Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:22:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054603.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_SRR054603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:22:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,252,471
Mapped reads	8,086,633 / 78.87%
Unmapped reads	2,165,838 / 21.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	292 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,611,453 / 15.72%
Duplication rate	14.8%
Clipped reads	699,515 / 6.82%

2.2. ACGT Content

Number/percentage of A's	115,997,703 / 30.39%
Number/percentage of C's	70,843,303 / 18.56%
Number/percentage of T's	116,855,583 / 30.62%
Number/percentage of G's	77,843,874 / 20.39%
Number/percentage of N's	147,238 / 0.04%
GC Percentage	38.96%

2.3. Coverage

Mean	0.1233

Standard Deviation	0.8393

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

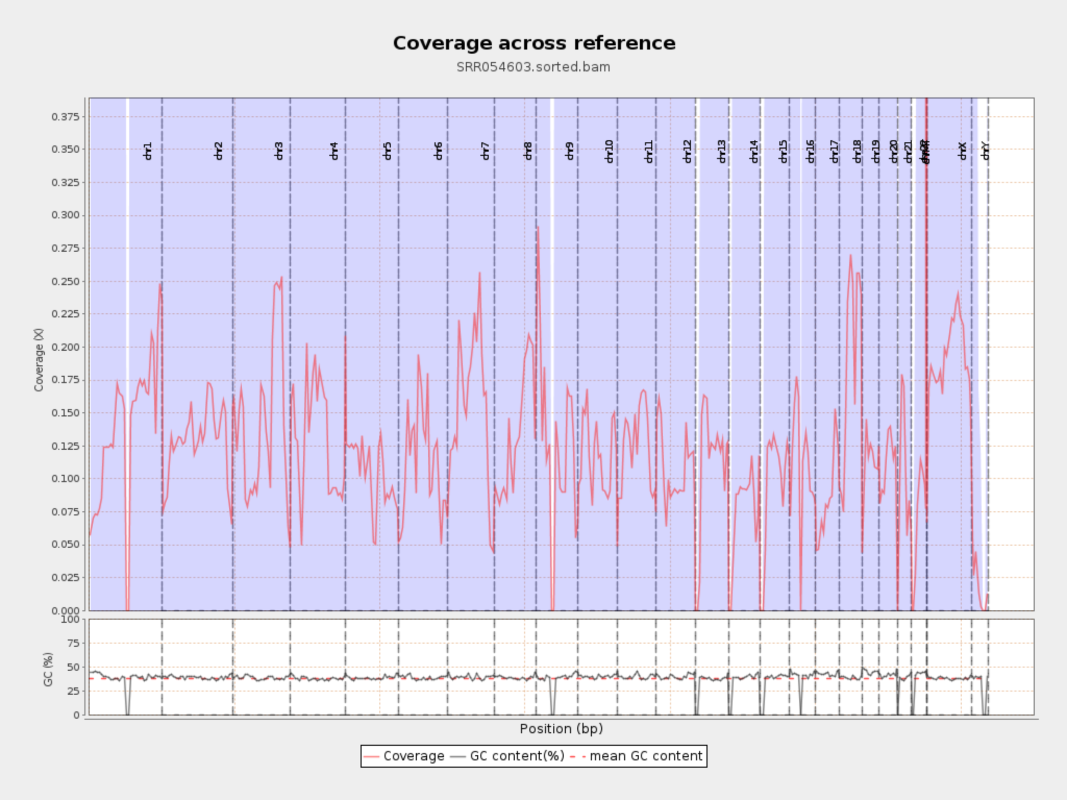
General error rate	0.49%
Mismatches	1,853,377
Insertions	17,228
Mapped reads with at least one insertion	0.21%
Deletions	56,053
Mapped reads with at least one deletion	0.69%
Homopolymer indels	49%

2.6. Chromosome stats

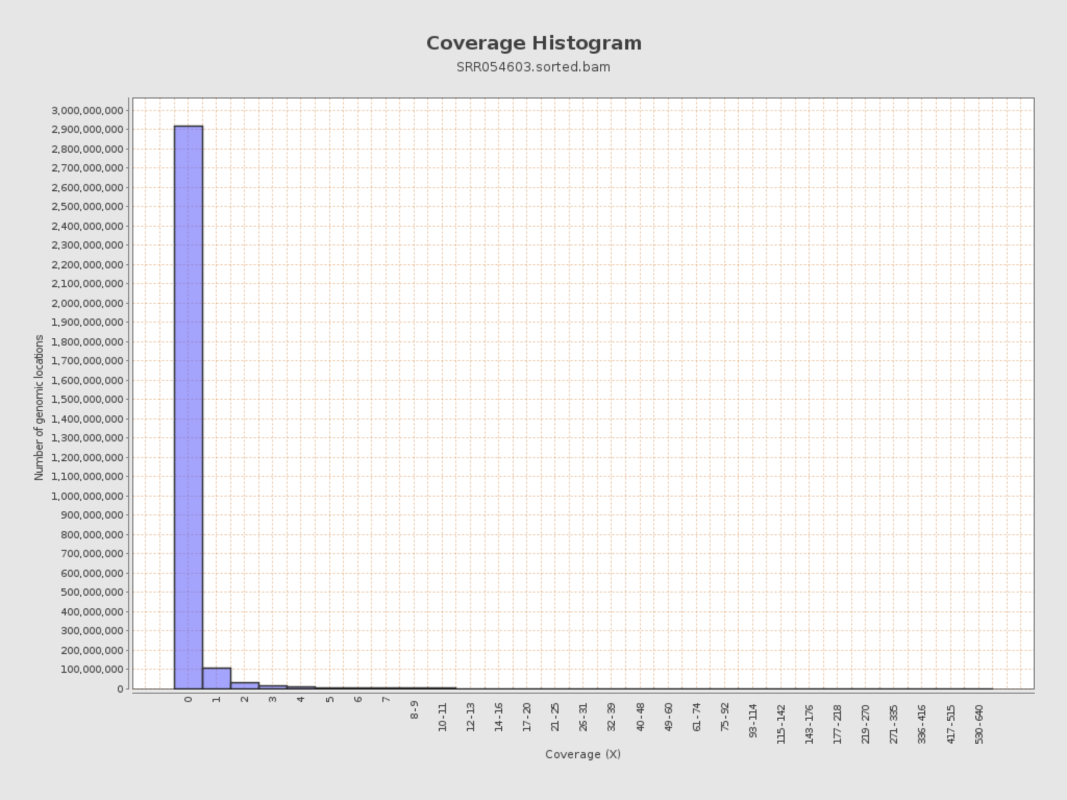
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34090728	0.1368	0.9358
chr2	243199373	31259501	0.1285	0.9068
chr3	198022430	28275673	0.1428	0.8439
chr4	191154276	24963731	0.1306	0.8407
chr5	180915260	18897615	0.1045	0.6731
chr6	171115067	19076689	0.1115	0.7742
chr7	159138663	25088174	0.1576	1.015

chr8	146364022	19684912	0.1345	0.9167
chr9	141213431	17974805	0.1273	0.8689
chr10	135534747	16156355	0.1192	0.8104
chr11	135006516	16926492	0.1254	0.8327
chr12	133851895	14405945	0.1076	0.6979
chr13	115169878	12509483	0.1086	0.7084
chr14	107349540	7940068	0.074	0.6285
chr15	102531392	9762601	0.0952	0.6479
chr16	90354753	10097332	0.1118	0.8052
chr17	81195210	6976625	0.0859	0.6001
chr18	78077248	14881890	0.1906	1.1904
chr19	59128983	6764526	0.1144	0.8318
chr20	63025520	6962799	0.1105	0.7386
chr21	48129895	4825446	0.1003	0.8024
chr22	51304566	3448454	0.0672	0.5224
chrMT	16571	123277	7.4393	13.86
chrX	155270560	29626585	0.1908	1.0852
chrY	59373566	1050929	0.0177	0.3756

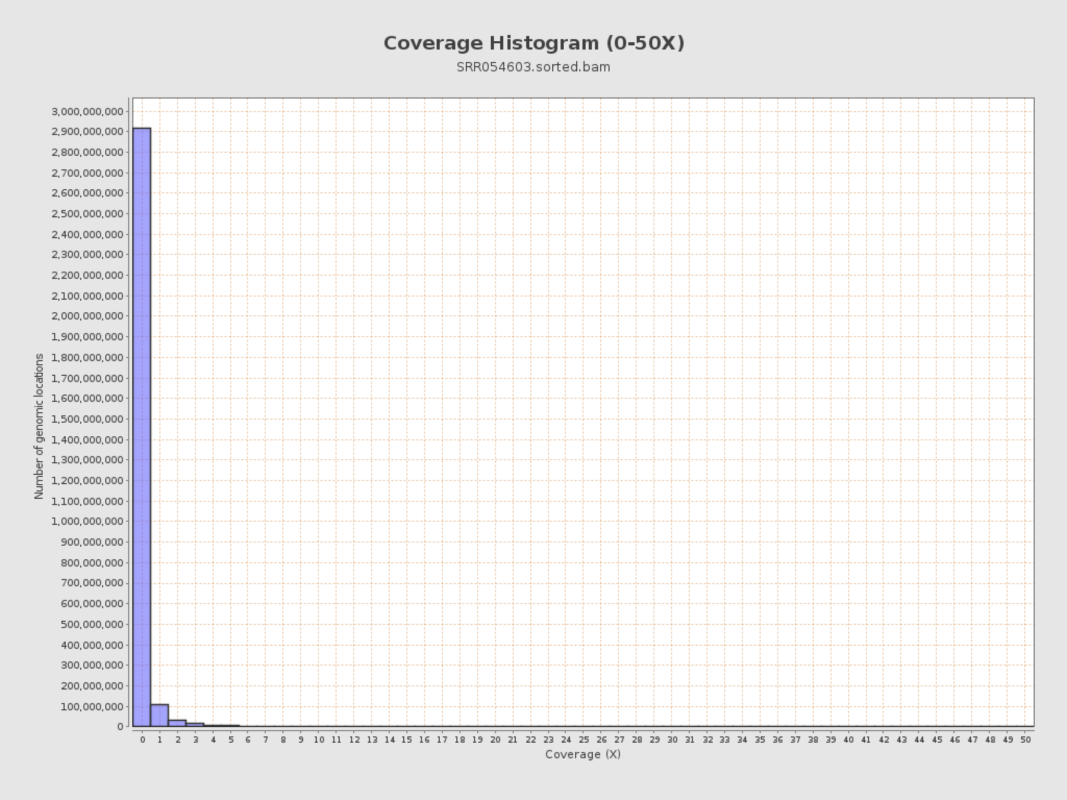
3. Results : Coverage across reference



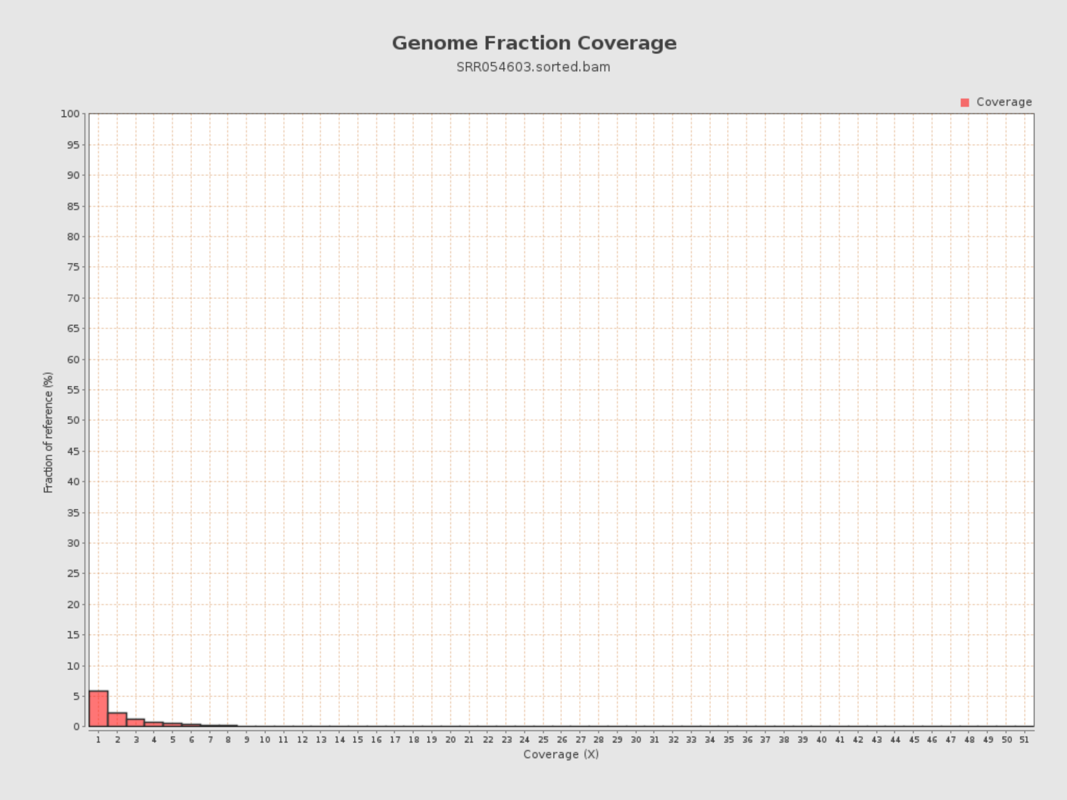
4. Results : Coverage Histogram



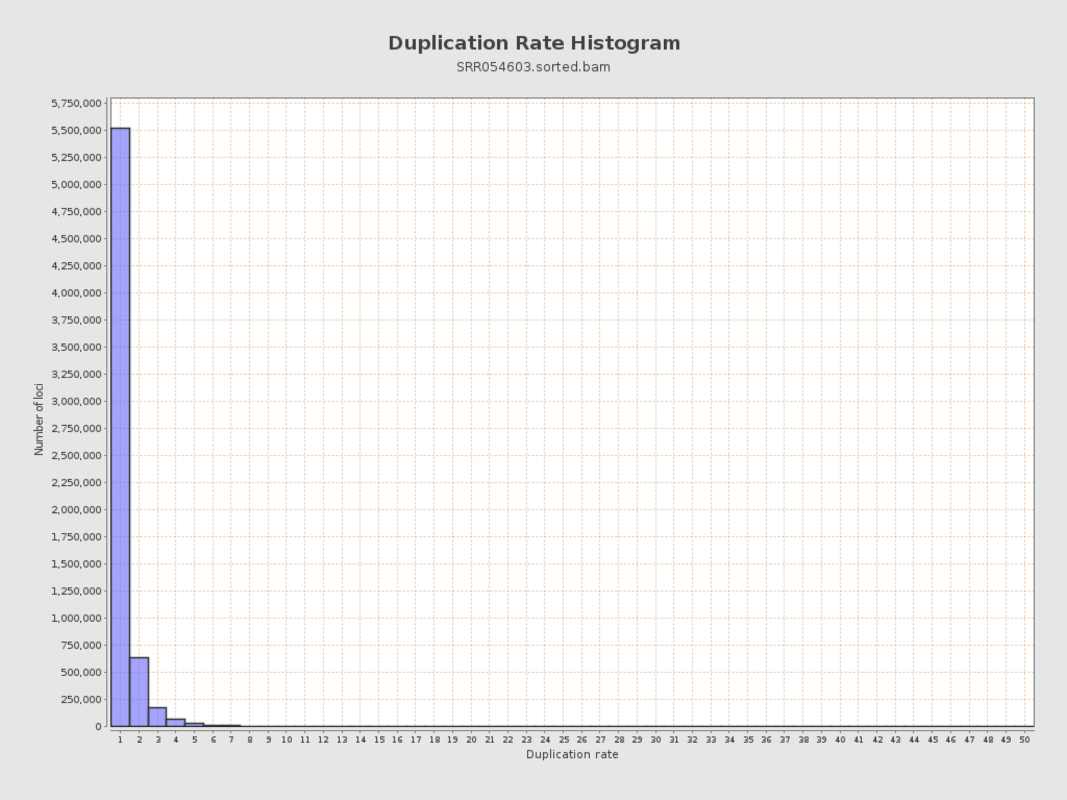
5. Results : Coverage Histogram (0-50X)



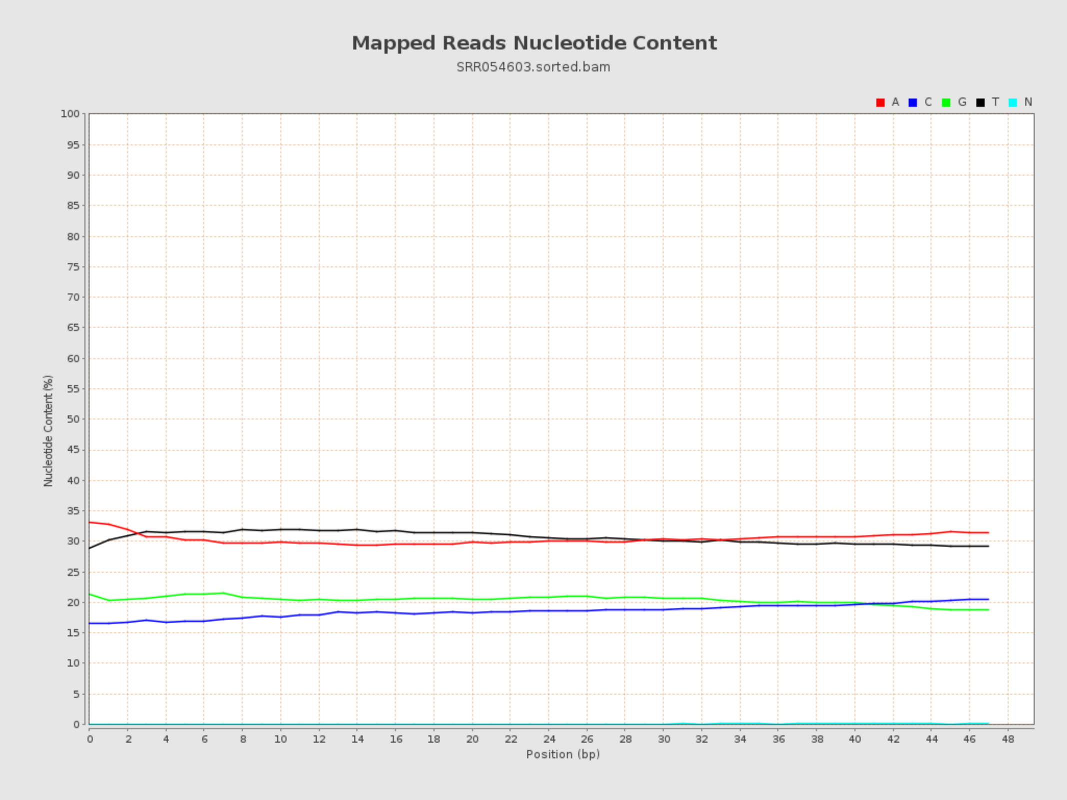
6. Results : Genome Fraction Coverage



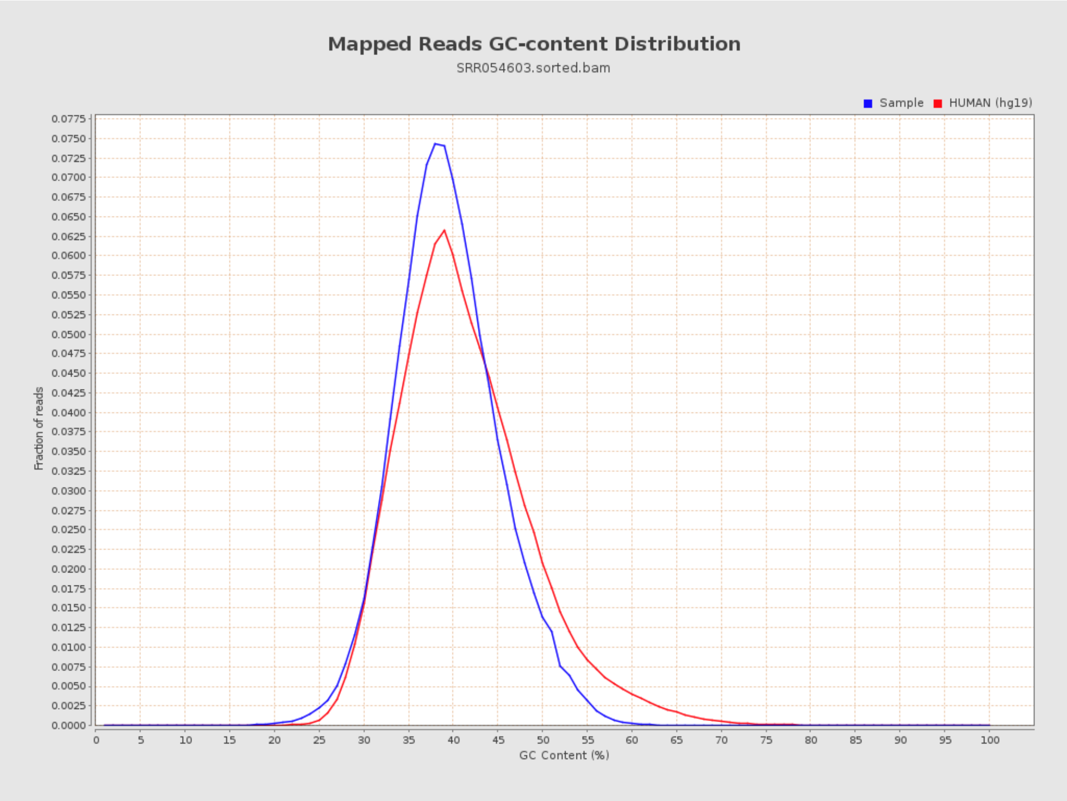
7. Results : Duplication Rate Histogram



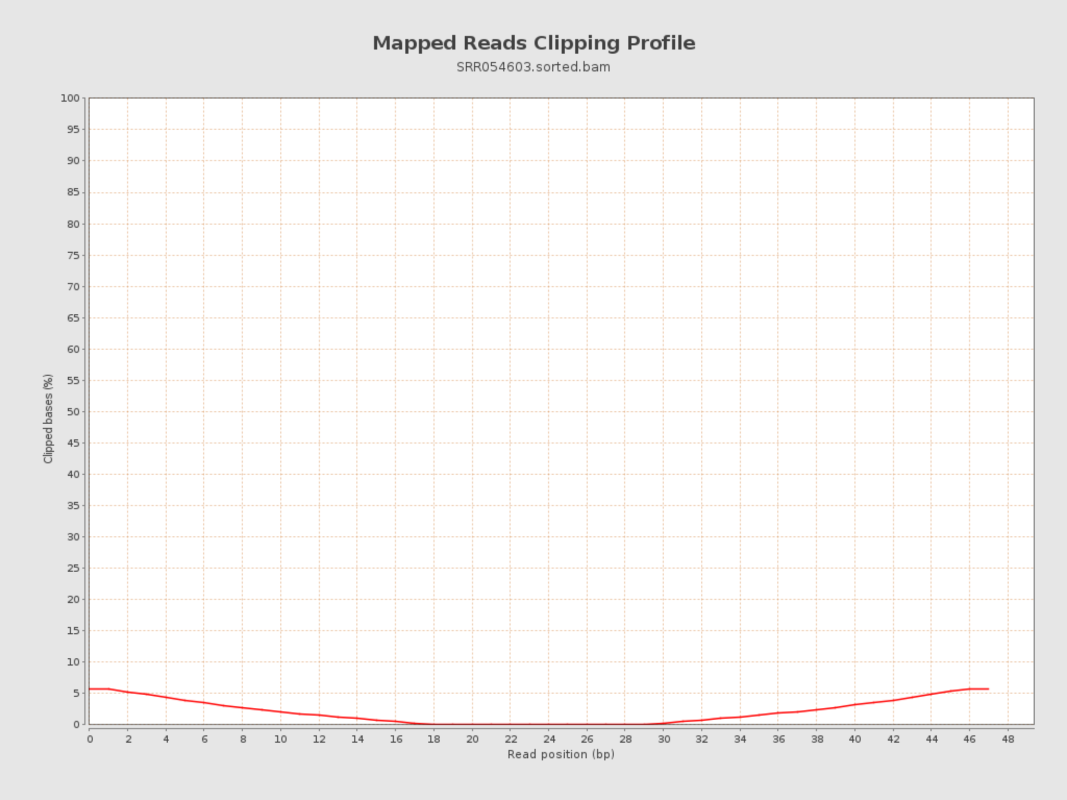
8. Results : Mapped Reads Nucleotide Content



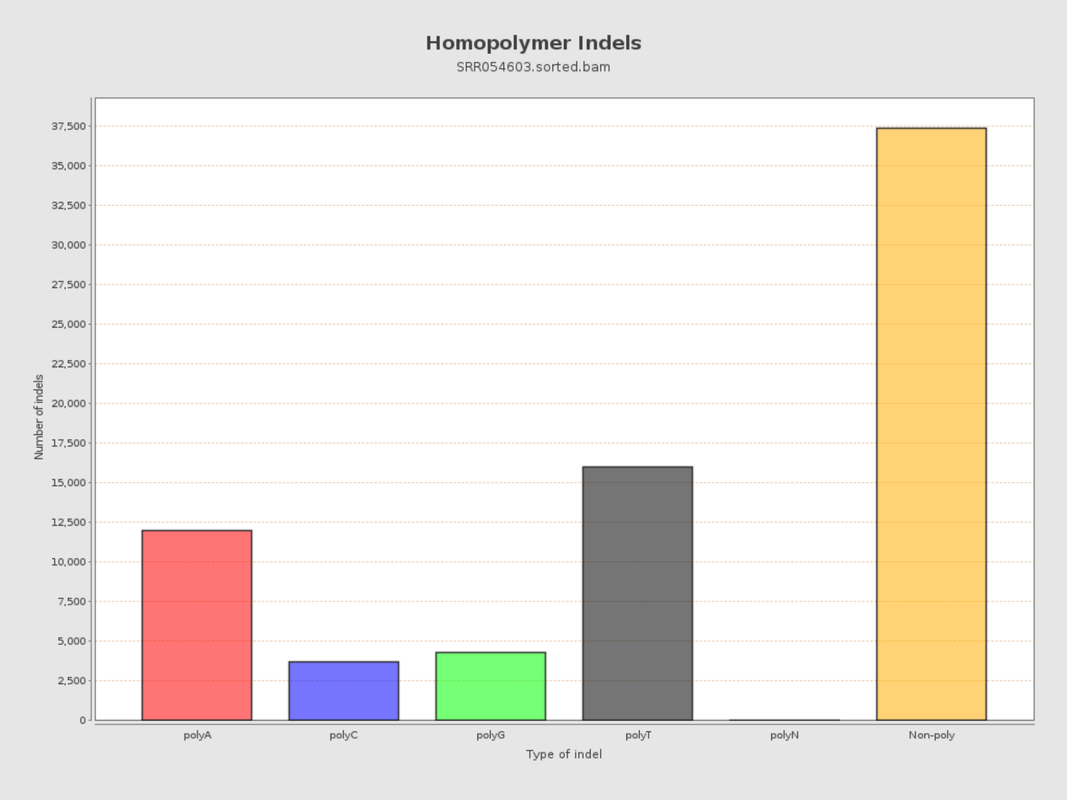
9. Results : Mapped Reads GC-content Distribution



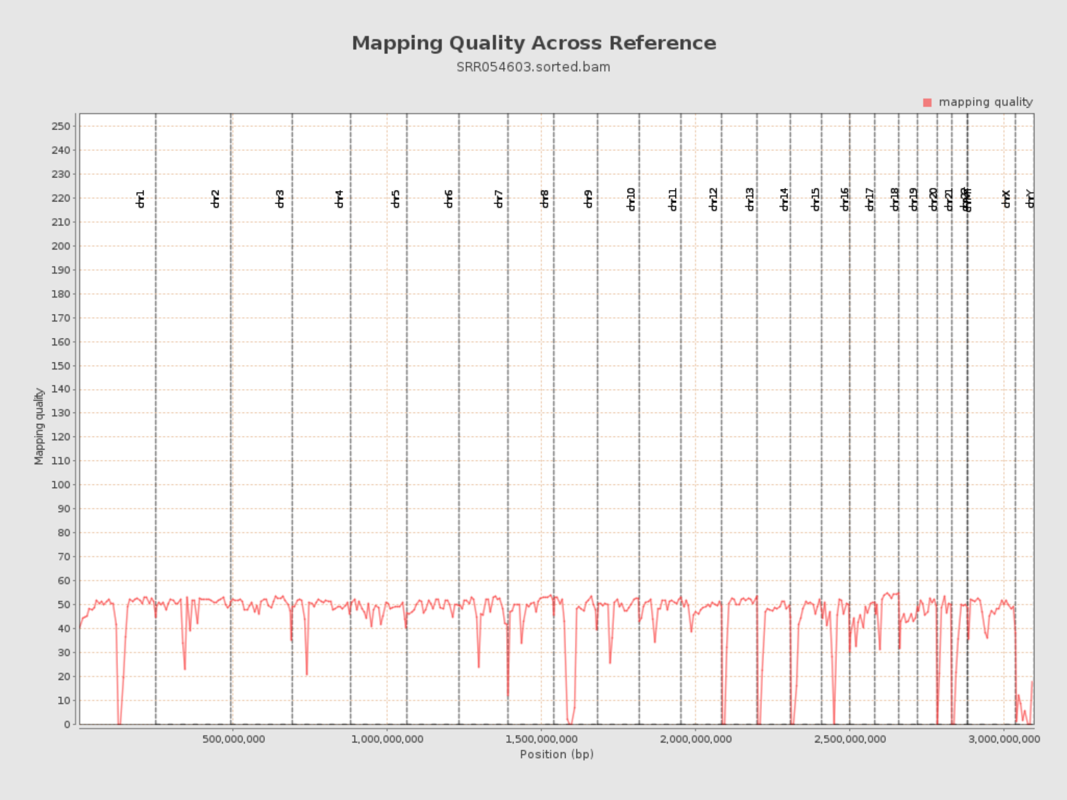
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram