Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 07:50:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514718.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_SRR5514718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 07:50:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,643,161
Mapped reads	57,305,095 / 94.5%
Unmapped reads	3,338,066 / 5.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,234,895 / 5.33%
Read min/max/mean length	30 / 100 / 100.67
Duplicated reads (estimated)	45,394,421 / 74.85%
Duplication rate	36.36%
Clipped reads	17,437,713 / 28.75%

2.2. ACGT Content

Number/percentage of A's	1,404,383,948 / 26.56%
Number/percentage of C's	1,197,966,552 / 22.66%
Number/percentage of T's	1,417,629,071 / 26.81%
Number/percentage of G's	1,203,504,684 / 22.76%
Number/percentage of N's	63,843,919 / 1.21%
GC Percentage	45.42%

2.3. Coverage

Mean	1.7099

Standard Deviation	125.2974

2.4. Mapping Quality

Mean Mapping Quality	48.71

2.5. Mismatches and indels

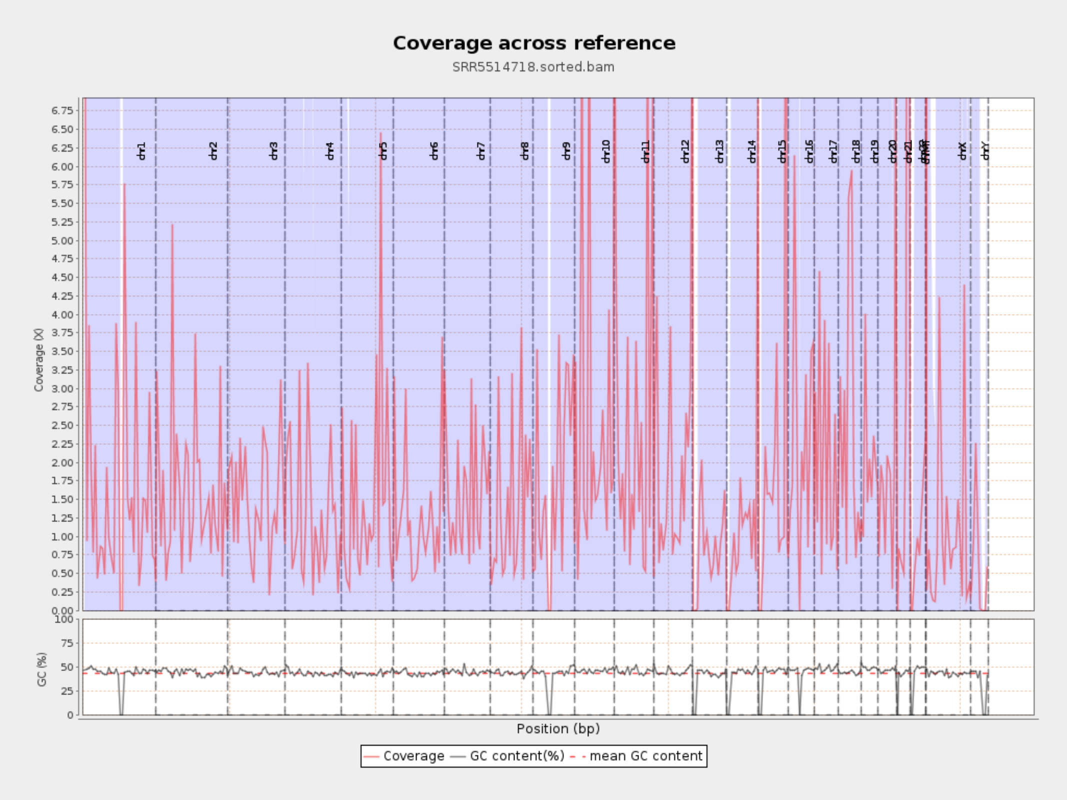
General error rate	1.13%
Mismatches	53,819,326
Insertions	2,887,127
Mapped reads with at least one insertion	4.79%
Deletions	2,250,298
Mapped reads with at least one deletion	3.63%
Homopolymer indels	33.48%

2.6. Chromosome stats

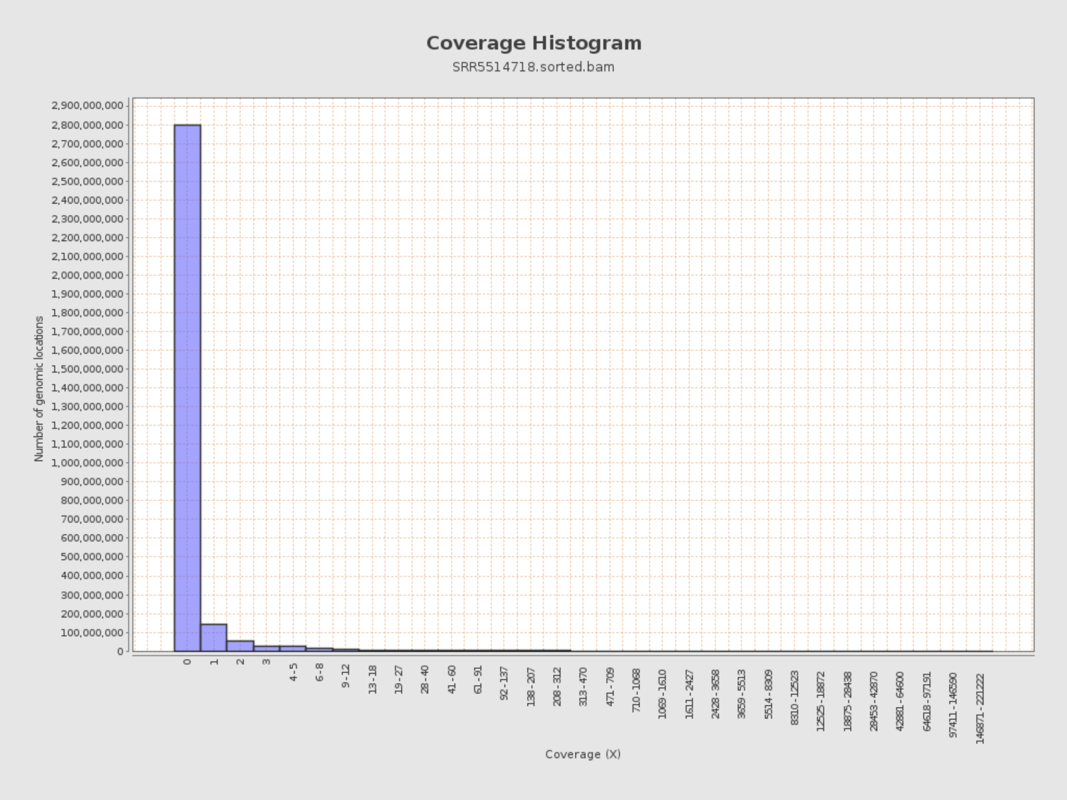
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	462010144	1.8536	210.5387
chr2	243199373	400181467	1.6455	70.9876
chr3	198022430	297310315	1.5014	32.75
chr4	191154276	251985651	1.3182	49.6146
chr5	180915260	277913587	1.5362	67.7057
chr6	171115067	216725302	1.2665	51.7953
chr7	159138663	260386841	1.6362	40.9149

chr8	146364022	209066122	1.4284	46.3003
chr9	141213431	252236515	1.7862	87.6278
chr10	135534747	349859052	2.5813	126.1575
chr11	135006516	353050121	2.6151	146.7688
chr12	133851895	270545484	2.0212	47.635
chr13	115169878	97617517	0.8476	35.1992
chr14	107349540	103160336	0.961	23.1732
chr15	102531392	233497545	2.2773	274.9734
chr16	90354753	202085360	2.2366	74.5583
chr17	81195210	172372119	2.1229	41.5877
chr18	78077248	190962165	2.4458	67.8365
chr19	59128983	117010274	1.9789	45.9171
chr20	63025520	109989313	1.7452	61.5314
chr21	48129895	219019896	4.5506	603.7048
chr22	51304566	47017757	0.9164	23.4418
chrMT	16571	2418620	145.955	212.7178
chrX	155270560	156597363	1.0085	49.8546
chrY	59373566	40336860	0.6794	27.8381

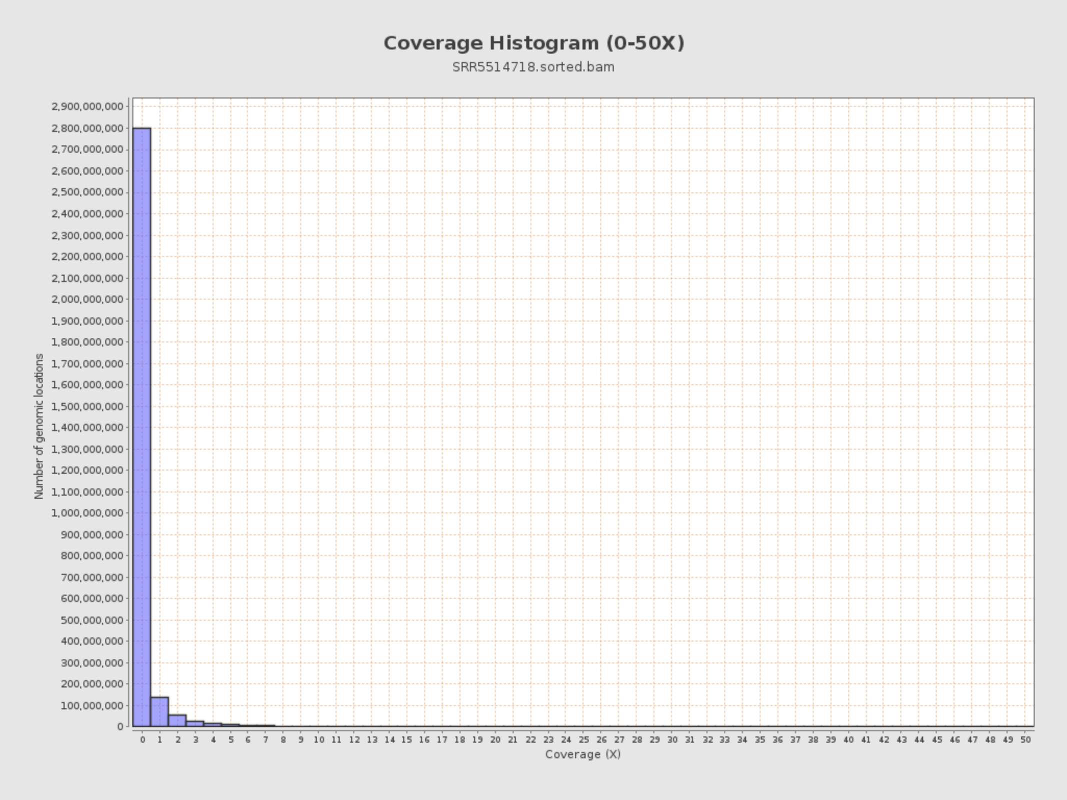
3. Results : Coverage across reference



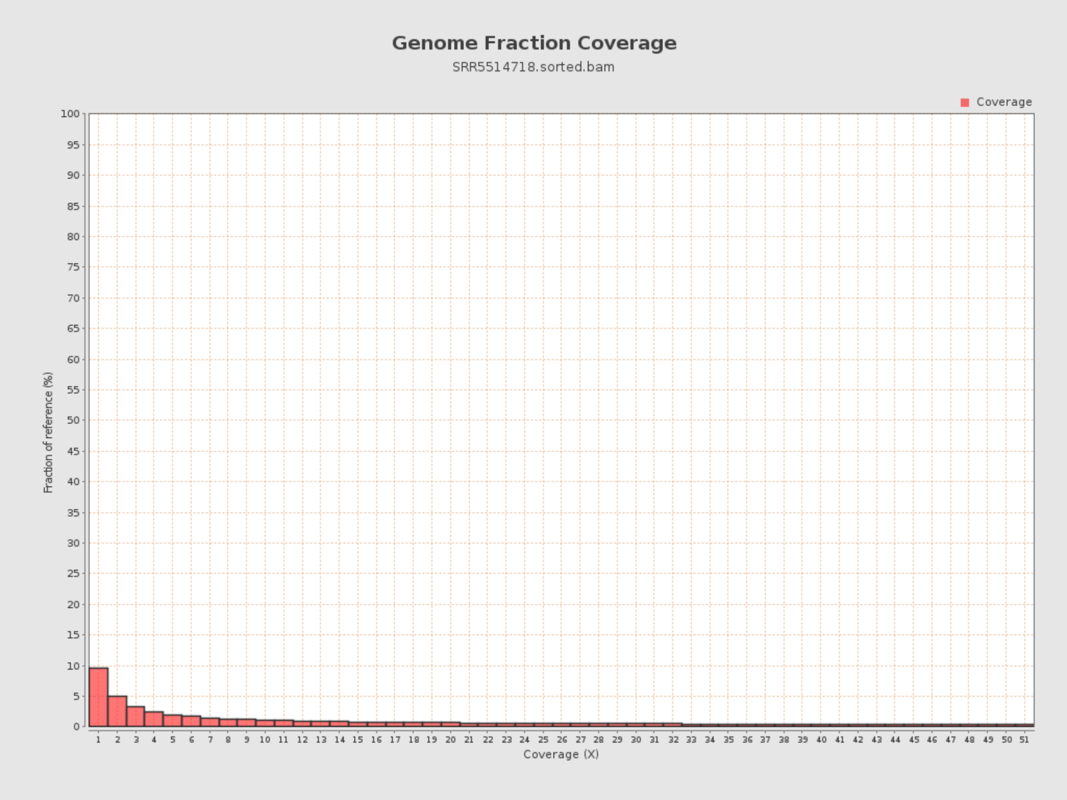
4. Results : Coverage Histogram



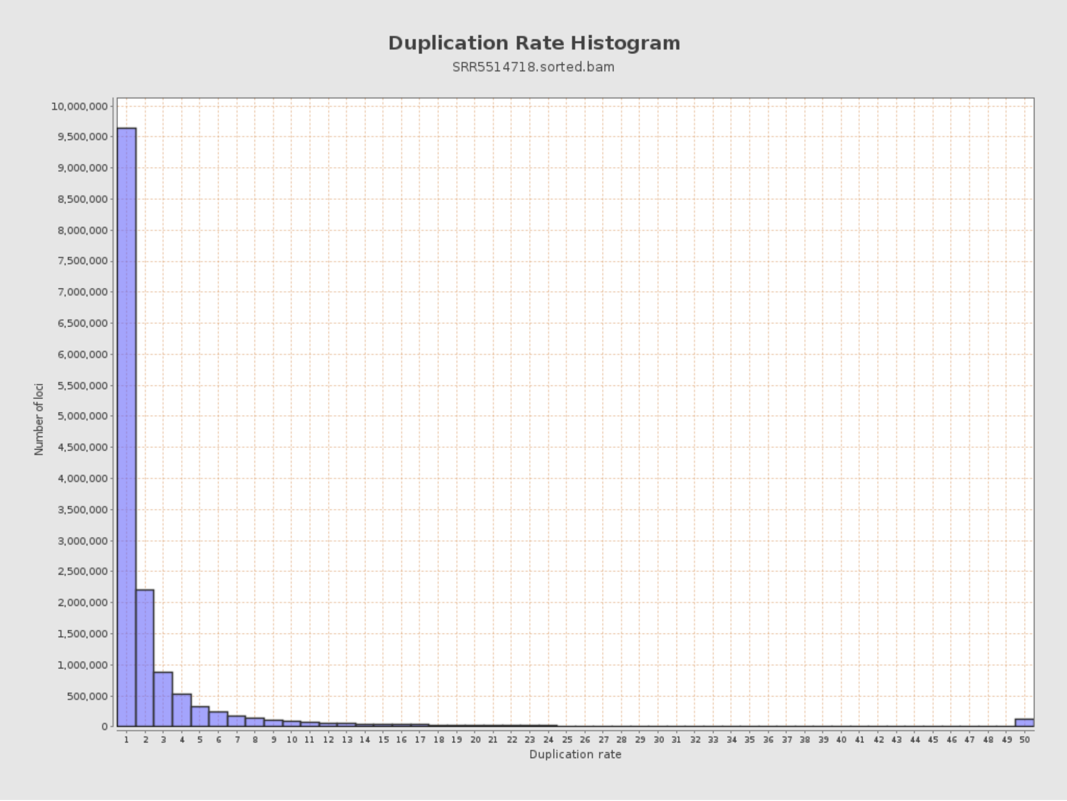
5. Results : Coverage Histogram (0-50X)



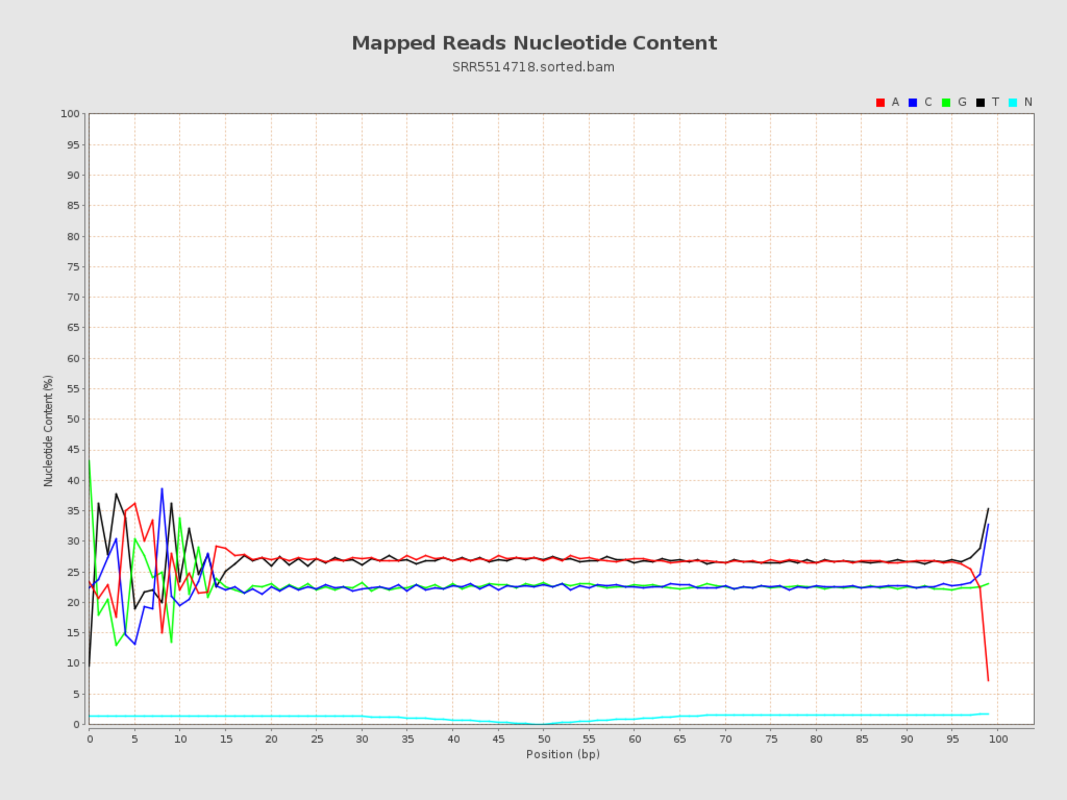
6. Results : Genome Fraction Coverage



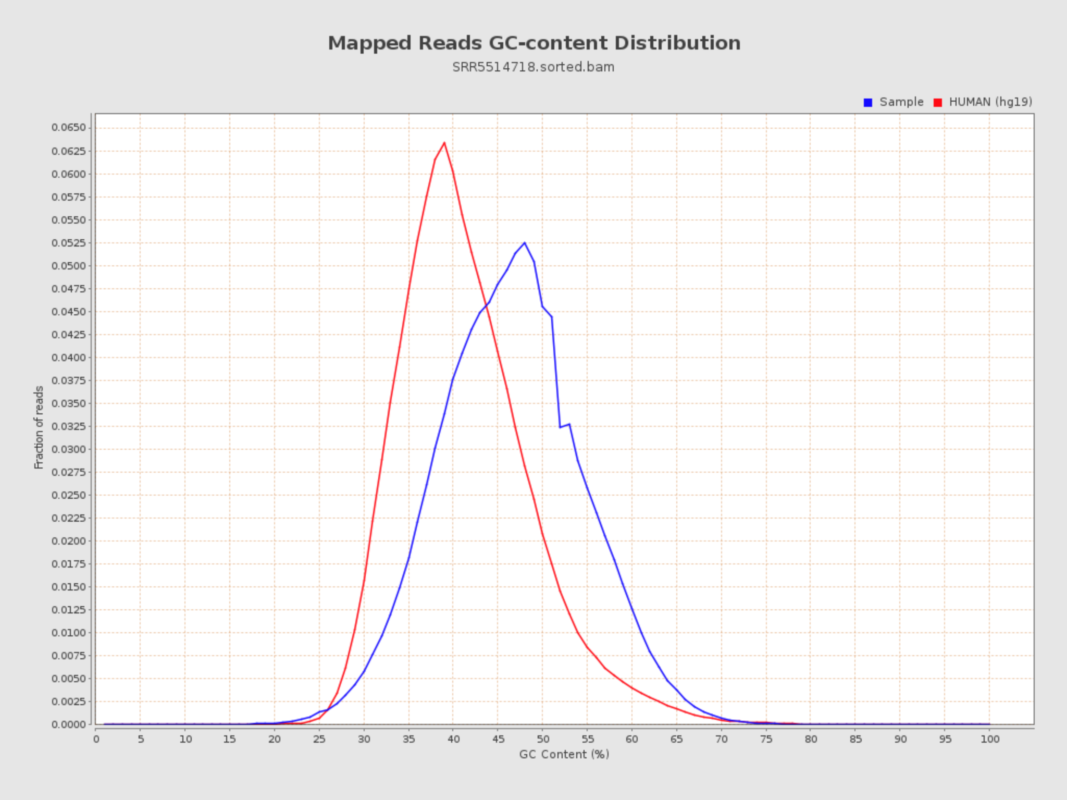
7. Results : Duplication Rate Histogram



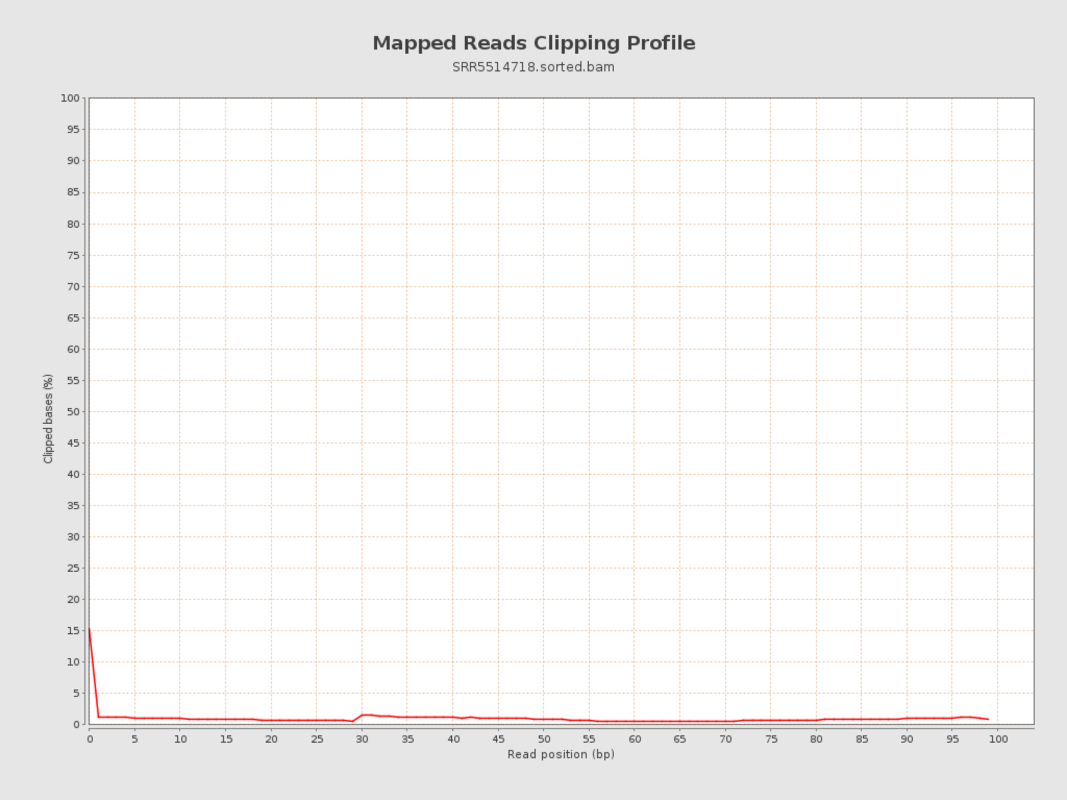
8. Results : Mapped Reads Nucleotide Content



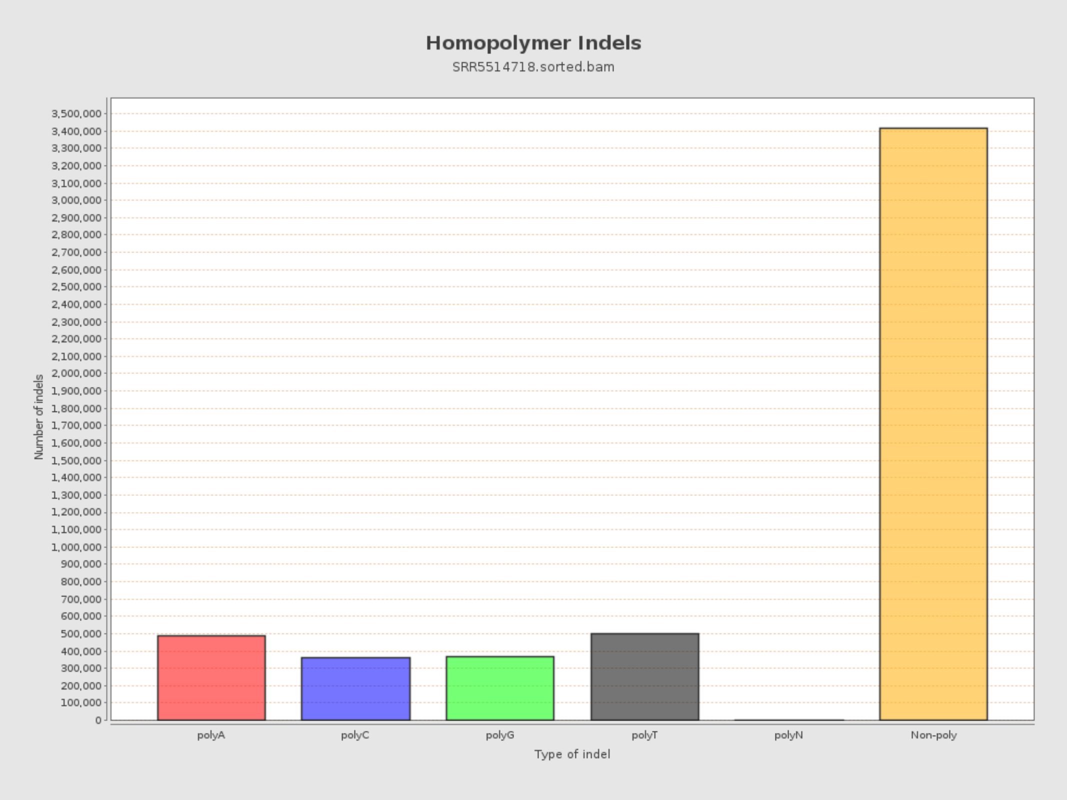
9. Results : Mapped Reads GC-content Distribution



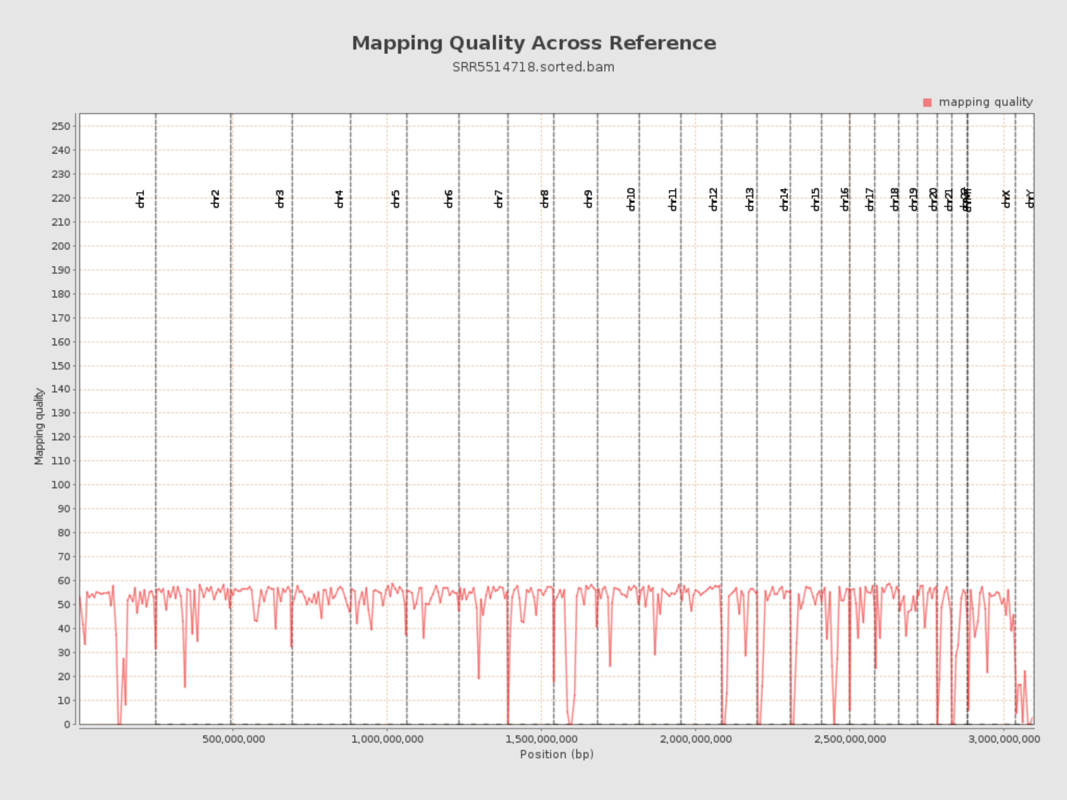
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram