Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 00:31:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053624.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_SRR053624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053624.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 00:31:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,232,679
Mapped reads	10,208,474 / 71.73%
Unmapped reads	4,024,205 / 28.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	302 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,770,419 / 19.47%
Duplication rate	18.62%
Clipped reads	852,452 / 5.99%

2.2. ACGT Content

Number/percentage of A's	143,889,964 / 29.84%
Number/percentage of C's	90,659,922 / 18.8%
Number/percentage of T's	147,816,953 / 30.66%
Number/percentage of G's	99,616,972 / 20.66%
Number/percentage of N's	147,921 / 0.03%
GC Percentage	39.47%

2.3. Coverage

Mean	0.1558

Standard Deviation	1.152

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

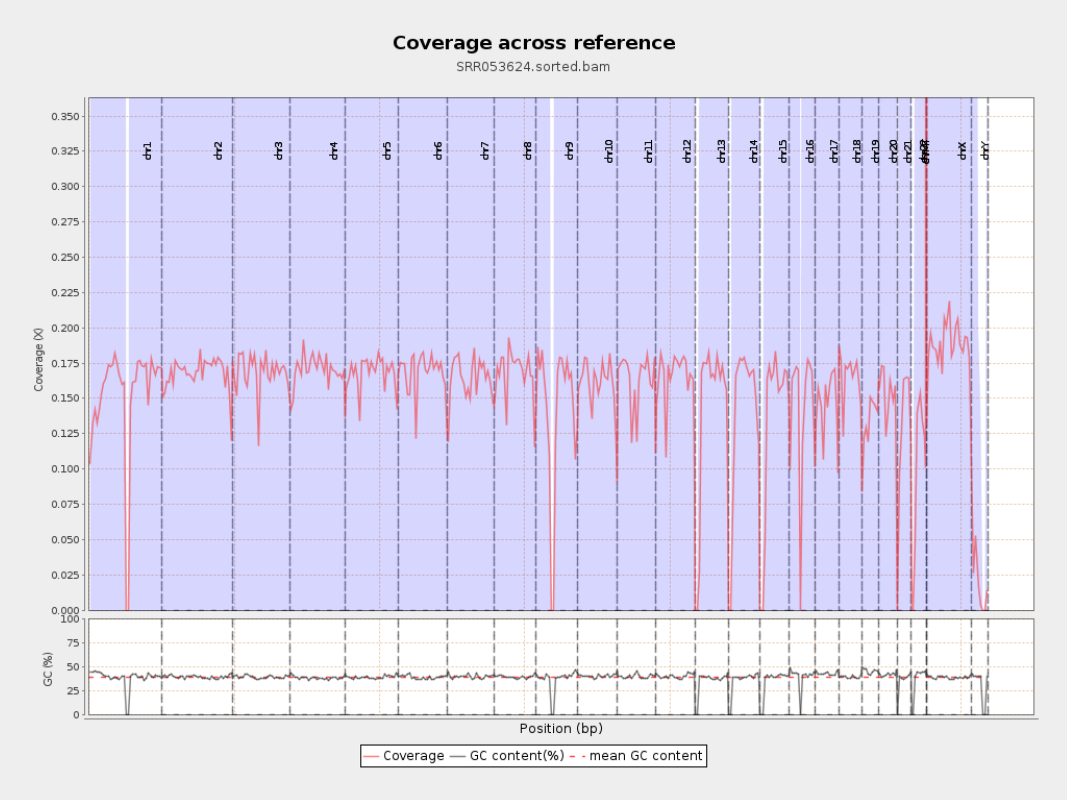
General error rate	0.63%
Mismatches	3,019,073
Insertions	21,706
Mapped reads with at least one insertion	0.21%
Deletions	68,678
Mapped reads with at least one deletion	0.67%
Homopolymer indels	48.17%

2.6. Chromosome stats

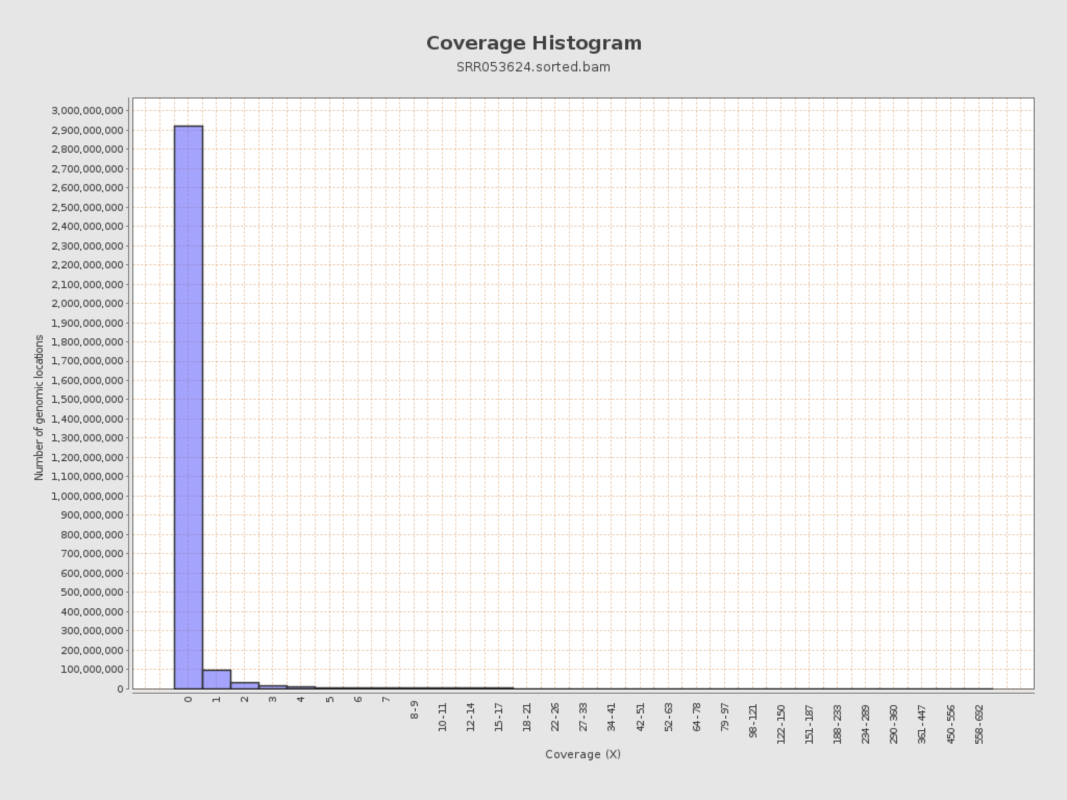
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37780079	0.1516	1.215
chr2	243199373	40862808	0.168	1.2452
chr3	198022430	33457255	0.169	1.1415
chr4	191154276	32546143	0.1703	1.2031
chr5	180915260	30427611	0.1682	1.1302
chr6	171115067	28861975	0.1687	1.198
chr7	159138663	26346181	0.1656	1.2202

chr8	146364022	24649881	0.1684	1.2259
chr9	141213431	19907453	0.141	1.0621
chr10	135534747	22078586	0.1629	1.2047
chr11	135006516	21946690	0.1626	1.1706
chr12	133851895	22132512	0.1654	1.1223
chr13	115169878	16157590	0.1403	1.0511
chr14	107349540	14849253	0.1383	1.1296
chr15	102531392	13689995	0.1335	0.9855
chr16	90354753	12949804	0.1433	1.0938
chr17	81195210	11821075	0.1456	1.0089
chr18	78077248	12921593	0.1655	1.2911
chr19	59128983	7989729	0.1351	1.1396
chr20	63025520	9534243	0.1513	1.0629
chr21	48129895	6130827	0.1274	1.0191
chr22	51304566	4841725	0.0944	0.8055
chrMT	16571	29352	1.7713	4.3411
chrX	155270560	29096780	0.1874	1.2874
chrY	59373566	1223827	0.0206	0.4047

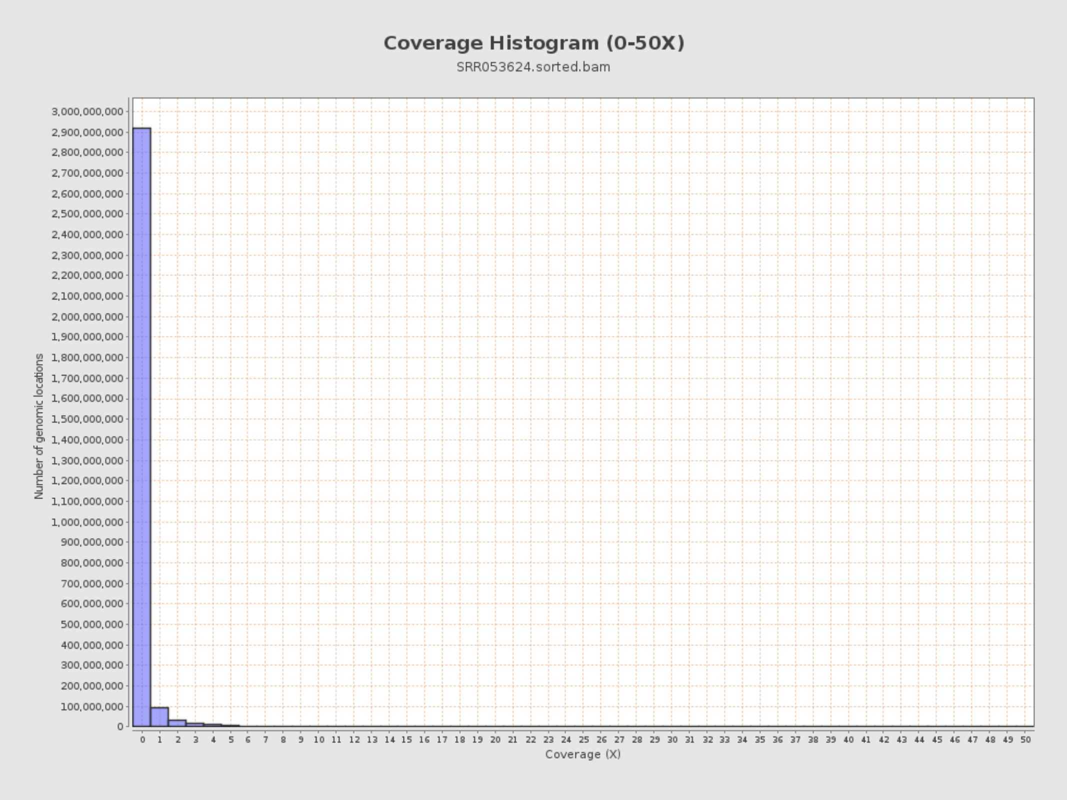
3. Results : Coverage across reference



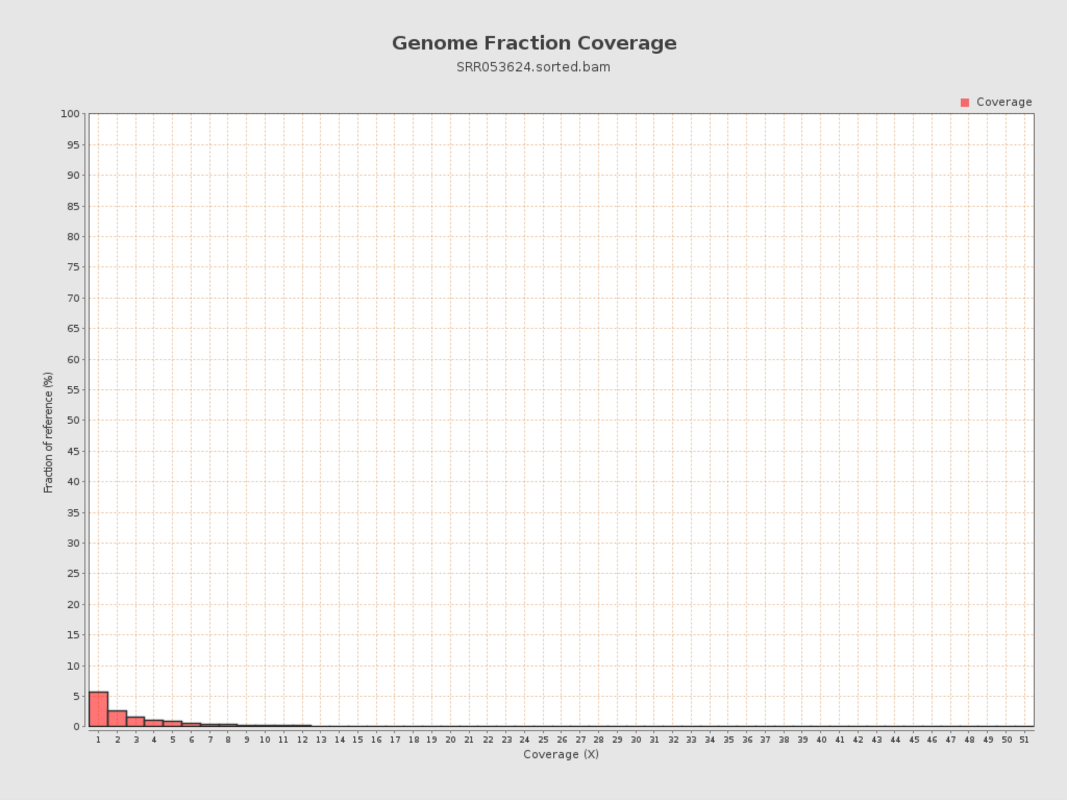
4. Results : Coverage Histogram



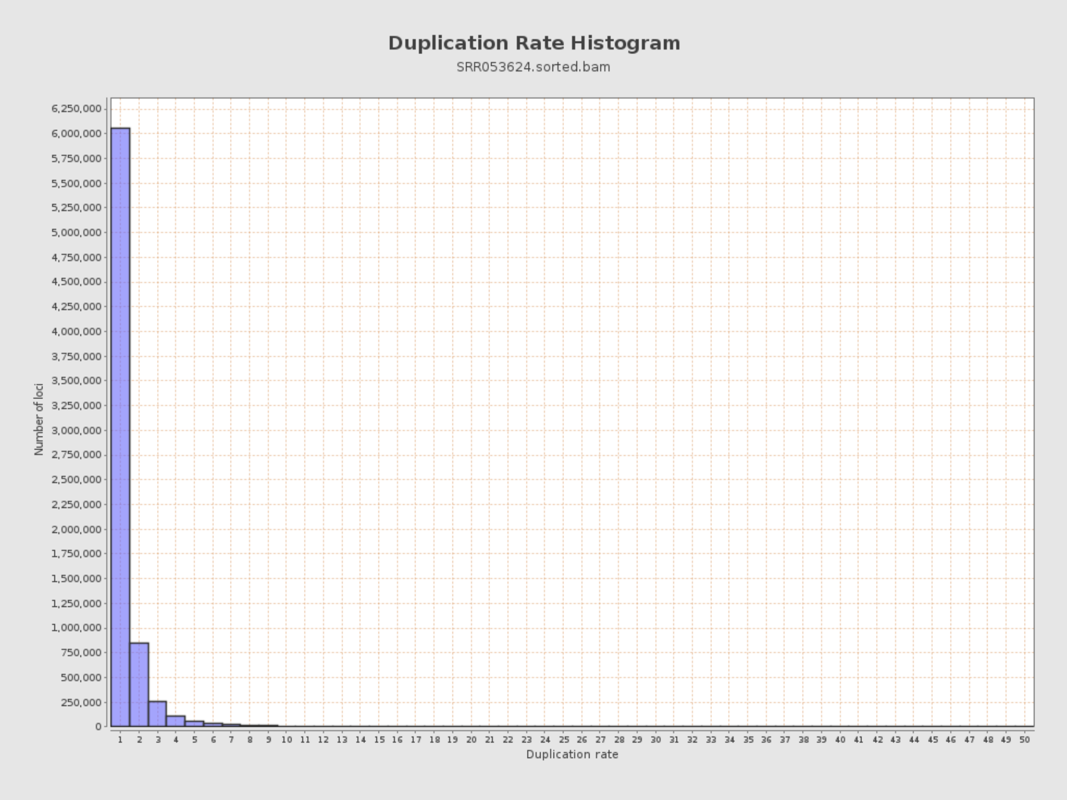
5. Results : Coverage Histogram (0-50X)



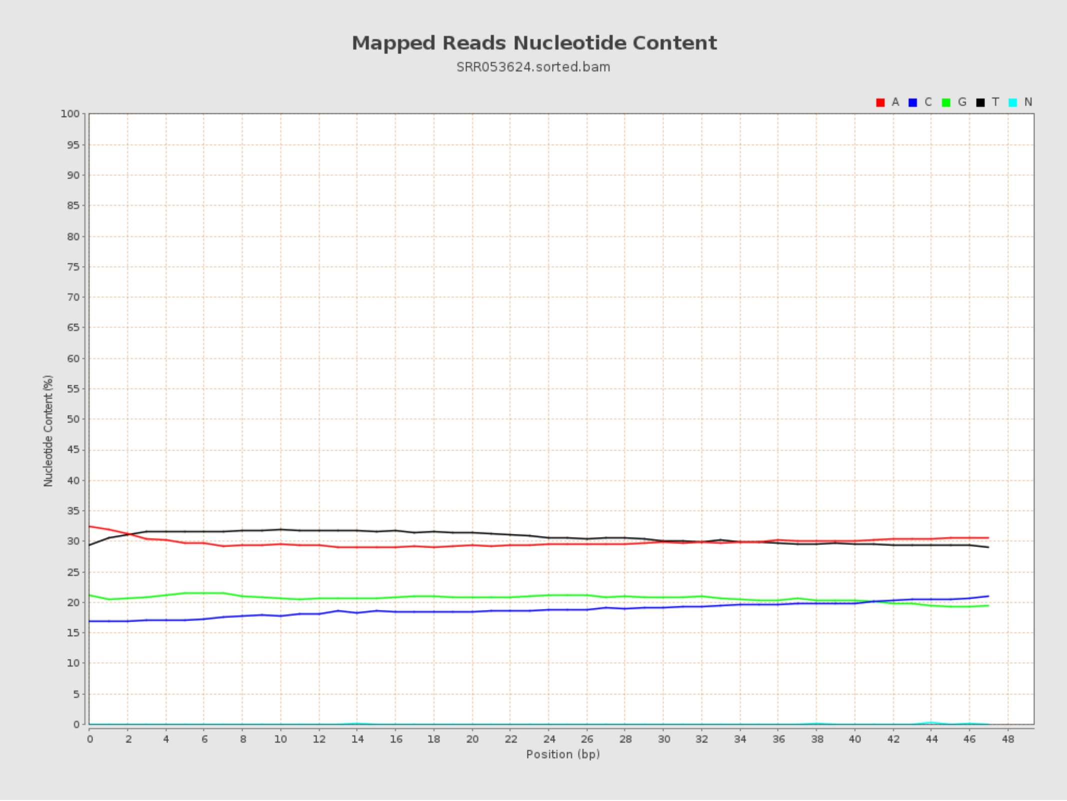
6. Results : Genome Fraction Coverage



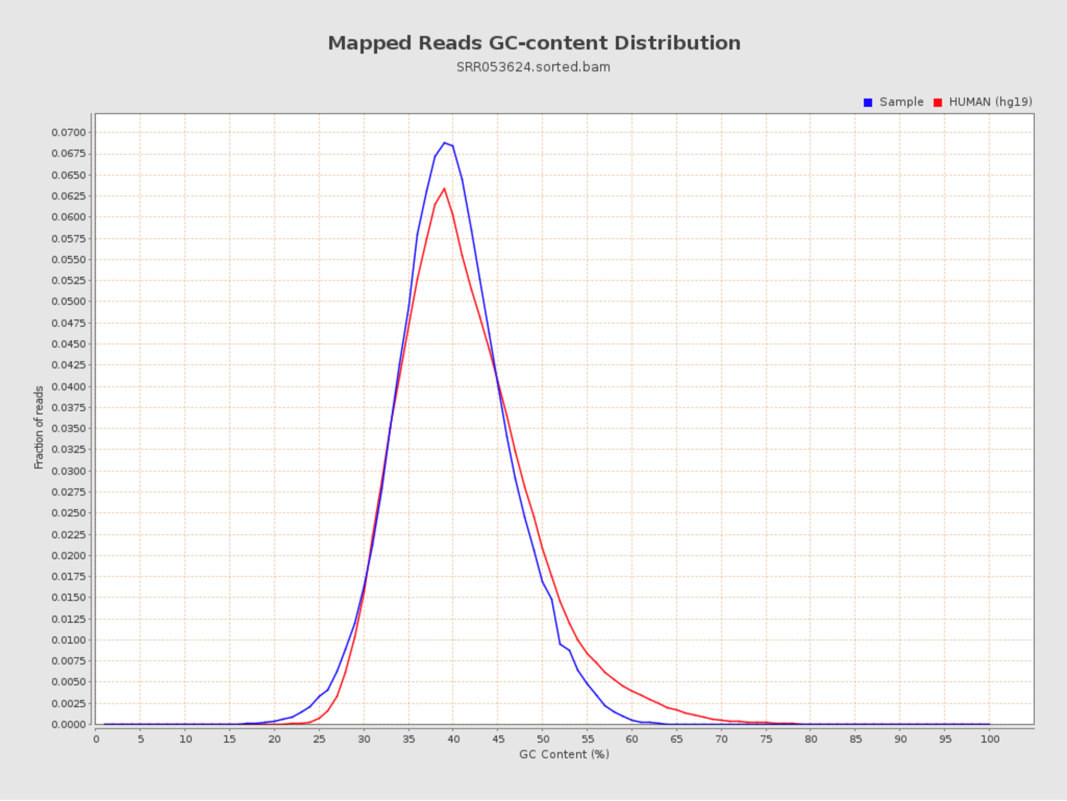
7. Results : Duplication Rate Histogram



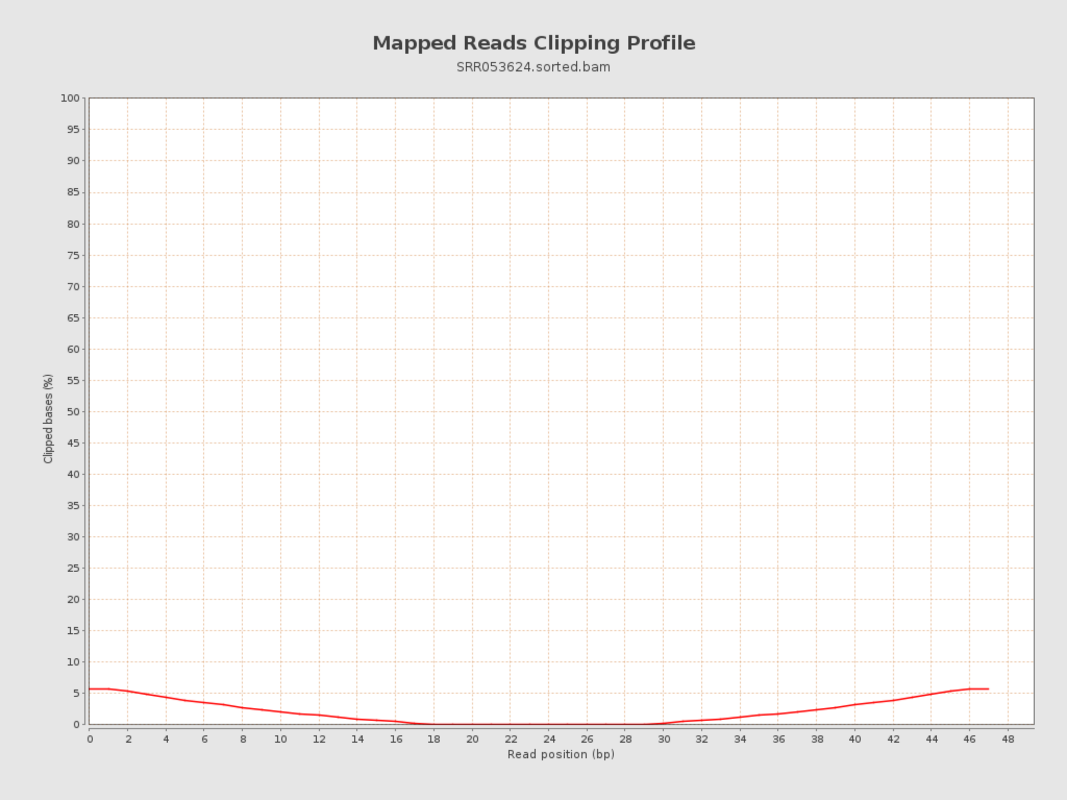
8. Results : Mapped Reads Nucleotide Content



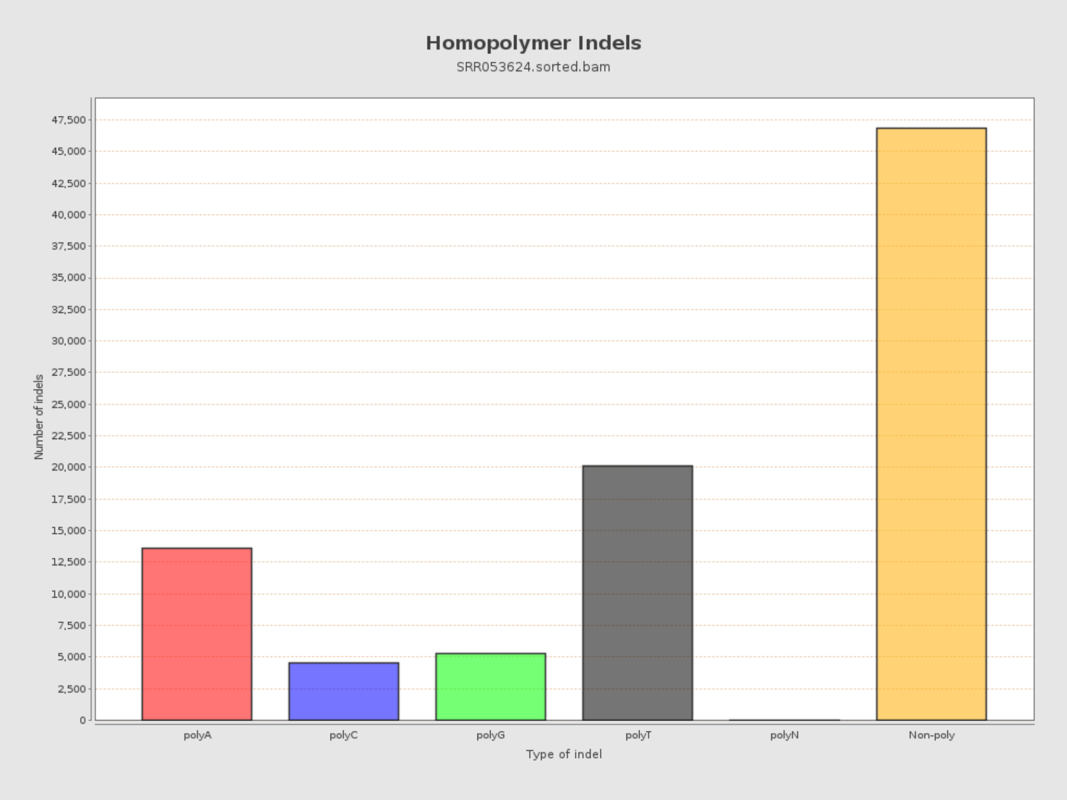
9. Results : Mapped Reads GC-content Distribution



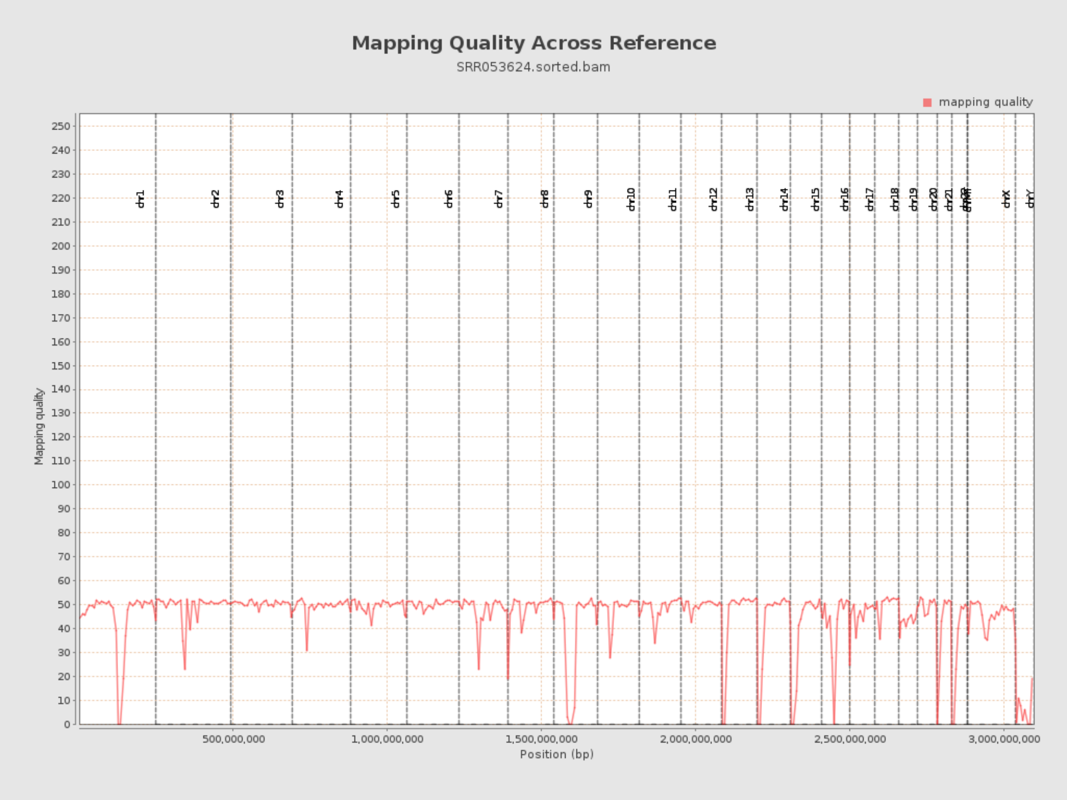
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram