Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 21:02:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514763.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_SRR5514763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 21:02:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,826,883
Mapped reads	15,725,907 / 83.53%
Unmapped reads	3,100,976 / 16.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,539,897 / 13.49%
Read min/max/mean length	30 / 100 / 104.48
Duplicated reads (estimated)	10,161,943 / 53.98%
Duplication rate	35.34%
Clipped reads	8,574,991 / 45.55%

2.2. ACGT Content

Number/percentage of A's	463,229,854 / 31.24%
Number/percentage of C's	274,972,590 / 18.54%
Number/percentage of T's	458,508,304 / 30.92%
Number/percentage of G's	286,220,270 / 19.3%
Number/percentage of N's	97,119 / 0.01%
GC Percentage	37.84%

2.3. Coverage

Mean	0.4795

Standard Deviation	23.5729

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

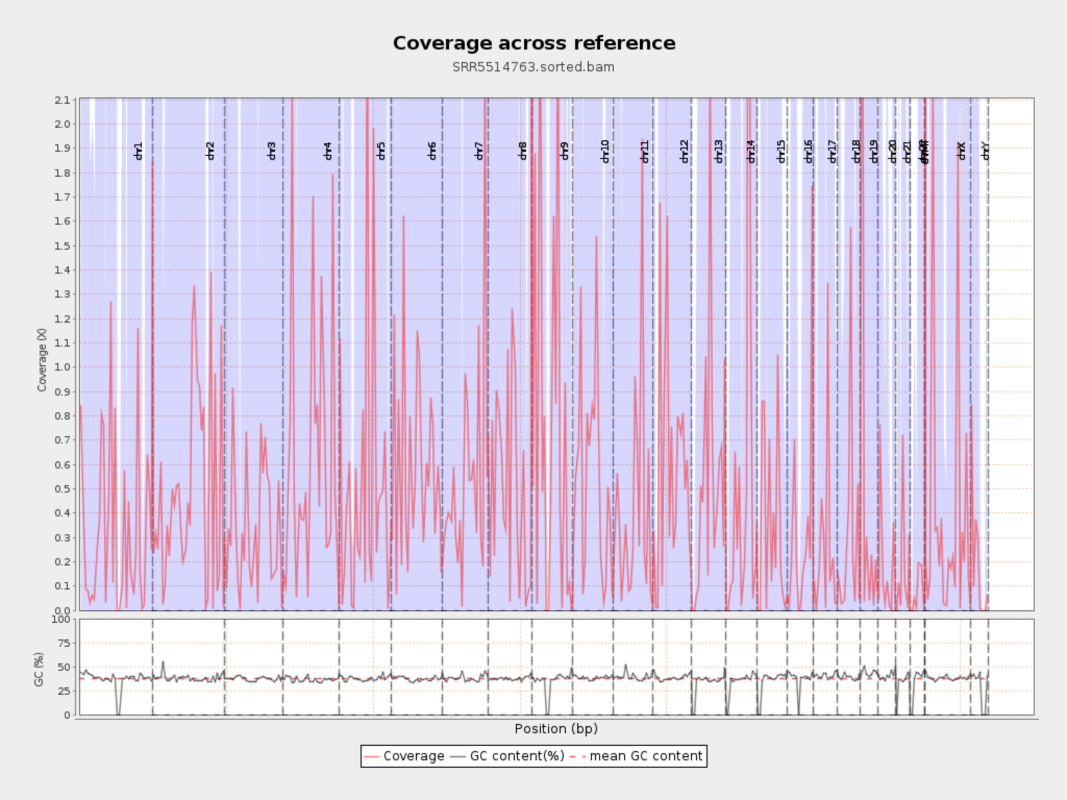
General error rate	0.67%
Mismatches	8,426,015
Insertions	881,248
Mapped reads with at least one insertion	5.35%
Deletions	423,454
Mapped reads with at least one deletion	2.49%
Homopolymer indels	46.95%

2.6. Chromosome stats

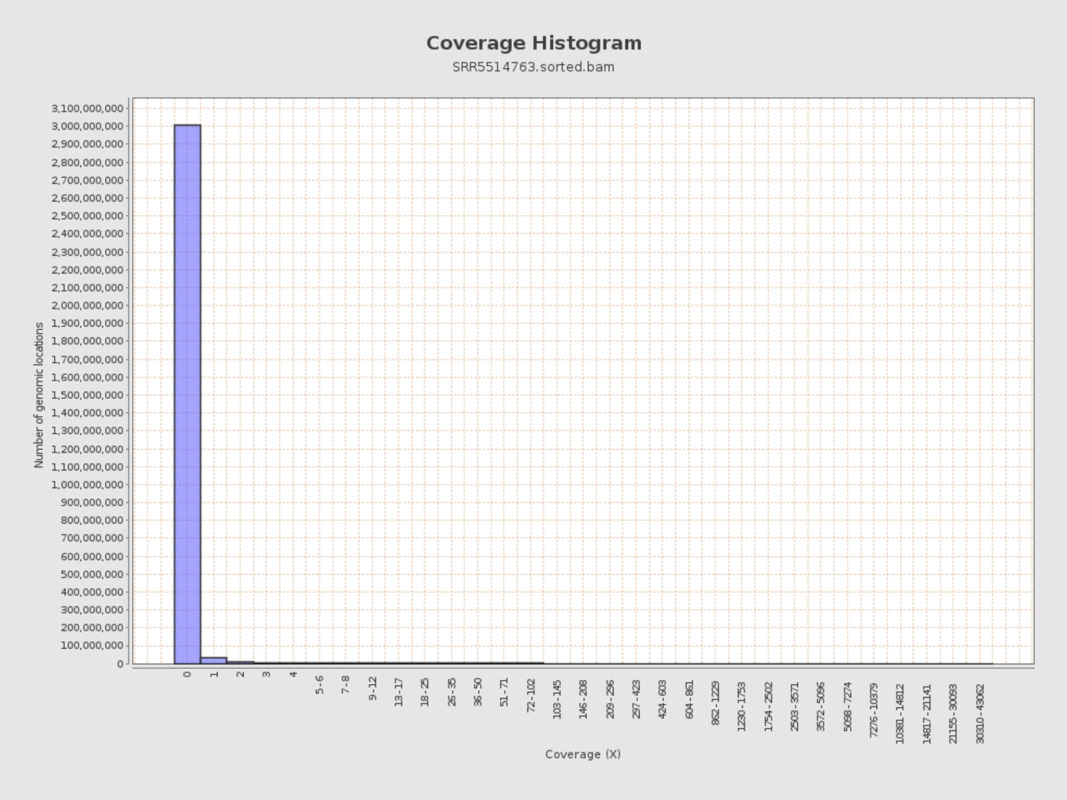
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	86581169	0.3474	10.2319
chr2	243199373	119230603	0.4903	12.217
chr3	198022430	67454972	0.3406	7.549
chr4	191154276	121080376	0.6334	9.4484
chr5	180915260	93199731	0.5152	15.03
chr6	171115067	105259300	0.6151	28.9556
chr7	159138663	88444268	0.5558	49.139

chr8	146364022	71421153	0.488	10.0144
chr9	141213431	108959730	0.7716	18.1268
chr10	135534747	75806832	0.5593	17.7413
chr11	135006516	55293368	0.4096	9.3621
chr12	133851895	78182716	0.5841	12.0462
chr13	115169878	61477153	0.5338	10.1684
chr14	107349540	60350939	0.5622	10.0933
chr15	102531392	34261361	0.3342	8.6598
chr16	90354753	30161984	0.3338	42.3092
chr17	81195210	21940161	0.2702	5.773
chr18	78077248	25519462	0.3268	7.1434
chr19	59128983	33650755	0.5691	78.9882
chr20	63025520	11213251	0.1779	5.8531
chr21	48129895	9122473	0.1895	4.363
chr22	51304566	3715038	0.0724	3.1661
chrMT	16571	50700812	3,059.6109	3,387.2628
chrX	155270560	60322831	0.3885	7.1393
chrY	59373566	10967689	0.1847	4.6925

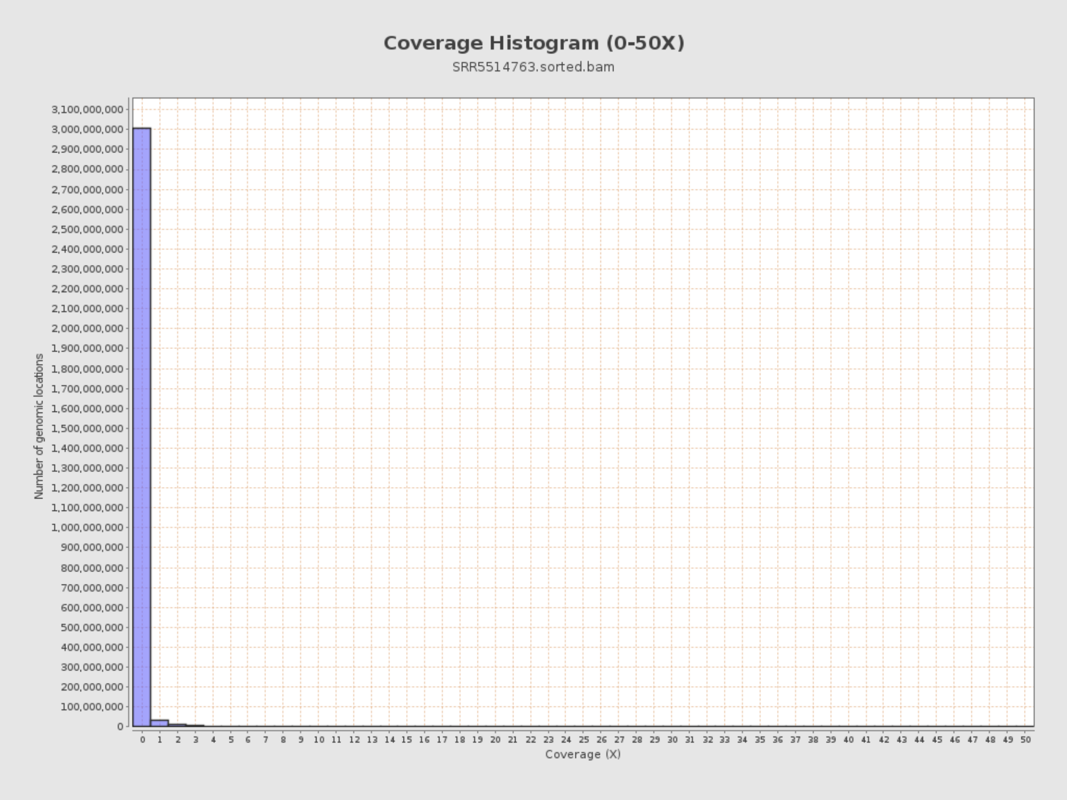
3. Results : Coverage across reference



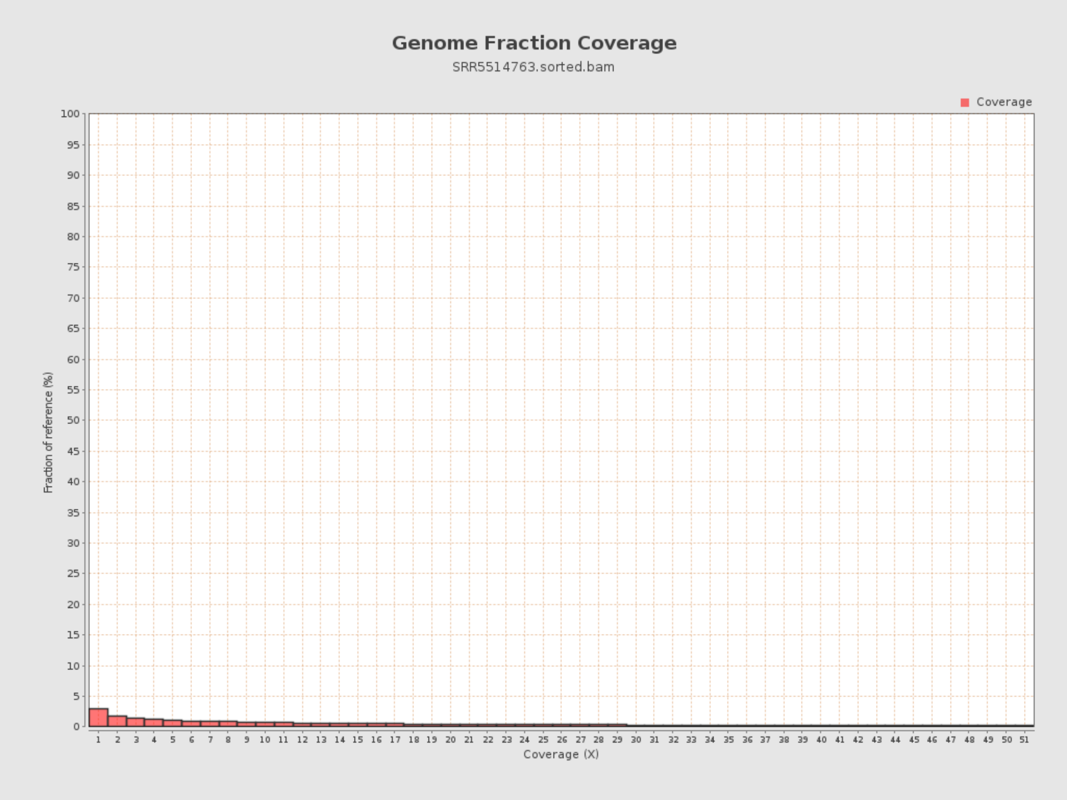
4. Results : Coverage Histogram



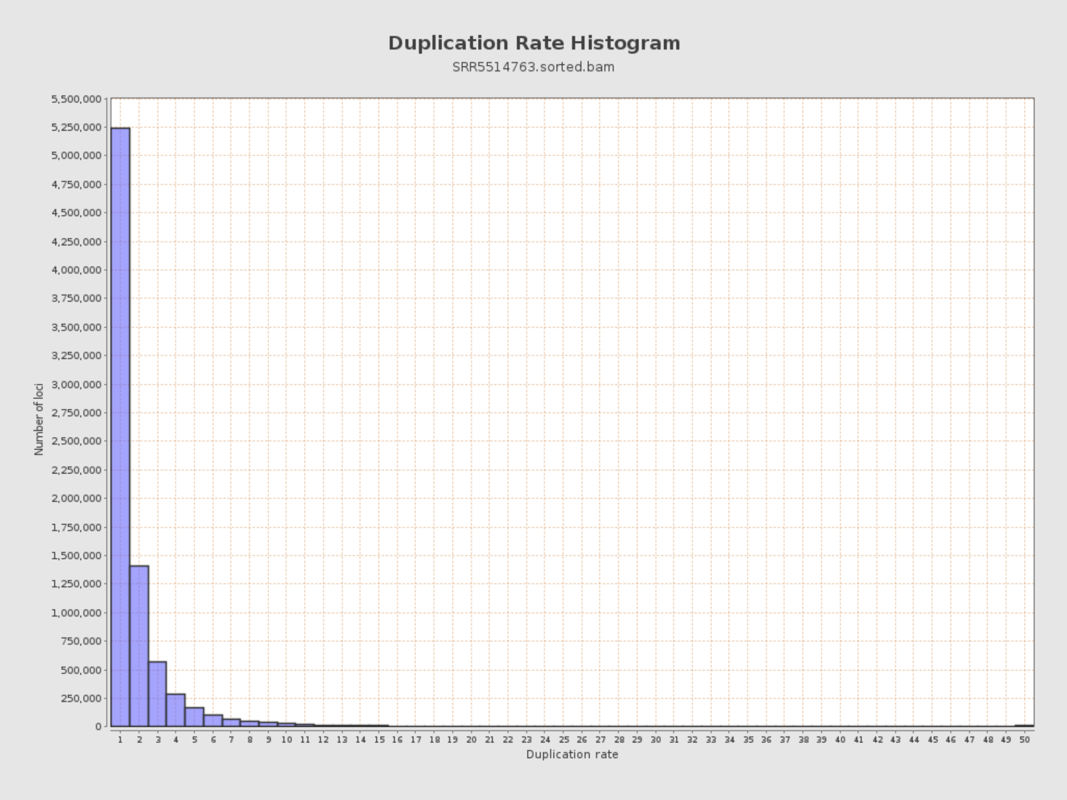
5. Results : Coverage Histogram (0-50X)



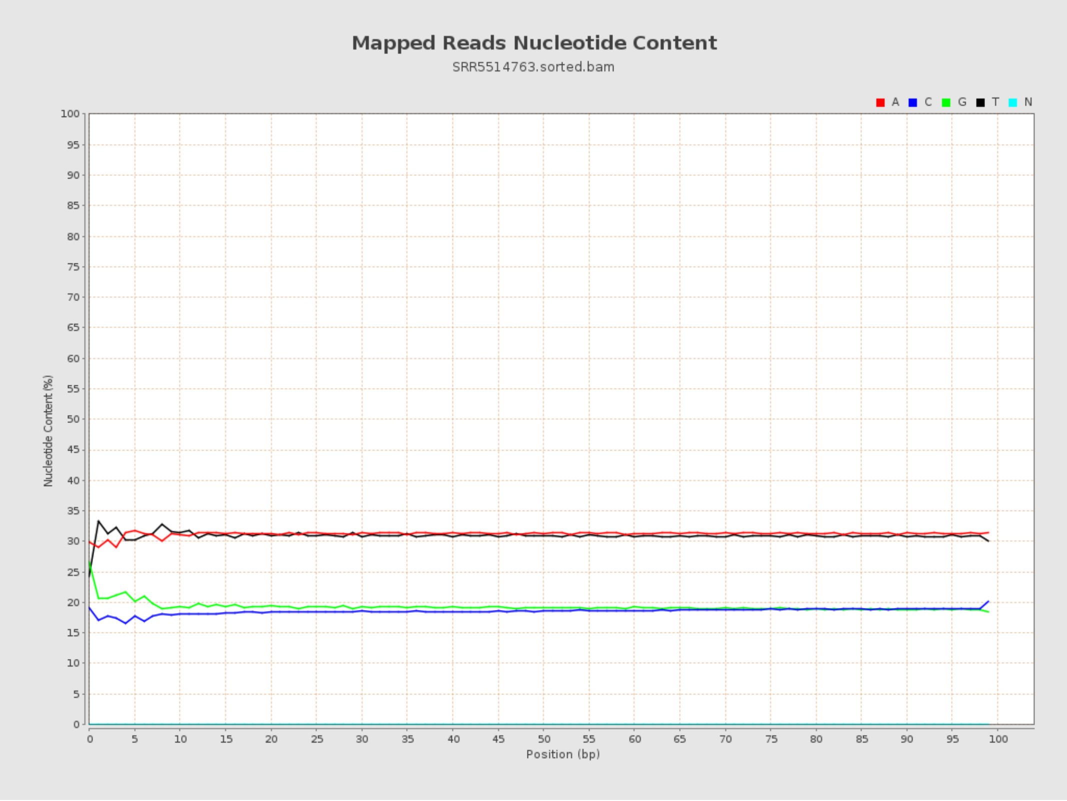
6. Results : Genome Fraction Coverage



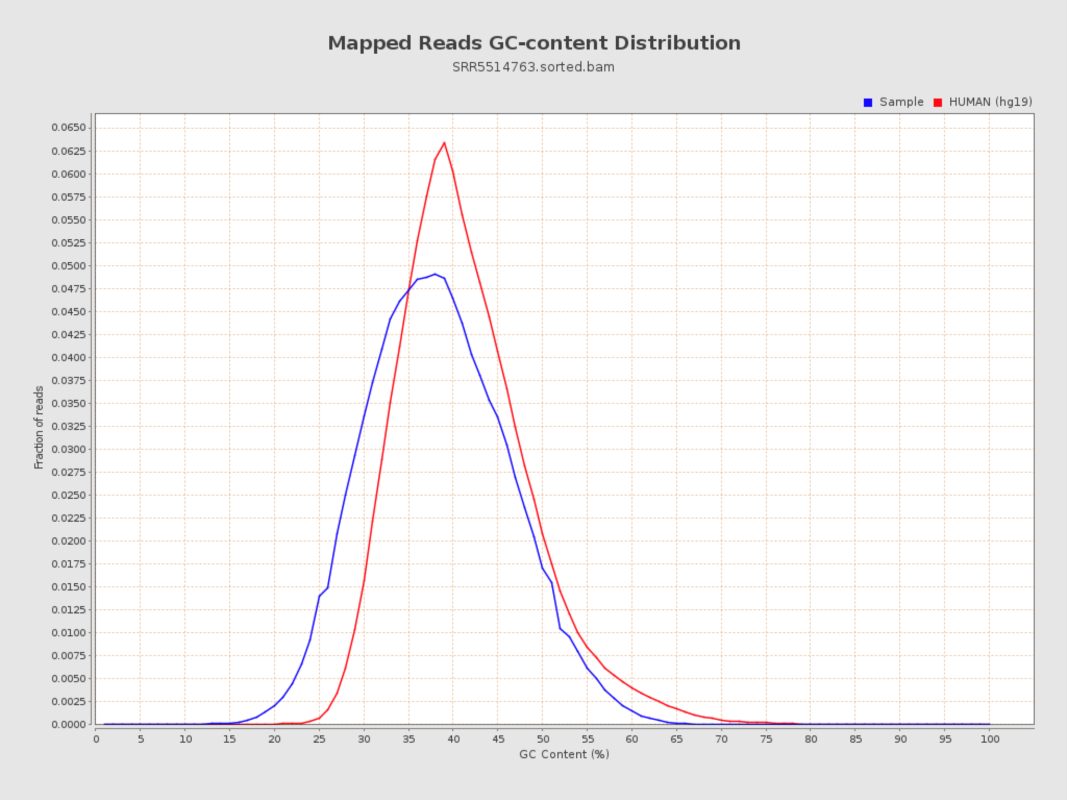
7. Results : Duplication Rate Histogram



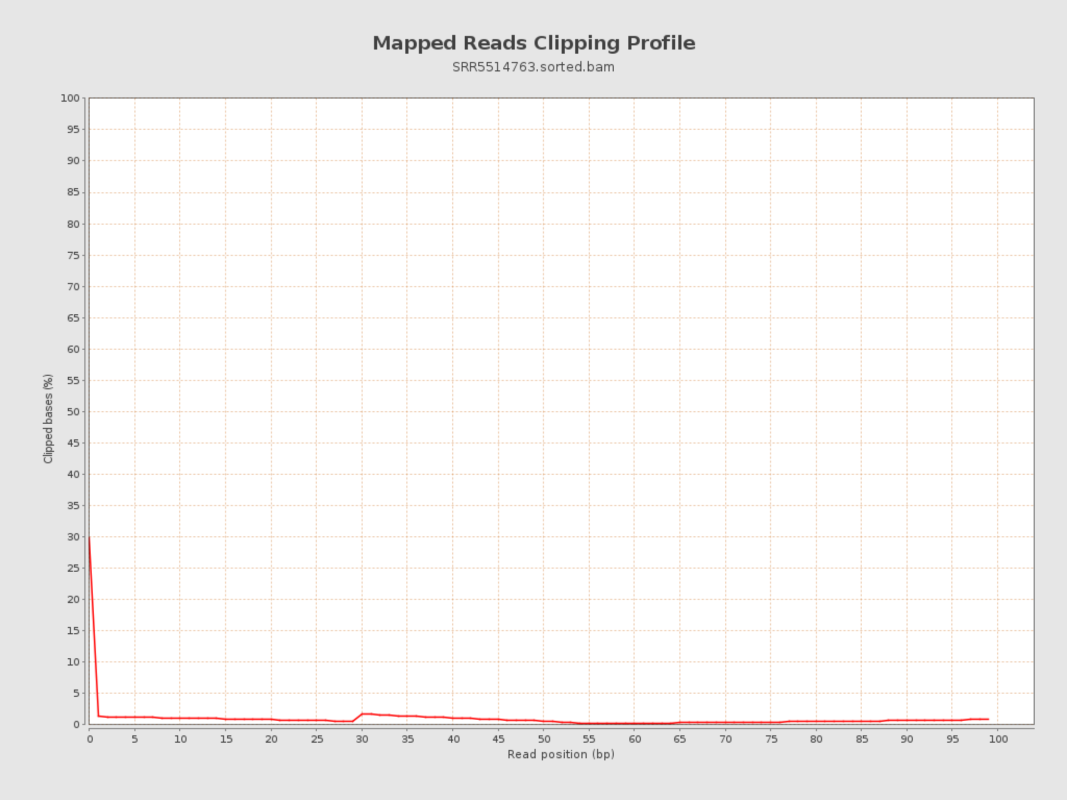
8. Results : Mapped Reads Nucleotide Content



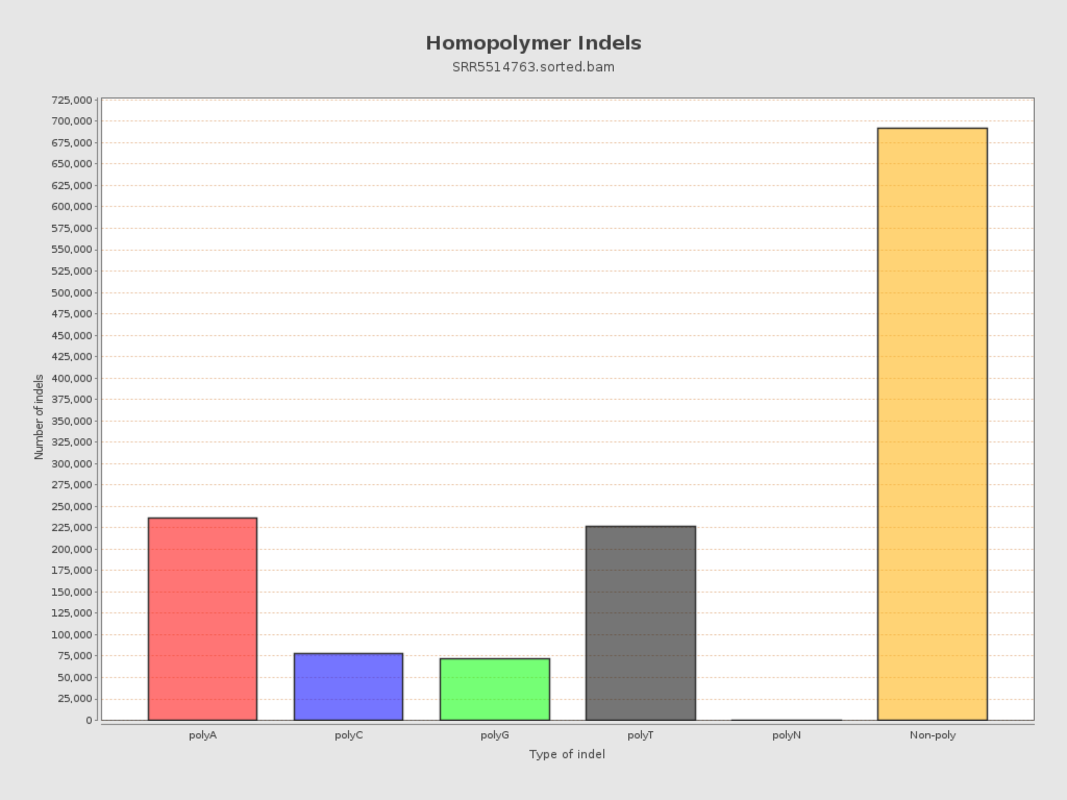
9. Results : Mapped Reads GC-content Distribution



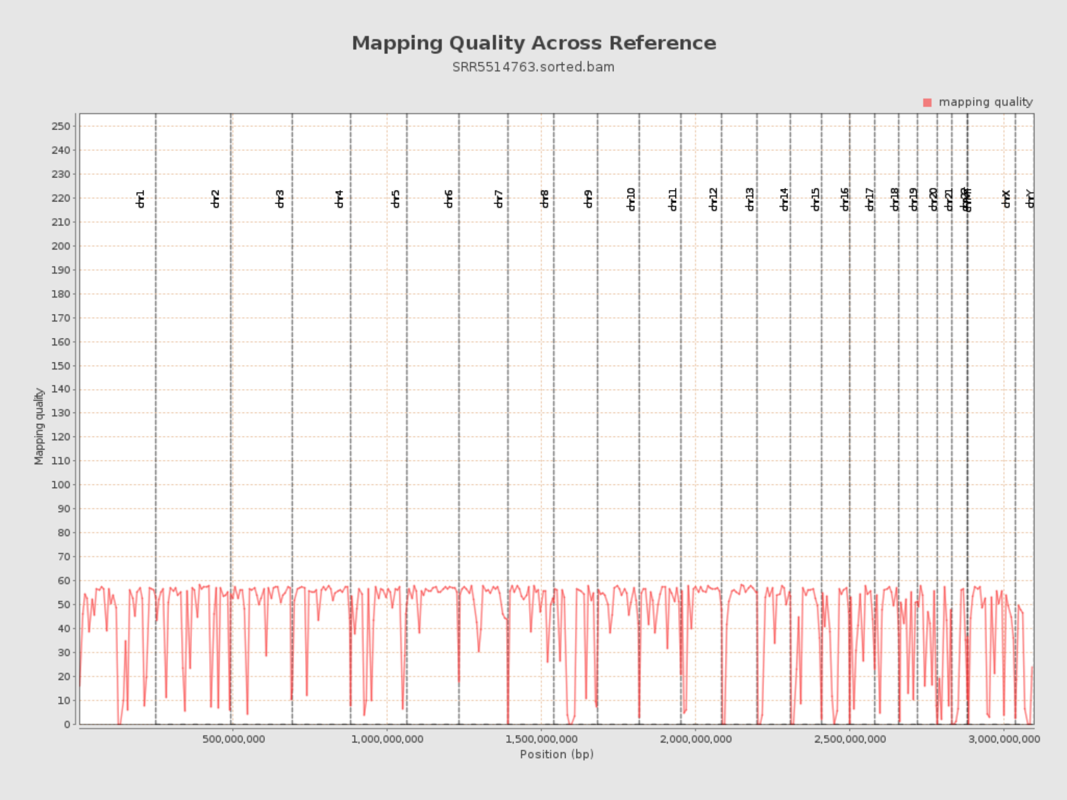
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram