Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 07:54:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054614.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_SRR054614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054614.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 07:54:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,536,473
Mapped reads	12,863,092 / 82.79%
Unmapped reads	2,673,381 / 17.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	359 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,642,579 / 23.45%
Duplication rate	19.37%
Clipped reads	1,061,174 / 6.83%

2.2. ACGT Content

Number/percentage of A's	179,046,977 / 29.45%
Number/percentage of C's	119,334,790 / 19.63%
Number/percentage of T's	179,832,325 / 29.58%
Number/percentage of G's	129,662,736 / 21.33%
Number/percentage of N's	103,501 / 0.02%
GC Percentage	40.95%

2.3. Coverage

Mean	0.1964

Standard Deviation	1.4587

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

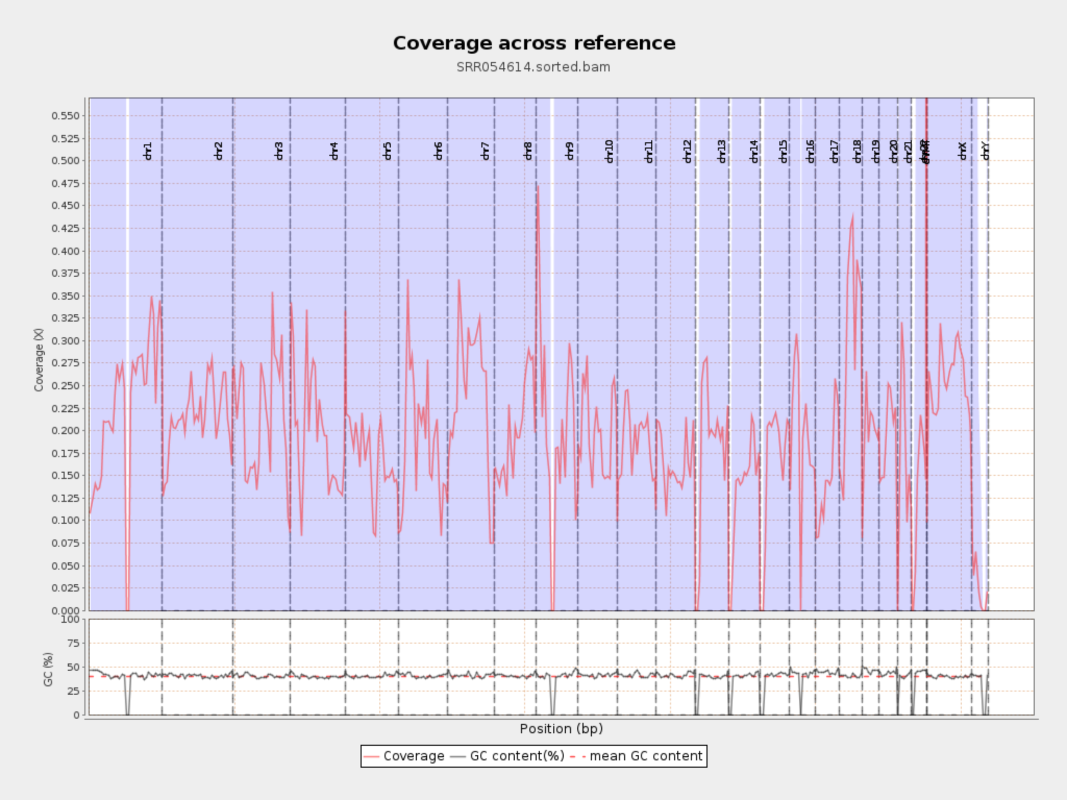
General error rate	0.48%
Mismatches	2,875,517
Insertions	23,613
Mapped reads with at least one insertion	0.18%
Deletions	83,510
Mapped reads with at least one deletion	0.65%
Homopolymer indels	46.72%

2.6. Chromosome stats

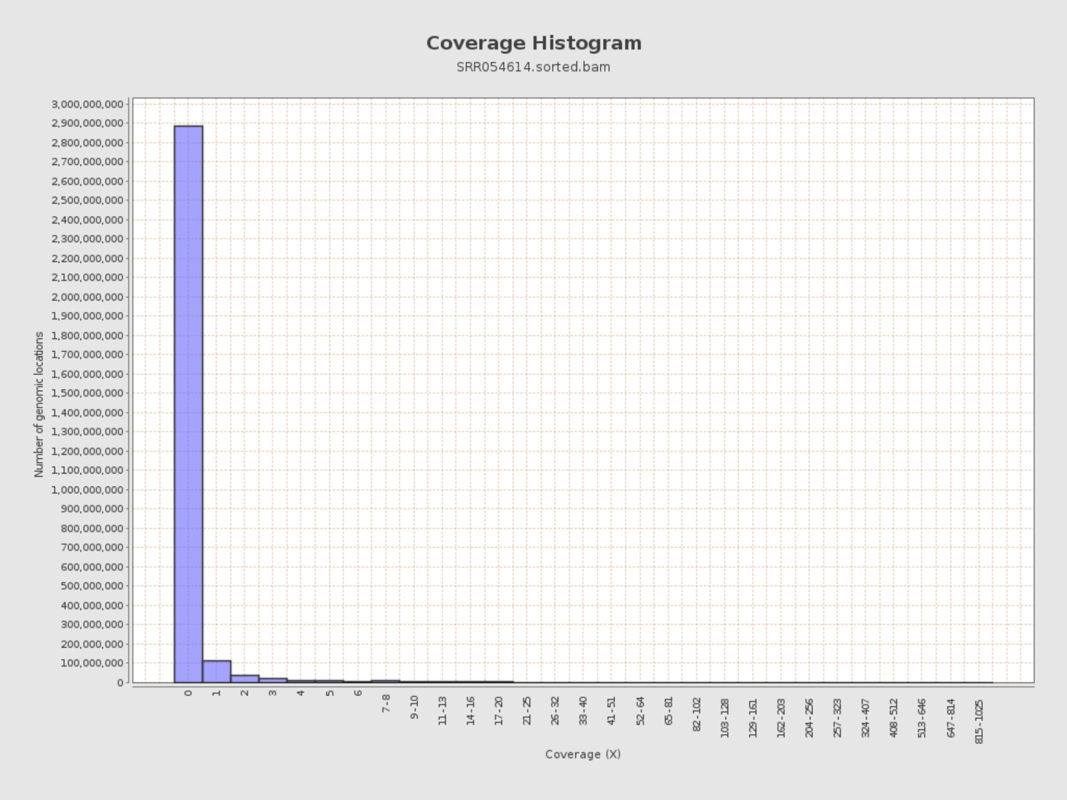
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55676325	0.2234	1.6767
chr2	243199373	52451332	0.2157	1.5989
chr3	198022430	42908209	0.2167	1.4708
chr4	191154276	37549179	0.1964	1.4221
chr5	180915260	31014275	0.1714	1.2186
chr6	171115067	31791814	0.1858	1.4197
chr7	159138663	39202357	0.2463	1.7309

chr8	146364022	29453274	0.2012	1.4558
chr9	141213431	28869287	0.2044	1.5171
chr10	135534747	27180101	0.2005	1.4498
chr11	135006516	25348264	0.1878	1.3963
chr12	133851895	21971804	0.1642	1.1998
chr13	115169878	20455479	0.1776	1.2872
chr14	107349540	14387756	0.134	1.1803
chr15	102531392	16341837	0.1594	1.1623
chr16	90354753	17660485	0.1955	1.454
chr17	81195210	12210506	0.1504	1.0995
chr18	78077248	23722270	0.3038	1.9672
chr19	59128983	11990731	0.2028	1.5311
chr20	63025520	12262211	0.1946	1.4531
chr21	48129895	8272051	0.1719	1.5584
chr22	51304566	6325228	0.1233	1.0231
chrMT	16571	41716	2.5174	6.0821
chrX	155270560	39529507	0.2546	1.6902
chrY	59373566	1489741	0.0251	0.5991

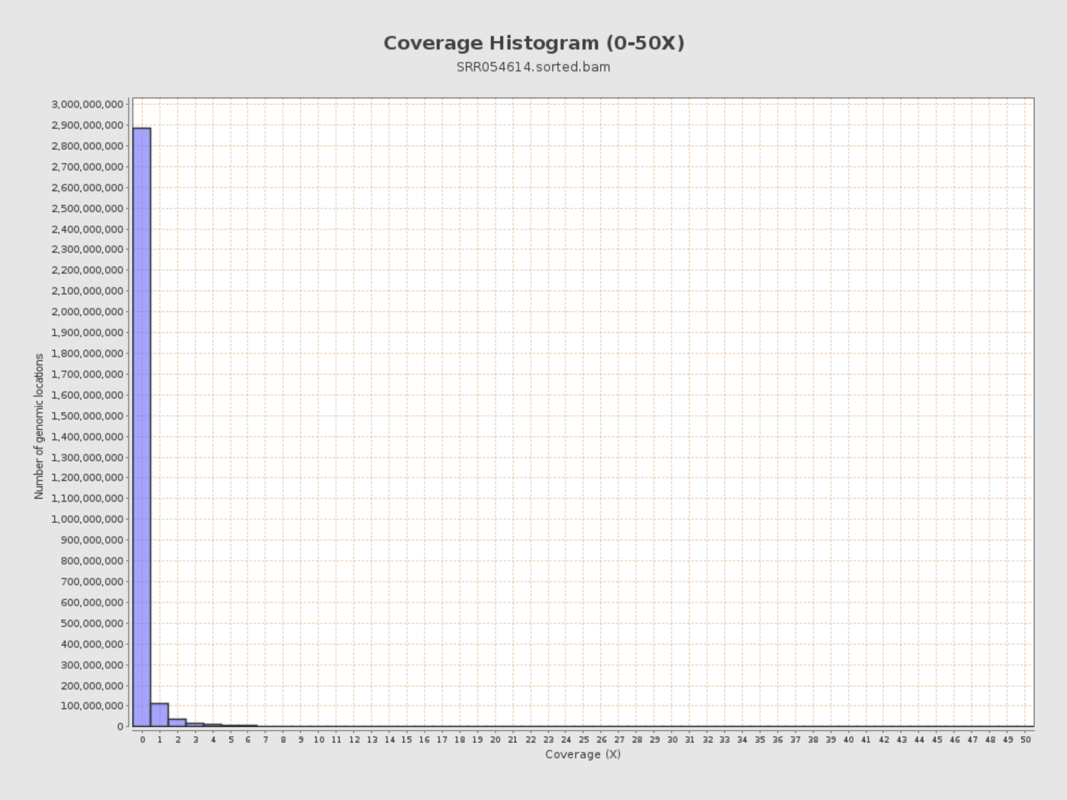
3. Results : Coverage across reference



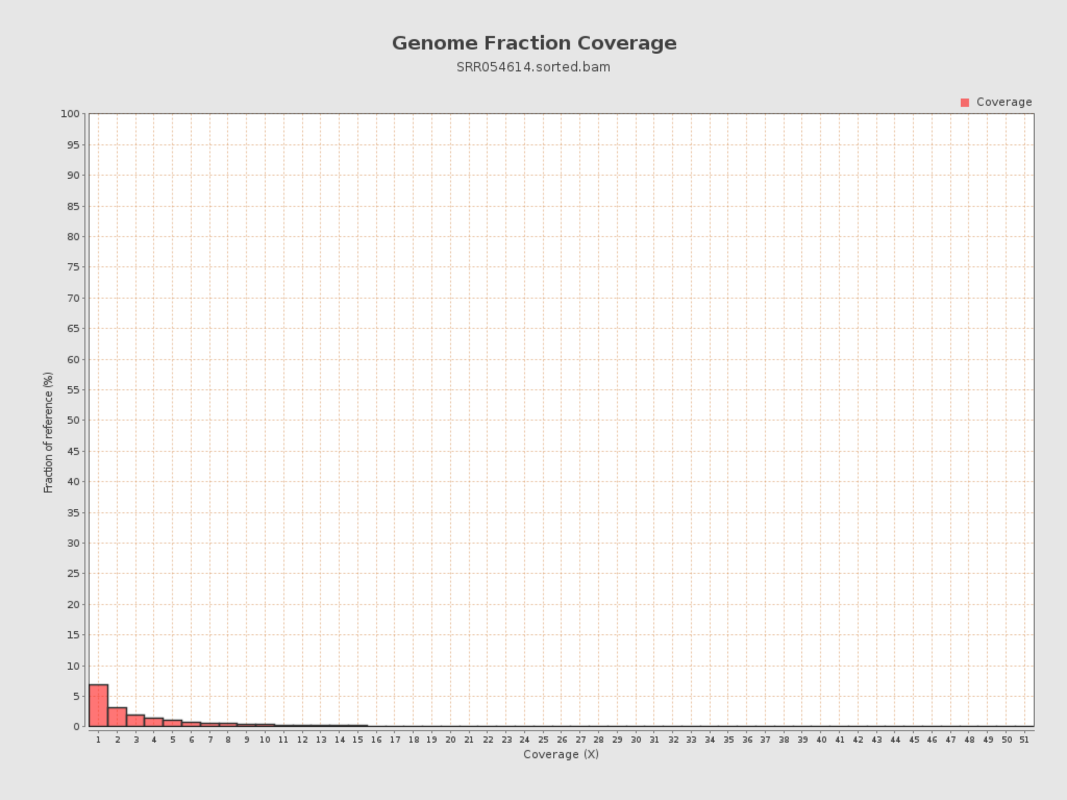
4. Results : Coverage Histogram



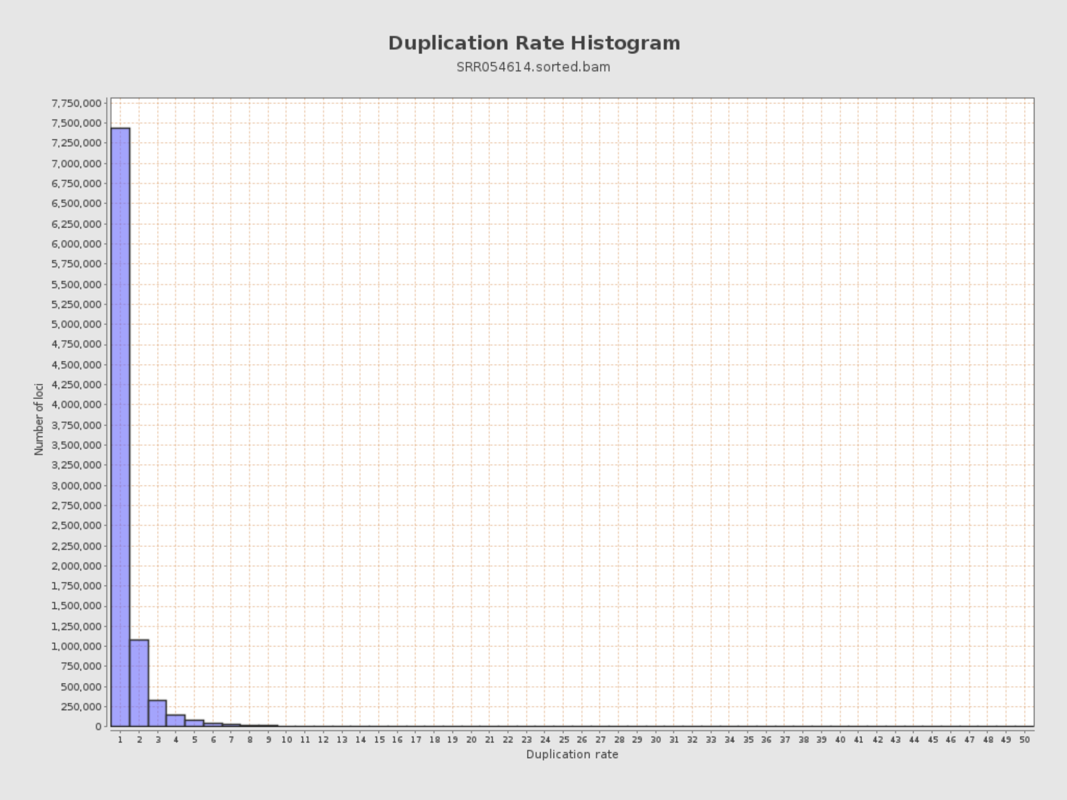
5. Results : Coverage Histogram (0-50X)



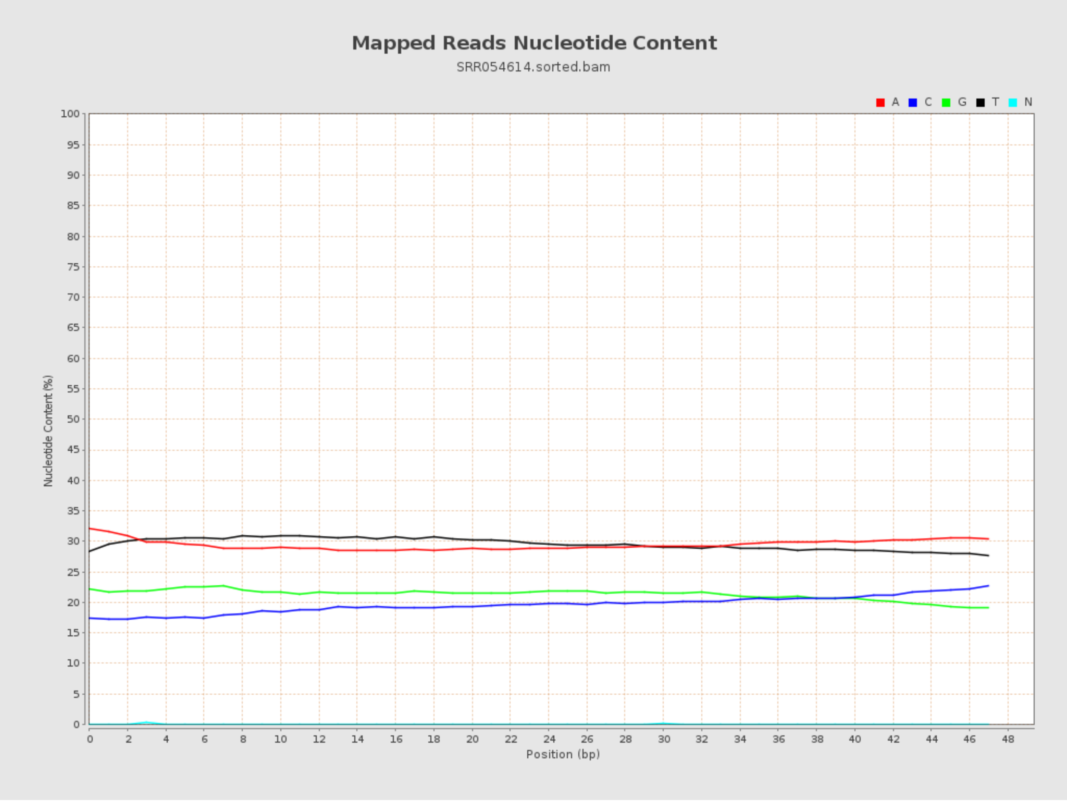
6. Results : Genome Fraction Coverage



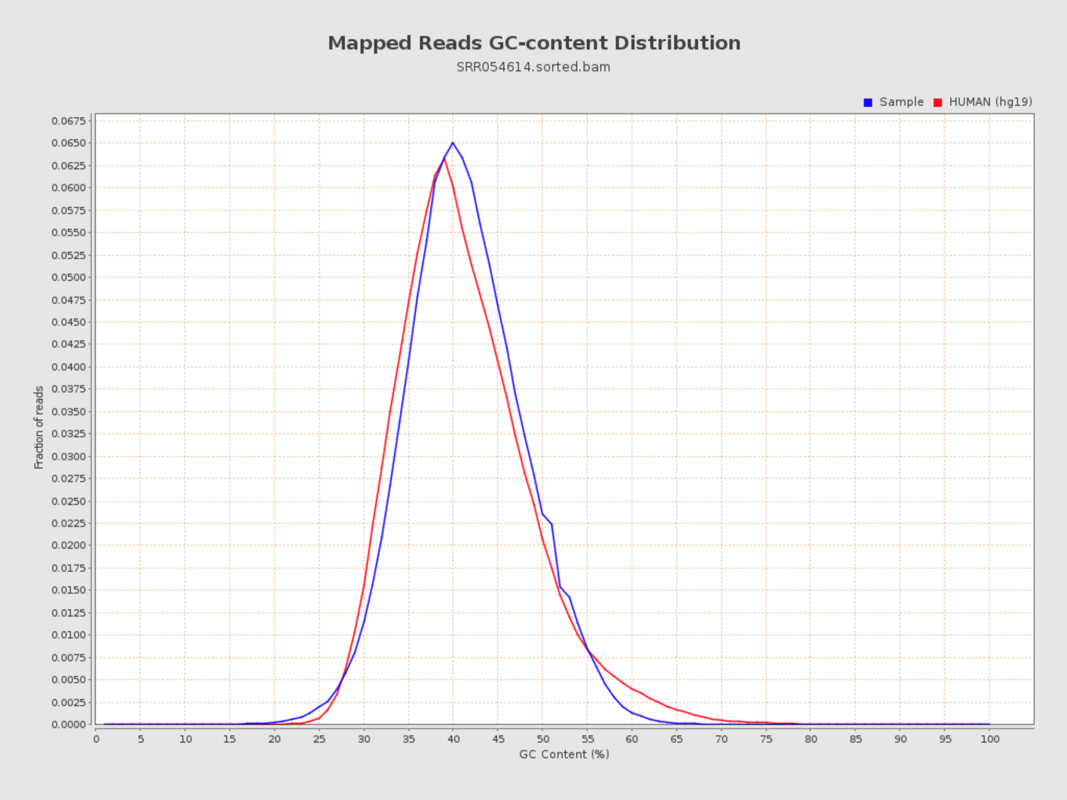
7. Results : Duplication Rate Histogram



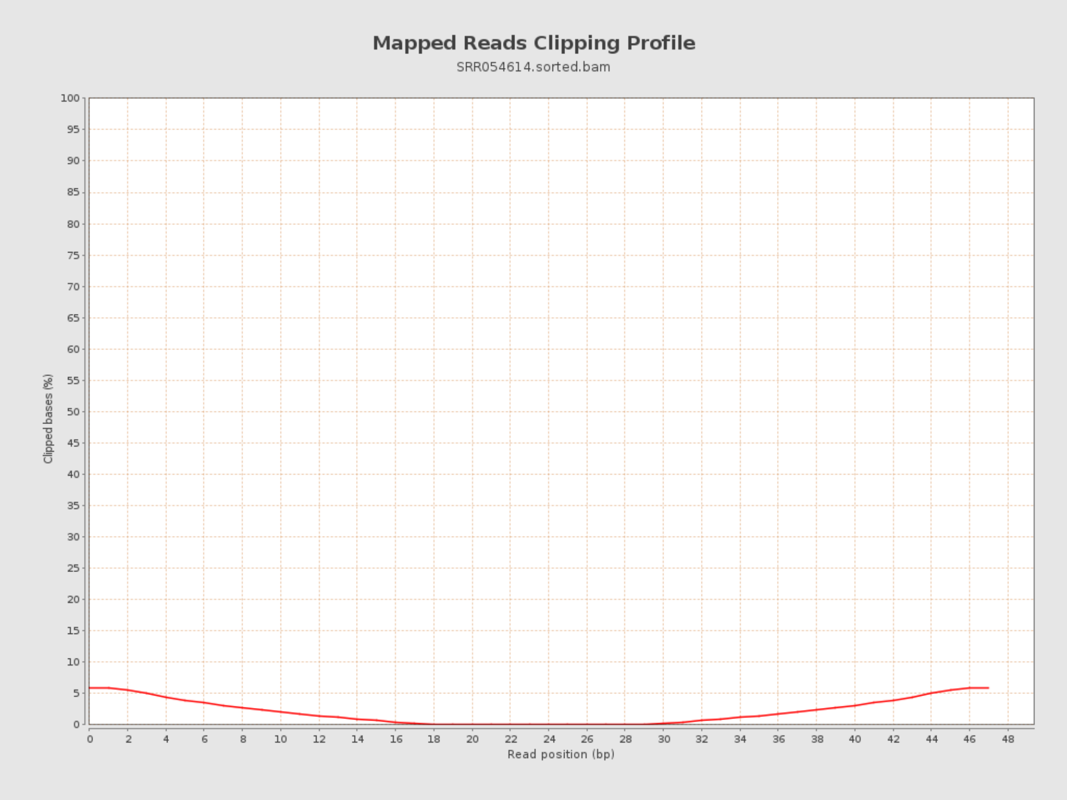
8. Results : Mapped Reads Nucleotide Content



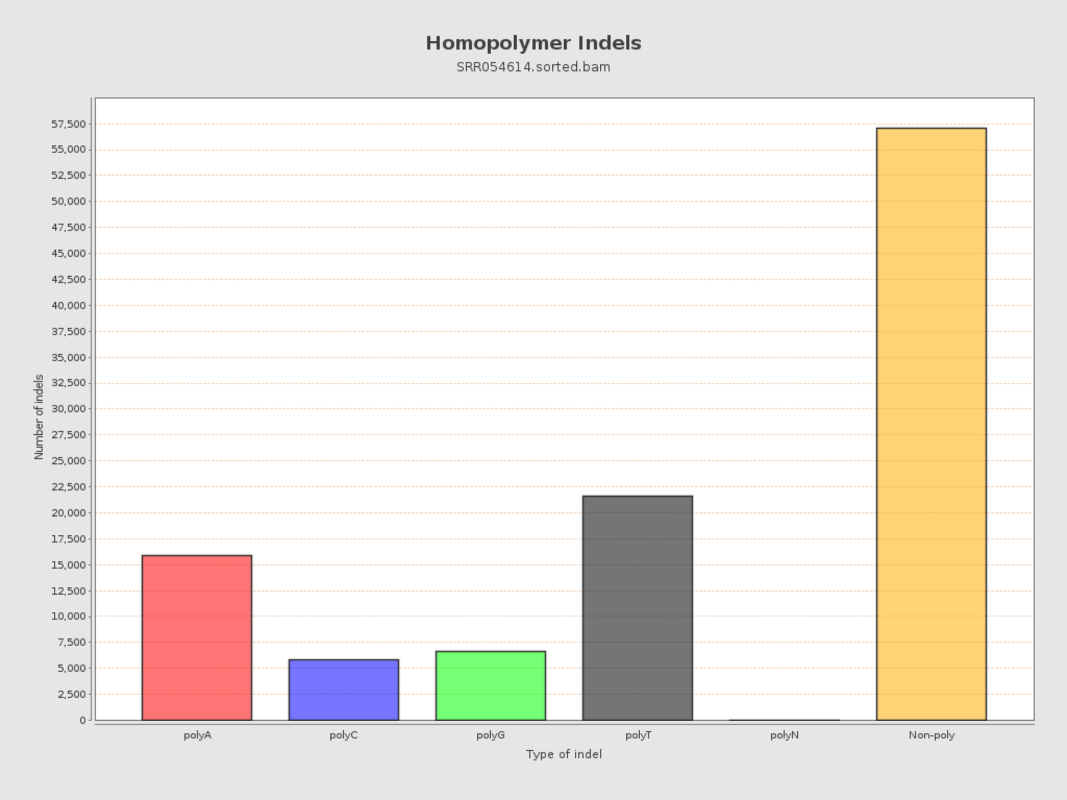
9. Results : Mapped Reads GC-content Distribution



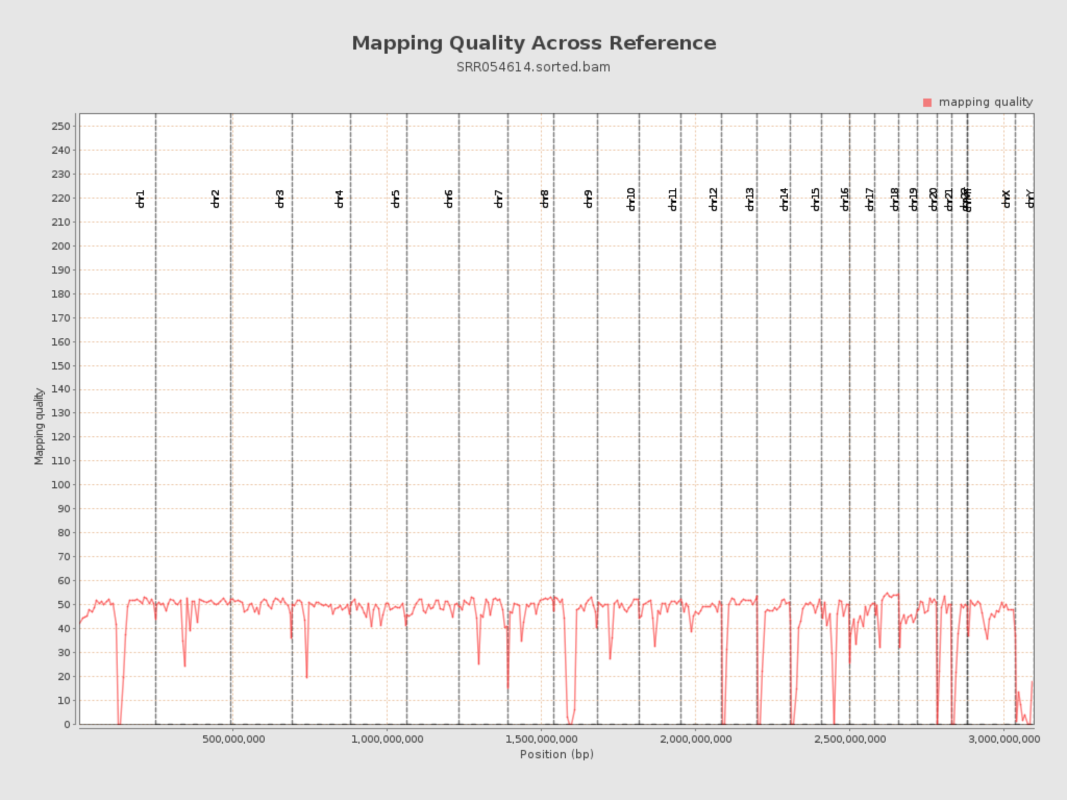
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram