Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:52:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054597.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_SRR054597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:52:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,261,041
Mapped reads	2,583,187 / 79.21%
Unmapped reads	677,854 / 20.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	103 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	296,087 / 9.08%
Duplication rate	9.43%
Clipped reads	254,336 / 7.8%

2.2. ACGT Content

Number/percentage of A's	36,095,619 / 29.65%
Number/percentage of C's	23,645,955 / 19.42%
Number/percentage of T's	36,518,341 / 30%
Number/percentage of G's	25,471,263 / 20.92%
Number/percentage of N's	994 / 0%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.3348

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

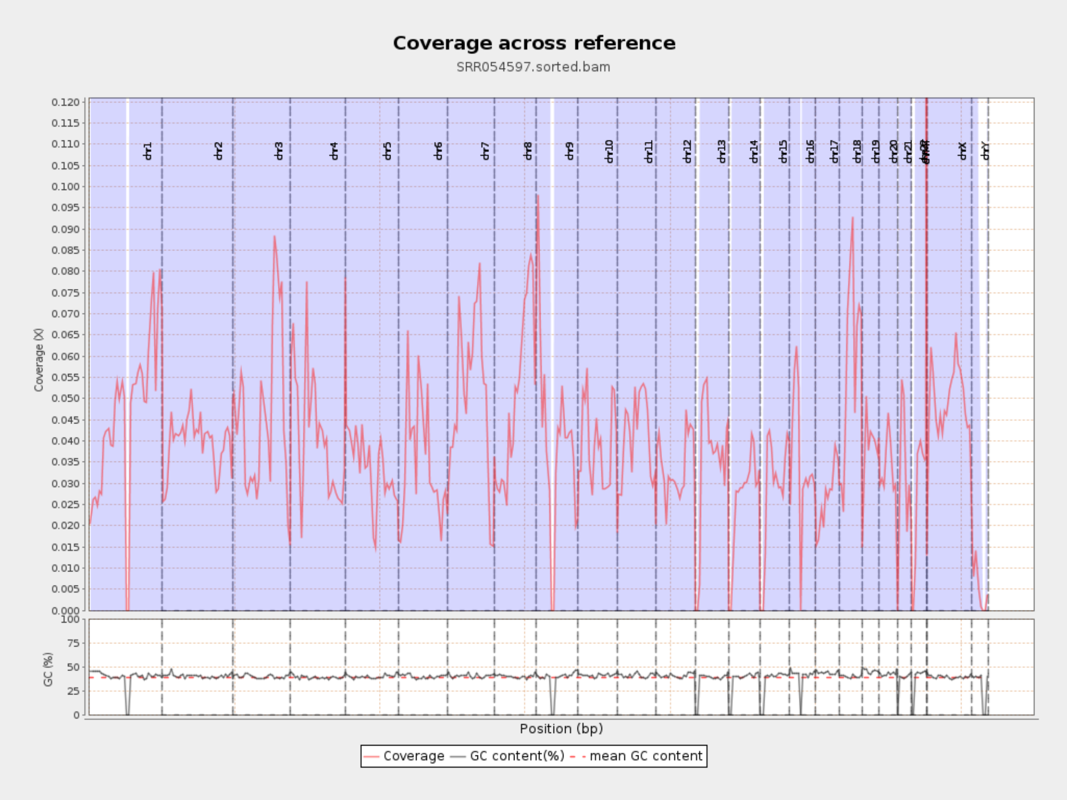
General error rate	0.74%
Mismatches	897,468
Insertions	5,228
Mapped reads with at least one insertion	0.2%
Deletions	17,118
Mapped reads with at least one deletion	0.66%
Homopolymer indels	46.02%

2.6. Chromosome stats

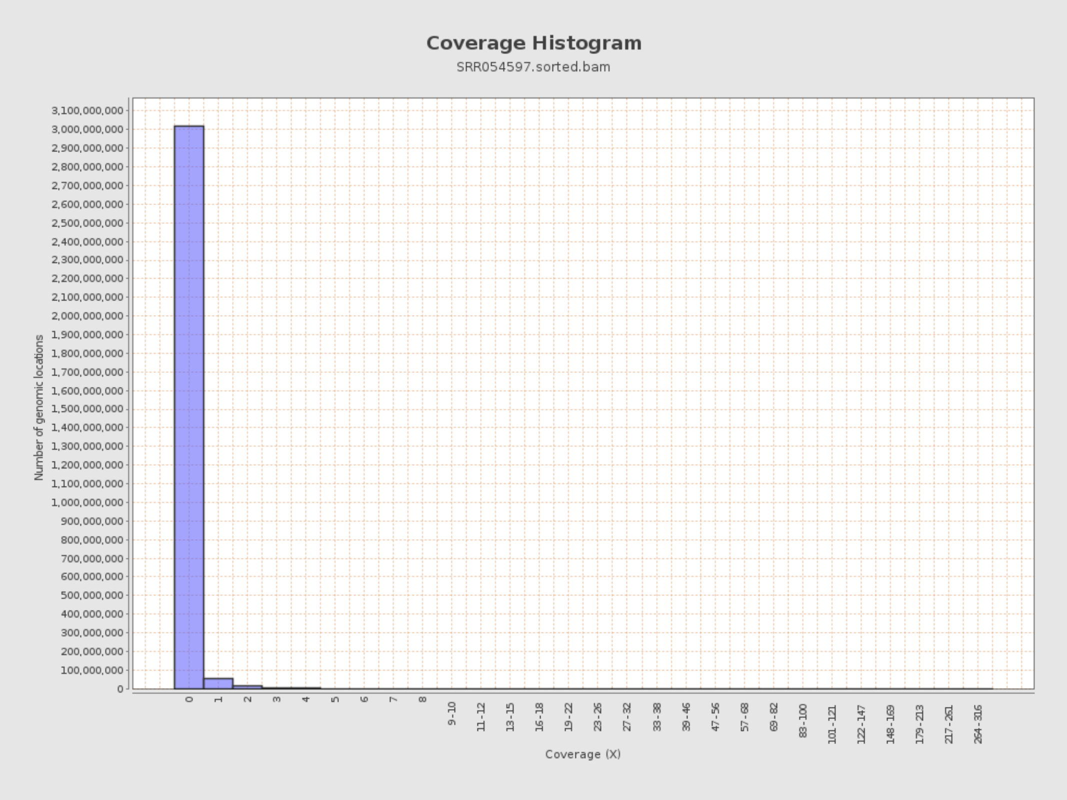
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11400914	0.0457	0.3766
chr2	243199373	9624284	0.0396	0.3969
chr3	198022430	9188837	0.0464	0.3485
chr4	191154276	7880945	0.0412	0.3339
chr5	180915260	6091744	0.0337	0.2797
chr6	171115067	5908189	0.0345	0.3041
chr7	159138663	8184780	0.0514	0.398

chr8	146364022	7462032	0.051	0.3806
chr9	141213431	5694148	0.0403	0.3326
chr10	135534747	5376419	0.0397	0.3276
chr11	135006516	5541342	0.041	0.3345
chr12	133851895	4554624	0.034	0.2846
chr13	115169878	3977649	0.0345	0.2914
chr14	107349540	2819560	0.0263	0.2841
chr15	102531392	2909727	0.0284	0.2559
chr16	90354753	3223038	0.0357	0.3121
chr17	81195210	2186319	0.0269	0.2451
chr18	78077248	4574383	0.0586	0.421
chr19	59128983	2317403	0.0392	0.3578
chr20	63025520	2105406	0.0334	0.2891
chr21	48129895	1512983	0.0314	0.3126
chr22	51304566	1316189	0.0257	0.2466
chrMT	16571	6293	0.3798	0.9231
chrX	155270560	7589687	0.0489	0.3673
chrY	59373566	310335	0.0052	0.1239

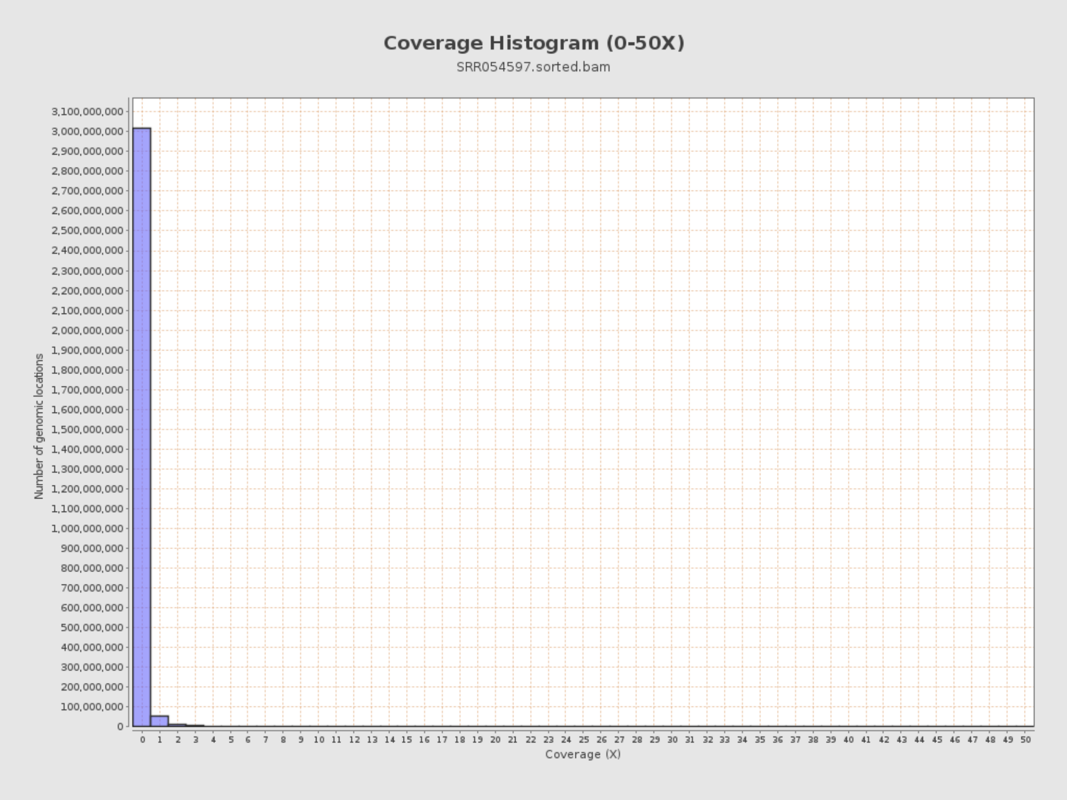
3. Results : Coverage across reference



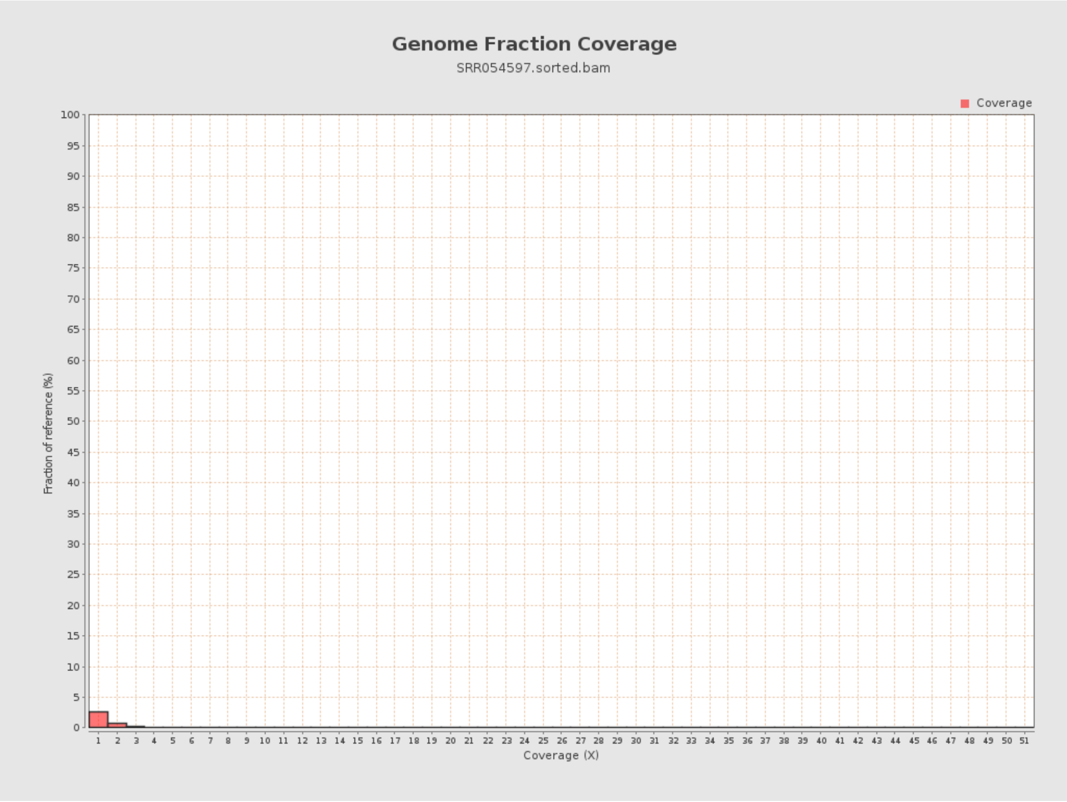
4. Results : Coverage Histogram



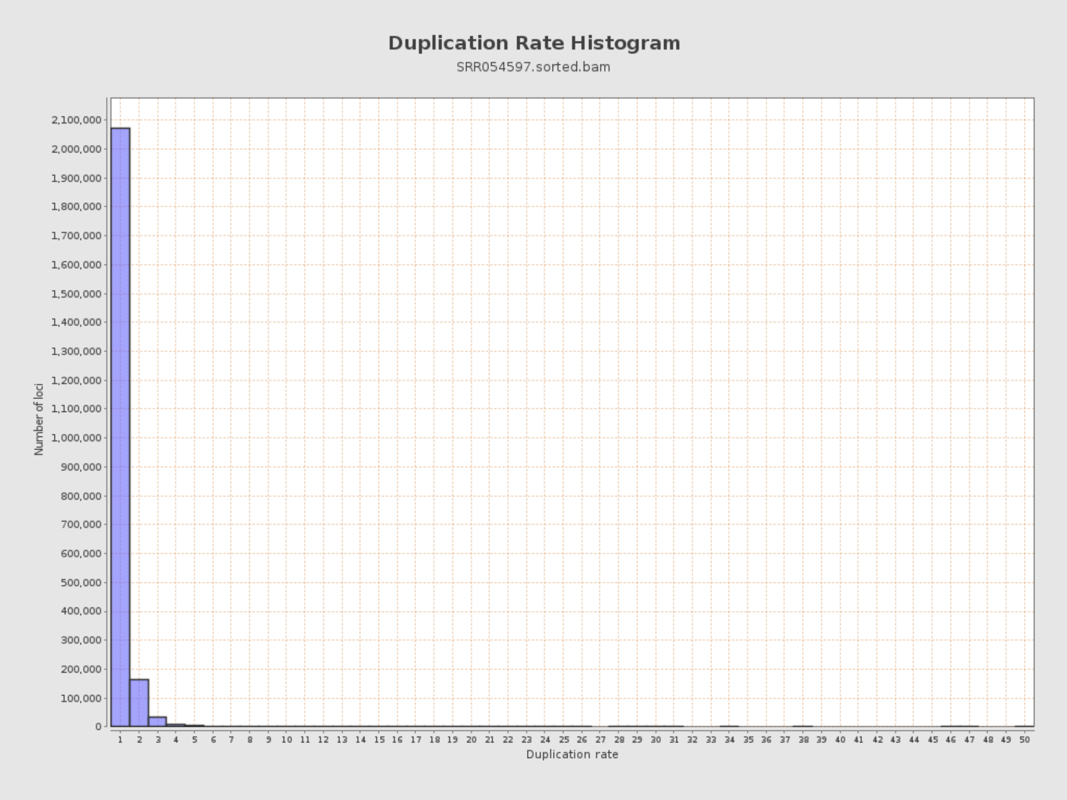
5. Results : Coverage Histogram (0-50X)



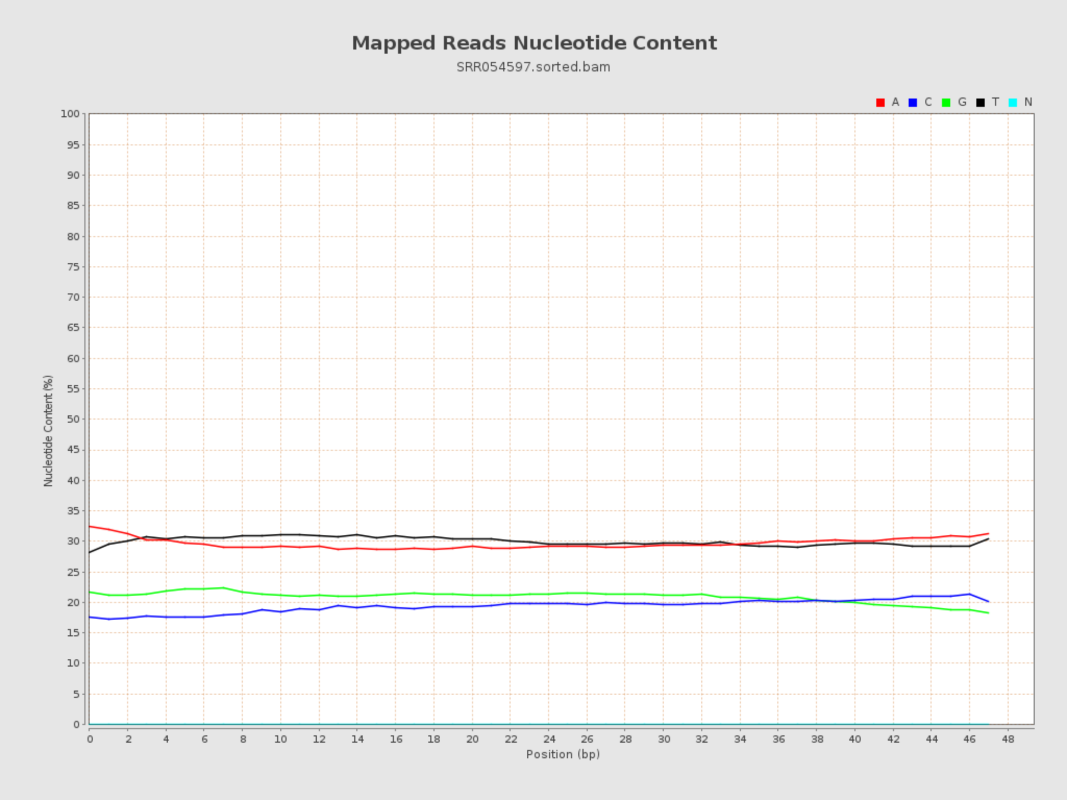
6. Results : Genome Fraction Coverage



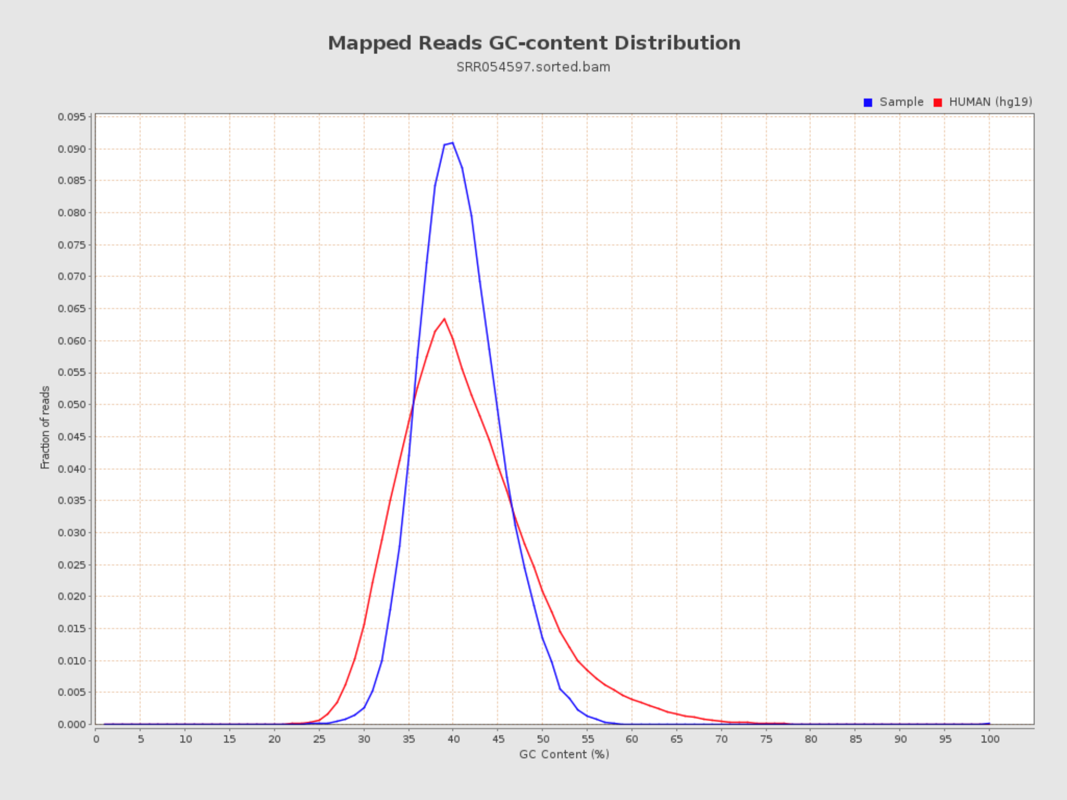
7. Results : Duplication Rate Histogram



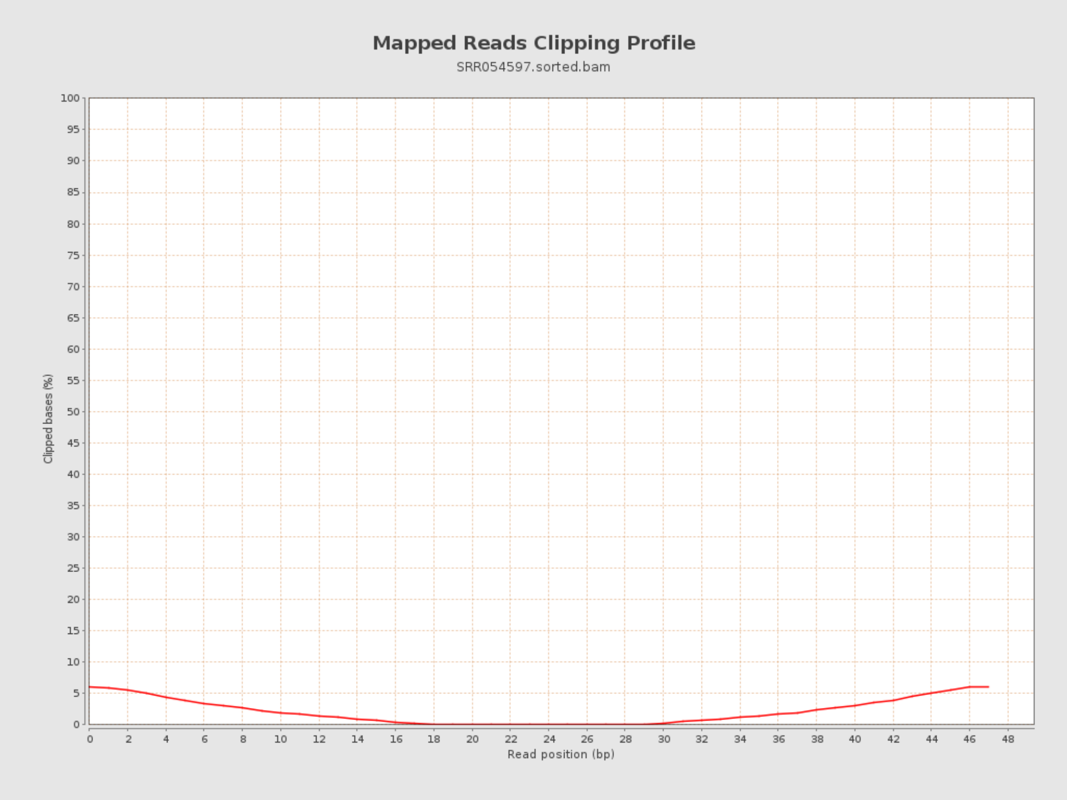
8. Results : Mapped Reads Nucleotide Content



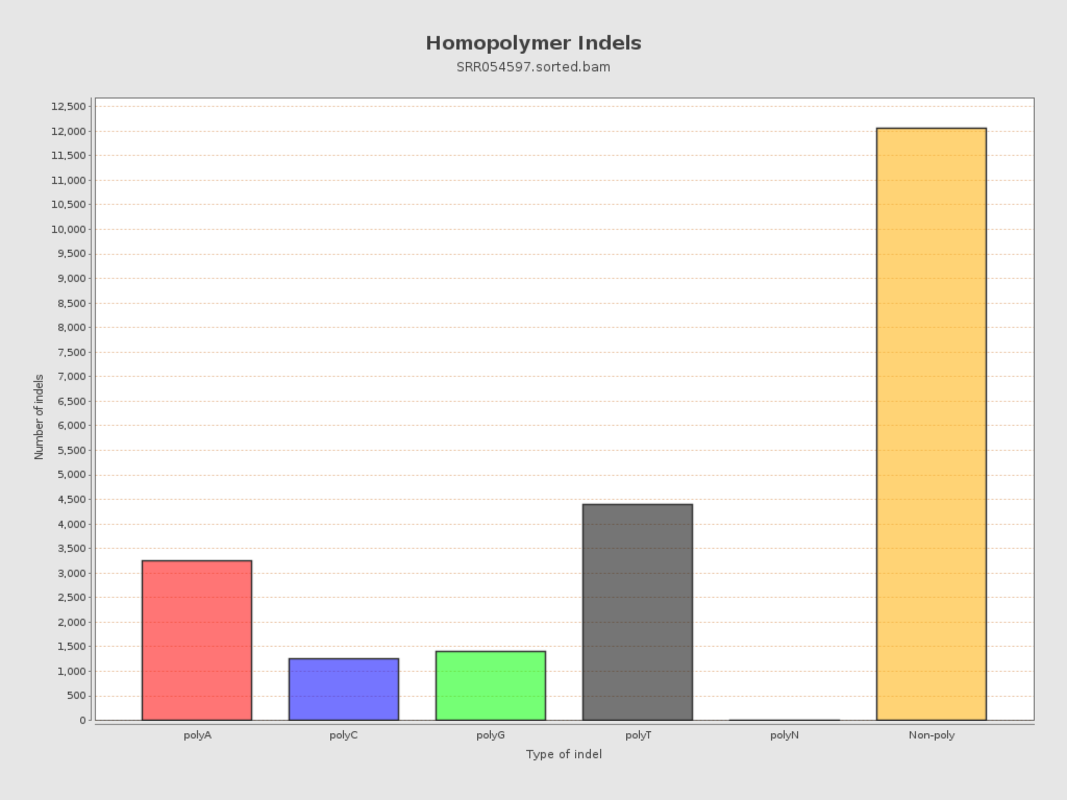
9. Results : Mapped Reads GC-content Distribution



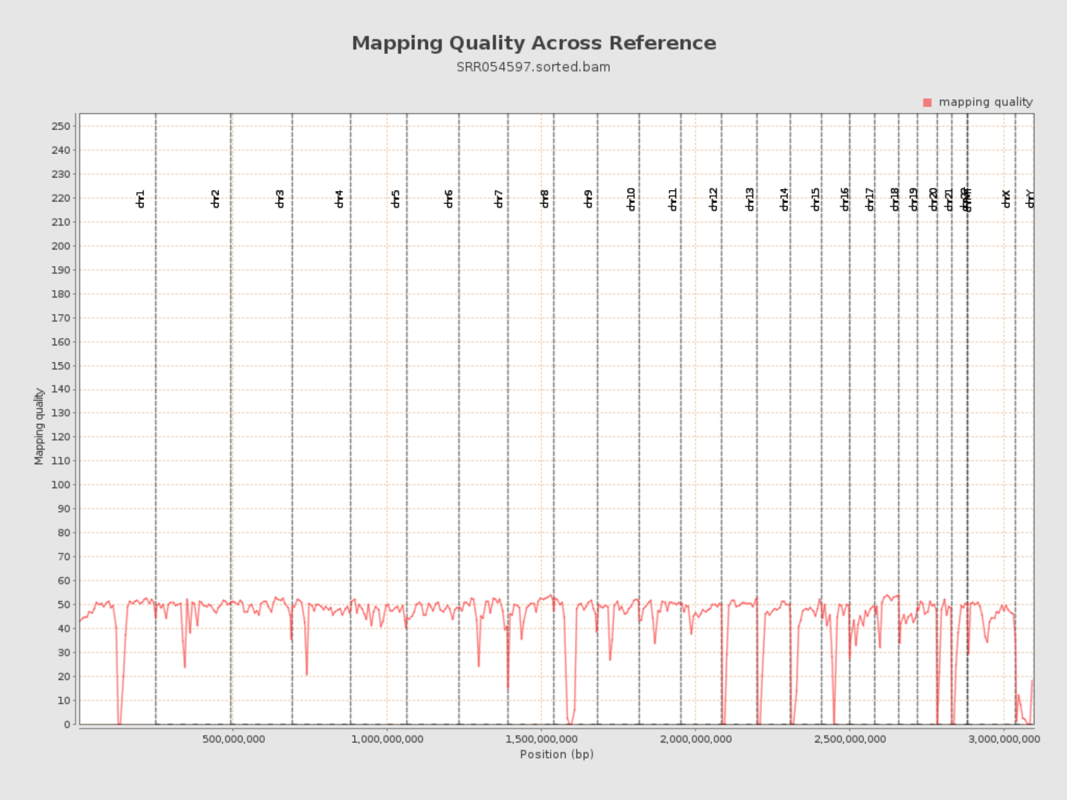
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram