Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 23:13:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514704.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_SRR5514704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514704.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 23:13:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,964,776
Mapped reads	40,599,449 / 99.11%
Unmapped reads	365,327 / 0.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,972,695 / 4.82%
Read min/max/mean length	30 / 100 / 99.68
Duplicated reads (estimated)	23,381,213 / 57.08%
Duplication rate	37.67%
Clipped reads	8,919,995 / 21.77%

2.2. ACGT Content

Number/percentage of A's	1,133,994,585 / 29.45%
Number/percentage of C's	789,638,489 / 20.51%
Number/percentage of T's	1,118,868,266 / 29.06%
Number/percentage of G's	798,613,470 / 20.74%
Number/percentage of N's	9,153,799 / 0.24%
GC Percentage	41.25%

2.3. Coverage

Mean	1.2447

Standard Deviation	85.1116

2.4. Mapping Quality

Mean Mapping Quality	31.42

2.5. Mismatches and indels

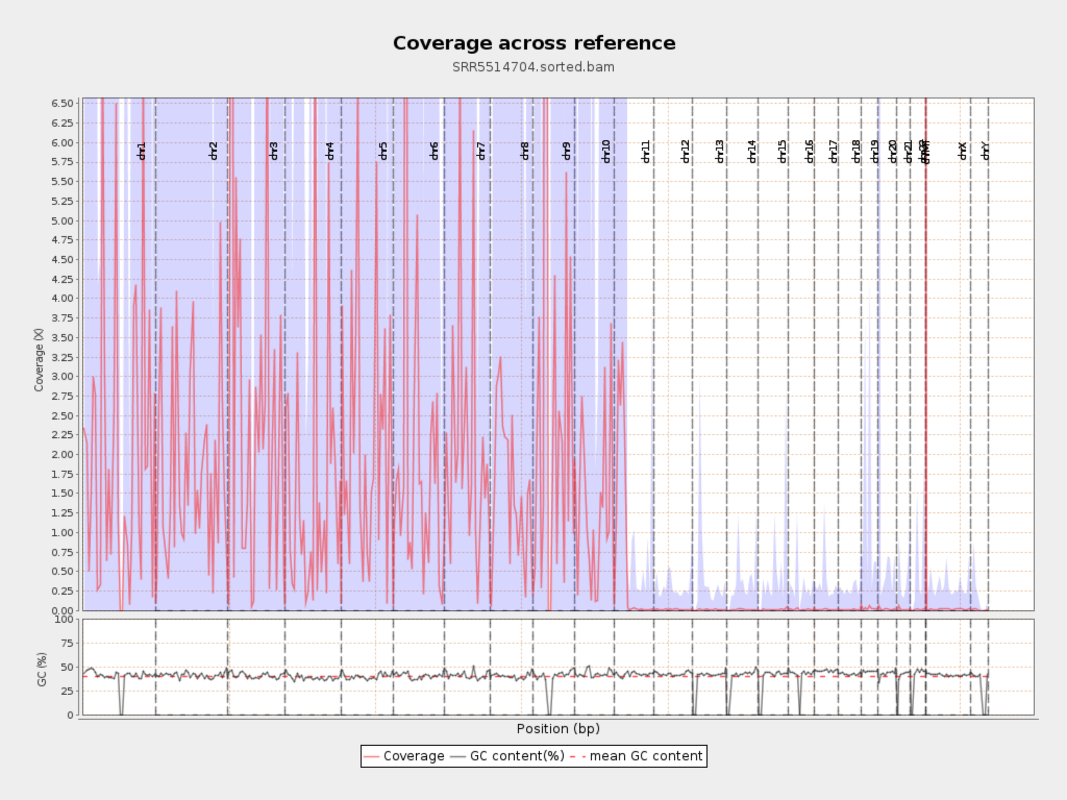
General error rate	0.68%
Mismatches	23,825,624
Insertions	1,317,794
Mapped reads with at least one insertion	3.14%
Deletions	1,338,143
Mapped reads with at least one deletion	3.17%
Homopolymer indels	42.01%

2.6. Chromosome stats

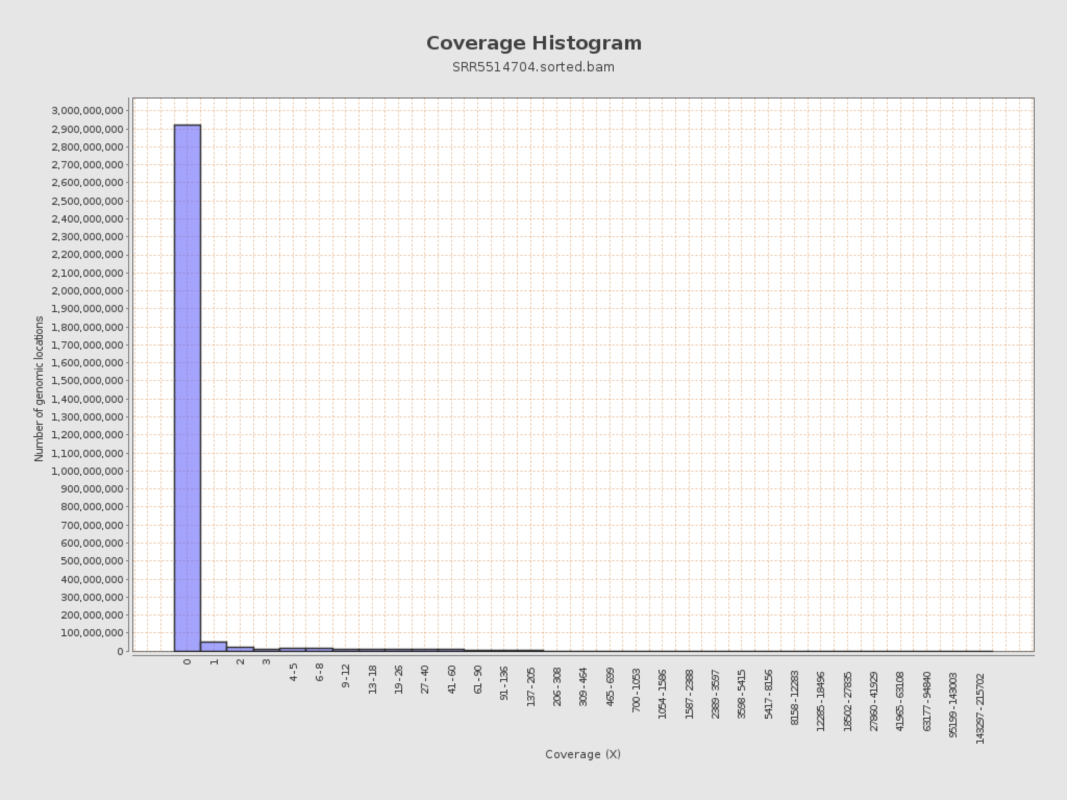
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	519962628	2.0861	35.1527
chr2	243199373	446873583	1.8375	37.8148
chr3	198022430	530725694	2.6801	193.4972
chr4	191154276	310401507	1.6238	22.1519
chr5	180915260	408508467	2.258	19.6672
chr6	171115067	364711086	2.1314	227.1126
chr7	159138663	338240569	2.1254	25.4692

chr8	146364022	231336486	1.5806	21.5256
chr9	141213431	405066475	2.8685	189.8635
chr10	135534747	180018418	1.3282	22.257
chr11	135006516	100335745	0.7432	14.9603
chr12	133851895	2015379	0.0151	0.3568
chr13	115169878	1240925	0.0108	0.8484
chr14	107349540	1287283	0.012	0.5408
chr15	102531392	1448472	0.0141	0.9009
chr16	90354753	1213716	0.0134	0.4363
chr17	81195210	1128711	0.0139	0.4934
chr18	78077248	979051	0.0125	0.2709
chr19	59128983	1603959	0.0271	2.085
chr20	63025520	1306906	0.0207	6.2588
chr21	48129895	923925	0.0192	0.5726
chr22	51304566	542508	0.0106	0.9447
chrMT	16571	139387	8.4115	24.6822
chrX	155270560	2710804	0.0175	0.3489
chrY	59373566	471821	0.0079	0.3418

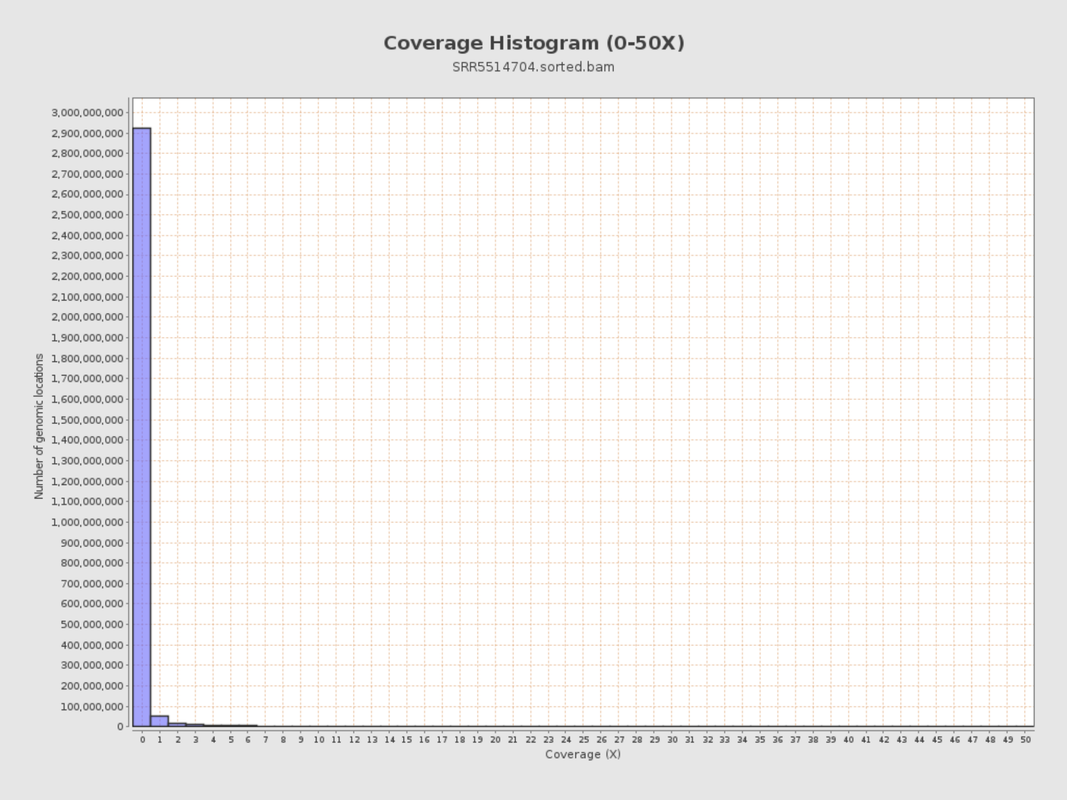
3. Results : Coverage across reference



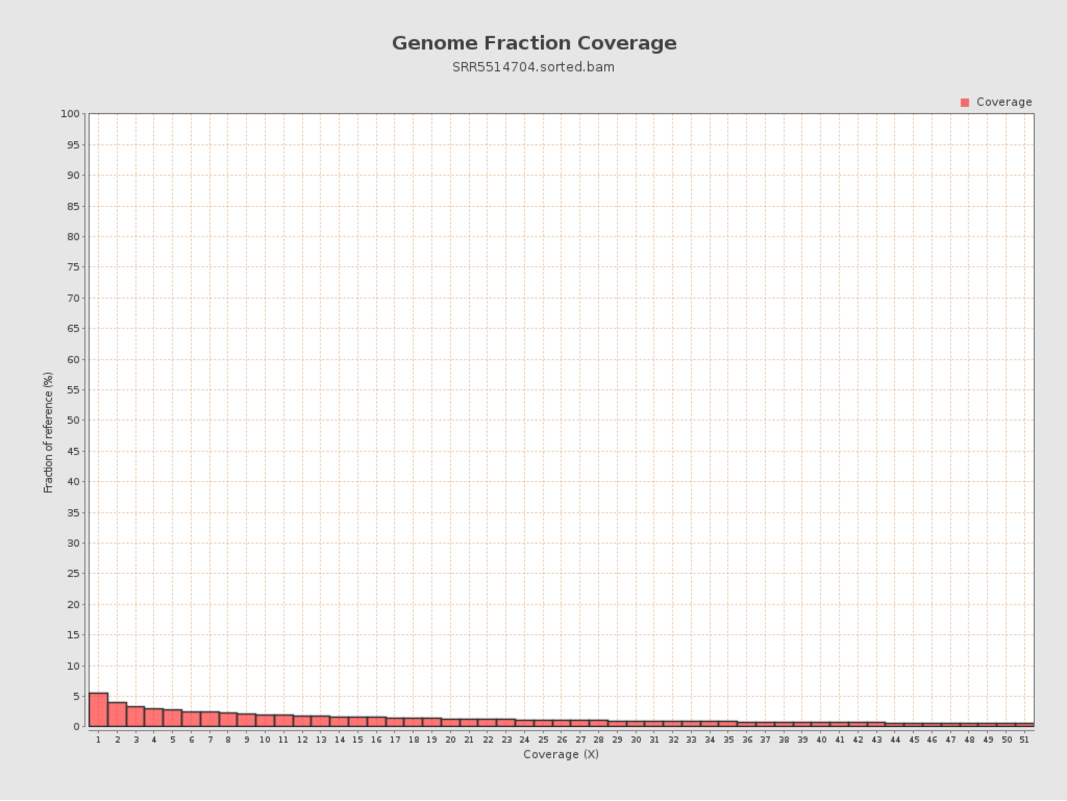
4. Results : Coverage Histogram



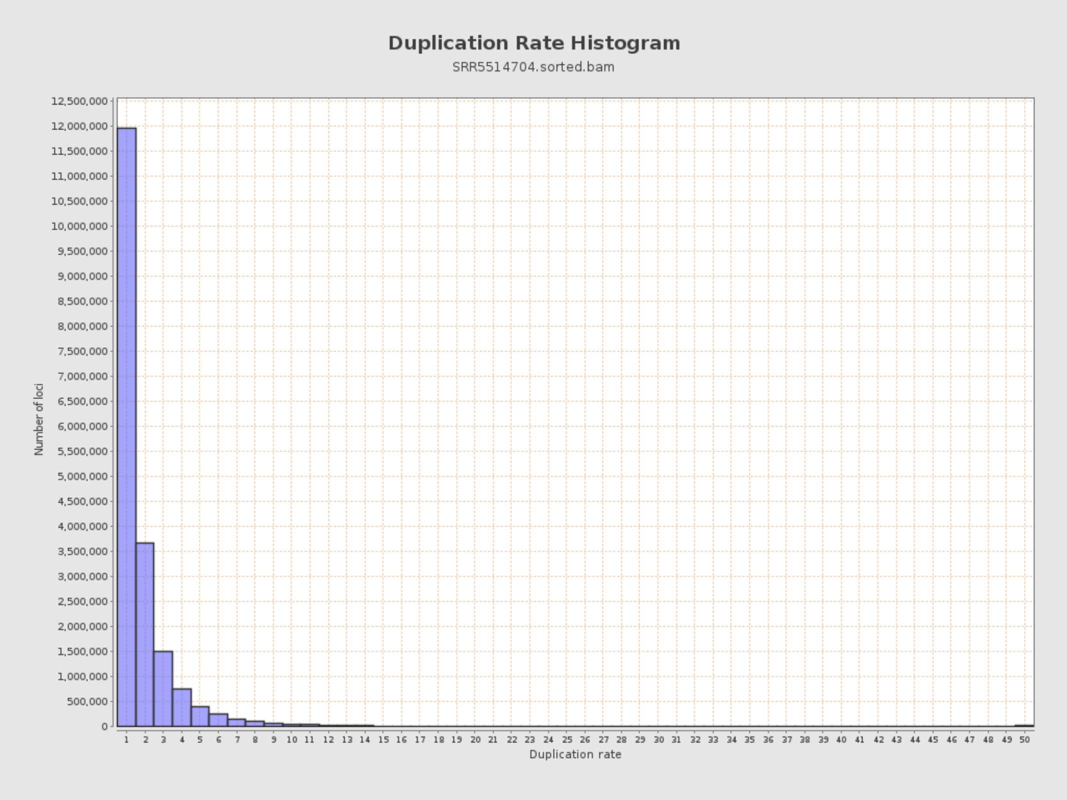
5. Results : Coverage Histogram (0-50X)



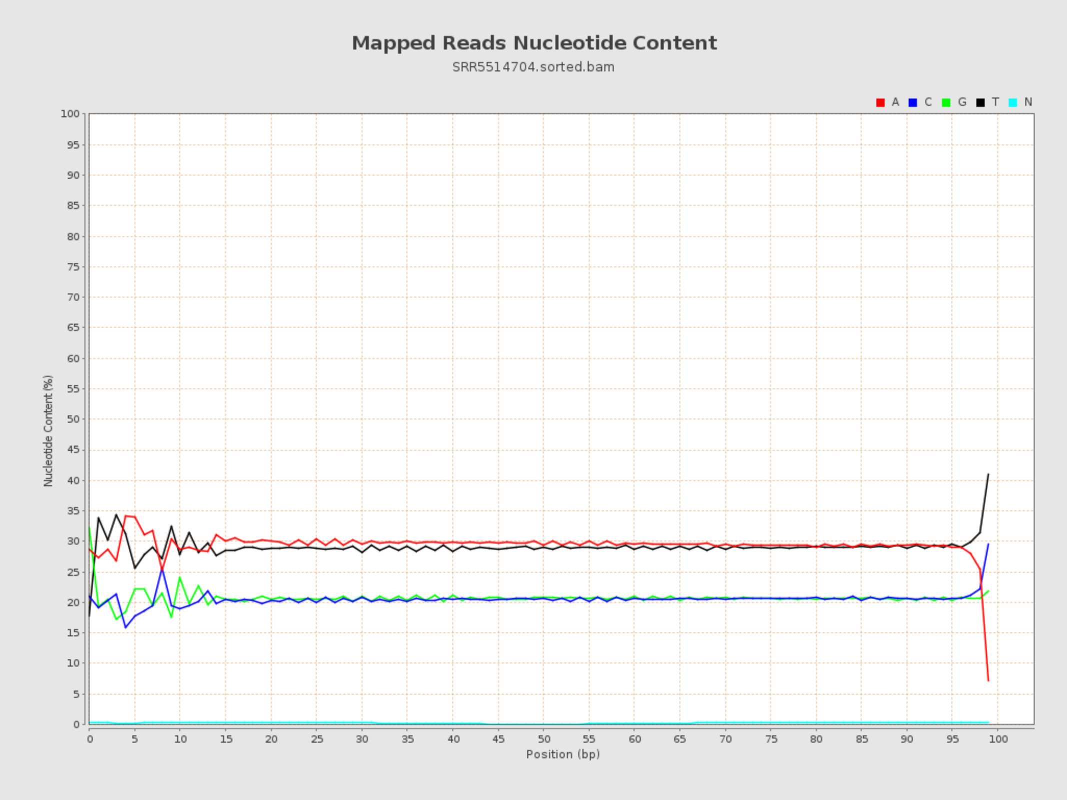
6. Results : Genome Fraction Coverage



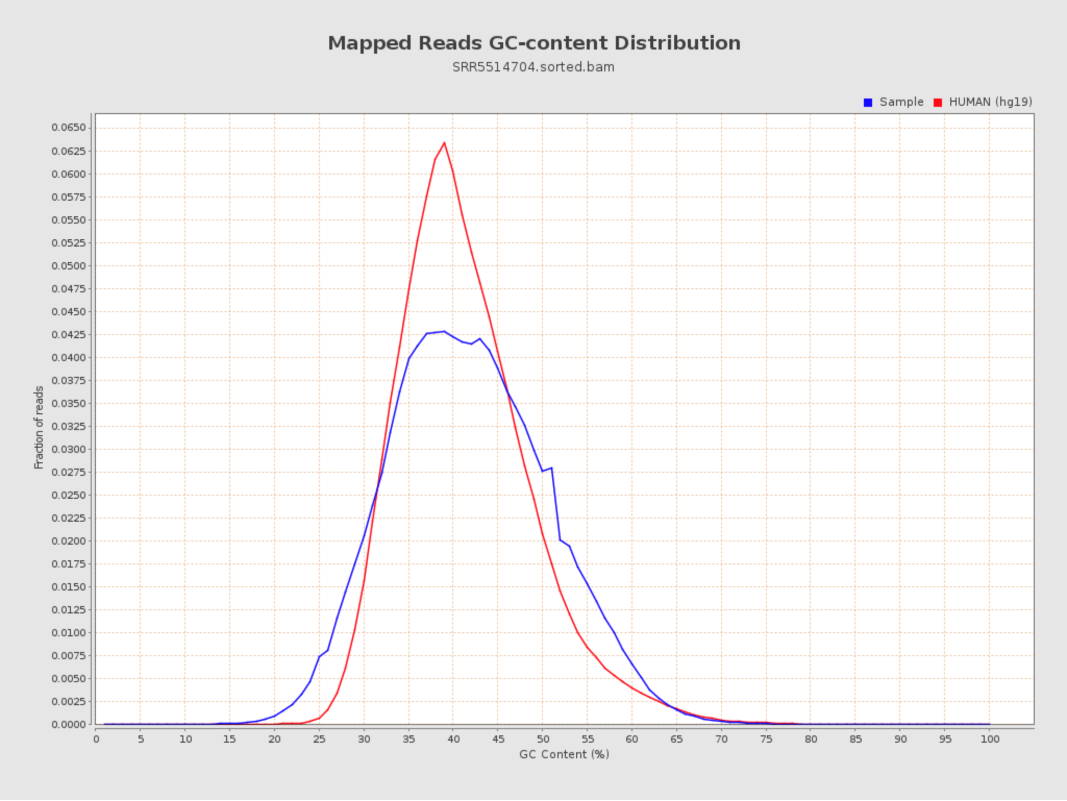
7. Results : Duplication Rate Histogram



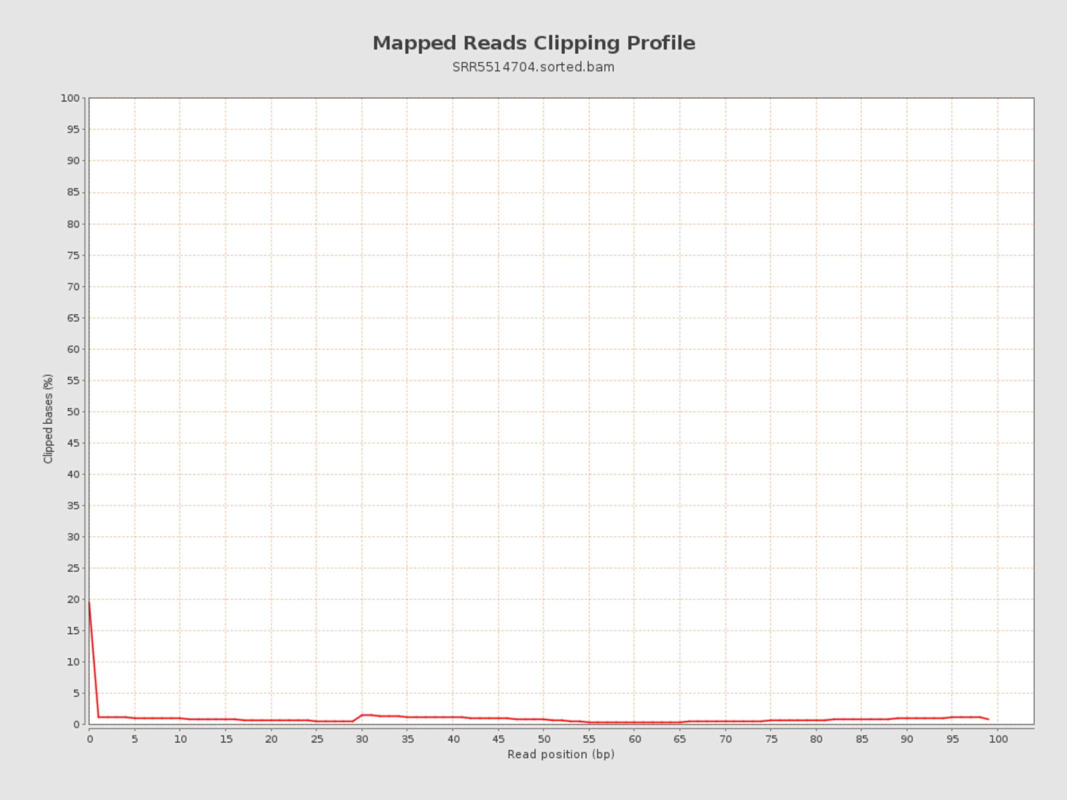
8. Results : Mapped Reads Nucleotide Content



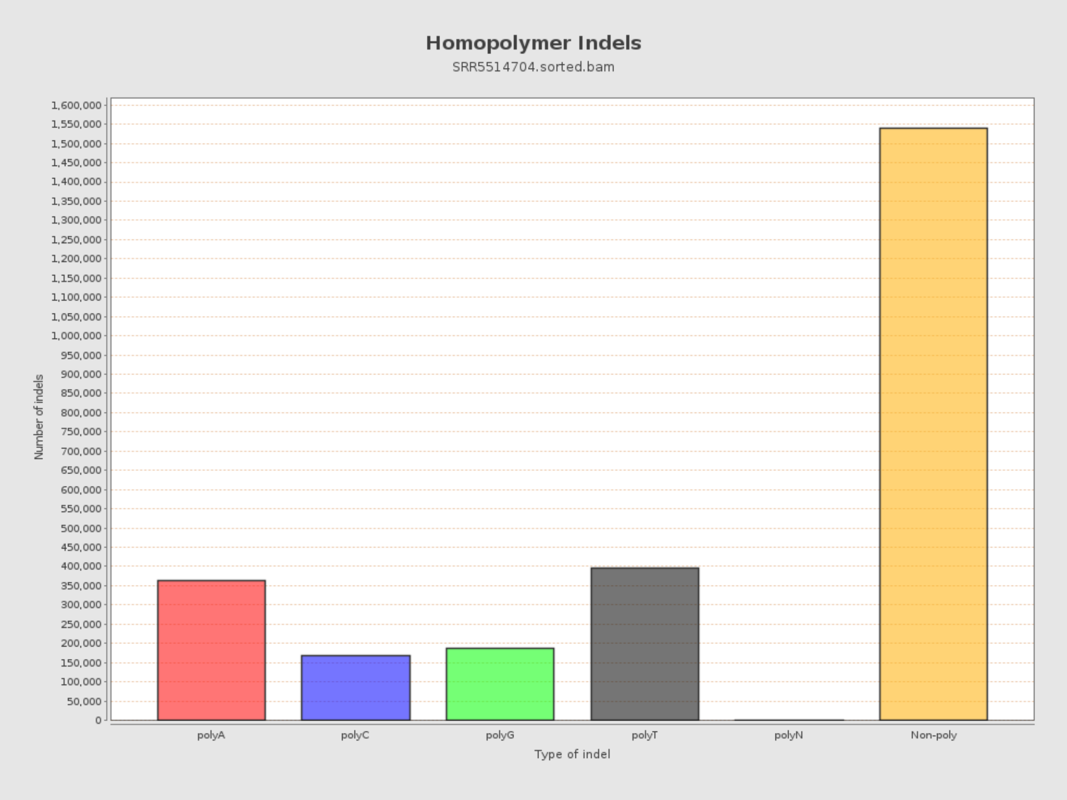
9. Results : Mapped Reads GC-content Distribution



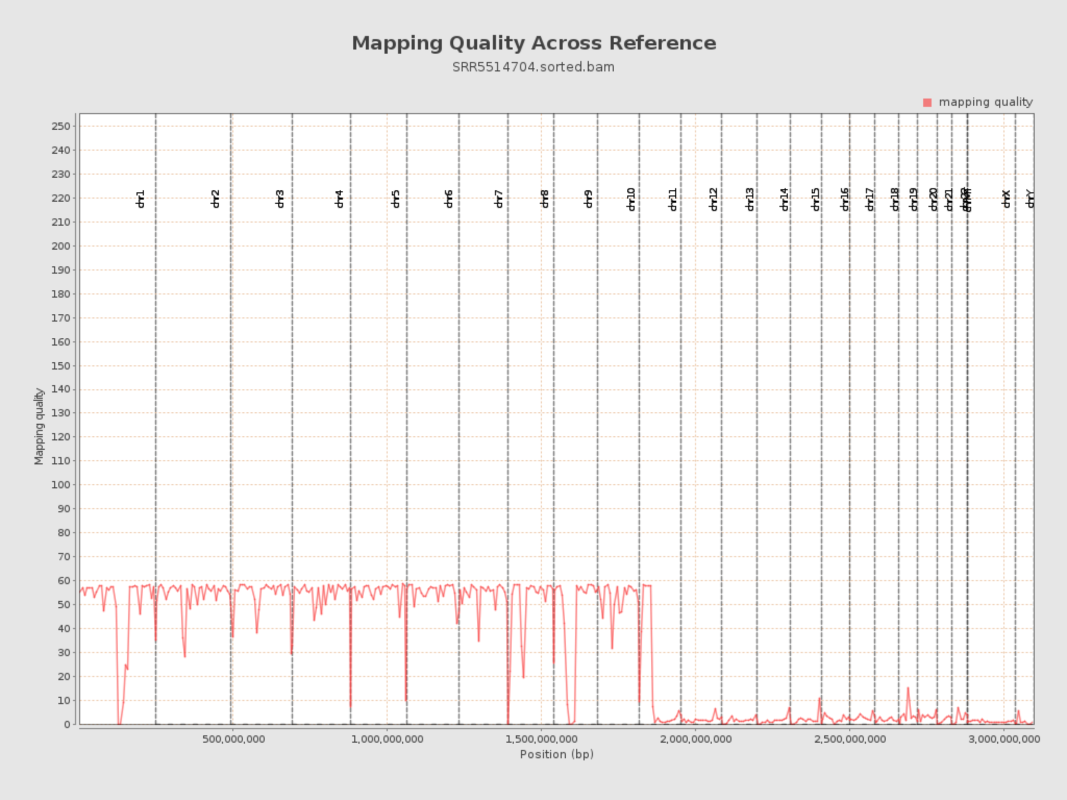
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram