Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 01:12:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514707.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_SRR5514707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 01:12:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,538,672
Mapped reads	74,848,939 / 99.09%
Unmapped reads	689,733 / 0.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,870,296 / 5.12%
Read min/max/mean length	30 / 100 / 99.8
Duplicated reads (estimated)	37,555,154 / 49.72%
Duplication rate	33.19%
Clipped reads	16,814,053 / 22.26%

2.2. ACGT Content

Number/percentage of A's	2,108,139,717 / 29.64%
Number/percentage of C's	1,440,419,588 / 20.25%
Number/percentage of T's	2,086,999,489 / 29.34%
Number/percentage of G's	1,467,126,529 / 20.63%
Number/percentage of N's	10,161,667 / 0.14%
GC Percentage	40.88%

2.3. Coverage

Mean	2.2997

Standard Deviation	150.1757

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

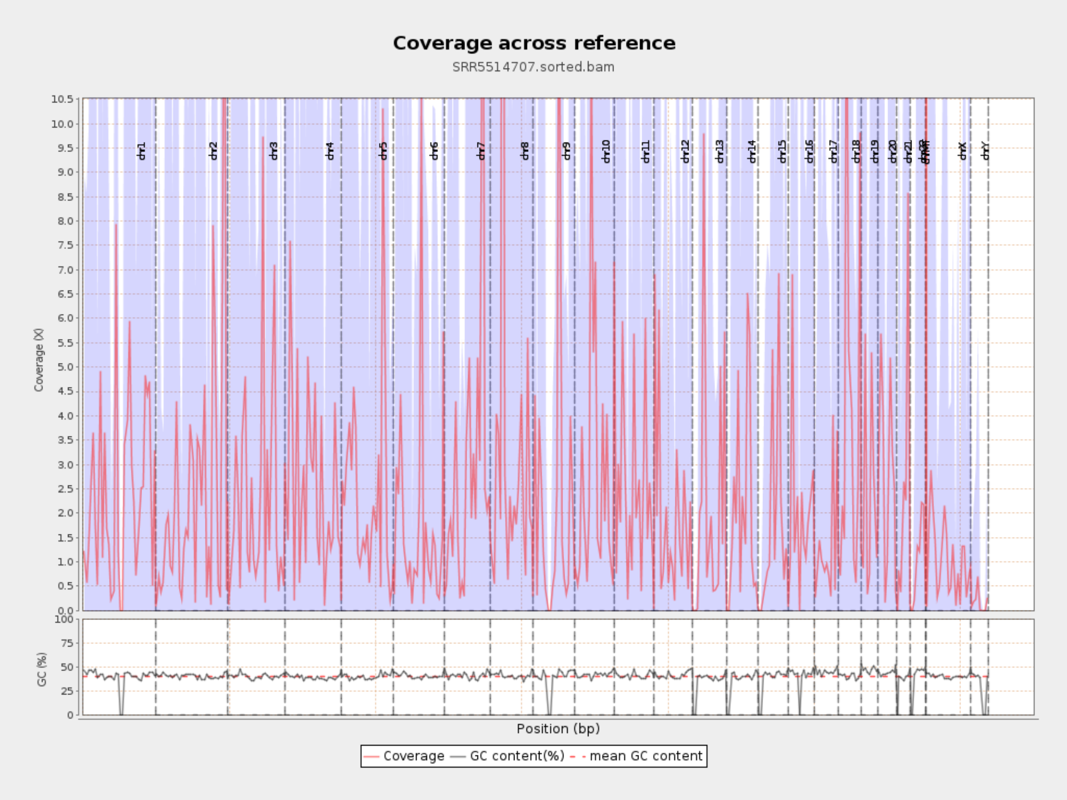
General error rate	0.69%
Mismatches	44,515,535
Insertions	2,599,908
Mapped reads with at least one insertion	3.31%
Deletions	2,658,596
Mapped reads with at least one deletion	3.34%
Homopolymer indels	39.79%

2.6. Chromosome stats

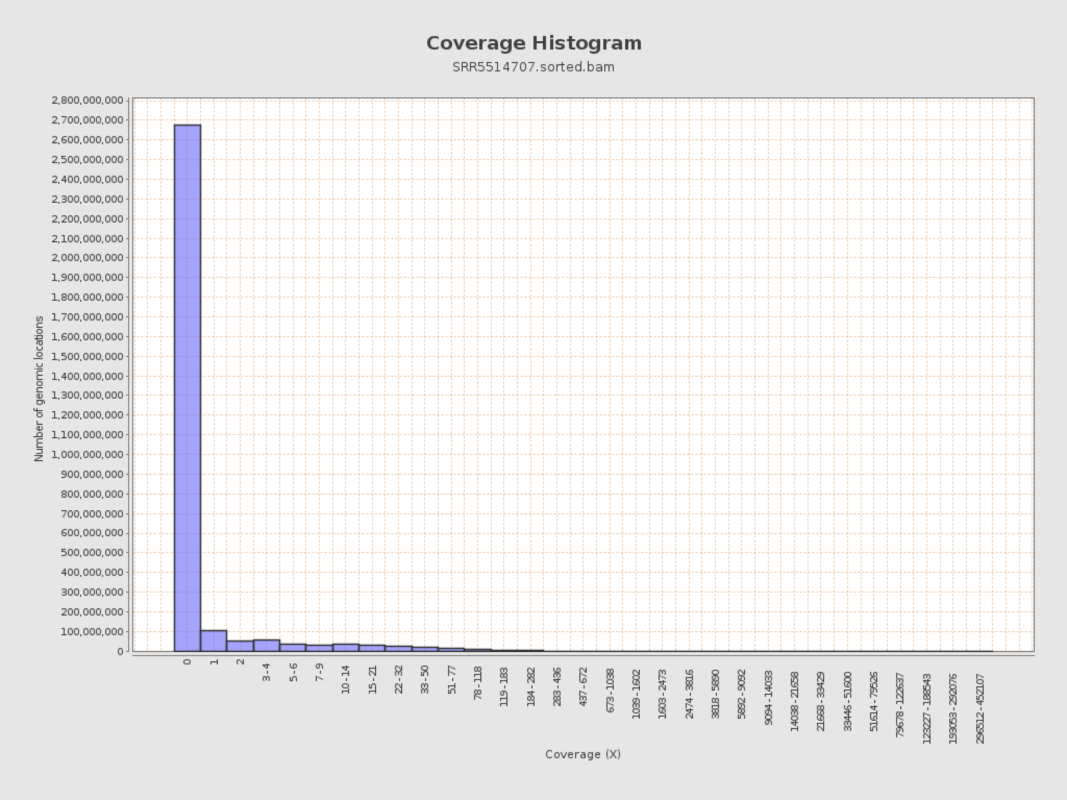
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	604415805	2.4249	22.8325
chr2	243199373	606821285	2.4952	121.9002
chr3	198022430	461160869	2.3288	28.0034
chr4	191154276	486508677	2.5451	14.7069
chr5	180915260	443347778	2.4506	15.7116
chr6	171115067	303799163	1.7754	17.315
chr7	159138663	455424800	2.8618	57.9767

chr8	146364022	538890082	3.6818	621.0072
chr9	141213431	309522861	2.1919	184.4946
chr10	135534747	389609094	2.8746	17.8249
chr11	135006516	349766295	2.5907	76.7963
chr12	133851895	258695341	1.9327	14.4131
chr13	115169878	245856290	2.1347	34.3894
chr14	107349540	226216896	2.1073	14.4277
chr15	102531392	179262483	1.7484	13.7477
chr16	90354753	182473176	2.0195	34.6942
chr17	81195210	99228127	1.2221	12.2143
chr18	78077248	304132852	3.8953	20.9105
chr19	59128983	138040421	2.3346	25.8137
chr20	63025520	188832230	2.9961	18.2278
chr21	48129895	114318613	2.3752	235.8499
chr22	51304566	55582510	1.0834	27.6379
chrMT	16571	1678681	101.3023	65.4382
chrX	155270560	164633862	1.0603	9.6105
chrY	59373566	10987508	0.1851	2.4264

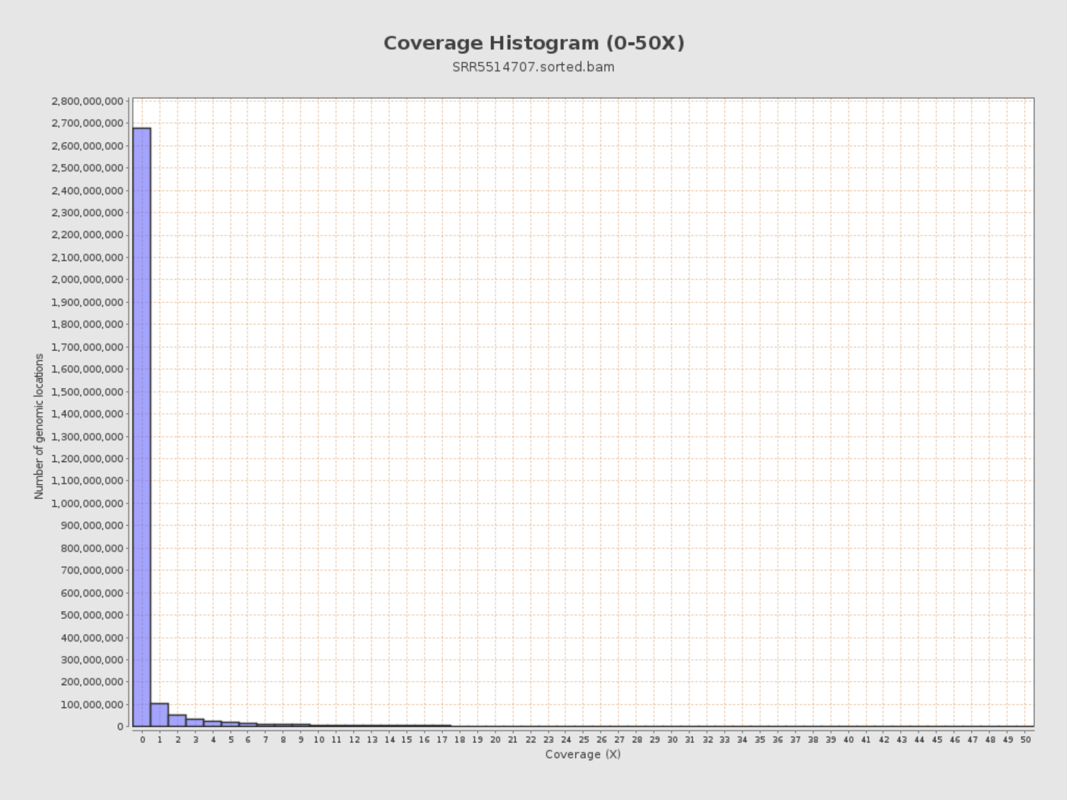
3. Results : Coverage across reference



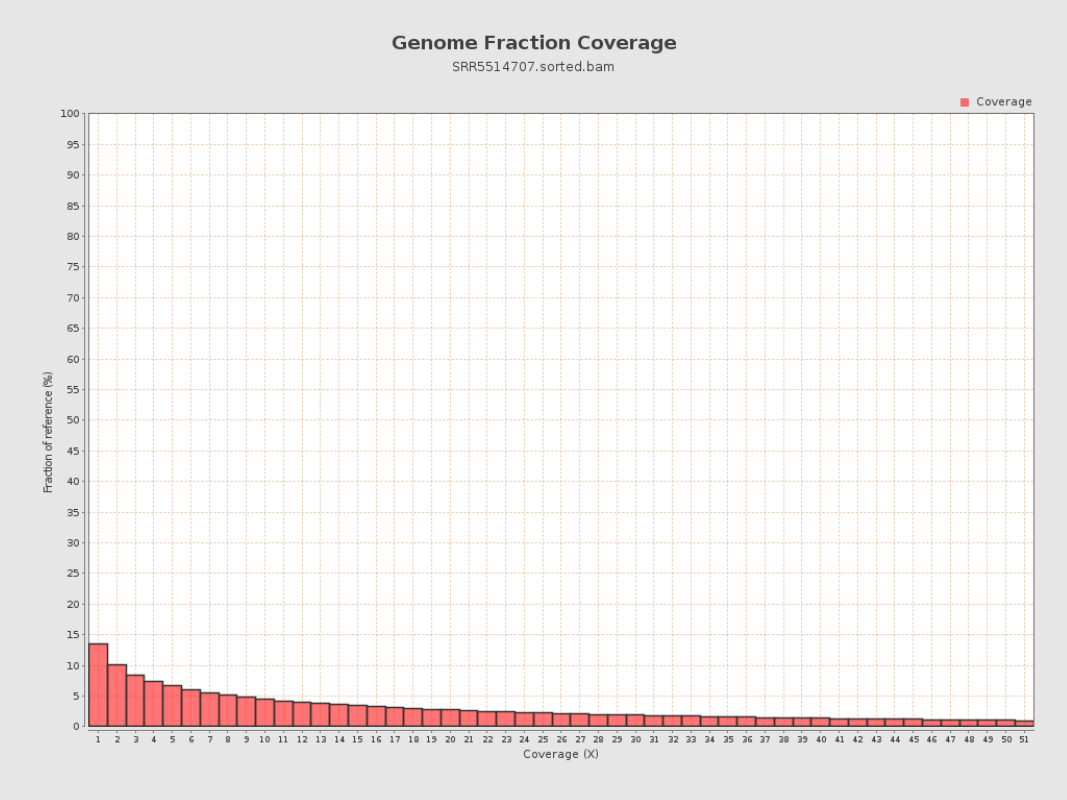
4. Results : Coverage Histogram



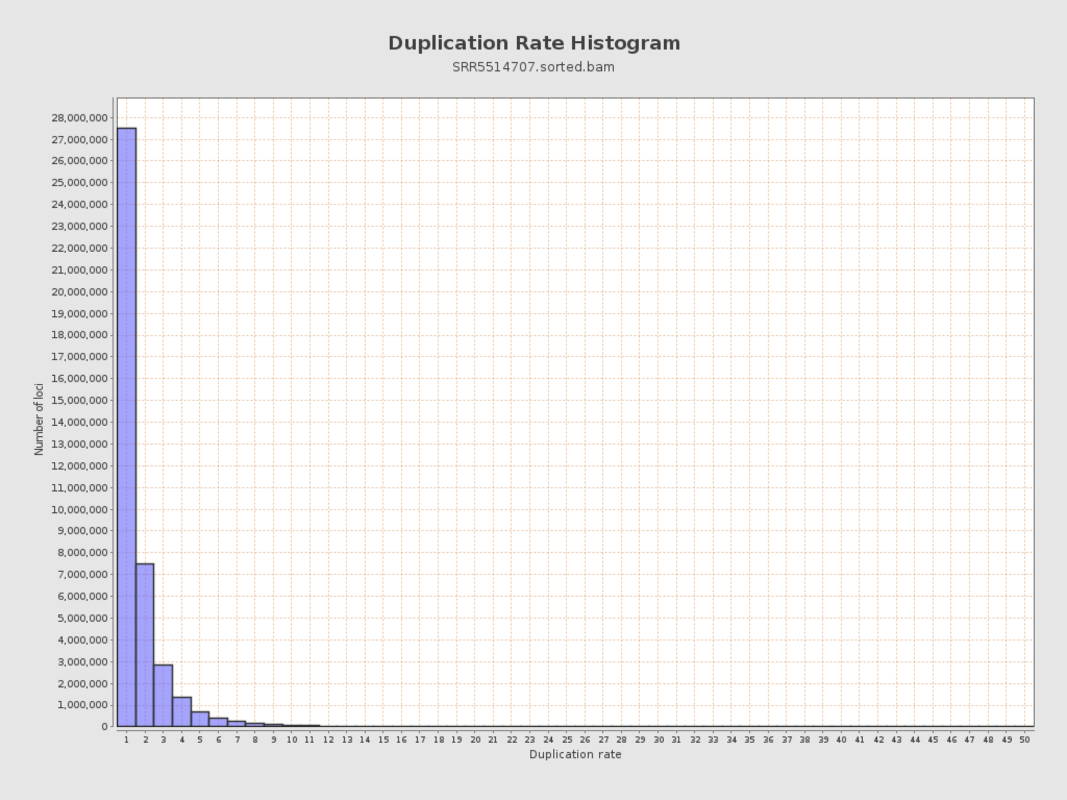
5. Results : Coverage Histogram (0-50X)



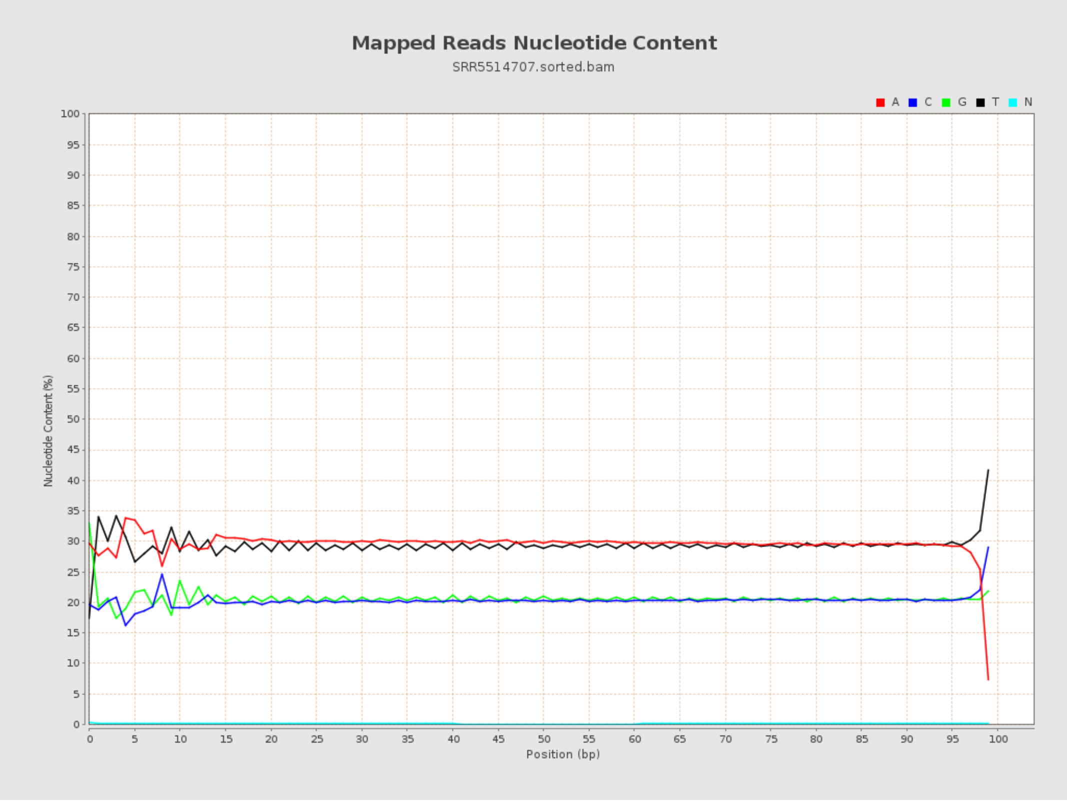
6. Results : Genome Fraction Coverage



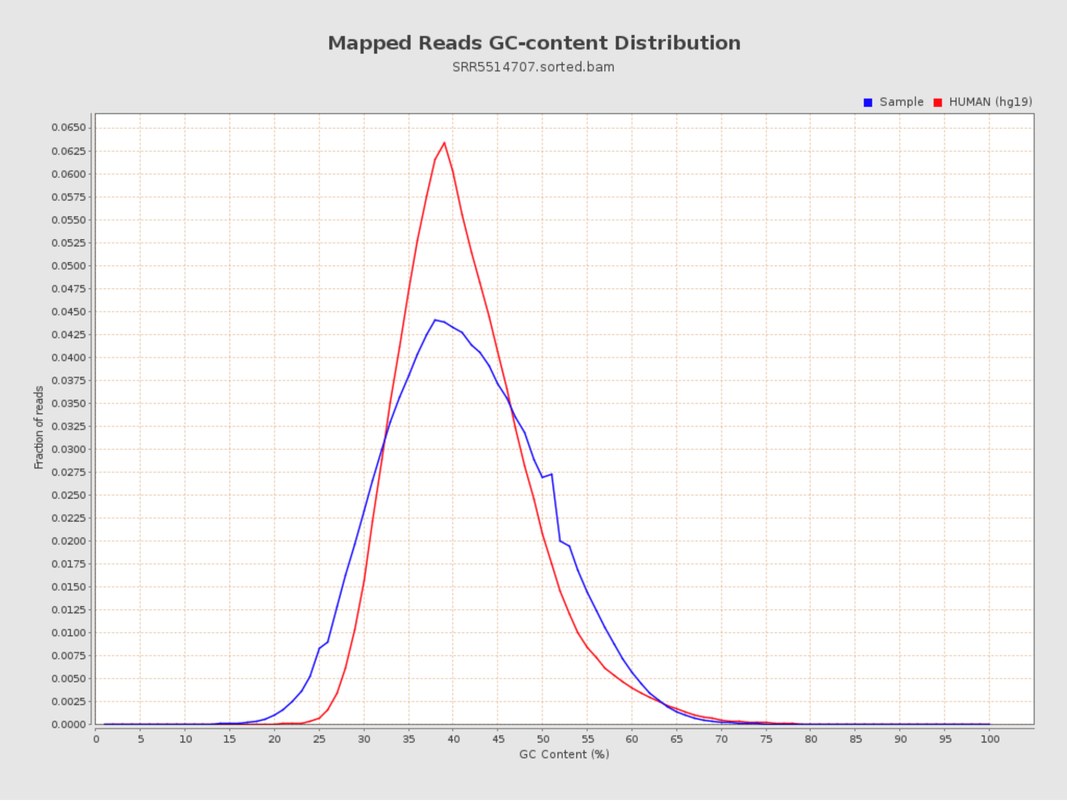
7. Results : Duplication Rate Histogram



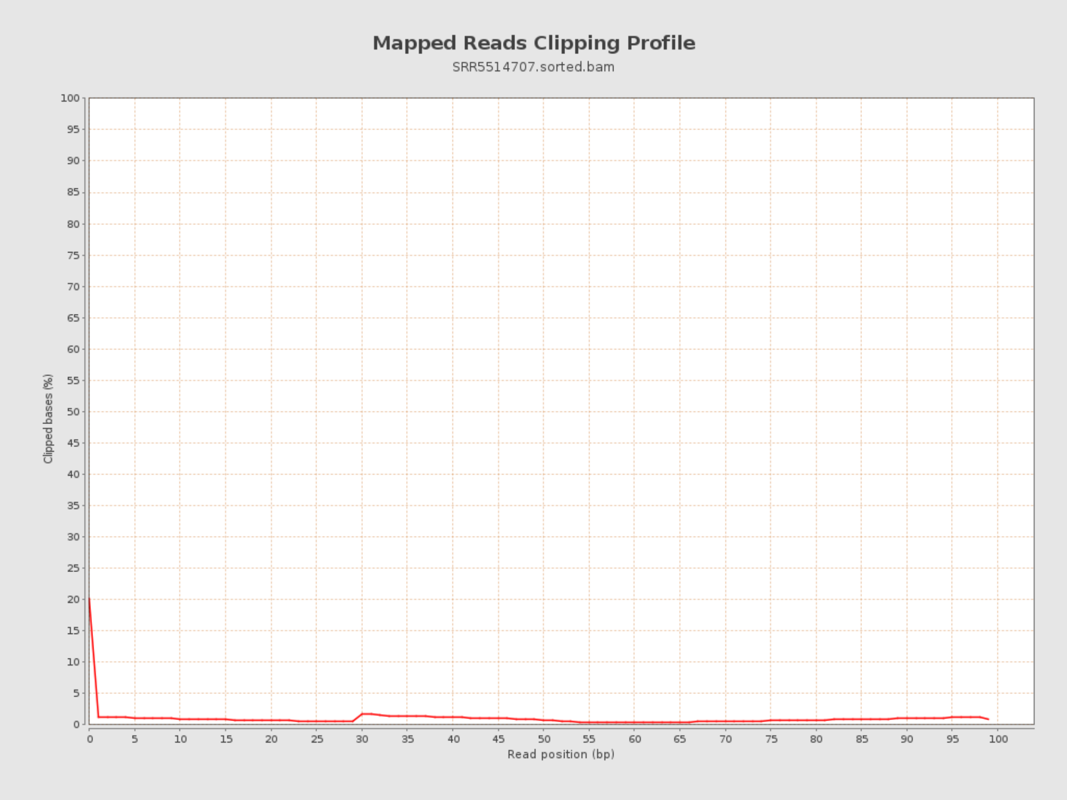
8. Results : Mapped Reads Nucleotide Content



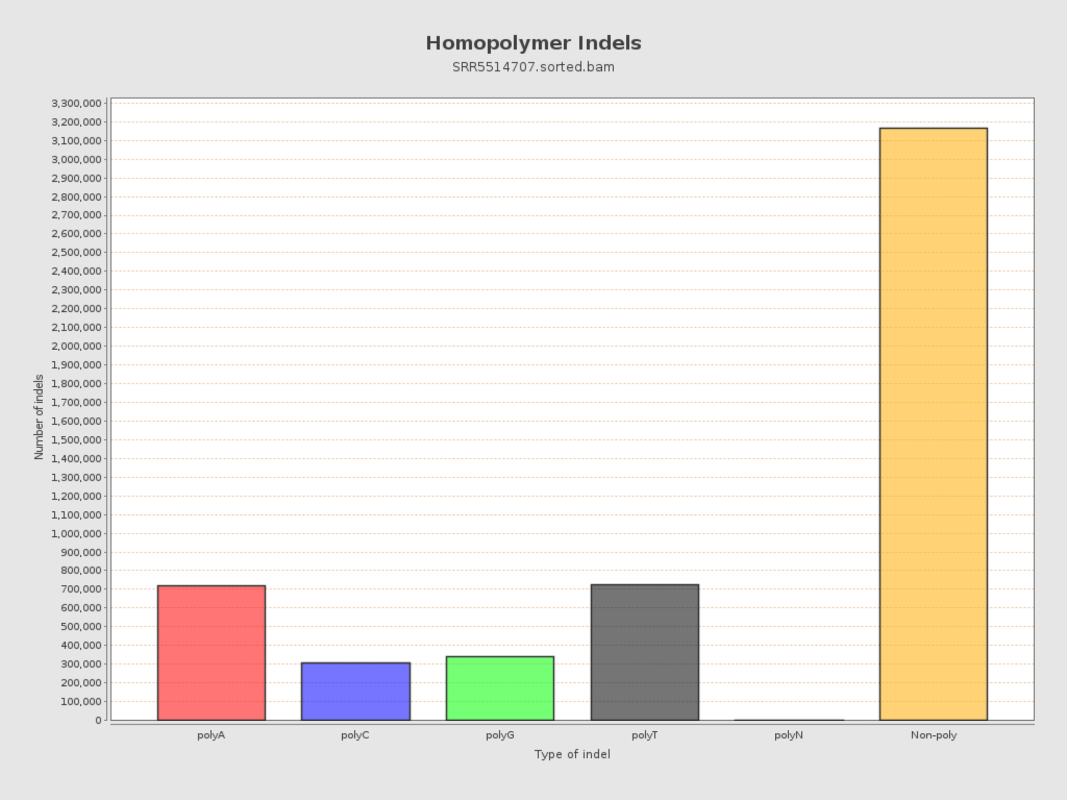
9. Results : Mapped Reads GC-content Distribution



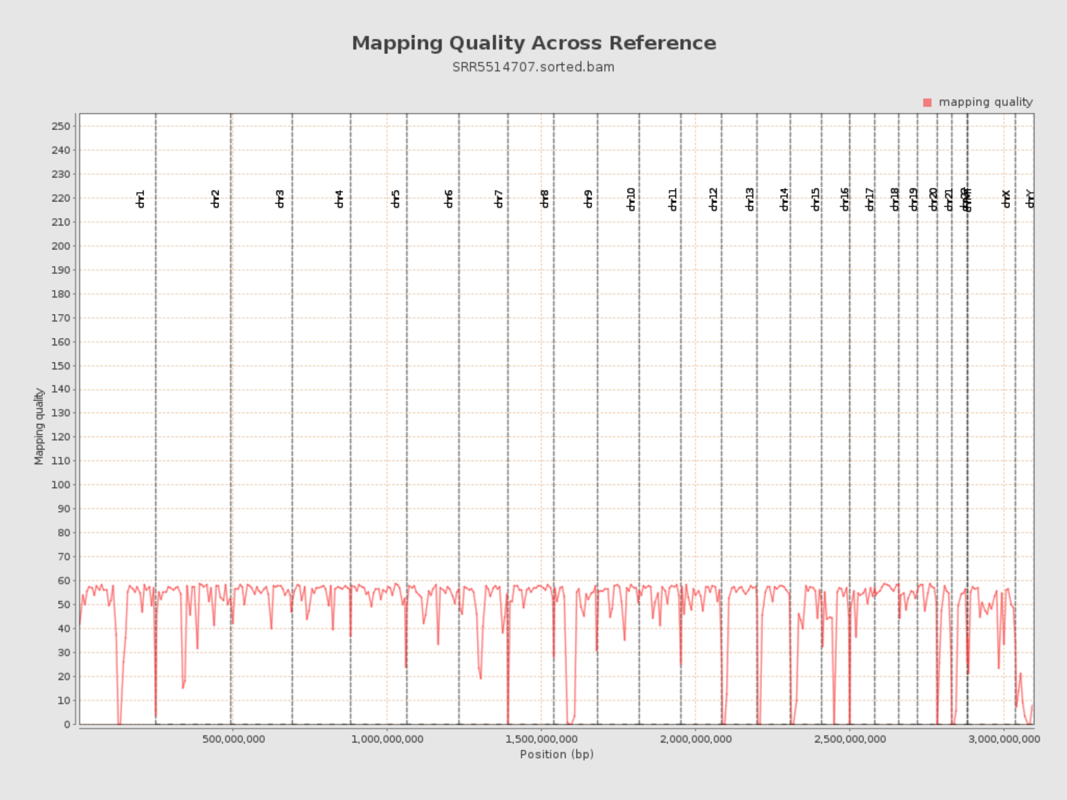
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram