Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 15:26:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514744.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_SRR5514744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514744.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 15:26:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,320,948
Mapped reads	12,887,458 / 84.12%
Unmapped reads	2,433,490 / 15.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,411,071 / 15.74%
Read min/max/mean length	30 / 100 / 105.6
Duplicated reads (estimated)	11,164,551 / 72.87%
Duplication rate	41.01%
Clipped reads	8,619,042 / 56.26%

2.2. ACGT Content

Number/percentage of A's	352,524,766 / 29.91%
Number/percentage of C's	219,431,322 / 18.62%
Number/percentage of T's	362,477,264 / 30.75%
Number/percentage of G's	244,203,306 / 20.72%
Number/percentage of N's	78,946 / 0.01%
GC Percentage	39.33%

2.3. Coverage

Mean	0.3813

Standard Deviation	61.0063

2.4. Mapping Quality

Mean Mapping Quality	38.51

2.5. Mismatches and indels

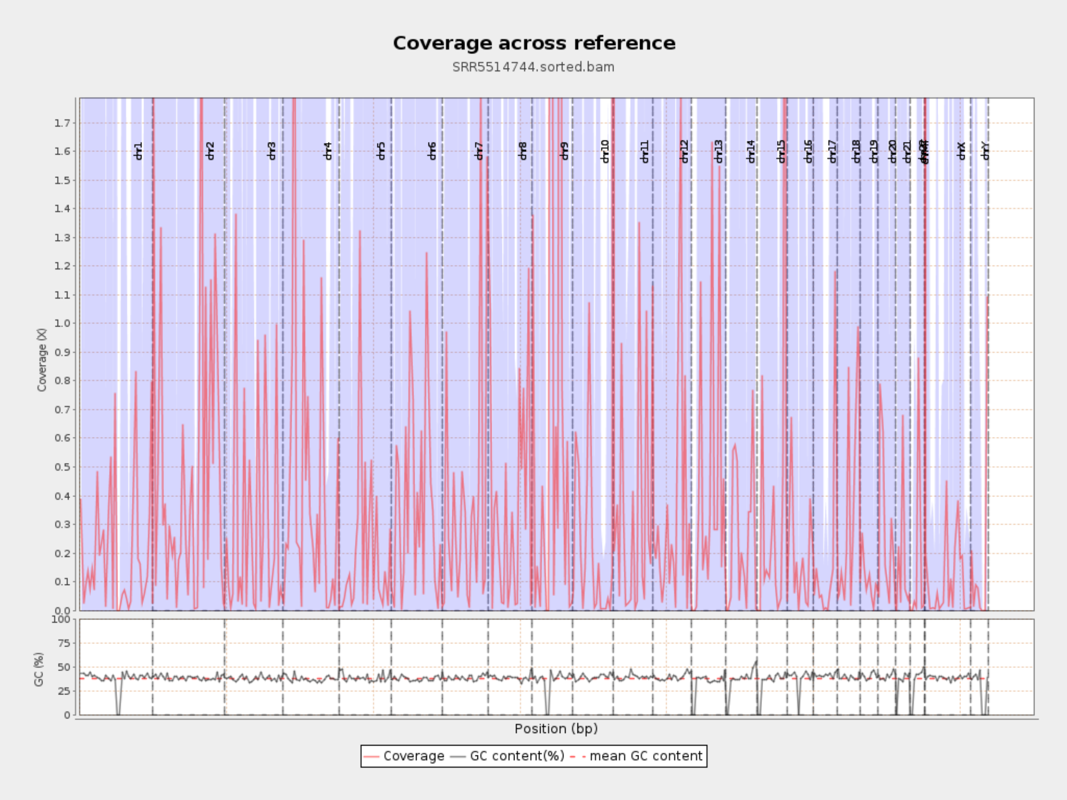
General error rate	1.05%
Mismatches	9,891,791
Insertions	1,134,711
Mapped reads with at least one insertion	7.99%
Deletions	563,065
Mapped reads with at least one deletion	4.06%
Homopolymer indels	34.66%

2.6. Chromosome stats

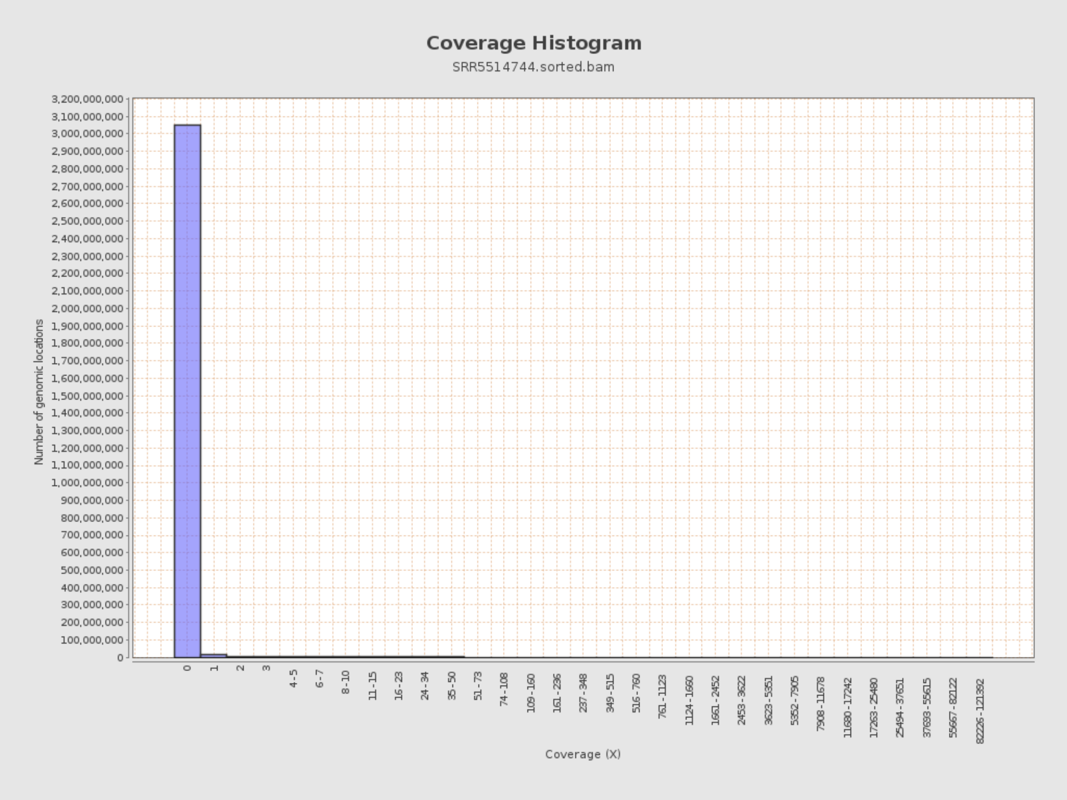
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54354896	0.2181	10.408
chr2	243199373	126328862	0.5194	27.8198
chr3	198022430	59771391	0.3018	12.4611
chr4	191154276	85213068	0.4458	50.1984
chr5	180915260	36241444	0.2003	8.7574
chr6	171115067	65366934	0.382	11.328
chr7	159138663	61625034	0.3872	24.7065

chr8	146364022	52511500	0.3588	11.872
chr9	141213431	120951269	0.8565	180.0458
chr10	135534747	27987979	0.2065	7.2354
chr11	135006516	160057407	1.1856	184.1147
chr12	133851895	43908964	0.328	14.9356
chr13	115169878	52311293	0.4542	11.6191
chr14	107349540	27330848	0.2546	16.1191
chr15	102531392	48325892	0.4713	104.0703
chr16	90354753	17295013	0.1914	11.1493
chr17	81195210	14309587	0.1762	35.2303
chr18	78077248	28370187	0.3634	13.8689
chr19	59128983	6375230	0.1078	5.3429
chr20	63025520	17326244	0.2749	10.7659
chr21	48129895	8389955	0.1743	5.694
chr22	51304566	7566404	0.1475	18.5938
chrMT	16571	32387833	1,954.4887	2,069.0005
chrX	155270560	15175395	0.0977	4.5239
chrY	59373566	11022288	0.1856	6.2894

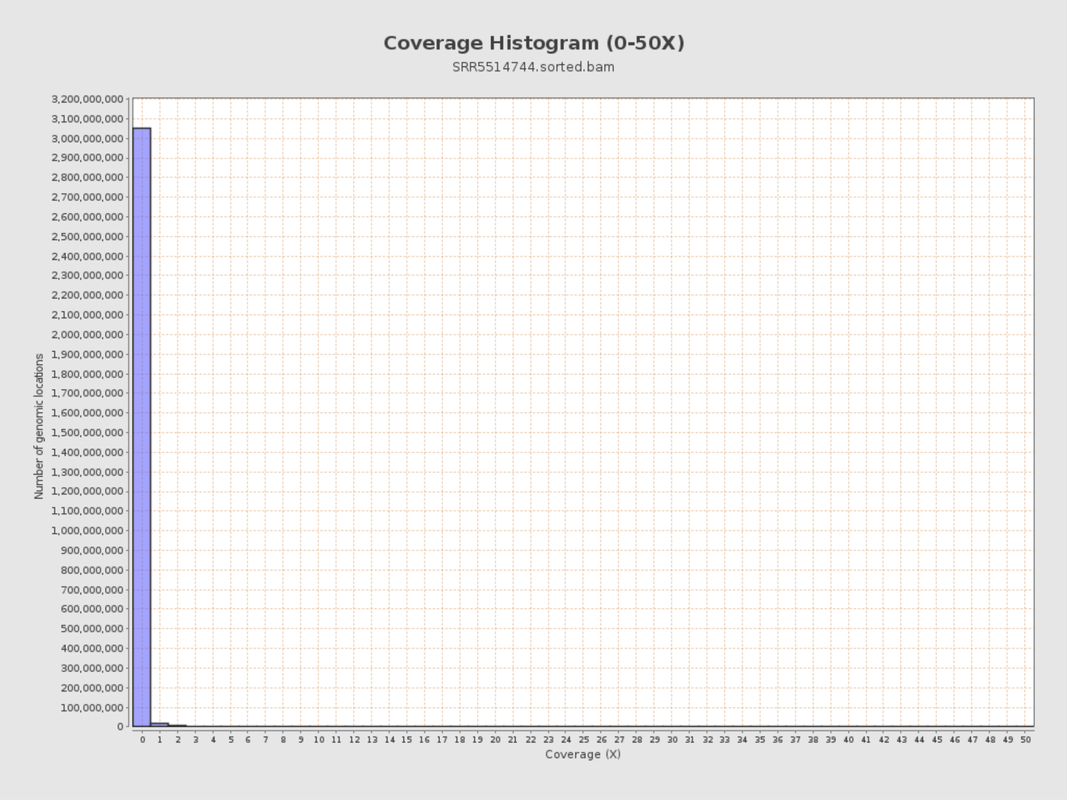
3. Results : Coverage across reference



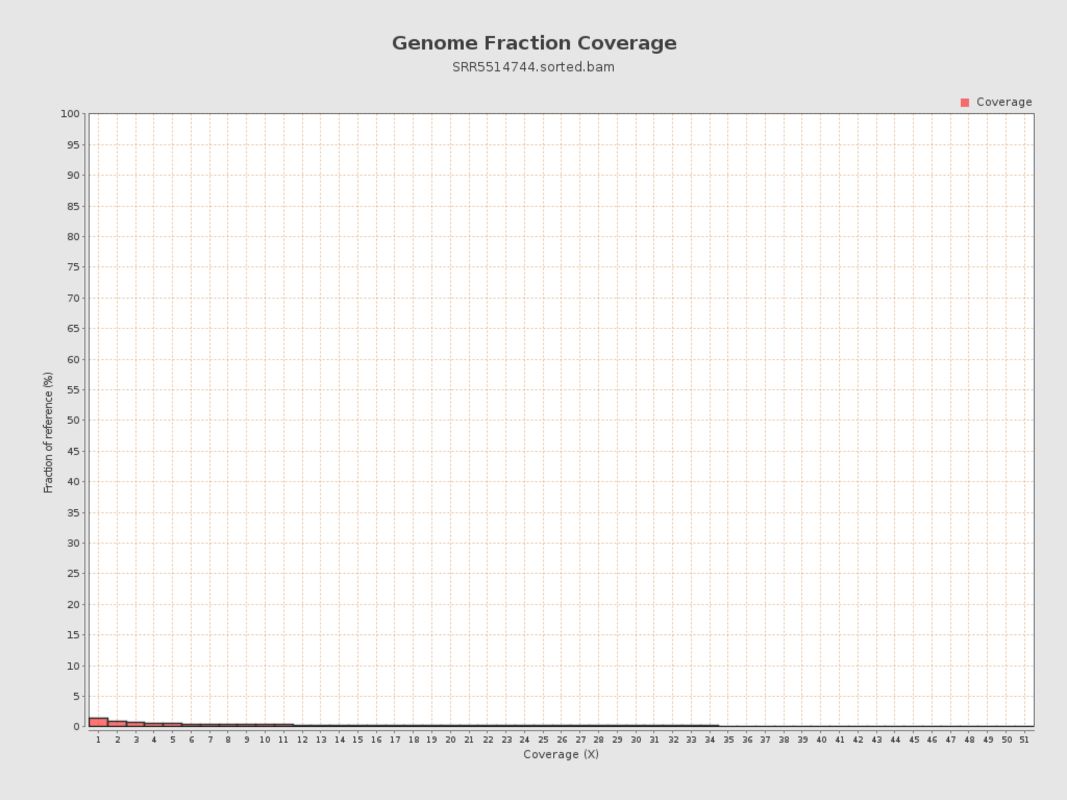
4. Results : Coverage Histogram



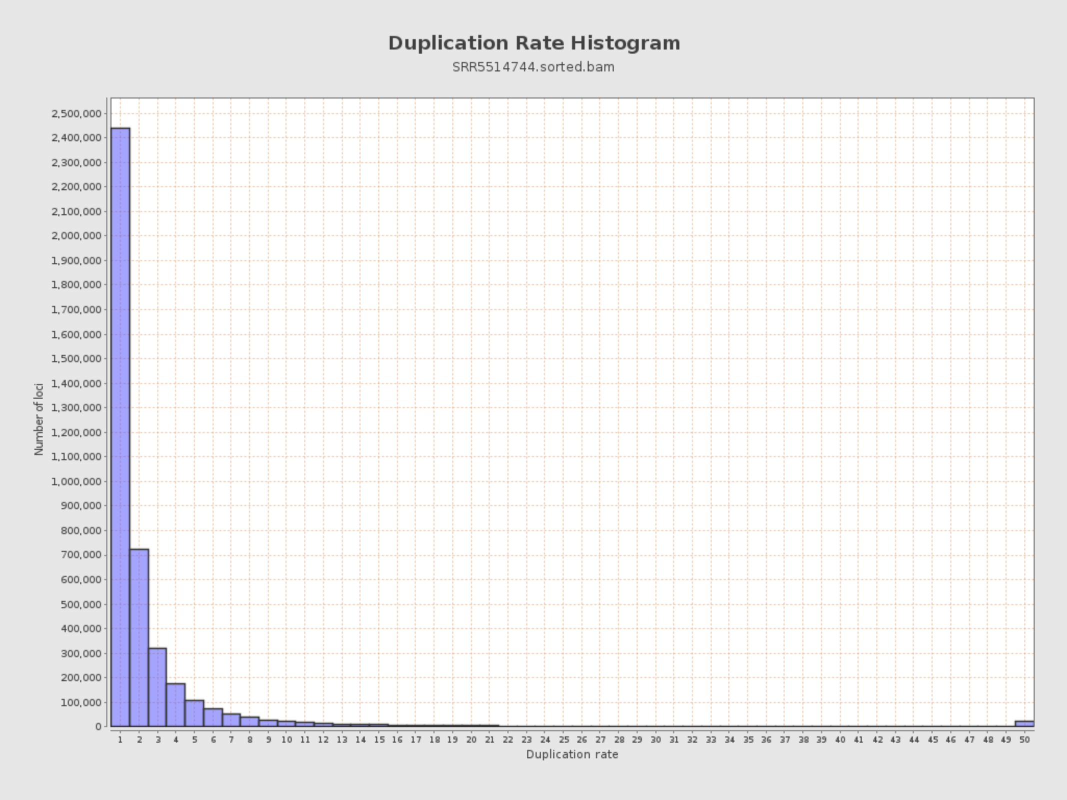
5. Results : Coverage Histogram (0-50X)



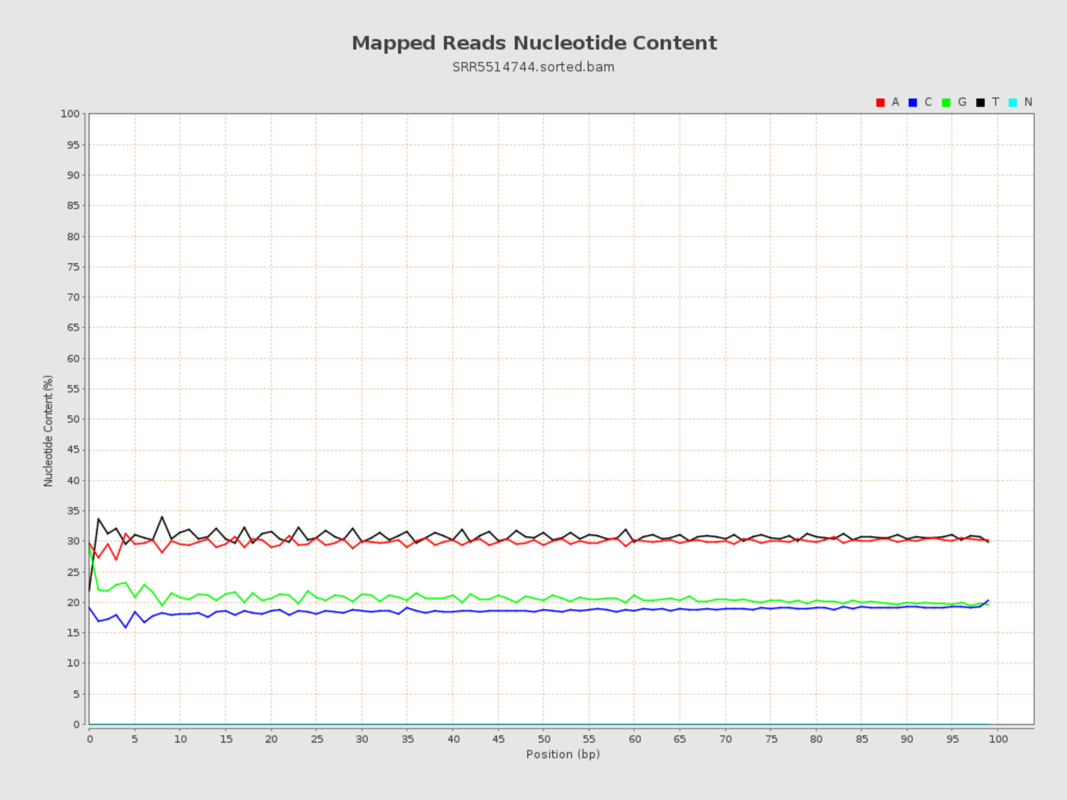
6. Results : Genome Fraction Coverage



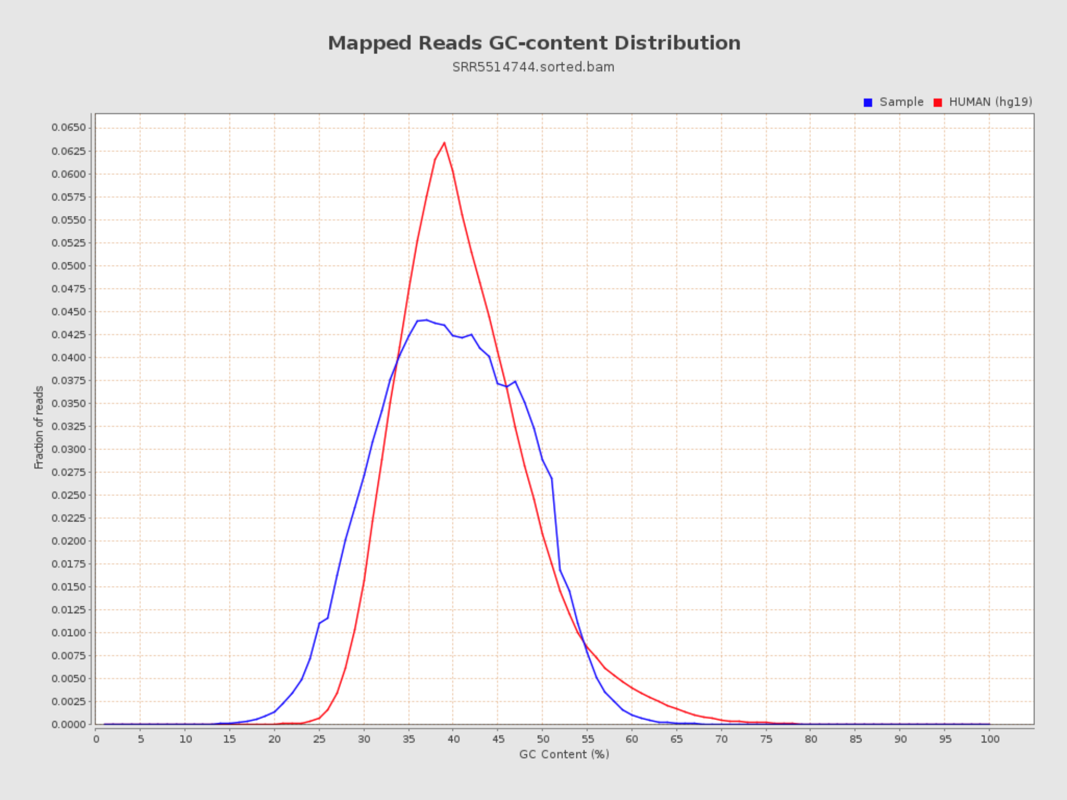
7. Results : Duplication Rate Histogram



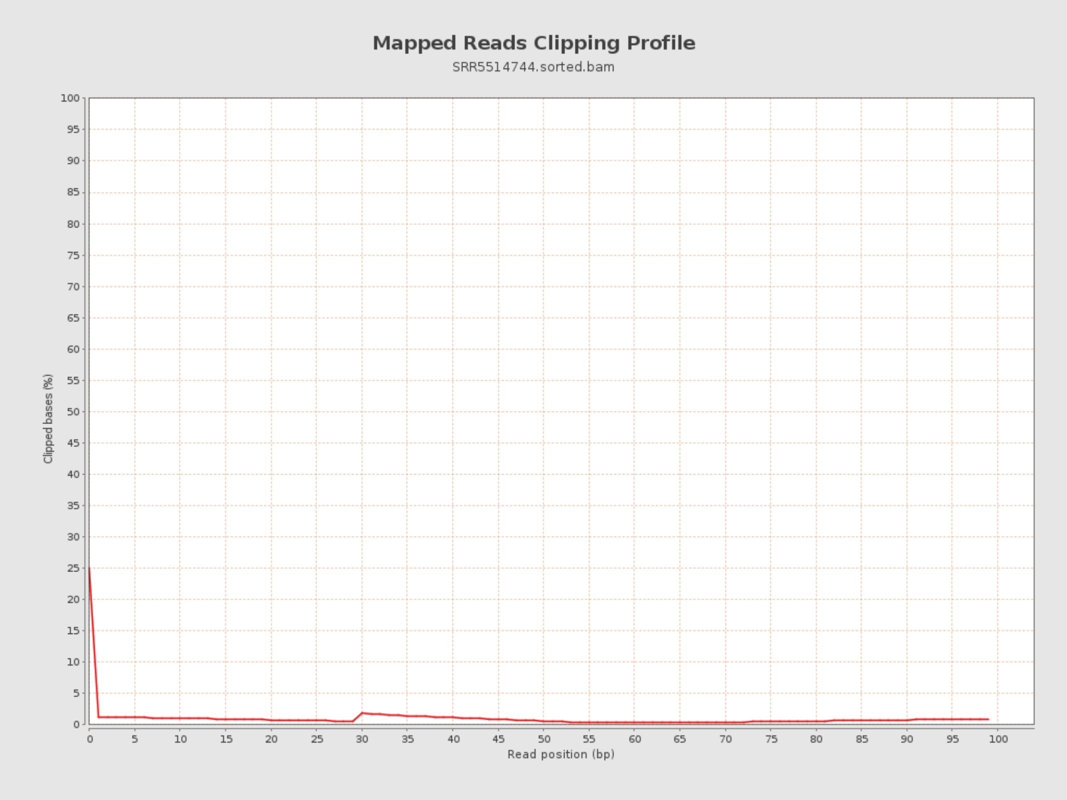
8. Results : Mapped Reads Nucleotide Content



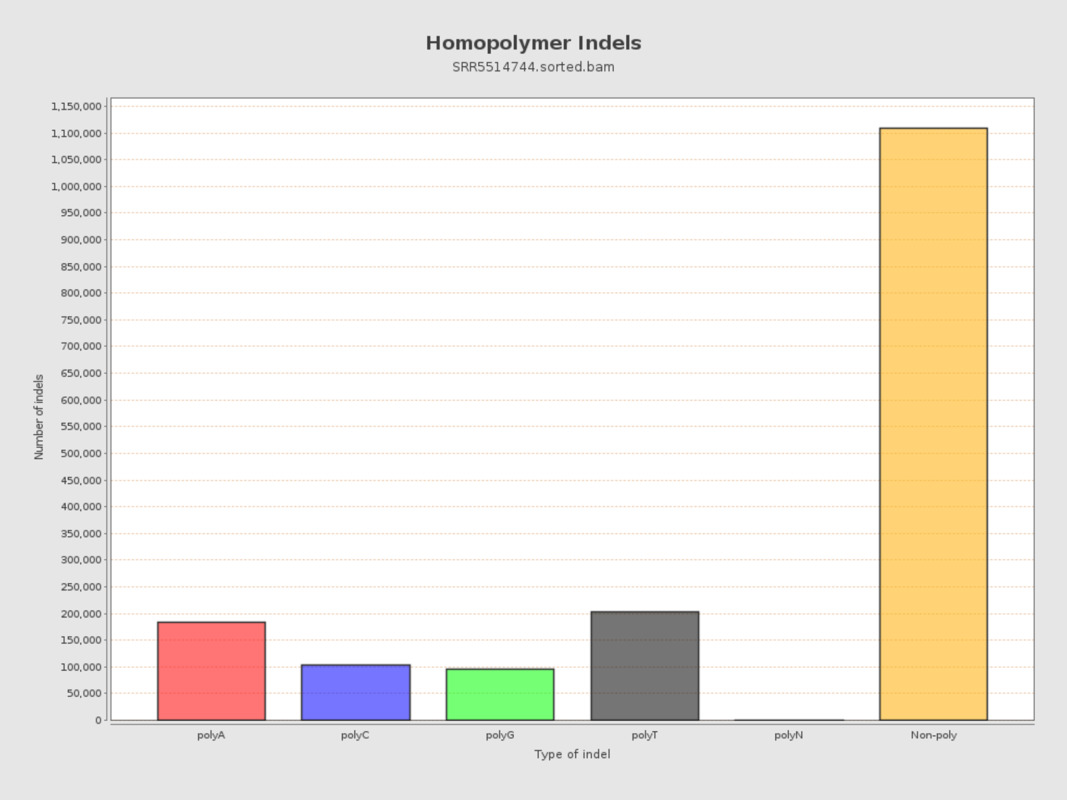
9. Results : Mapped Reads GC-content Distribution



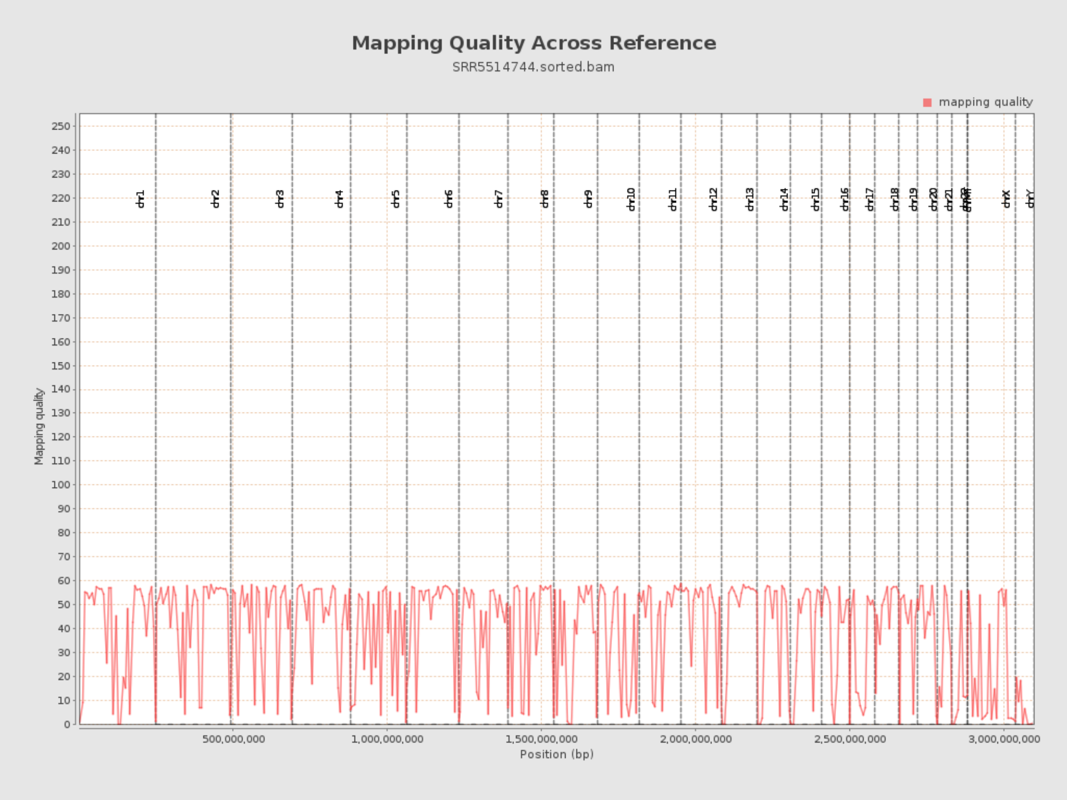
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram