Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 19:24:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089664.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_SRR089664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 19:24:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,269,964
Mapped reads	17,919,308 / 84.25%
Unmapped reads	3,350,656 / 15.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	709 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,482,785 / 6.97%
Duplication rate	5.98%
Clipped reads	1,929,130 / 9.07%

2.2. ACGT Content

Number/percentage of A's	246,155,336 / 29.23%
Number/percentage of C's	175,493,676 / 20.84%
Number/percentage of T's	239,948,720 / 28.49%
Number/percentage of G's	180,516,901 / 21.44%
Number/percentage of N's	16,520 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.2721

Standard Deviation	1.5616

2.4. Mapping Quality

Mean Mapping Quality	42.32

2.5. Mismatches and indels

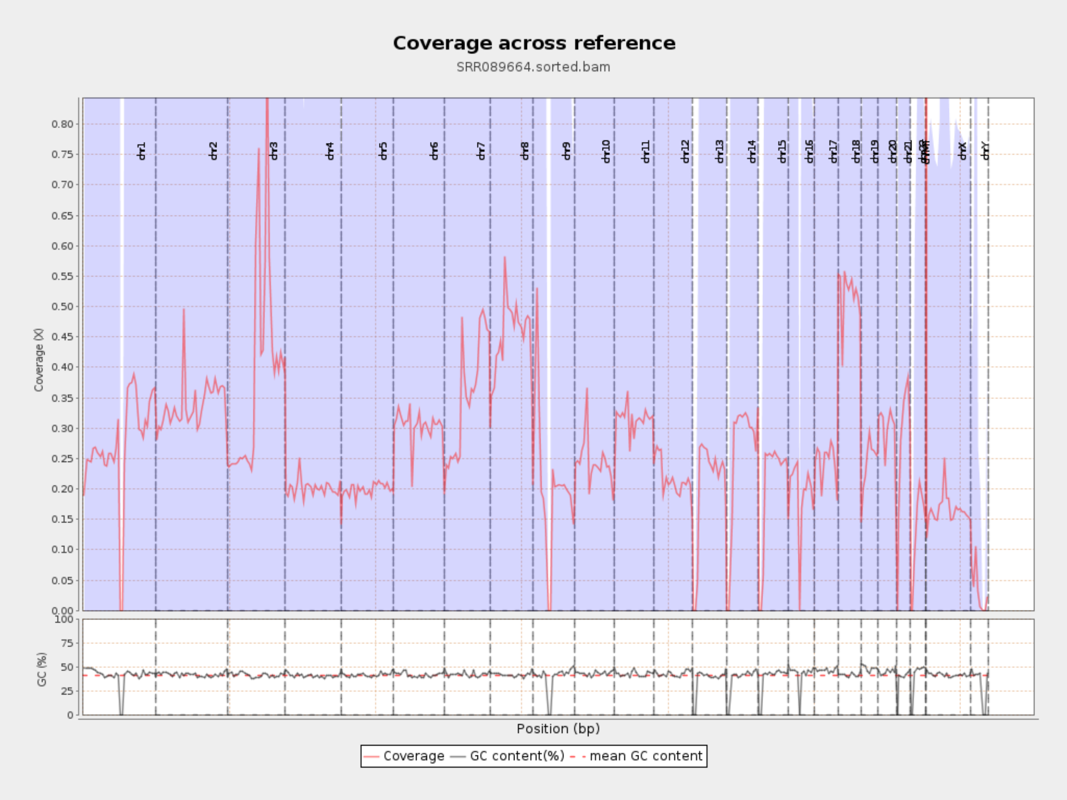
General error rate	0.53%
Mismatches	4,377,225
Insertions	34,705
Mapped reads with at least one insertion	0.19%
Deletions	114,287
Mapped reads with at least one deletion	0.64%
Homopolymer indels	45.54%

2.6. Chromosome stats

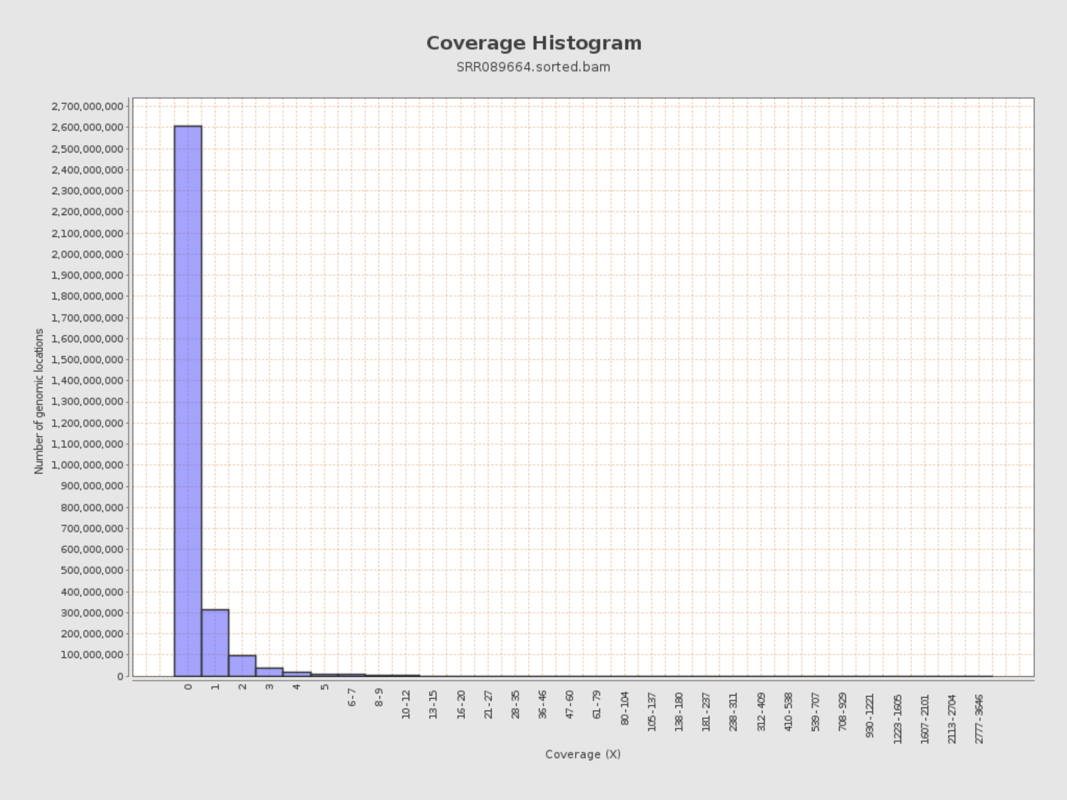
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68243058	0.2738	1.9575
chr2	243199373	82301672	0.3384	2.5546
chr3	198022430	76480855	0.3862	1.1045
chr4	191154276	38587093	0.2019	0.7599
chr5	180915260	36108358	0.1996	0.7211
chr6	171115067	52059057	0.3042	1.1019
chr7	159138663	56232941	0.3534	2.619

chr8	146364022	66647996	0.4554	2.2966
chr9	141213431	29419693	0.2083	1.5818
chr10	135534747	33227703	0.2452	1.5427
chr11	135006516	42294064	0.3133	1.537
chr12	133851895	29241294	0.2185	0.8019
chr13	115169878	23653106	0.2054	0.7165
chr14	107349540	27563090	0.2568	0.9954
chr15	102531392	20670330	0.2016	0.7131
chr16	90354753	16966270	0.1878	0.8546
chr17	81195210	20121029	0.2478	0.9659
chr18	78077248	40528805	0.5191	2.3439
chr19	59128983	14606826	0.247	1.9157
chr20	63025520	18937335	0.3005	0.9671
chr21	48129895	13318593	0.2767	1.0296
chr22	51304566	6788231	0.1323	0.566
chrMT	16571	566471	34.1845	26.5548
chrX	155270560	25775029	0.166	1.1377
chrY	59373566	1961417	0.033	0.568

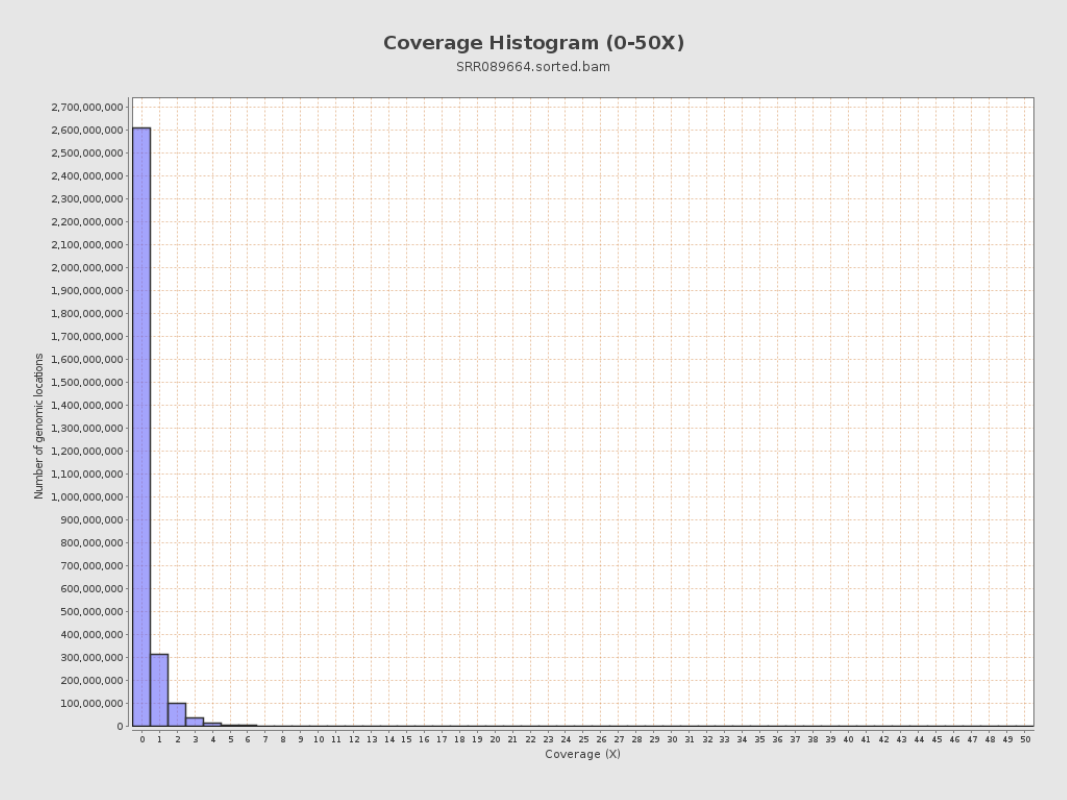
3. Results : Coverage across reference



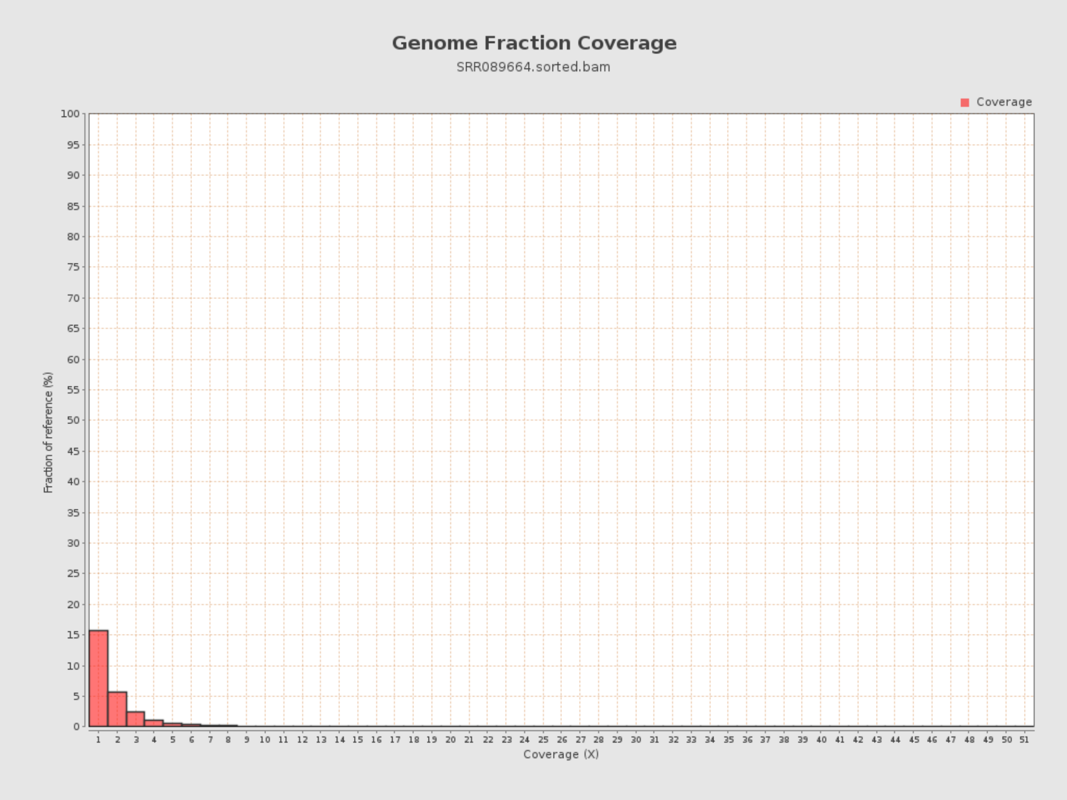
4. Results : Coverage Histogram



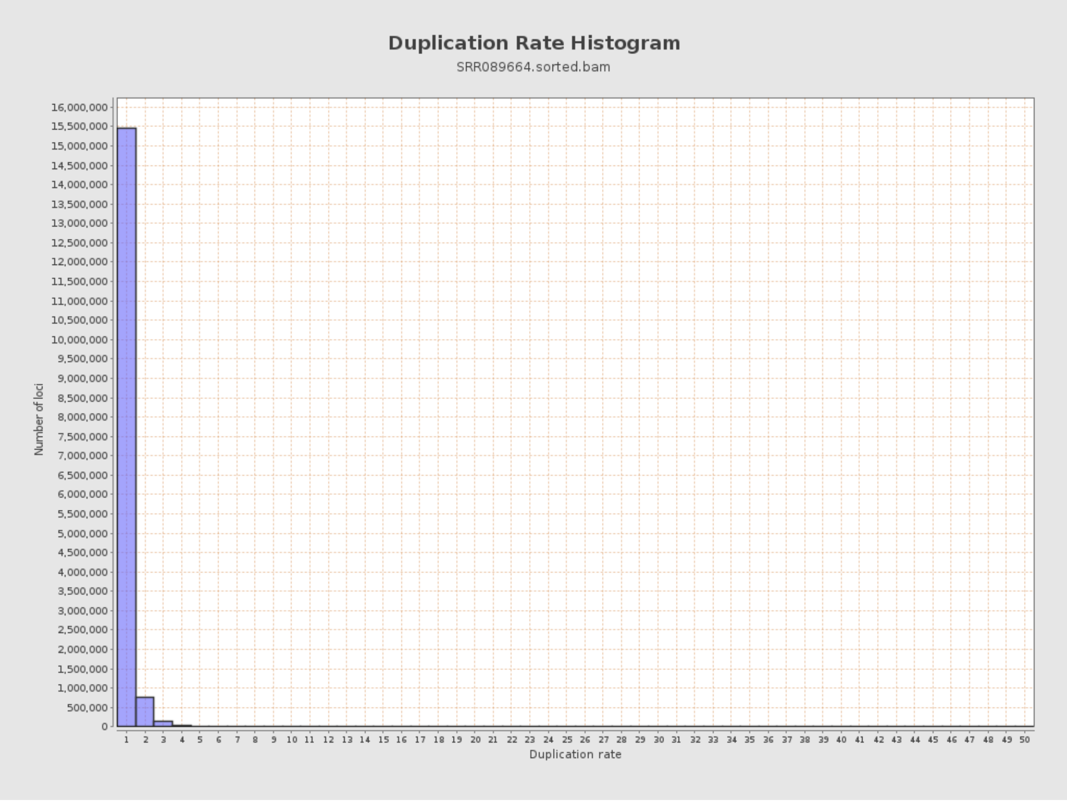
5. Results : Coverage Histogram (0-50X)



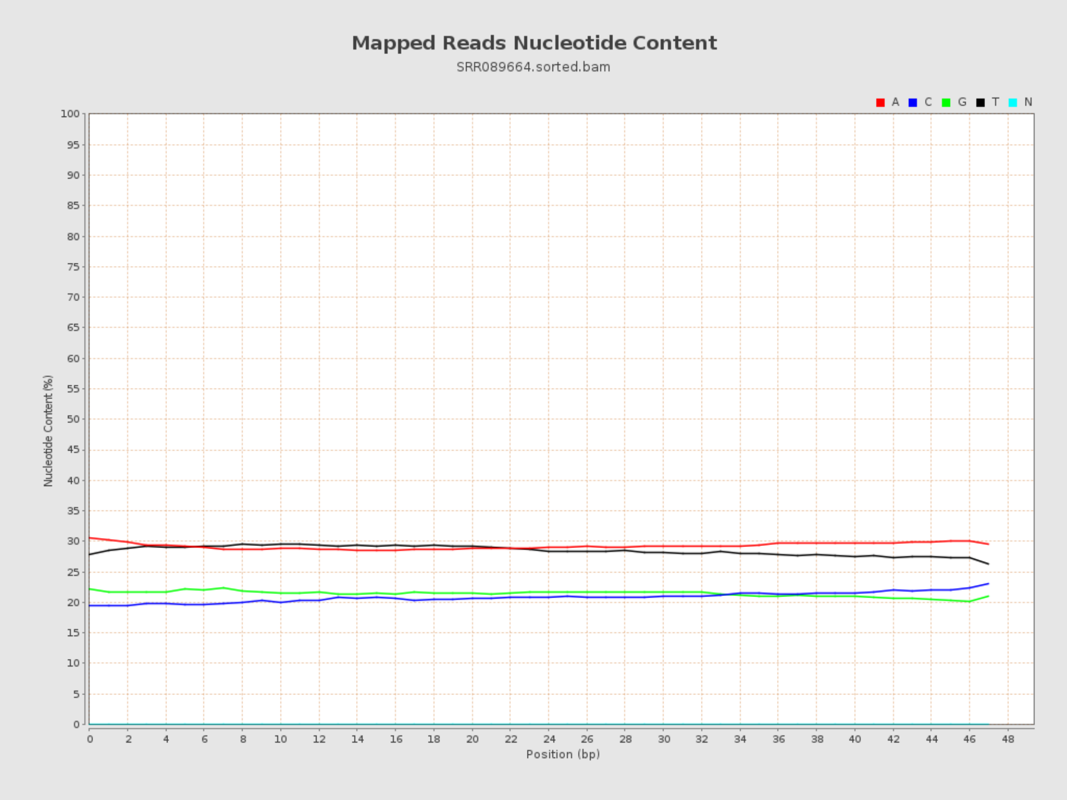
6. Results : Genome Fraction Coverage



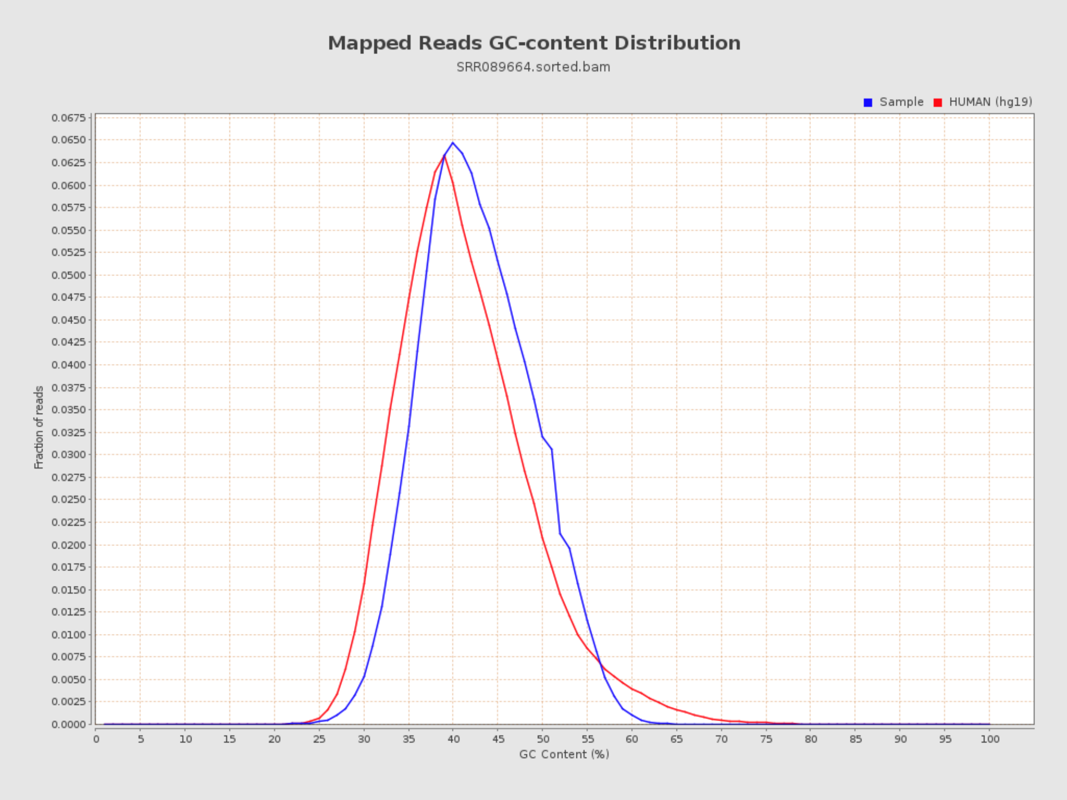
7. Results : Duplication Rate Histogram



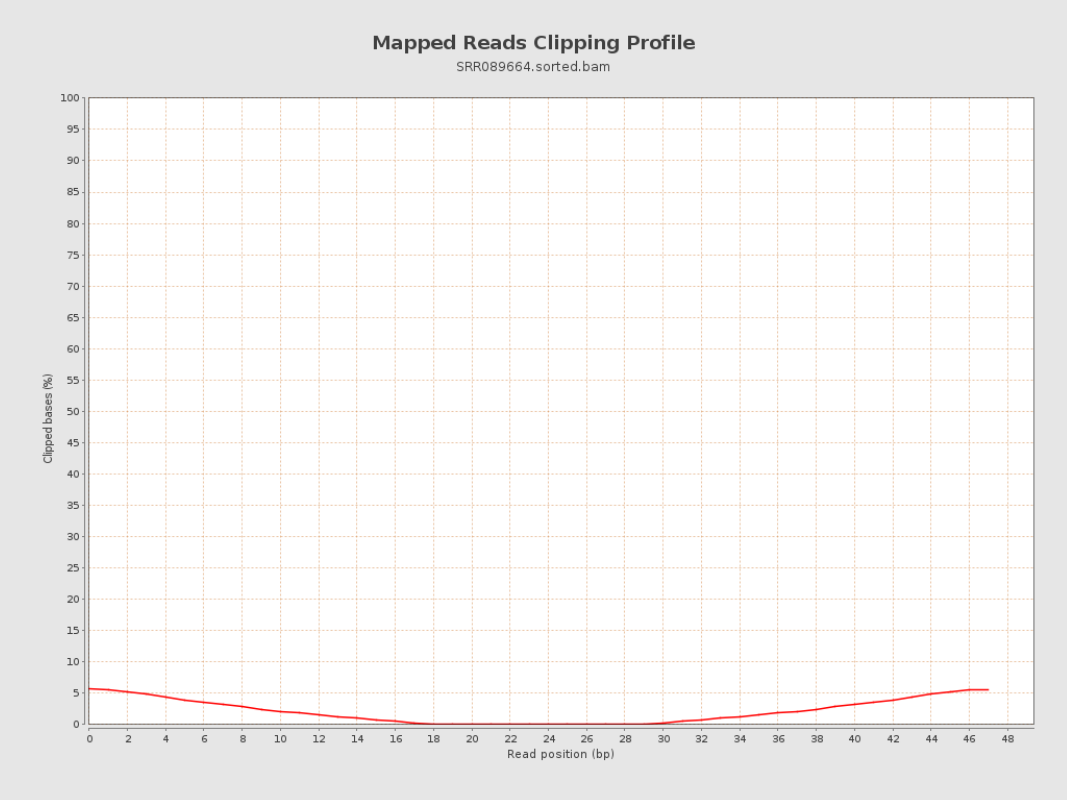
8. Results : Mapped Reads Nucleotide Content



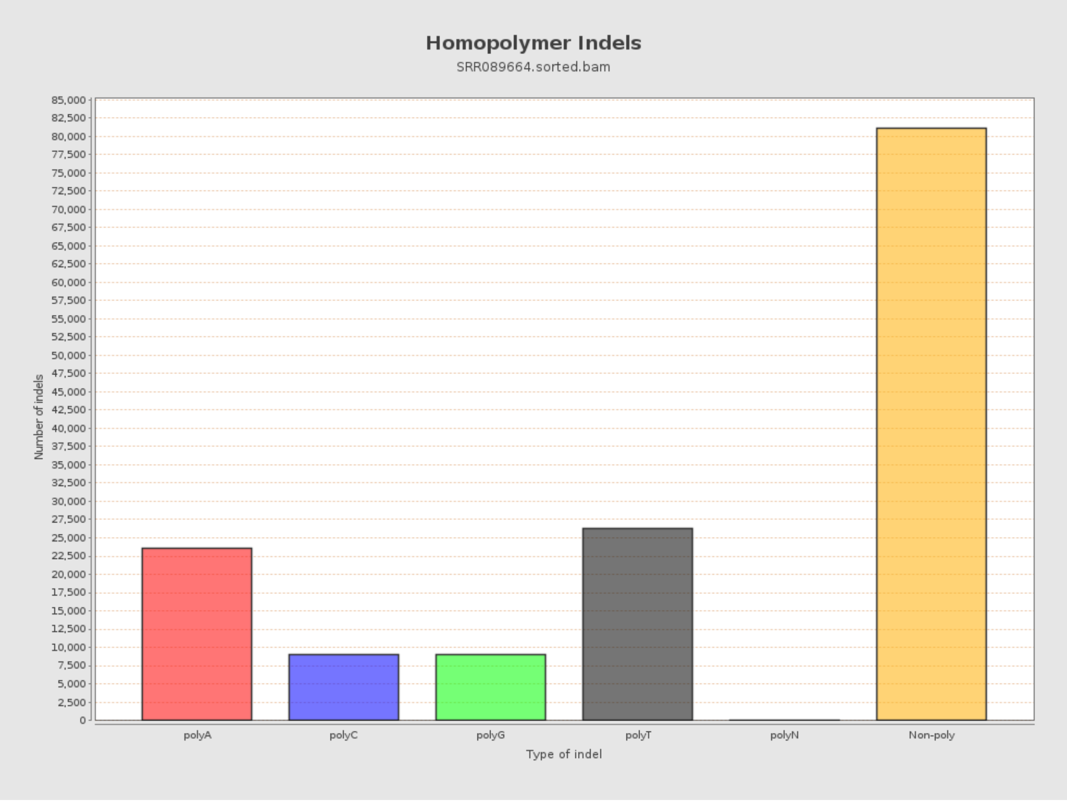
9. Results : Mapped Reads GC-content Distribution



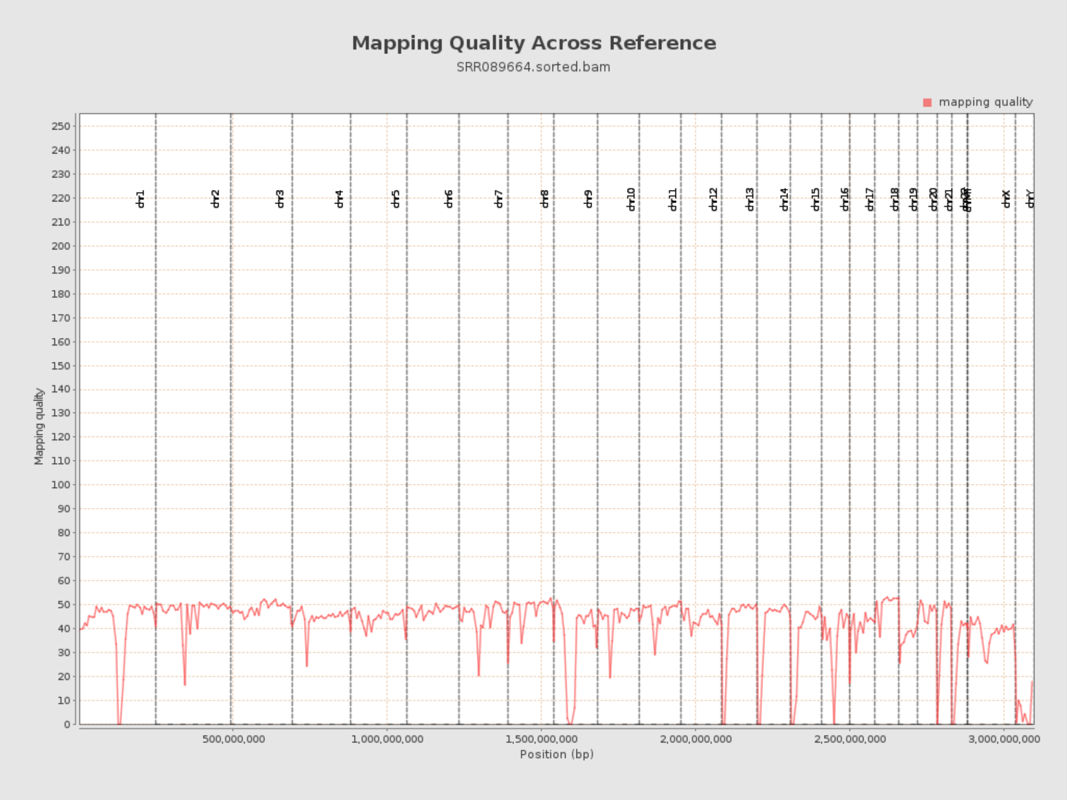
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram