Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 06:02:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514764.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_SRR5514764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 06:02:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,268,265
Mapped reads	10,952,130 / 76.76%
Unmapped reads	3,316,135 / 23.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,944,273 / 13.63%
Read min/max/mean length	30 / 100 / 104.54
Duplicated reads (estimated)	7,313,300 / 51.26%
Duplication rate	31.49%
Clipped reads	6,929,105 / 48.56%

2.2. ACGT Content

Number/percentage of A's	308,171,484 / 30.7%
Number/percentage of C's	187,816,632 / 18.71%
Number/percentage of T's	308,608,610 / 30.74%
Number/percentage of G's	199,173,451 / 19.84%
Number/percentage of N's	66,486 / 0.01%
GC Percentage	38.55%

2.3. Coverage

Mean	0.3246

Standard Deviation	38.1619

2.4. Mapping Quality

Mean Mapping Quality	43.88

2.5. Mismatches and indels

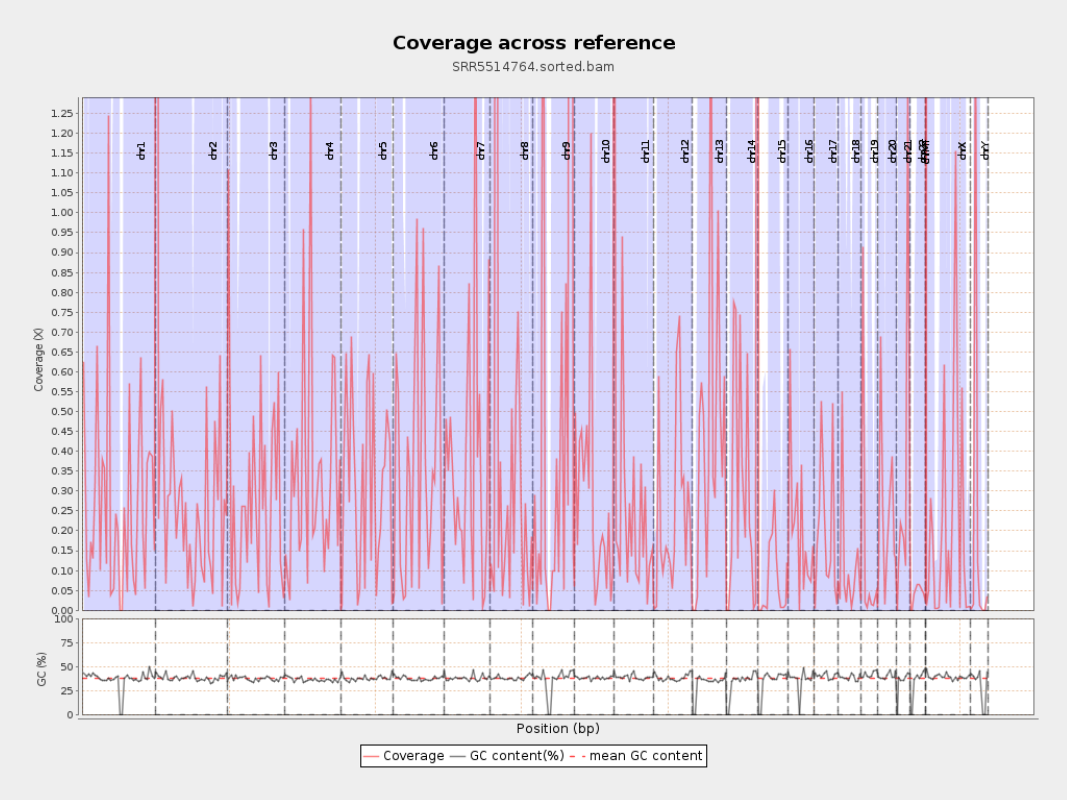
General error rate	0.74%
Mismatches	6,252,594
Insertions	665,822
Mapped reads with at least one insertion	5.79%
Deletions	358,181
Mapped reads with at least one deletion	3.02%
Homopolymer indels	39.73%

2.6. Chromosome stats

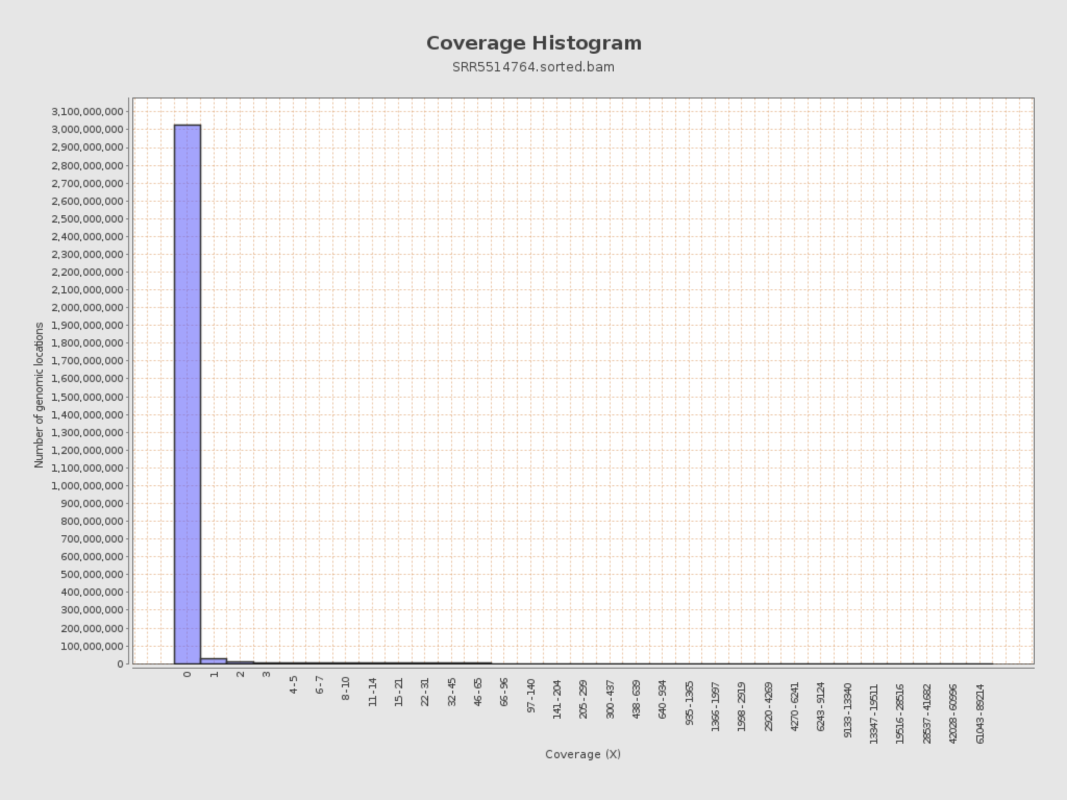
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	69088162	0.2772	9.2617
chr2	243199373	100136158	0.4117	47.1406
chr3	198022430	55722213	0.2814	5.994
chr4	191154276	65711115	0.3438	5.8549
chr5	180915260	56750290	0.3137	5.5931
chr6	171115067	62418742	0.3648	6.6881
chr7	159138663	62536299	0.393	7.4696

chr8	146364022	60665399	0.4145	67.0984
chr9	141213431	99373458	0.7037	143.0725
chr10	135534747	37975730	0.2802	5.201
chr11	135006516	36748200	0.2722	18.0882
chr12	133851895	32430223	0.2423	4.6742
chr13	115169878	53563311	0.4651	7.2326
chr14	107349540	37372991	0.3481	6.3212
chr15	102531392	7312036	0.0713	3.2285
chr16	90354753	17871535	0.1978	4.9147
chr17	81195210	16025904	0.1974	4.7064
chr18	78077248	8781618	0.1125	2.8552
chr19	59128983	8235731	0.1393	33.6876
chr20	63025520	15933166	0.2528	11.0882
chr21	48129895	16025459	0.333	16.7913
chr22	51304566	2122933	0.0414	1.7953
chrMT	16571	36611673	2,209.3822	2,433.7492
chrX	155270560	32241464	0.2076	5.2192
chrY	59373566	13299174	0.224	19.4667

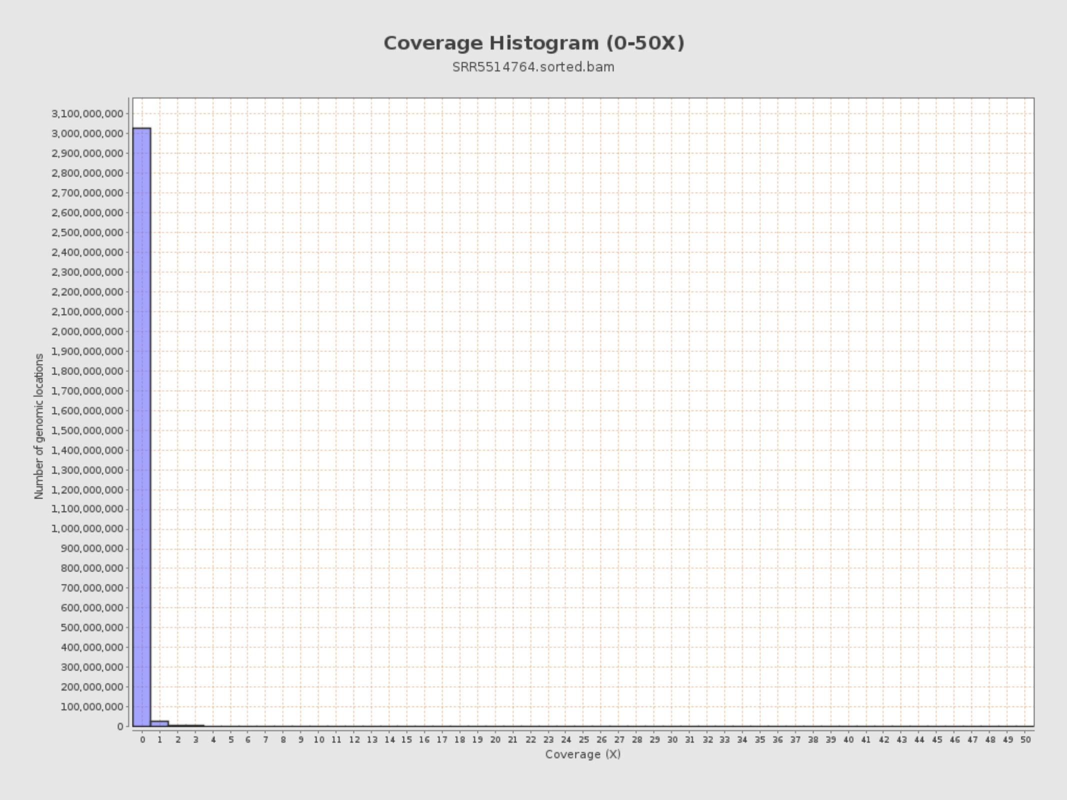
3. Results : Coverage across reference



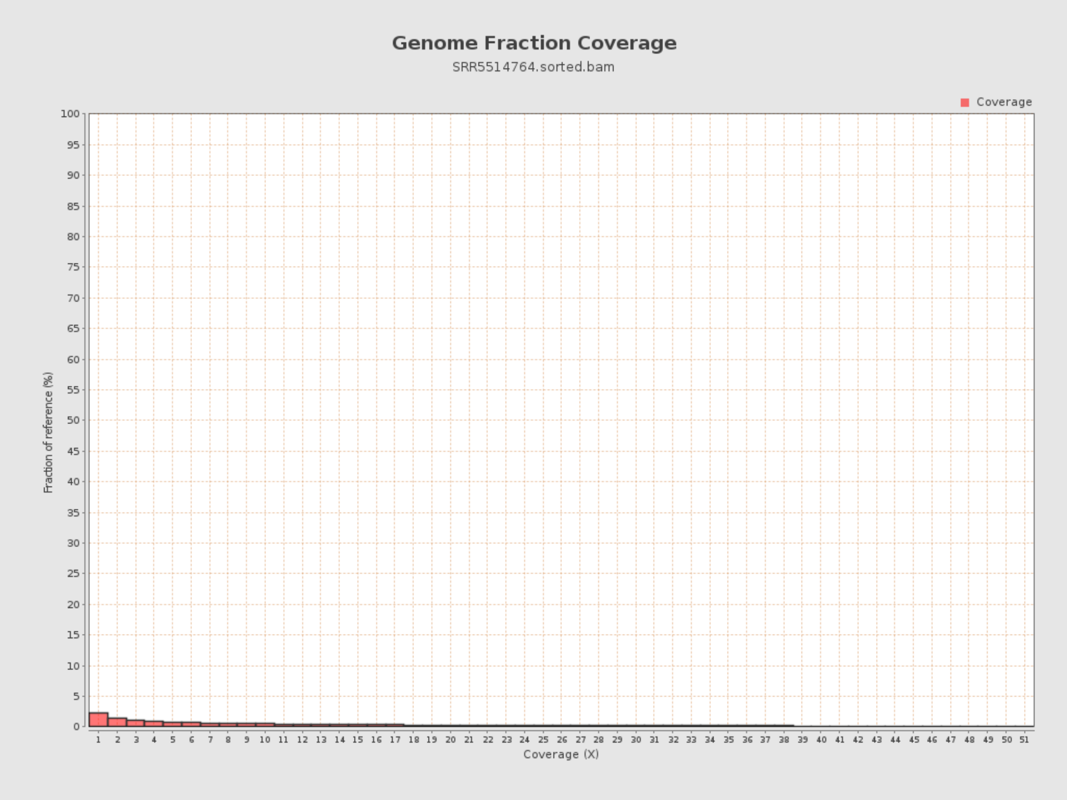
4. Results : Coverage Histogram



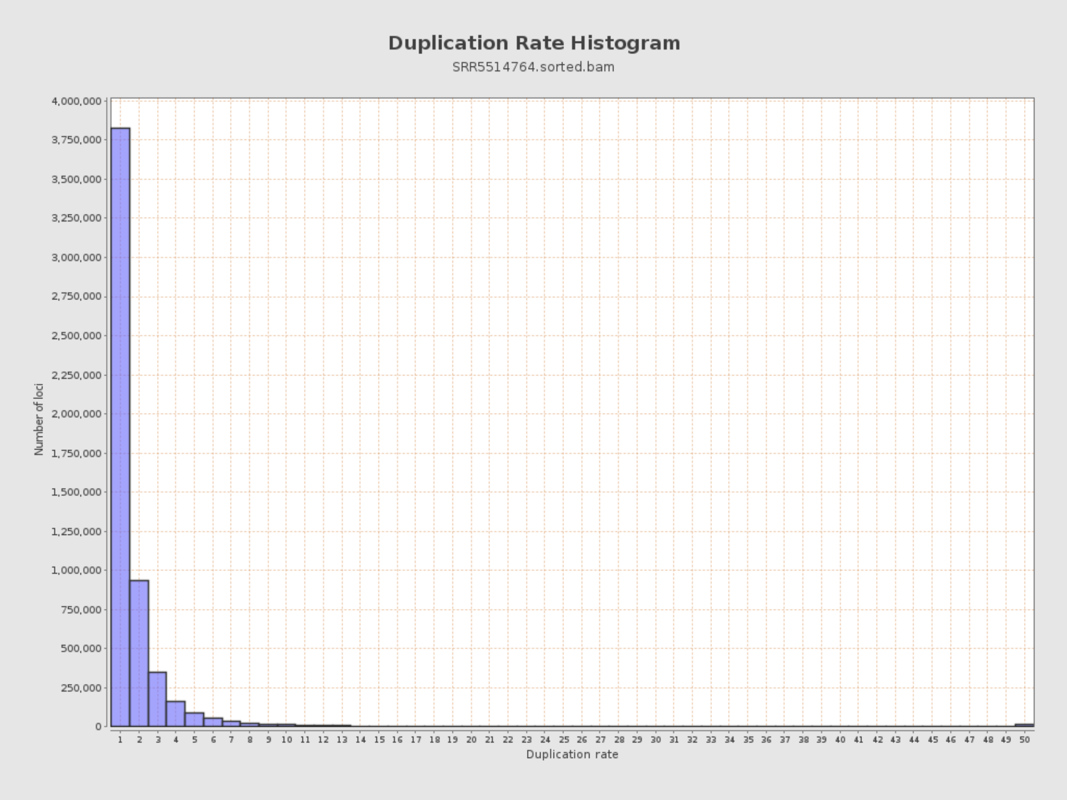
5. Results : Coverage Histogram (0-50X)



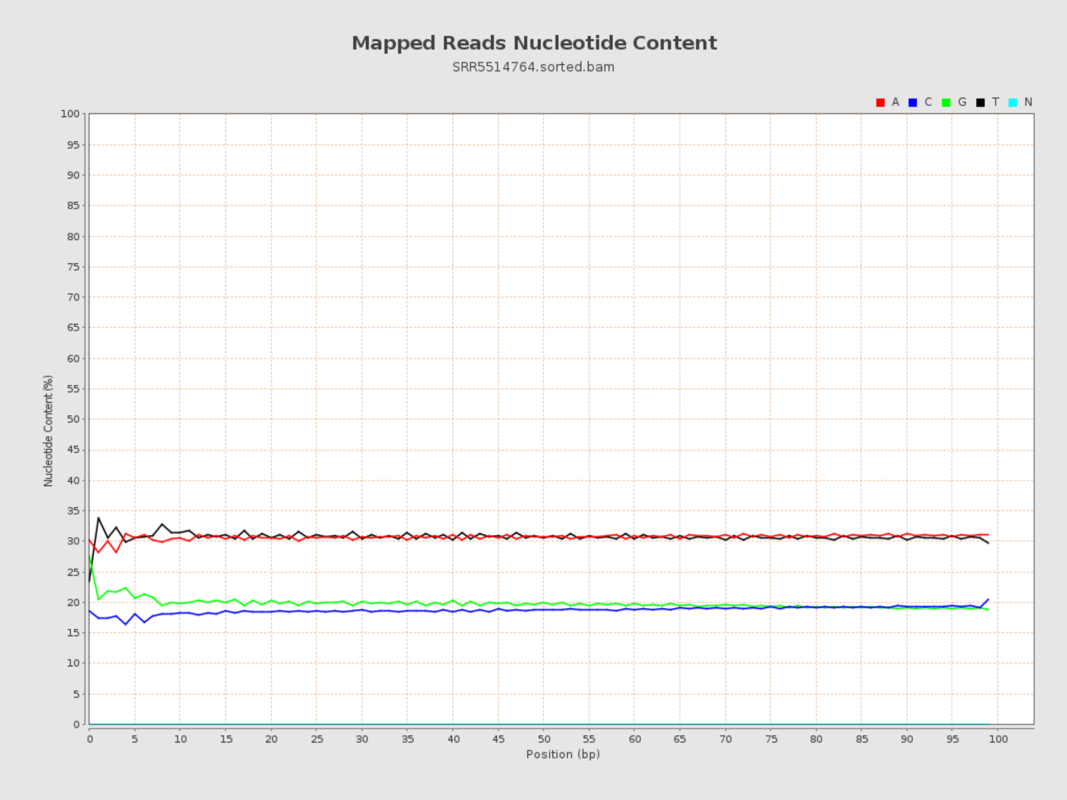
6. Results : Genome Fraction Coverage



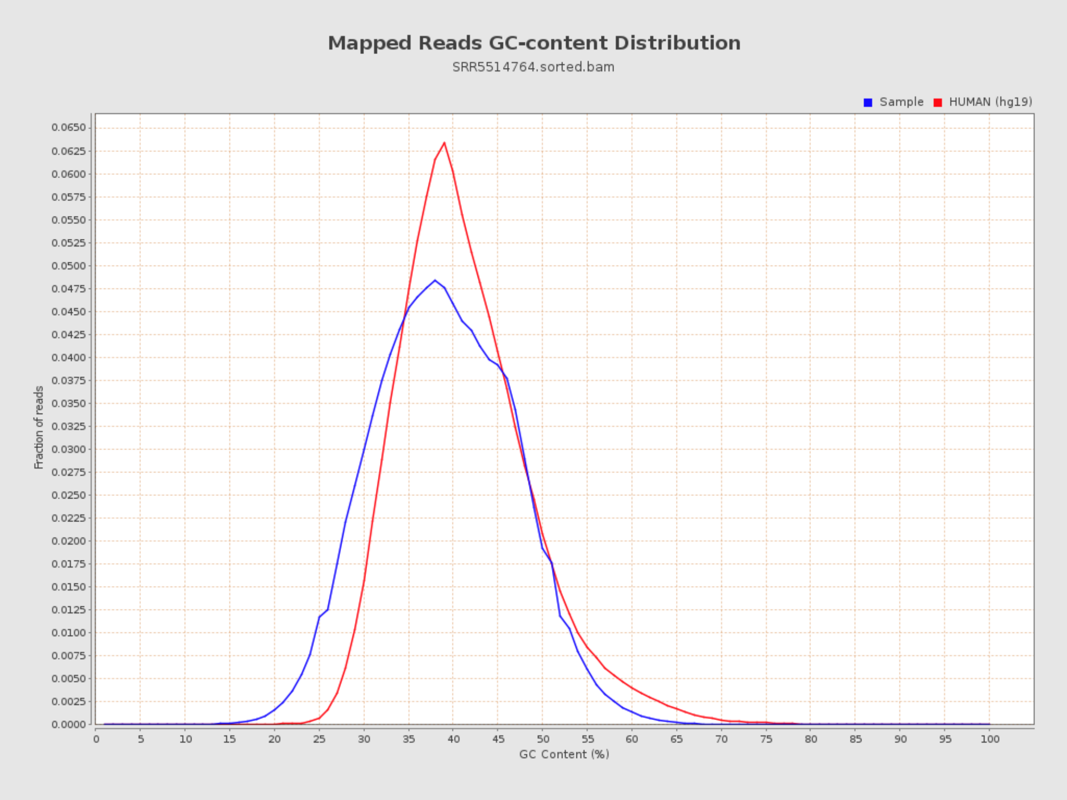
7. Results : Duplication Rate Histogram



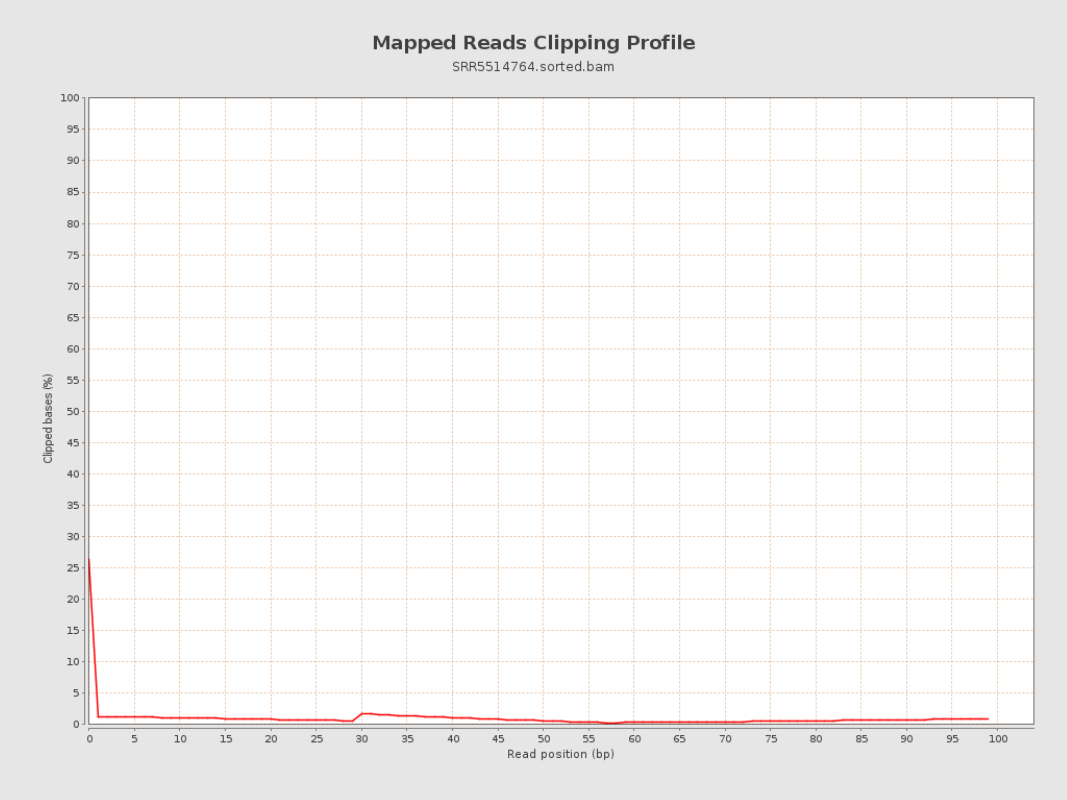
8. Results : Mapped Reads Nucleotide Content



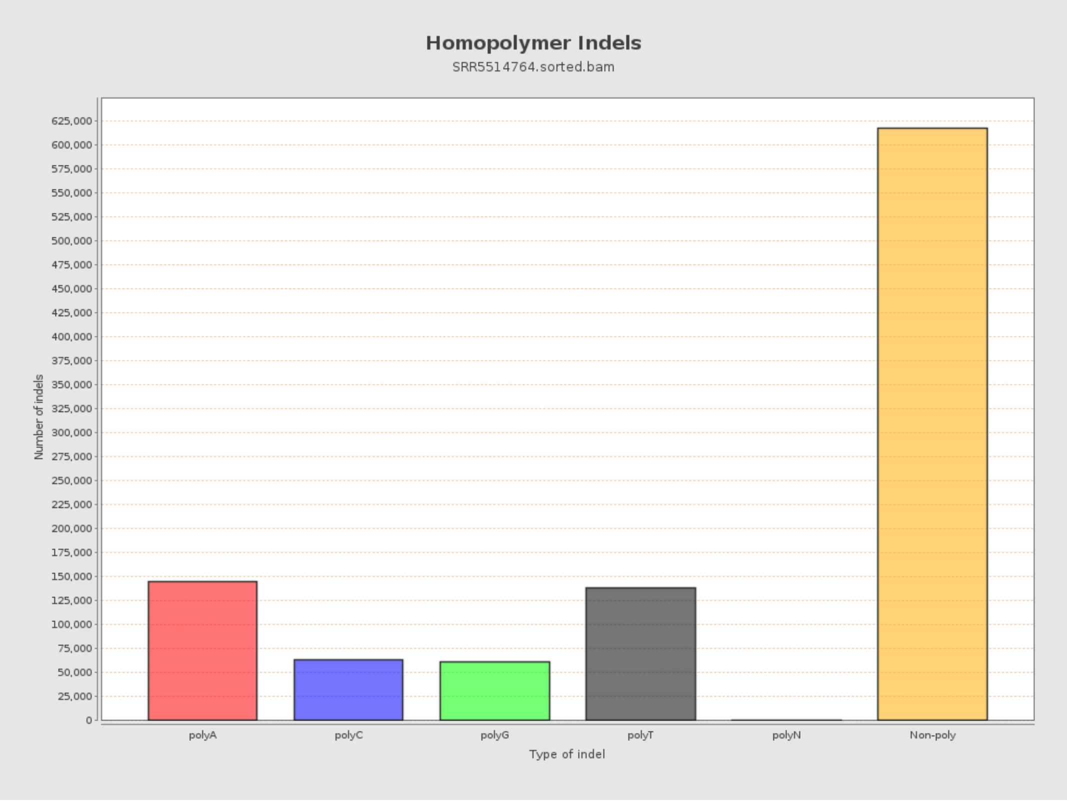
9. Results : Mapped Reads GC-content Distribution



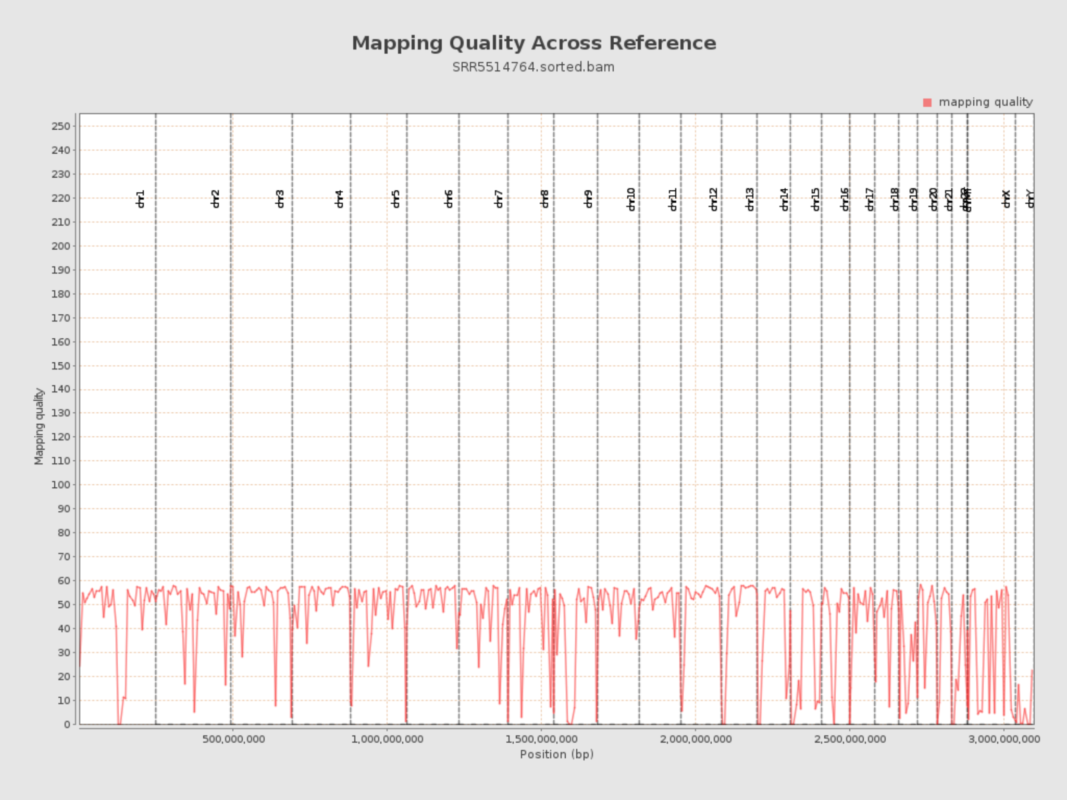
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram