Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 19:47:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514712.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_SRR5514712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 19:47:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,292,808
Mapped reads	47,281,298 / 97.91%
Unmapped reads	1,011,510 / 2.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,788,932 / 7.85%
Read min/max/mean length	30 / 100 / 101.01
Duplicated reads (estimated)	45,900,096 / 95.05%
Duplication rate	51%
Clipped reads	15,685,471 / 32.48%

2.2. ACGT Content

Number/percentage of A's	1,269,629,995 / 28.59%
Number/percentage of C's	942,960,769 / 21.23%
Number/percentage of T's	1,265,860,012 / 28.5%
Number/percentage of G's	961,527,947 / 21.65%
Number/percentage of N's	1,121,644 / 0.03%
GC Percentage	42.88%

2.3. Coverage

Mean	1.4358

Standard Deviation	271.1535

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

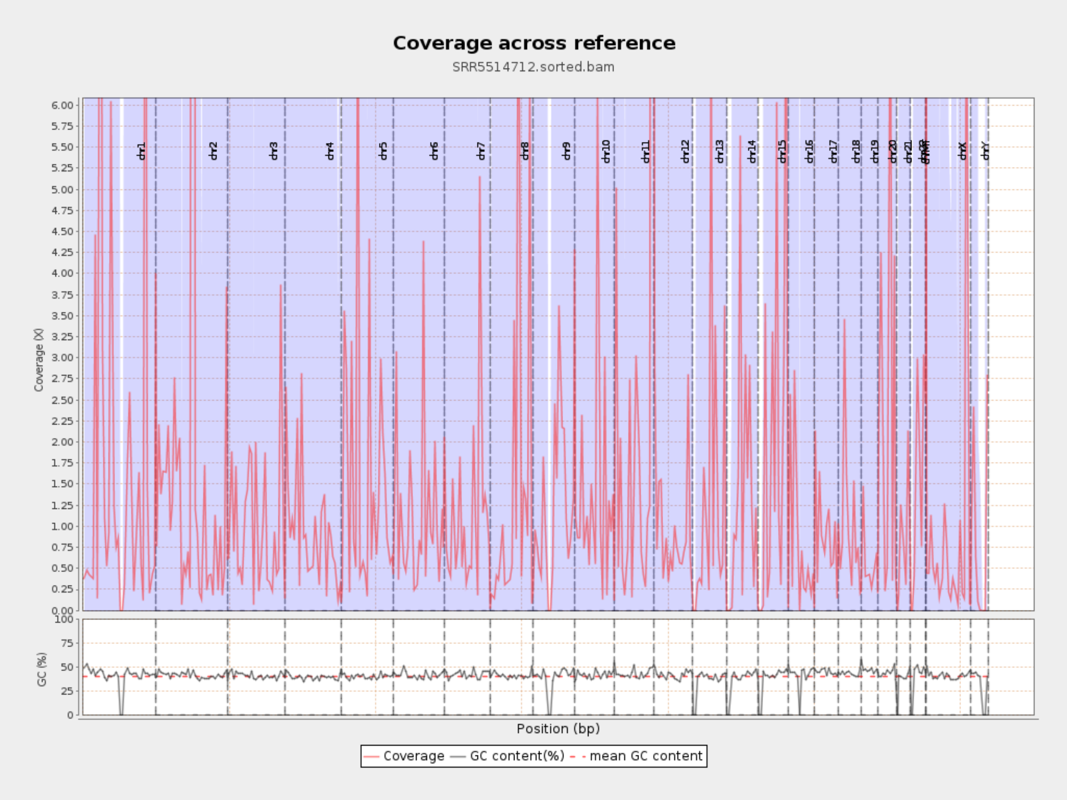
General error rate	0.84%
Mismatches	32,685,779
Insertions	2,286,801
Mapped reads with at least one insertion	4.67%
Deletions	1,404,073
Mapped reads with at least one deletion	2.85%
Homopolymer indels	38.27%

2.6. Chromosome stats

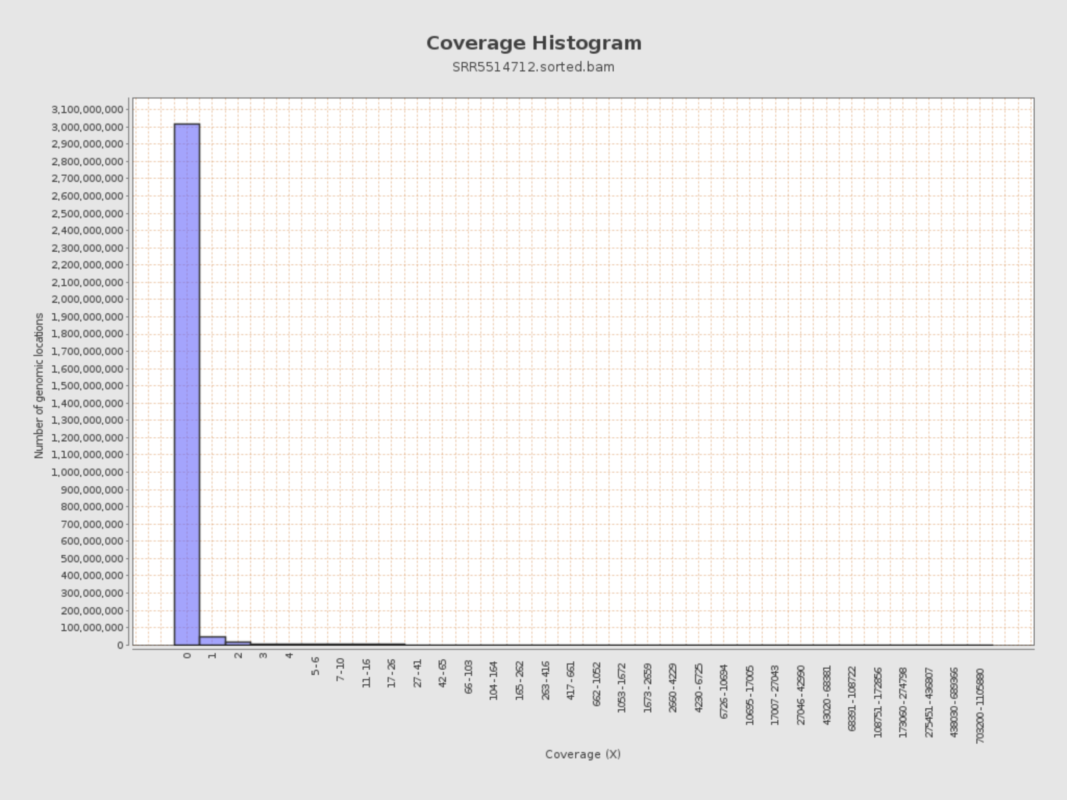
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	441597422	1.7717	181.9718
chr2	243199373	553807161	2.2772	610.9281
chr3	198022430	201460718	1.0174	51.2566
chr4	191154276	180798927	0.9458	47.3505
chr5	180915260	298522874	1.6501	93.0151
chr6	171115067	198598457	1.1606	58.1196
chr7	159138663	181163364	1.1384	77.4563

chr8	146364022	216425575	1.4787	129.0406
chr9	141213431	173192985	1.2265	78.5719
chr10	135534747	186345062	1.3749	110.117
chr11	135006516	421692664	3.1235	881.3034
chr12	133851895	131775348	0.9845	52.2187
chr13	115169878	156574754	1.3595	98.5611
chr14	107349540	150797724	1.4047	95.3487
chr15	102531392	224395460	2.1886	229.2089
chr16	90354753	70572867	0.7811	60.6298
chr17	81195210	77975114	0.9603	41.2212
chr18	78077248	84964083	1.0882	49.1938
chr19	59128983	32978448	0.5577	30.1528
chr20	63025520	165915631	2.6325	226.1136
chr21	48129895	39604803	0.8229	47.4942
chr22	51304566	76034765	1.482	94.353
chrMT	16571	260230	15.7039	41.8641
chrX	155270560	127432968	0.8207	121.0985
chrY	59373566	51890189	0.874	41.3716

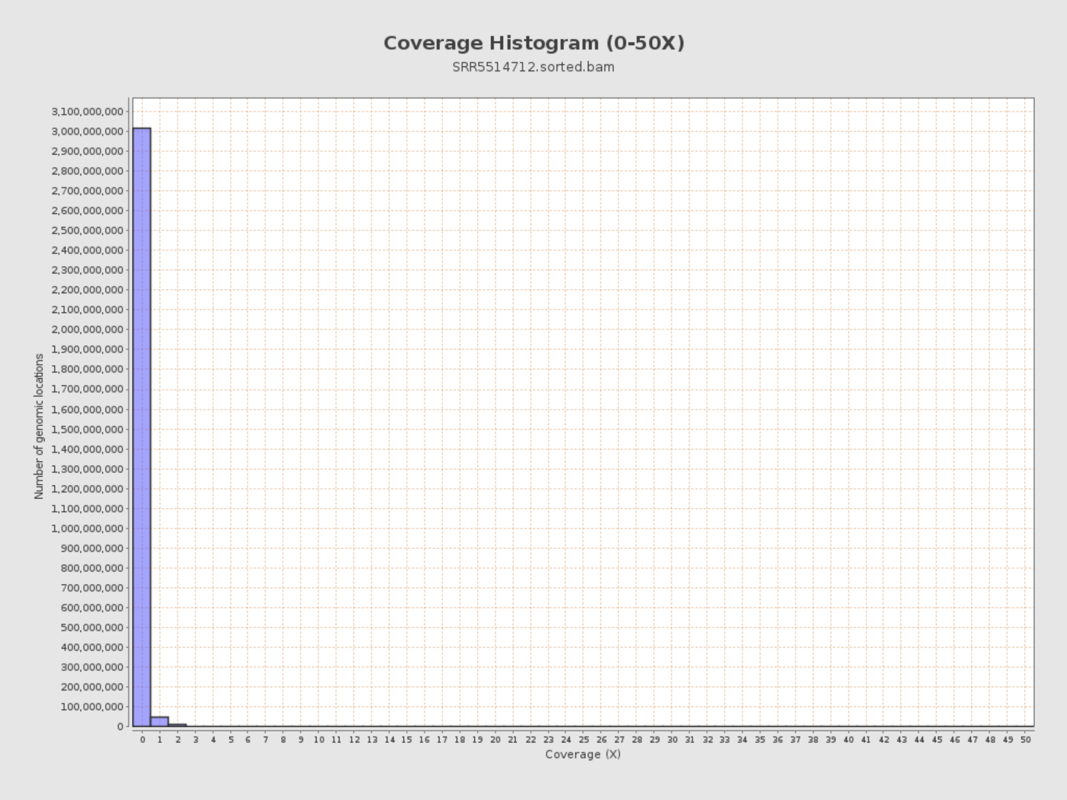
3. Results : Coverage across reference



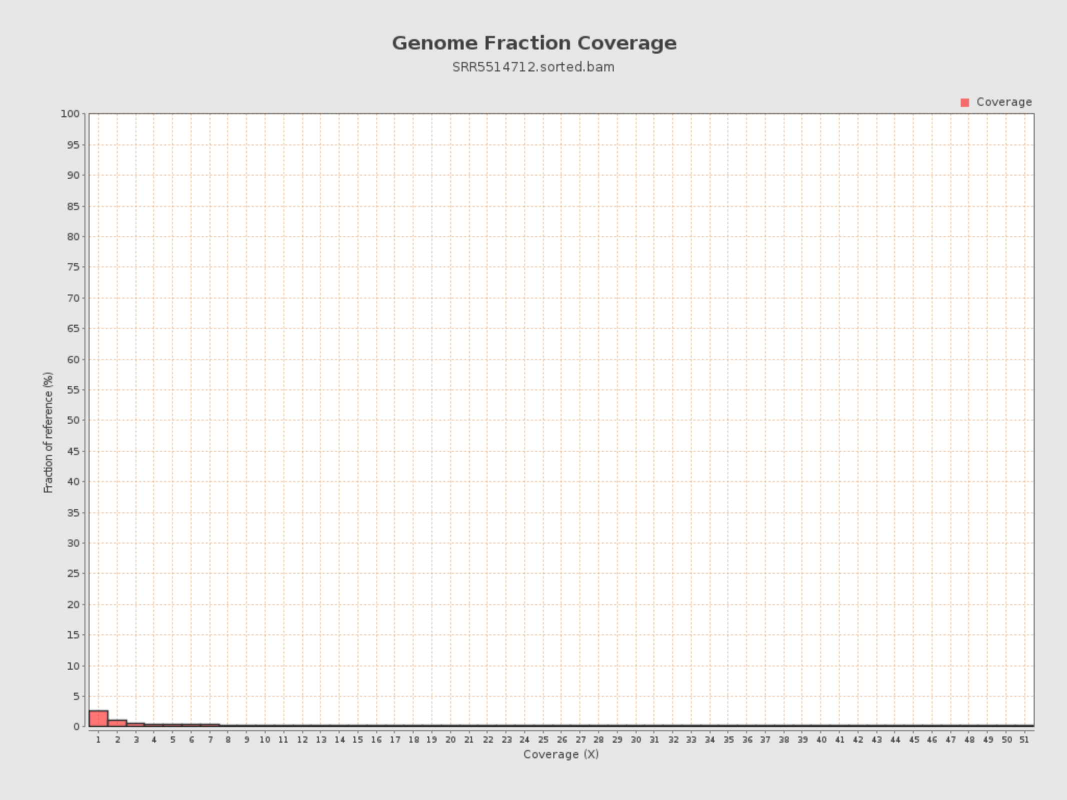
4. Results : Coverage Histogram



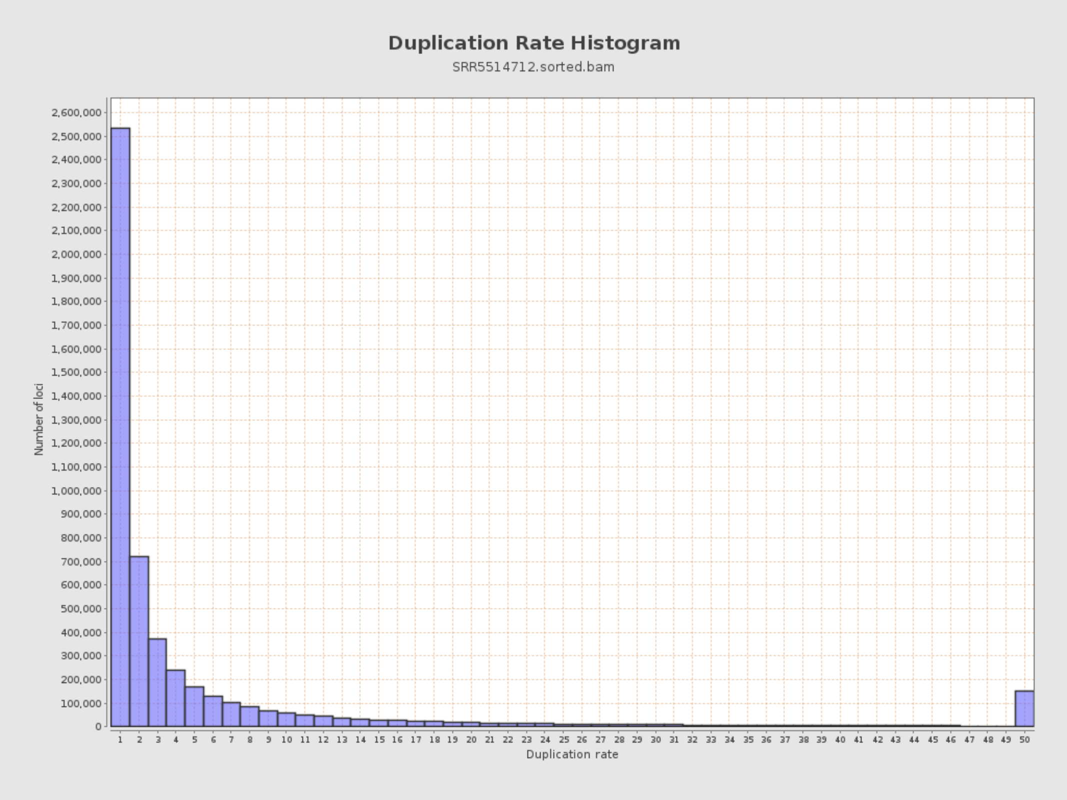
5. Results : Coverage Histogram (0-50X)



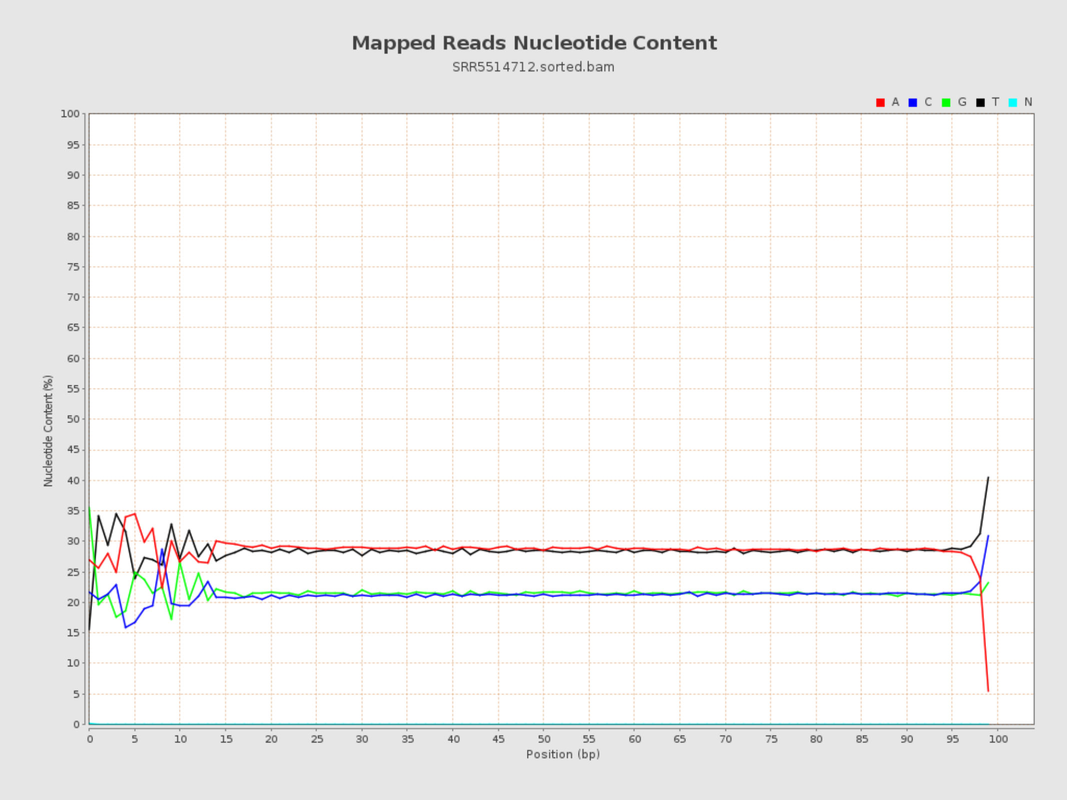
6. Results : Genome Fraction Coverage



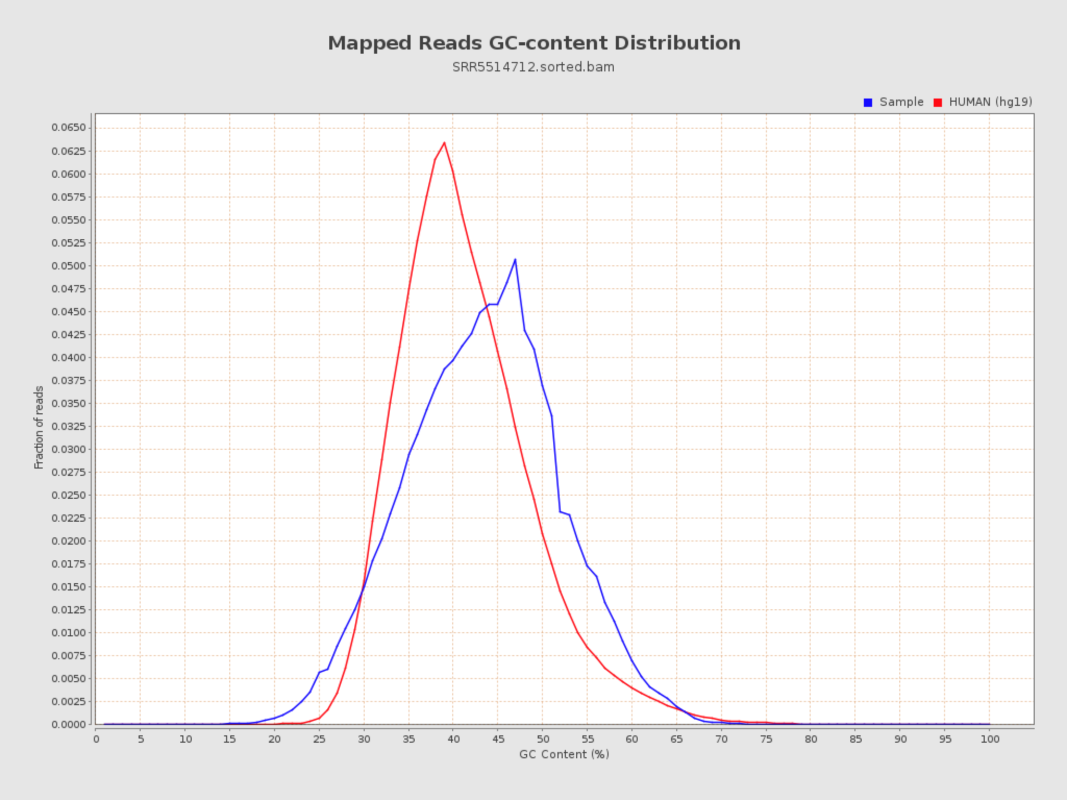
7. Results : Duplication Rate Histogram



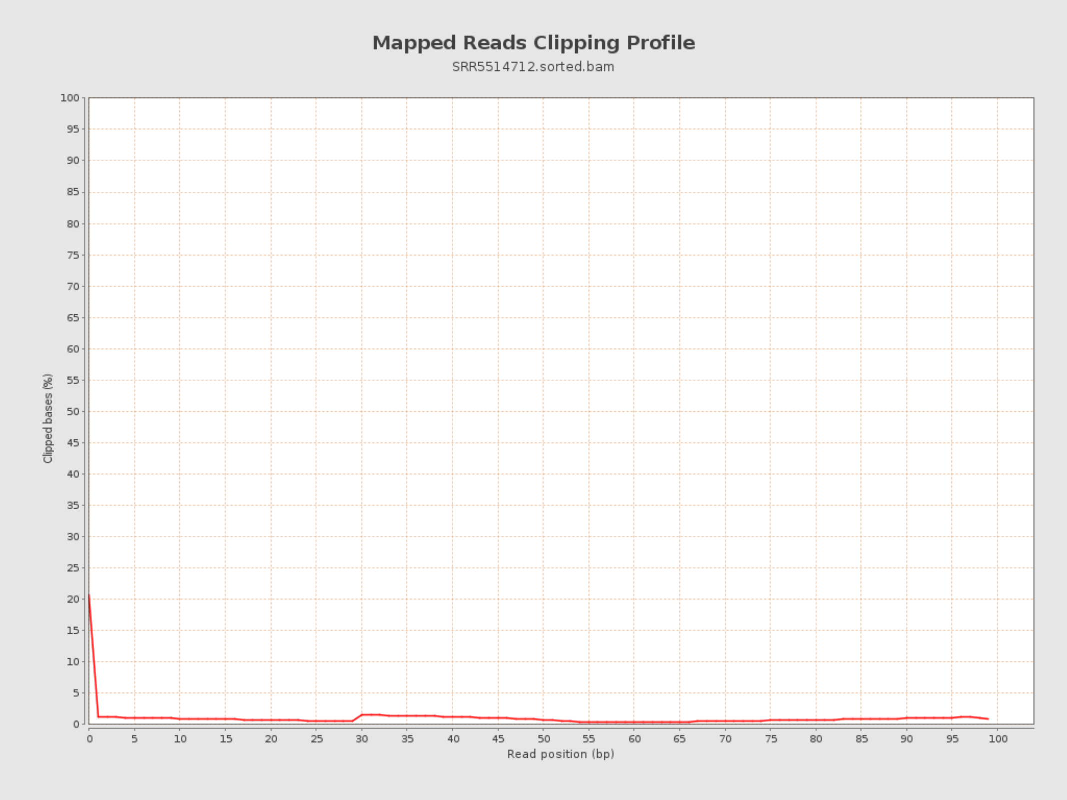
8. Results : Mapped Reads Nucleotide Content



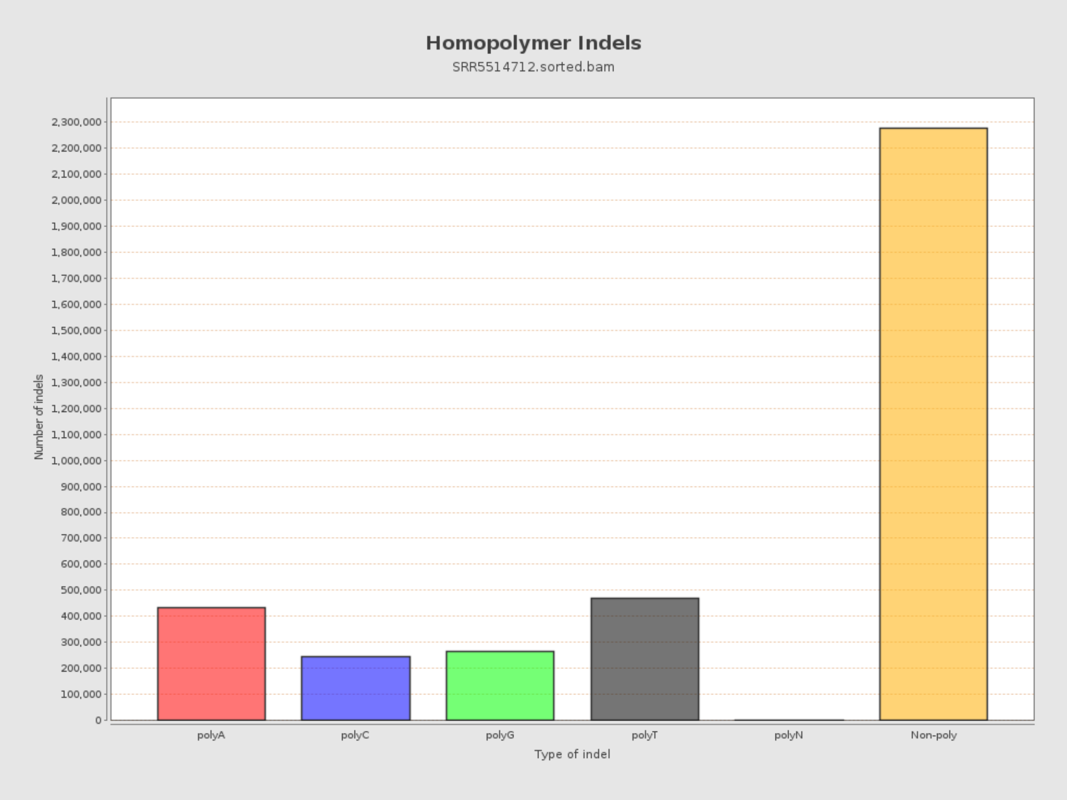
9. Results : Mapped Reads GC-content Distribution



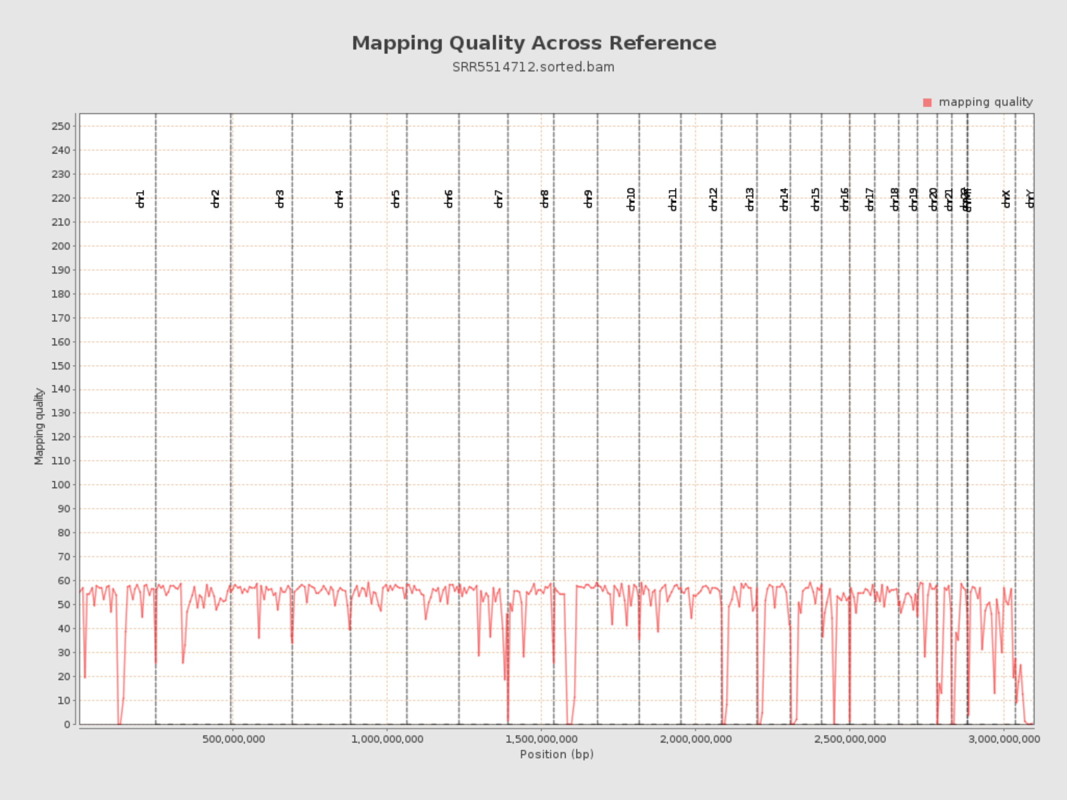
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram