Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 07:35:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514770.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_SRR5514770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 07:35:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	73,212,771
Mapped reads	72,635,238 / 99.21%
Unmapped reads	577,533 / 0.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,000,995 / 6.83%
Read min/max/mean length	30 / 100 / 100.55
Duplicated reads (estimated)	65,800,965 / 89.88%
Duplication rate	52.52%
Clipped reads	19,263,171 / 26.31%

2.2. ACGT Content

Number/percentage of A's	2,044,854,051 / 29.51%
Number/percentage of C's	1,419,380,792 / 20.48%
Number/percentage of T's	2,018,110,936 / 29.12%
Number/percentage of G's	1,446,171,761 / 20.87%
Number/percentage of N's	1,347,724 / 0.02%
GC Percentage	41.35%

2.3. Coverage

Mean	2.2401

Standard Deviation	180.7973

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

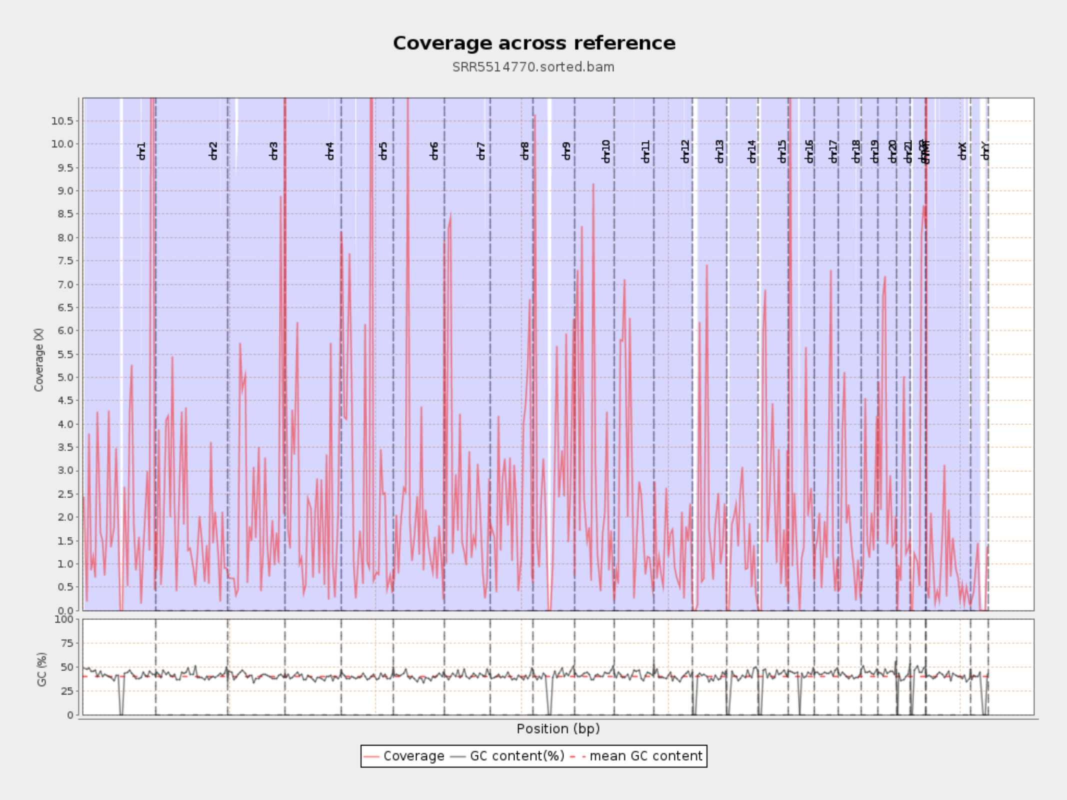
General error rate	0.68%
Mismatches	42,740,255
Insertions	3,305,098
Mapped reads with at least one insertion	4.39%
Deletions	2,234,285
Mapped reads with at least one deletion	2.96%
Homopolymer indels	43.96%

2.6. Chromosome stats

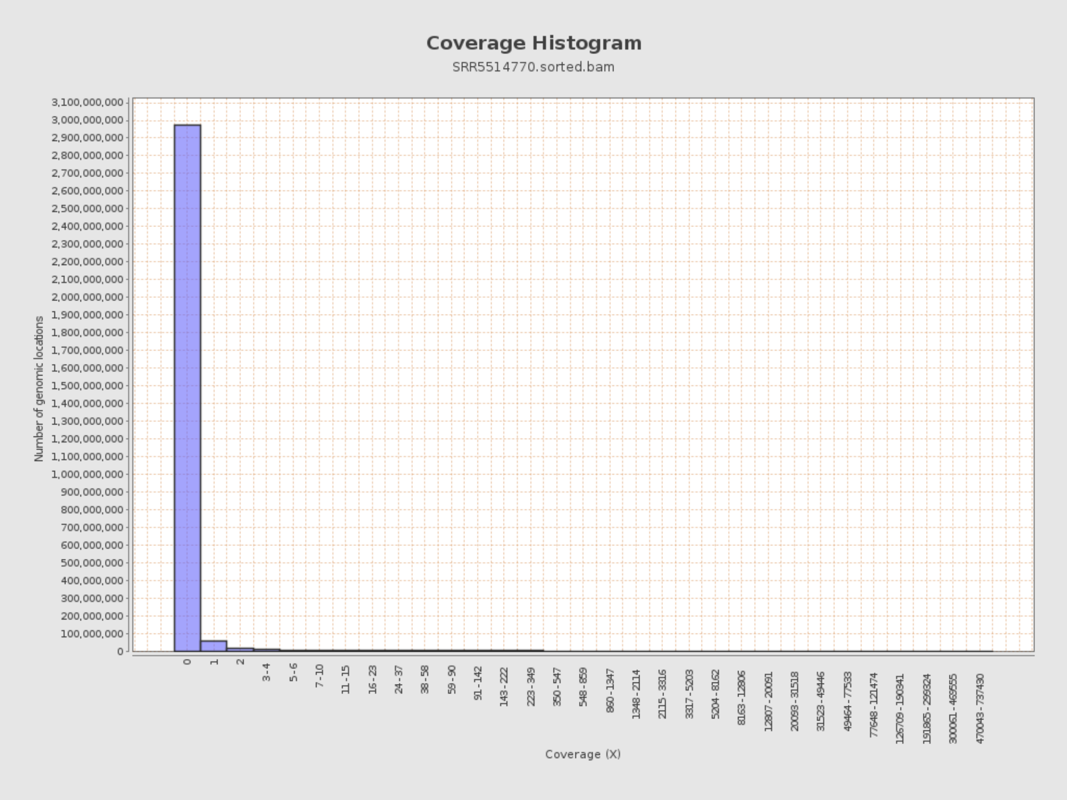
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	603906630	2.4229	511.271
chr2	243199373	479034085	1.9697	71.3385
chr3	198022430	448396798	2.2644	92.9604
chr4	191154276	434398123	2.2725	113.7631
chr5	180915260	553836978	3.0613	237.7844
chr6	171115067	348824576	2.0385	73.5329
chr7	159138663	414920484	2.6073	104.959

chr8	146364022	383879592	2.6228	86.1033
chr9	141213431	428771499	3.0363	133.0575
chr10	135534747	415651617	3.0668	122.2617
chr11	135006516	337387541	2.499	92.6008
chr12	133851895	178395833	1.3328	43.1343
chr13	115169878	218076118	1.8935	76.9196
chr14	107349540	147648769	1.3754	48.9372
chr15	102531392	248170502	2.4204	81.9988
chr16	90354753	234399032	2.5942	148.3445
chr17	81195210	166994583	2.0567	72.4149
chr18	78077248	135927288	1.7409	51.4766
chr19	59128983	124642352	2.108	82.1023
chr20	63025520	214142425	3.3977	135.2829
chr21	48129895	78673440	1.6346	65.1984
chr22	51304566	168076976	3.2761	290.3436
chrMT	16571	3134102	189.1317	318.9141
chrX	155270560	134187623	0.8642	45.4796
chrY	59373566	33185734	0.5589	23.8867

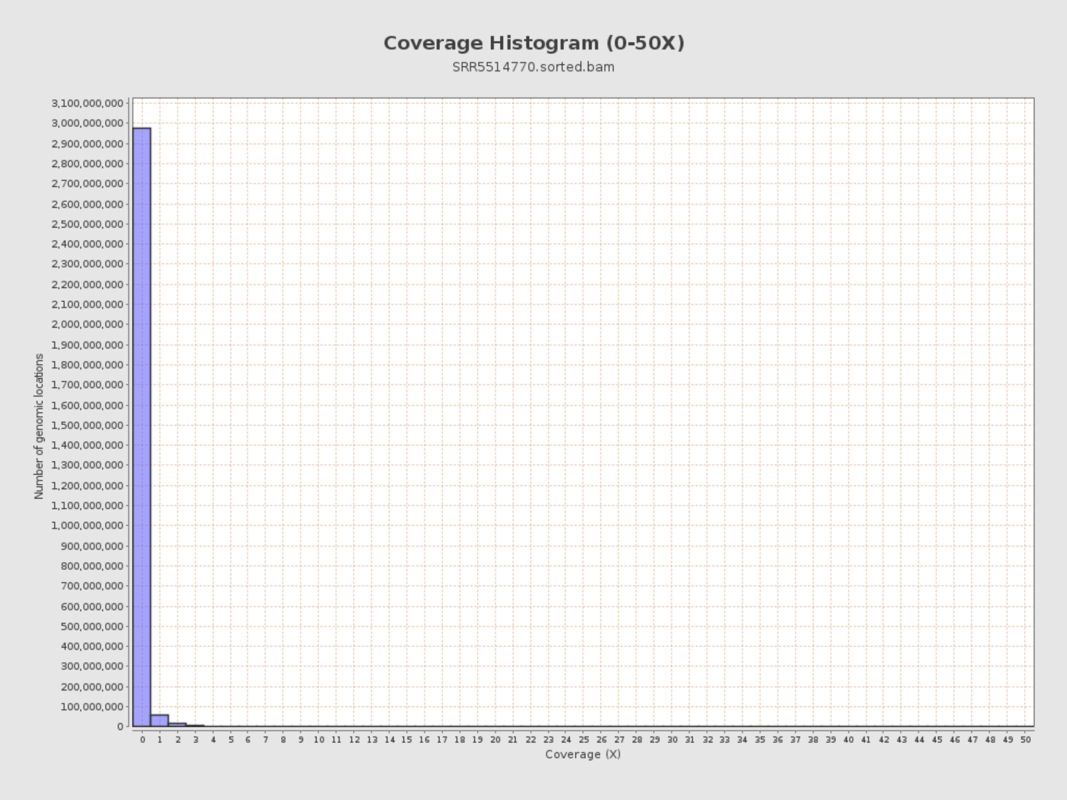
3. Results : Coverage across reference



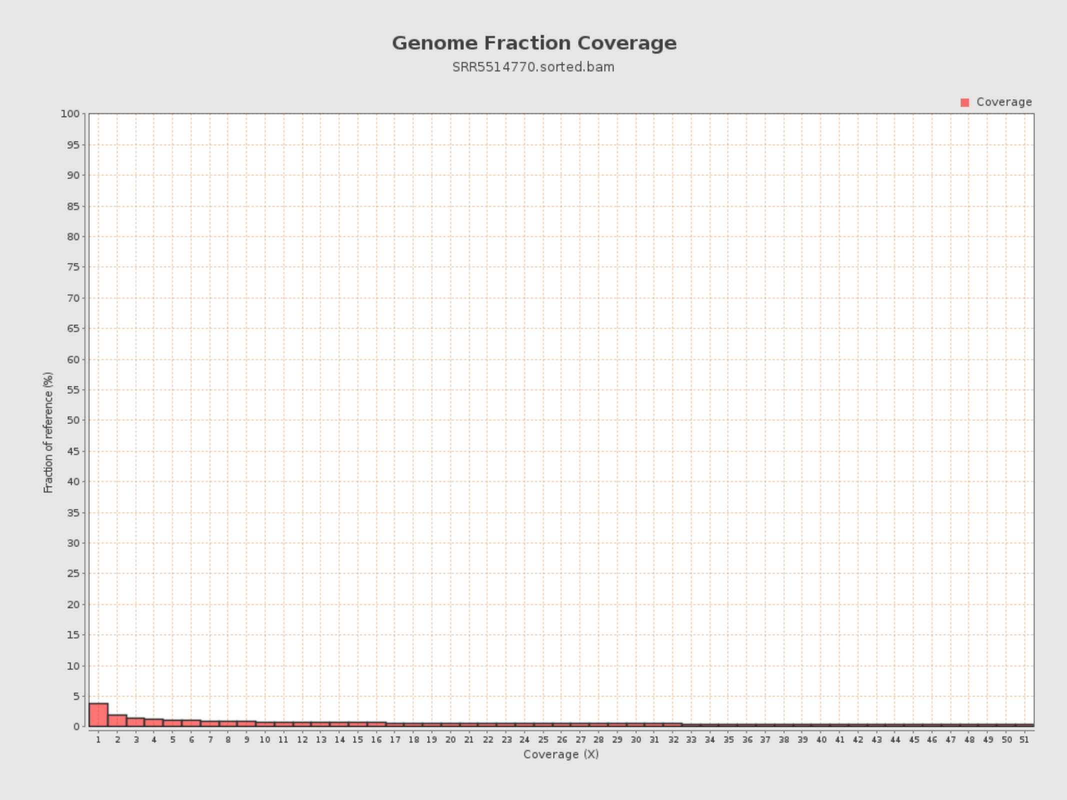
4. Results : Coverage Histogram



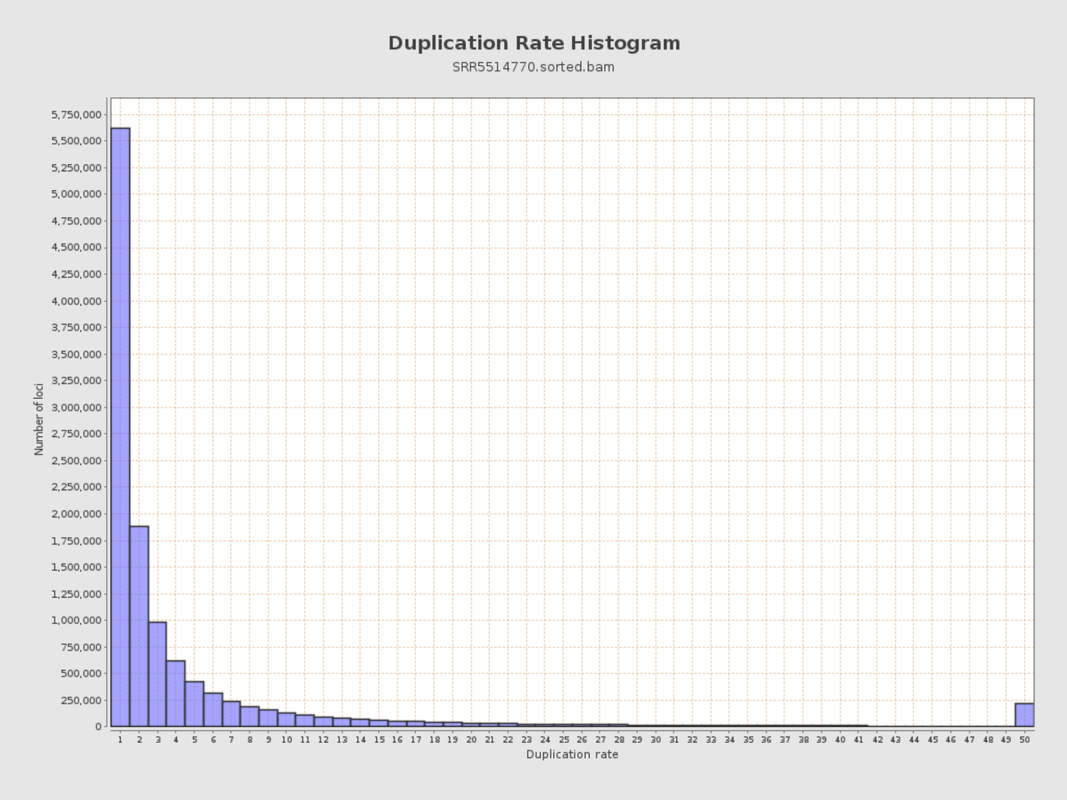
5. Results : Coverage Histogram (0-50X)



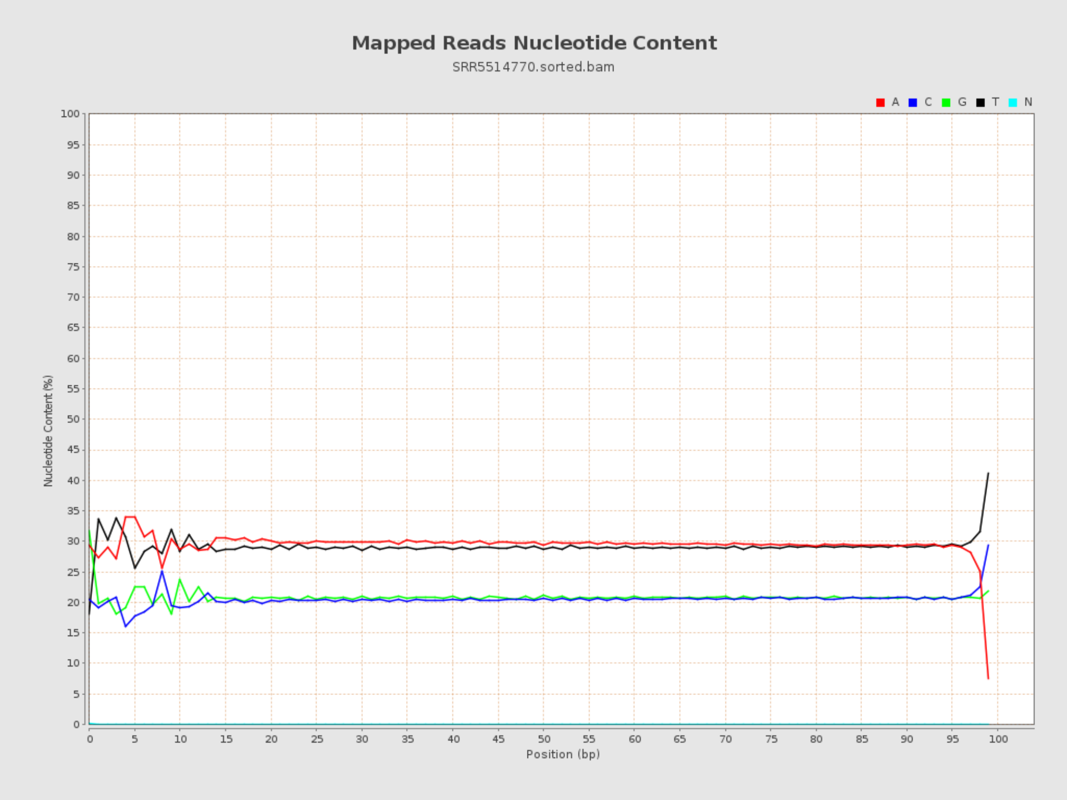
6. Results : Genome Fraction Coverage



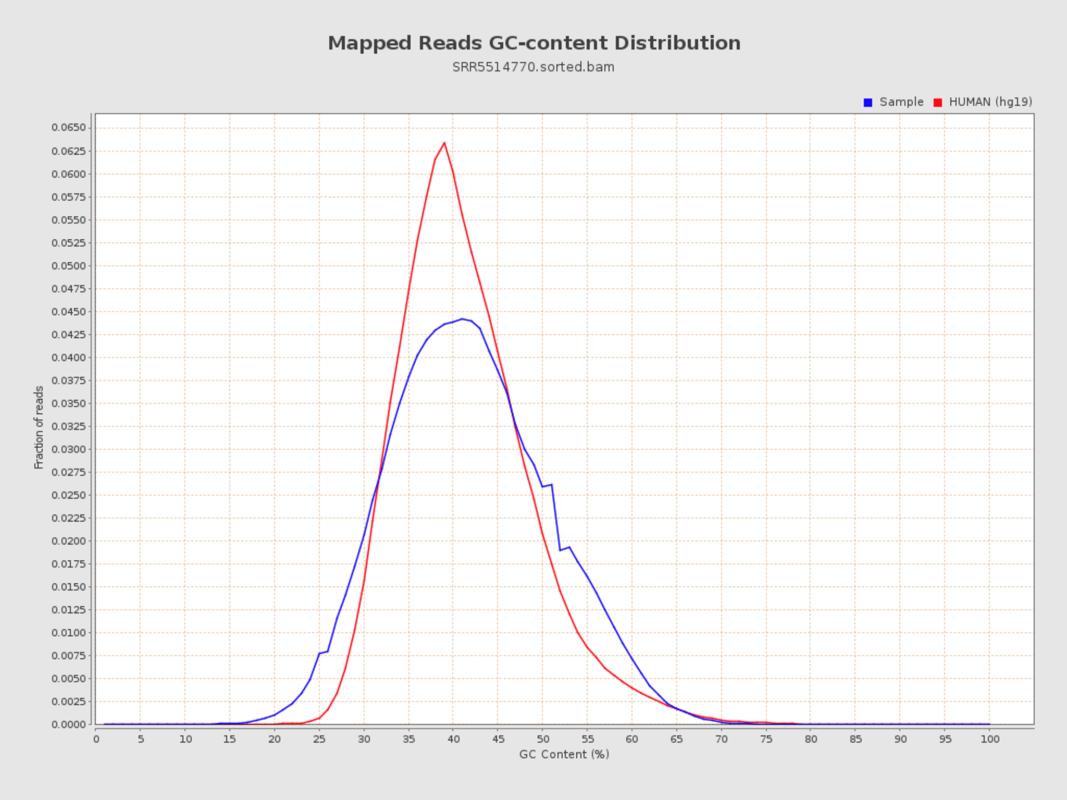
7. Results : Duplication Rate Histogram



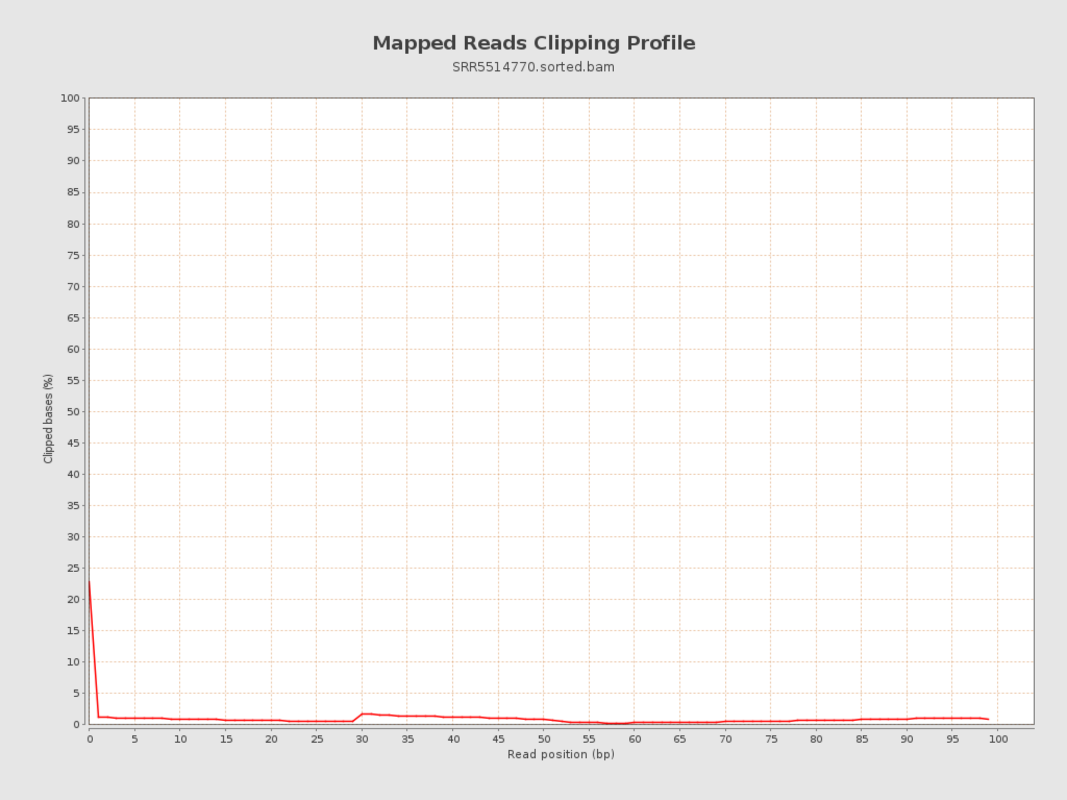
8. Results : Mapped Reads Nucleotide Content



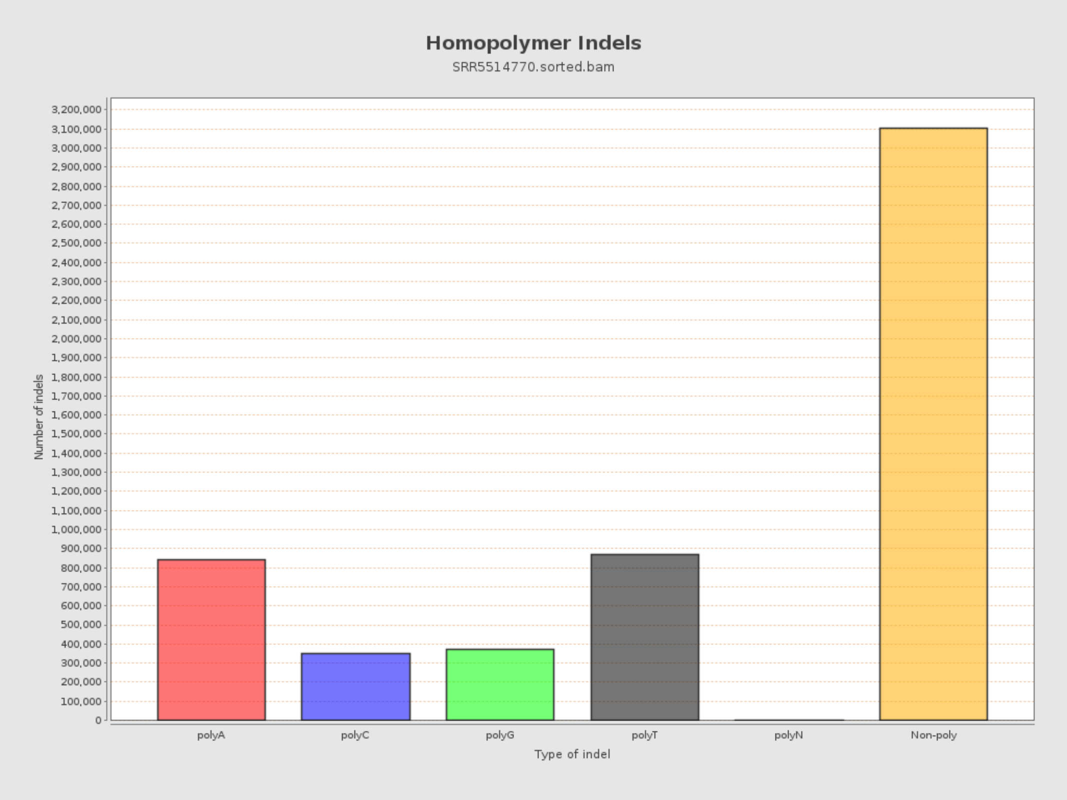
9. Results : Mapped Reads GC-content Distribution



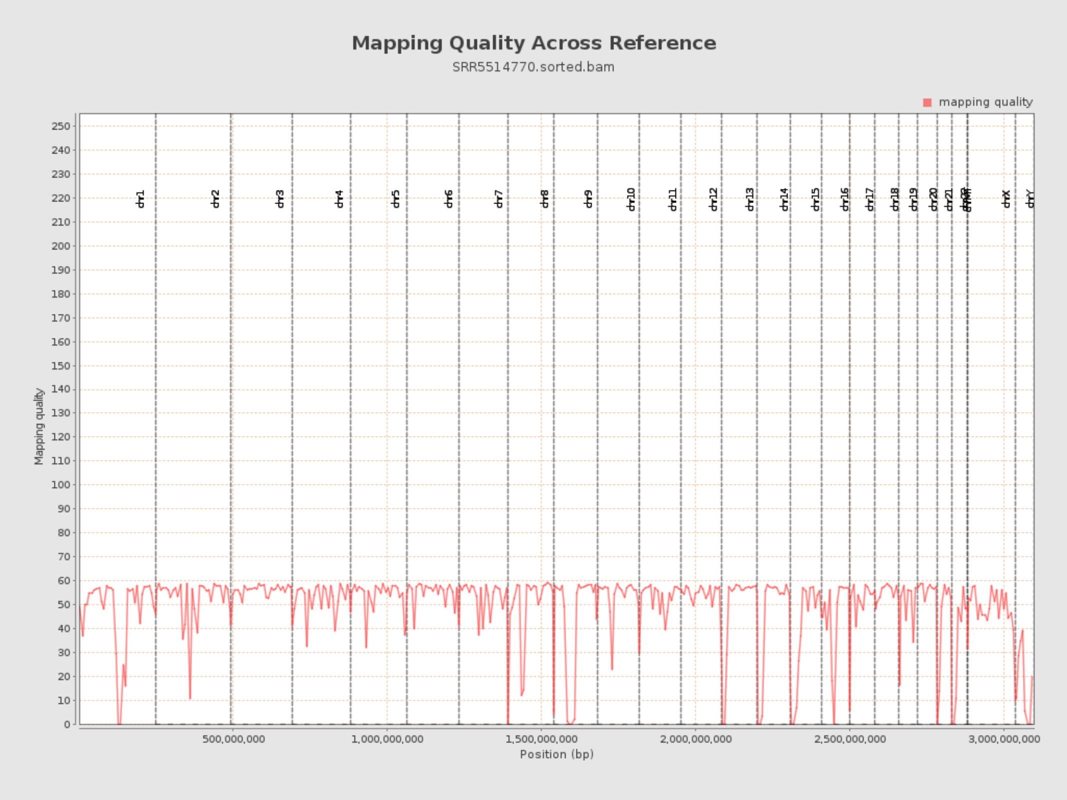
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram