Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:44:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054622.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_SRR054622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054622.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:44:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,789,858
Mapped reads	2,056,756 / 73.72%
Unmapped reads	733,102 / 26.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	128 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	480,605 / 17.23%
Duplication rate	15.78%
Clipped reads	494,145 / 17.71%

2.2. ACGT Content

Number/percentage of A's	31,200,095 / 33.2%
Number/percentage of C's	19,748,342 / 21.01%
Number/percentage of T's	25,120,843 / 26.73%
Number/percentage of G's	17,897,488 / 19.04%
Number/percentage of N's	19,279 / 0.02%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.7697

2.4. Mapping Quality

Mean Mapping Quality	41.45

2.5. Mismatches and indels

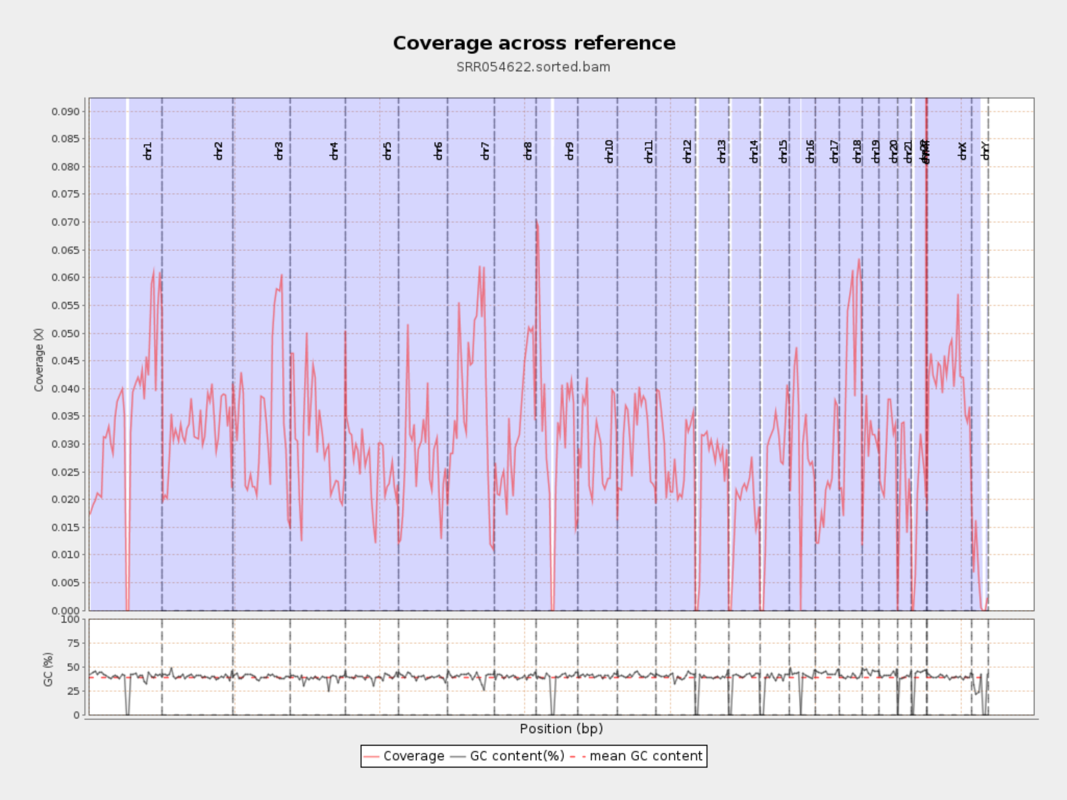
General error rate	0.65%
Mismatches	604,911
Insertions	5,189
Mapped reads with at least one insertion	0.25%
Deletions	11,921
Mapped reads with at least one deletion	0.58%
Homopolymer indels	40.08%

2.6. Chromosome stats

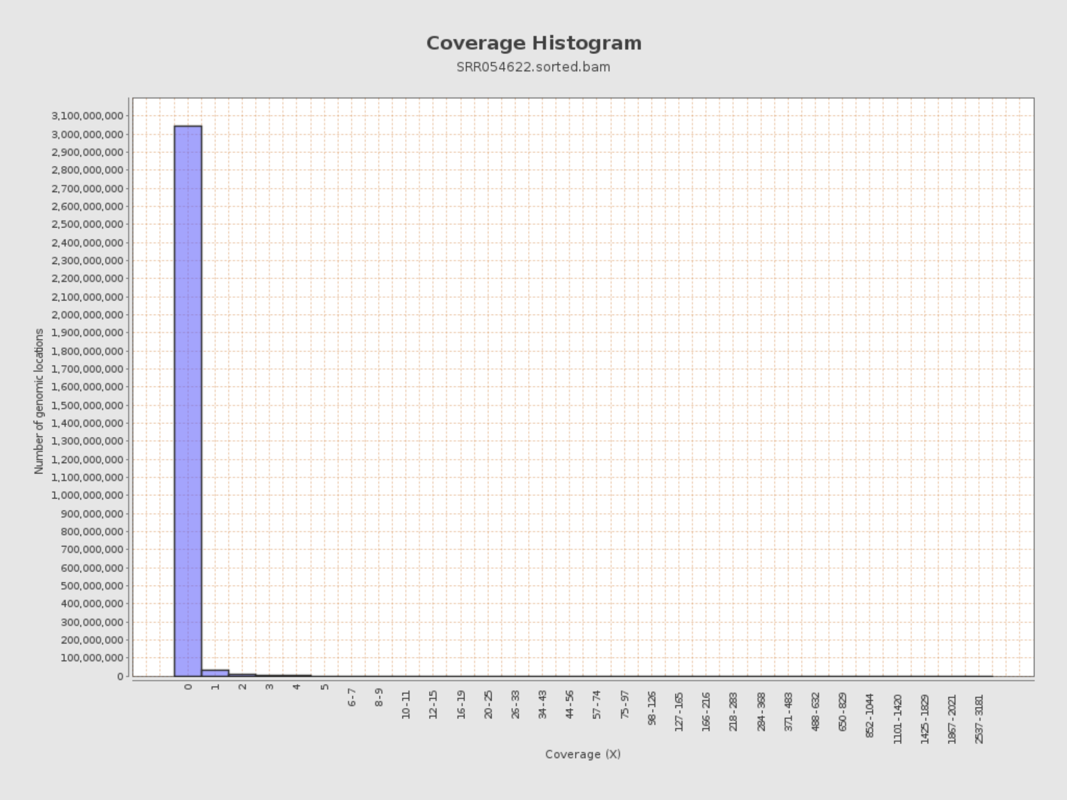
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8600045	0.0345	0.7936
chr2	243199373	7871665	0.0324	0.5791
chr3	198022430	6902528	0.0349	0.5204
chr4	191154276	5797393	0.0303	1.3161
chr5	180915260	4717436	0.0261	0.5213
chr6	171115067	4598437	0.0269	0.5861
chr7	159138663	6271850	0.0394	1.9838

chr8	146364022	4828006	0.033	0.5608
chr9	141213431	4507125	0.0319	0.5322
chr10	135534747	4095019	0.0302	0.4996
chr11	135006516	4186481	0.031	0.4319
chr12	133851895	3785634	0.0283	0.6053
chr13	115169878	2796478	0.0243	0.395
chr14	107349540	1880780	0.0175	0.31
chr15	102531392	2660277	0.0259	0.6832
chr16	90354753	2687509	0.0297	0.617
chr17	81195210	1849201	0.0228	0.3692
chr18	78077248	3549794	0.0455	0.5986
chr19	59128983	1818840	0.0308	0.4716
chr20	63025520	1833609	0.0291	0.5973
chr21	48129895	1045883	0.0217	0.5265
chr22	51304566	906786	0.0177	0.2508
chrMT	16571	7060	0.426	1.6511
chrX	155270560	6499007	0.0419	0.6286
chrY	59373566	306958	0.0052	0.5681

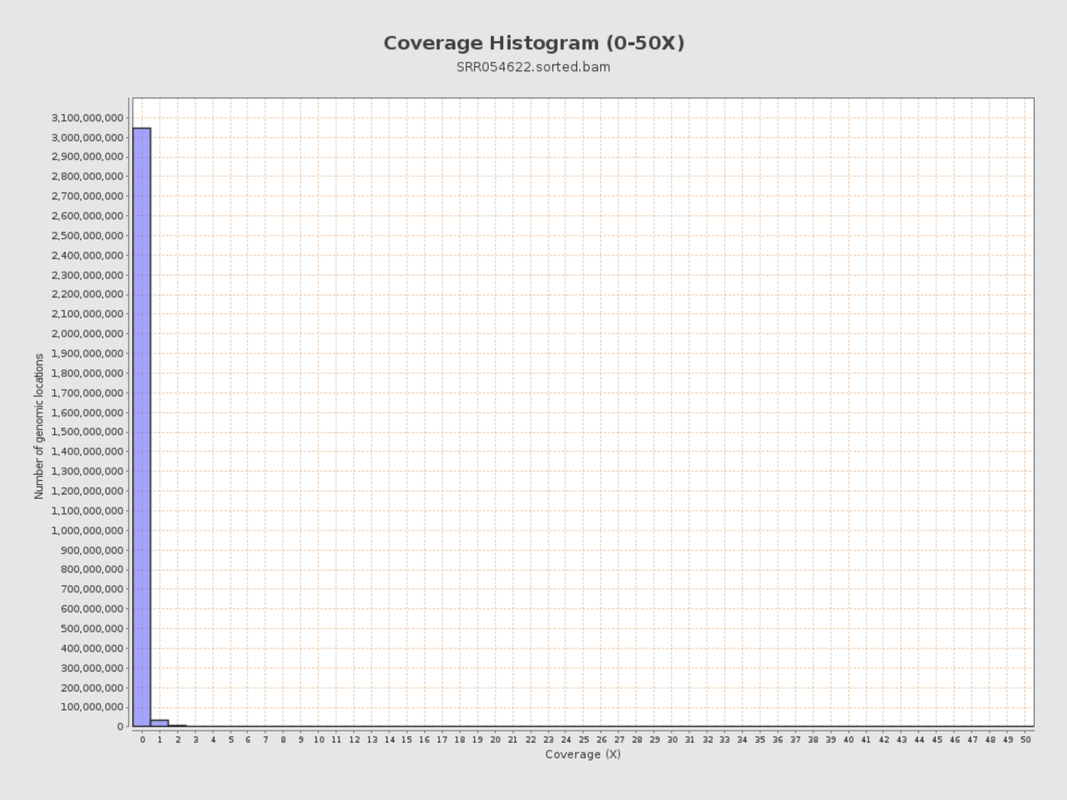
3. Results : Coverage across reference



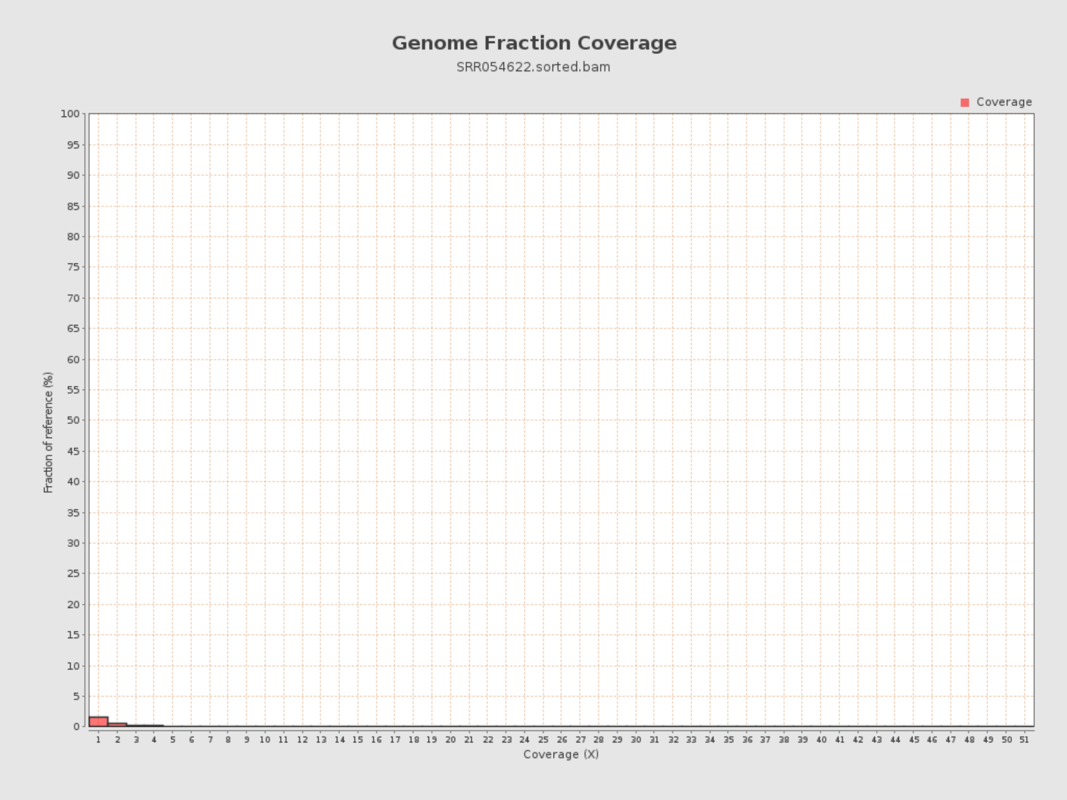
4. Results : Coverage Histogram



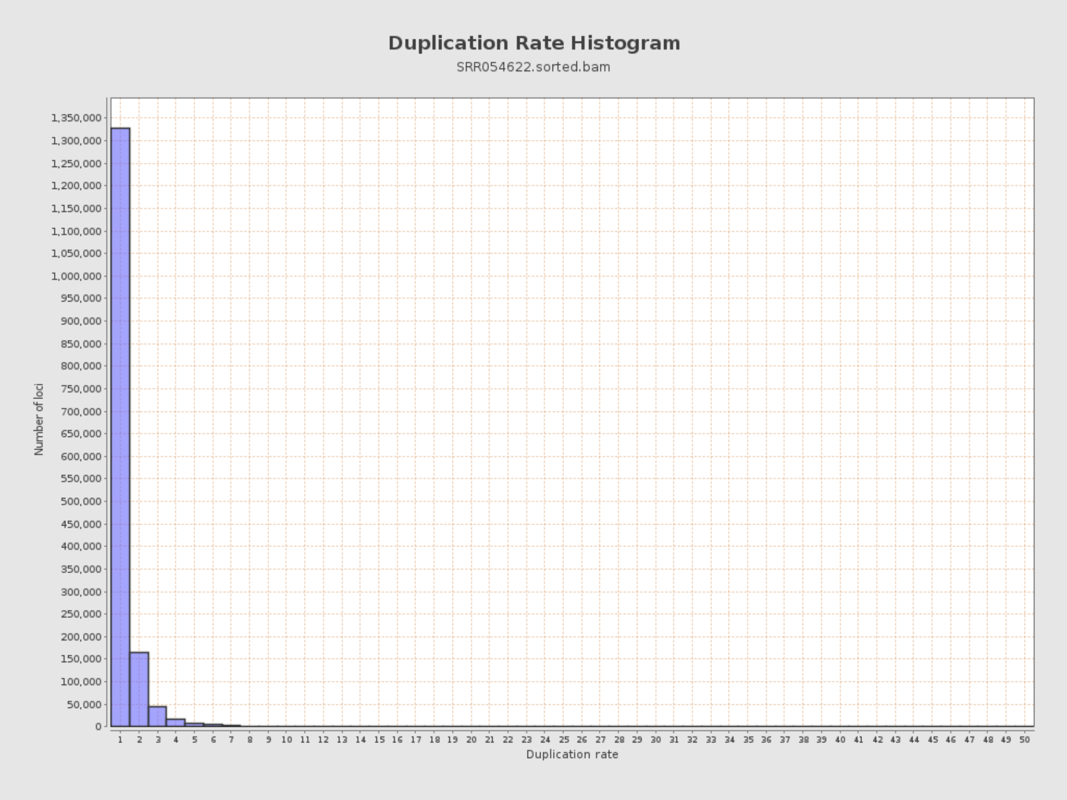
5. Results : Coverage Histogram (0-50X)



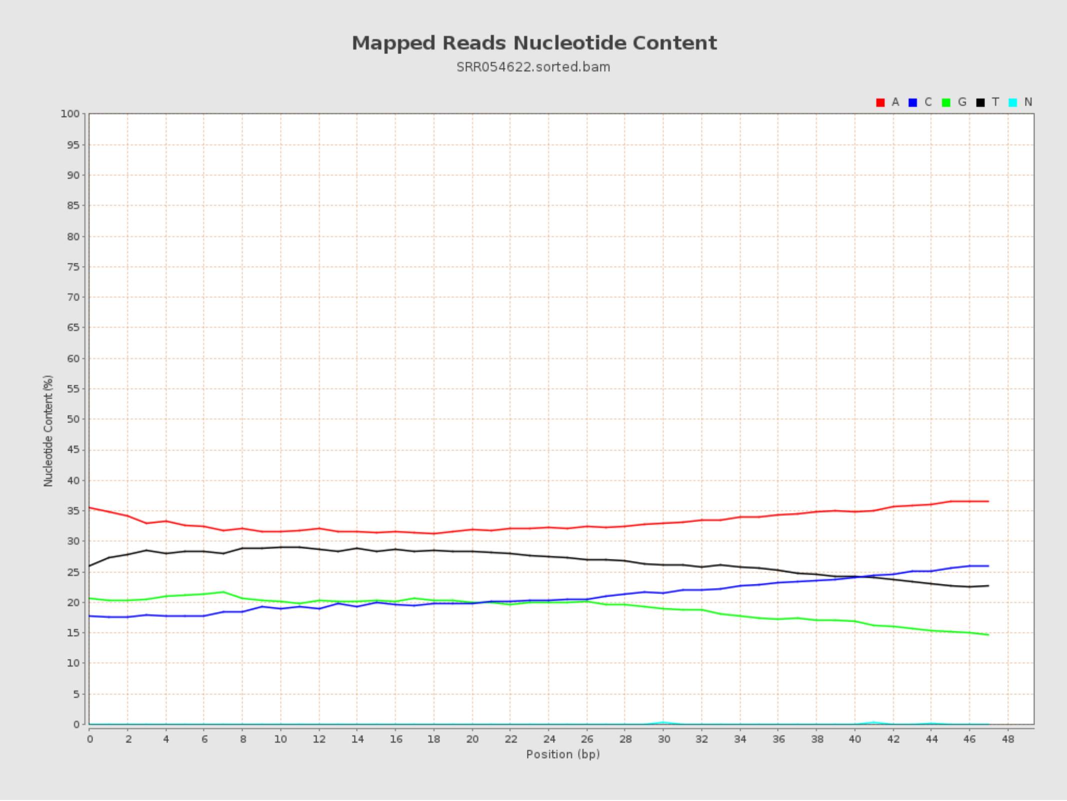
6. Results : Genome Fraction Coverage



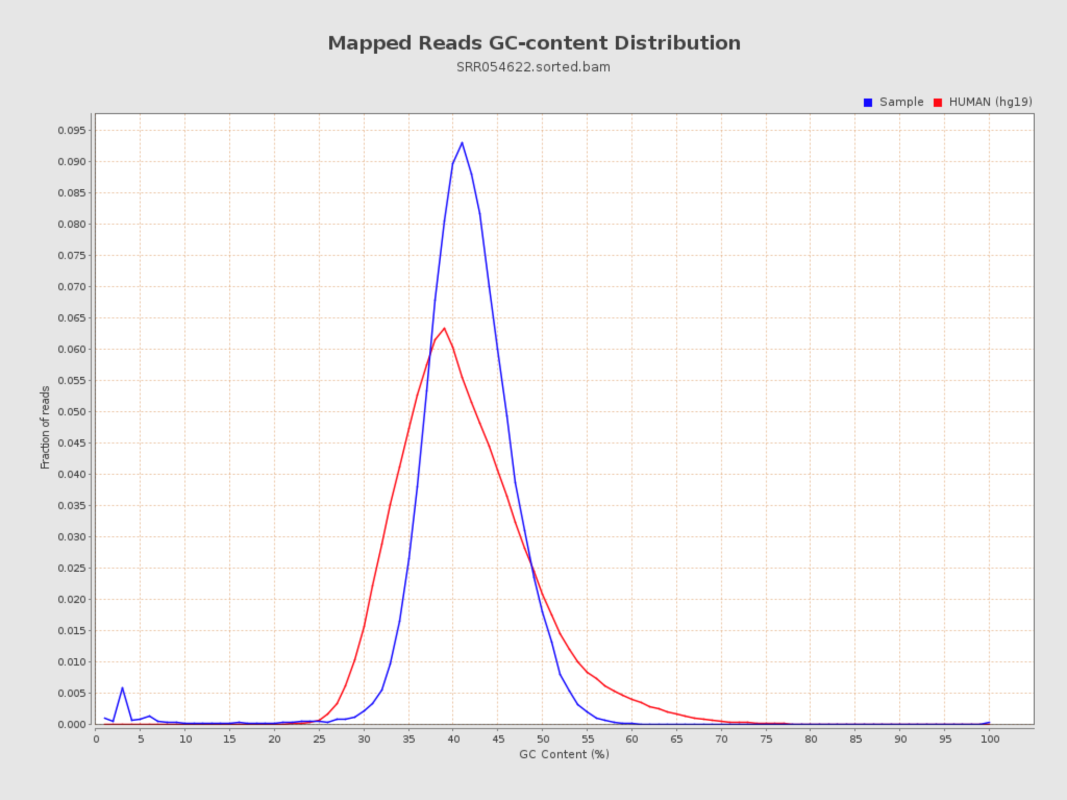
7. Results : Duplication Rate Histogram



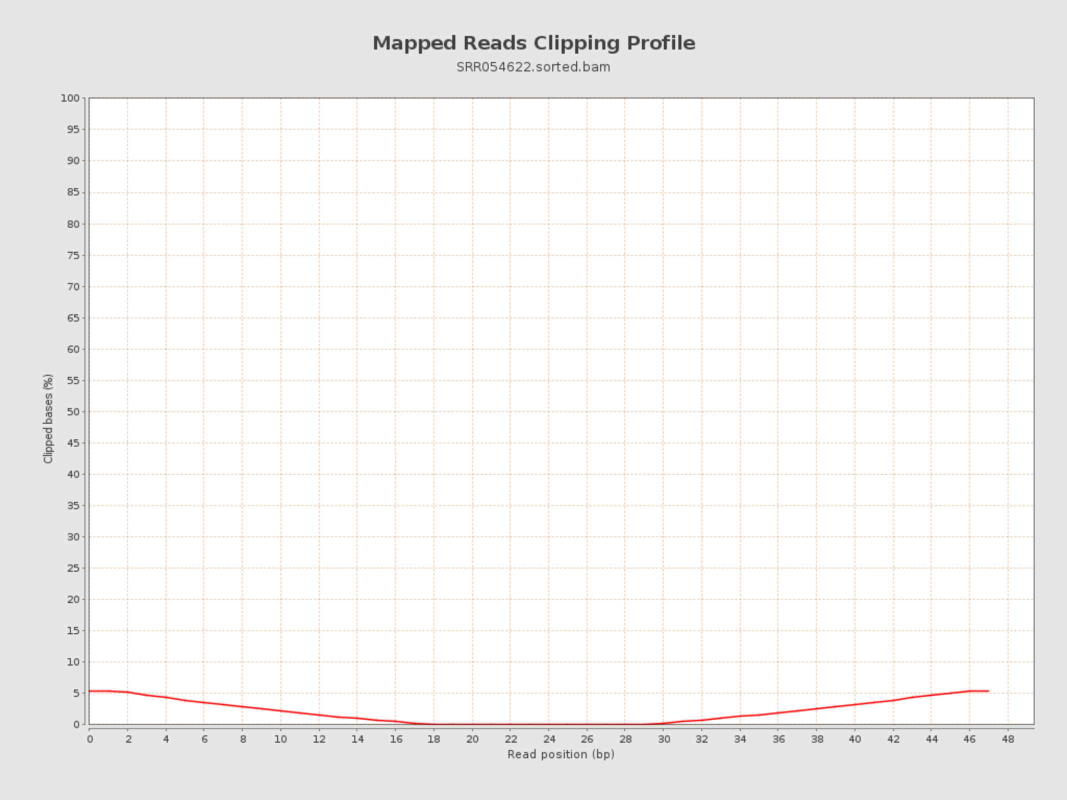
8. Results : Mapped Reads Nucleotide Content



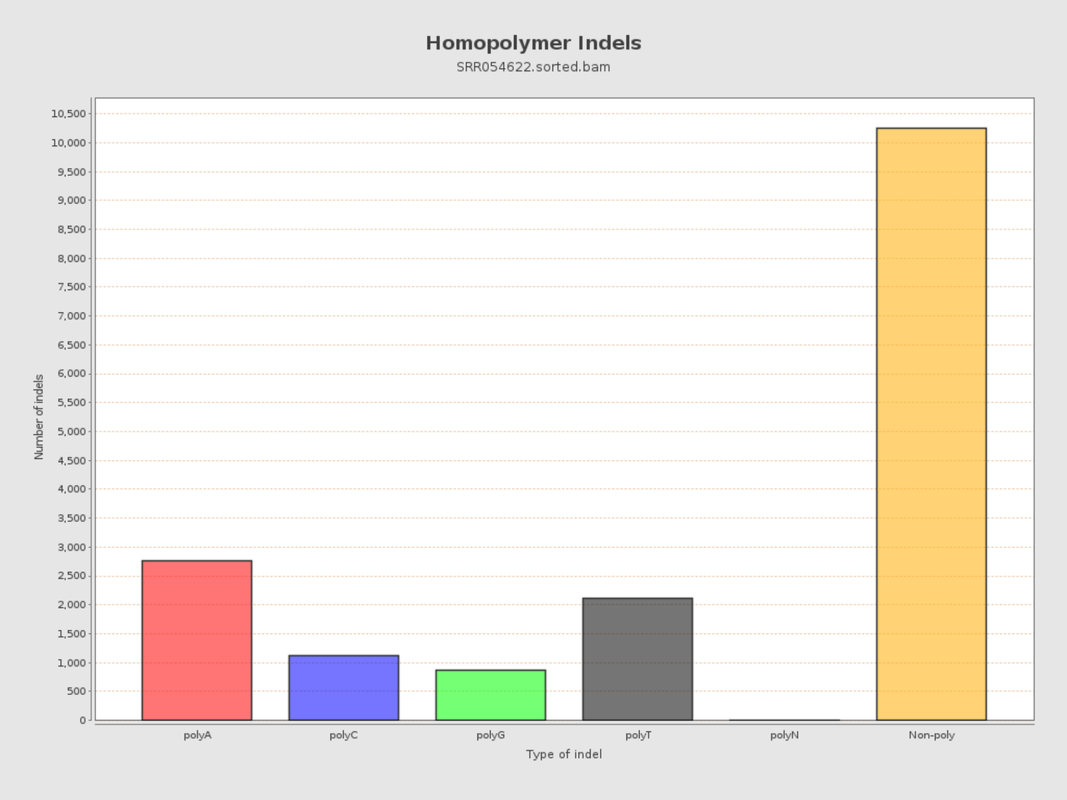
9. Results : Mapped Reads GC-content Distribution



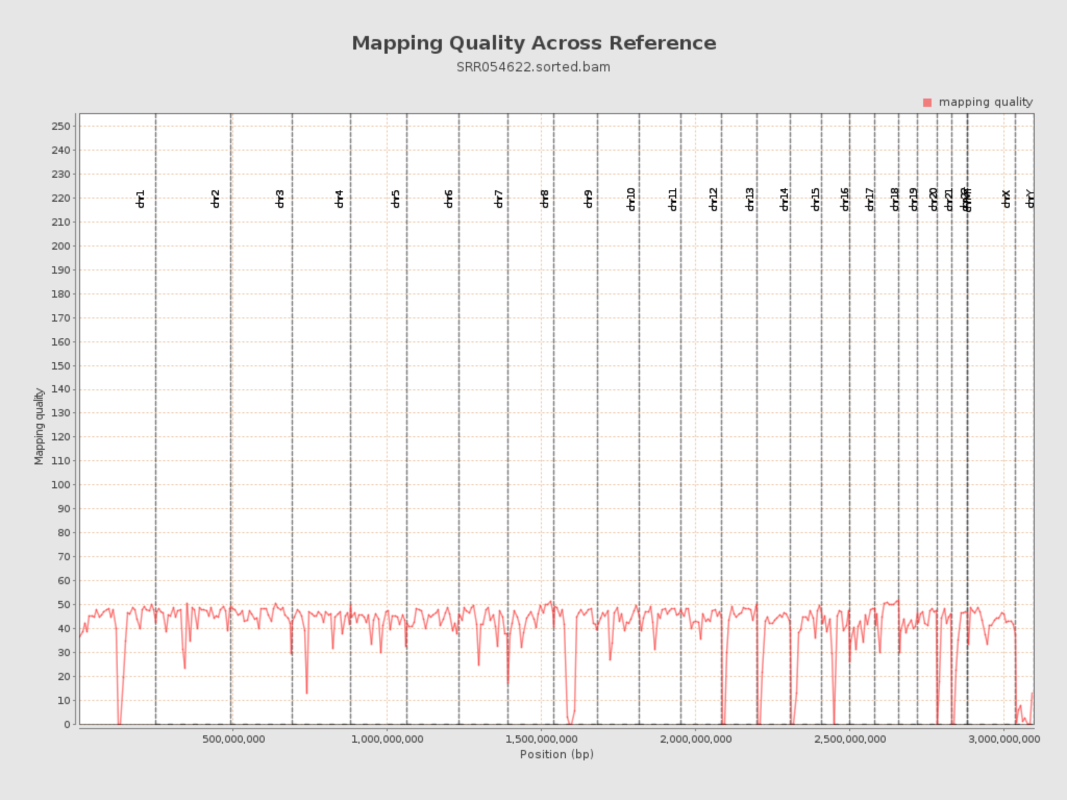
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram