Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 13:40:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514728.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_SRR5514728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514728.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 13:40:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,271,360
Mapped reads	52,939,086 / 95.78%
Unmapped reads	2,332,274 / 4.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,490,959 / 2.7%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	38,586,234 / 69.81%
Duplication rate	42.73%
Clipped reads	8,978,640 / 16.24%

2.2. ACGT Content

Number/percentage of A's	1,319,397,850 / 26.2%
Number/percentage of C's	1,174,006,985 / 23.32%
Number/percentage of T's	1,334,724,735 / 26.51%
Number/percentage of G's	1,177,098,374 / 23.38%
Number/percentage of N's	30,145,168 / 0.6%
GC Percentage	46.69%

2.3. Coverage

Mean	1.6273

Standard Deviation	59.587

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

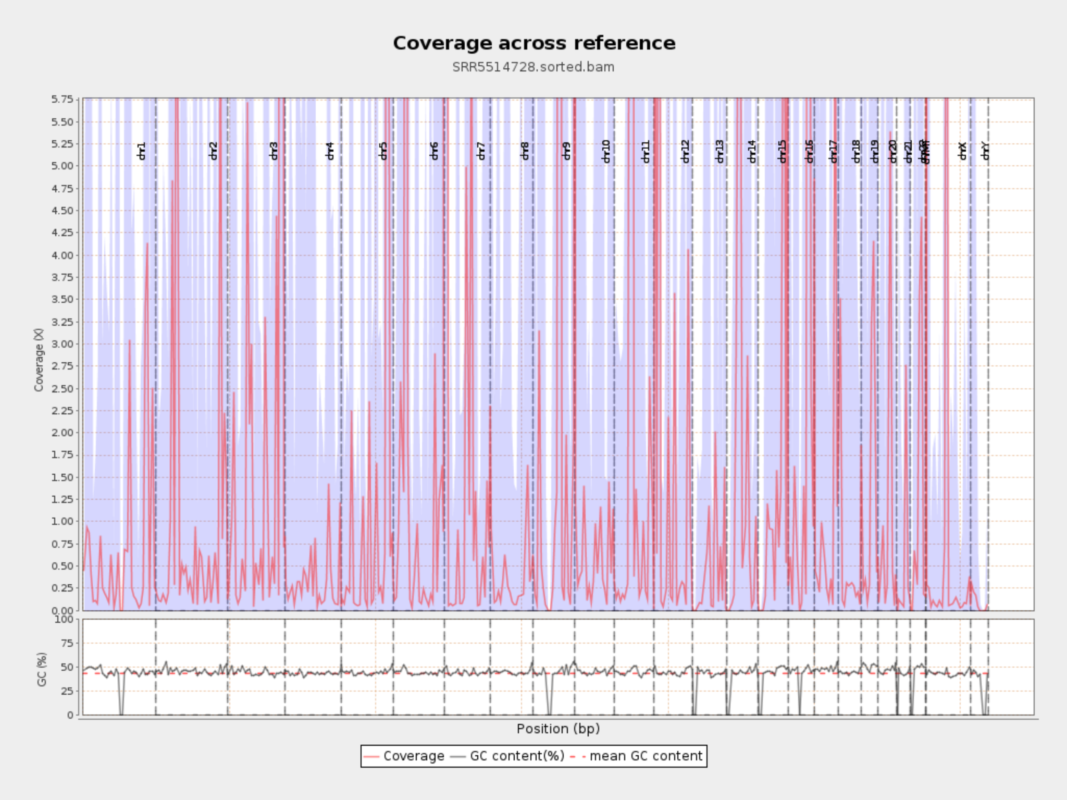
General error rate	0.86%
Mismatches	40,988,851
Insertions	1,731,620
Mapped reads with at least one insertion	3.17%
Deletions	1,285,805
Mapped reads with at least one deletion	2.36%
Homopolymer indels	45.25%

2.6. Chromosome stats

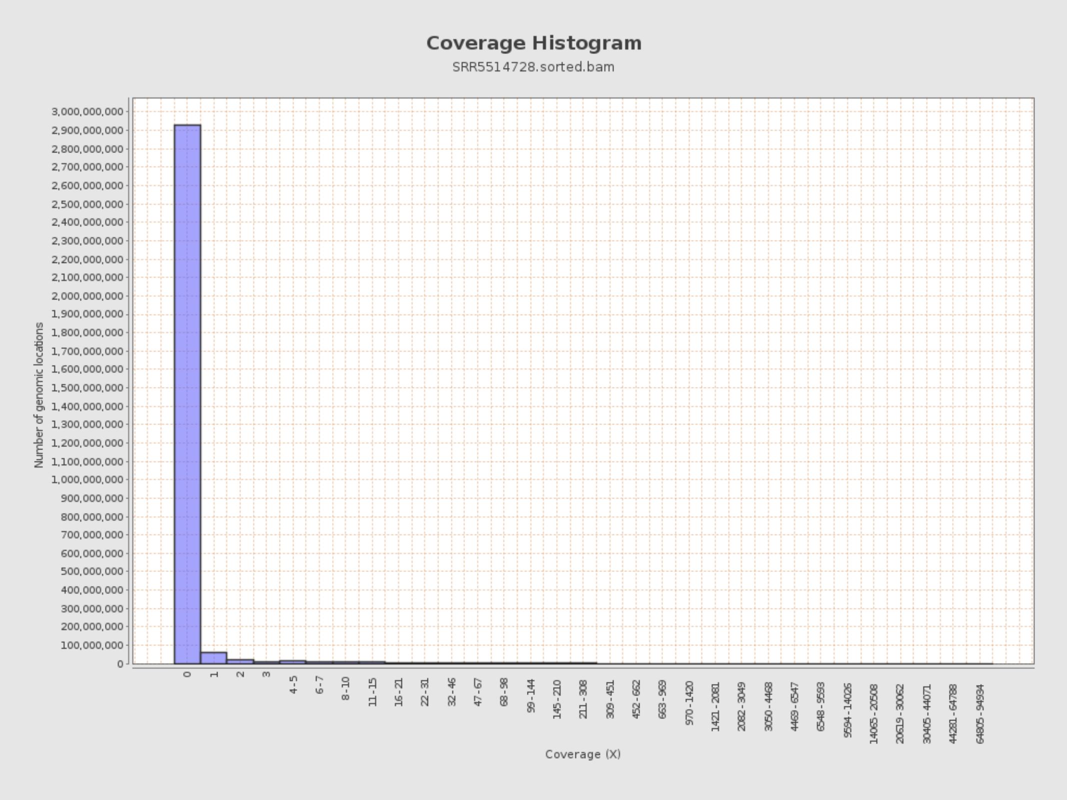
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	168344606	0.6754	11.7799
chr2	243199373	262300605	1.0785	22.2949
chr3	198022430	774103329	3.9092	84.1665
chr4	191154276	66061101	0.3456	6.6062
chr5	180915260	208364756	1.1517	23.6747
chr6	171115067	271012470	1.5838	29.4876
chr7	159138663	821859146	5.1644	64.4221

chr8	146364022	53952792	0.3686	8.9324
chr9	141213431	346527596	2.4539	215.9686
chr10	135534747	78654817	0.5803	21.3118
chr11	135006516	580627421	4.3007	88.8557
chr12	133851895	284933527	2.1287	38.1312
chr13	115169878	54287261	0.4714	13.2811
chr14	107349540	192432912	1.7926	29.1246
chr15	102531392	166417683	1.6231	29.059
chr16	90354753	220127600	2.4363	45.4729
chr17	81195210	86991658	1.0714	13.9353
chr18	78077248	47149183	0.6039	29.0313
chr19	59128983	74769396	1.2645	27.2934
chr20	63025520	61258825	0.972	19.0472
chr21	48129895	25983273	0.5399	8.1921
chr22	51304566	70971743	1.3833	13.3629
chrMT	16571	4566159	275.5512	127.8276
chrX	155270560	110660959	0.7127	15.5228
chrY	59373566	5405007	0.091	7.7951

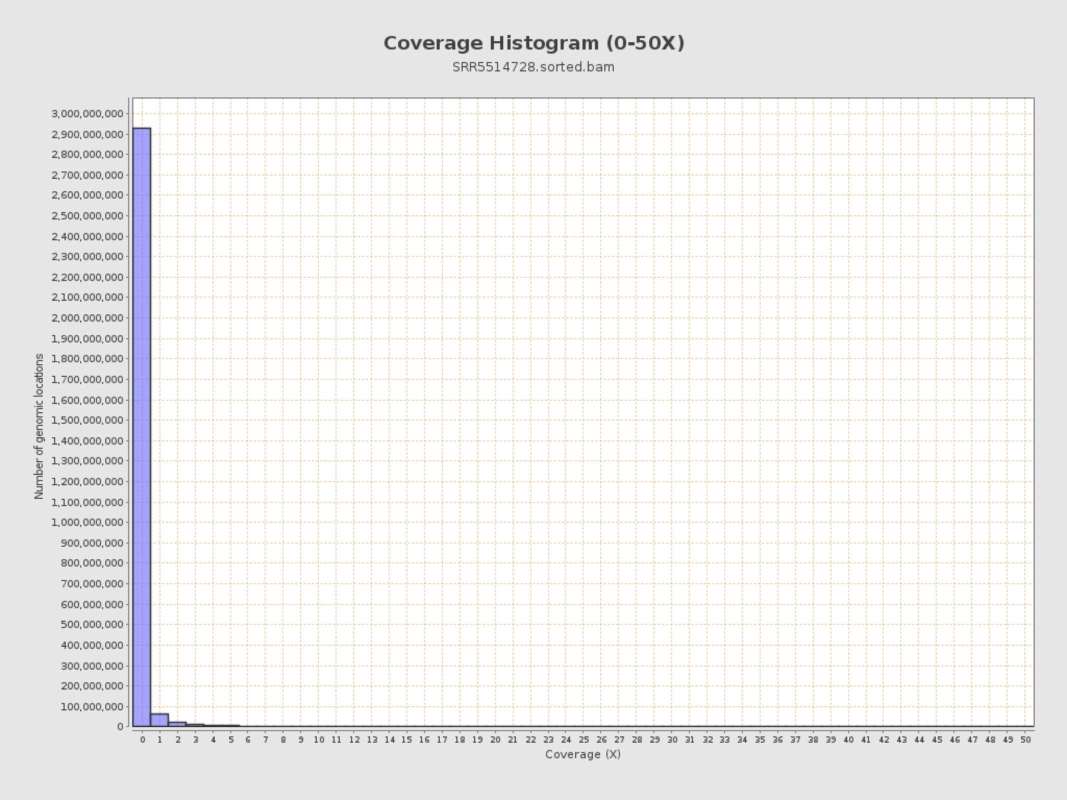
3. Results : Coverage across reference



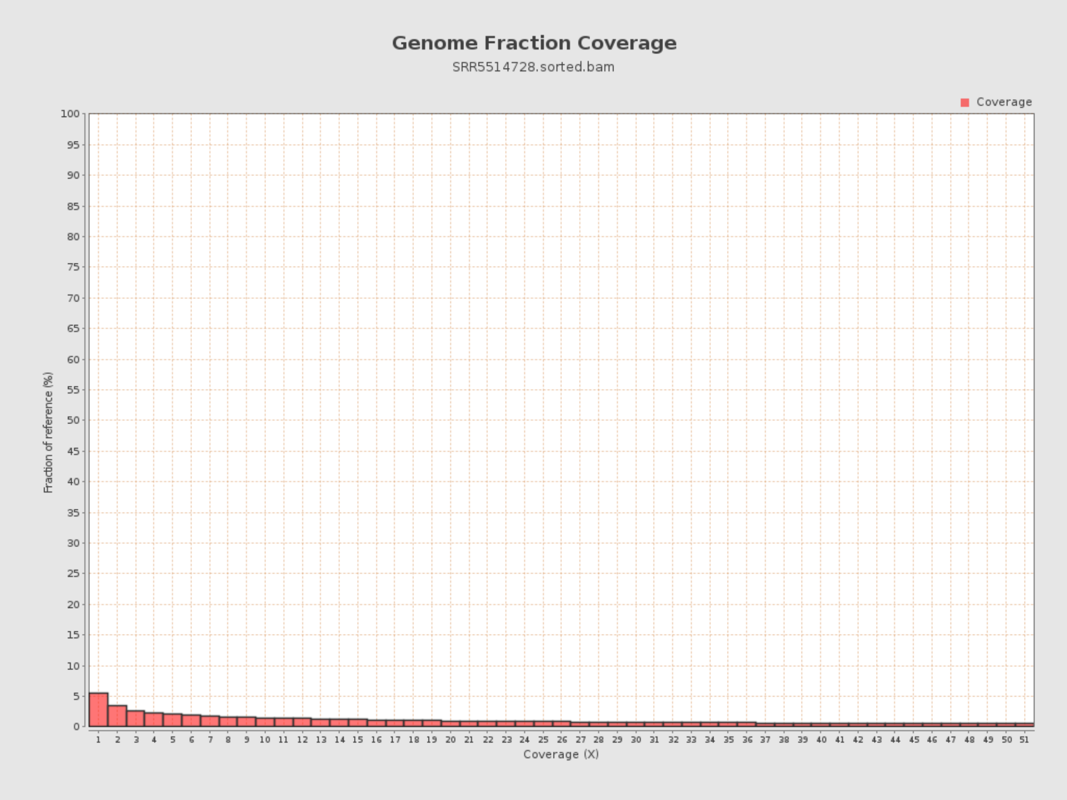
4. Results : Coverage Histogram



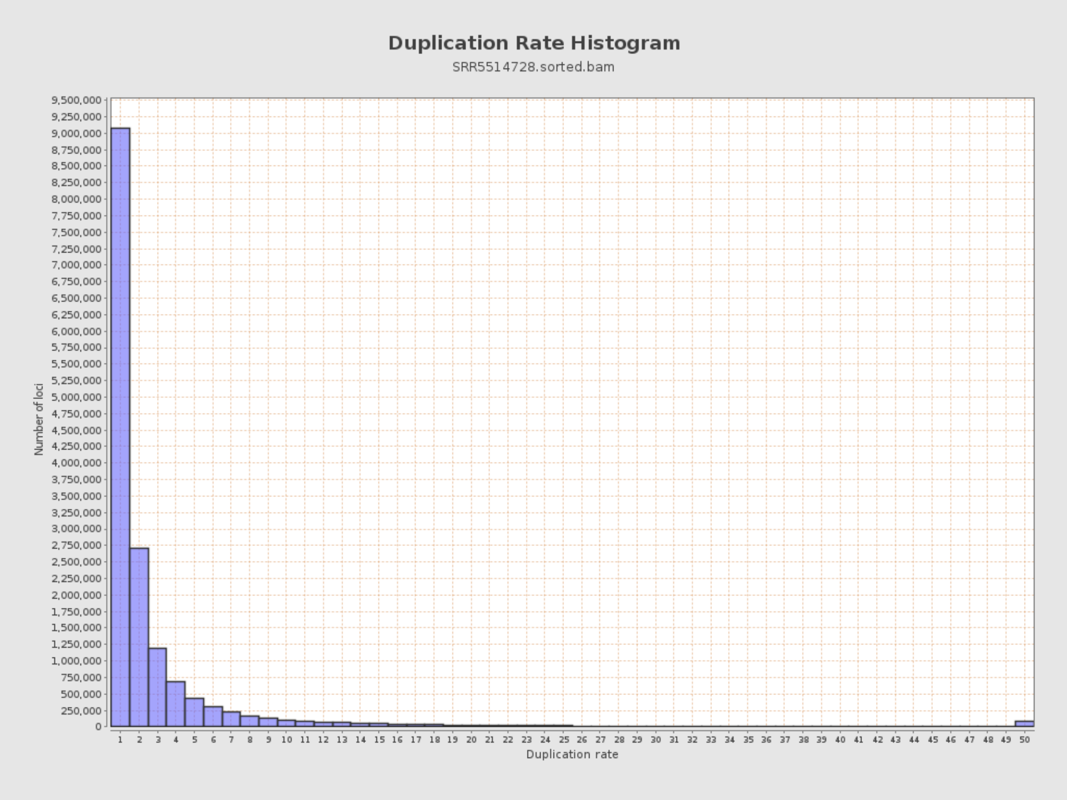
5. Results : Coverage Histogram (0-50X)



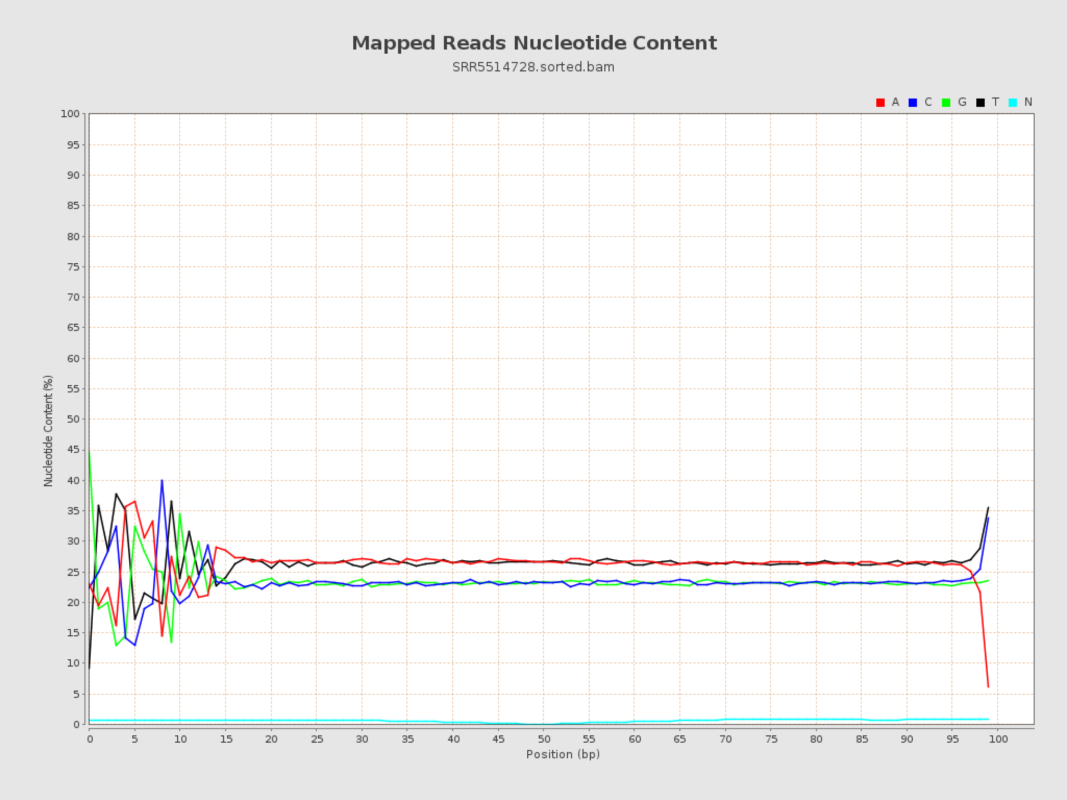
6. Results : Genome Fraction Coverage



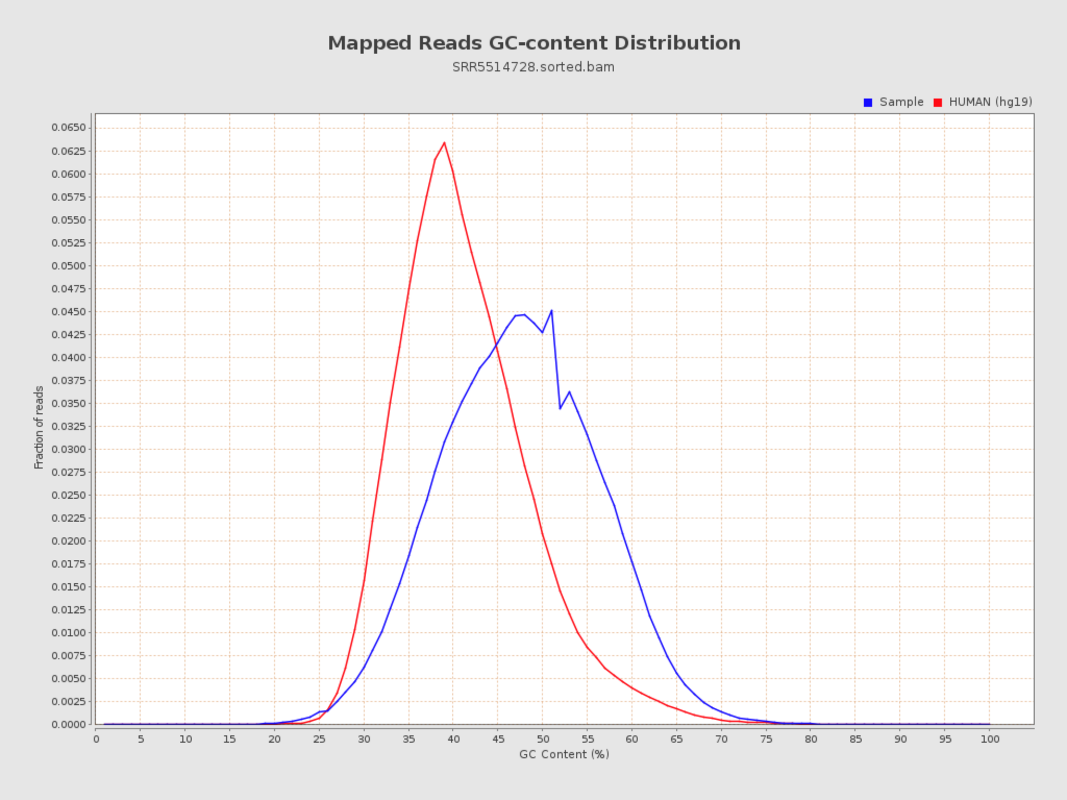
7. Results : Duplication Rate Histogram



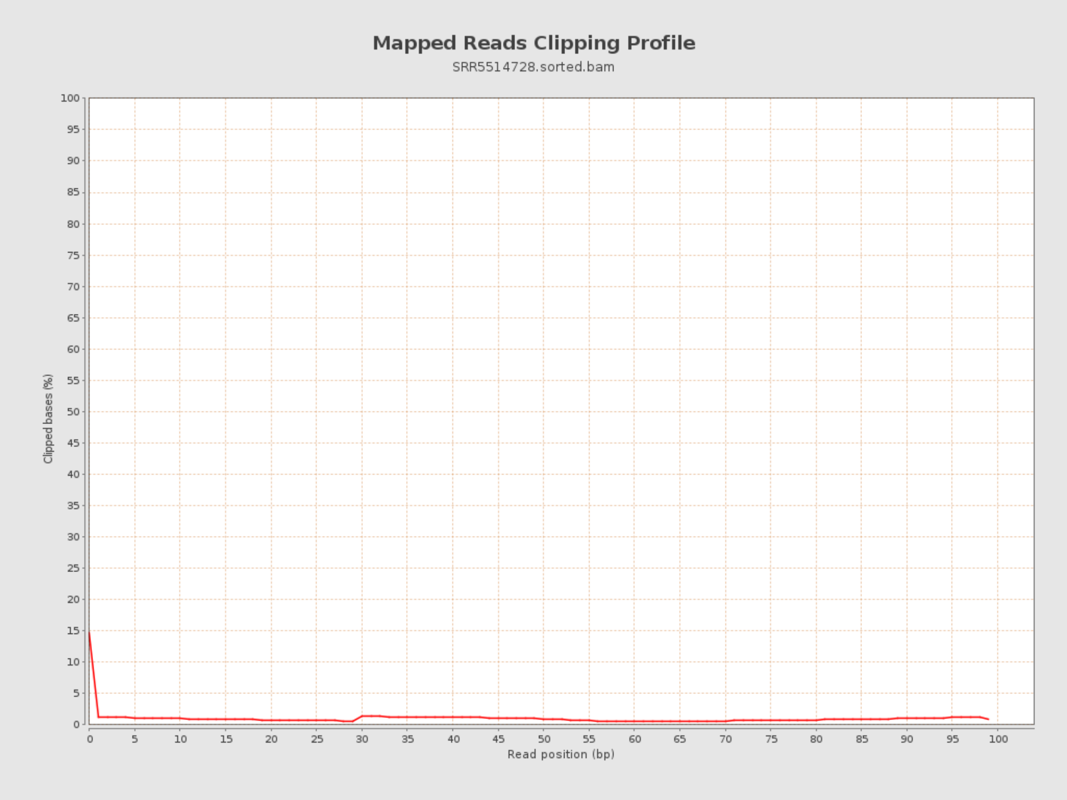
8. Results : Mapped Reads Nucleotide Content



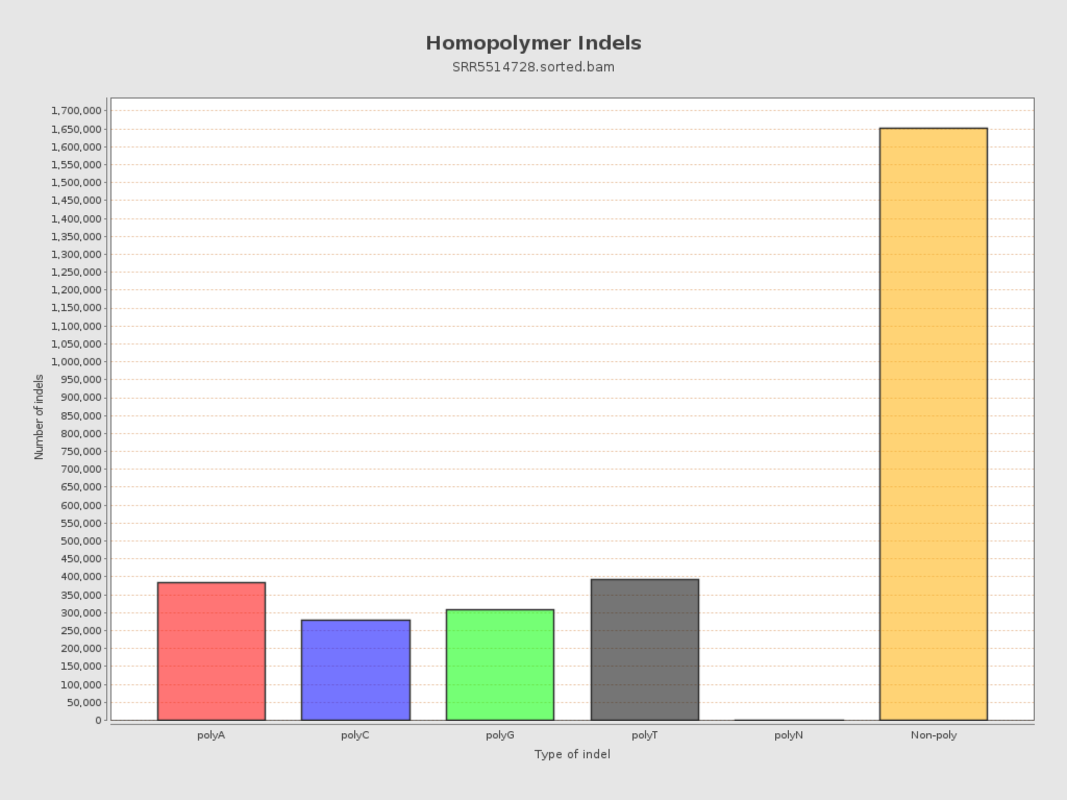
9. Results : Mapped Reads GC-content Distribution



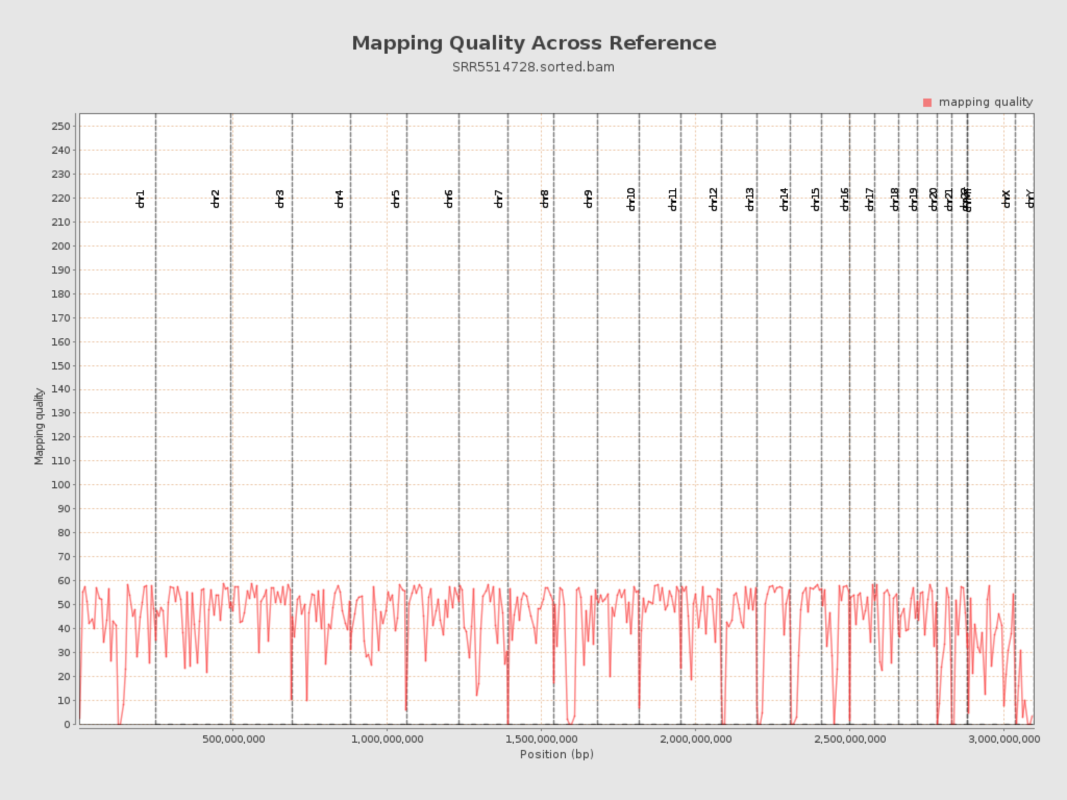
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram