Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 09:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514732.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_SRR5514732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514732.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 09:17:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,556,393
Mapped reads	46,691,869 / 96.16%
Unmapped reads	1,864,524 / 3.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,435,463 / 2.96%
Read min/max/mean length	30 / 100 / 99.03
Duplicated reads (estimated)	35,566,403 / 73.25%
Duplication rate	44.49%
Clipped reads	9,018,862 / 18.57%

2.2. ACGT Content

Number/percentage of A's	1,135,177,224 / 25.88%
Number/percentage of C's	1,034,697,208 / 23.59%
Number/percentage of T's	1,147,832,325 / 26.17%
Number/percentage of G's	1,039,718,387 / 23.7%
Number/percentage of N's	29,459,159 / 0.67%
GC Percentage	47.29%

2.3. Coverage

Mean	1.4179

Standard Deviation	55.6473

2.4. Mapping Quality

Mean Mapping Quality	39.99

2.5. Mismatches and indels

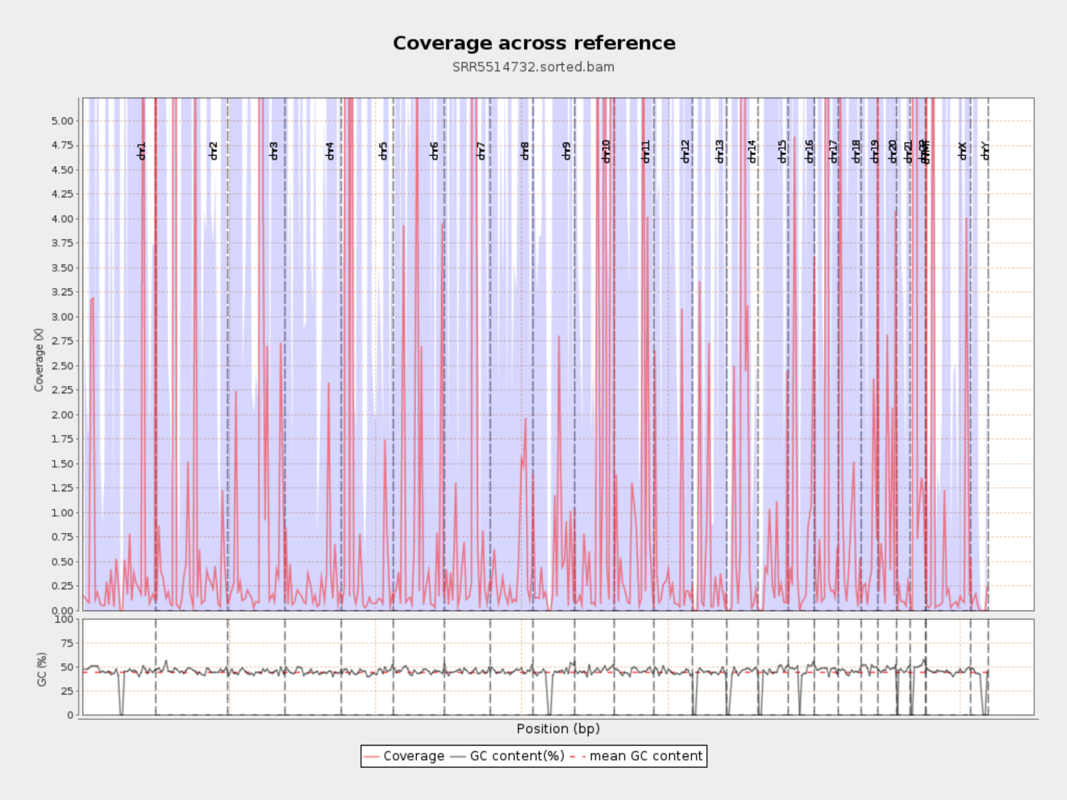
General error rate	1.01%
Mismatches	41,685,057
Insertions	1,640,082
Mapped reads with at least one insertion	3.34%
Deletions	1,268,308
Mapped reads with at least one deletion	2.63%
Homopolymer indels	42.51%

2.6. Chromosome stats

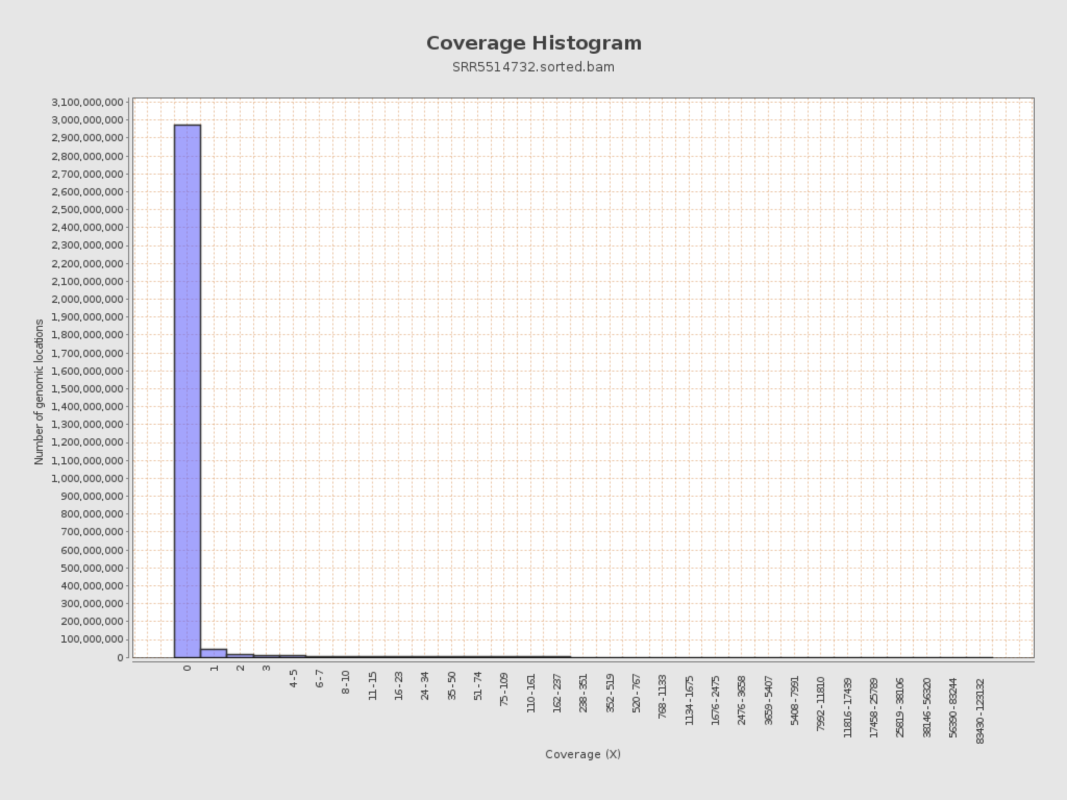
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	175981268	0.706	12.6774
chr2	243199373	308647320	1.2691	45.8607
chr3	198022430	773284444	3.905	56.6041
chr4	191154276	58318339	0.3051	24.6372
chr5	180915260	327233927	1.8088	52.7899
chr6	171115067	157675346	0.9215	121.6654
chr7	159138663	264833709	1.6642	52.4961

chr8	146364022	66485318	0.4542	12.7335
chr9	141213431	67640023	0.479	51.8681
chr10	135534747	811887084	5.9903	146.483
chr11	135006516	144272602	1.0686	33.6528
chr12	133851895	64629943	0.4828	19.6714
chr13	115169878	64321296	0.5585	16.3695
chr14	107349540	237980087	2.2169	58.0655
chr15	102531392	37880094	0.3694	15.4528
chr16	90354753	84937879	0.94	23.9597
chr17	81195210	141614953	1.7441	50.2673
chr18	78077248	85212656	1.0914	15.9155
chr19	59128983	47795875	0.8083	15.5423
chr20	63025520	65800049	1.044	11.5929
chr21	48129895	6978080	0.145	6.4313
chr22	51304566	275164147	5.3633	99.2427
chrMT	16571	2925132	176.5212	109.8392
chrX	155270560	113221850	0.7292	19.4518
chrY	59373566	4709819	0.0793	5.8983

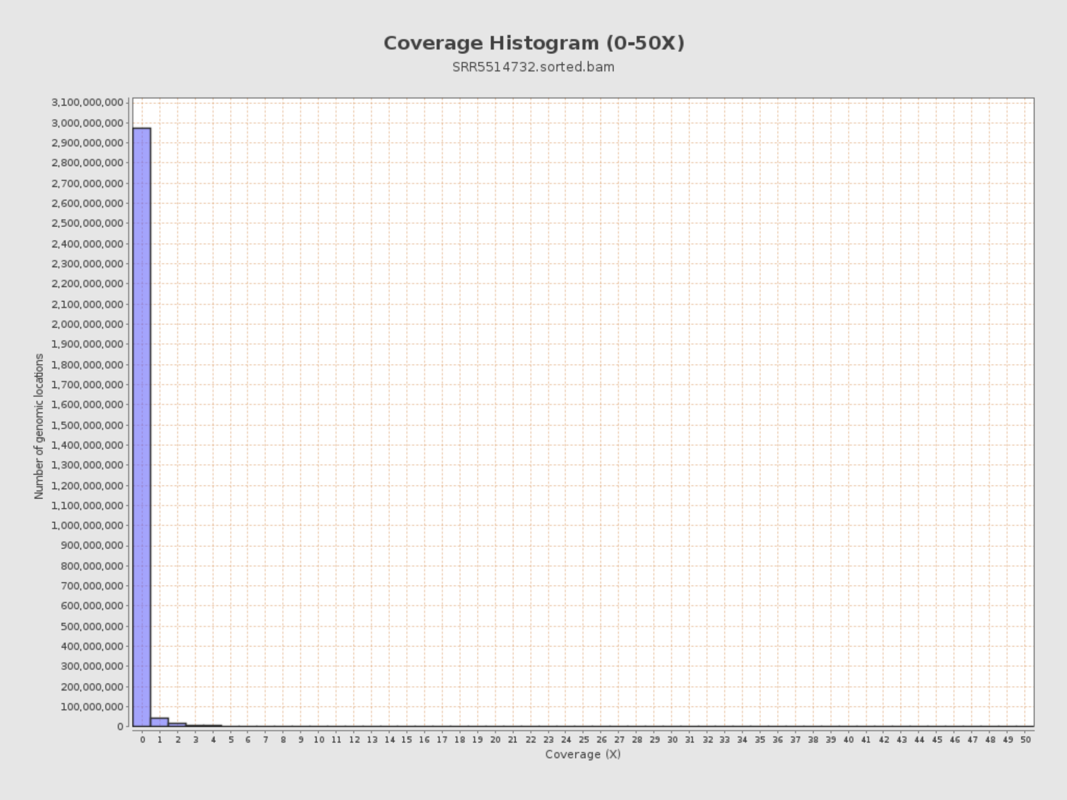
3. Results : Coverage across reference



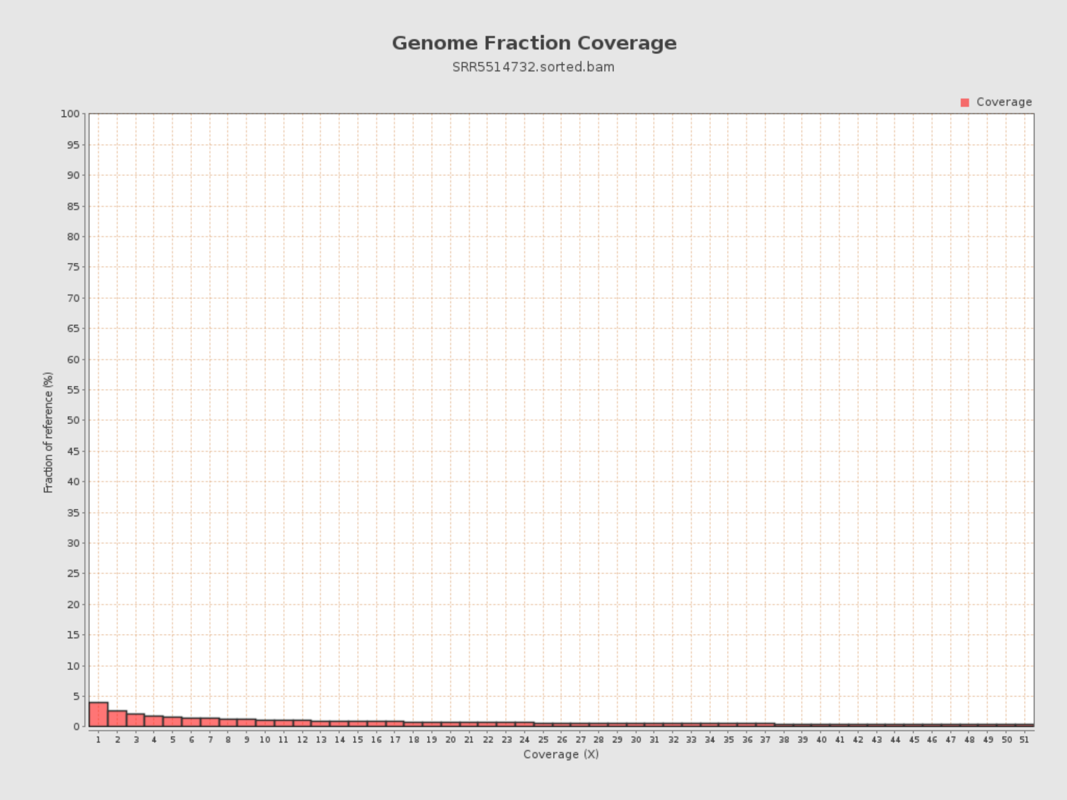
4. Results : Coverage Histogram



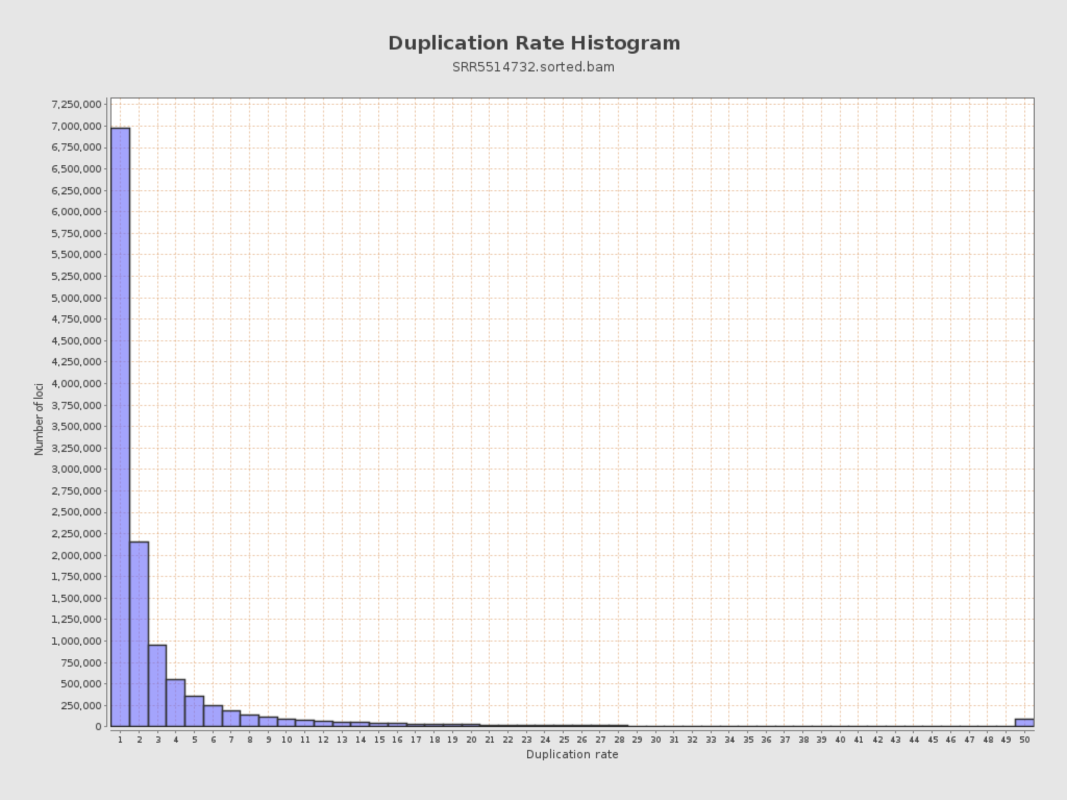
5. Results : Coverage Histogram (0-50X)



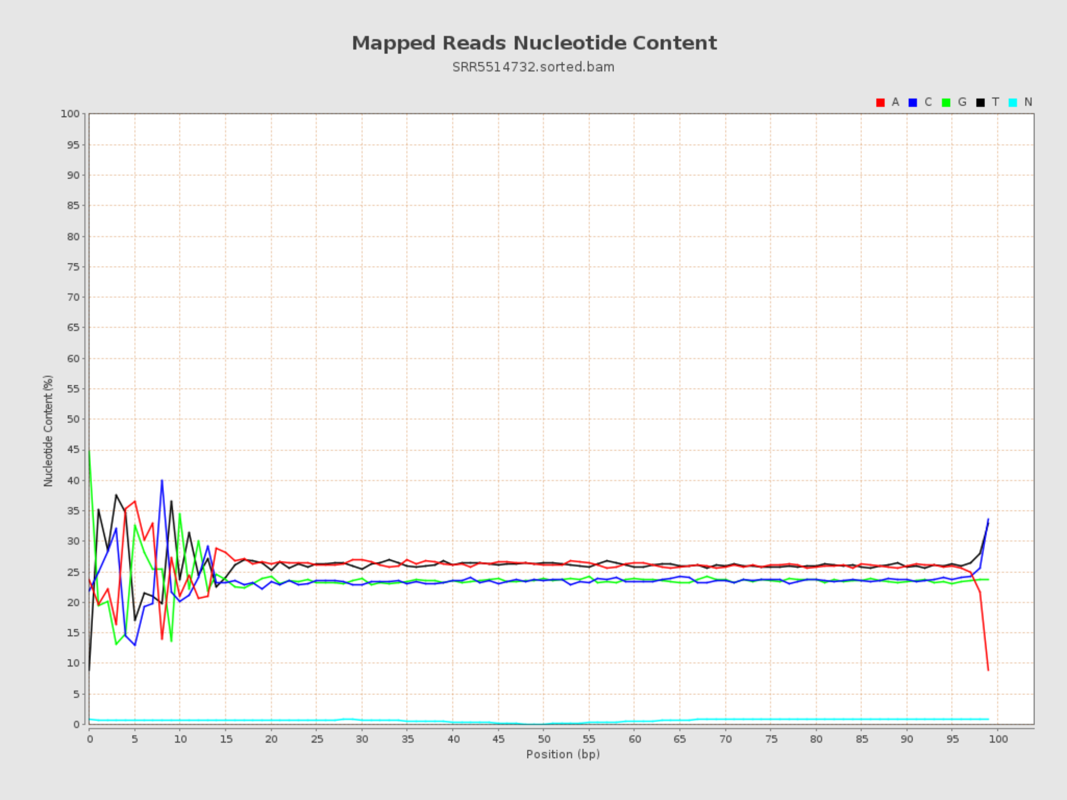
6. Results : Genome Fraction Coverage



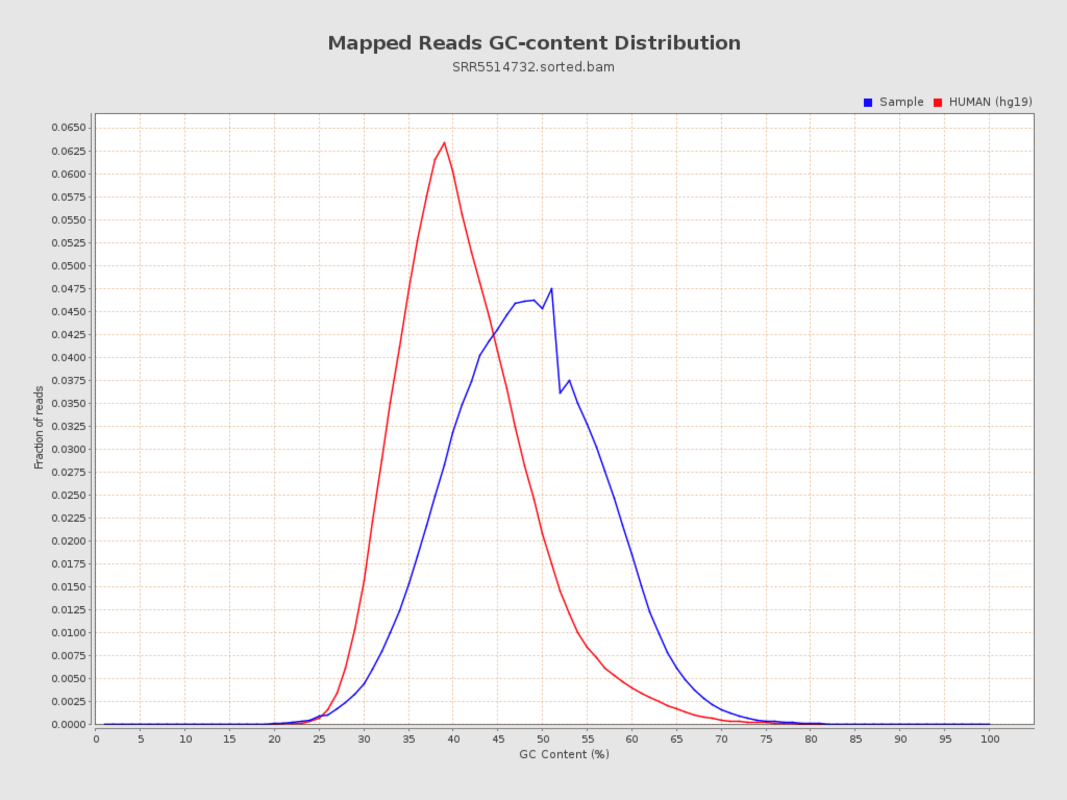
7. Results : Duplication Rate Histogram



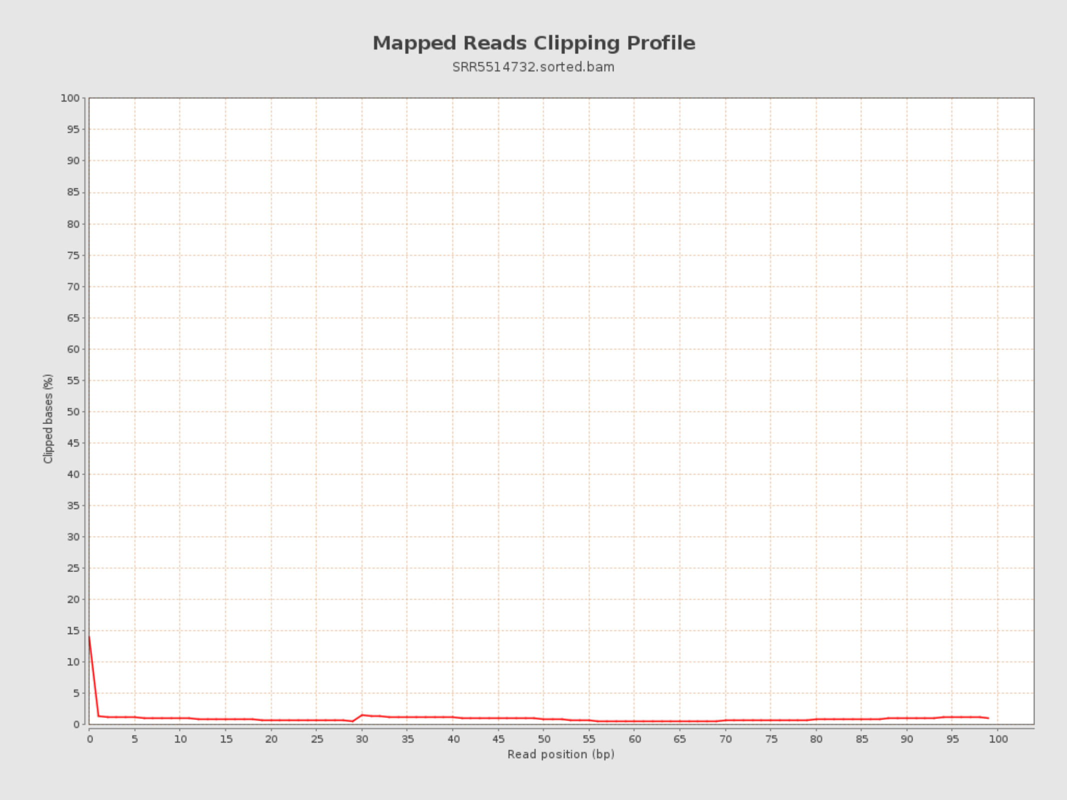
8. Results : Mapped Reads Nucleotide Content



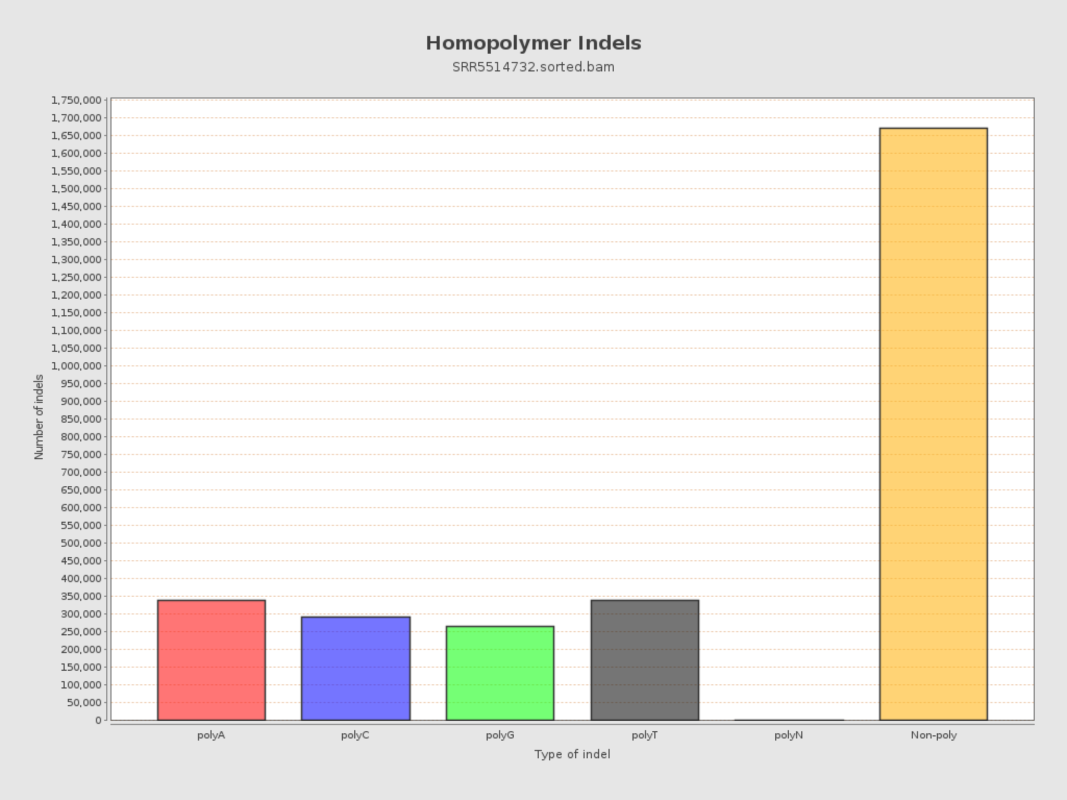
9. Results : Mapped Reads GC-content Distribution



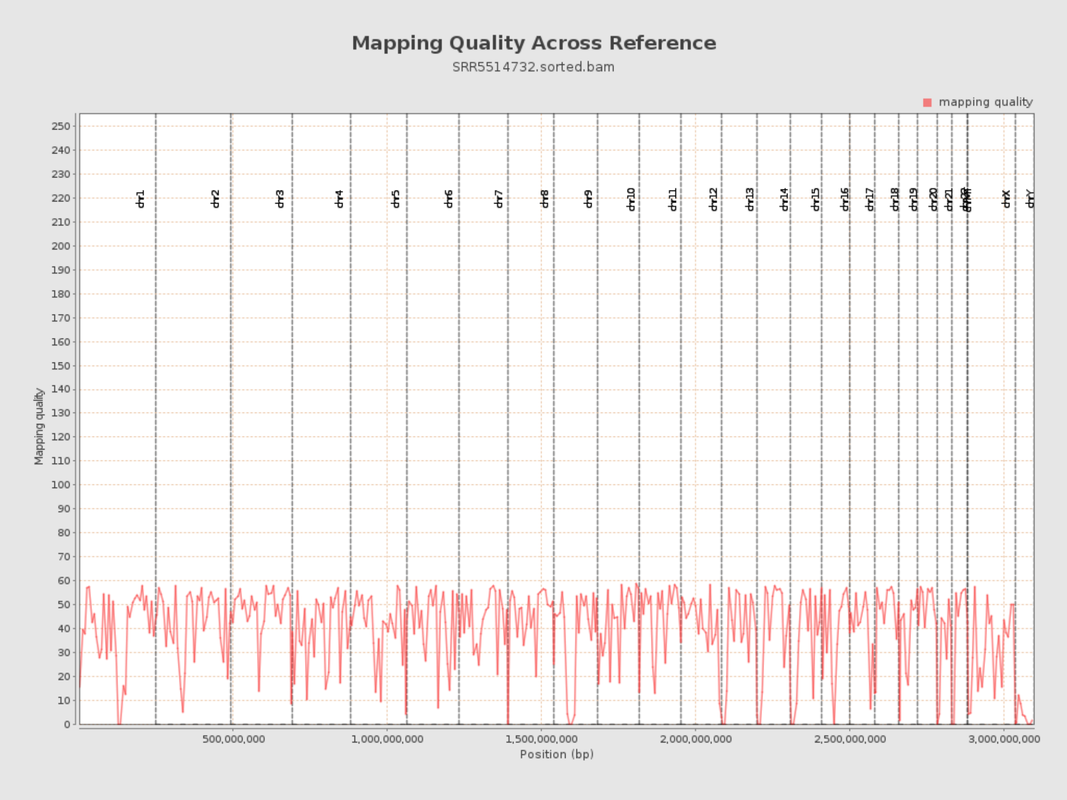
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram