Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:04:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004055.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_SRR6004055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:04:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,296,279
Mapped reads	2,032,372 / 88.51%
Unmapped reads	263,907 / 11.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,273 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	72,625 / 3.16%
Duplication rate	2.75%
Clipped reads	963,915 / 41.98%

2.2. ACGT Content

Number/percentage of A's	37,199,798 / 27.63%
Number/percentage of C's	25,587,610 / 19.01%
Number/percentage of T's	41,429,073 / 30.77%
Number/percentage of G's	30,394,298 / 22.58%
Number/percentage of N's	23,816 / 0.02%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0435

Standard Deviation	0.3568

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

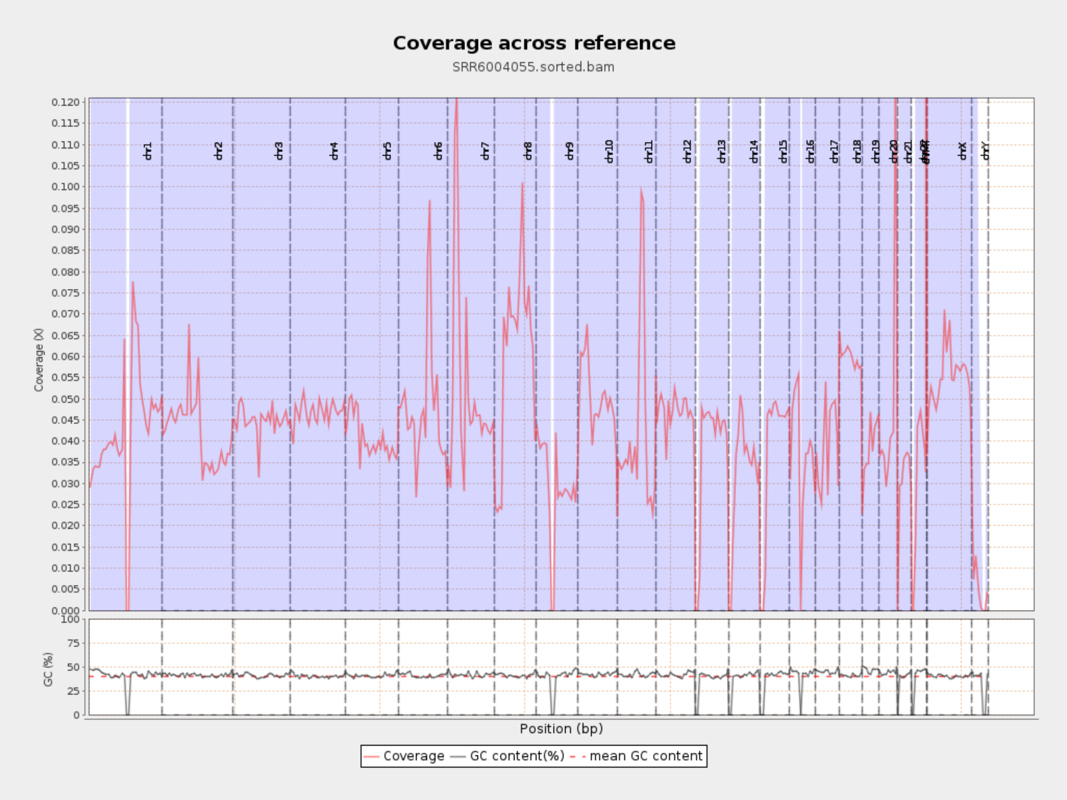
General error rate	0.87%
Mismatches	1,160,905
Insertions	9,759
Mapped reads with at least one insertion	0.48%
Deletions	31,551
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.48%

2.6. Chromosome stats

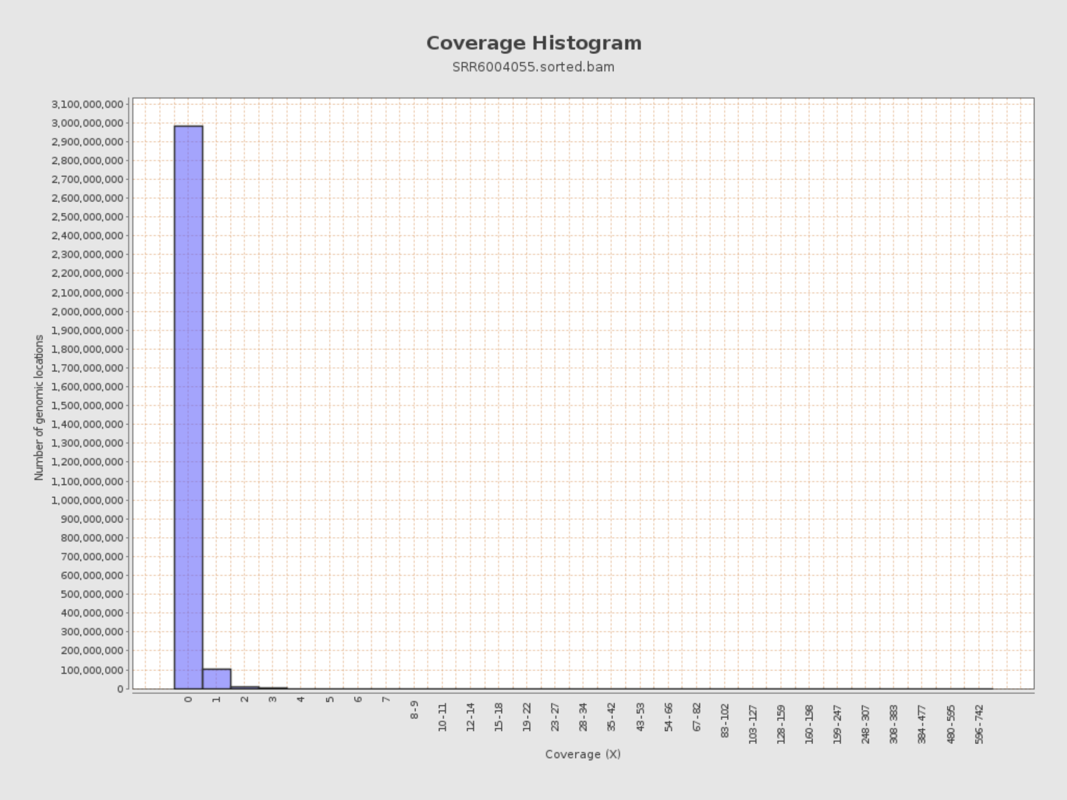
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10517448	0.0422	0.5752
chr2	243199373	10246335	0.0421	0.4488
chr3	198022430	8904727	0.045	0.2365
chr4	191154276	8940407	0.0468	0.253
chr5	180915260	7375195	0.0408	0.2269
chr6	171115067	8213468	0.048	0.2719
chr7	159138663	8457119	0.0531	0.545

chr8	146364022	8832790	0.0603	0.4725
chr9	141213431	4019920	0.0285	0.3237
chr10	135534747	6885186	0.0508	0.3145
chr11	135006516	5721010	0.0424	0.3146
chr12	133851895	6263202	0.0468	0.2478
chr13	115169878	4300402	0.0373	0.2269
chr14	107349540	3460931	0.0322	0.2202
chr15	102531392	3830617	0.0374	0.2301
chr16	90354753	3393898	0.0376	0.2364
chr17	81195210	3207554	0.0395	0.2424
chr18	78077248	4674643	0.0599	0.5866
chr19	59128983	2299825	0.0389	0.4365
chr20	63025520	3230209	0.0513	0.271
chr21	48129895	1448493	0.0301	0.2066
chr22	51304566	1500834	0.0293	0.1909
chrMT	16571	70274	4.2408	3.7851
chrX	155270560	8568363	0.0552	0.2904
chrY	59373566	326184	0.0055	0.1013

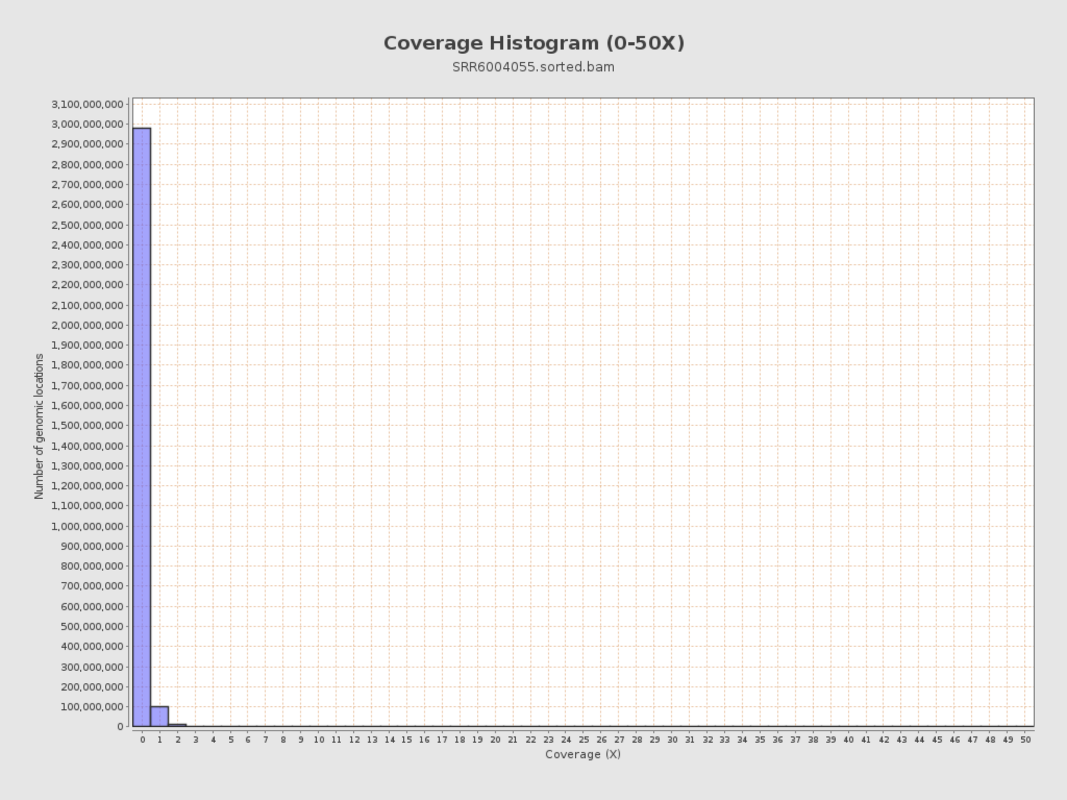
3. Results : Coverage across reference



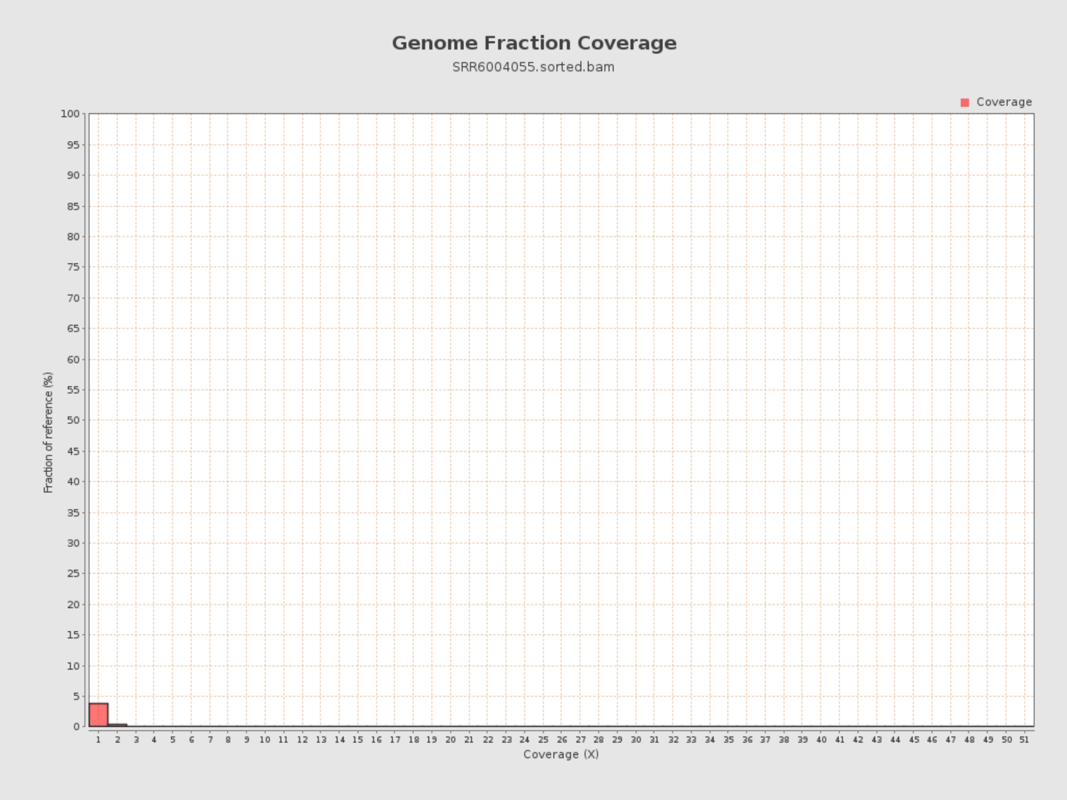
4. Results : Coverage Histogram



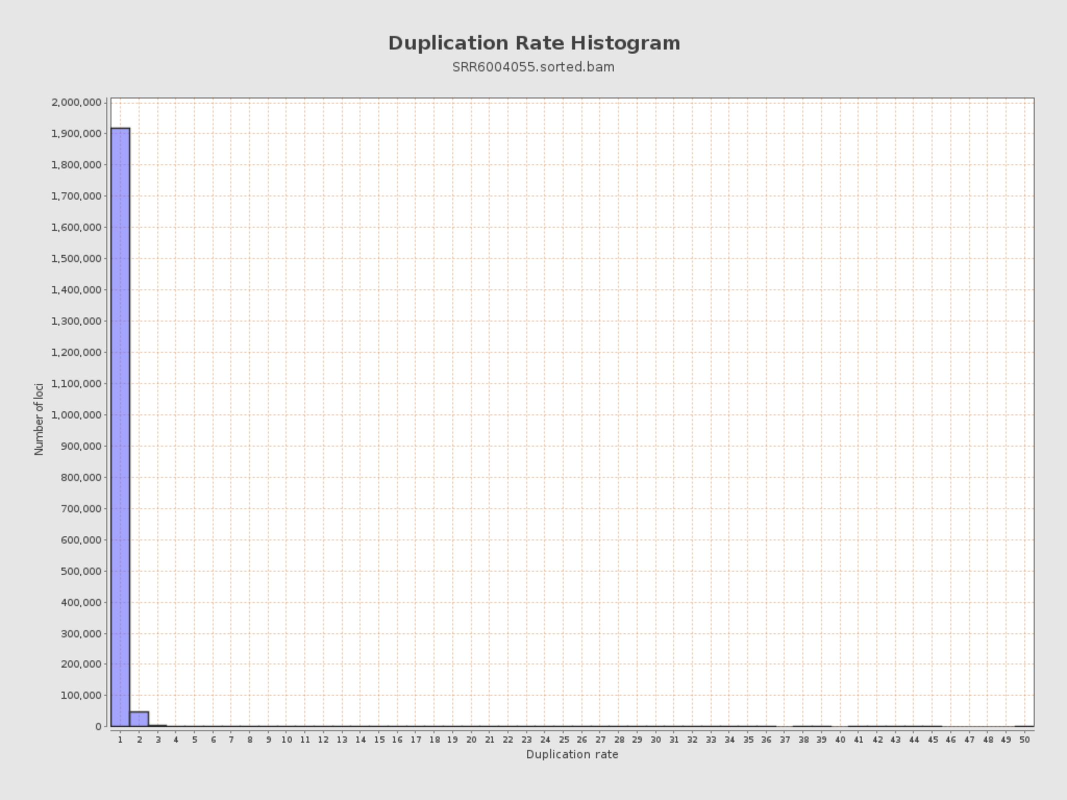
5. Results : Coverage Histogram (0-50X)



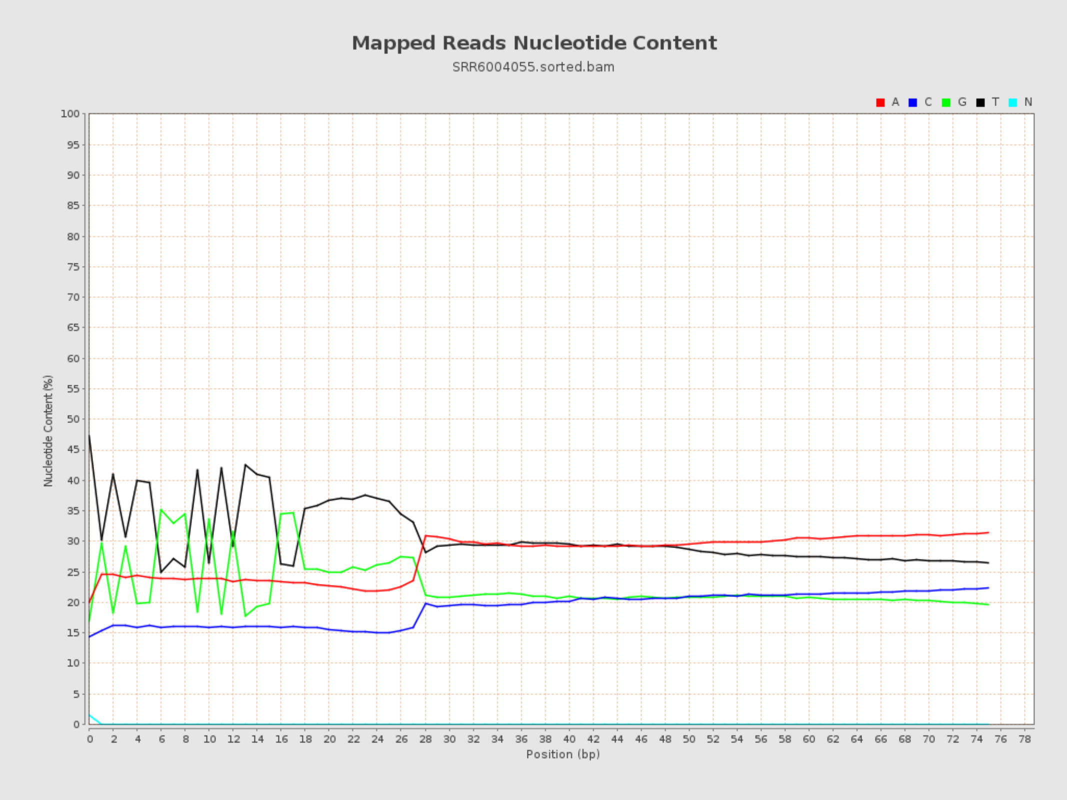
6. Results : Genome Fraction Coverage



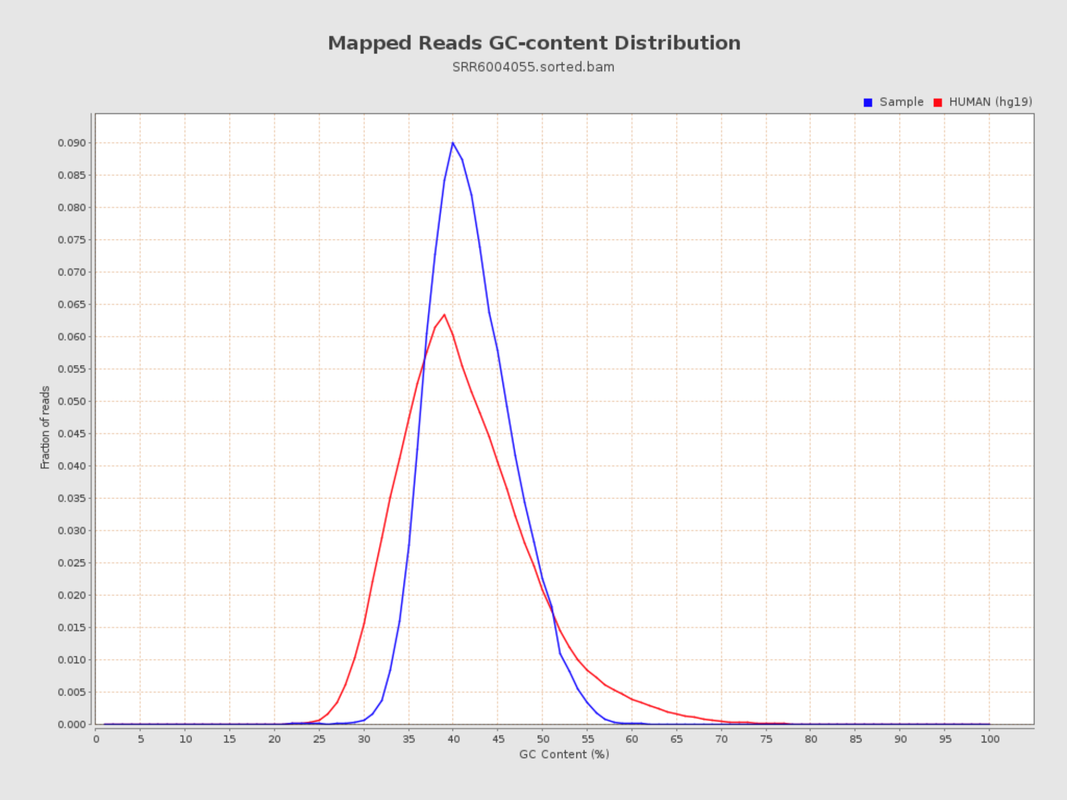
7. Results : Duplication Rate Histogram



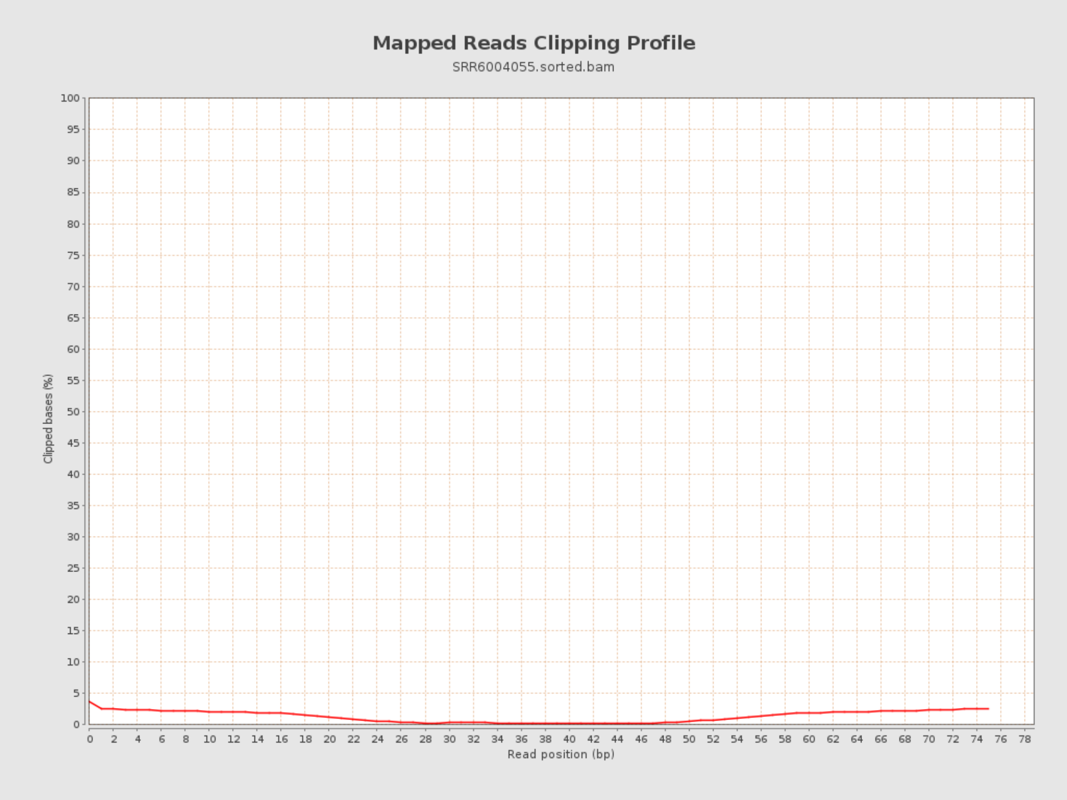
8. Results : Mapped Reads Nucleotide Content



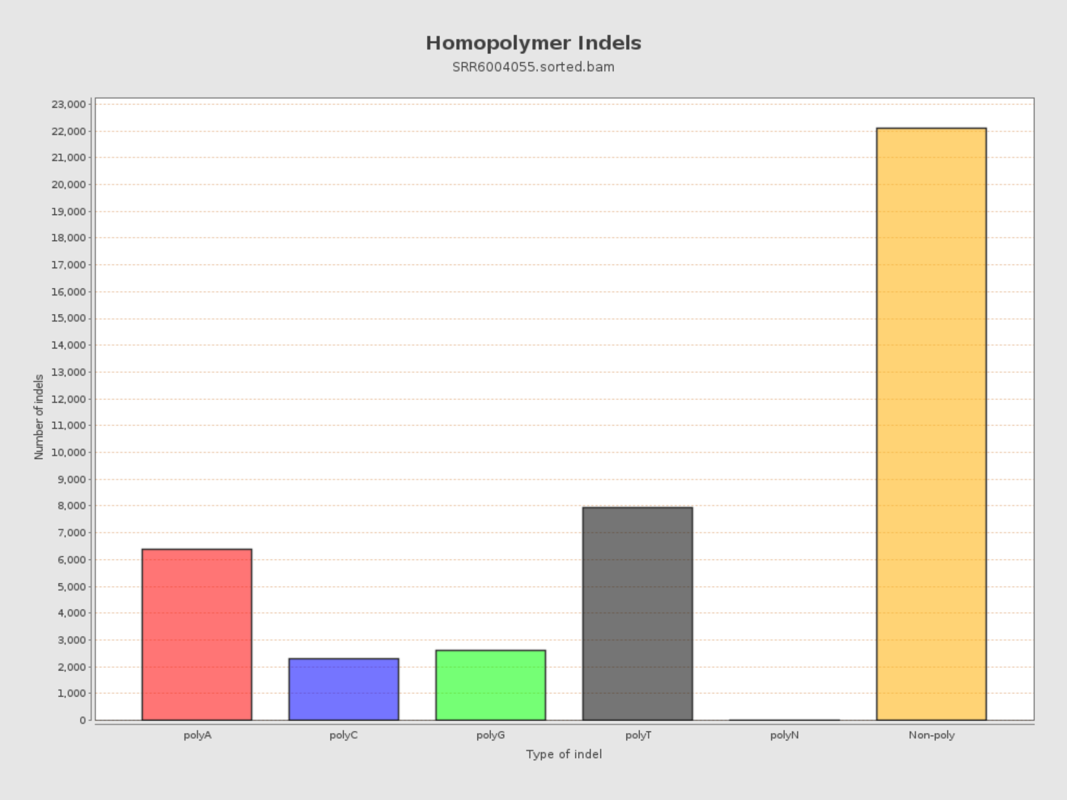
9. Results : Mapped Reads GC-content Distribution



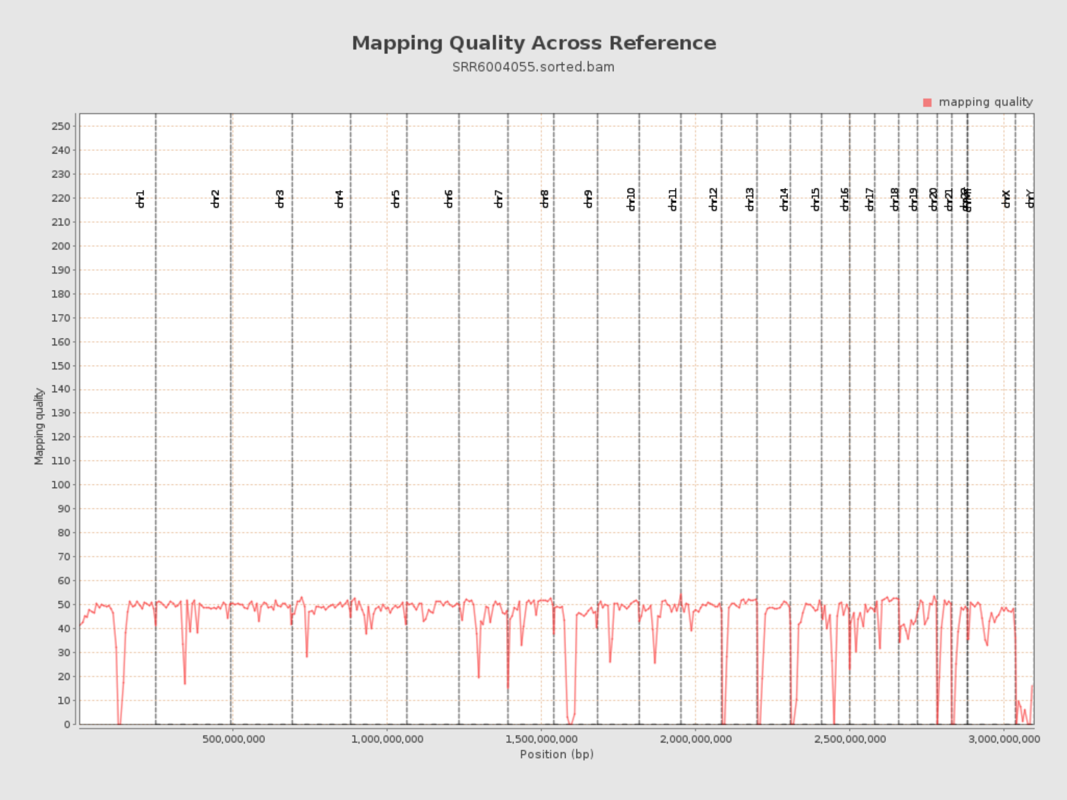
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram