Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 16:47:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514750.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_SRR5514750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 16:47:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,341,149
Mapped reads	52,666,195 / 93.48%
Unmapped reads	3,674,954 / 6.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,915,099 / 14.05%
Read min/max/mean length	30 / 100 / 104.98
Duplicated reads (estimated)	41,087,760 / 72.93%
Duplication rate	43.66%
Clipped reads	26,883,512 / 47.72%

2.2. ACGT Content

Number/percentage of A's	1,544,489,747 / 30.92%
Number/percentage of C's	934,263,913 / 18.7%
Number/percentage of T's	1,533,444,166 / 30.7%
Number/percentage of G's	982,613,274 / 19.67%
Number/percentage of N's	345,722 / 0.01%
GC Percentage	38.37%

2.3. Coverage

Mean	1.6148

Standard Deviation	82.8039

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

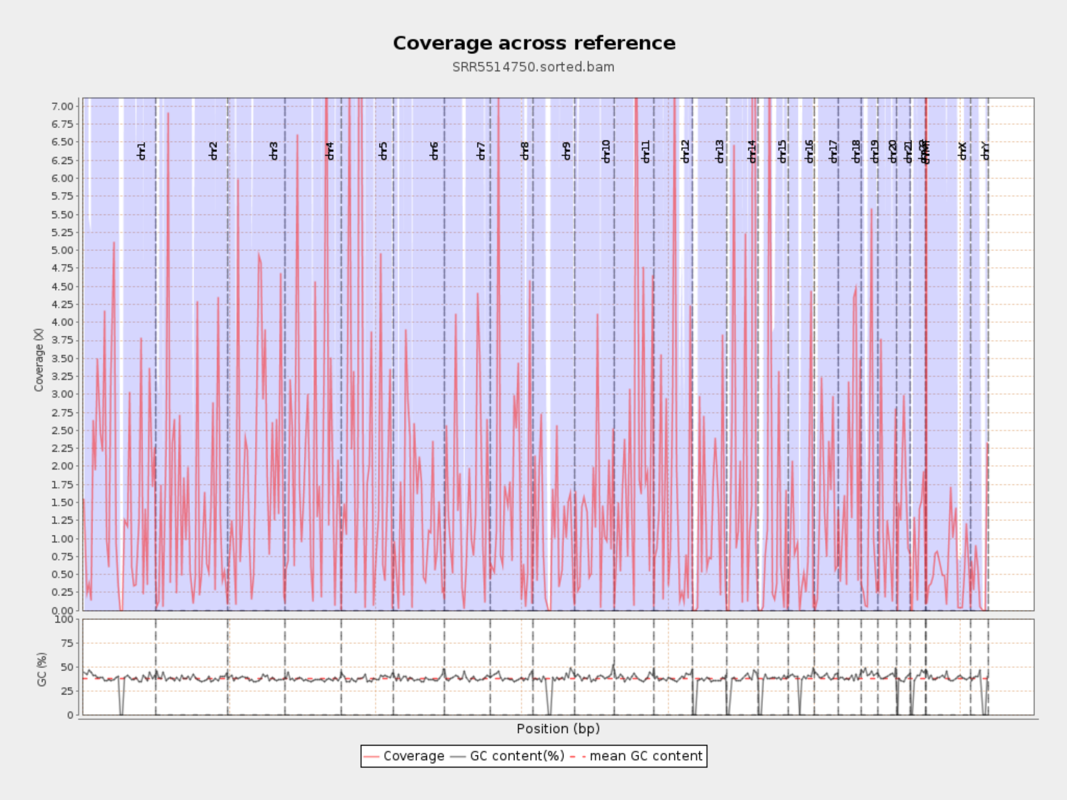
General error rate	0.67%
Mismatches	27,664,980
Insertions	3,569,848
Mapped reads with at least one insertion	6.49%
Deletions	1,328,896
Mapped reads with at least one deletion	2.37%
Homopolymer indels	52.19%

2.6. Chromosome stats

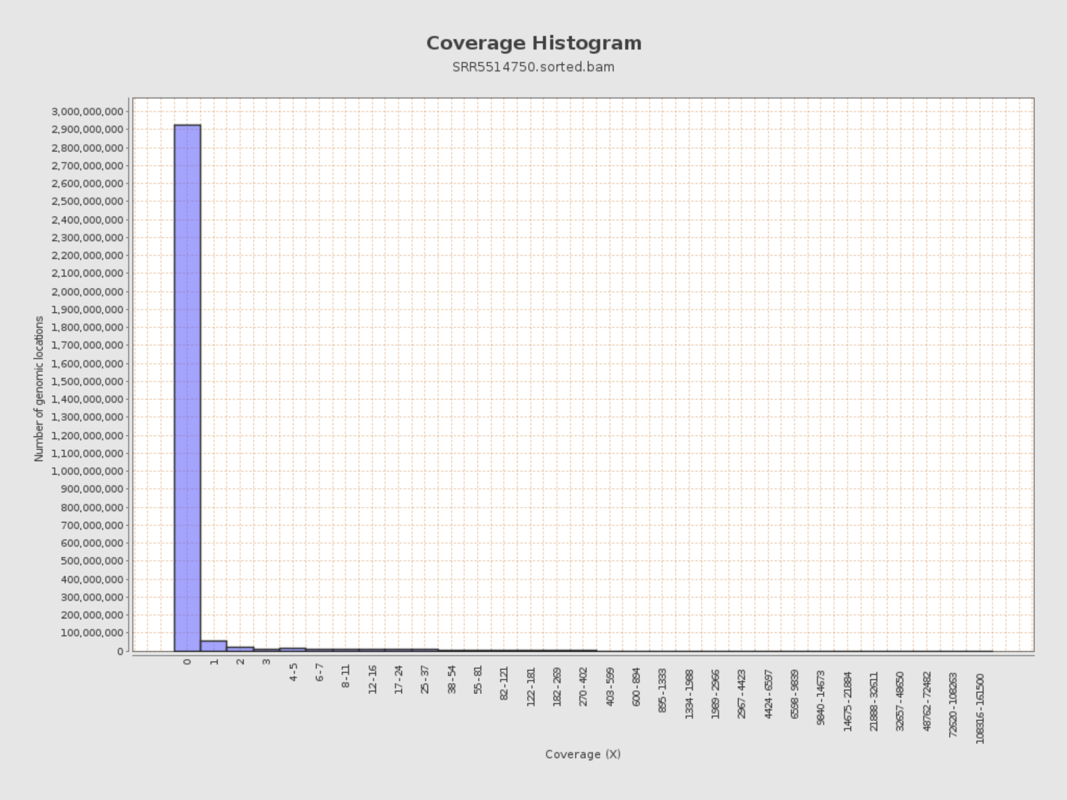
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	400099032	1.6052	52.9955
chr2	243199373	348960852	1.4349	23.6442
chr3	198022430	392929784	1.9843	46.798
chr4	191154276	423165598	2.2137	31.7659
chr5	180915260	426471355	2.3573	31.6689
chr6	171115067	227545351	1.3298	25.7168
chr7	159138663	243466528	1.5299	40.1841

chr8	146364022	244735825	1.6721	111.1321
chr9	141213431	156937972	1.1114	43.8307
chr10	135534747	175850146	1.2975	41.3185
chr11	135006516	298426623	2.2105	32.7776
chr12	133851895	225704108	1.6862	51.0104
chr13	115169878	146360913	1.2708	21.1527
chr14	107349540	327111457	3.0472	367.4161
chr15	102531392	127436392	1.2429	22.518
chr16	90354753	85316679	0.9442	16.0648
chr17	81195210	113431022	1.397	23.6721
chr18	78077248	154461418	1.9783	65.5812
chr19	59128983	74596143	1.2616	76.2663
chr20	63025520	80603710	1.2789	28.5334
chr21	48129895	68723205	1.4279	23.645
chr22	51304566	49184737	0.9587	54.1878
chrMT	16571	79563327	4,801.3594	4,960.0333
chrX	155270560	92227562	0.594	15.0865
chrY	59373566	35731373	0.6018	12.8502

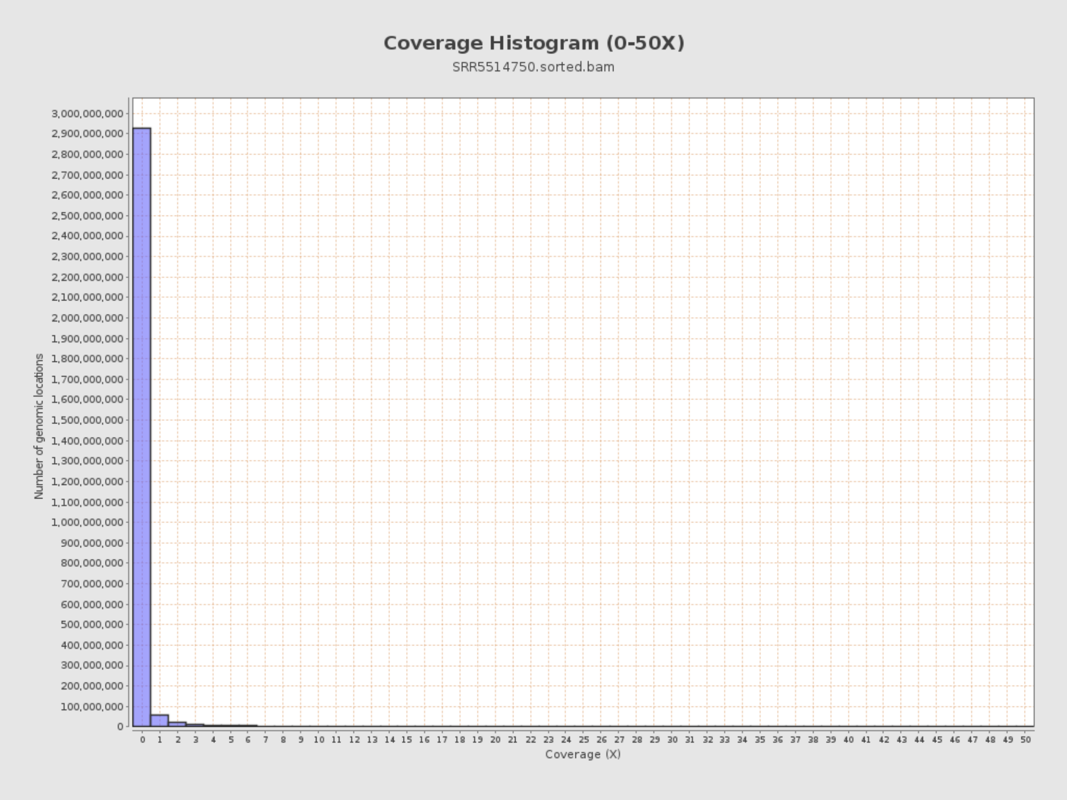
3. Results : Coverage across reference



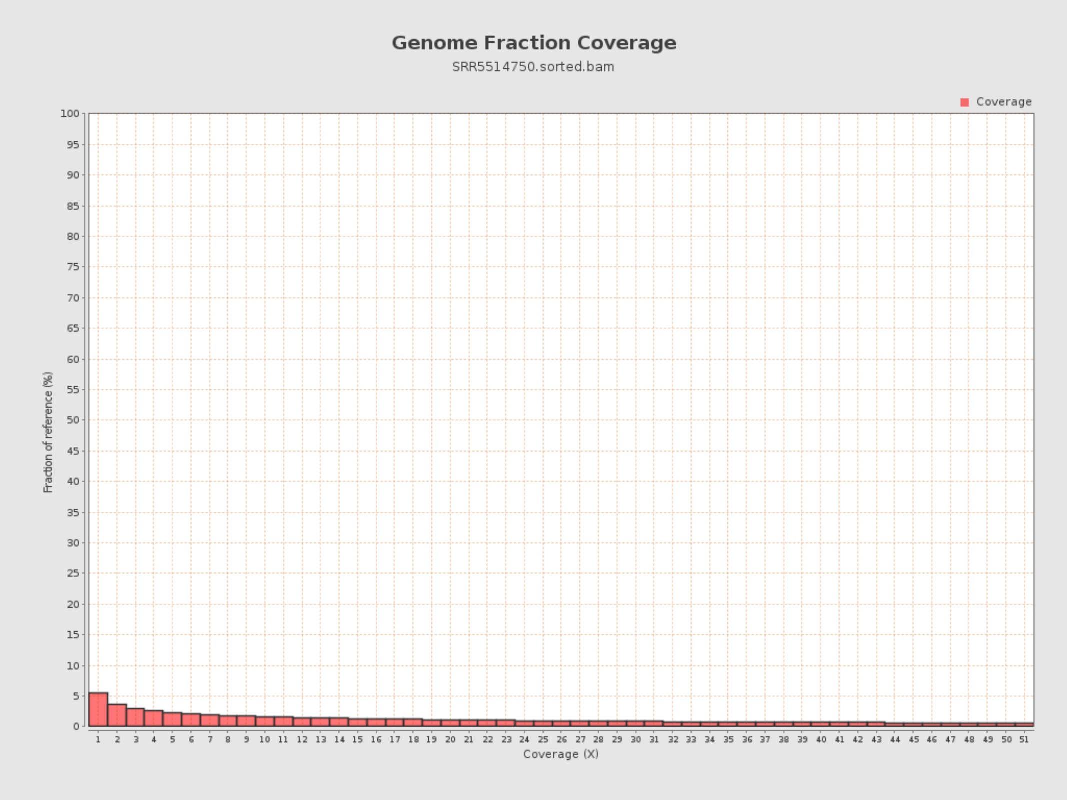
4. Results : Coverage Histogram



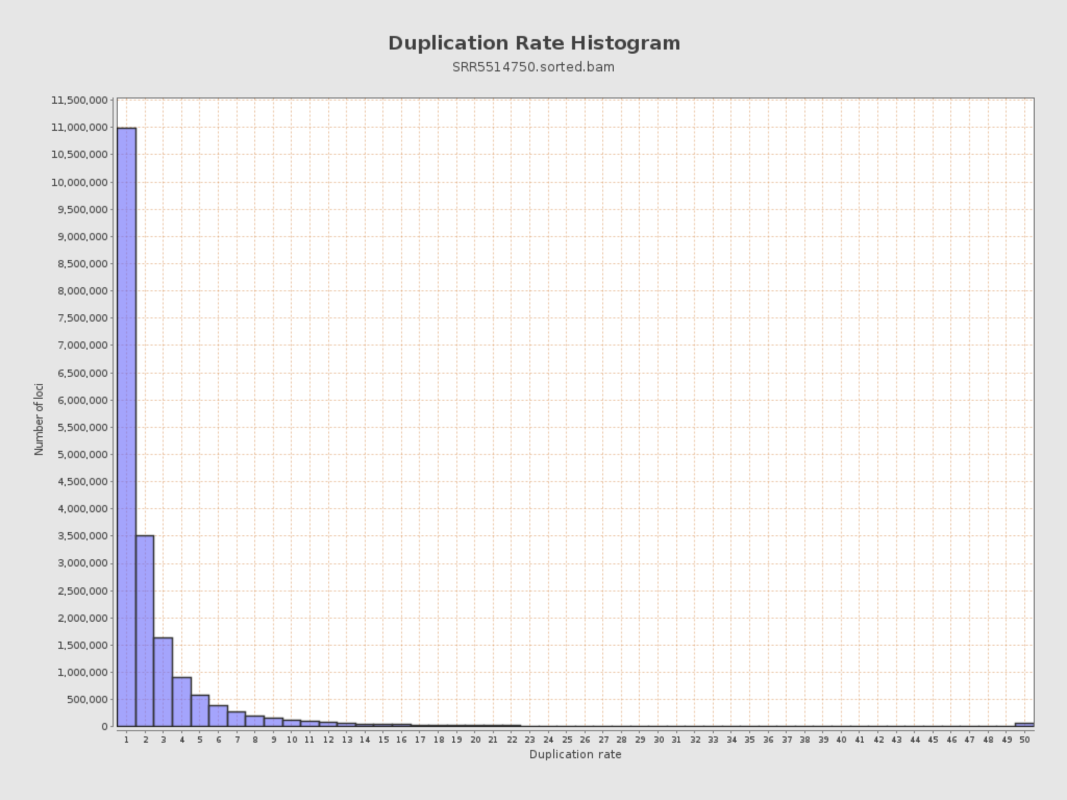
5. Results : Coverage Histogram (0-50X)



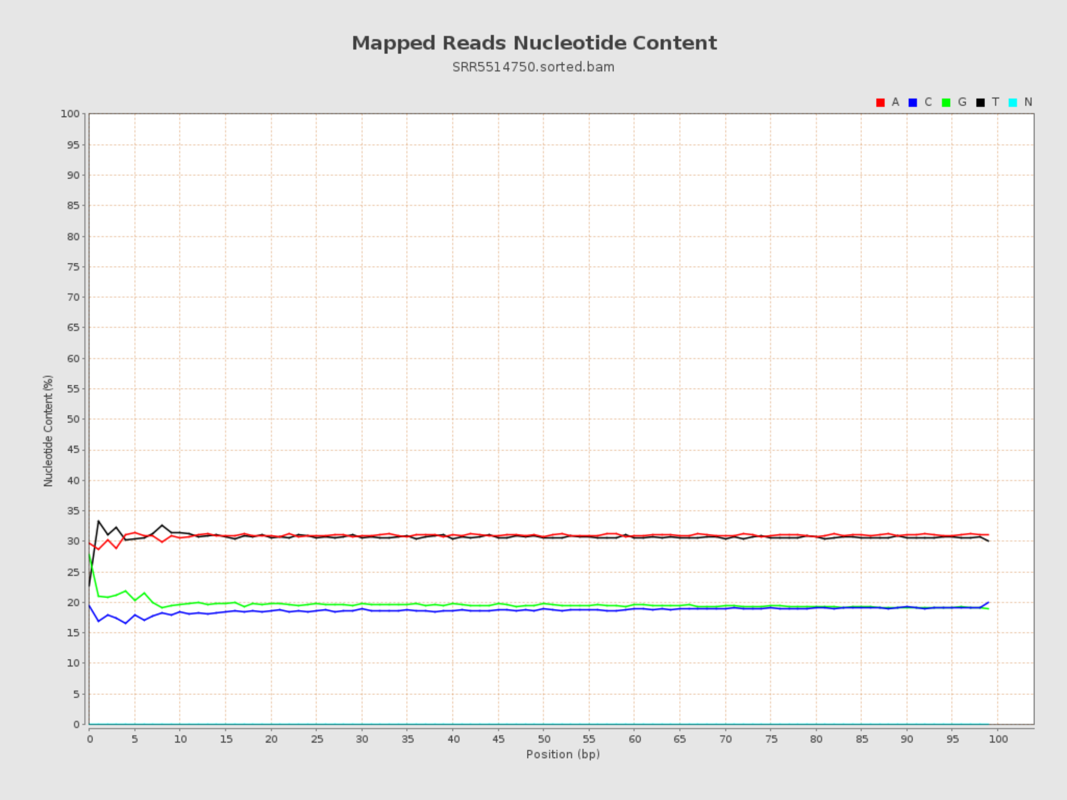
6. Results : Genome Fraction Coverage



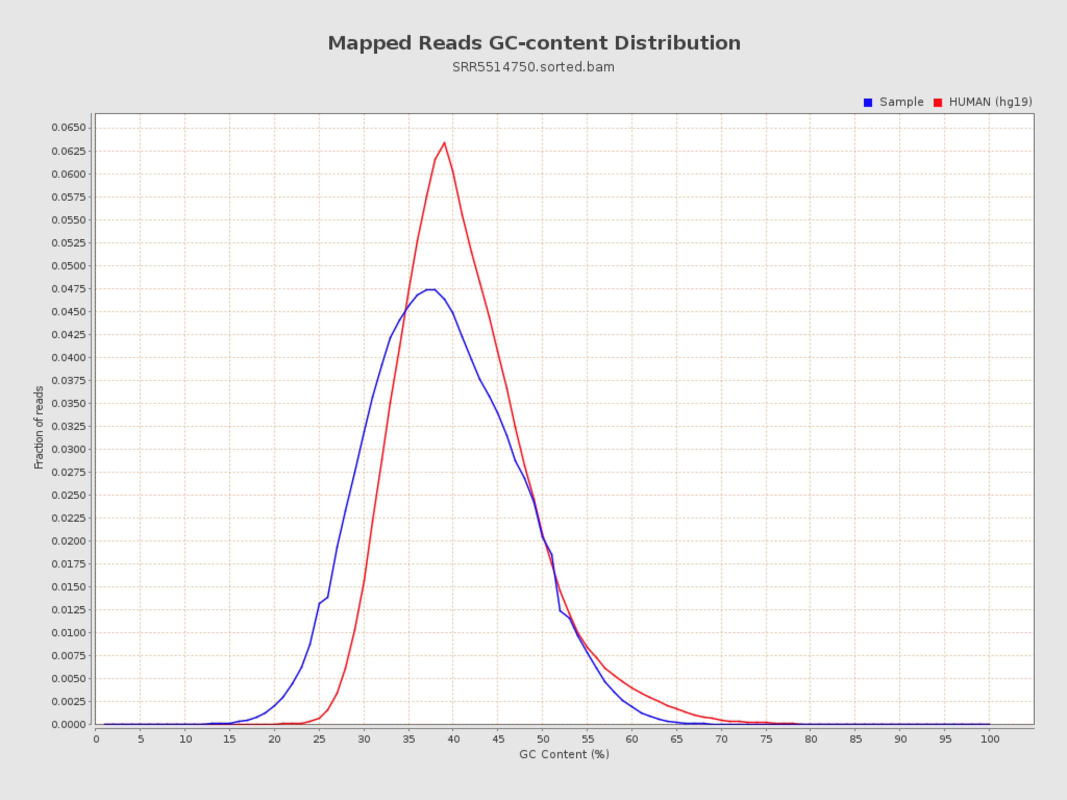
7. Results : Duplication Rate Histogram



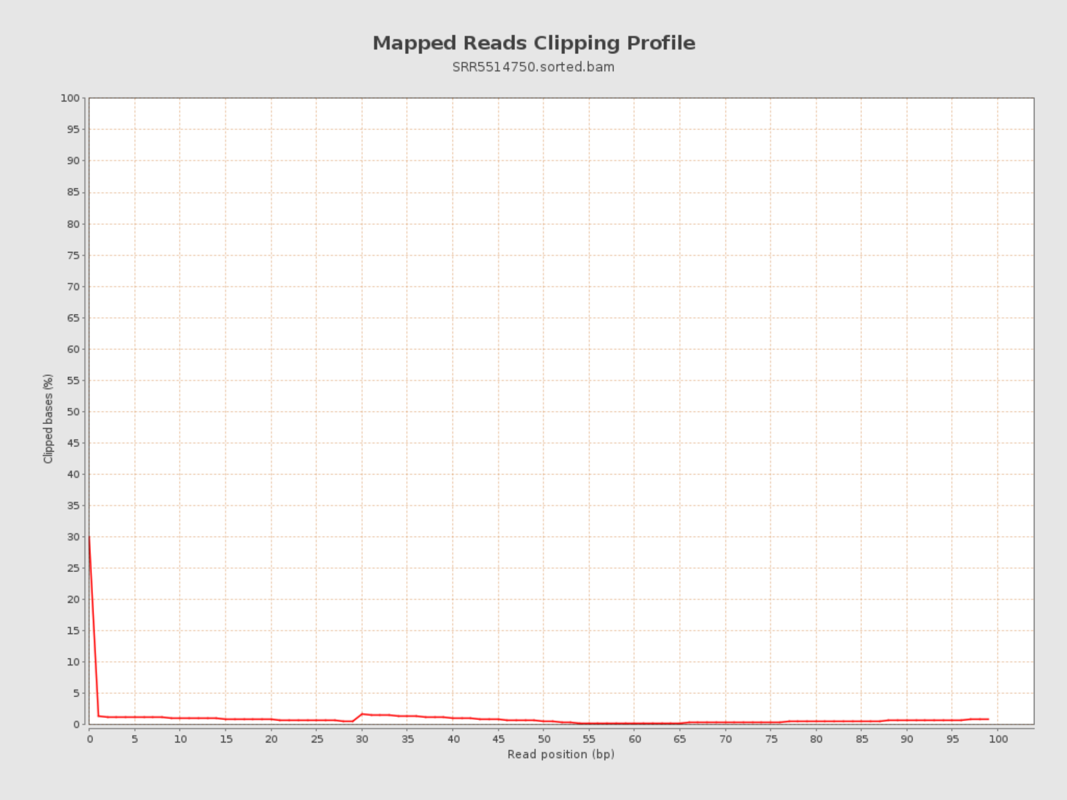
8. Results : Mapped Reads Nucleotide Content



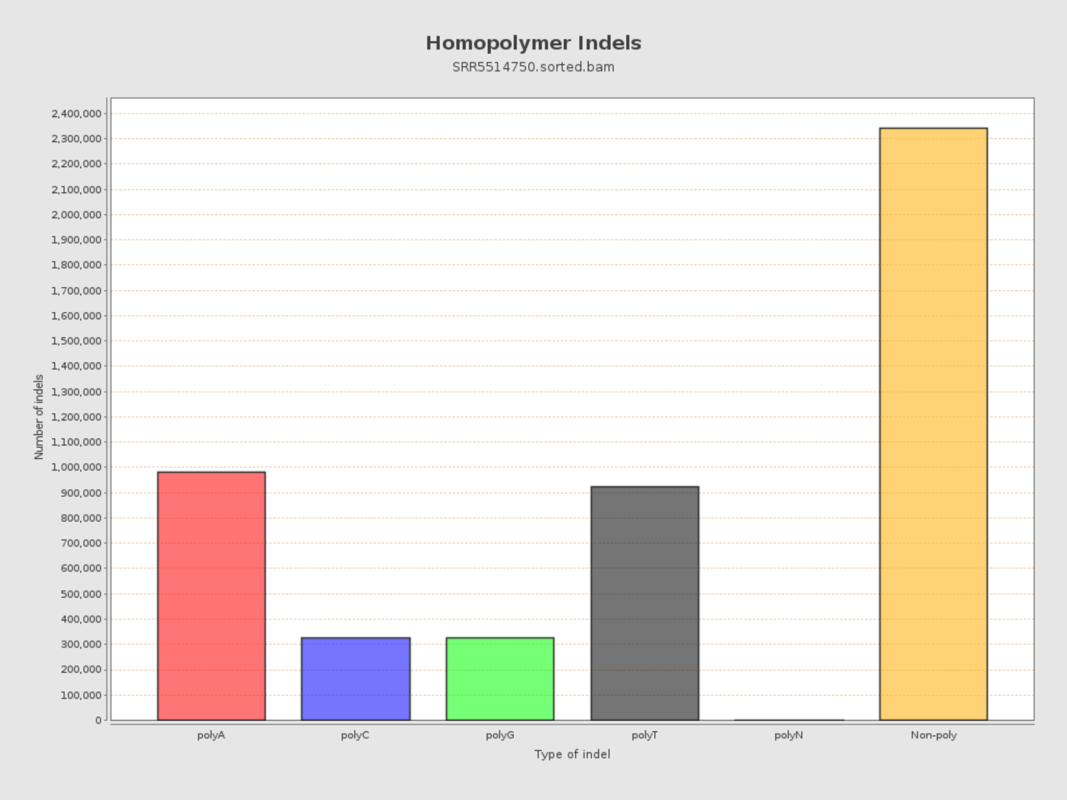
9. Results : Mapped Reads GC-content Distribution



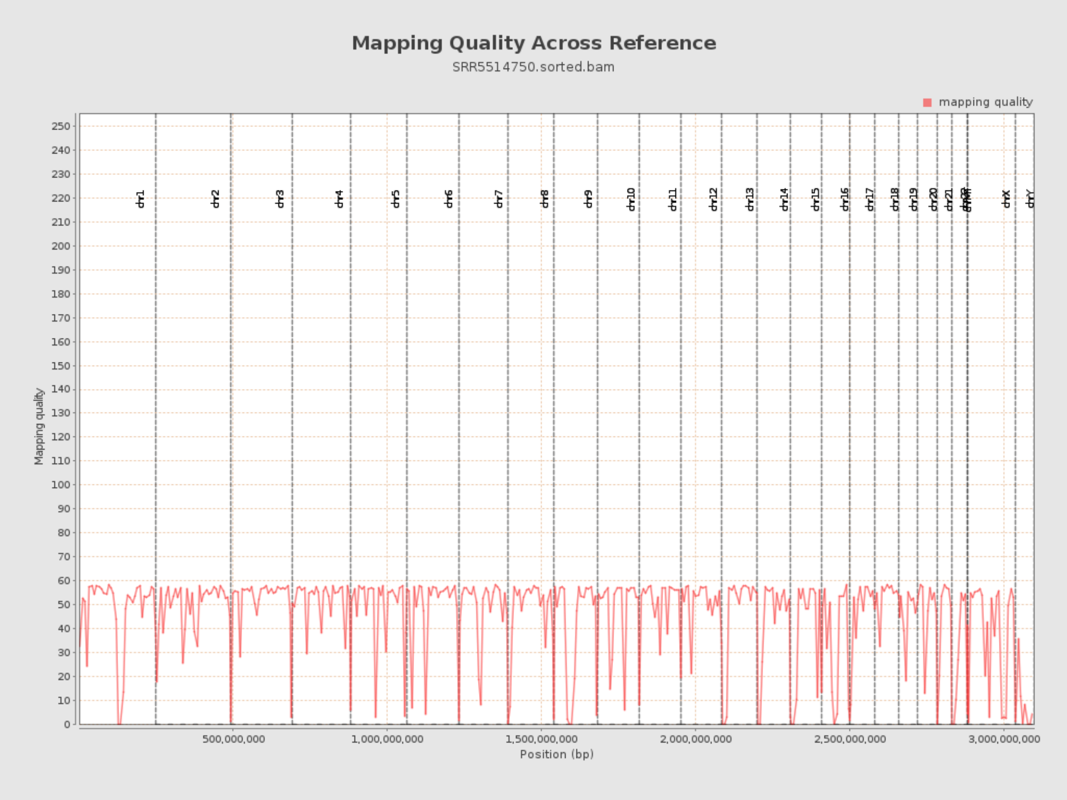
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram