Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 04:49:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514713.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_SRR5514713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 04:49:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	85,186,229
Mapped reads	84,420,512 / 99.1%
Unmapped reads	765,717 / 0.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,209,659 / 4.94%
Read min/max/mean length	30 / 100 / 99.75
Duplicated reads (estimated)	50,895,775 / 59.75%
Duplication rate	38.93%
Clipped reads	16,919,437 / 19.86%

2.2. ACGT Content

Number/percentage of A's	2,404,089,605 / 29.7%
Number/percentage of C's	1,652,086,432 / 20.41%
Number/percentage of T's	2,361,682,601 / 29.17%
Number/percentage of G's	1,675,630,246 / 20.7%
Number/percentage of N's	1,862,767 / 0.02%
GC Percentage	41.11%

2.3. Coverage

Mean	2.6174

Standard Deviation	127.3414

2.4. Mapping Quality

Mean Mapping Quality	49.47

2.5. Mismatches and indels

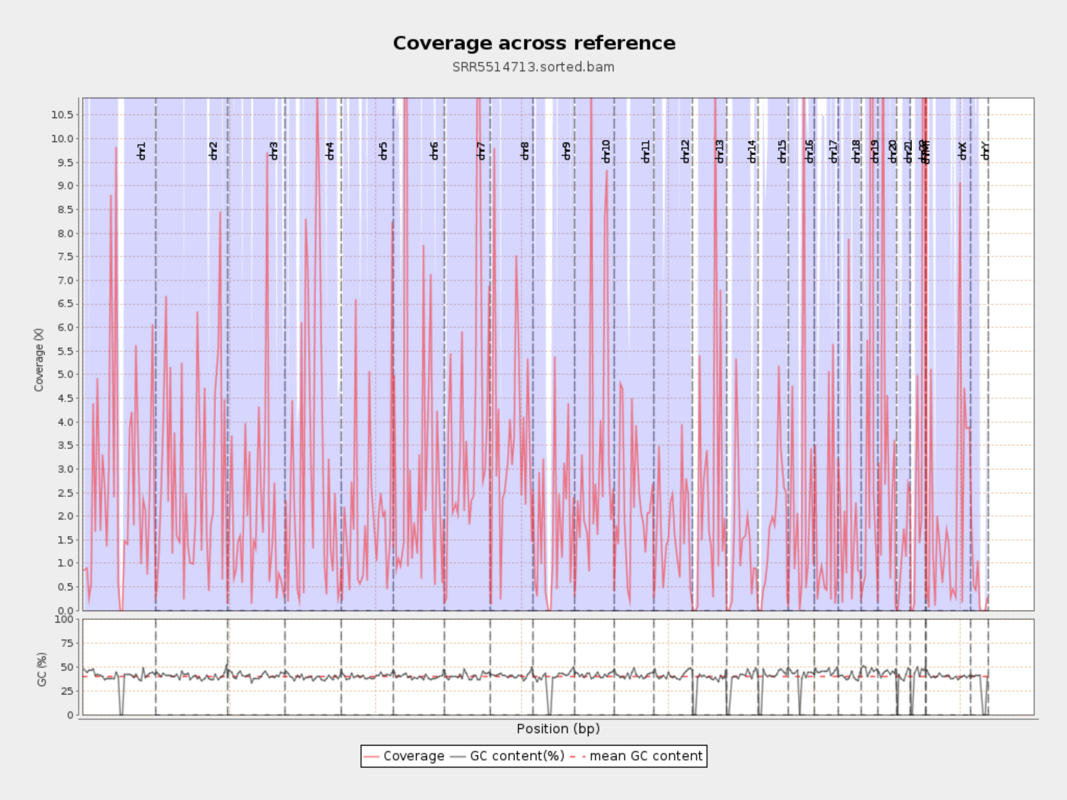
General error rate	0.68%
Mismatches	50,042,095
Insertions	2,774,680
Mapped reads with at least one insertion	3.14%
Deletions	2,844,160
Mapped reads with at least one deletion	3.15%
Homopolymer indels	41.49%

2.6. Chromosome stats

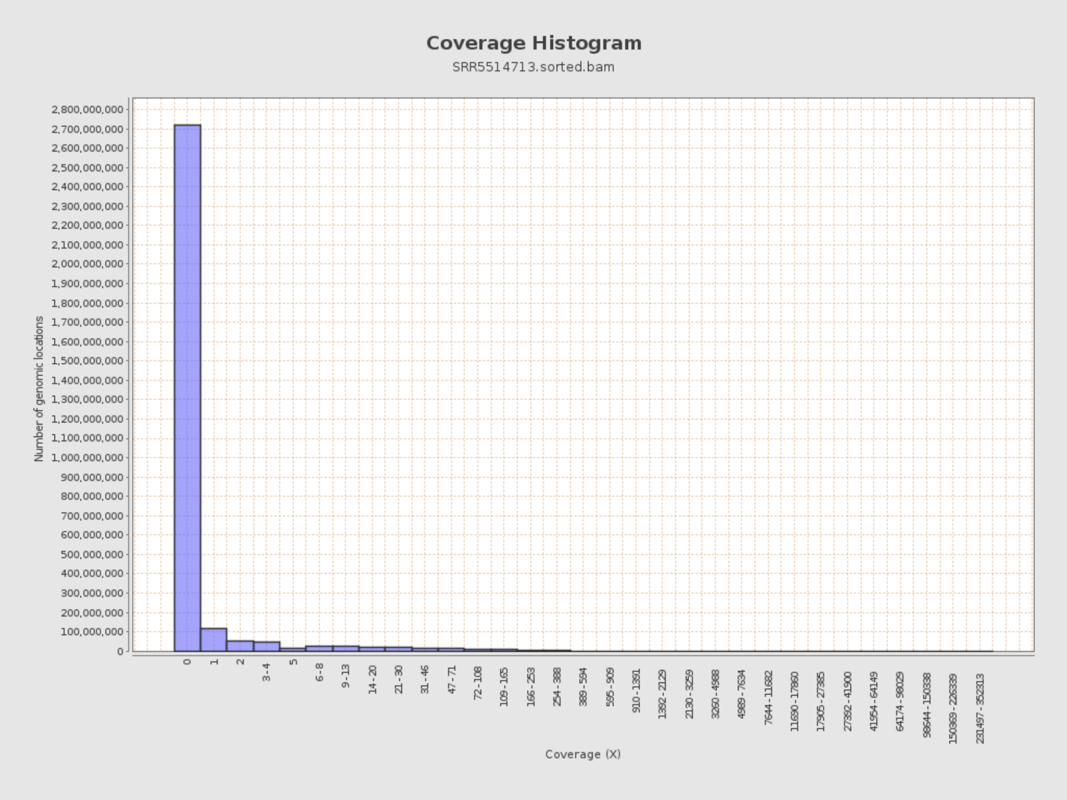
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	655215921	2.6287	37.8707
chr2	243199373	695951530	2.8617	26.7631
chr3	198022430	398014405	2.0099	20.6441
chr4	191154276	620816614	3.2477	30.2909
chr5	180915260	386339135	2.1355	26.5174
chr6	171115067	585020385	3.4189	322.8488
chr7	159138663	637444354	4.0056	34.7987

chr8	146364022	530792965	3.6265	37.0507
chr9	141213431	248631911	1.7607	20.8061
chr10	135534747	470269789	3.4697	28.6275
chr11	135006516	313086519	2.319	25.5459
chr12	133851895	232978920	1.7406	37.5633
chr13	115169878	303665798	2.6367	21.8052
chr14	107349540	157753961	1.4695	16.5503
chr15	102531392	184961838	1.804	21.3231
chr16	90354753	216785687	2.3993	51.0058
chr17	81195210	136069951	1.6758	31.016
chr18	78077248	155309179	1.9892	20.8163
chr19	59128983	275138016	4.6532	591.387
chr20	63025520	241379068	3.8299	81.209
chr21	48129895	63660957	1.3227	89.6595
chr22	51304566	220267780	4.2933	407.3079
chrMT	16571	5452526	329.0403	191.1347
chrX	155270560	341072869	2.1966	27.9982
chrY	59373566	26482991	0.446	8.6218

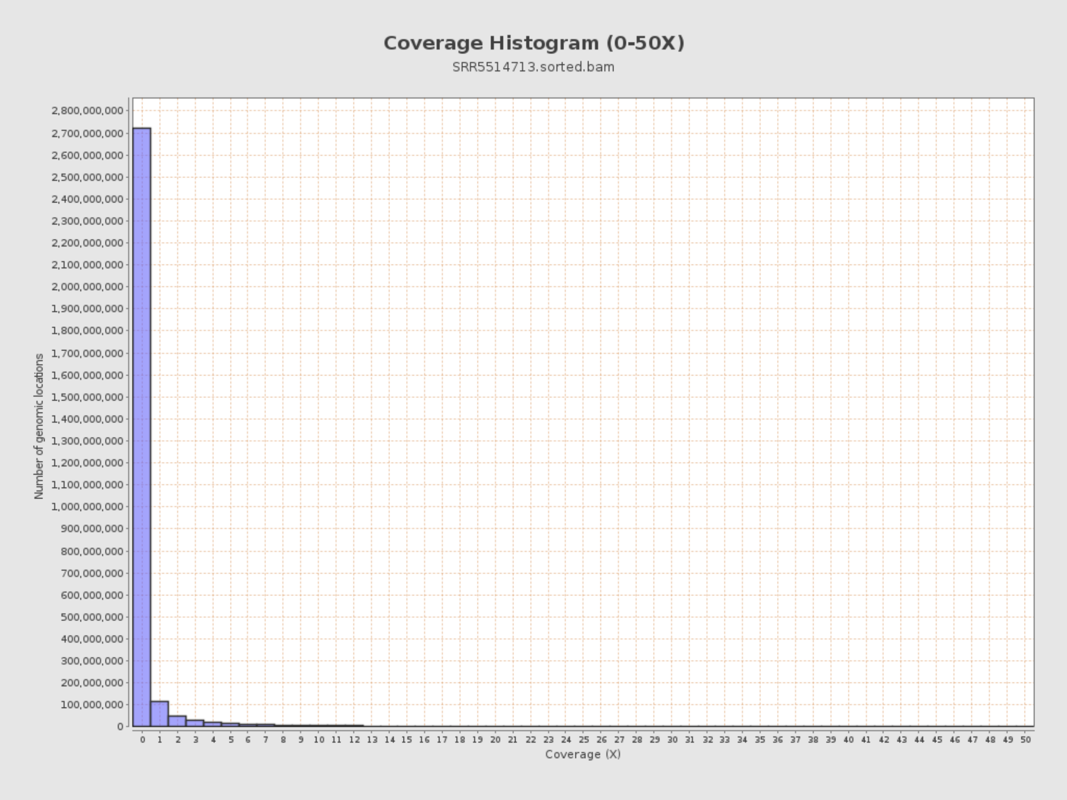
3. Results : Coverage across reference



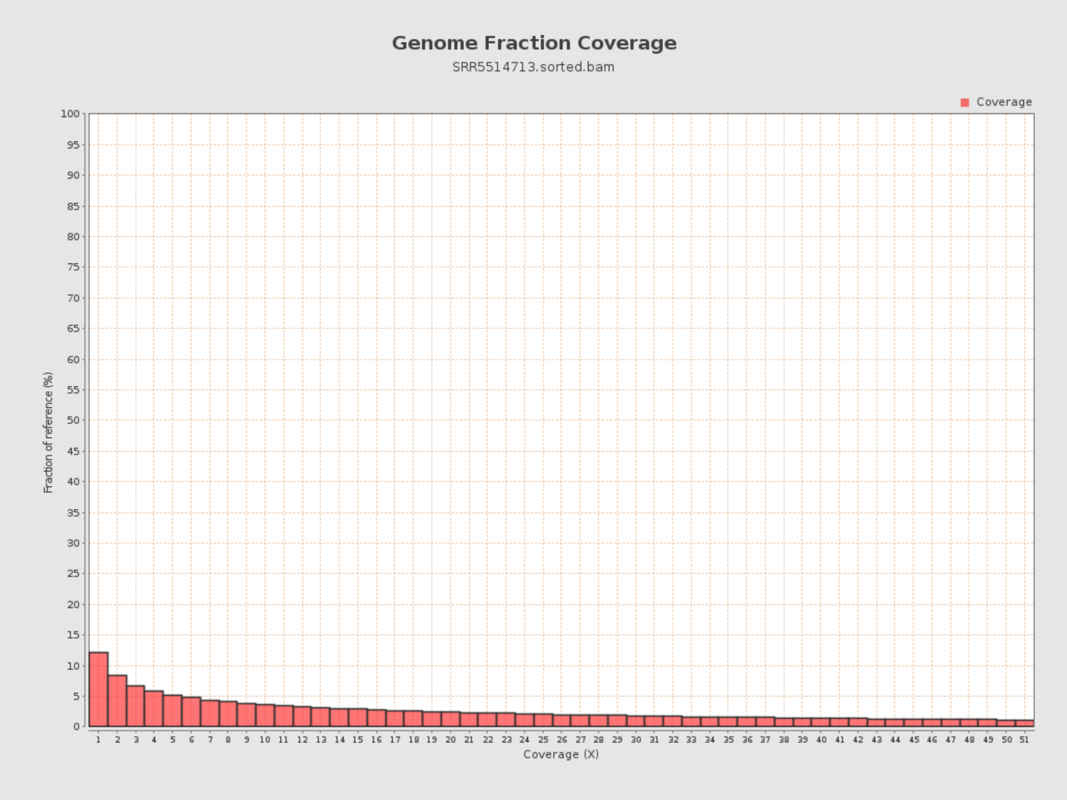
4. Results : Coverage Histogram



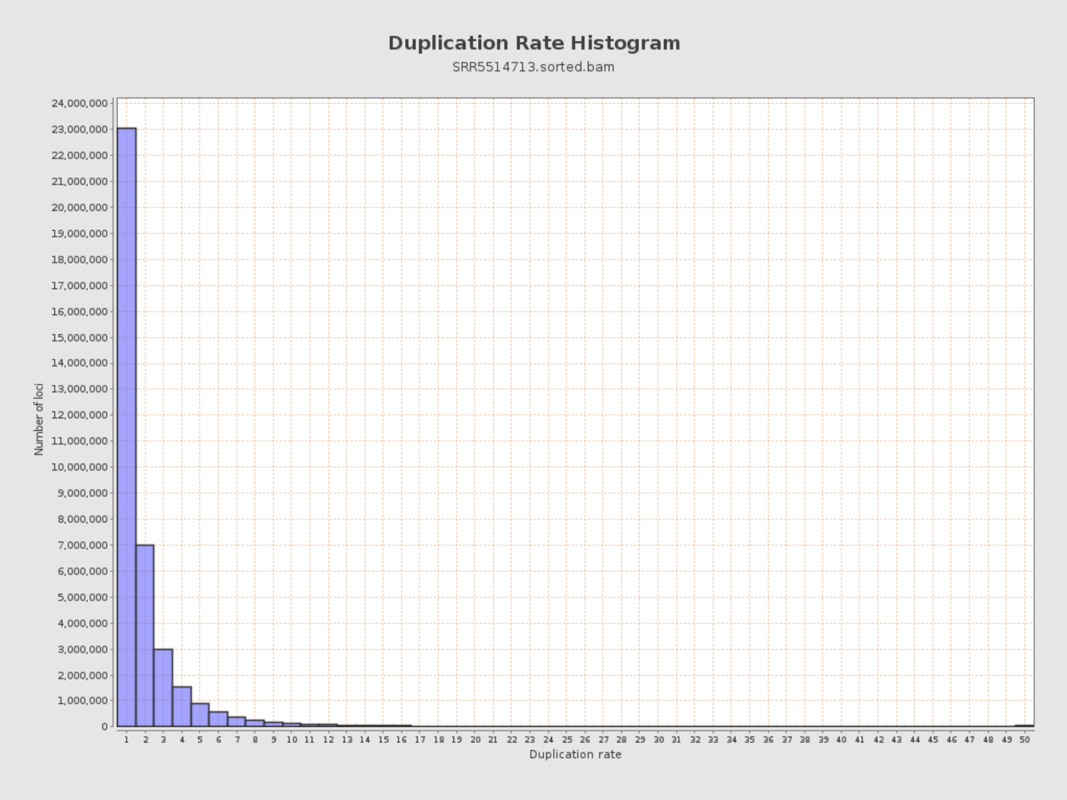
5. Results : Coverage Histogram (0-50X)



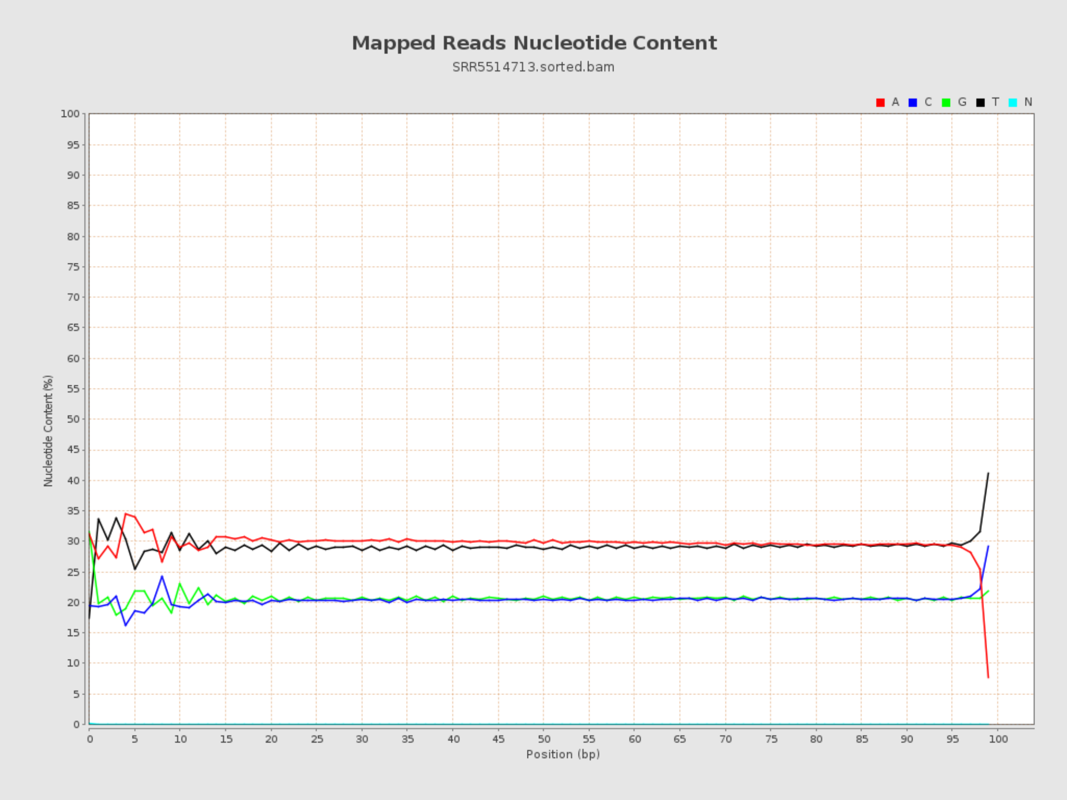
6. Results : Genome Fraction Coverage



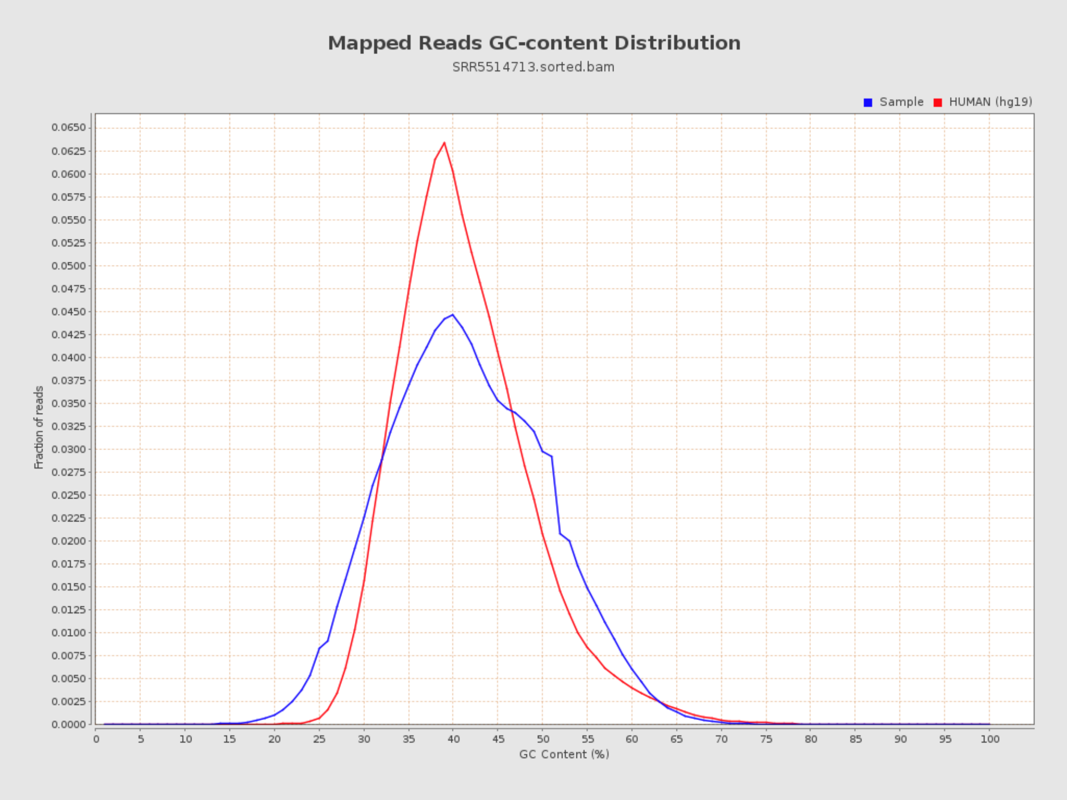
7. Results : Duplication Rate Histogram



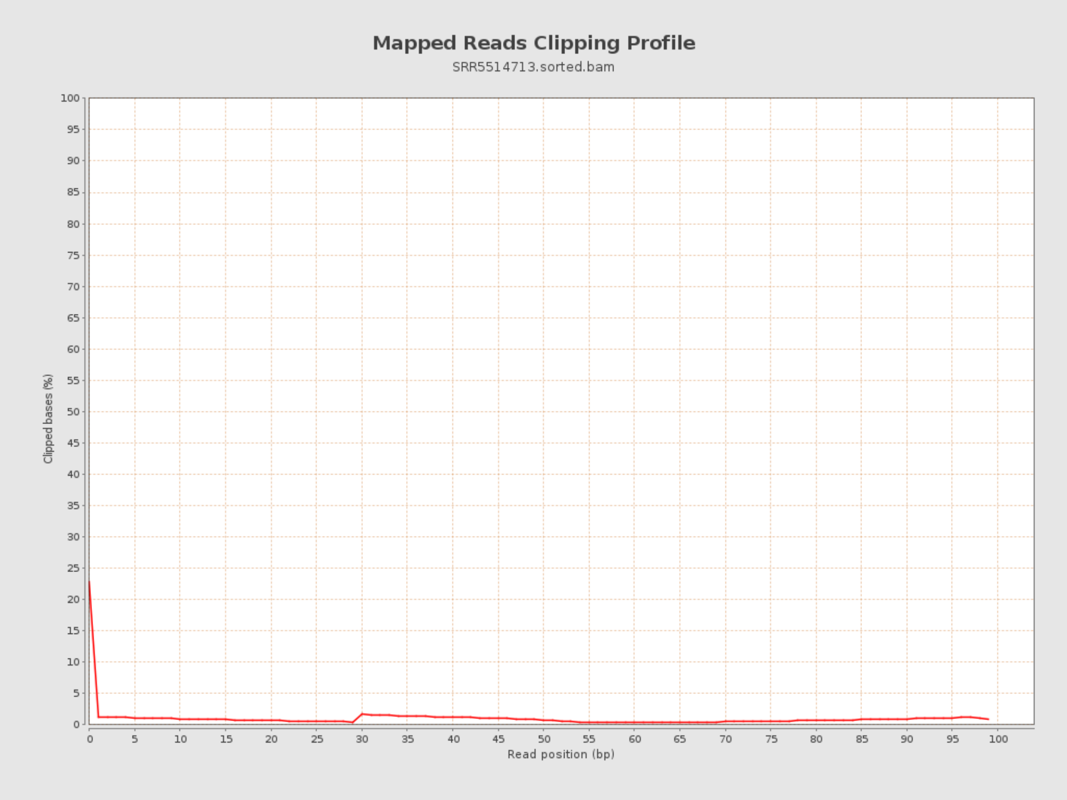
8. Results : Mapped Reads Nucleotide Content



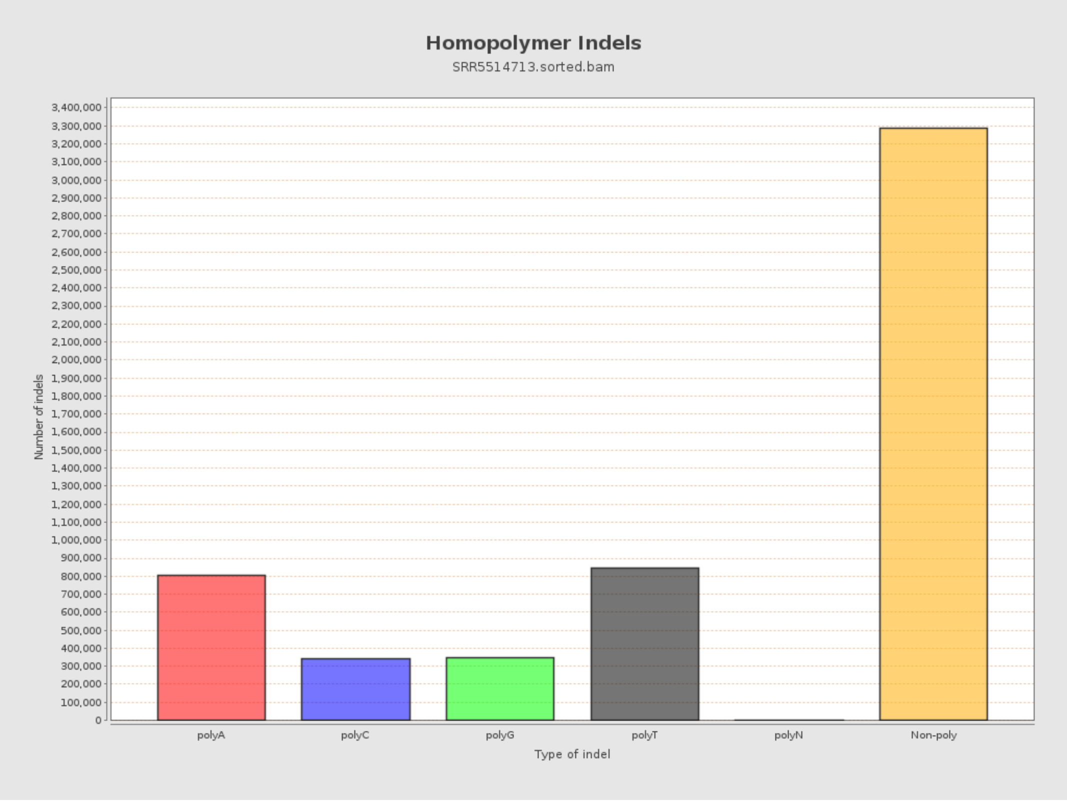
9. Results : Mapped Reads GC-content Distribution



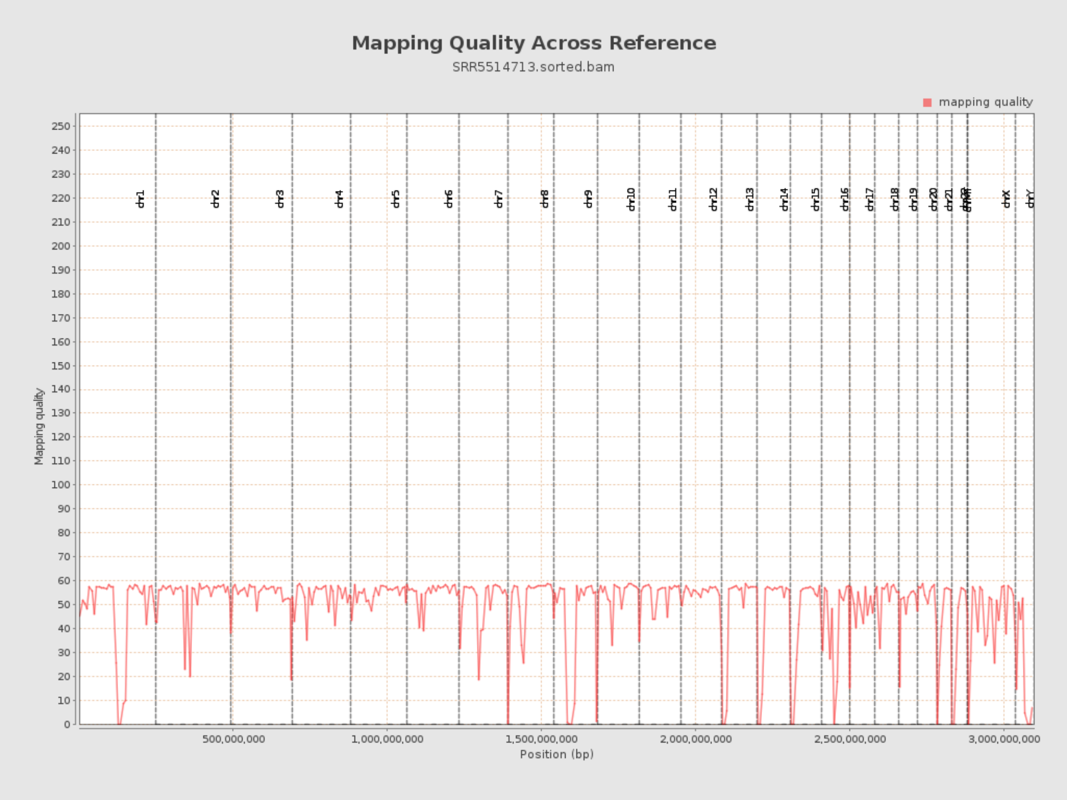
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram