Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:01:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053604.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_SRR053604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:01:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,084,818
Mapped reads	8,619,490 / 71.32%
Unmapped reads	3,465,328 / 28.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	241 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,434,714 / 20.15%
Duplication rate	20.11%
Clipped reads	748,167 / 6.19%

2.2. ACGT Content

Number/percentage of A's	119,496,887 / 29.35%
Number/percentage of C's	78,043,780 / 19.17%
Number/percentage of T's	122,005,469 / 29.96%
Number/percentage of G's	87,309,071 / 21.44%
Number/percentage of N's	313,982 / 0.08%
GC Percentage	40.61%

2.3. Coverage

Mean	0.1316

Standard Deviation	1.0224

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

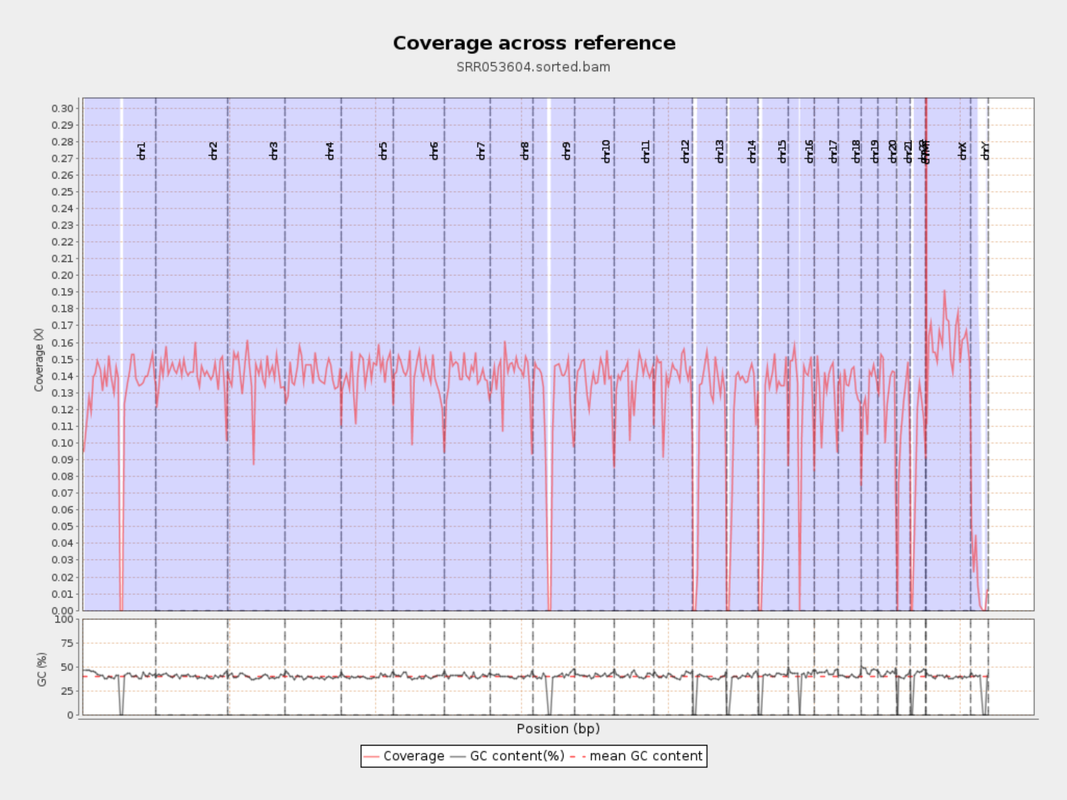
General error rate	0.68%
Mismatches	2,752,273
Insertions	17,977
Mapped reads with at least one insertion	0.21%
Deletions	54,282
Mapped reads with at least one deletion	0.63%
Homopolymer indels	47.81%

2.6. Chromosome stats

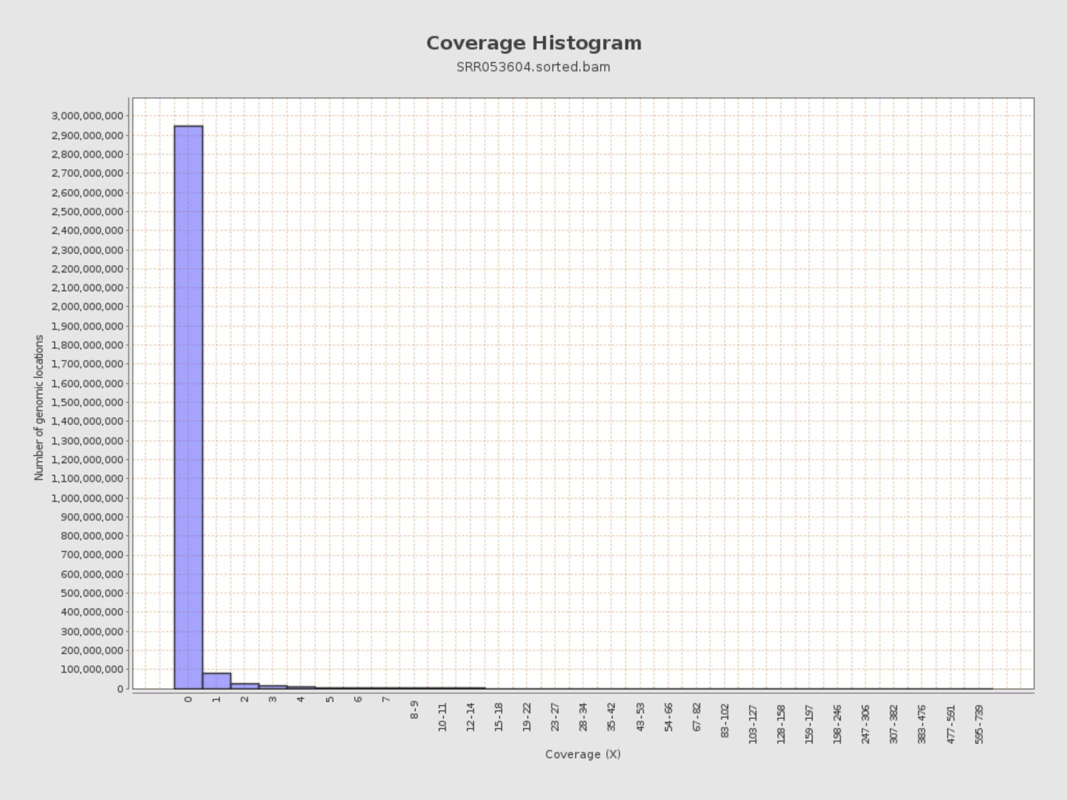
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32051539	0.1286	1.0649
chr2	243199373	34512110	0.1419	1.1774
chr3	198022430	27938750	0.1411	0.9832
chr4	191154276	27080386	0.1417	1.0185
chr5	180915260	25668796	0.1419	0.9918
chr6	171115067	23962285	0.14	1.0418
chr7	159138663	22278137	0.14	1.1604

chr8	146364022	20482804	0.1399	1.0498
chr9	141213431	16858374	0.1194	0.9635
chr10	135534747	18733480	0.1382	1.0507
chr11	135006516	18539180	0.1373	1.0562
chr12	133851895	18780354	0.1403	0.9782
chr13	115169878	13170334	0.1144	0.8987
chr14	107349540	12205996	0.1137	0.9976
chr15	102531392	11504858	0.1122	0.8676
chr16	90354753	11179629	0.1237	0.9586
chr17	81195210	10623996	0.1308	0.9377
chr18	78077248	10418225	0.1334	1.1125
chr19	59128983	7605067	0.1286	1.0507
chr20	63025520	8324228	0.1321	0.9696
chr21	48129895	5054940	0.105	0.9215
chr22	51304566	4366671	0.0851	0.7383
chrMT	16571	91355	5.5129	10.3325
chrX	155270560	24797098	0.1597	1.1203
chrY	59373566	1021872	0.0172	0.3585

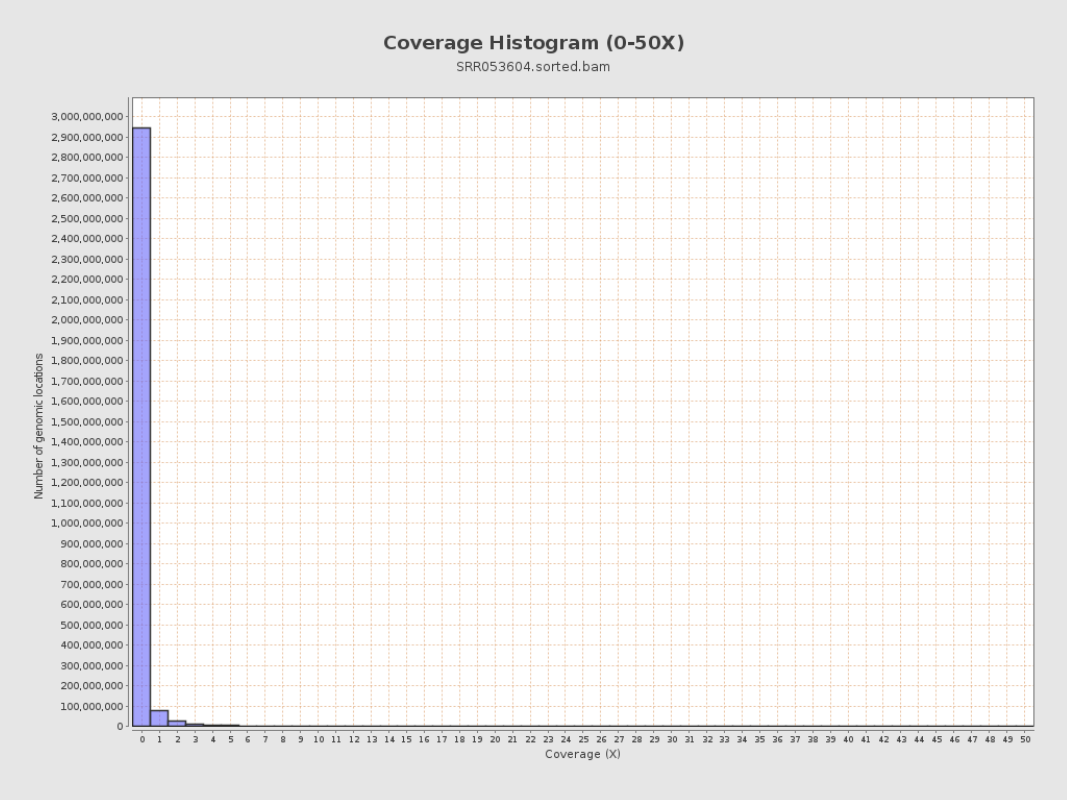
3. Results : Coverage across reference



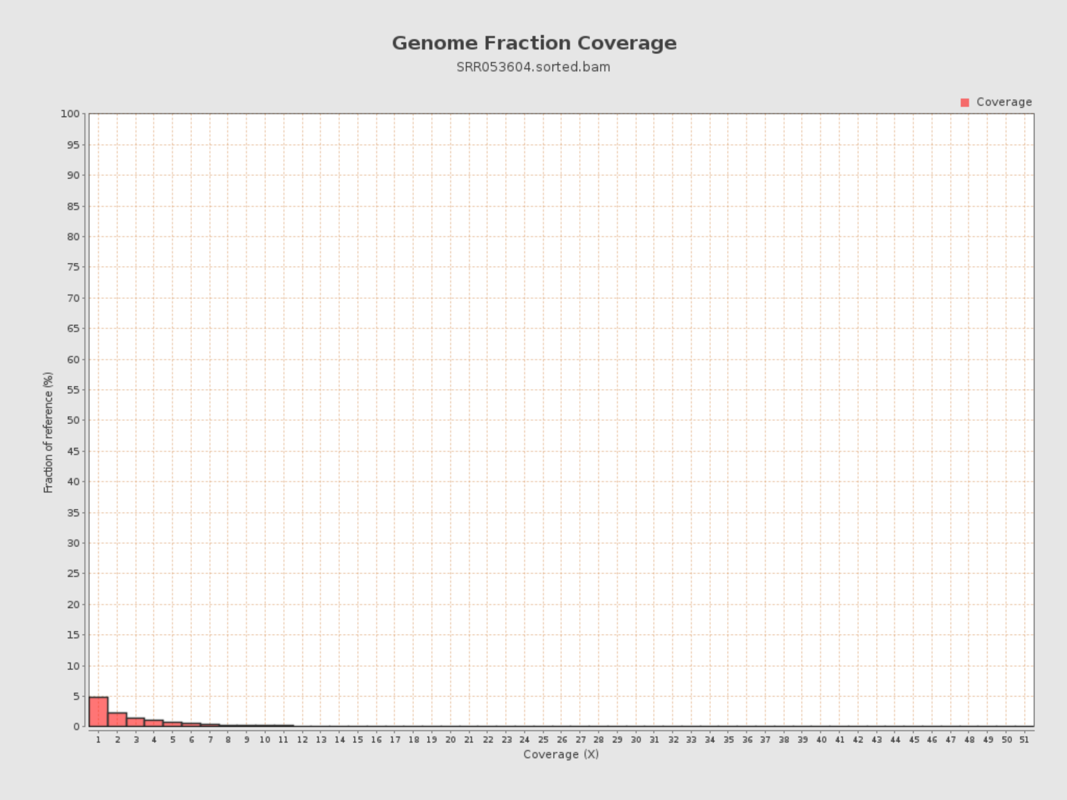
4. Results : Coverage Histogram



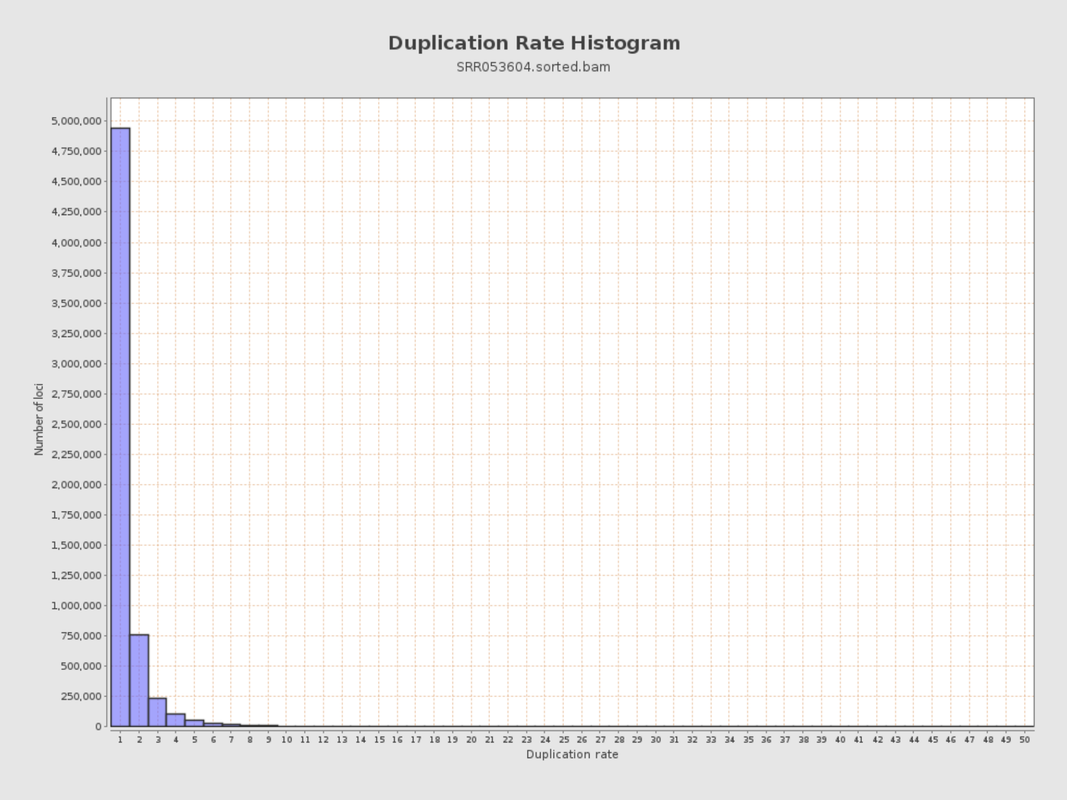
5. Results : Coverage Histogram (0-50X)



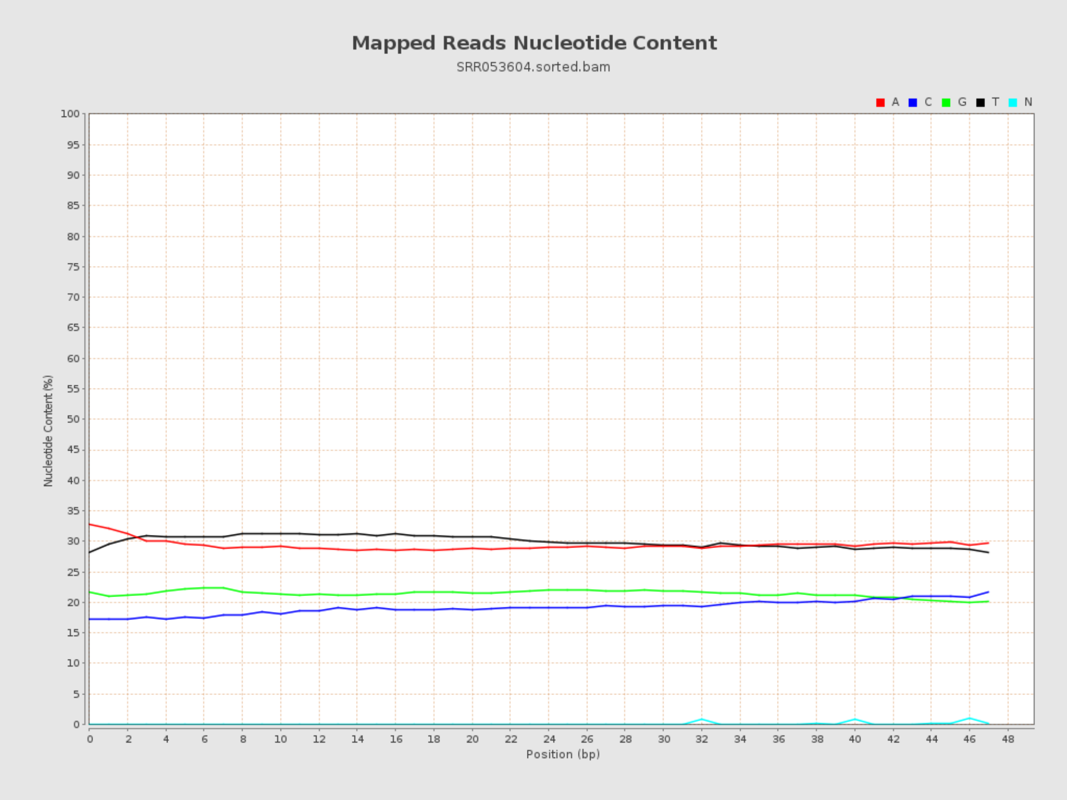
6. Results : Genome Fraction Coverage



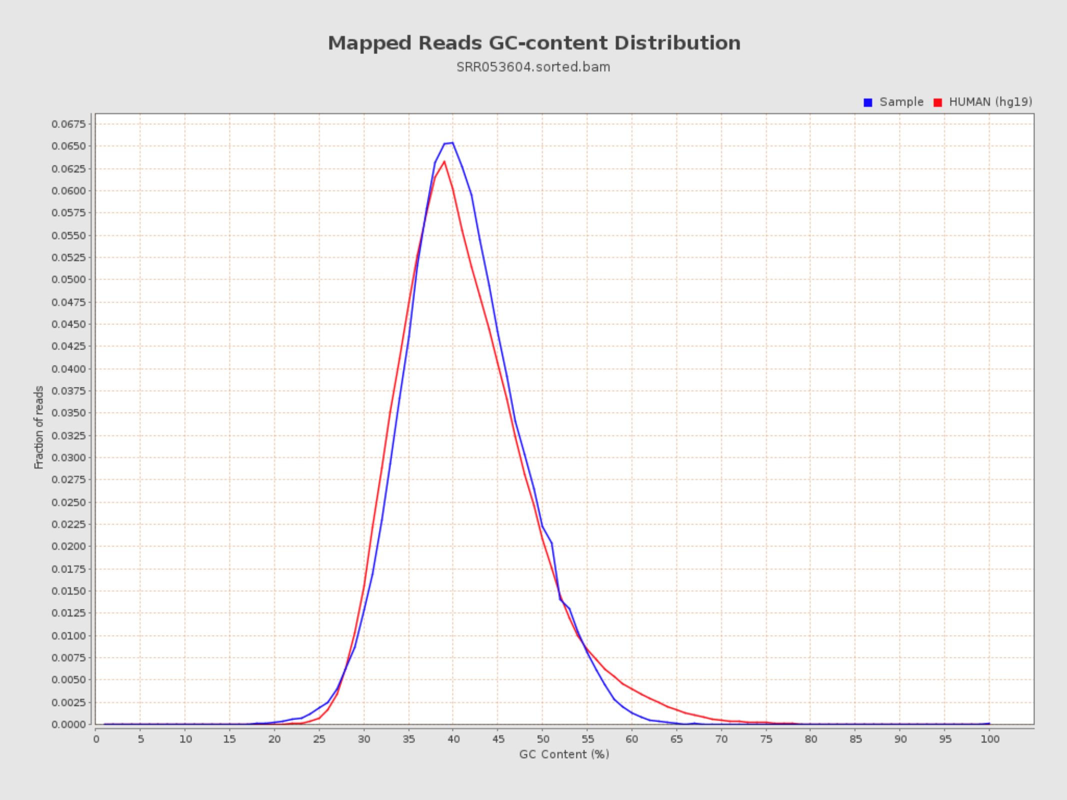
7. Results : Duplication Rate Histogram



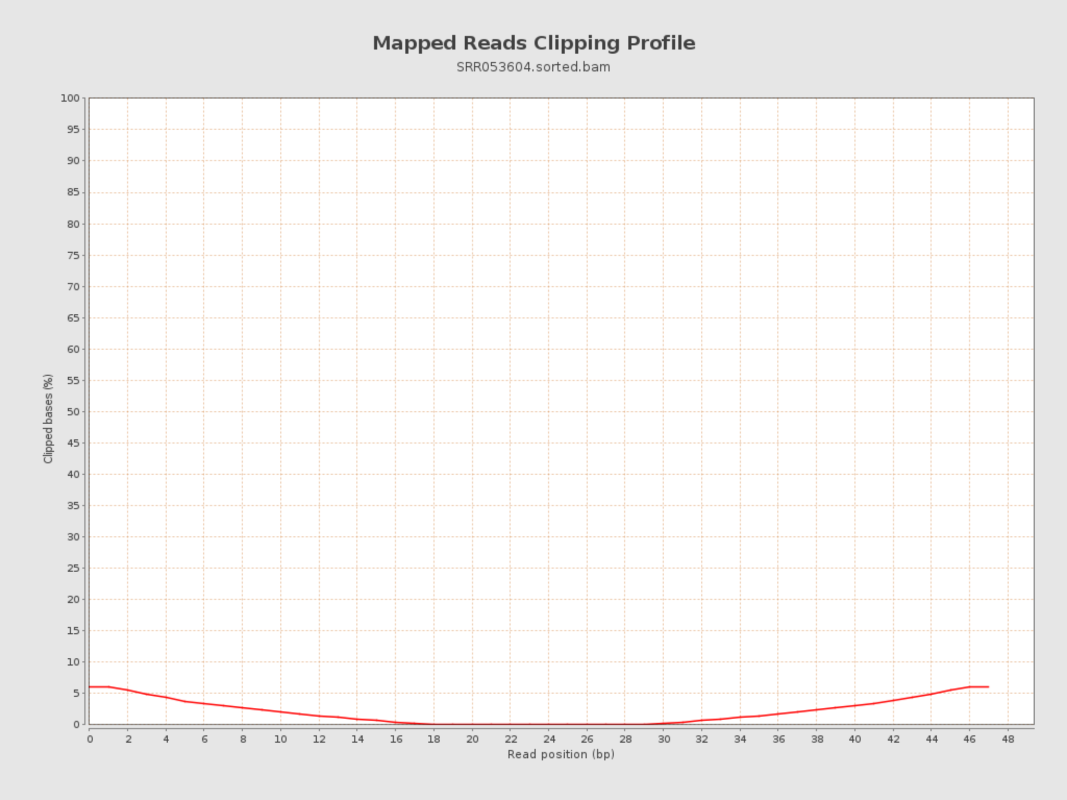
8. Results : Mapped Reads Nucleotide Content



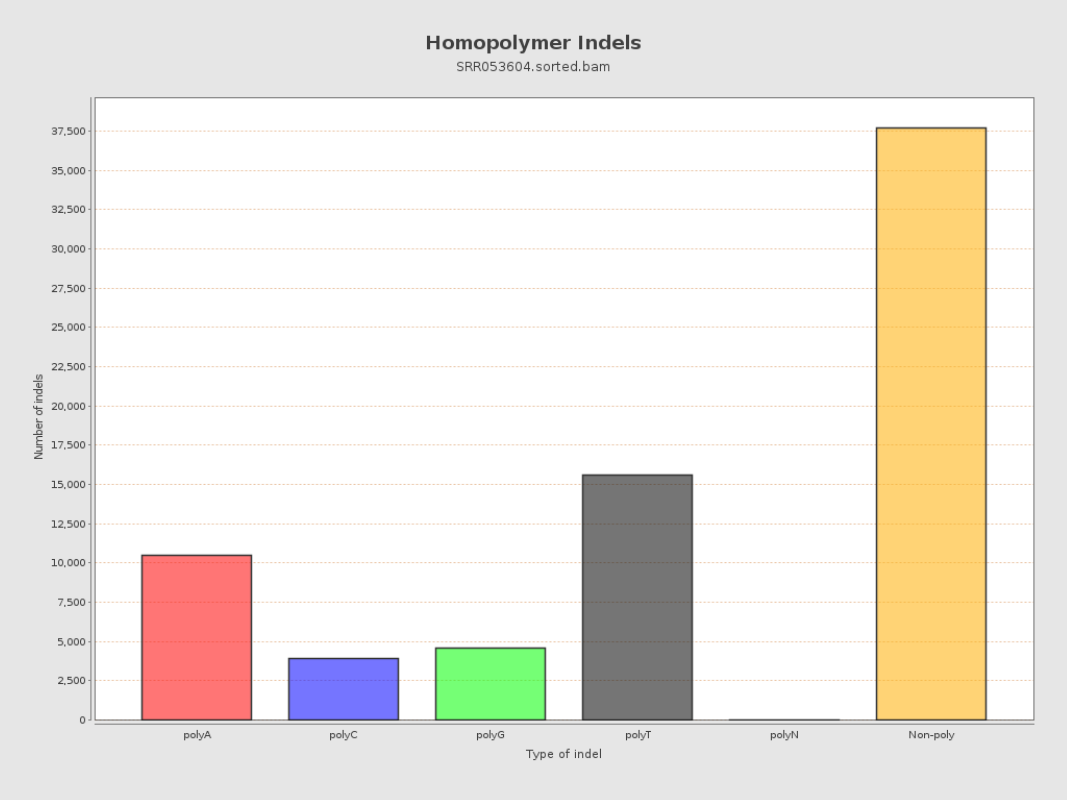
9. Results : Mapped Reads GC-content Distribution



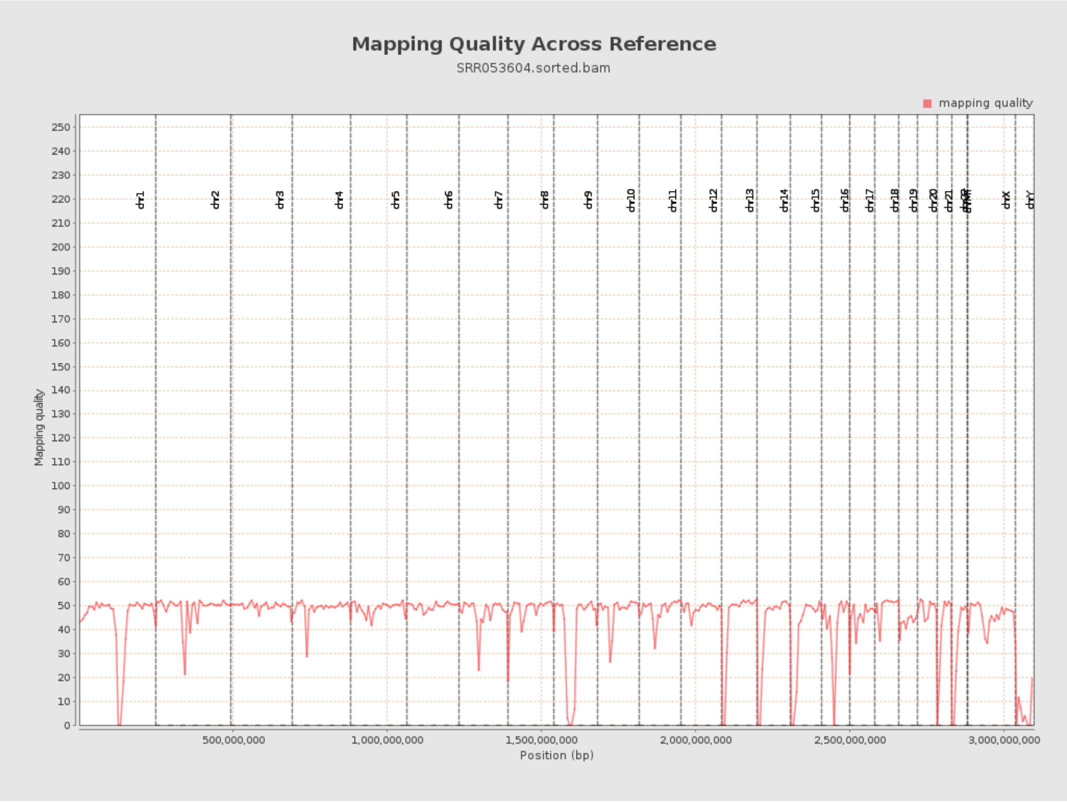
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram