Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/09 22:16:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514717.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_SRR5514717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 09 22:16:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,878,010
Mapped reads	73,327,108 / 92.96%
Unmapped reads	5,550,902 / 7.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,657,343 / 4.64%
Read min/max/mean length	30 / 100 / 100.43
Duplicated reads (estimated)	55,012,553 / 69.74%
Duplication rate	33.8%
Clipped reads	17,546,895 / 22.25%

2.2. ACGT Content

Number/percentage of A's	1,899,644,382 / 27.26%
Number/percentage of C's	1,570,292,552 / 22.53%
Number/percentage of T's	1,917,288,915 / 27.51%
Number/percentage of G's	1,581,728,502 / 22.7%
Number/percentage of N's	282,744 / 0%
GC Percentage	45.23%

2.3. Coverage

Mean	2.2529

Standard Deviation	104.6053

2.4. Mapping Quality

Mean Mapping Quality	49.14

2.5. Mismatches and indels

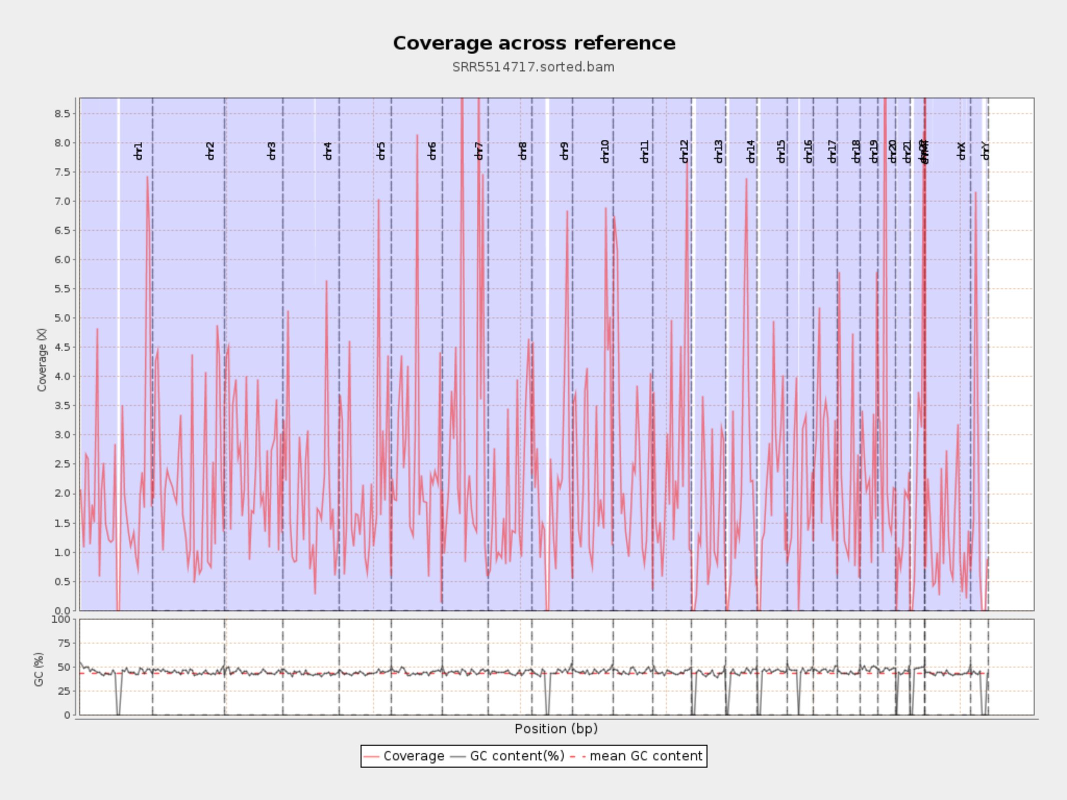
General error rate	1.04%
Mismatches	66,006,115
Insertions	3,668,290
Mapped reads with at least one insertion	4.73%
Deletions	2,192,106
Mapped reads with at least one deletion	2.82%
Homopolymer indels	40.69%

2.6. Chromosome stats

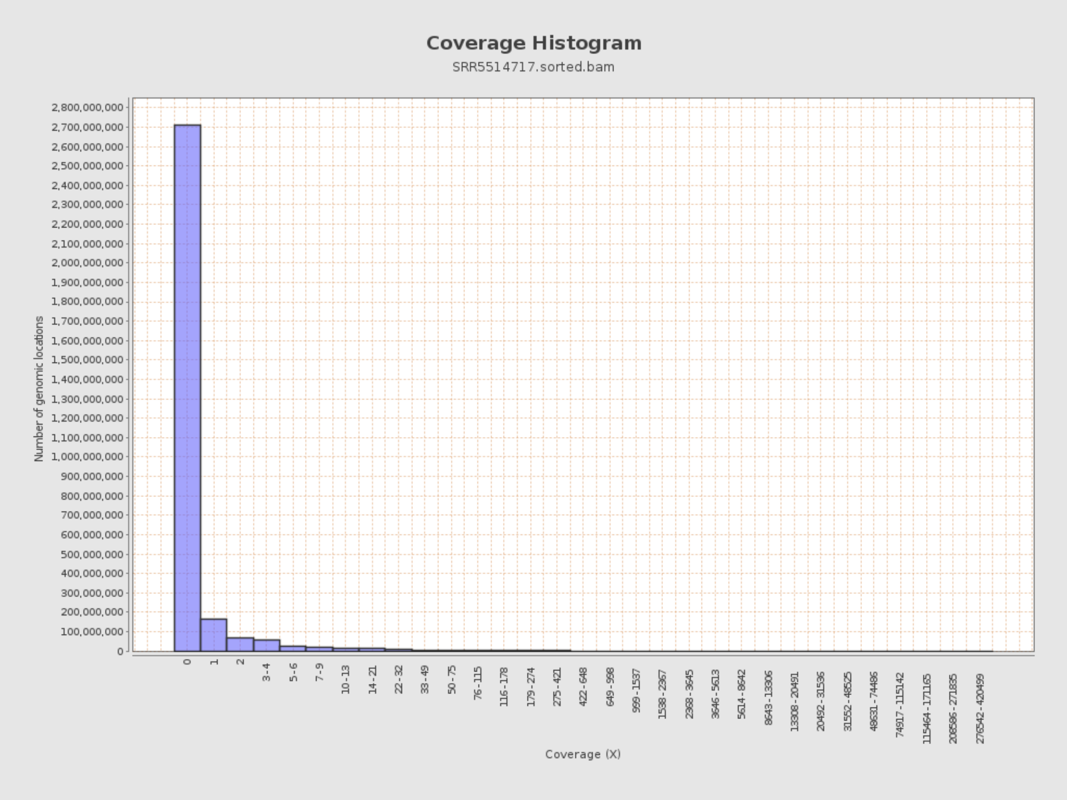
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	507510100	2.0361	59.7004
chr2	243199373	525445223	2.1606	100.9412
chr3	198022430	506371315	2.5571	56.2931
chr4	191154276	376625658	1.9703	57.1712
chr5	180915260	385221488	2.1293	57.4181
chr6	171115067	451128468	2.6364	135.3737
chr7	159138663	487464849	3.0631	129.4754

chr8	146364022	283669094	1.9381	62.6659
chr9	141213431	304369054	2.1554	77.2115
chr10	135534747	371868247	2.7437	55.585
chr11	135006516	362997682	2.6887	70.6388
chr12	133851895	349428780	2.6106	64.6832
chr13	115169878	174733699	1.5172	66.6766
chr14	107349540	242693970	2.2608	71.8857
chr15	102531392	218355057	2.1296	69.5709
chr16	90354753	176557085	1.954	74.6895
chr17	81195210	223502739	2.7527	78.1157
chr18	78077248	184972860	2.3691	55.7192
chr19	59128983	139175401	2.3538	78.0556
chr20	63025520	205204052	3.2559	482.0222
chr21	48129895	65074334	1.3521	61.7408
chr22	51304566	136740182	2.6653	171.6302
chrMT	16571	526892	31.796	21.8765
chrX	155270560	184960260	1.1912	35.717
chrY	59373566	109722710	1.848	37.543

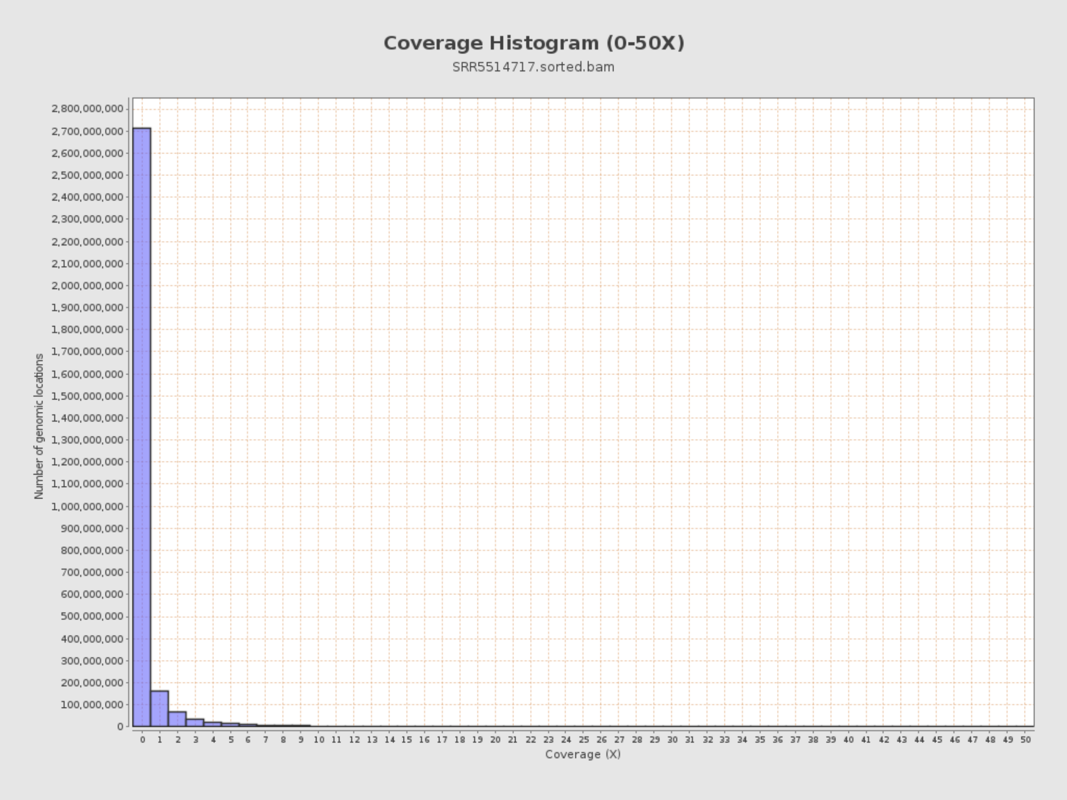
3. Results : Coverage across reference



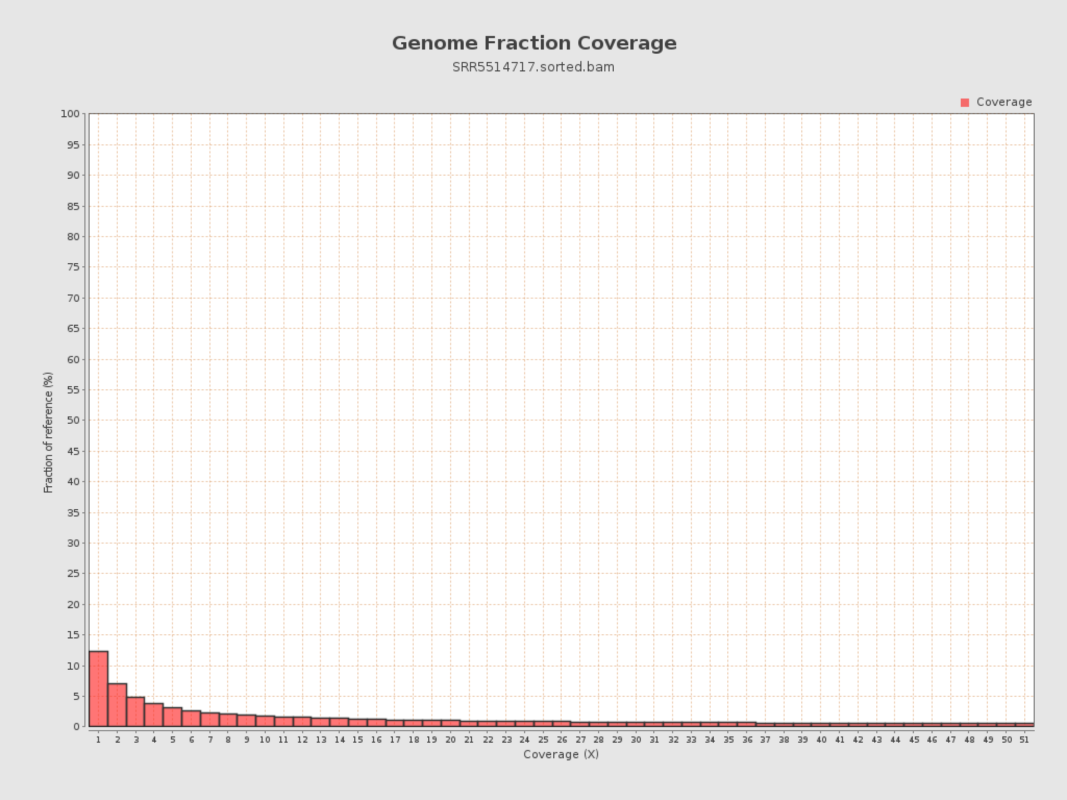
4. Results : Coverage Histogram



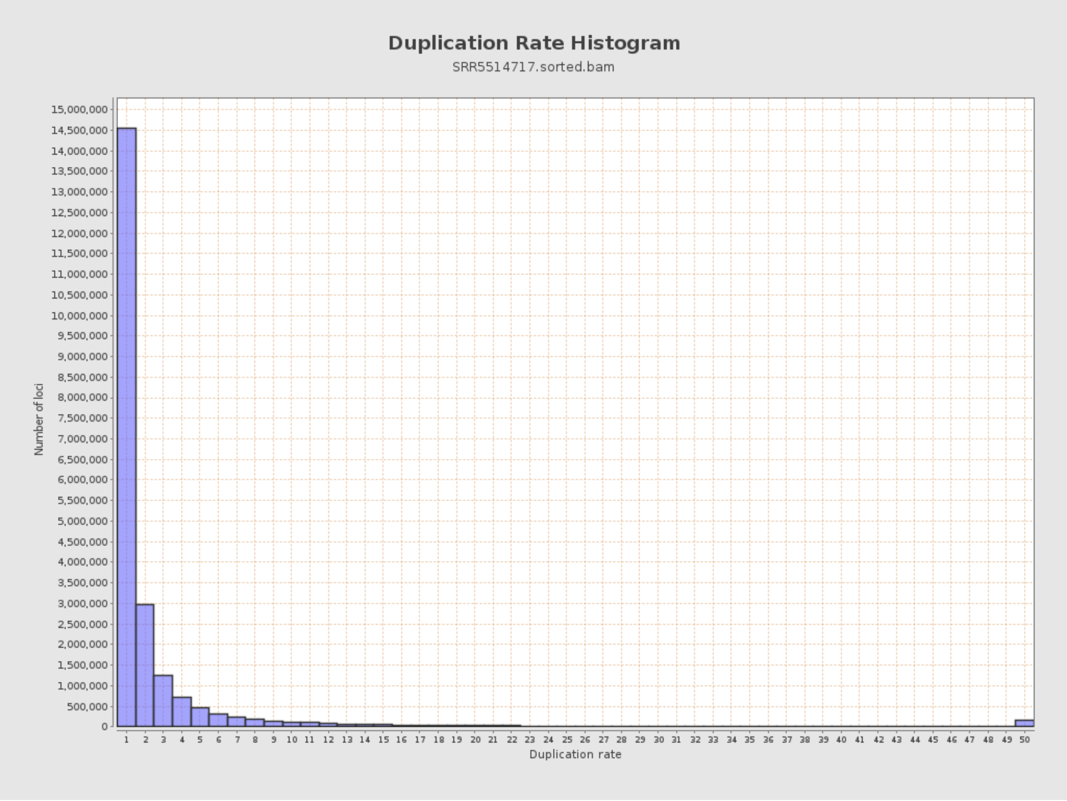
5. Results : Coverage Histogram (0-50X)



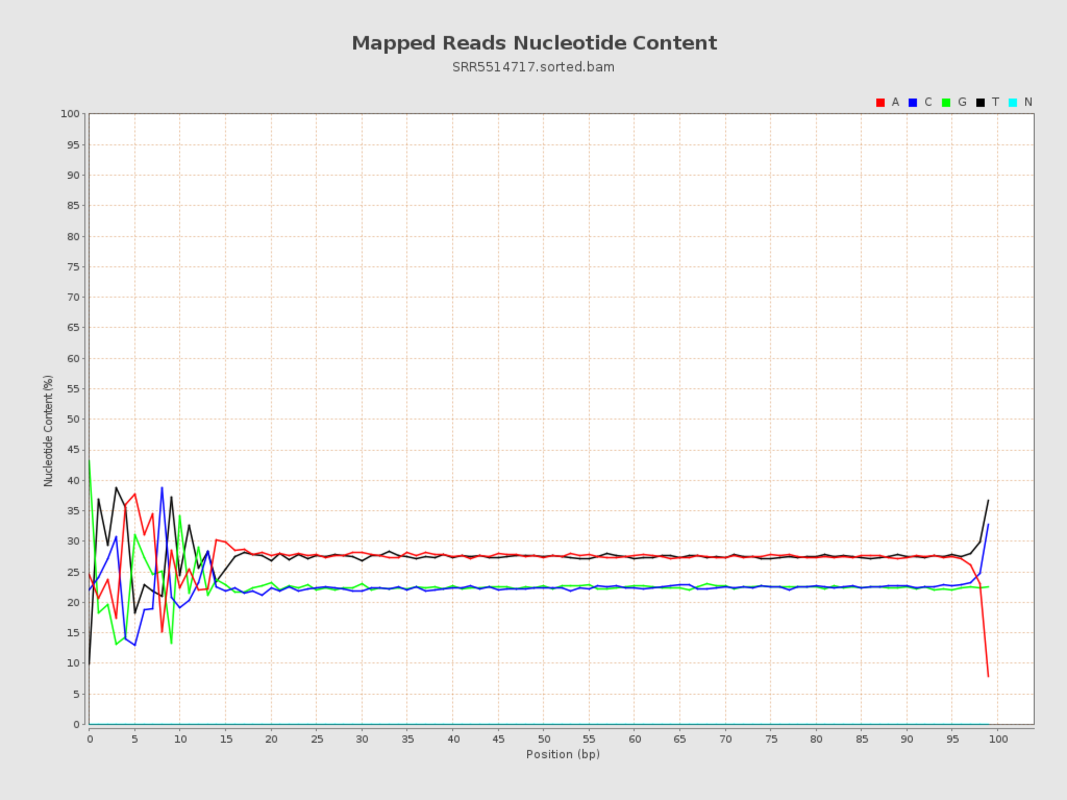
6. Results : Genome Fraction Coverage



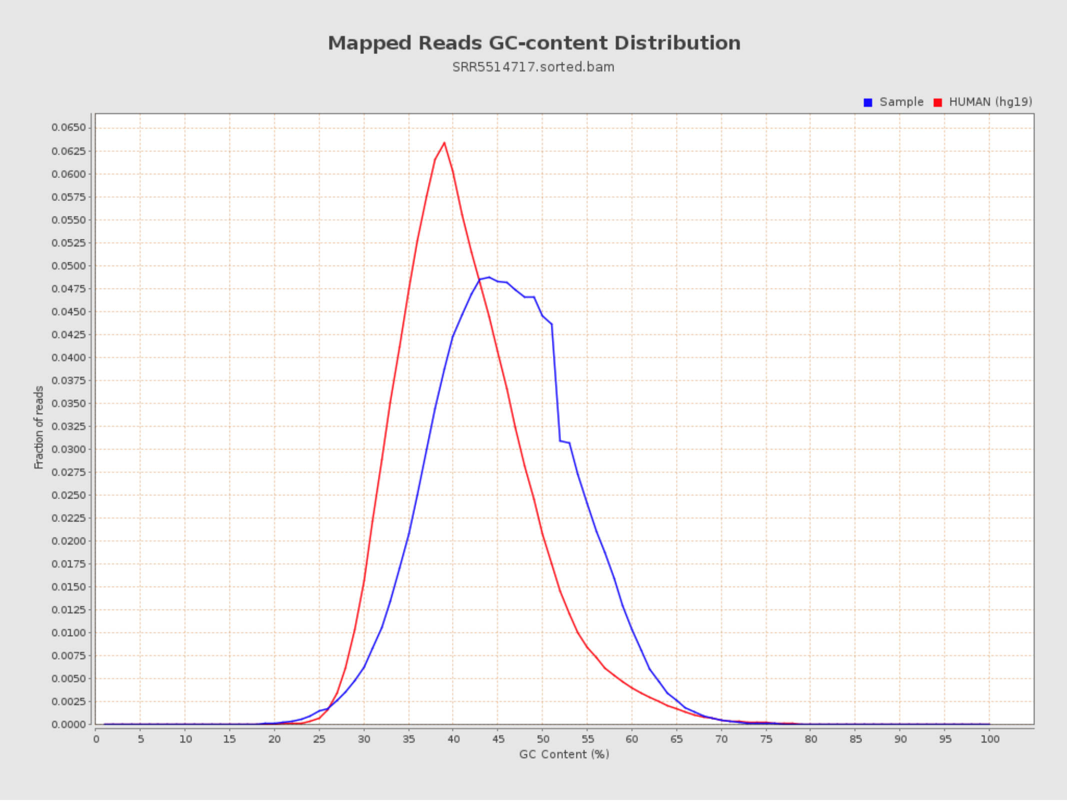
7. Results : Duplication Rate Histogram



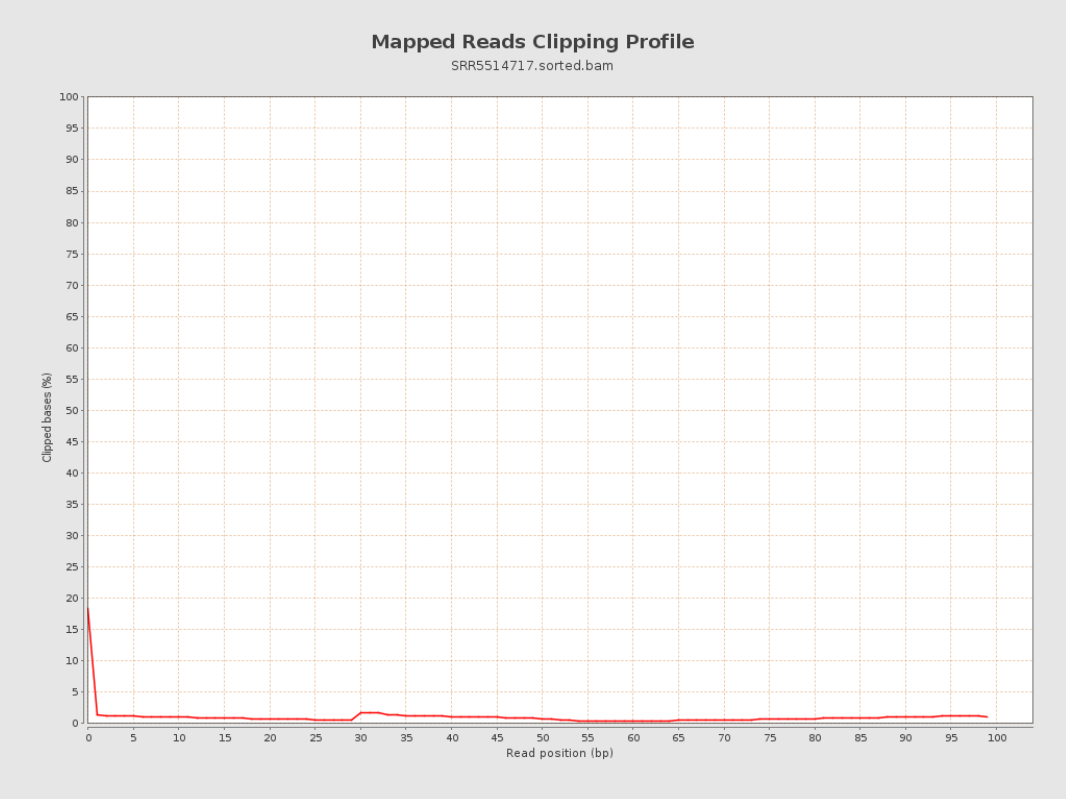
8. Results : Mapped Reads Nucleotide Content



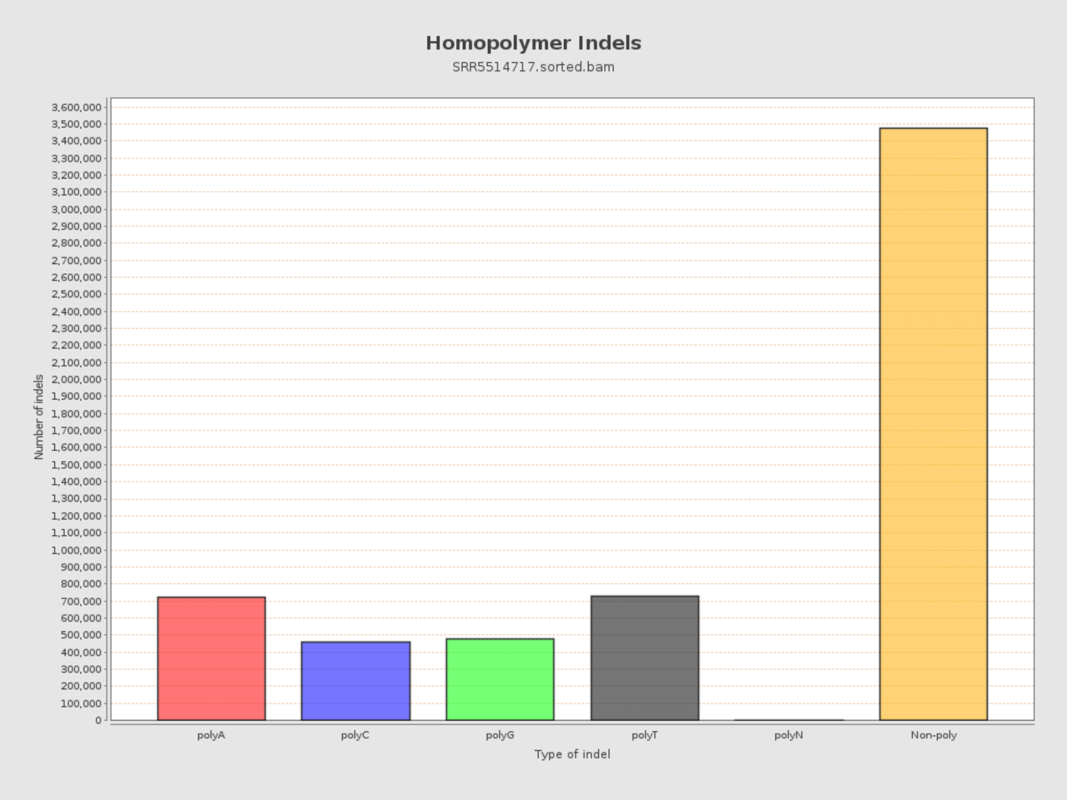
9. Results : Mapped Reads GC-content Distribution



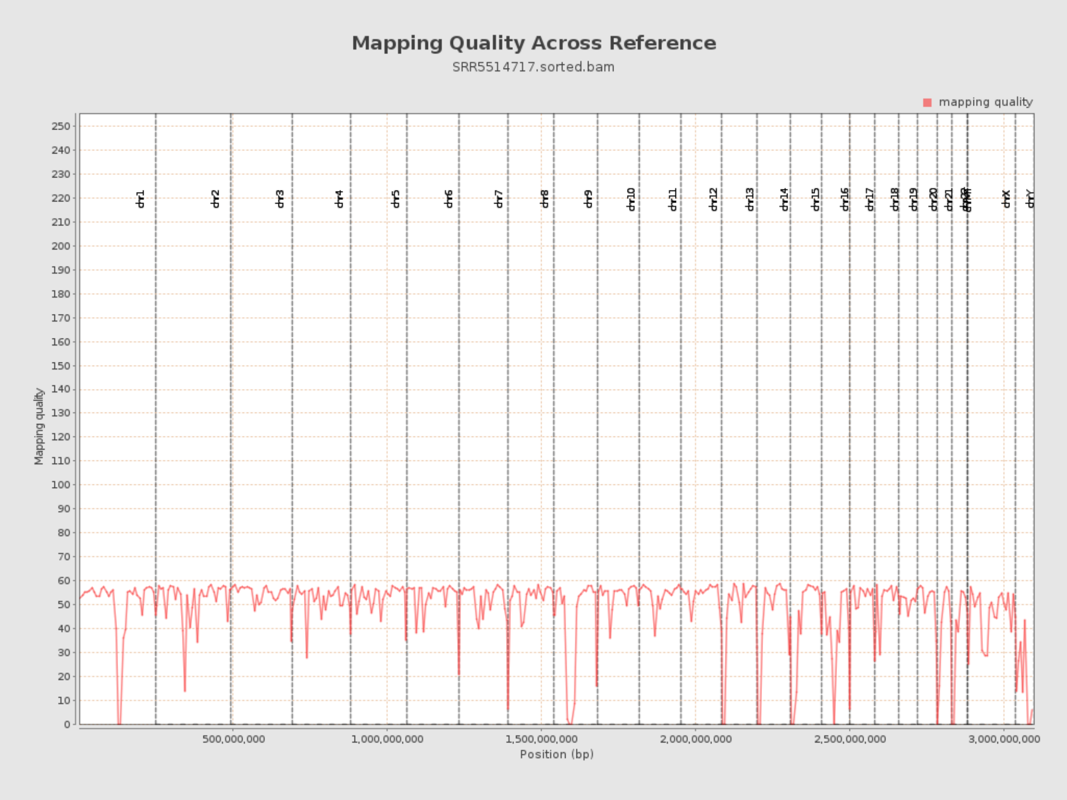
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram