Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053669.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_SRR053669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:32:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,875,392
Mapped reads	4,465,777 / 76.01%
Unmapped reads	1,409,615 / 23.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	149 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	608,654 / 10.36%
Duplication rate	10.73%
Clipped reads	439,195 / 7.48%

2.2. ACGT Content

Number/percentage of A's	63,523,959 / 30.19%
Number/percentage of C's	39,966,852 / 18.99%
Number/percentage of T's	64,653,448 / 30.73%
Number/percentage of G's	42,183,946 / 20.05%
Number/percentage of N's	89,288 / 0.04%
GC Percentage	39.04%

2.3. Coverage

Mean	0.068

Standard Deviation	0.4892

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

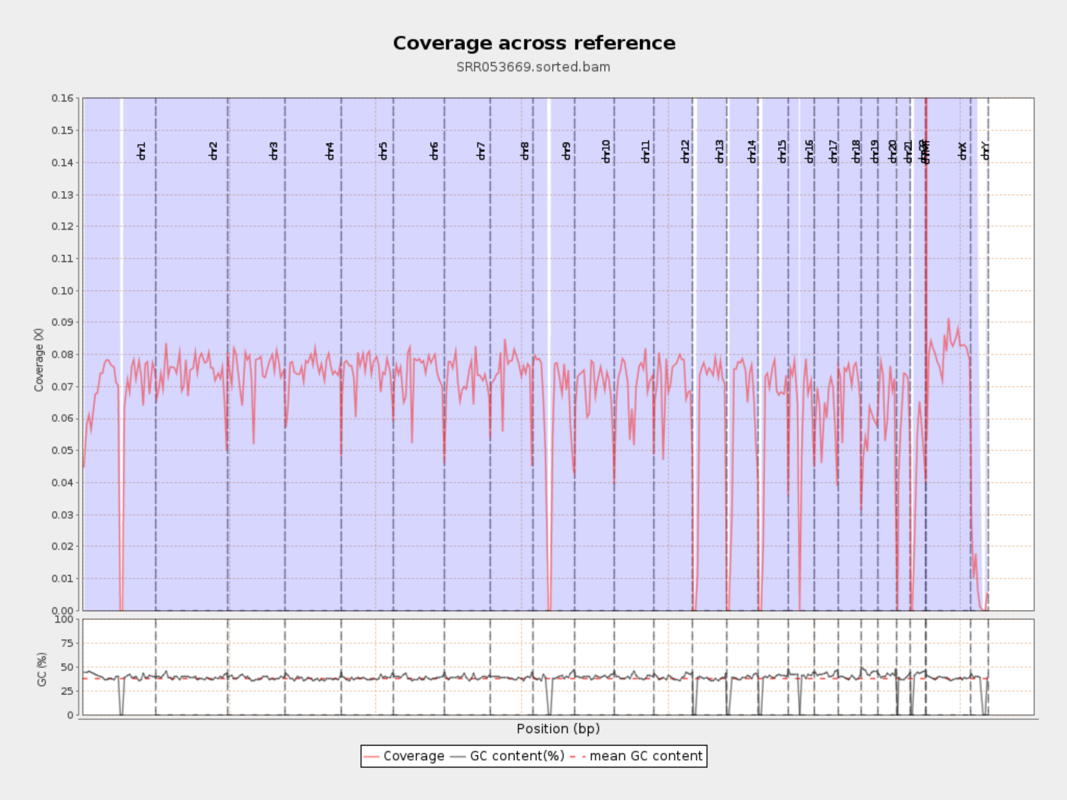
General error rate	0.7%
Mismatches	1,455,448
Insertions	8,884
Mapped reads with at least one insertion	0.2%
Deletions	27,507
Mapped reads with at least one deletion	0.61%
Homopolymer indels	47.25%

2.6. Chromosome stats

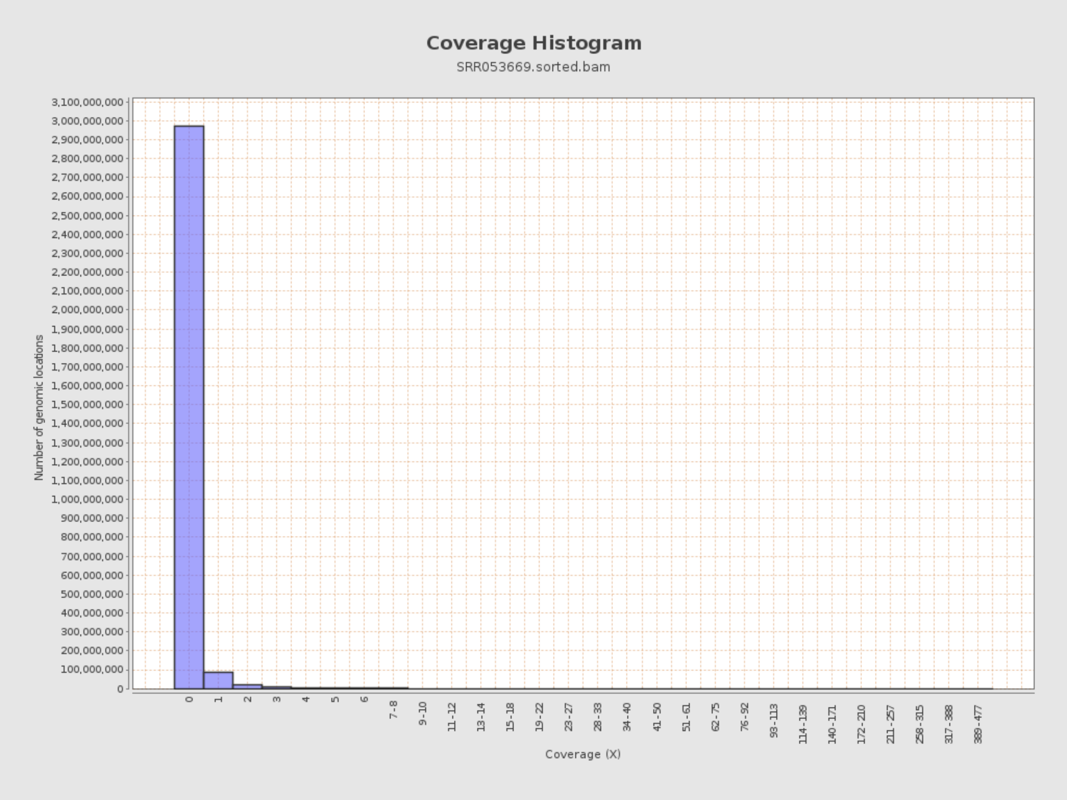
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16503380	0.0662	0.4949
chr2	243199373	18061162	0.0743	0.6084
chr3	198022430	14883330	0.0752	0.4821
chr4	191154276	14359939	0.0751	0.4951
chr5	180915260	13522951	0.0747	0.4792
chr6	171115067	12727496	0.0744	0.5197
chr7	159138663	11463265	0.072	0.5373

chr8	146364022	10862528	0.0742	0.5151
chr9	141213431	8652528	0.0613	0.4523
chr10	135534747	9543366	0.0704	0.4807
chr11	135006516	9459383	0.0701	0.4978
chr12	133851895	9587354	0.0716	0.4696
chr13	115169878	7114671	0.0618	0.4327
chr14	107349540	6425730	0.0599	0.4695
chr15	102531392	5898968	0.0575	0.4093
chr16	90354753	5462463	0.0605	0.4347
chr17	81195210	5040960	0.0621	0.4259
chr18	78077248	5624848	0.072	0.5256
chr19	59128983	3279670	0.0555	0.4434
chr20	63025520	4217615	0.0669	0.454
chr21	48129895	2730267	0.0567	0.4438
chr22	51304566	1998055	0.0389	0.3185
chrMT	16571	44979	2.7143	5.7039
chrX	155270560	12539008	0.0808	0.5301
chrY	59373566	454109	0.0076	0.1513

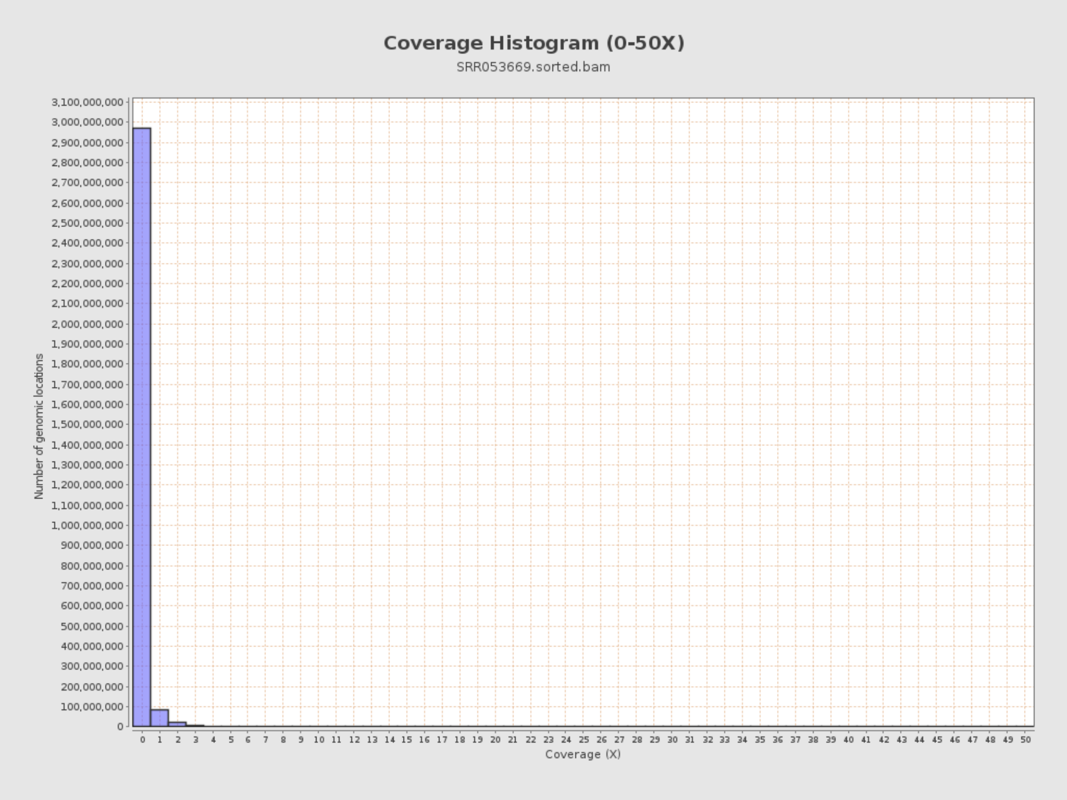
3. Results : Coverage across reference



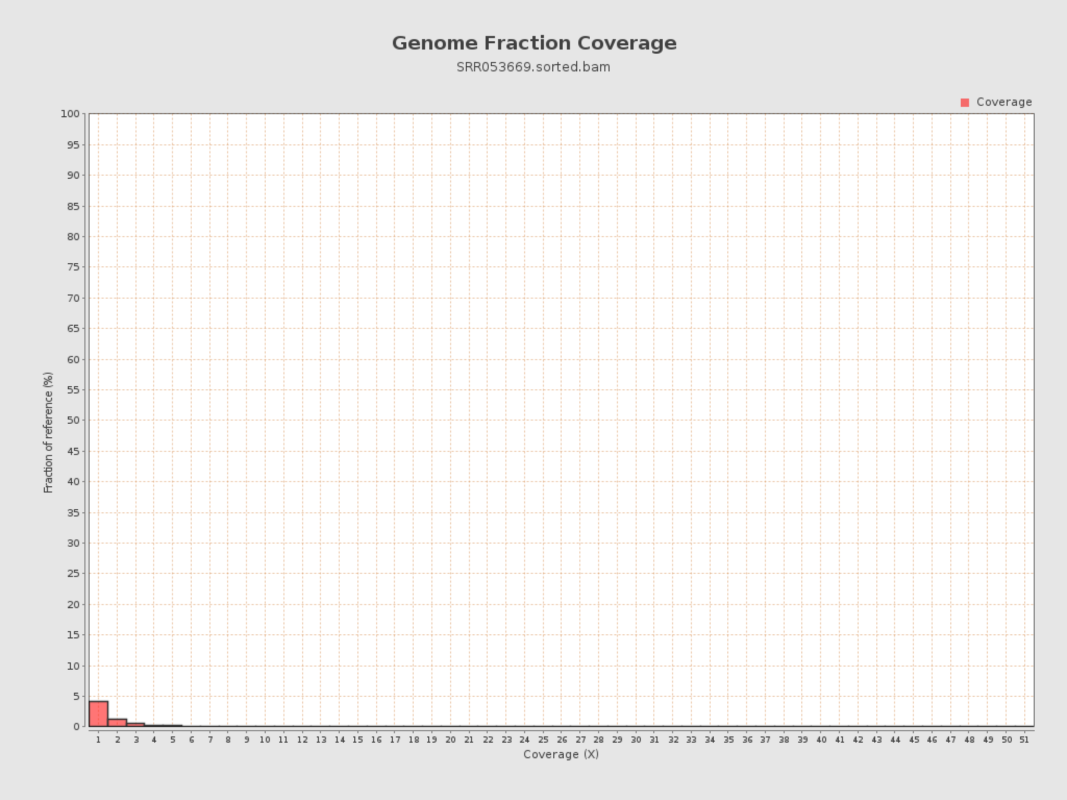
4. Results : Coverage Histogram



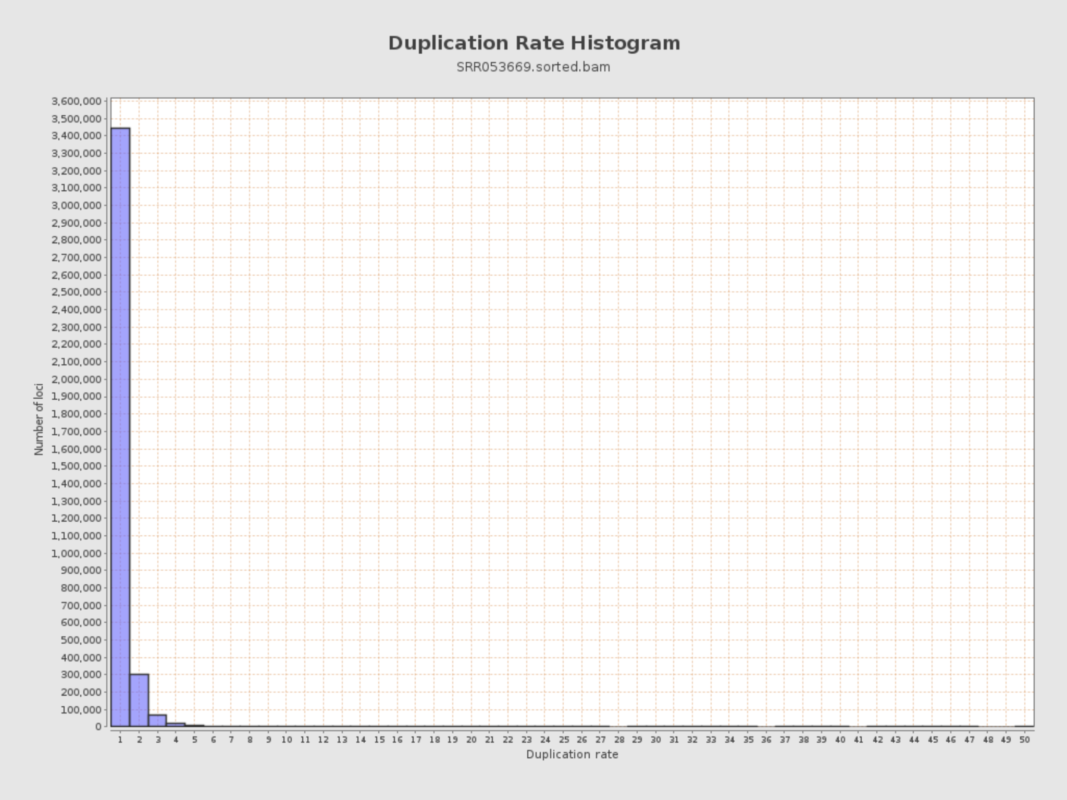
5. Results : Coverage Histogram (0-50X)



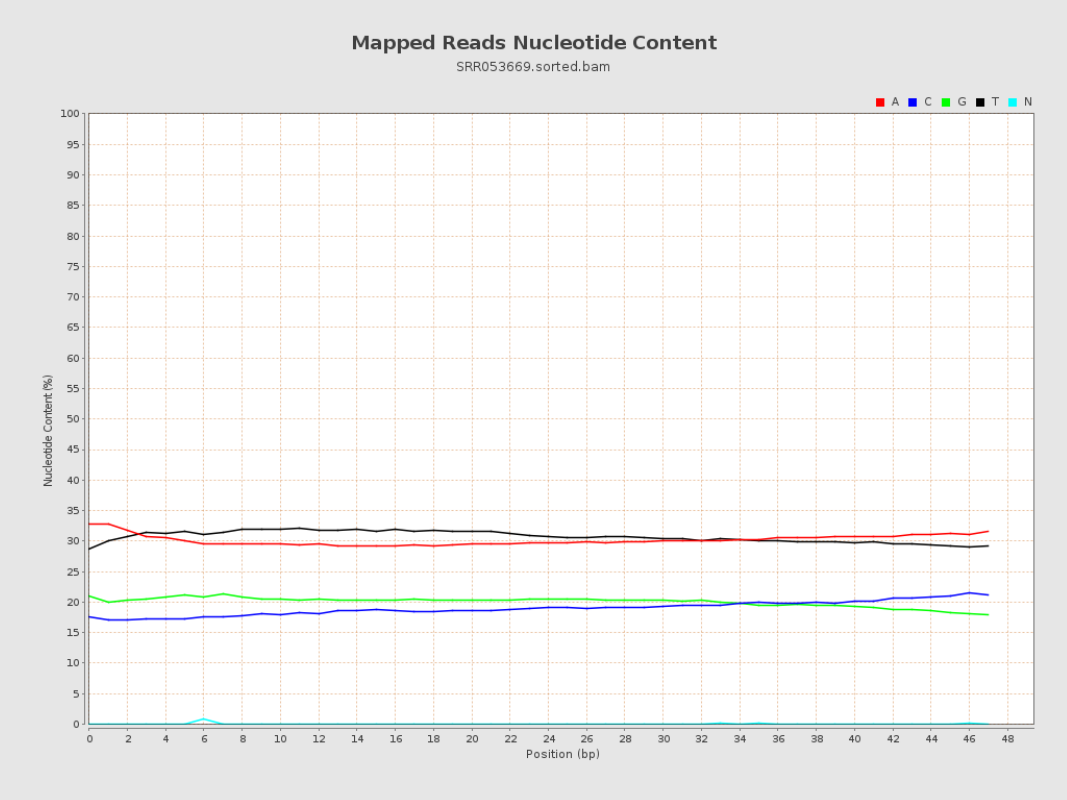
6. Results : Genome Fraction Coverage



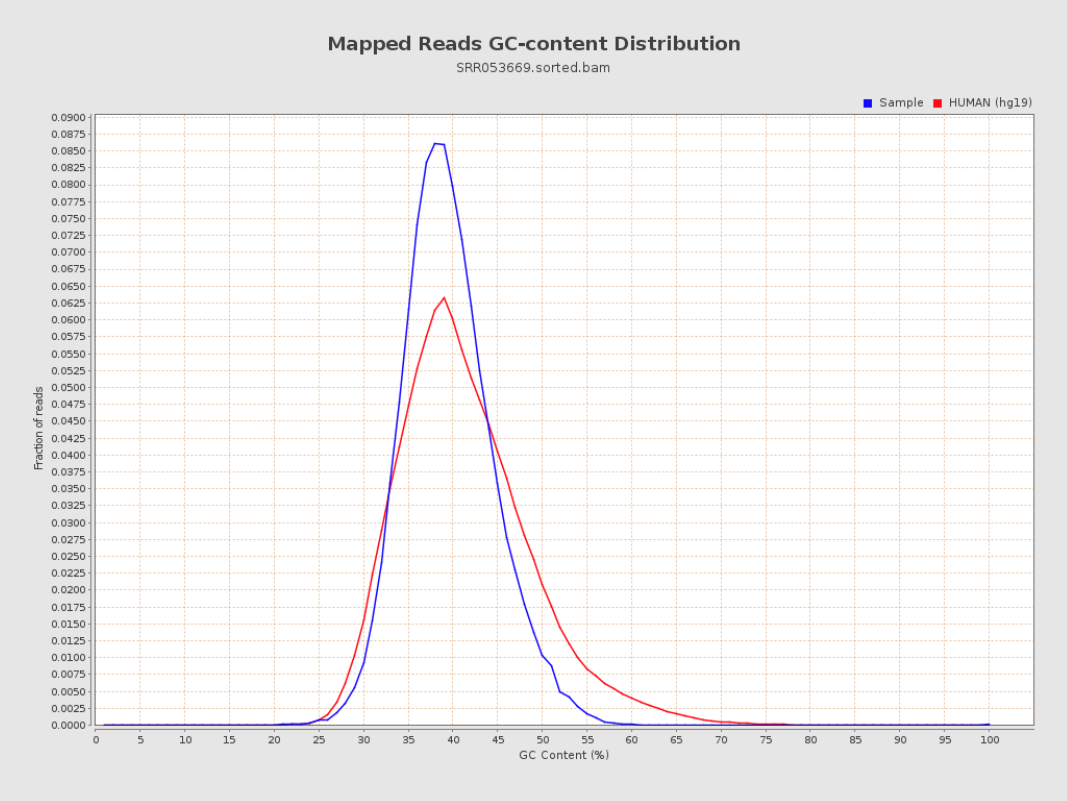
7. Results : Duplication Rate Histogram



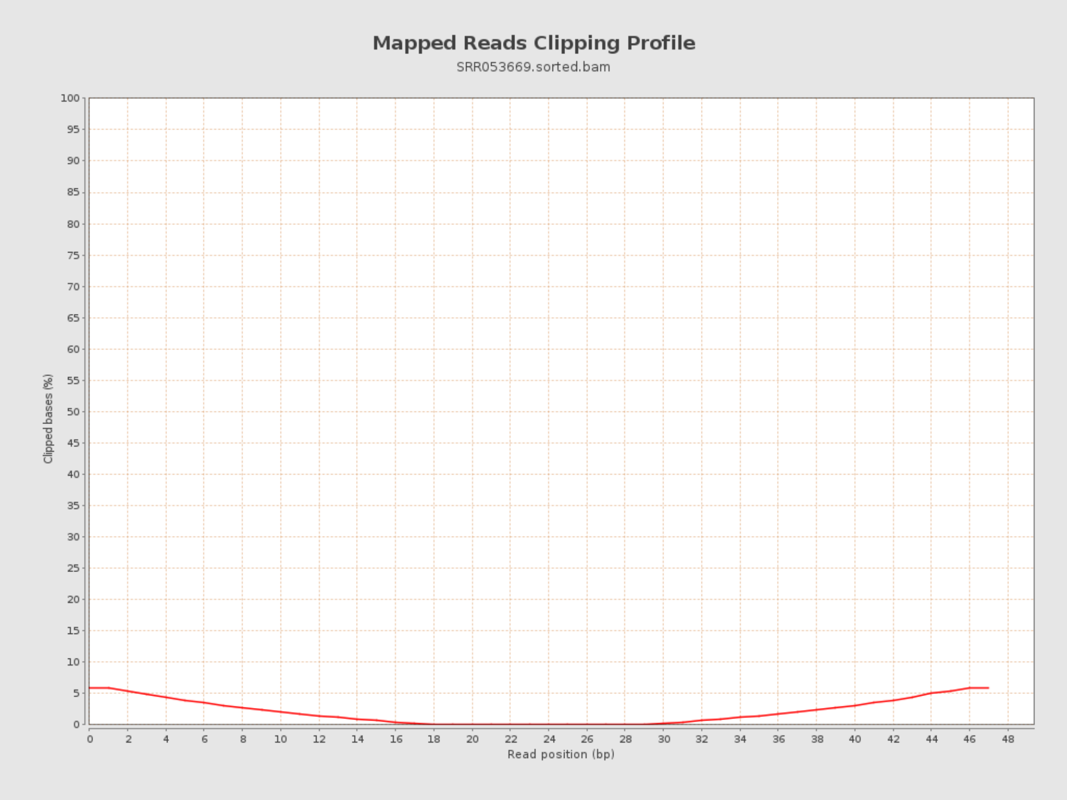
8. Results : Mapped Reads Nucleotide Content



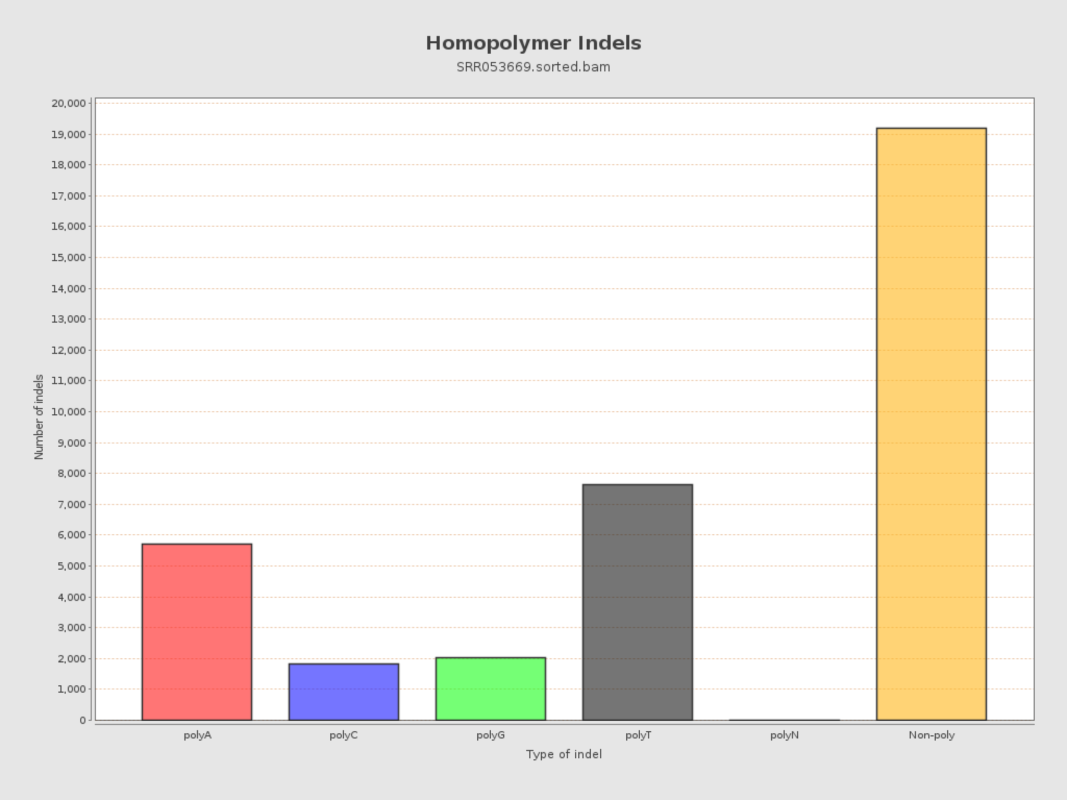
9. Results : Mapped Reads GC-content Distribution



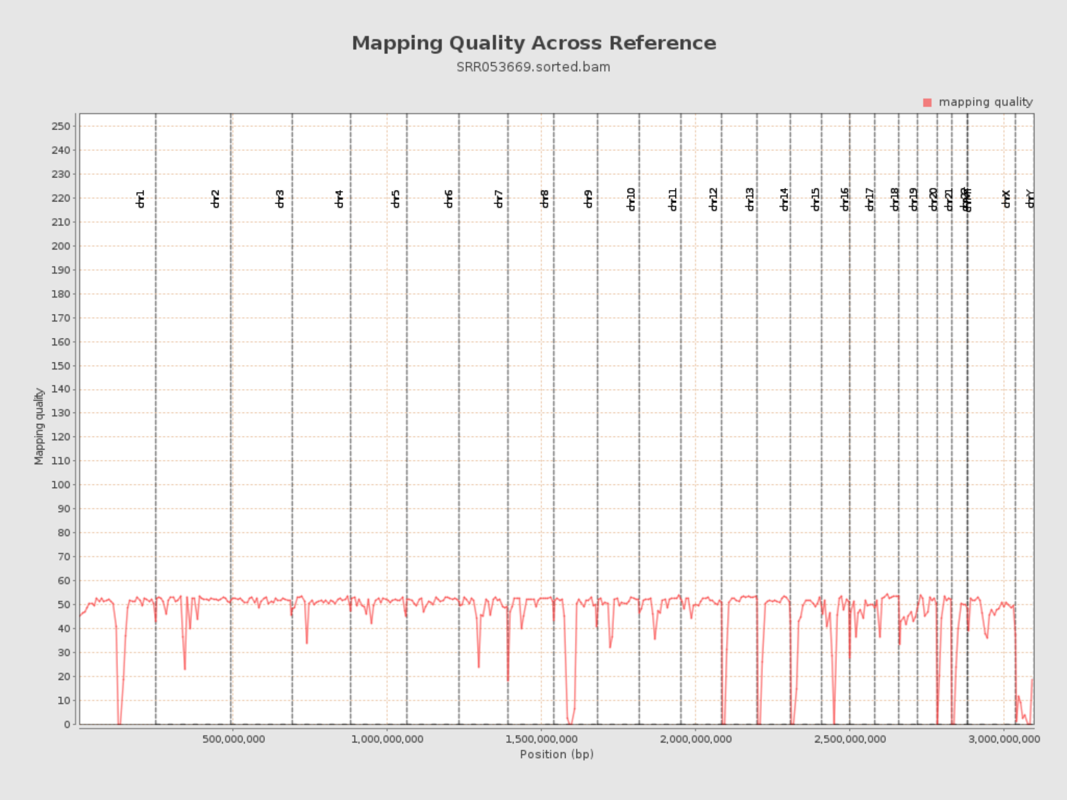
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram