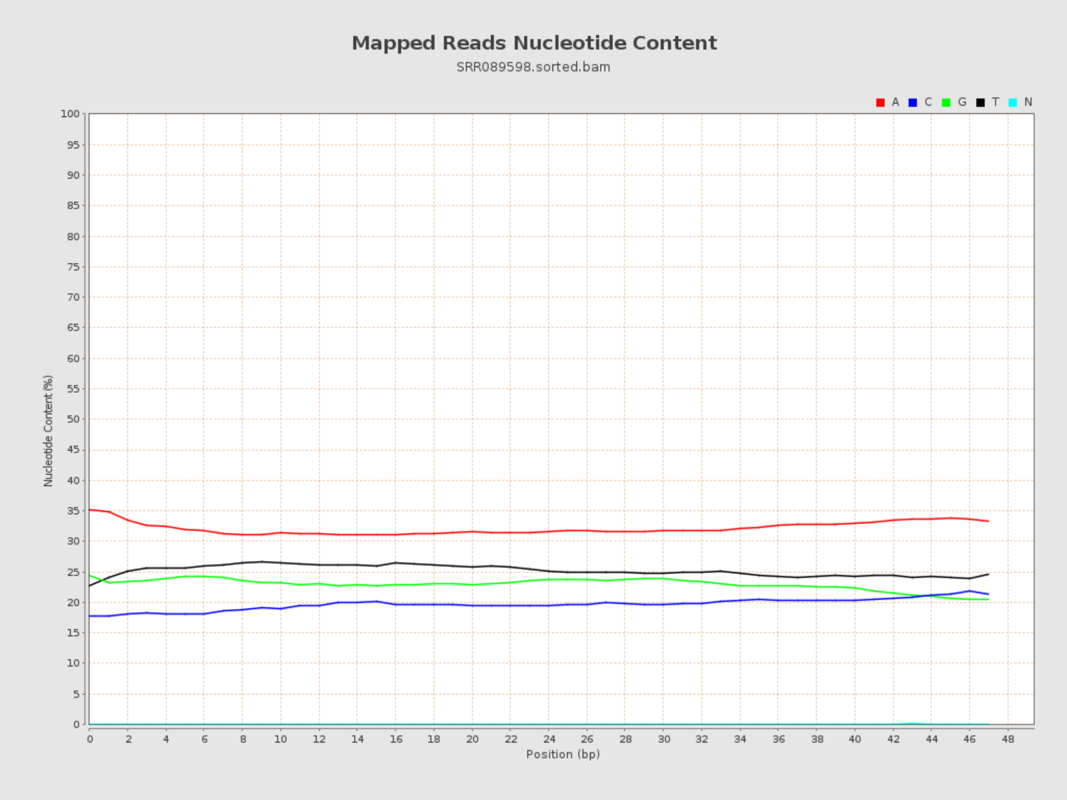
6. Results : Genome Fraction Coverage



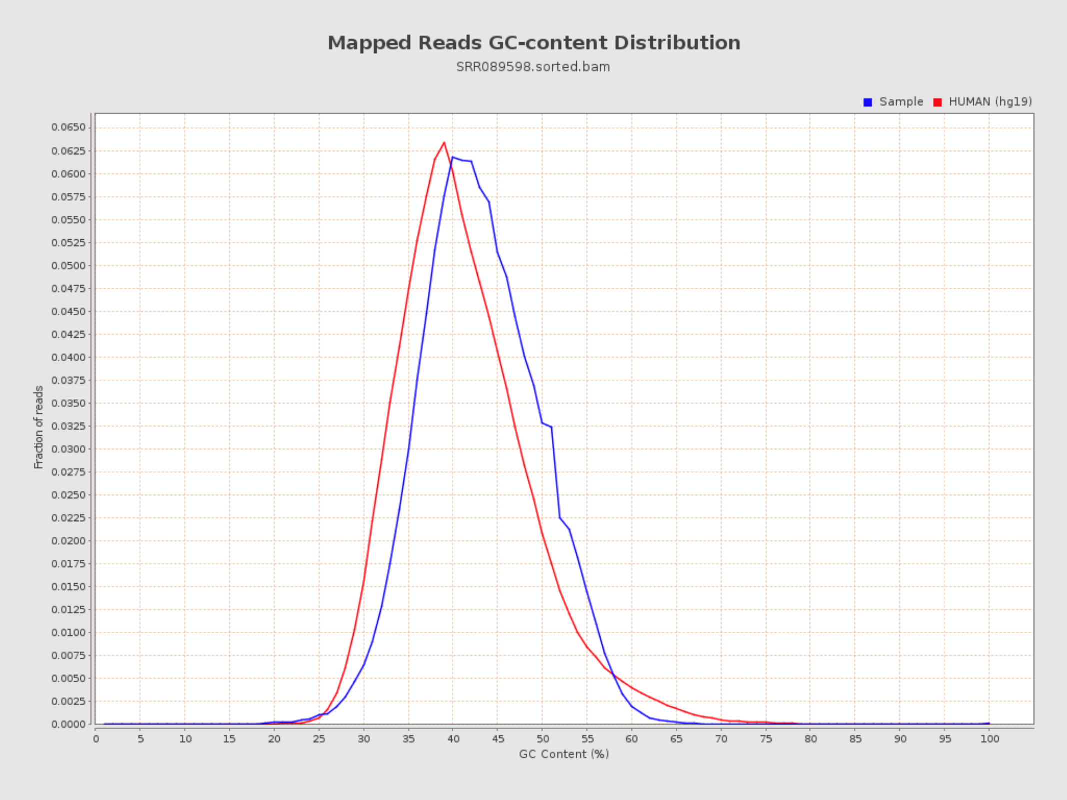
7. Results : Duplication Rate Histogram



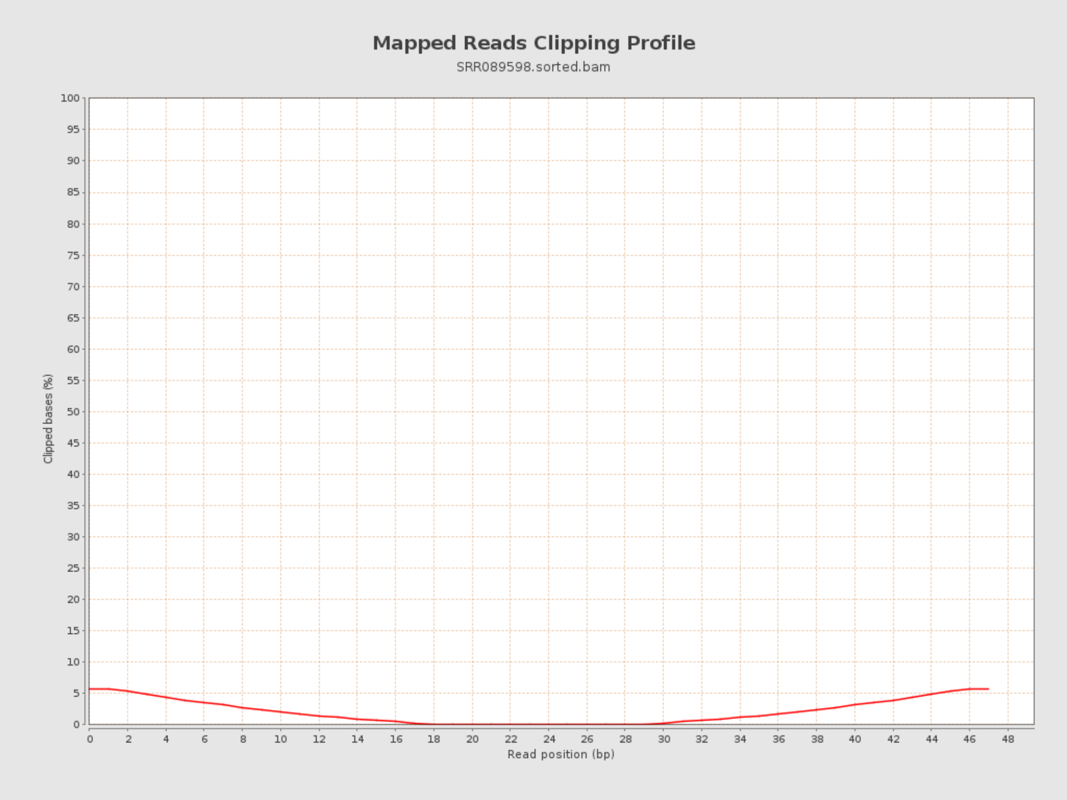
8. Results : Mapped Reads Nucleotide Content



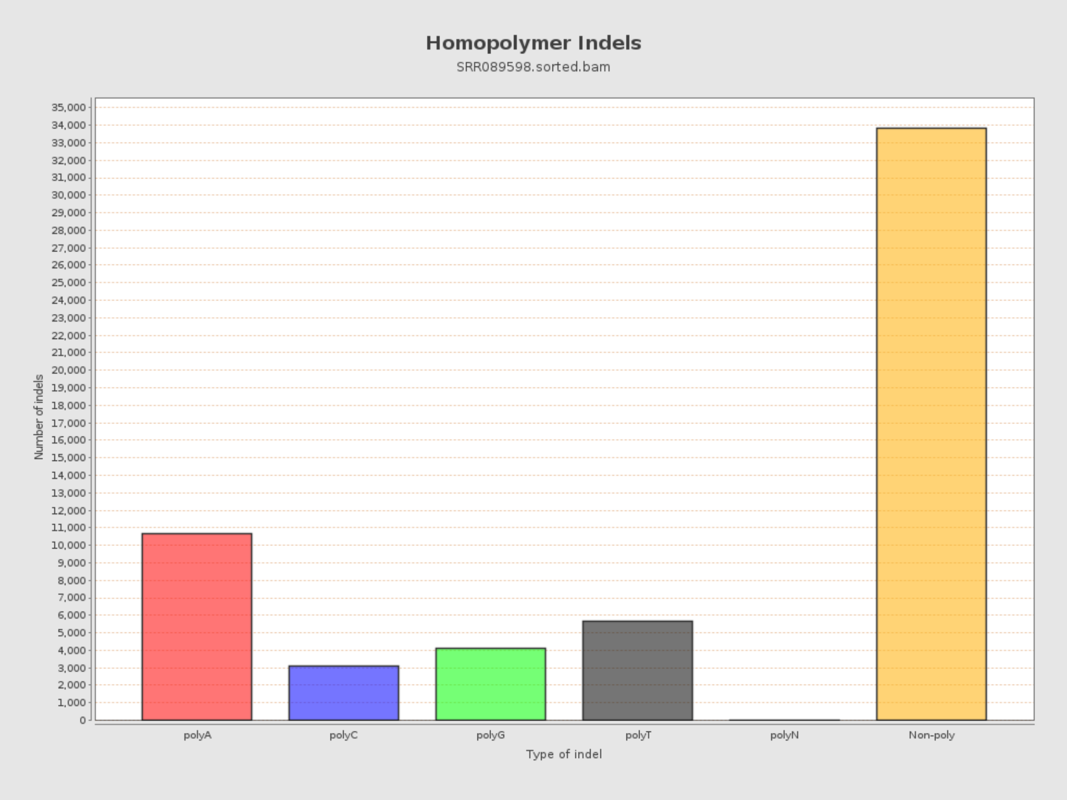
9. Results : Mapped Reads GC-content Distribution



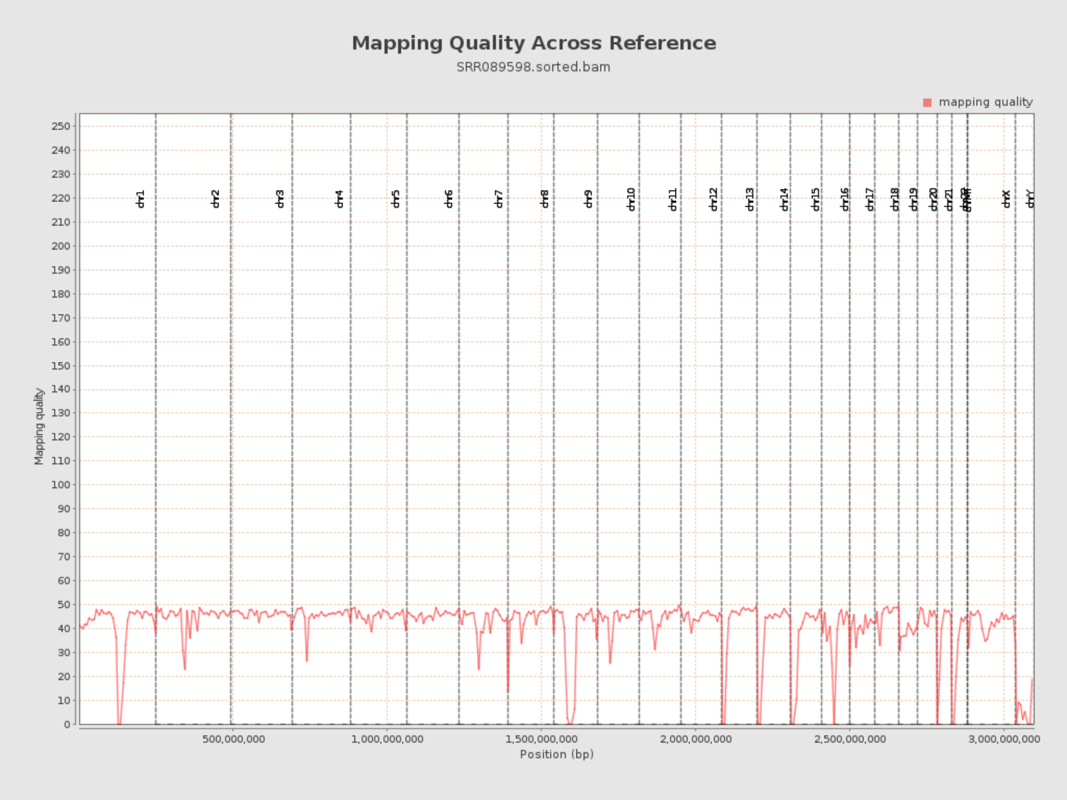
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram