Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 05:30:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514761.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_SRR5514761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 05:30:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,242,205
Mapped reads	17,269,163 / 81.3%
Unmapped reads	3,973,042 / 18.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,813,666 / 13.25%
Read min/max/mean length	30 / 100 / 104.51
Duplicated reads (estimated)	12,335,927 / 58.07%
Duplication rate	35.06%
Clipped reads	10,273,147 / 48.36%

2.2. ACGT Content

Number/percentage of A's	479,734,188 / 30.37%
Number/percentage of C's	294,852,824 / 18.66%
Number/percentage of T's	485,250,072 / 30.72%
Number/percentage of G's	319,777,627 / 20.24%
Number/percentage of N's	104,687 / 0.01%
GC Percentage	38.91%

2.3. Coverage

Mean	0.5109

Standard Deviation	70.5532

2.4. Mapping Quality

Mean Mapping Quality	43.46

2.5. Mismatches and indels

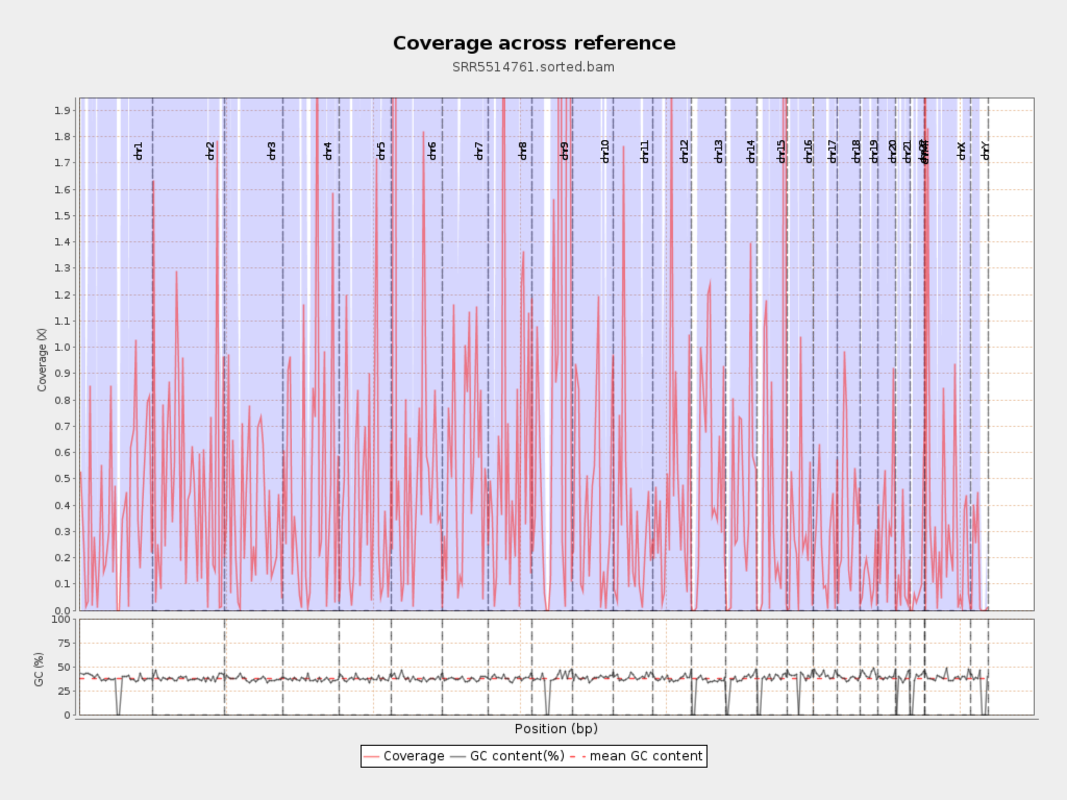
General error rate	0.75%
Mismatches	9,911,268
Insertions	1,119,800
Mapped reads with at least one insertion	6.16%
Deletions	553,573
Mapped reads with at least one deletion	2.97%
Homopolymer indels	40.16%

2.6. Chromosome stats

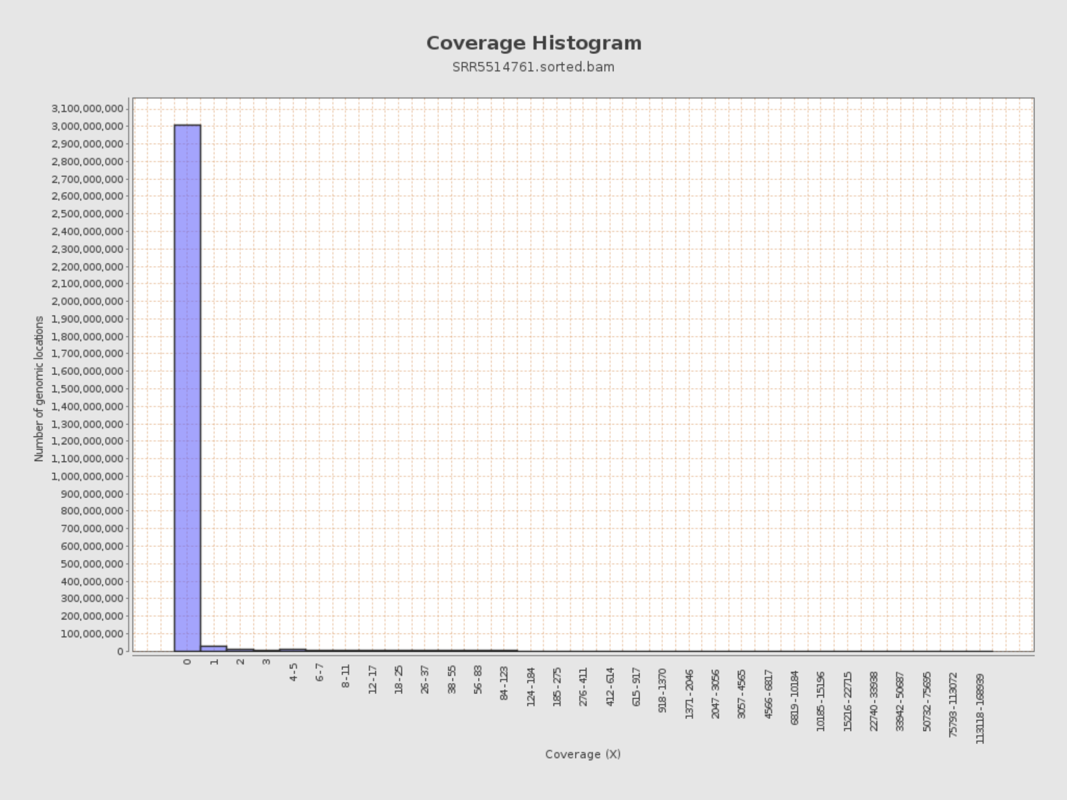
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	90301268	0.3623	9.5905
chr2	243199373	122617245	0.5042	9.3494
chr3	198022430	71074097	0.3589	8.8146
chr4	191154276	101040826	0.5286	9.9657
chr5	180915260	75393908	0.4167	13.9402
chr6	171115067	127106839	0.7428	122.4811
chr7	159138663	86424946	0.5431	10.4583

chr8	146364022	90416053	0.6177	22.3354
chr9	141213431	149595847	1.0594	121.4184
chr10	135534747	57476242	0.4241	10.4686
chr11	135006516	49044713	0.3633	15.2037
chr12	133851895	62882063	0.4698	8.3445
chr13	115169878	63546394	0.5518	24.6665
chr14	107349540	46839935	0.4363	11.061
chr15	102531392	150566214	1.4685	310.7861
chr16	90354753	25907947	0.2867	11.1098
chr17	81195210	20544551	0.253	6.0609
chr18	78077248	29413519	0.3767	6.6465
chr19	59128983	7311895	0.1237	7.0088
chr20	63025520	22274116	0.3534	6.6912
chr21	48129895	6322061	0.1314	5.0518
chr22	51304566	7845008	0.1529	32.3526
chrMT	16571	58906475	3,554.793	3,431.8532
chrX	155270560	49816089	0.3208	14.1955
chrY	59373566	8781151	0.1479	3.1958

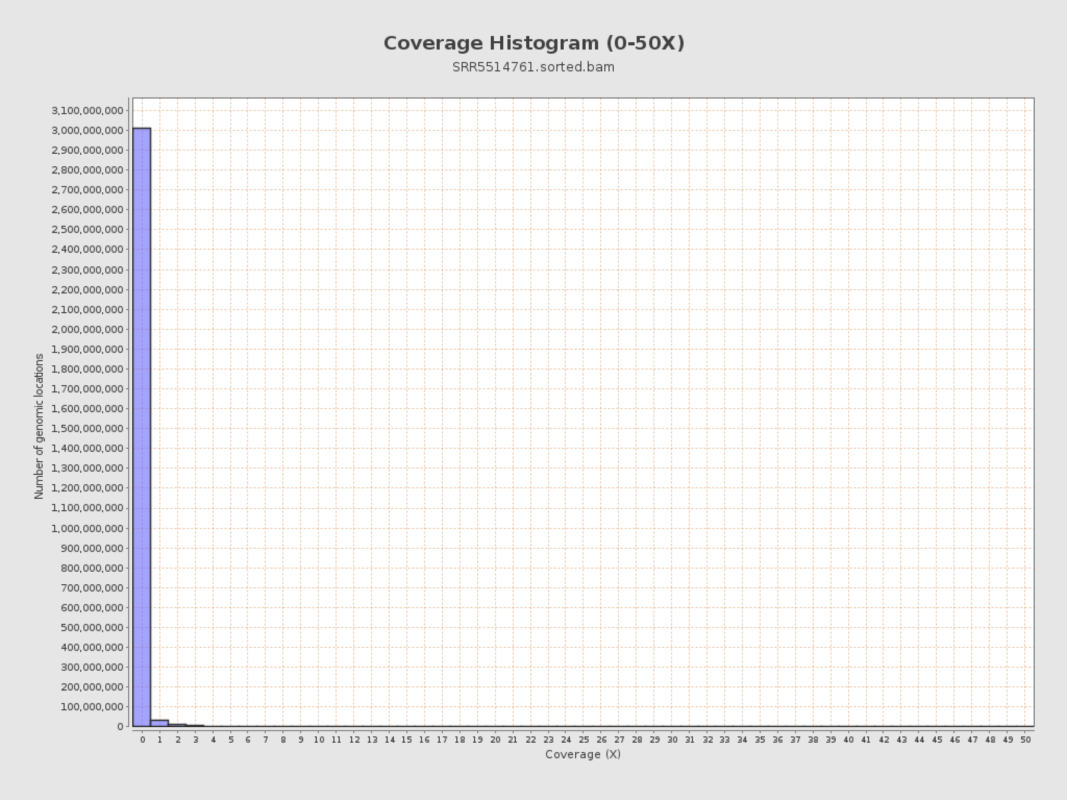
3. Results : Coverage across reference



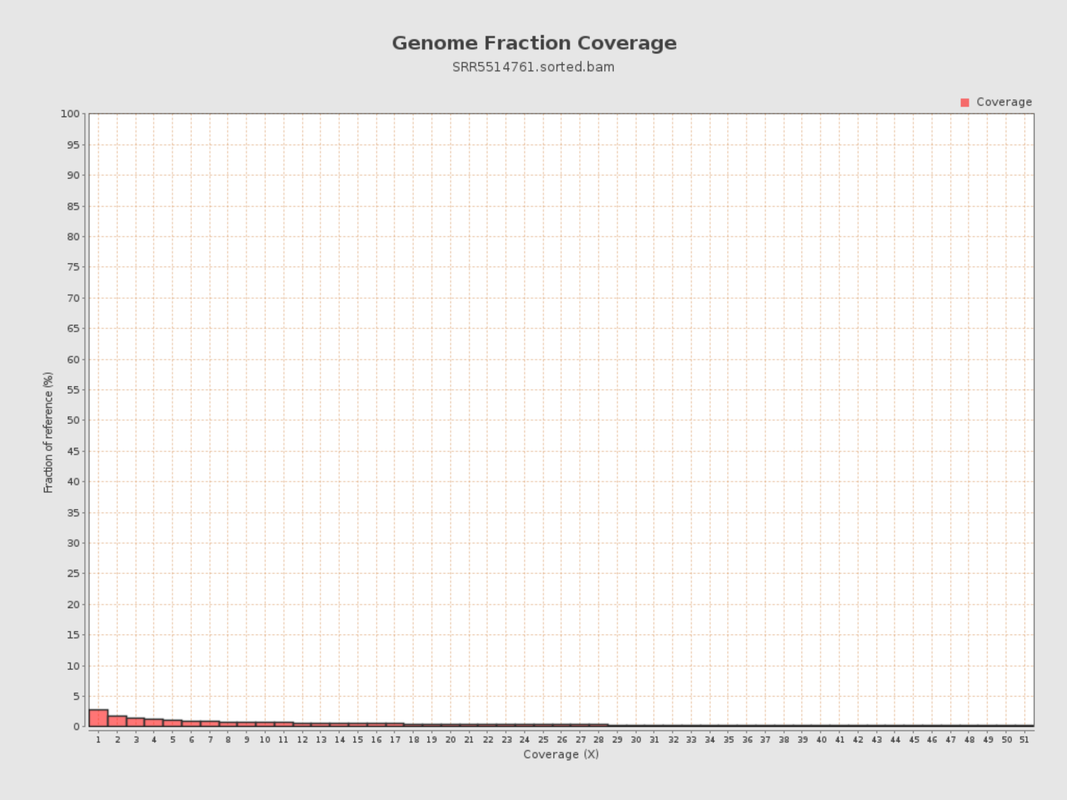
4. Results : Coverage Histogram



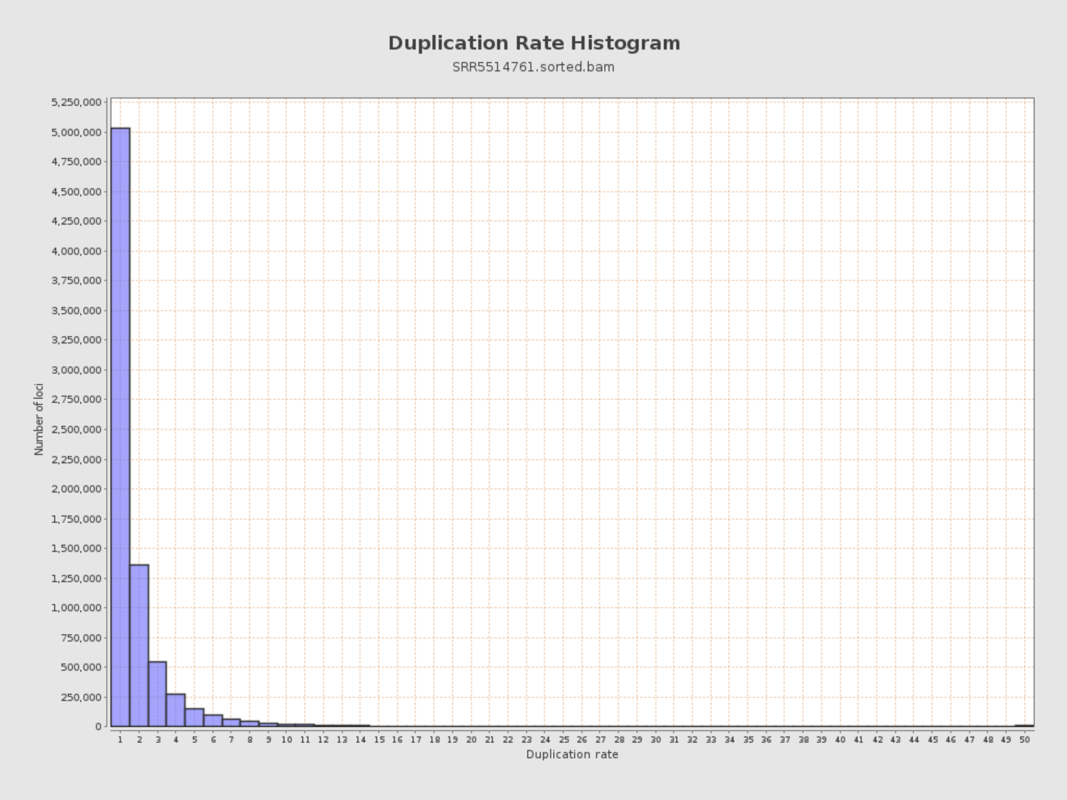
5. Results : Coverage Histogram (0-50X)



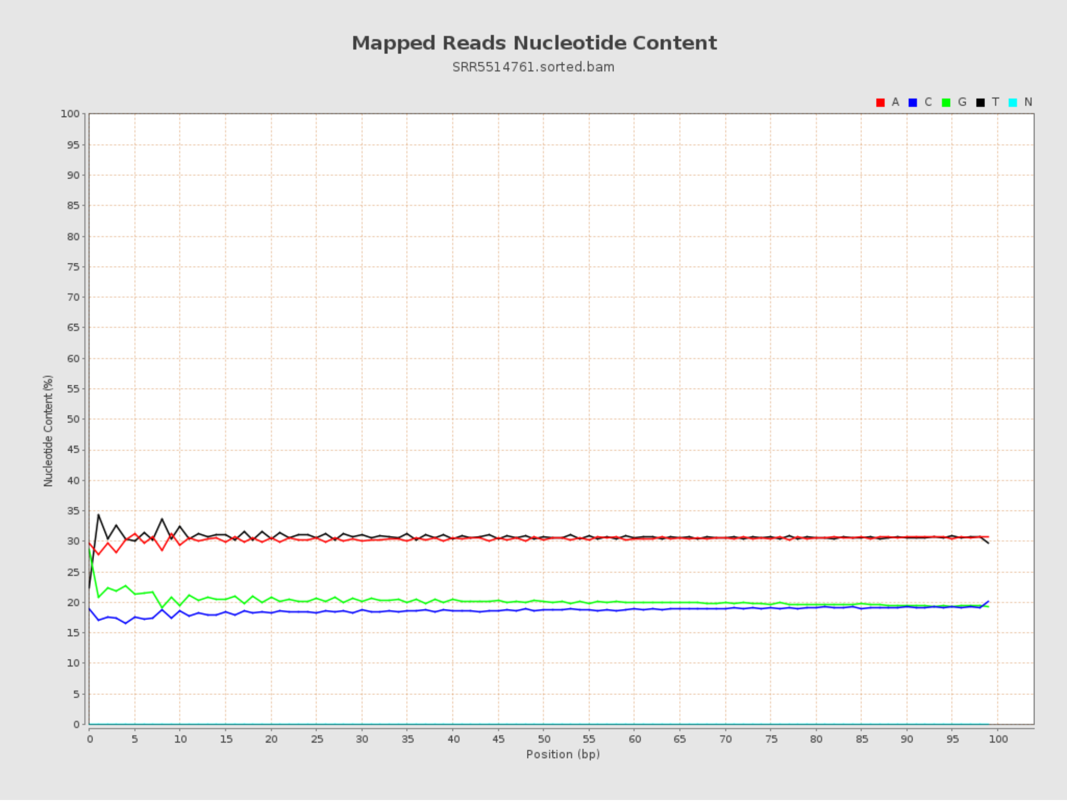
6. Results : Genome Fraction Coverage



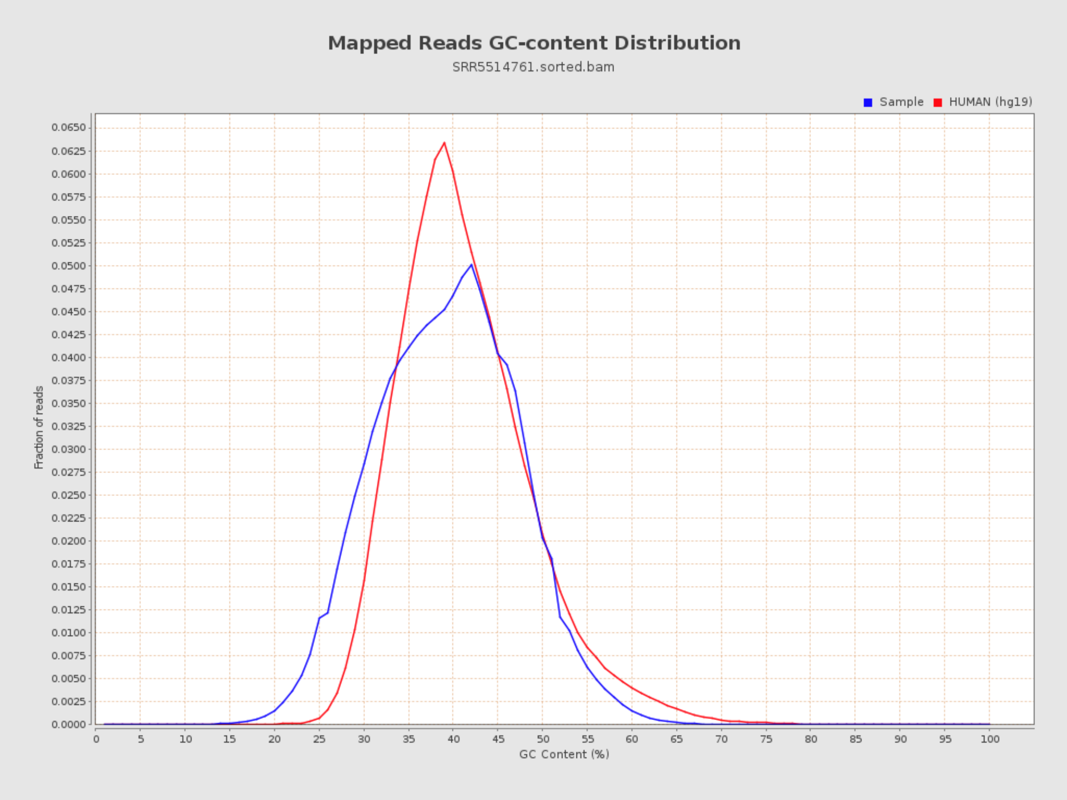
7. Results : Duplication Rate Histogram



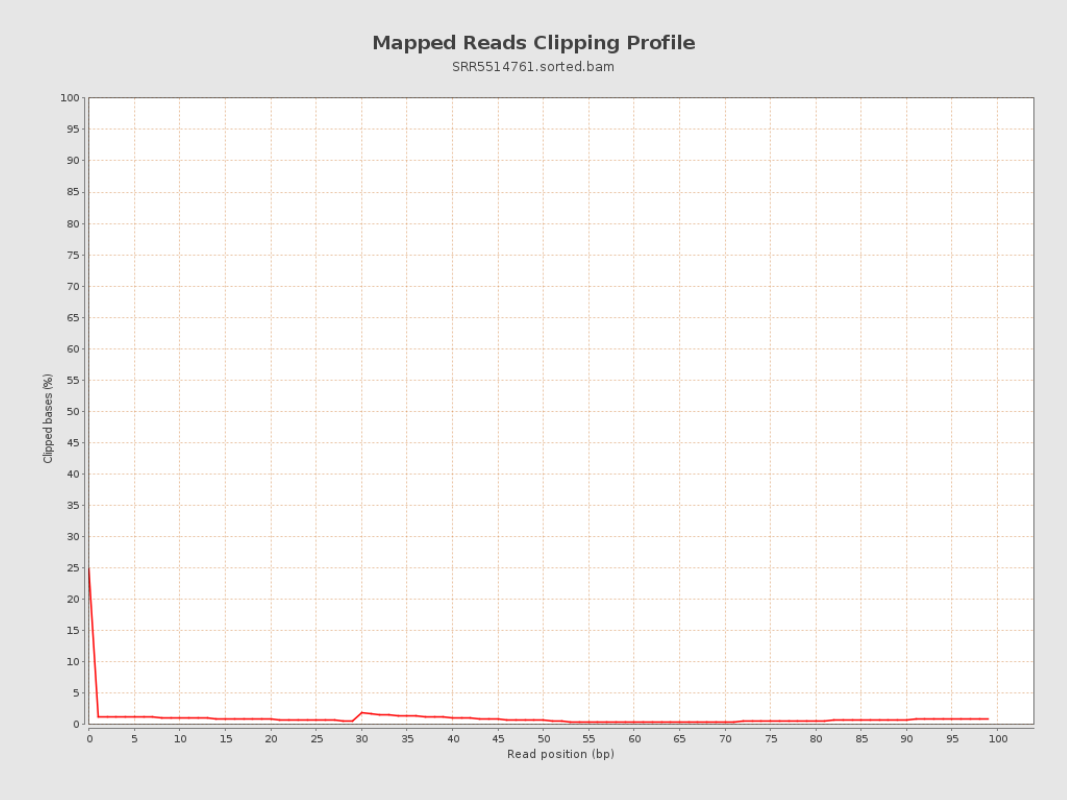
8. Results : Mapped Reads Nucleotide Content



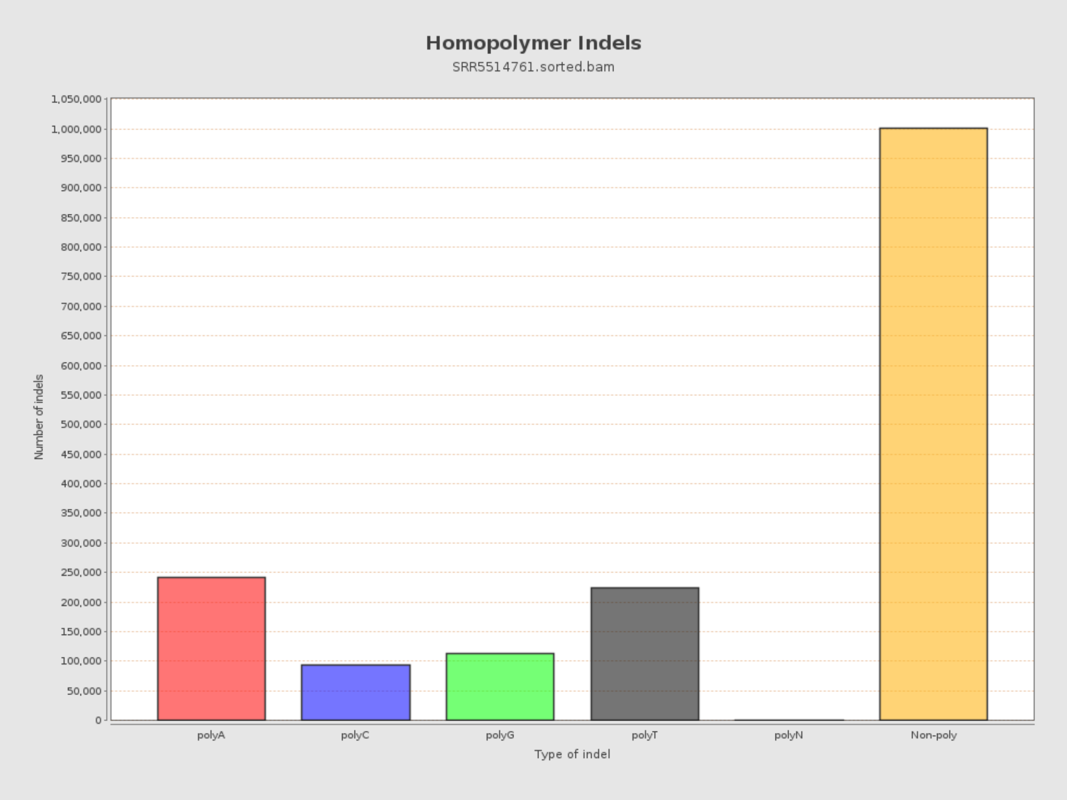
9. Results : Mapped Reads GC-content Distribution



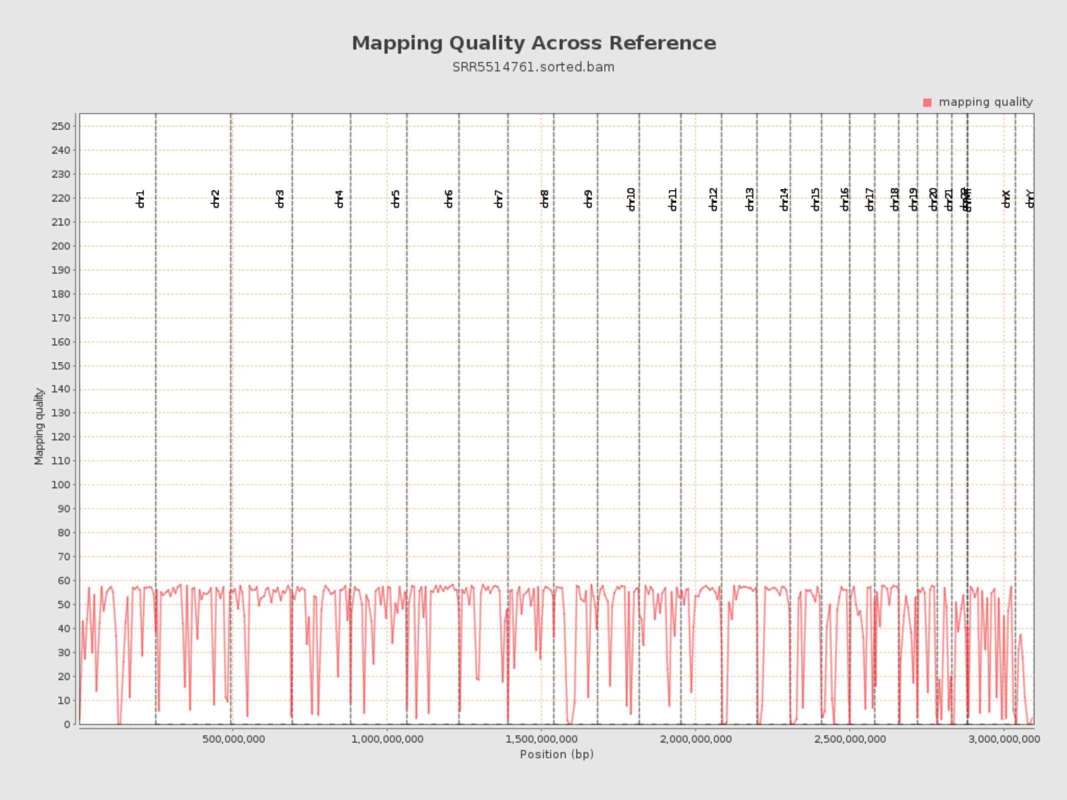
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram