Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 07:34:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054612.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_SRR054612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054612.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 07:34:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,877,465
Mapped reads	15,020,338 / 84.02%
Unmapped reads	2,857,127 / 15.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	481 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,228,170 / 23.65%
Duplication rate	19.52%
Clipped reads	959,117 / 5.36%

2.2. ACGT Content

Number/percentage of A's	212,589,202 / 29.85%
Number/percentage of C's	129,907,334 / 18.24%
Number/percentage of T's	223,702,594 / 31.41%
Number/percentage of G's	145,970,334 / 20.5%
Number/percentage of N's	4,293 / 0%
GC Percentage	38.74%

2.3. Coverage

Mean	0.2301

Standard Deviation	1.5668

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

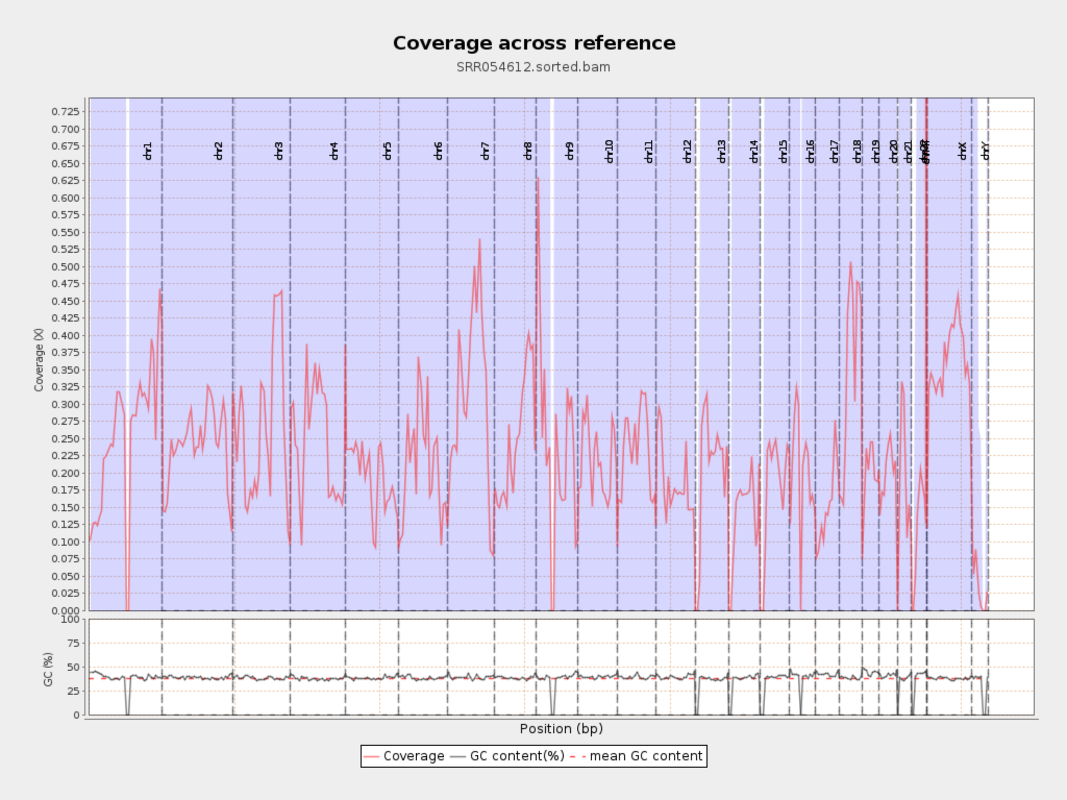
General error rate	0.42%
Mismatches	2,918,741
Insertions	29,180
Mapped reads with at least one insertion	0.19%
Deletions	103,334
Mapped reads with at least one deletion	0.69%
Homopolymer indels	49.98%

2.6. Chromosome stats

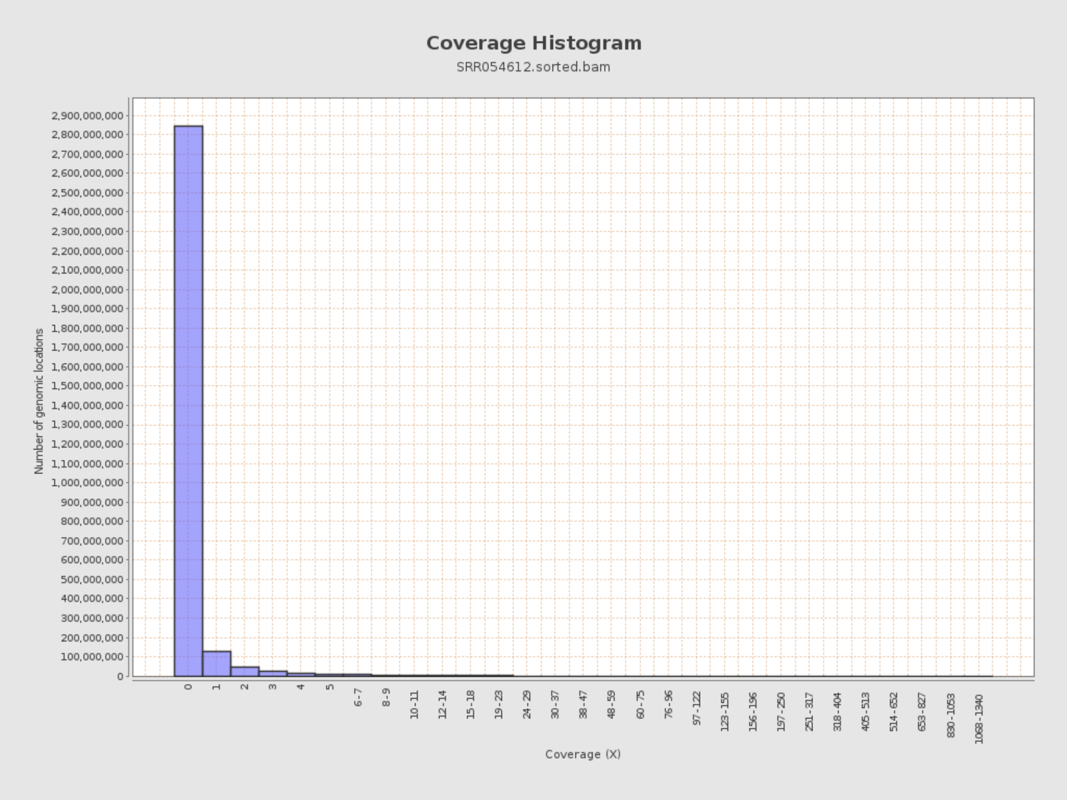
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62717306	0.2516	1.7476
chr2	243199373	58584196	0.2409	1.7086
chr3	198022430	52962646	0.2675	1.5569
chr4	191154276	46765504	0.2446	1.5379
chr5	180915260	35236242	0.1948	1.2345
chr6	171115067	35695517	0.2086	1.3894
chr7	159138663	50741755	0.3189	1.9831

chr8	146364022	36887061	0.252	1.616
chr9	141213431	34456586	0.244	1.6644
chr10	135534747	29985133	0.2212	1.5933
chr11	135006516	31662938	0.2345	1.5988
chr12	133851895	24802259	0.1853	1.2077
chr13	115169878	23317729	0.2025	1.2772
chr14	107349540	14612650	0.1361	1.3117
chr15	102531392	18090933	0.1764	1.1605
chr16	90354753	18371185	0.2033	1.4323
chr17	81195210	12312781	0.1516	1.0403
chr18	78077248	27777851	0.3558	2.3796
chr19	59128983	12002583	0.203	1.4749
chr20	63025520	12577381	0.1996	1.3297
chr21	48129895	8933217	0.1856	1.4783
chr22	51304566	5977194	0.1165	0.8624
chrMT	16571	89500	5.401	11.7481
chrX	155270560	55744376	0.359	2.0496
chrY	59373566	2023517	0.0341	0.7222

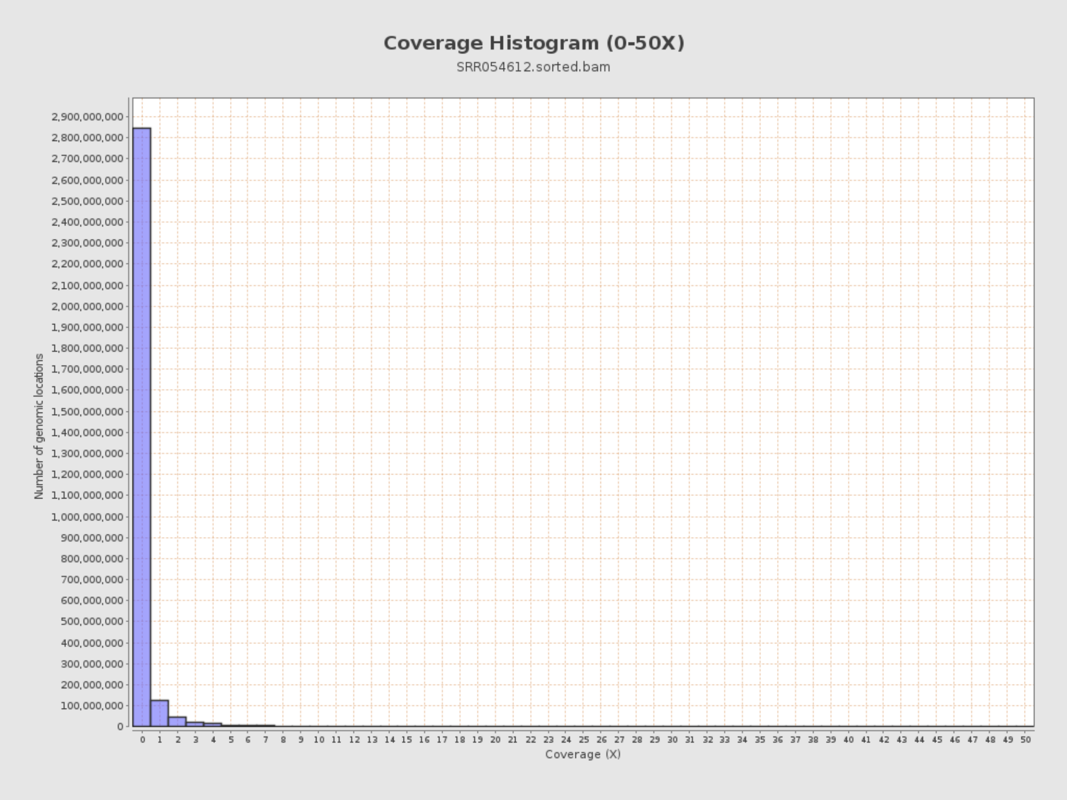
3. Results : Coverage across reference



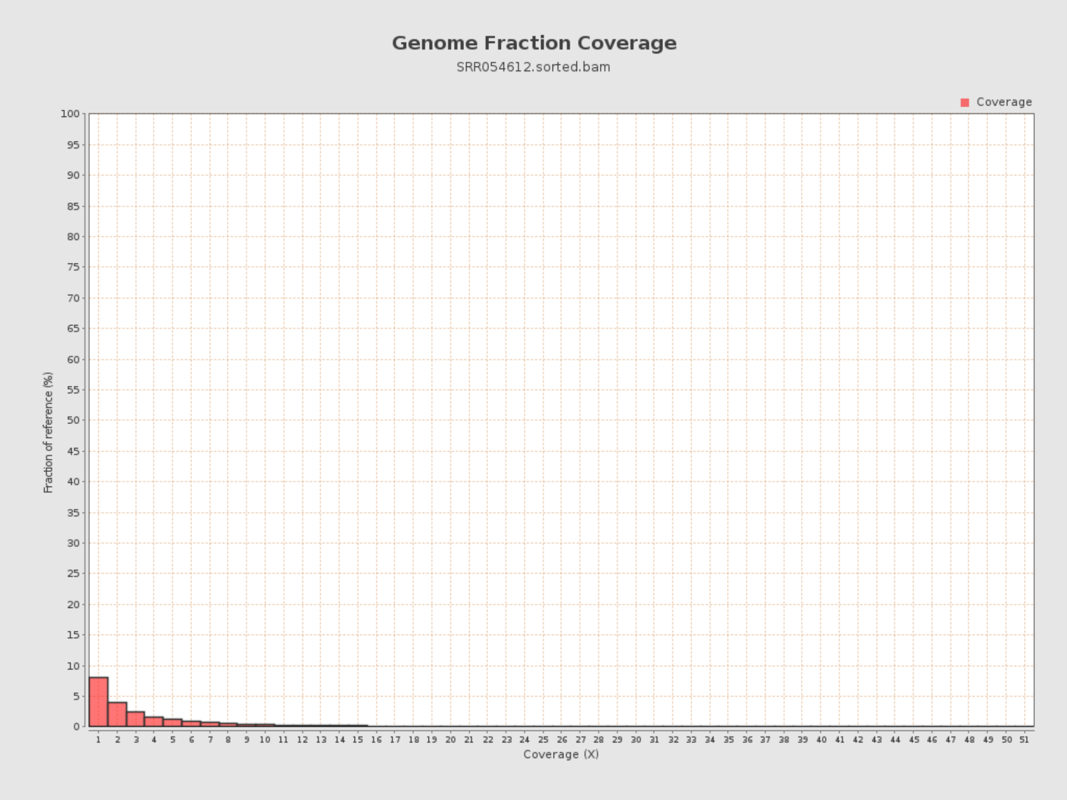
4. Results : Coverage Histogram



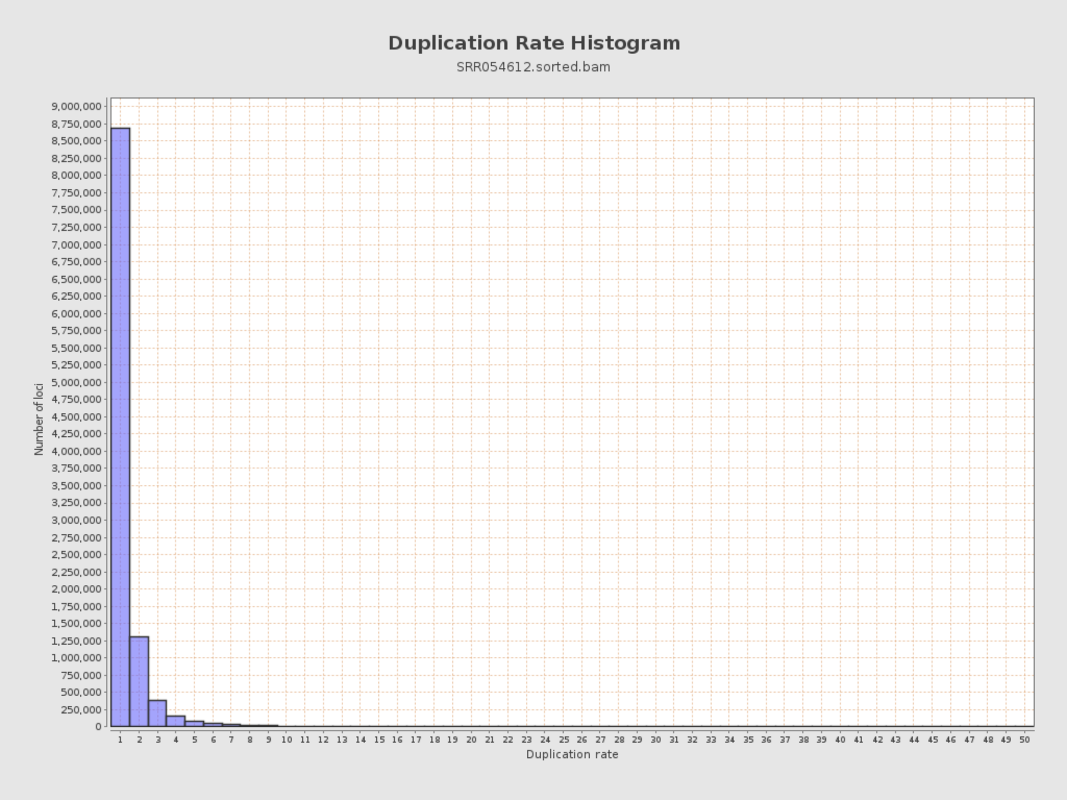
5. Results : Coverage Histogram (0-50X)



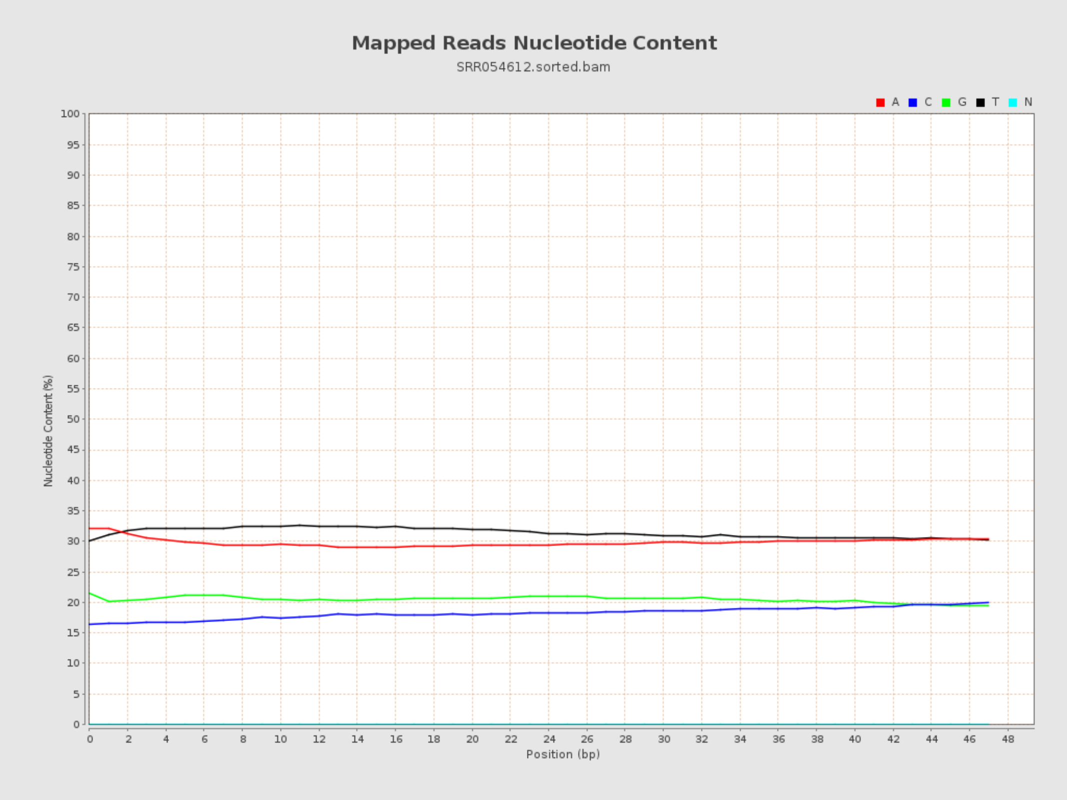
6. Results : Genome Fraction Coverage



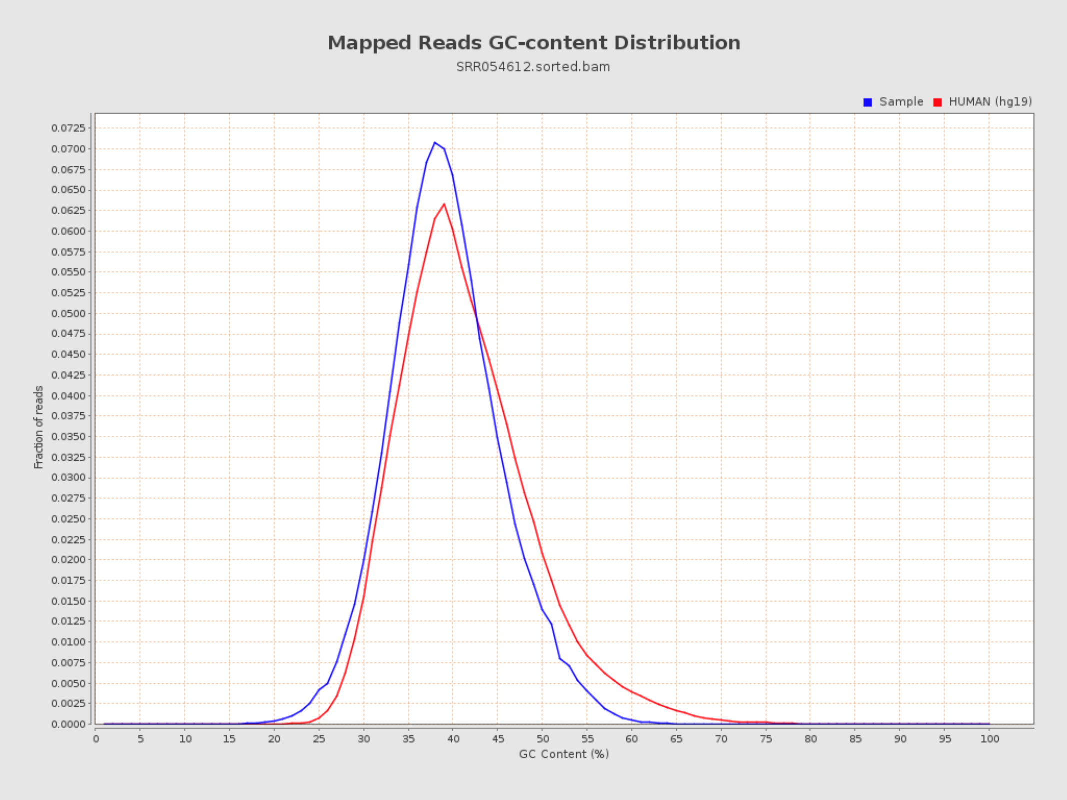
7. Results : Duplication Rate Histogram



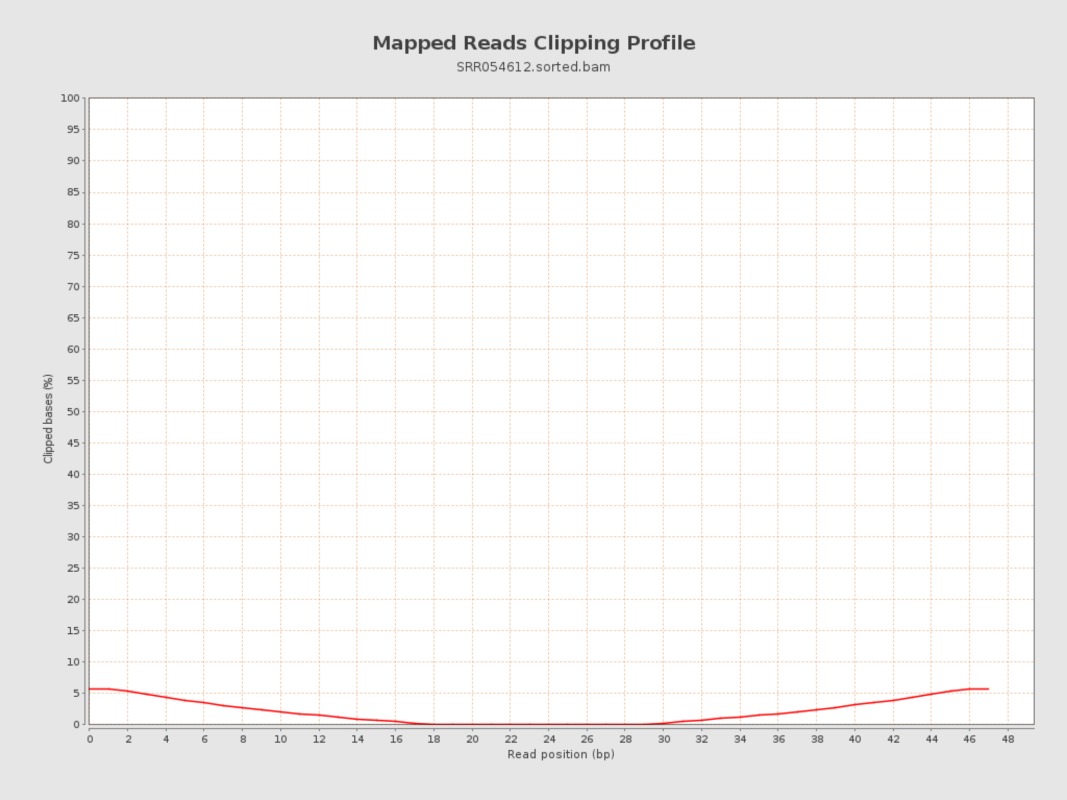
8. Results : Mapped Reads Nucleotide Content



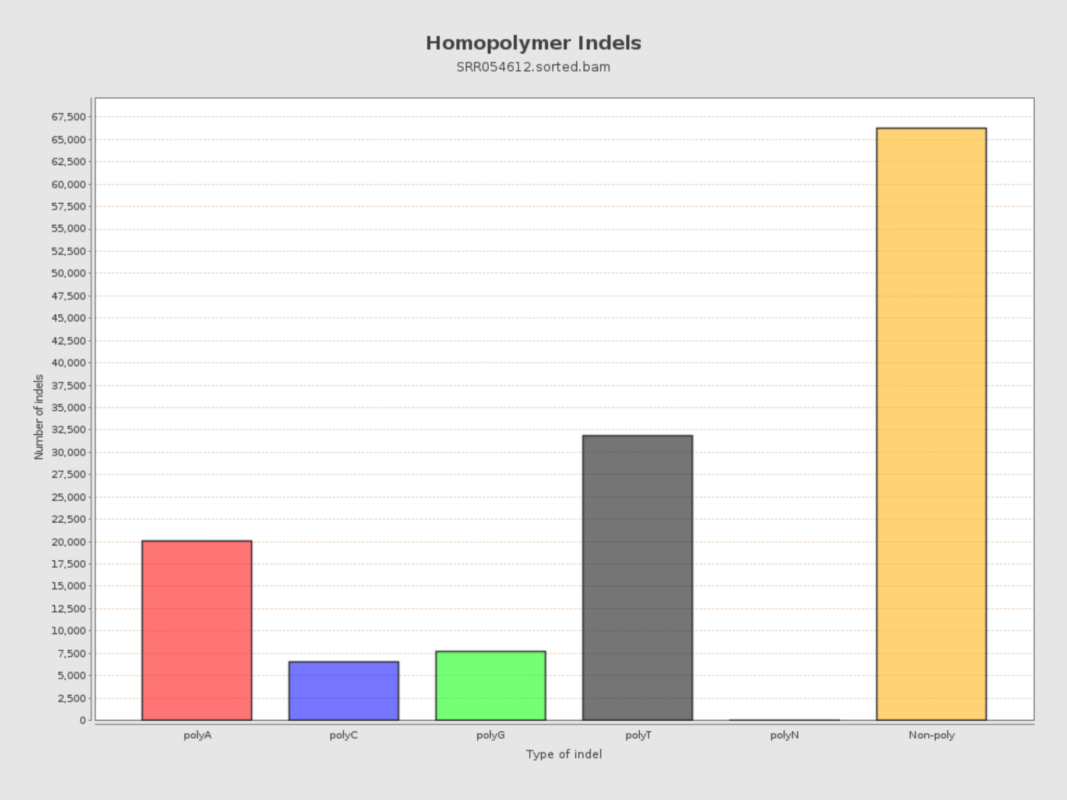
9. Results : Mapped Reads GC-content Distribution



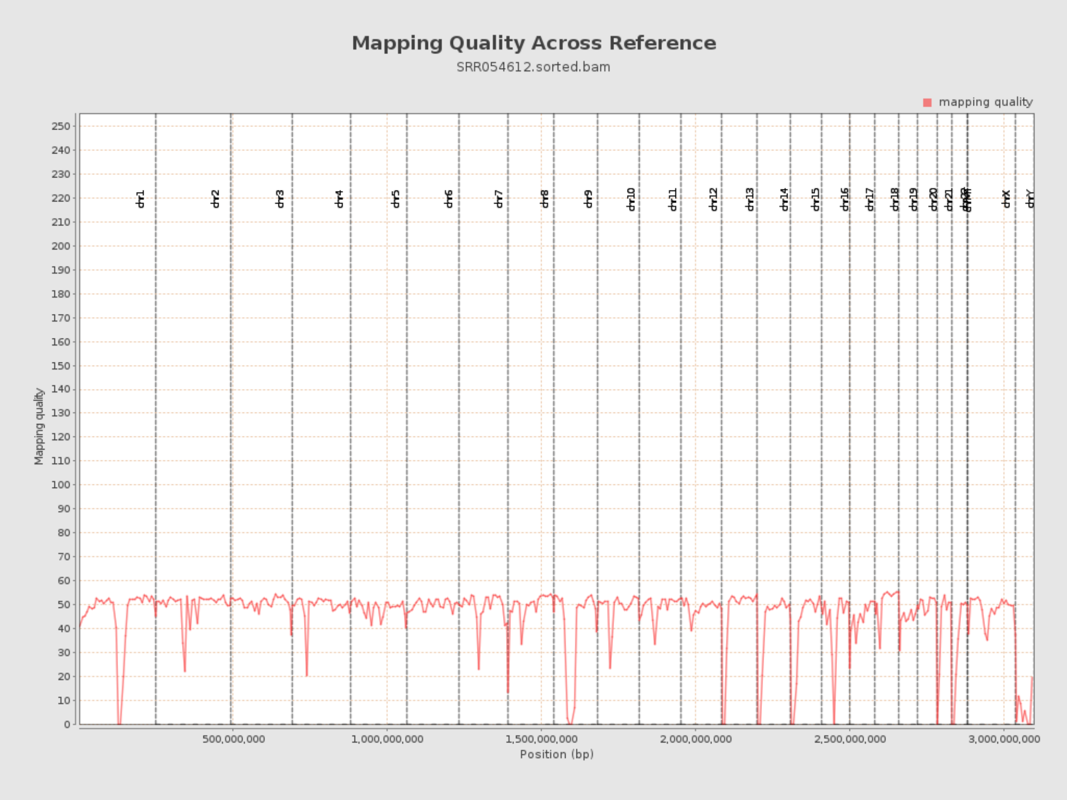
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram