Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:52:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054608.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_SRR054608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:52:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,218,012
Mapped reads	9,007,335 / 73.72%
Unmapped reads	3,210,677 / 26.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	197 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,862,753 / 15.25%
Duplication rate	14.95%
Clipped reads	664,596 / 5.44%

2.2. ACGT Content

Number/percentage of A's	129,708,810 / 30.41%
Number/percentage of C's	77,016,561 / 18.06%
Number/percentage of T's	135,033,064 / 31.66%
Number/percentage of G's	84,703,441 / 19.86%
Number/percentage of N's	3,228 / 0%
GC Percentage	37.92%

2.3. Coverage

Mean	0.1378

Standard Deviation	1.0224

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

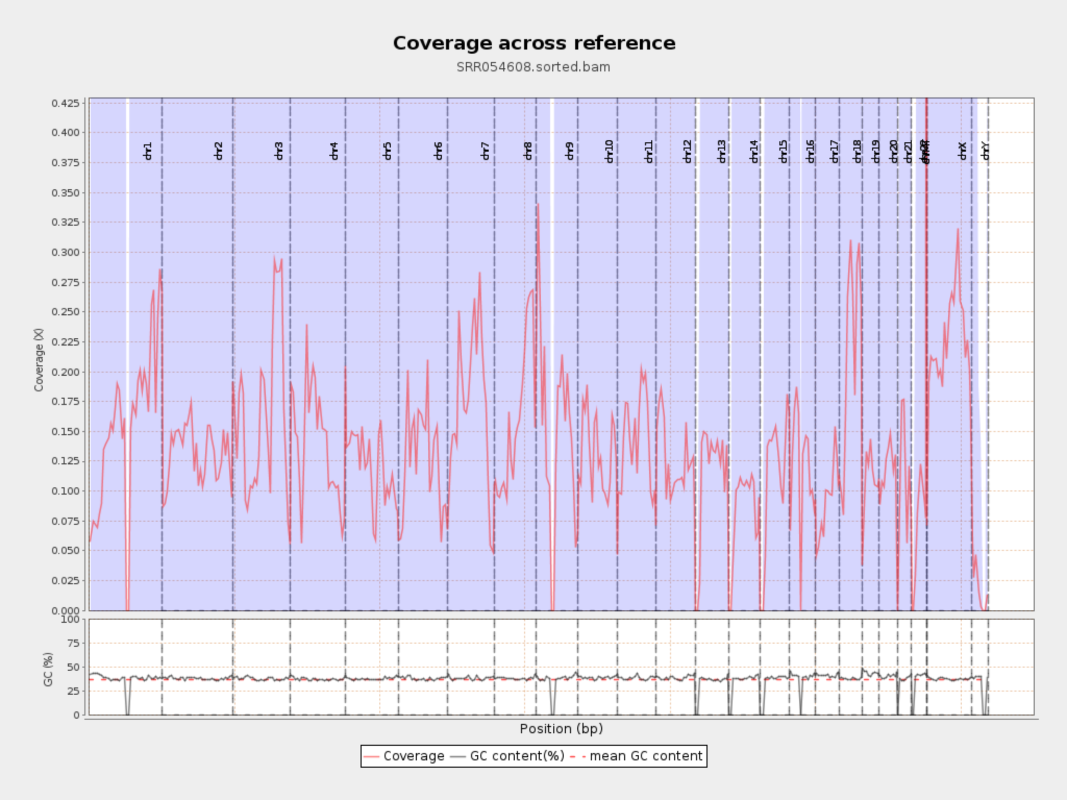
General error rate	0.55%
Mismatches	2,333,798
Insertions	17,567
Mapped reads with at least one insertion	0.19%
Deletions	60,402
Mapped reads with at least one deletion	0.67%
Homopolymer indels	49.92%

2.6. Chromosome stats

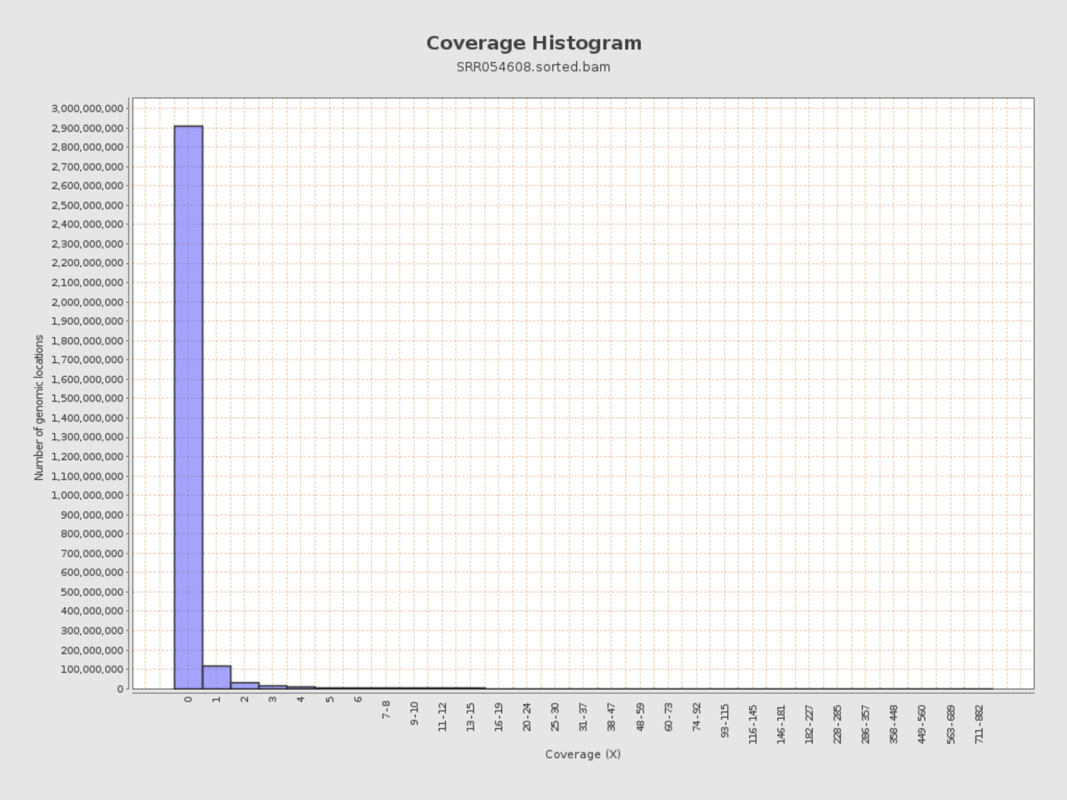
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38107630	0.1529	1.1481
chr2	243199373	32021699	0.1317	1.048
chr3	198022430	32663808	0.165	1.0555
chr4	191154276	26549522	0.1389	0.9952
chr5	180915260	21840739	0.1207	0.8489
chr6	171115067	21302094	0.1245	0.9586
chr7	159138663	27839244	0.1749	1.2357

chr8	146364022	23674730	0.1618	1.1383
chr9	141213431	21446215	0.1519	1.0762
chr10	135534747	18105236	0.1336	1.0309
chr11	135006516	19176361	0.142	1.0226
chr12	133851895	16804576	0.1255	0.8727
chr13	115169878	12861524	0.1117	0.8279
chr14	107349540	8825259	0.0822	0.8506
chr15	102531392	11358653	0.1108	0.8032
chr16	90354753	10866112	0.1203	0.9214
chr17	81195210	7475330	0.0921	0.7097
chr18	78077248	16832396	0.2156	1.3829
chr19	59128983	6638092	0.1123	0.9729
chr20	63025520	7424394	0.1178	0.8647
chr21	48129895	5199816	0.108	0.9019
chr22	51304566	3485586	0.0679	0.5676
chrMT	16571	34901	2.1061	4.8985
chrX	155270560	34909148	0.2248	1.3848
chrY	59373566	1110336	0.0187	0.3805

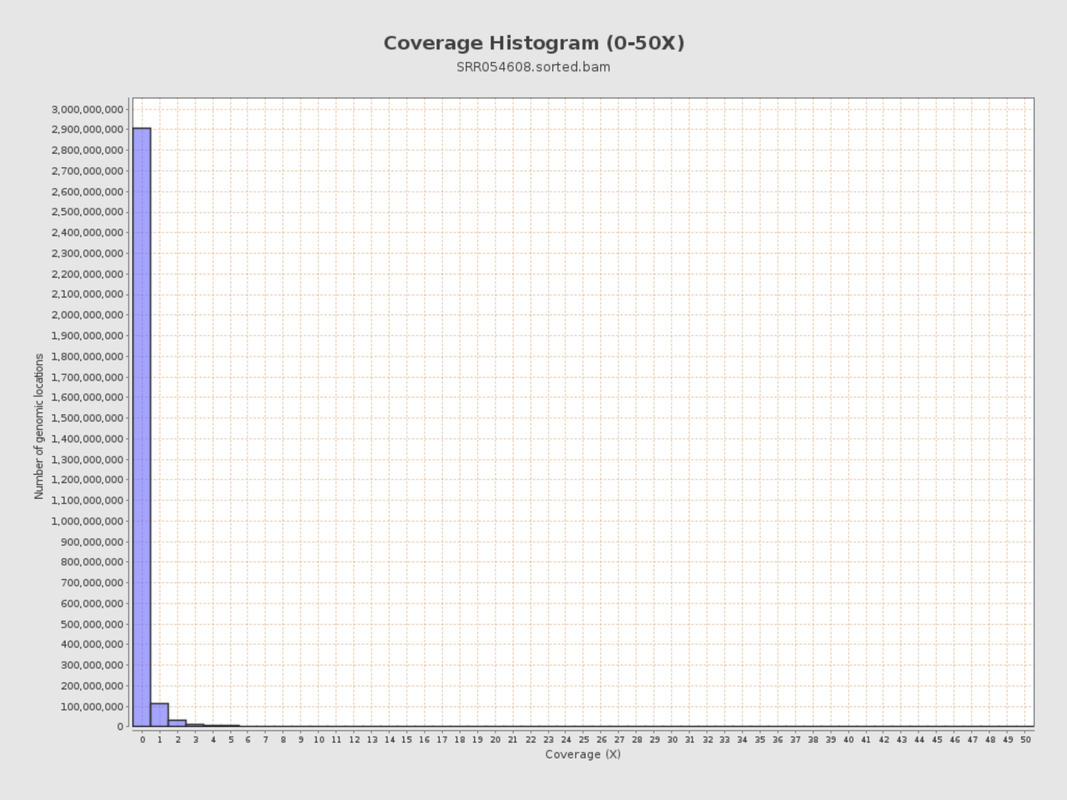
3. Results : Coverage across reference



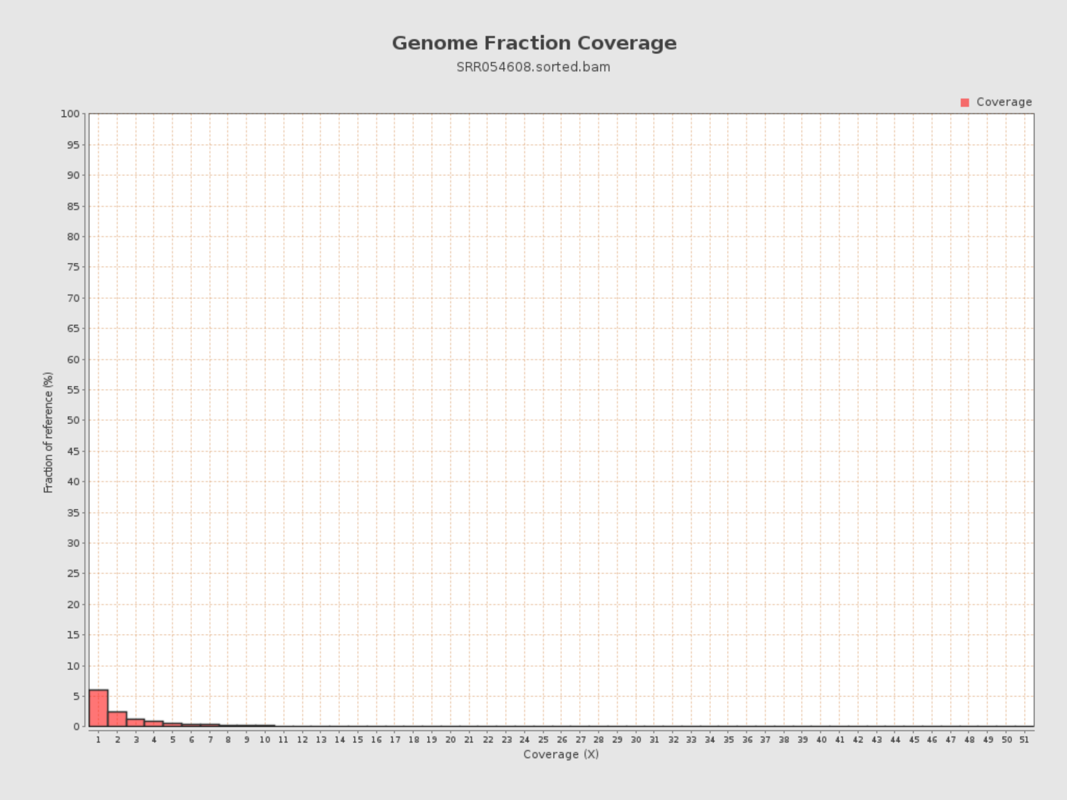
4. Results : Coverage Histogram



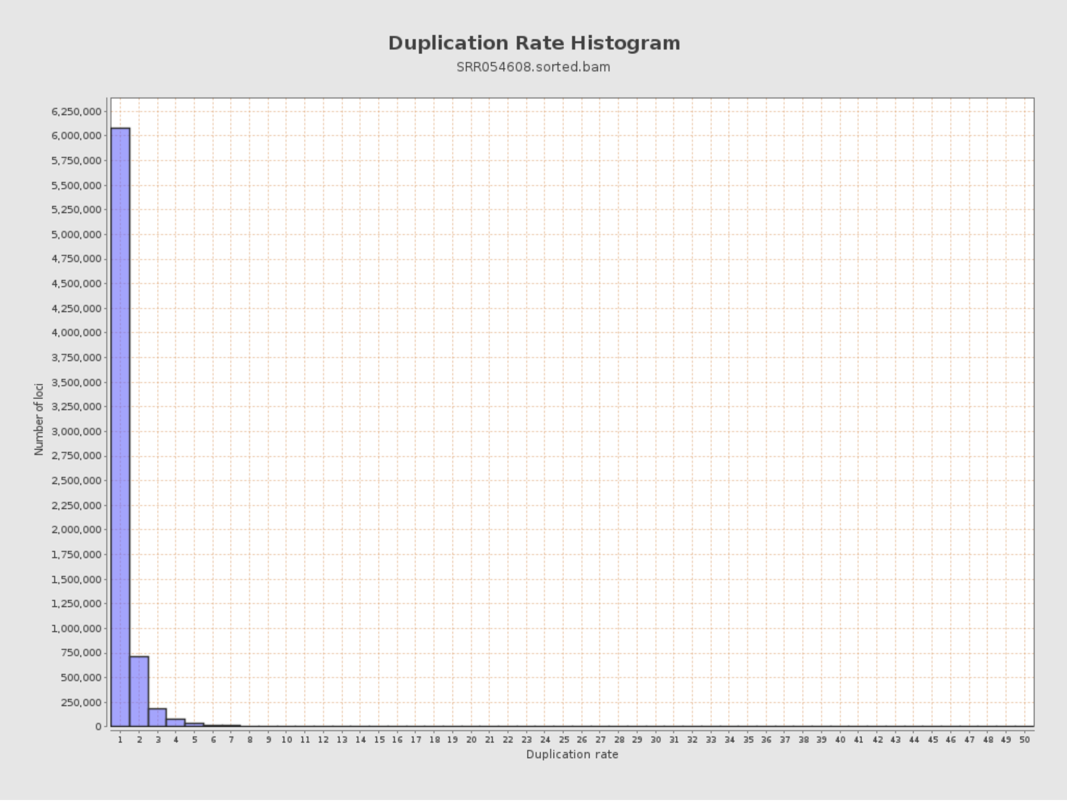
5. Results : Coverage Histogram (0-50X)



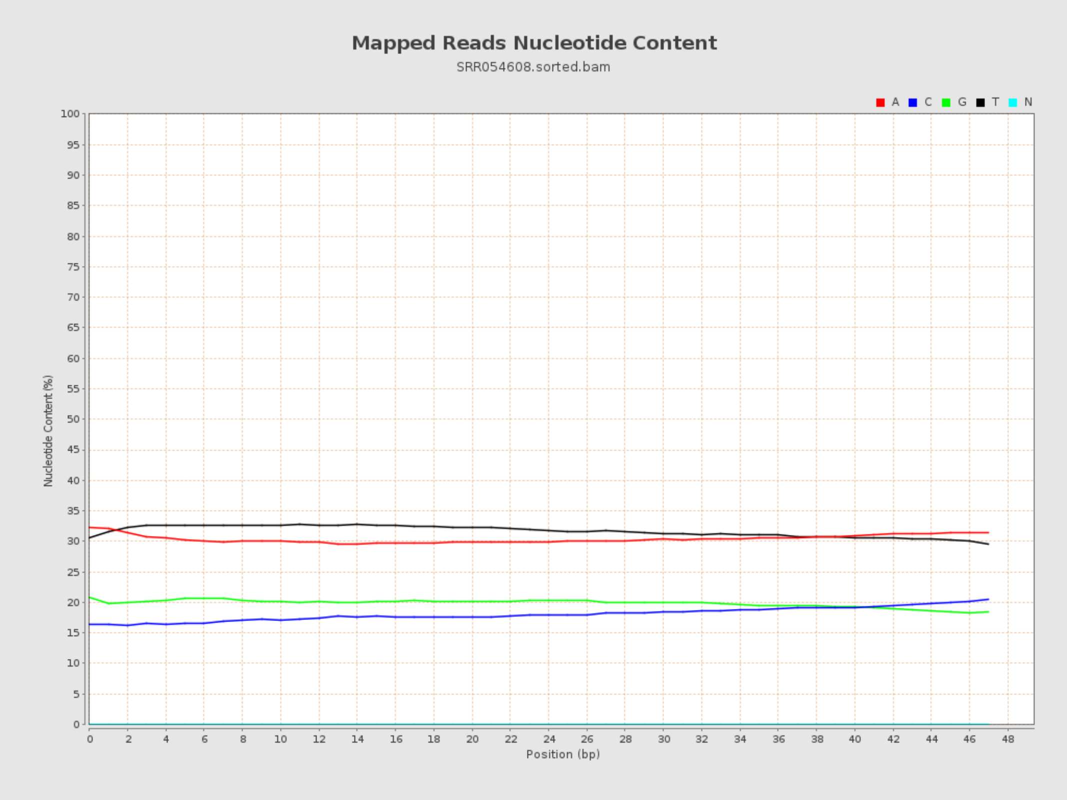
6. Results : Genome Fraction Coverage



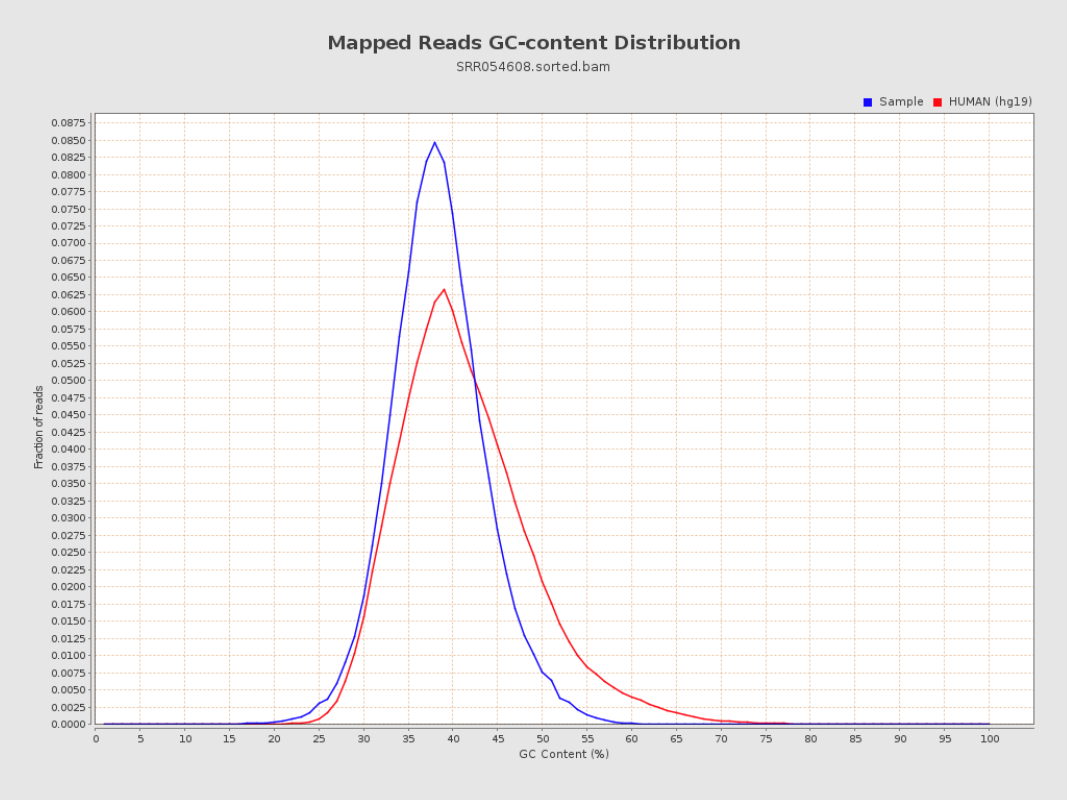
7. Results : Duplication Rate Histogram



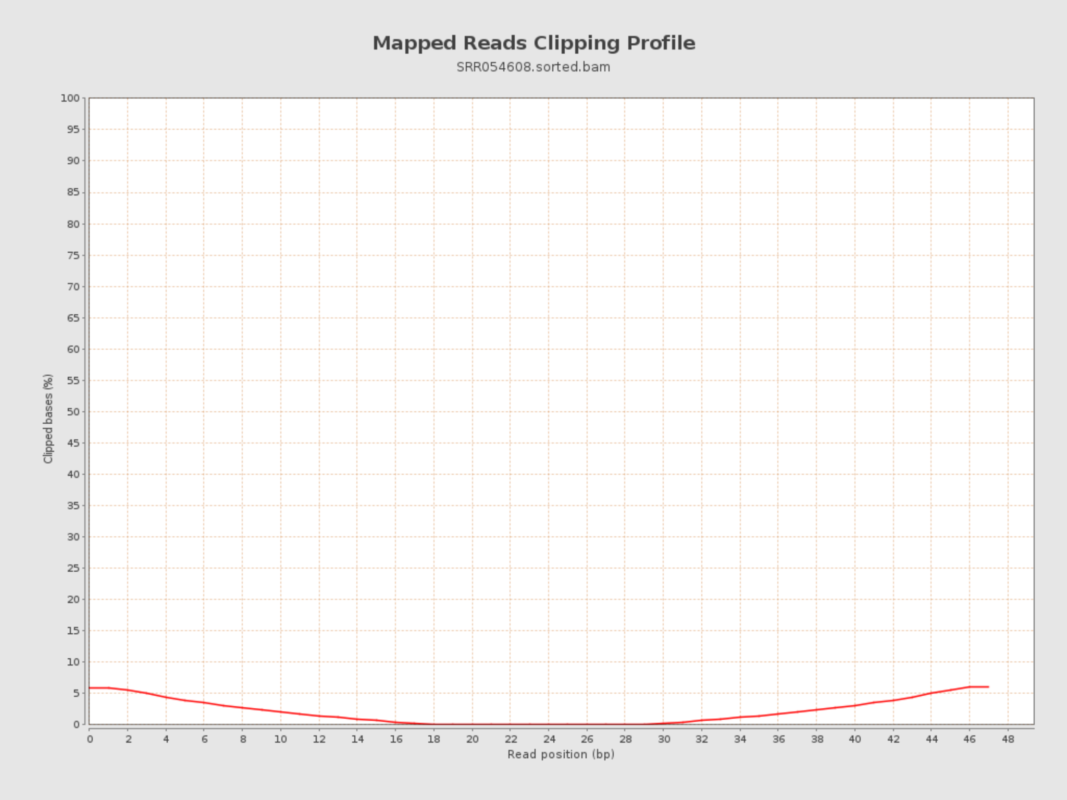
8. Results : Mapped Reads Nucleotide Content



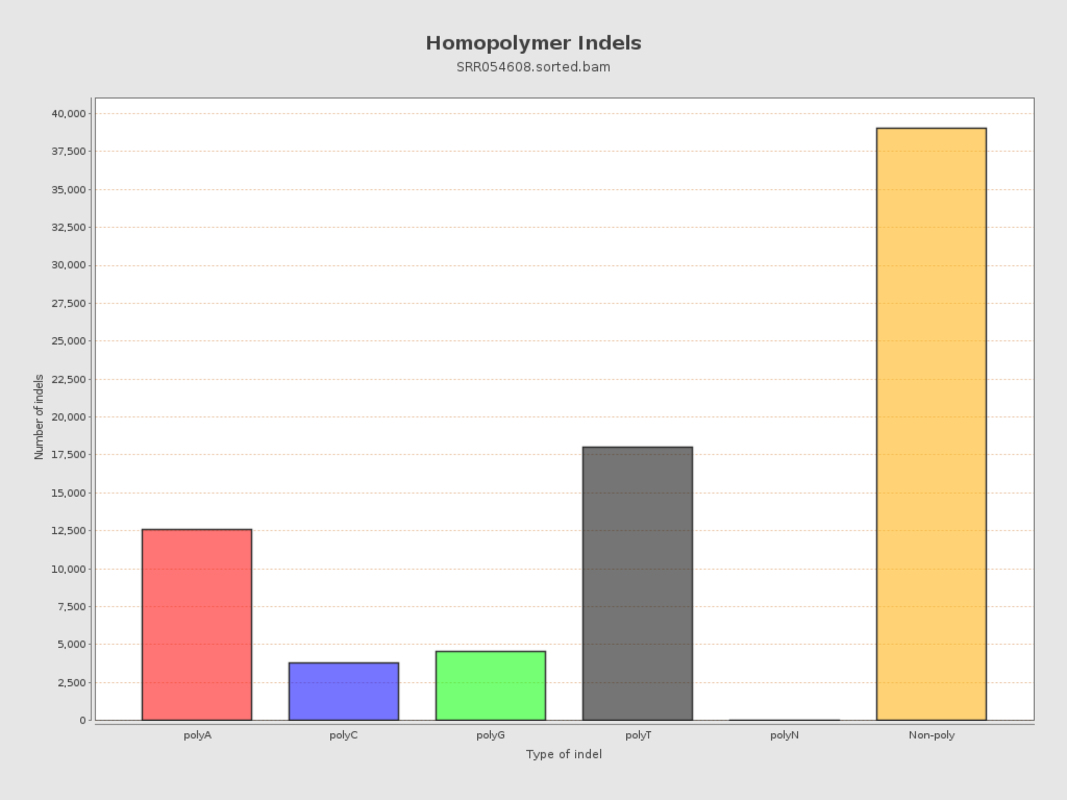
9. Results : Mapped Reads GC-content Distribution



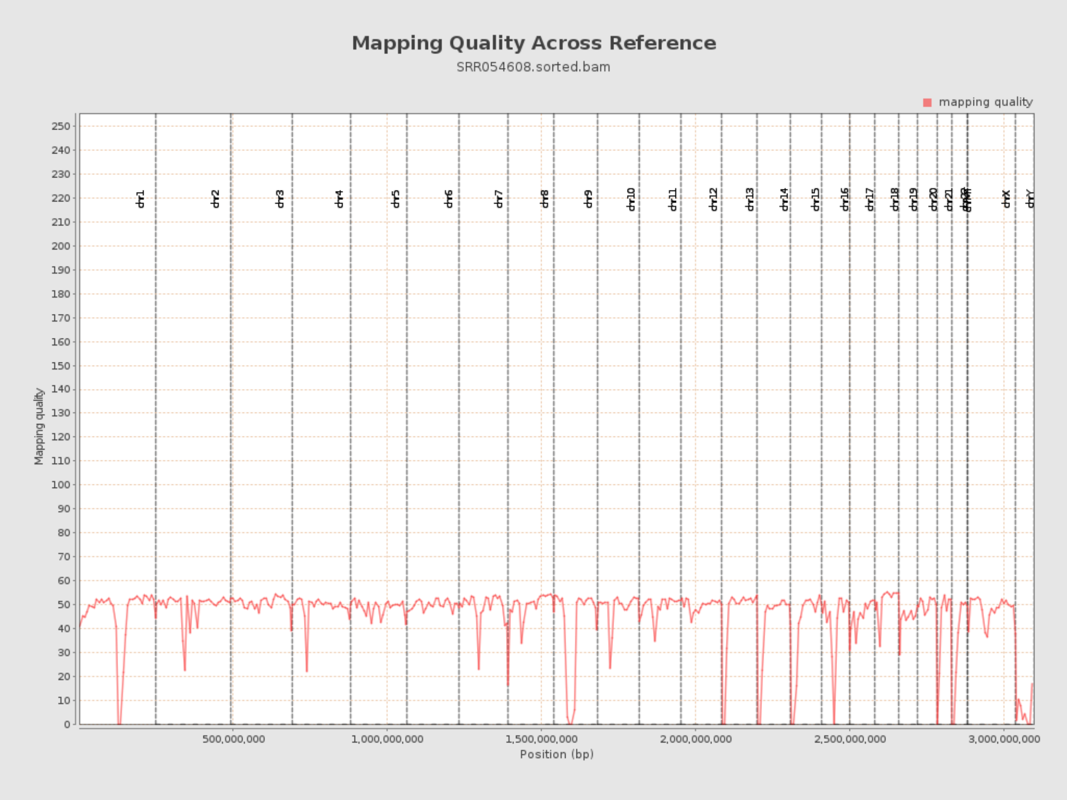
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram