Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 04:48:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514724.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_SRR5514724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514724.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 04:48:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	160,598,618
Mapped reads	152,196,654 / 94.77%
Unmapped reads	8,401,964 / 5.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,442,198 / 5.26%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	143,571,783 / 89.4%
Duplication rate	54.11%
Clipped reads	43,972,349 / 27.38%

2.2. ACGT Content

Number/percentage of A's	3,732,983,328 / 26.48%
Number/percentage of C's	3,210,482,711 / 22.77%
Number/percentage of T's	3,772,417,695 / 26.76%
Number/percentage of G's	3,225,239,542 / 22.88%
Number/percentage of N's	155,682,925 / 1.1%
GC Percentage	45.65%

2.3. Coverage

Mean	4.5577

Standard Deviation	323.0007

2.4. Mapping Quality

Mean Mapping Quality	46.9

2.5. Mismatches and indels

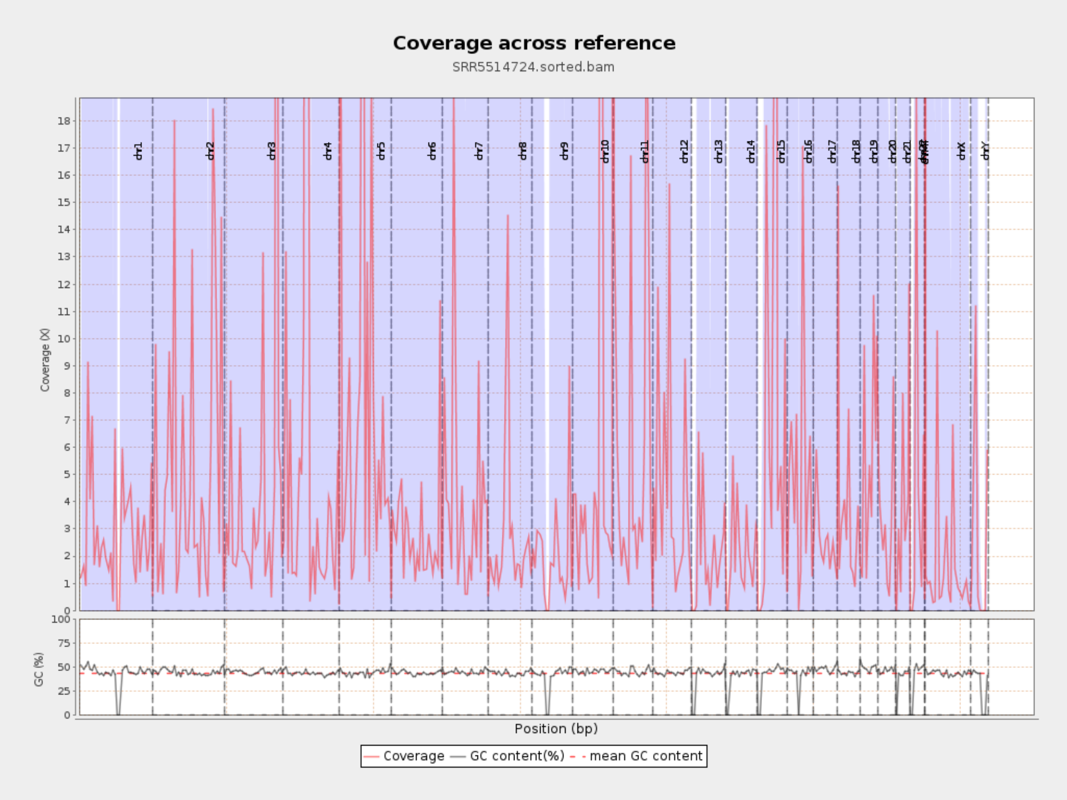
General error rate	1.04%
Mismatches	132,982,917
Insertions	7,430,443
Mapped reads with at least one insertion	4.64%
Deletions	4,987,459
Mapped reads with at least one deletion	3.1%
Homopolymer indels	38.85%

2.6. Chromosome stats

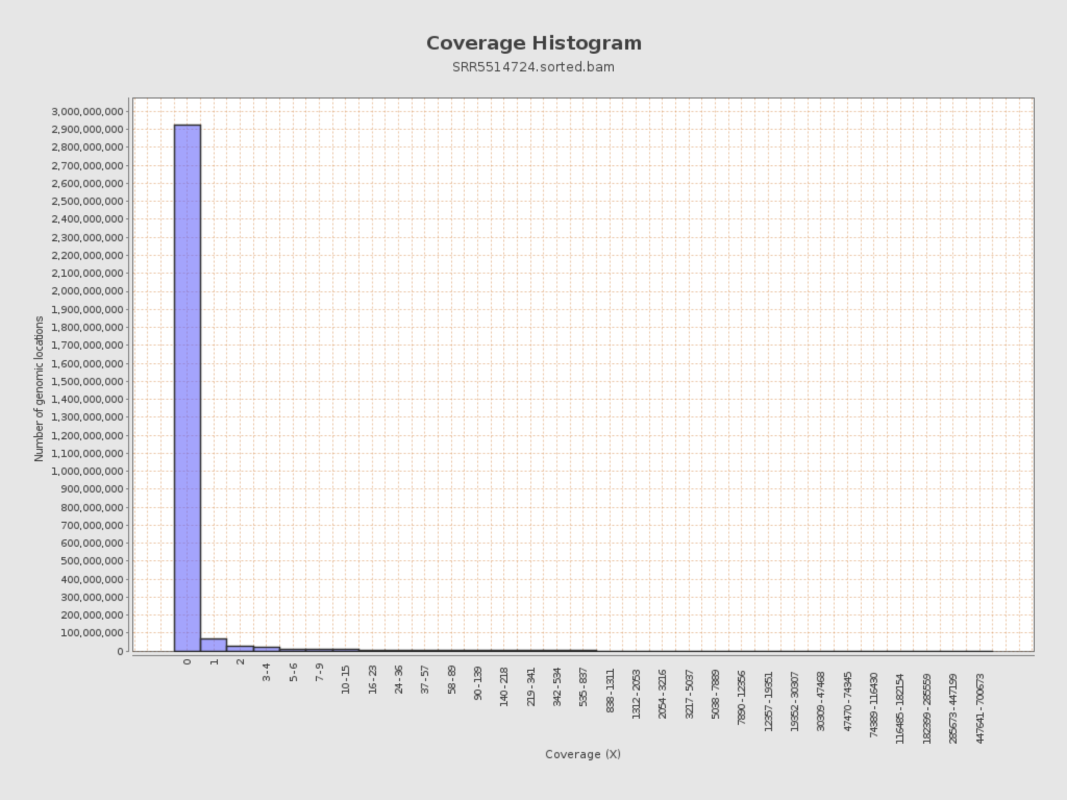
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	721819580	2.896	131.1111
chr2	243199373	1320237122	5.4286	323.6988
chr3	198022430	985963037	4.979	113.9699
chr4	191154276	1508815347	7.8932	918.0545
chr5	180915260	1488332240	8.2267	587.9965
chr6	171115067	495343045	2.8948	94.0157
chr7	159138663	685285750	4.3062	129.4528

chr8	146364022	424806863	2.9024	100.3833
chr9	141213431	286433255	2.0284	84.215
chr10	135534747	753076931	5.5563	151.5633
chr11	135006516	1117917599	8.2805	412.3806
chr12	133851895	613627206	4.5844	151.3602
chr13	115169878	231427309	2.0094	81.5991
chr14	107349540	231926072	2.1605	85.0734
chr15	102531392	909181334	8.8673	282.8705
chr16	90354753	432936508	4.7915	208.4596
chr17	81195210	210838358	2.5967	92.8807
chr18	78077248	274469335	3.5154	131.2212
chr19	59128983	326110159	5.5152	247.7653
chr20	63025520	202548043	3.2137	144.0086
chr21	48129895	200452234	4.1648	267.2408
chr22	51304566	244752714	4.7706	209.2806
chrMT	16571	2374464	143.2903	323.1431
chrX	155270560	256685828	1.6532	135.4489
chrY	59373566	183907219	3.0975	182.3085

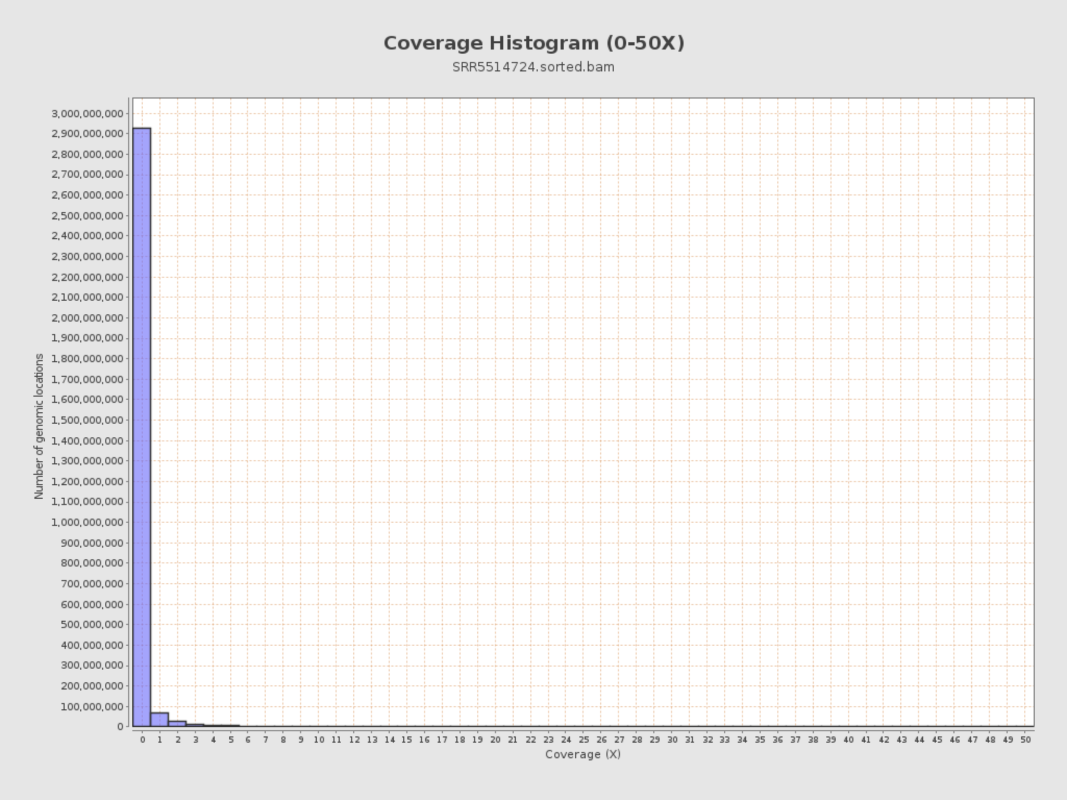
3. Results : Coverage across reference



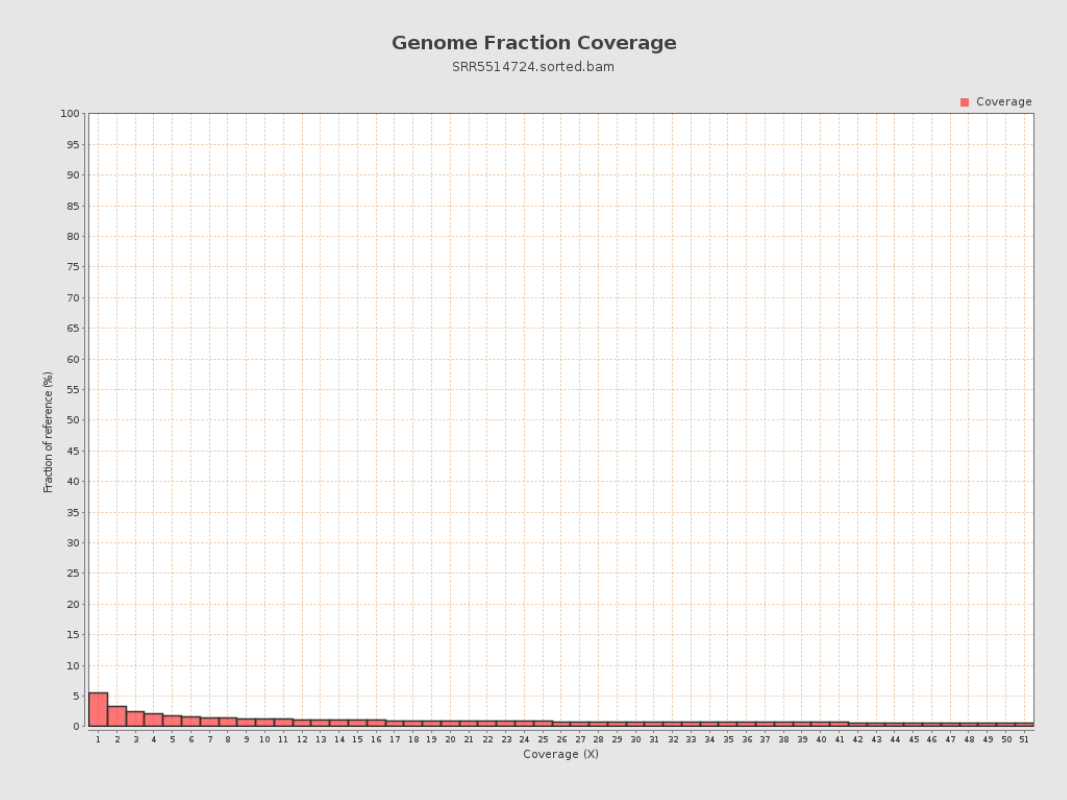
4. Results : Coverage Histogram



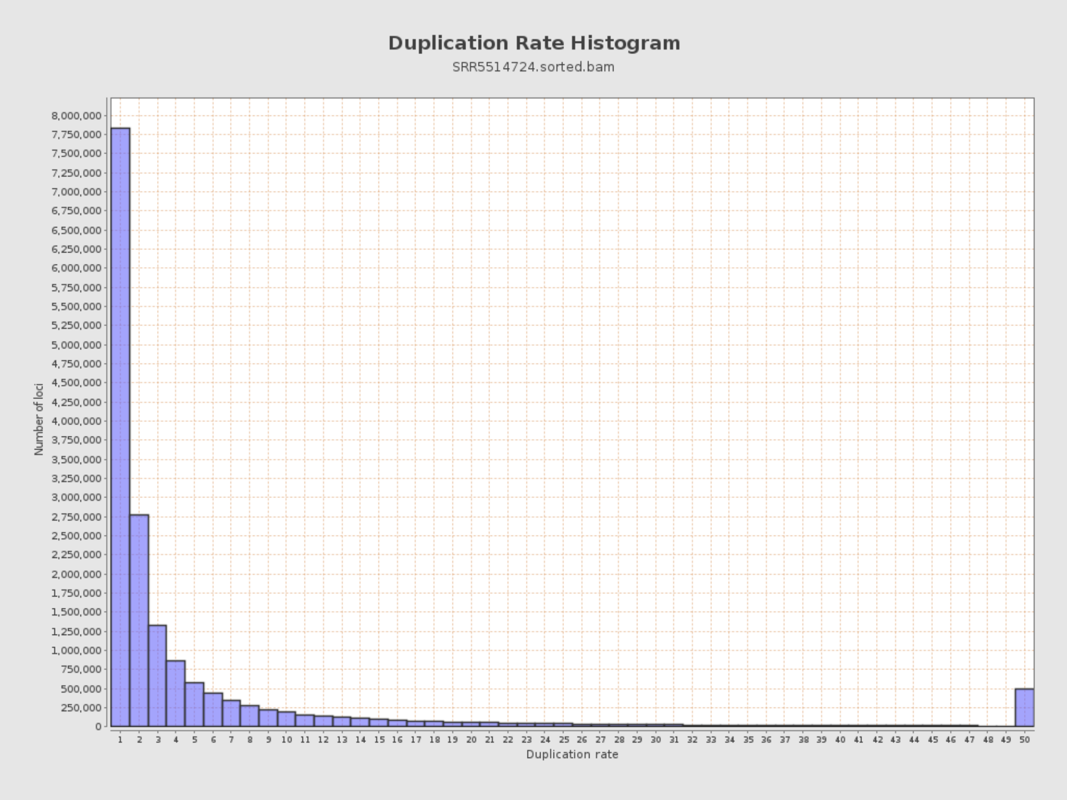
5. Results : Coverage Histogram (0-50X)



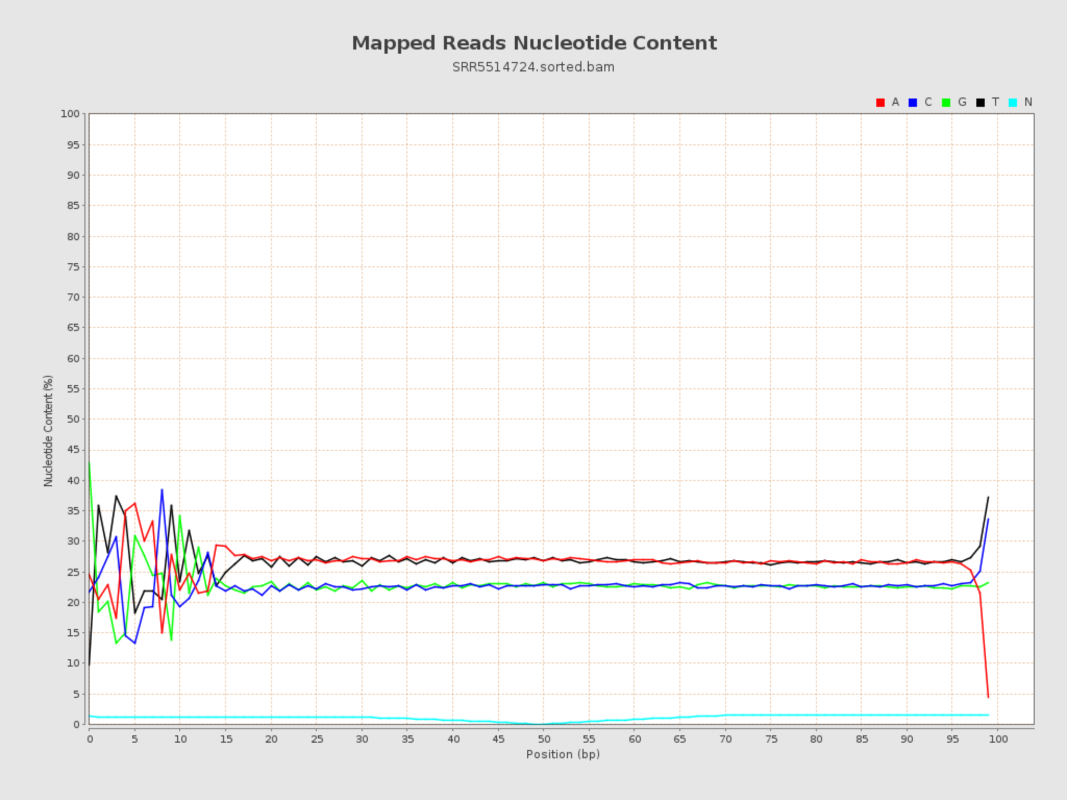
6. Results : Genome Fraction Coverage



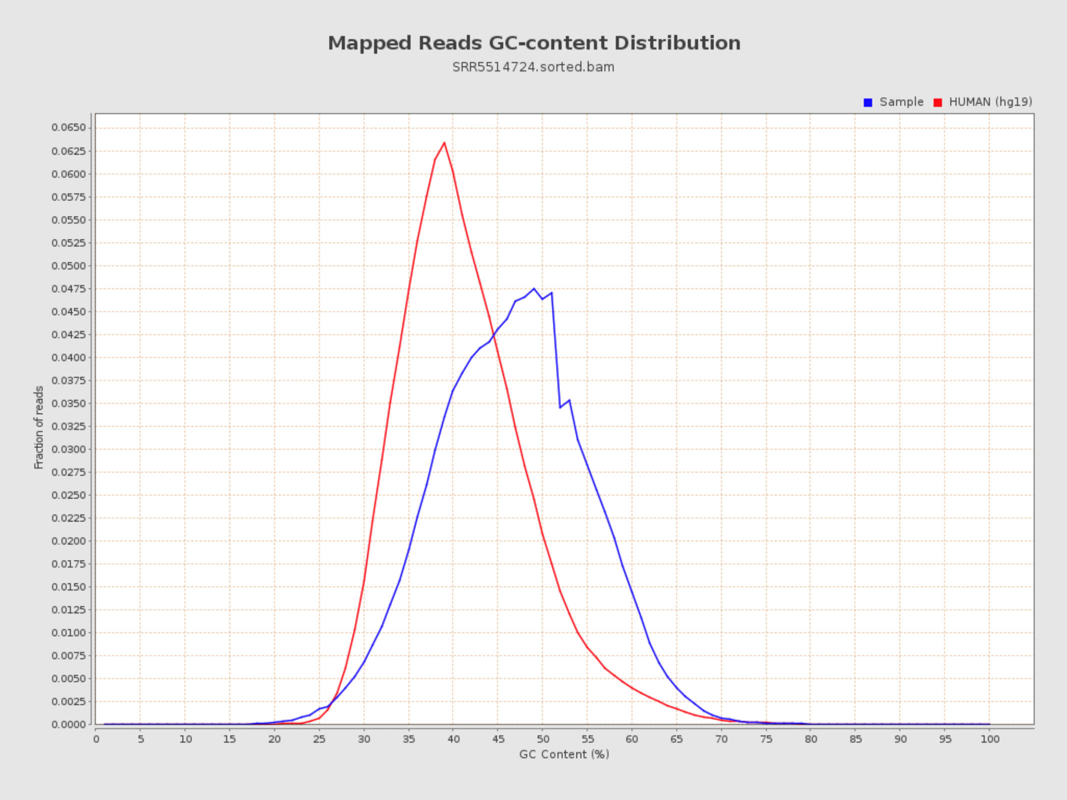
7. Results : Duplication Rate Histogram



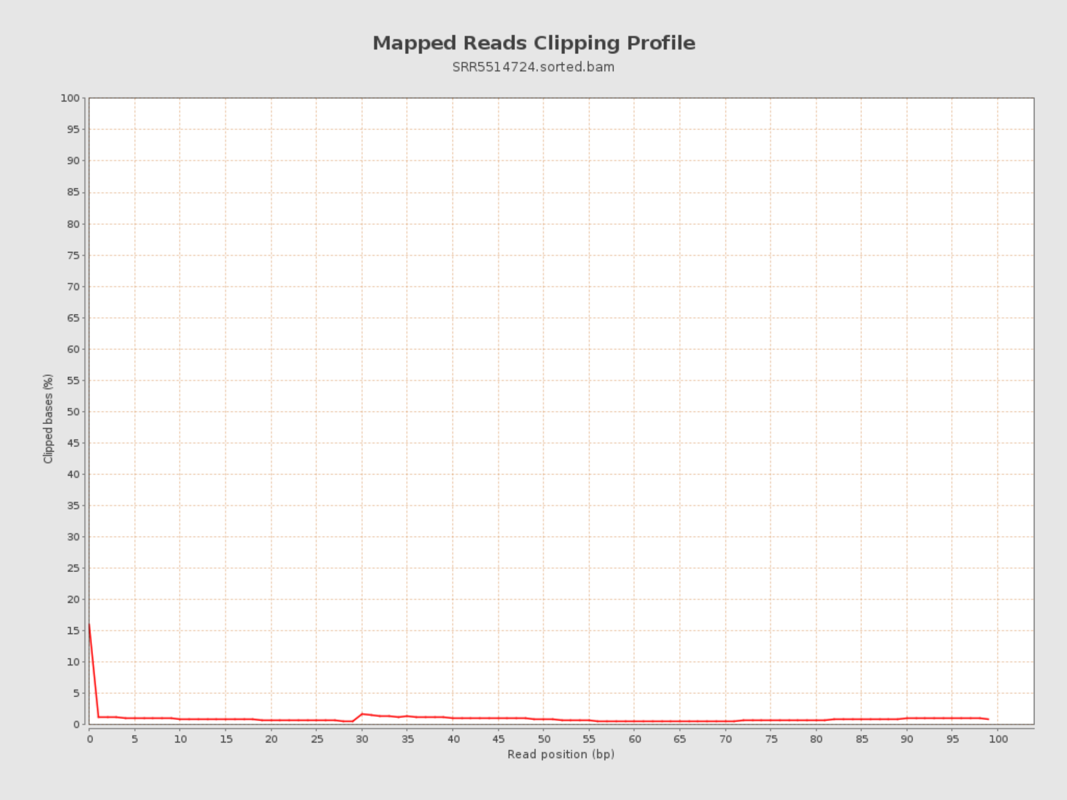
8. Results : Mapped Reads Nucleotide Content



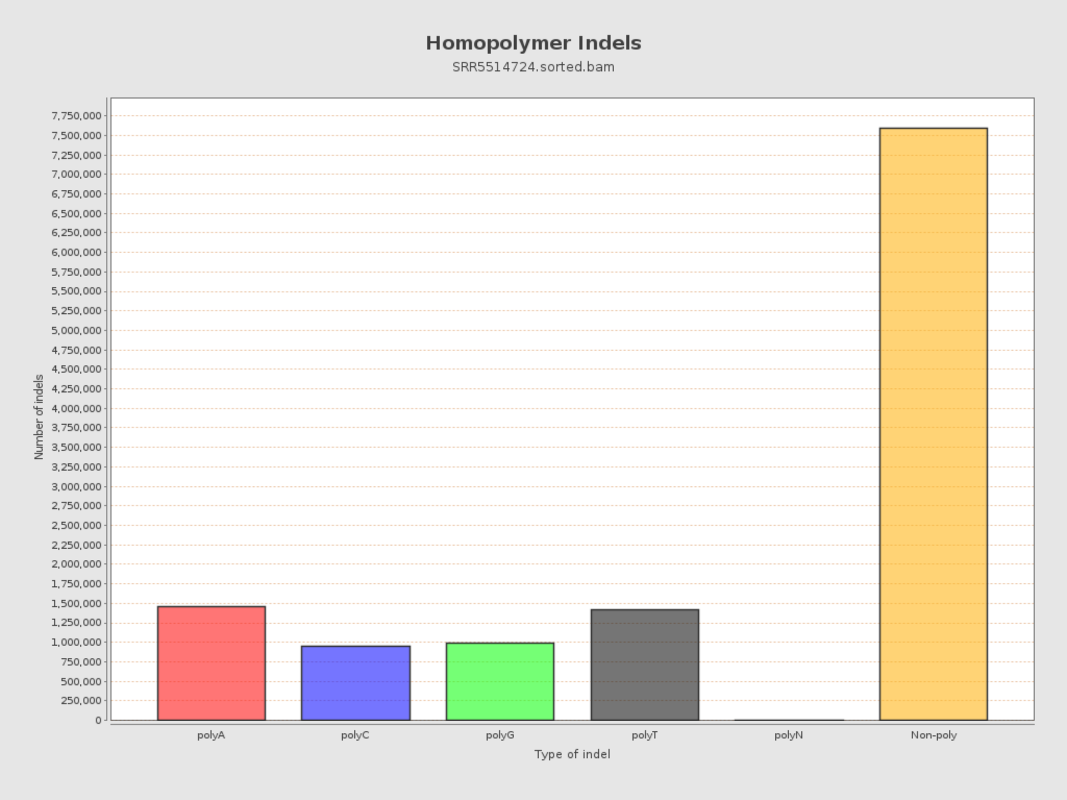
9. Results : Mapped Reads GC-content Distribution



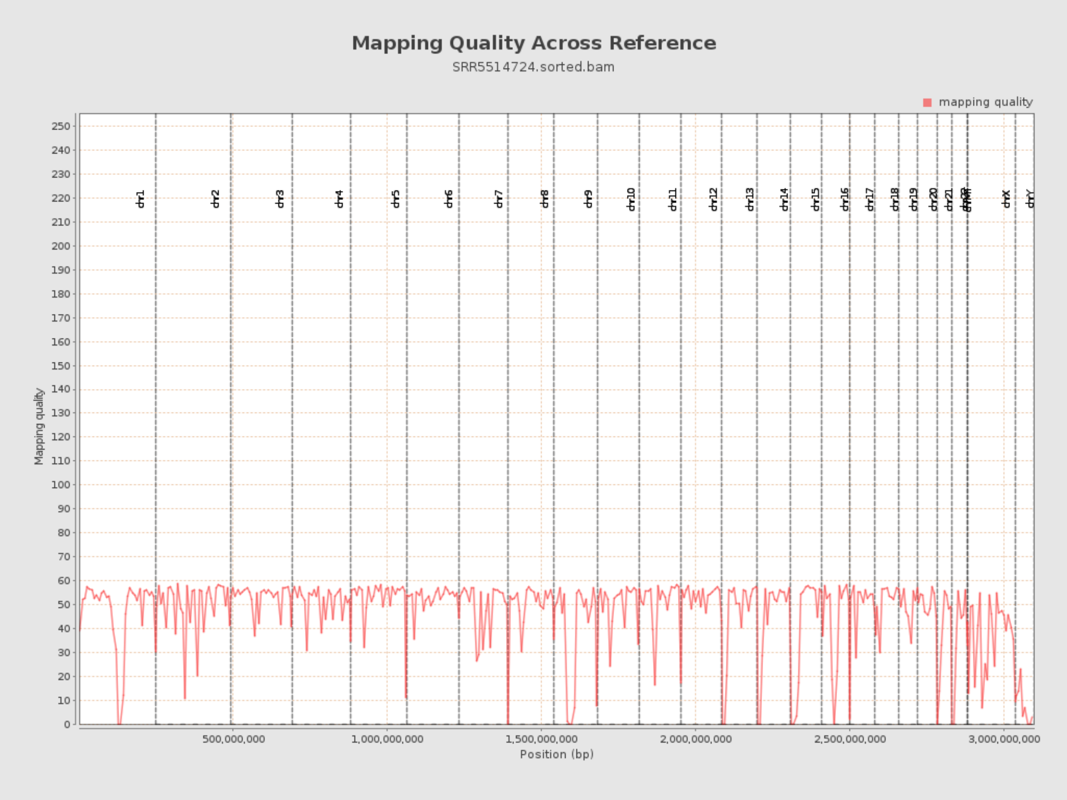
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram