Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 02:11:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514753.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_SRR5514753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 02:11:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	79,277,973
Mapped reads	75,125,323 / 94.76%
Unmapped reads	4,152,650 / 5.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,535,786 / 13.29%
Read min/max/mean length	30 / 100 / 104.52
Duplicated reads (estimated)	60,480,487 / 76.29%
Duplication rate	47.05%
Clipped reads	35,527,109 / 44.81%

2.2. ACGT Content

Number/percentage of A's	2,232,441,410 / 31.15%
Number/percentage of C's	1,344,308,133 / 18.76%
Number/percentage of T's	2,201,642,000 / 30.72%
Number/percentage of G's	1,388,718,824 / 19.37%
Number/percentage of N's	492,682 / 0.01%
GC Percentage	38.13%

2.3. Coverage

Mean	2.3168

Standard Deviation	76.5188

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

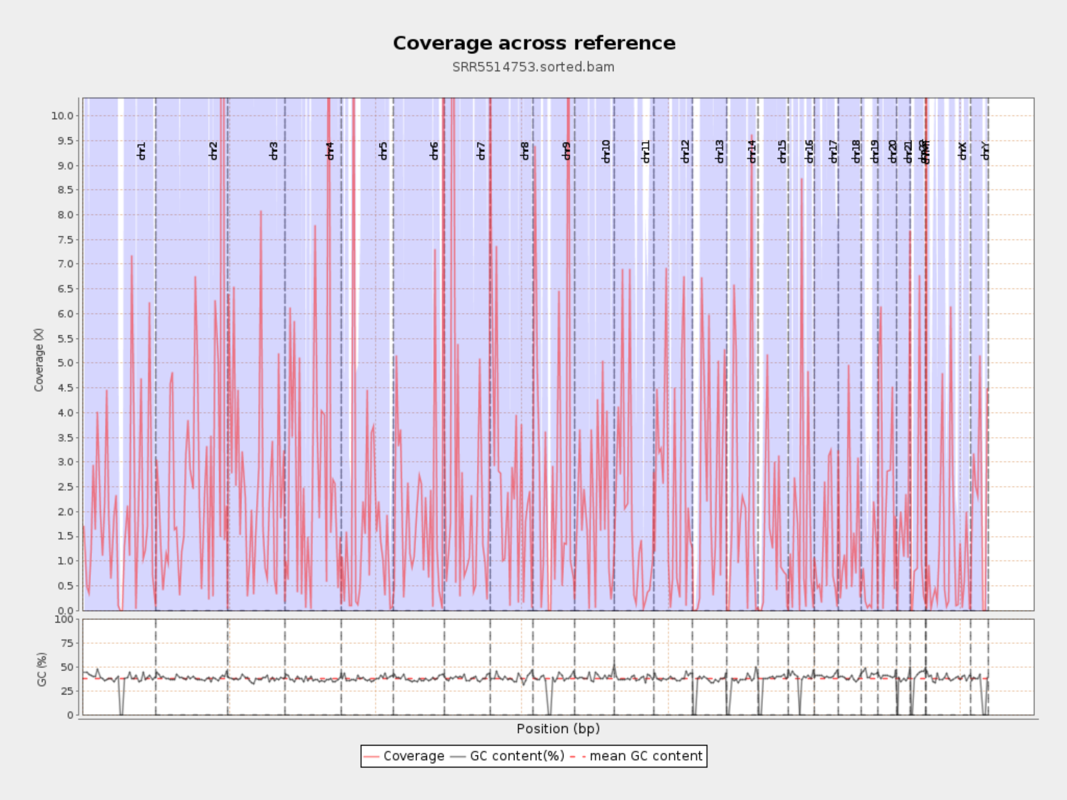
General error rate	0.63%
Mismatches	37,984,791
Insertions	4,708,125
Mapped reads with at least one insertion	6.01%
Deletions	1,699,682
Mapped reads with at least one deletion	2.14%
Homopolymer indels	54.3%

2.6. Chromosome stats

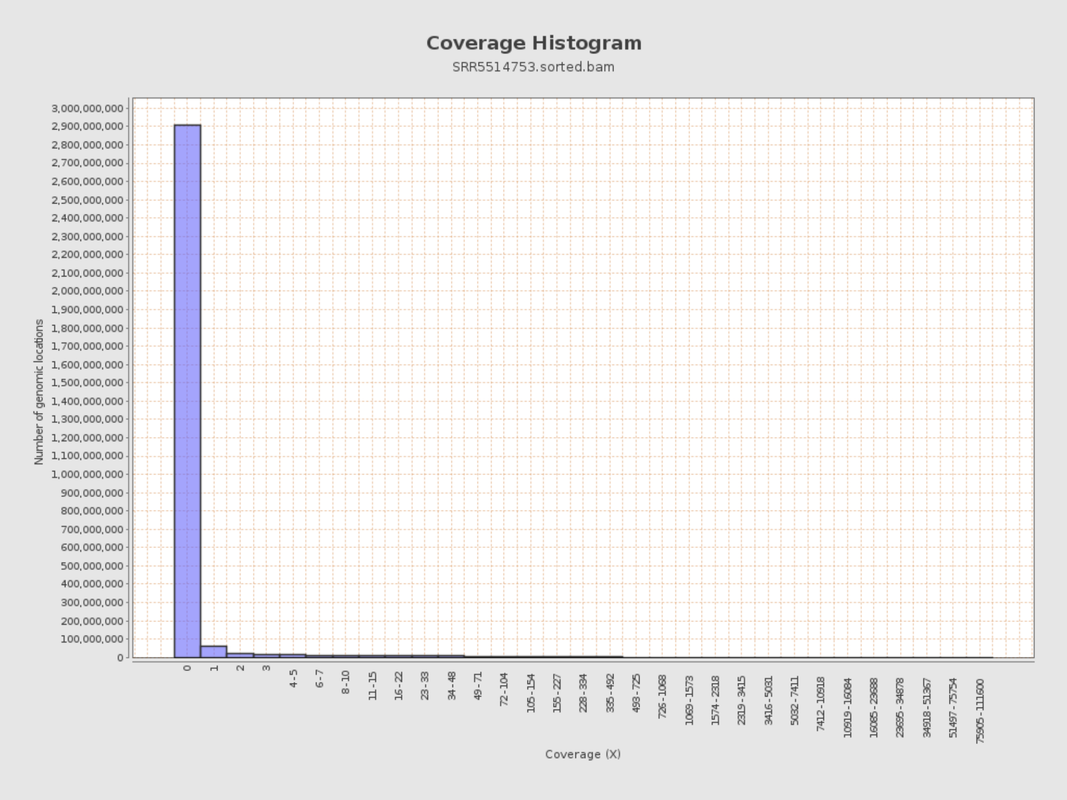
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	487917857	1.9575	41.0683
chr2	243199373	823826257	3.3875	186.6682
chr3	198022430	509902818	2.575	36.5951
chr4	191154276	592968108	3.102	41.1185
chr5	180915260	320996630	1.7743	31.751
chr6	171115067	383830752	2.2431	35.0739
chr7	159138663	391453242	2.4598	39.3934

chr8	146364022	373351432	2.5508	92.3376
chr9	141213431	422924363	2.9949	81.3994
chr10	135534747	280191959	2.0673	48.4535
chr11	135006516	270092658	2.0006	36.1074
chr12	133851895	346831352	2.5912	39.7416
chr13	115169878	300916520	2.6128	40.9499
chr14	107349540	267927992	2.4958	36.4204
chr15	102531392	154844794	1.5102	25.3691
chr16	90354753	160636959	1.7778	47.7689
chr17	81195210	98396639	1.2119	24.1327
chr18	78077248	116803705	1.496	32.7693
chr19	59128983	37977165	0.6423	17.2412
chr20	63025520	176719935	2.8039	65.9268
chr21	48129895	97056721	2.0166	77.2706
chr22	51304566	75272030	1.4672	91.6214
chrMT	16571	169683850	10,239.8075	9,157.6634
chrX	155270560	168409428	1.0846	21.9905
chrY	59373566	143285118	2.4133	52.415

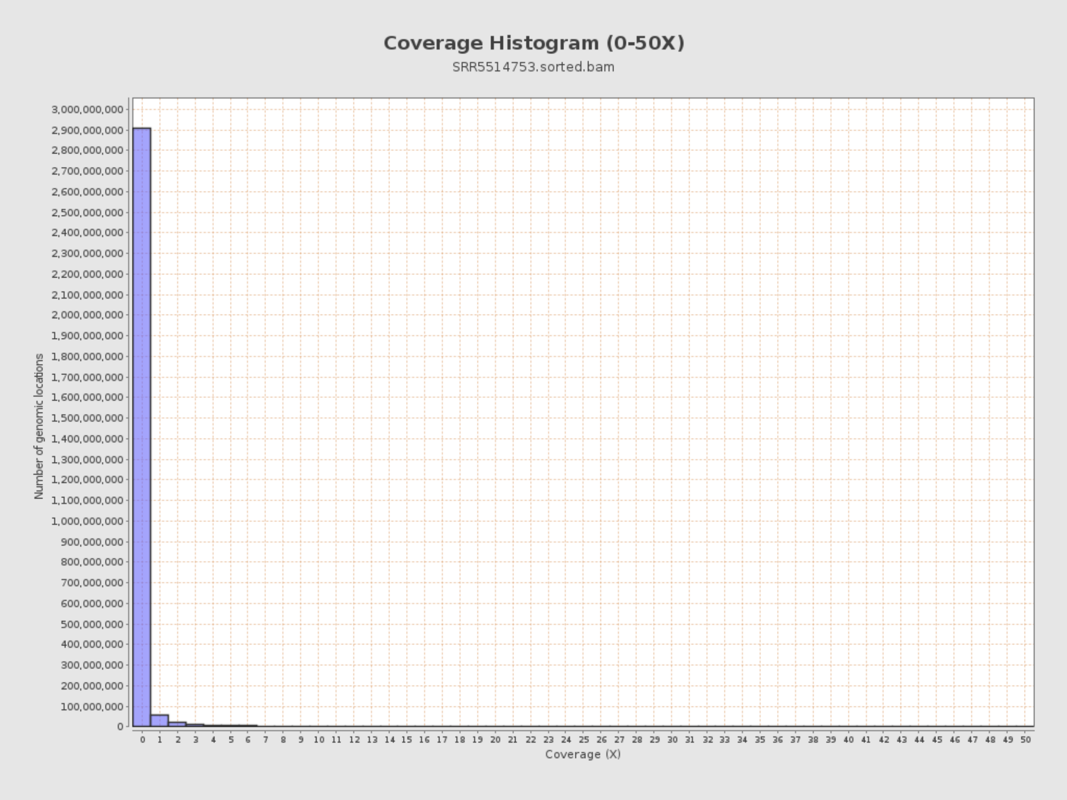
3. Results : Coverage across reference



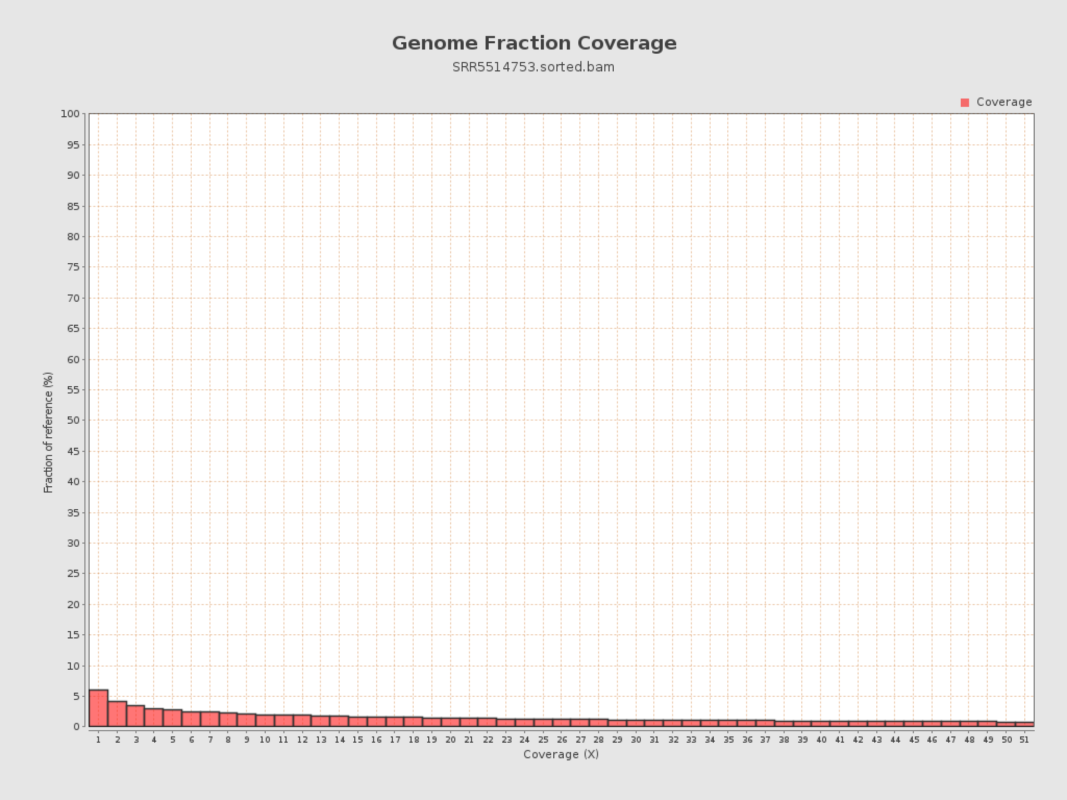
4. Results : Coverage Histogram



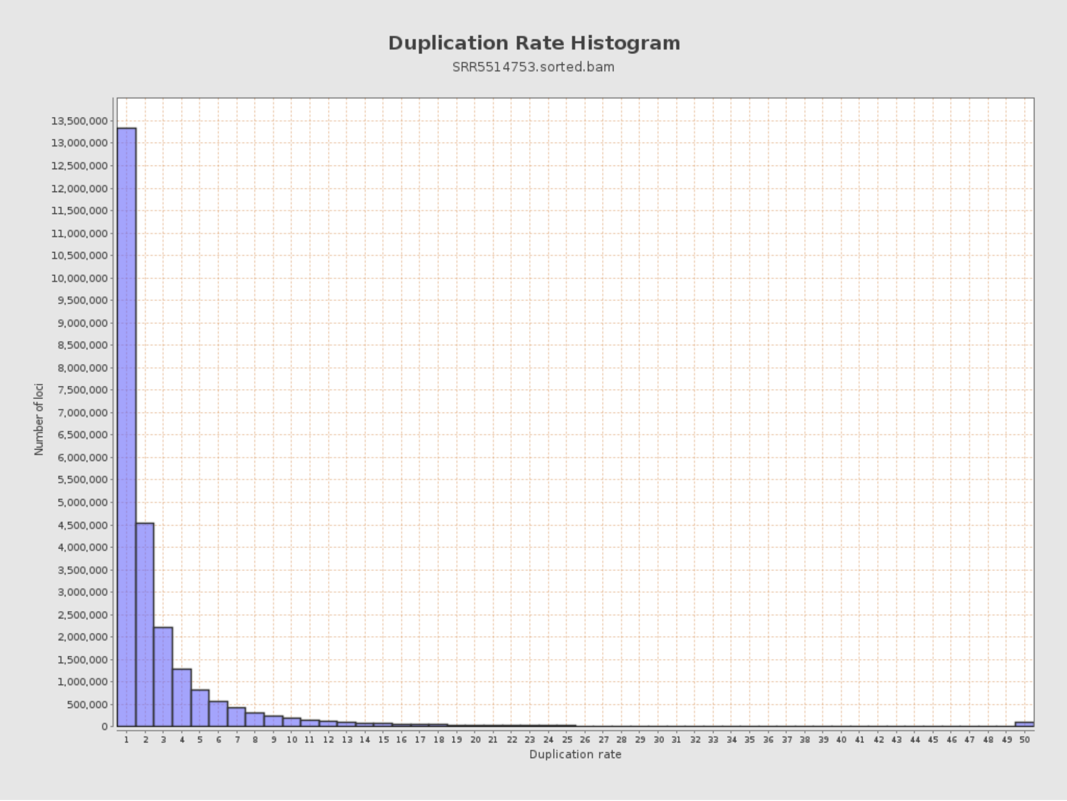
5. Results : Coverage Histogram (0-50X)



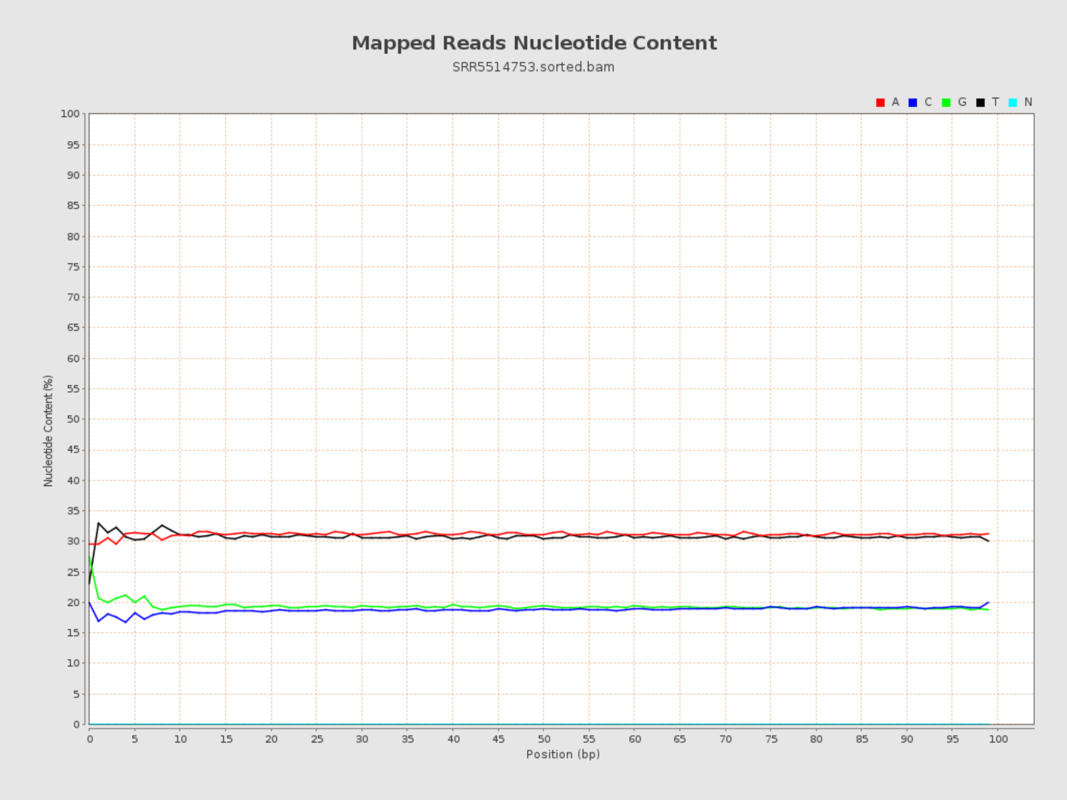
6. Results : Genome Fraction Coverage



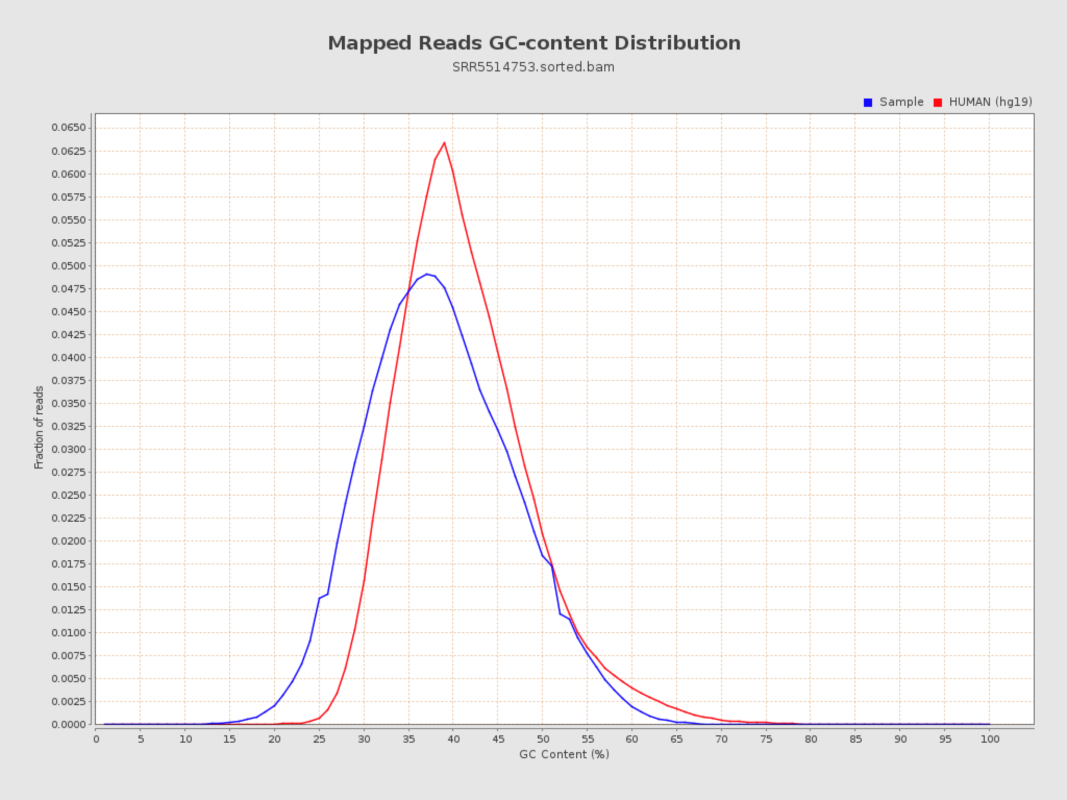
7. Results : Duplication Rate Histogram



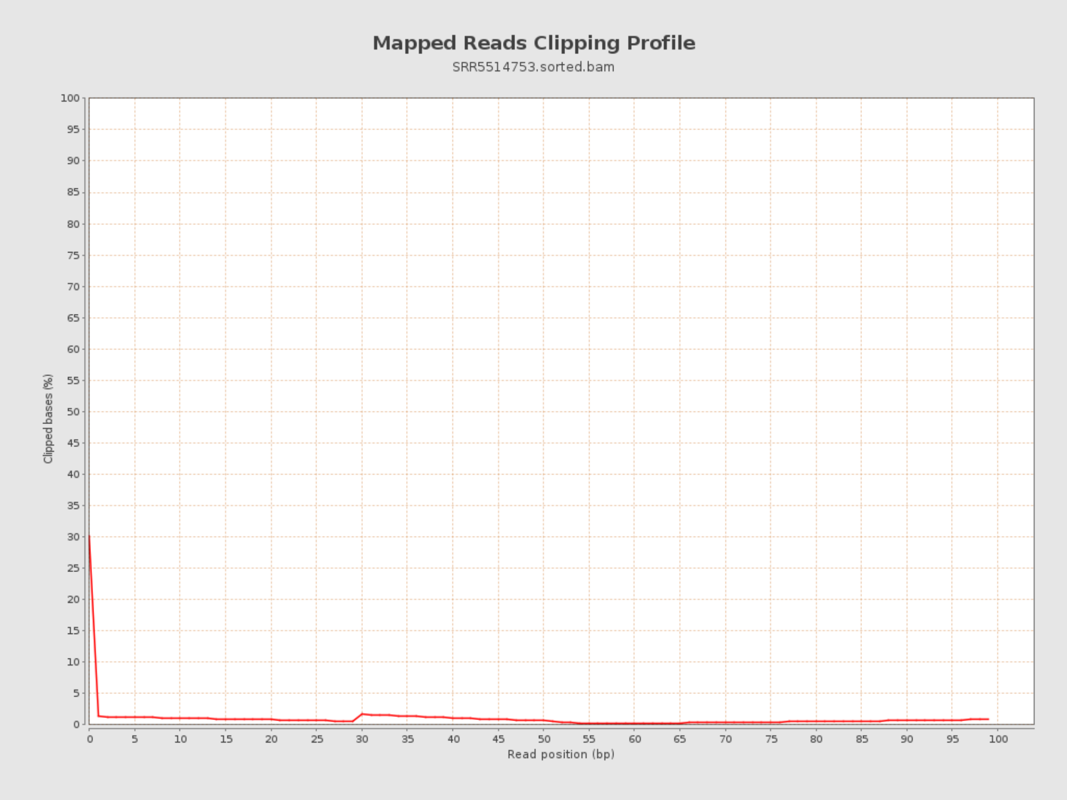
8. Results : Mapped Reads Nucleotide Content



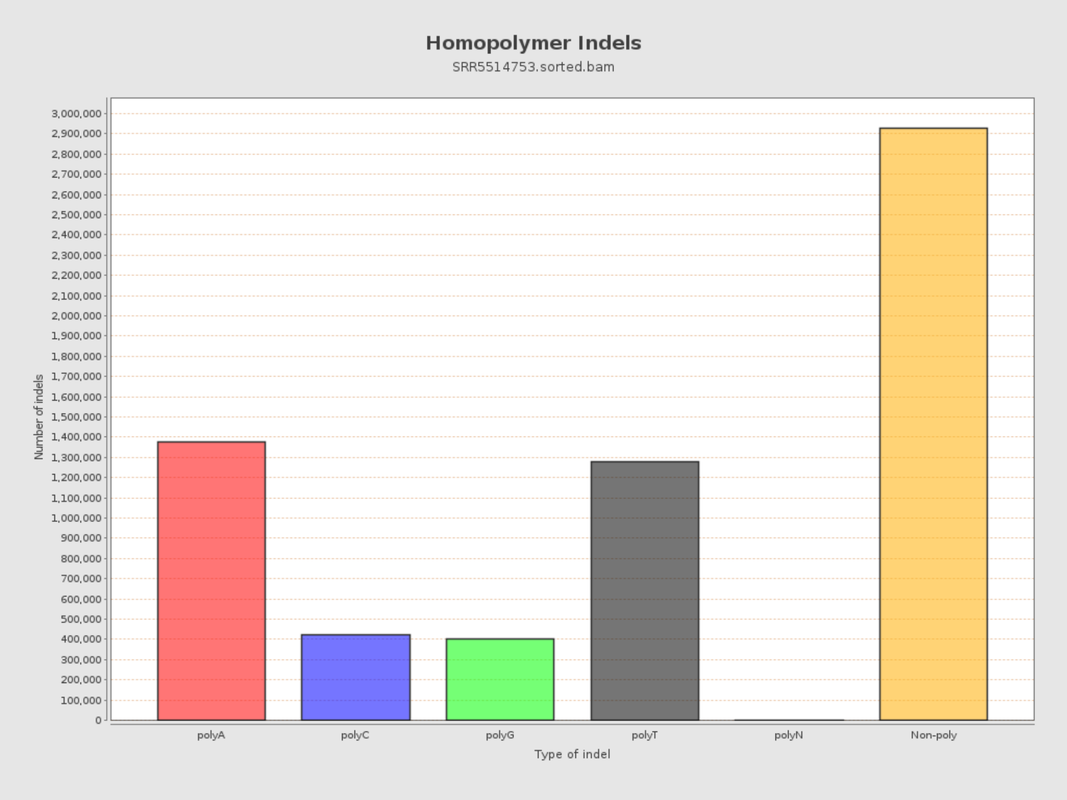
9. Results : Mapped Reads GC-content Distribution



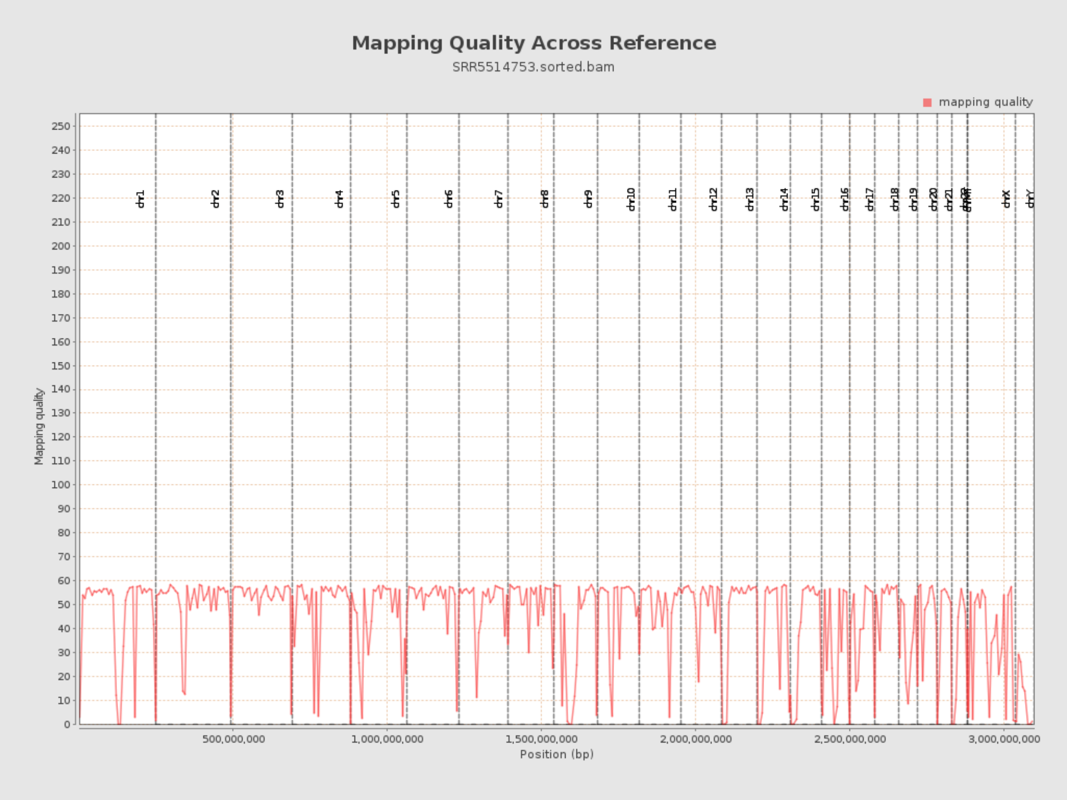
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram