Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 07:02:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514768.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_SRR5514768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514768.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 07:02:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,751,133
Mapped reads	3,404,954 / 28.98%
Unmapped reads	8,346,179 / 71.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	565,883 / 4.82%
Read min/max/mean length	30 / 100 / 100.86
Duplicated reads (estimated)	1,590,644 / 13.54%
Duplication rate	23.25%
Clipped reads	2,085,877 / 17.75%

2.2. ACGT Content

Number/percentage of A's	95,940,346 / 30.95%
Number/percentage of C's	57,957,158 / 18.7%
Number/percentage of T's	94,721,609 / 30.56%
Number/percentage of G's	61,298,211 / 19.78%
Number/percentage of N's	20,760 / 0.01%
GC Percentage	38.48%

2.3. Coverage

Mean	0.1002

Standard Deviation	10.1662

2.4. Mapping Quality

Mean Mapping Quality	43.23

2.5. Mismatches and indels

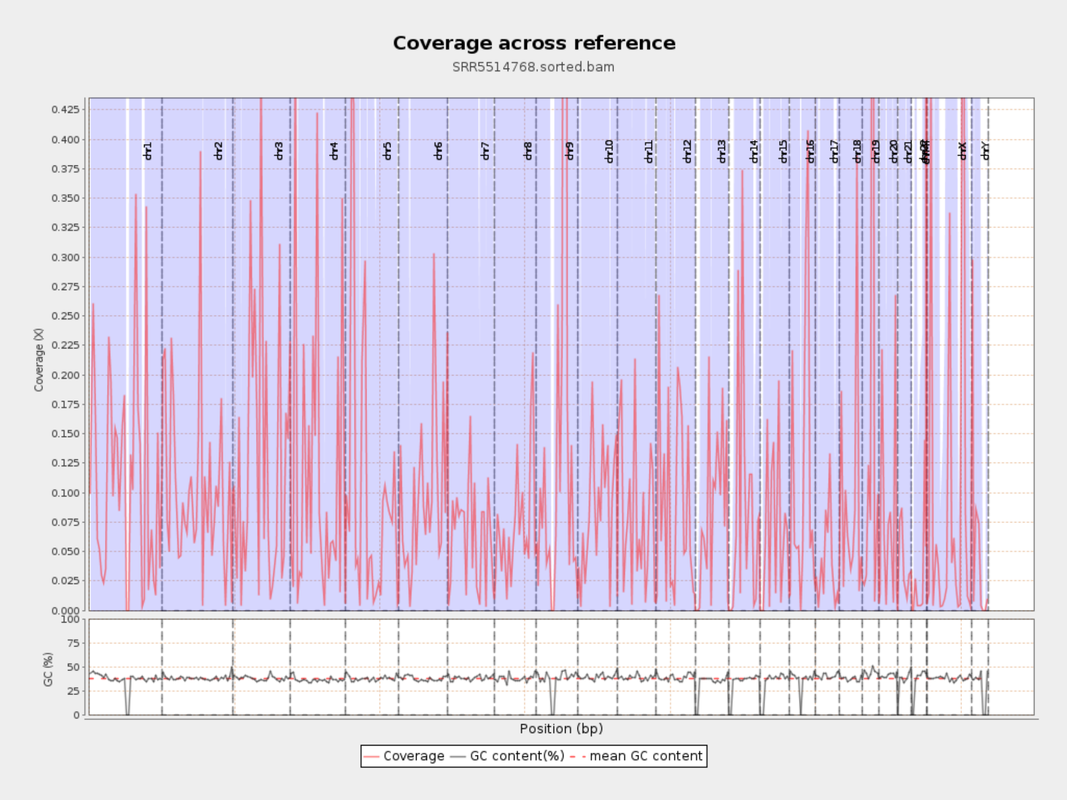
General error rate	0.7%
Mismatches	1,850,937
Insertions	174,865
Mapped reads with at least one insertion	4.89%
Deletions	87,098
Mapped reads with at least one deletion	2.37%
Homopolymer indels	44.17%

2.6. Chromosome stats

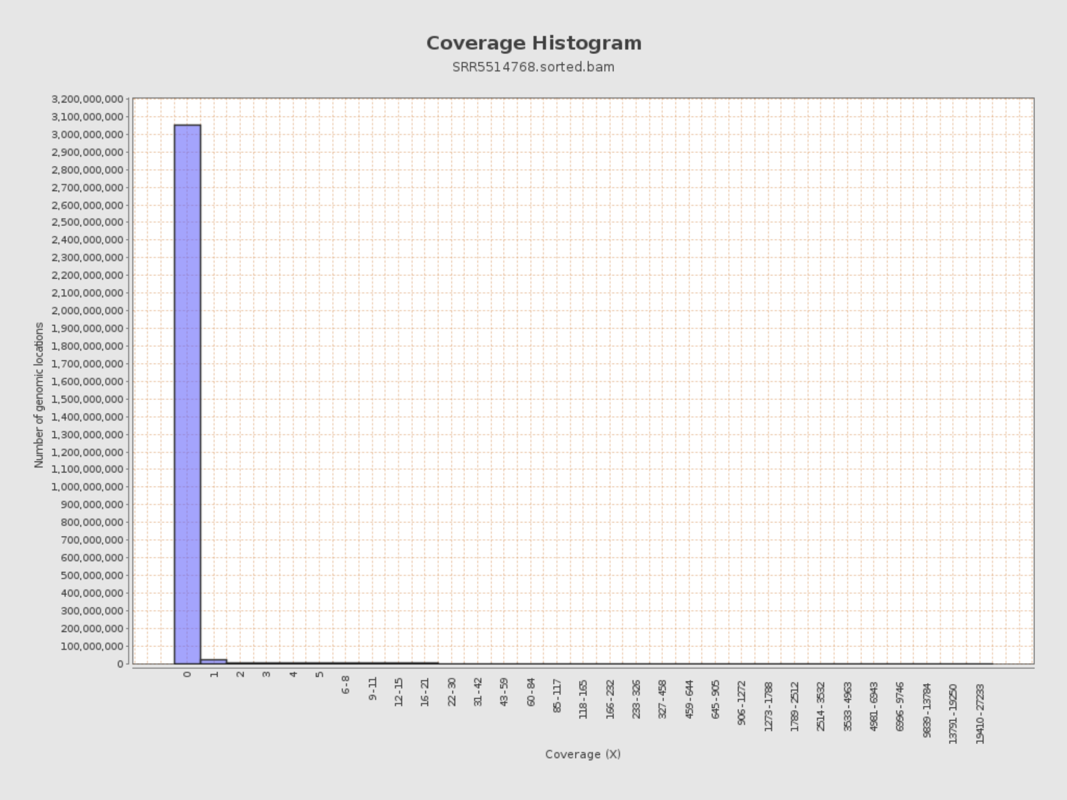
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27696905	0.1111	3.4526
chr2	243199373	25725356	0.1058	4.1162
chr3	198022430	24965082	0.1261	2.6969
chr4	191154276	23125323	0.121	2.6849
chr5	180915260	18912924	0.1045	2.4774
chr6	171115067	15995867	0.0935	3.2673
chr7	159138663	10543742	0.0663	1.568

chr8	146364022	10787640	0.0737	1.8643
chr9	141213431	25008163	0.1771	38.0139
chr10	135534747	11618209	0.0857	3.8557
chr11	135006516	10660521	0.079	1.8182
chr12	133851895	12430003	0.0929	3.0196
chr13	115169878	9866630	0.0857	1.9001
chr14	107349540	9656907	0.09	2.1284
chr15	102531392	6993527	0.0682	1.8679
chr16	90354753	10213724	0.113	2.8017
chr17	81195210	3348666	0.0412	1.3143
chr18	78077248	7589413	0.0972	2.0257
chr19	59128983	9602383	0.1624	36.9961
chr20	63025520	5719034	0.0907	2.8313
chr21	48129895	1950793	0.0405	3.0431
chr22	51304566	1549810	0.0302	3.1538
chrMT	16571	8554557	516.2366	709.4141
chrX	155270560	14733265	0.0949	2.0379
chrY	59373566	2957964	0.0498	1.9789

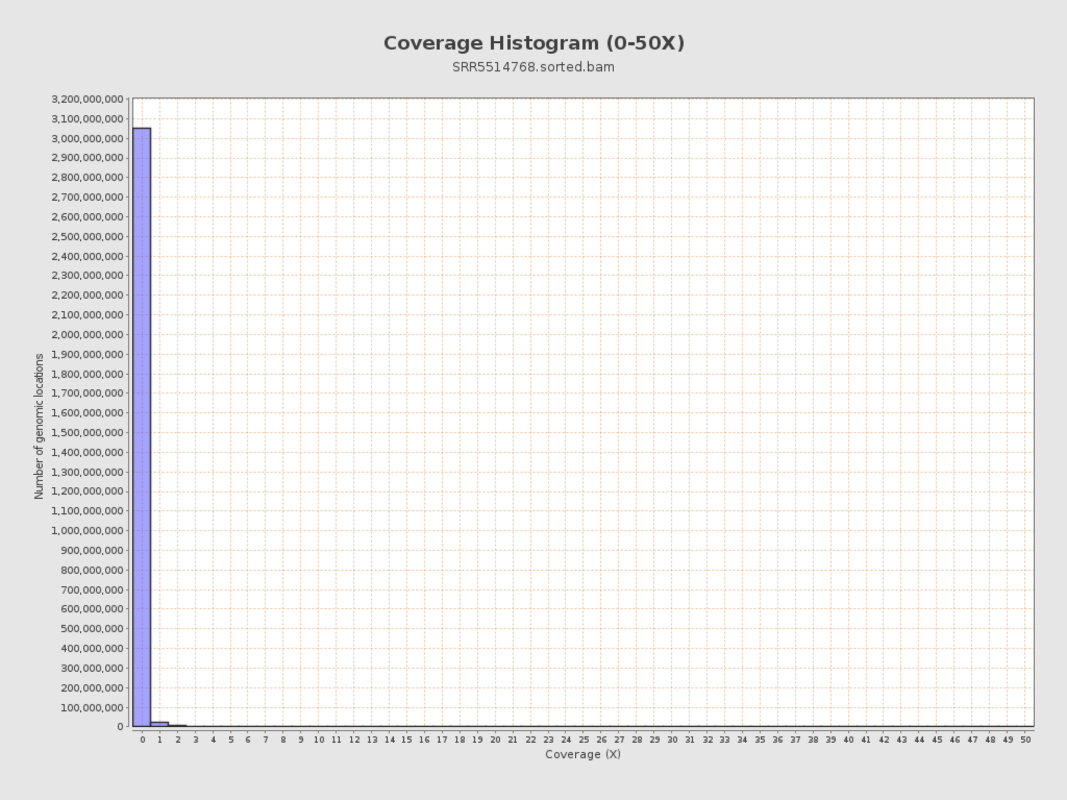
3. Results : Coverage across reference



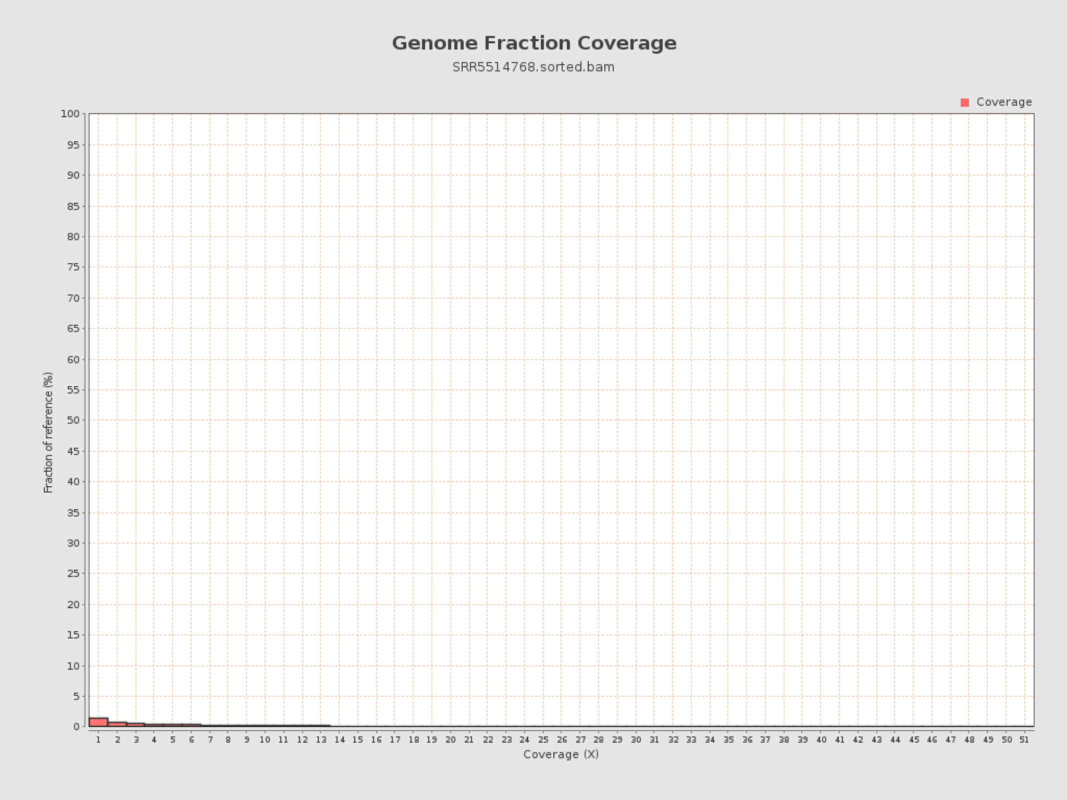
4. Results : Coverage Histogram



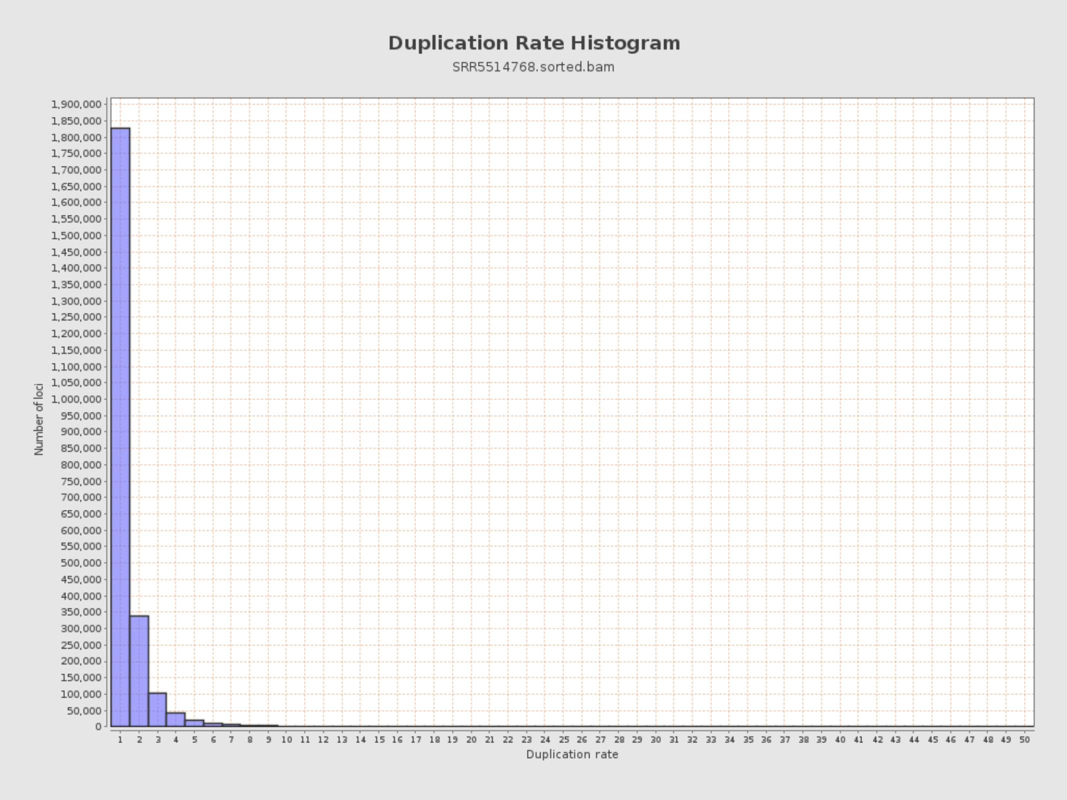
5. Results : Coverage Histogram (0-50X)



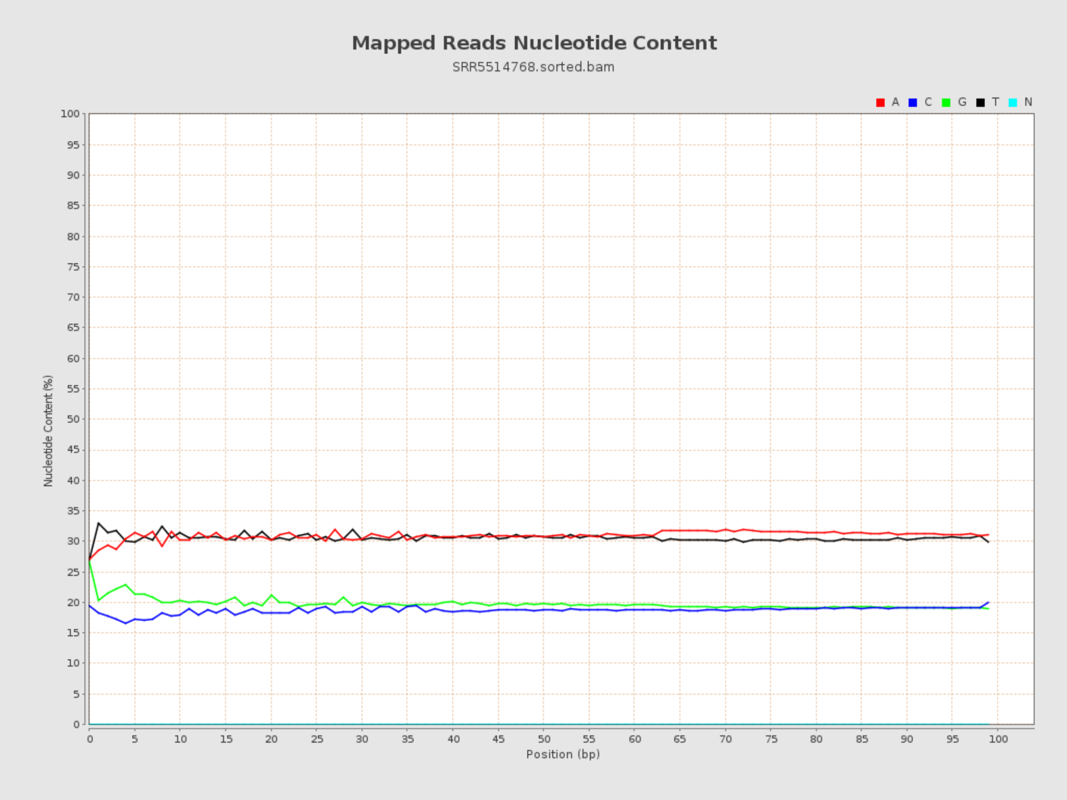
6. Results : Genome Fraction Coverage



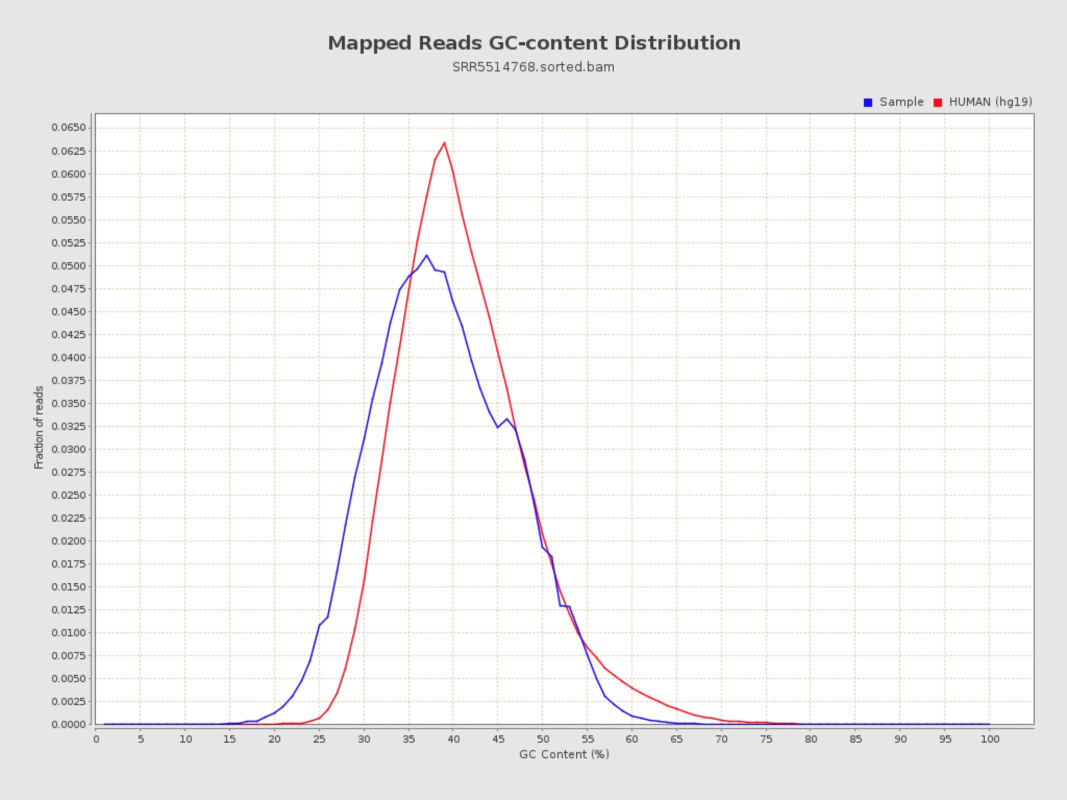
7. Results : Duplication Rate Histogram



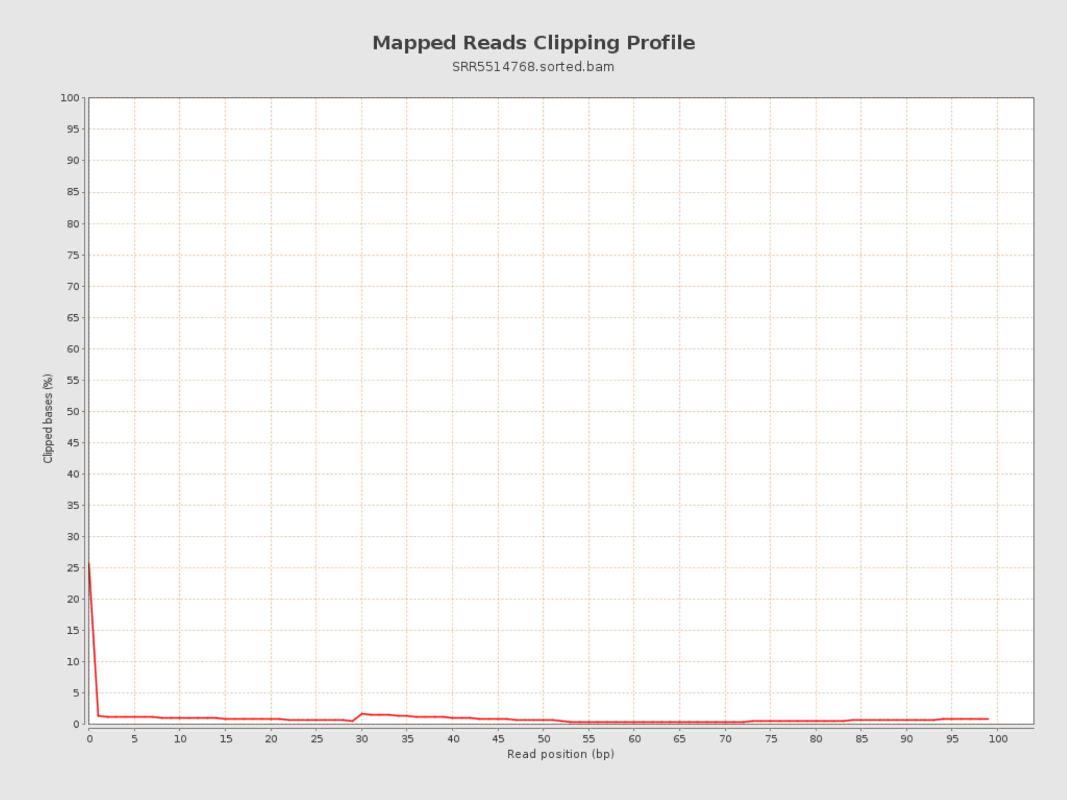
8. Results : Mapped Reads Nucleotide Content



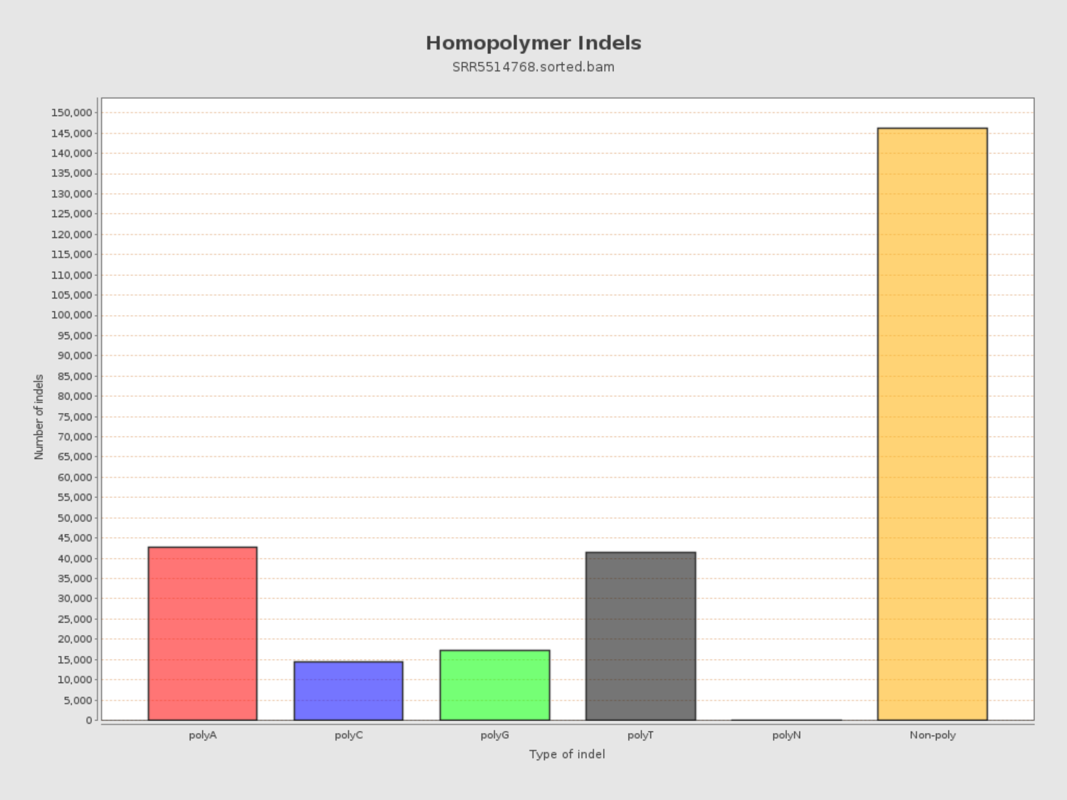
9. Results : Mapped Reads GC-content Distribution



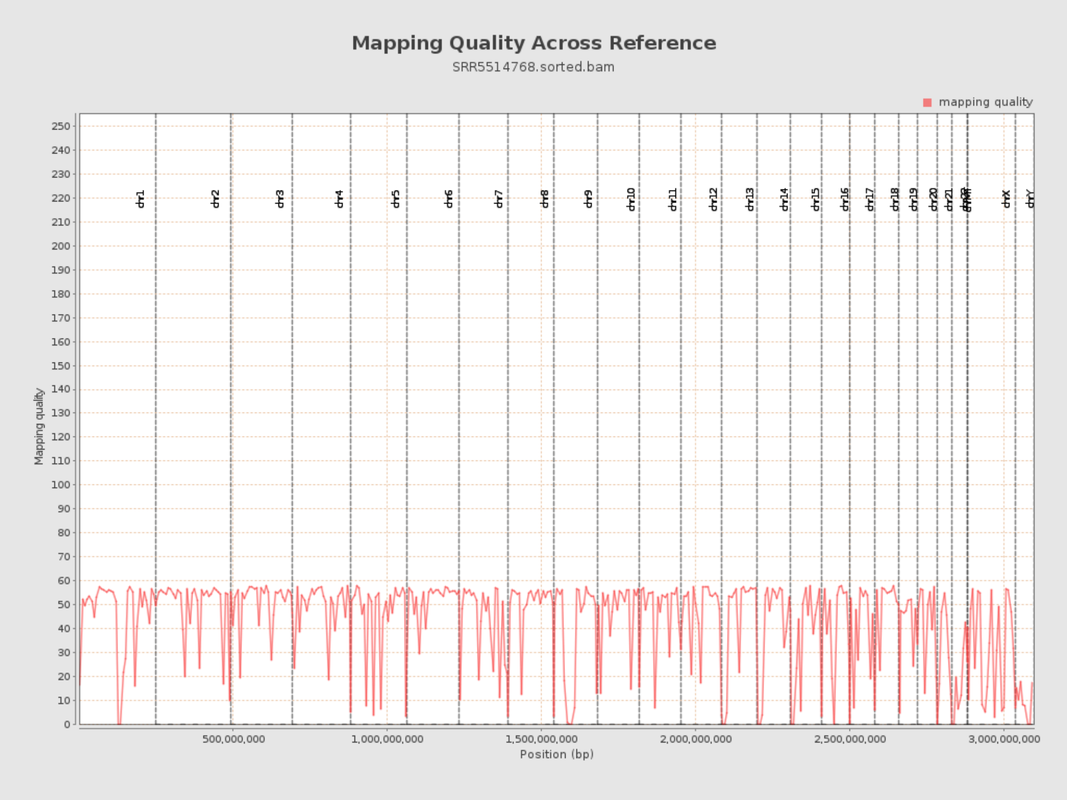
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram