Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:27:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053668.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_SRR053668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053668.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:27:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,985,600
Mapped reads	5,773,825 / 72.3%
Unmapped reads	2,211,775 / 27.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	185 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,615,279 / 20.23%
Duplication rate	21.47%
Clipped reads	471,635 / 5.91%

2.2. ACGT Content

Number/percentage of A's	79,421,997 / 29.1%
Number/percentage of C's	52,387,239 / 19.19%
Number/percentage of T's	83,195,175 / 30.48%
Number/percentage of G's	57,836,504 / 21.19%
Number/percentage of N's	124,453 / 0.05%
GC Percentage	40.38%

2.3. Coverage

Mean	0.0882

Standard Deviation	0.7276

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

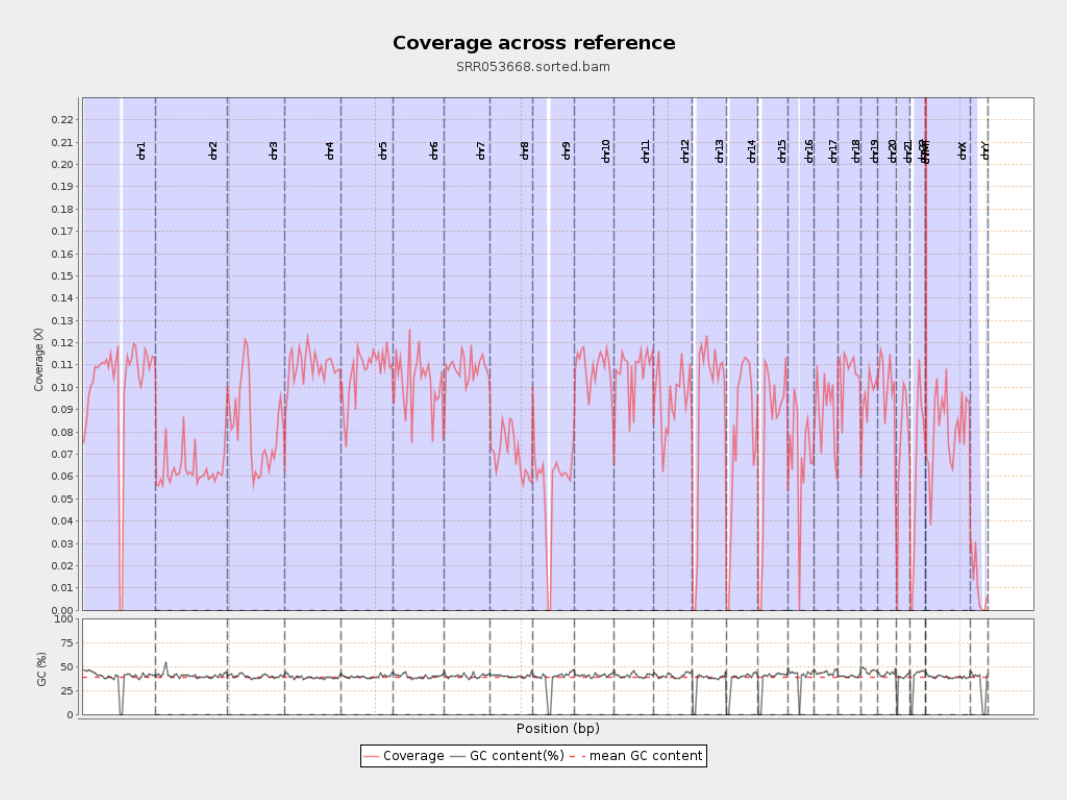
General error rate	0.65%
Mismatches	1,765,988
Insertions	12,546
Mapped reads with at least one insertion	0.22%
Deletions	39,917
Mapped reads with at least one deletion	0.69%
Homopolymer indels	48.66%

2.6. Chromosome stats

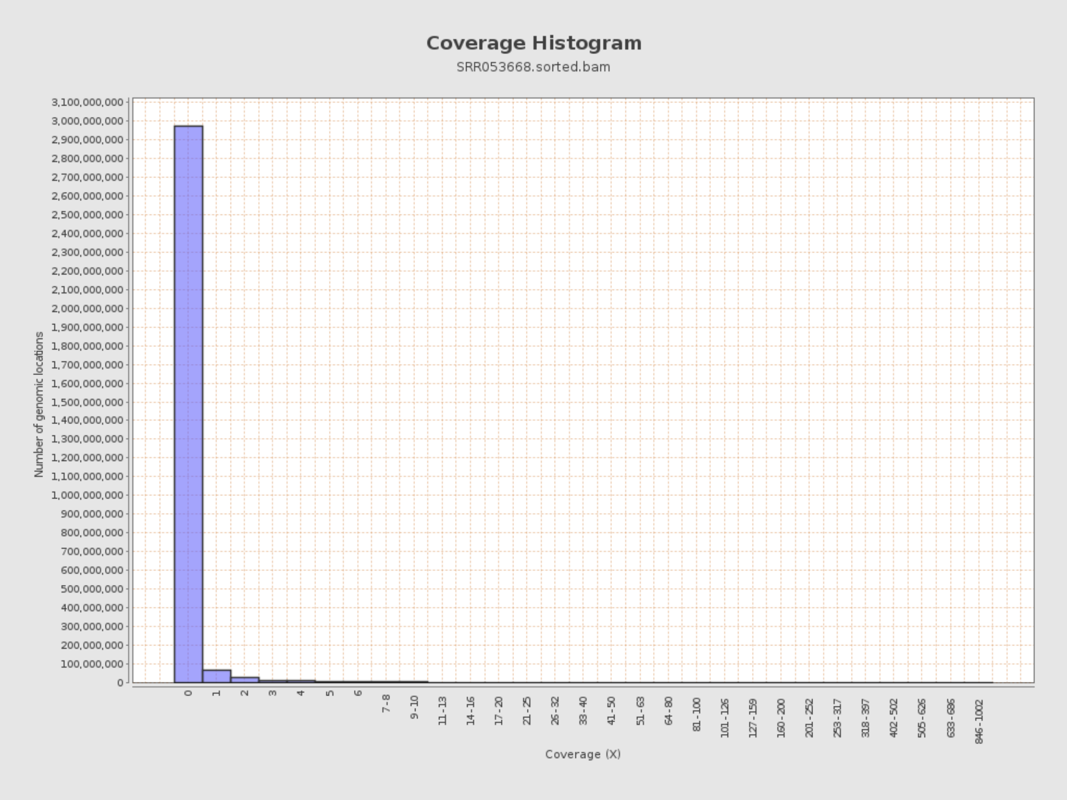
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25177747	0.101	0.8444
chr2	243199373	15386593	0.0633	0.979
chr3	198022430	16231109	0.082	0.6077
chr4	191154276	20961892	0.1097	0.7514
chr5	180915260	19379009	0.1071	0.7116
chr6	171115067	17454976	0.102	0.8071
chr7	159138663	17221895	0.1082	0.8775

chr8	146364022	10274370	0.0702	0.6364
chr9	141213431	7895882	0.0559	0.5218
chr10	135534747	14739431	0.1088	0.7759
chr11	135006516	14433317	0.1069	0.7687
chr12	133851895	12751287	0.0953	0.669
chr13	115169878	10637286	0.0924	0.6688
chr14	107349540	8495037	0.0791	0.6146
chr15	102531392	8148033	0.0795	0.5959
chr16	90354753	6133104	0.0679	0.5554
chr17	81195210	7299511	0.0899	0.6189
chr18	78077248	8368911	0.1072	0.8202
chr19	59128983	5700651	0.0964	0.7449
chr20	63025520	6382050	0.1013	0.6937
chr21	48129895	3568451	0.0741	0.6037
chr22	51304566	3258089	0.0635	0.5157
chrMT	16571	19660	1.1864	2.3614
chrX	155270560	12470533	0.0803	0.6394
chrY	59373566	635033	0.0107	0.2364

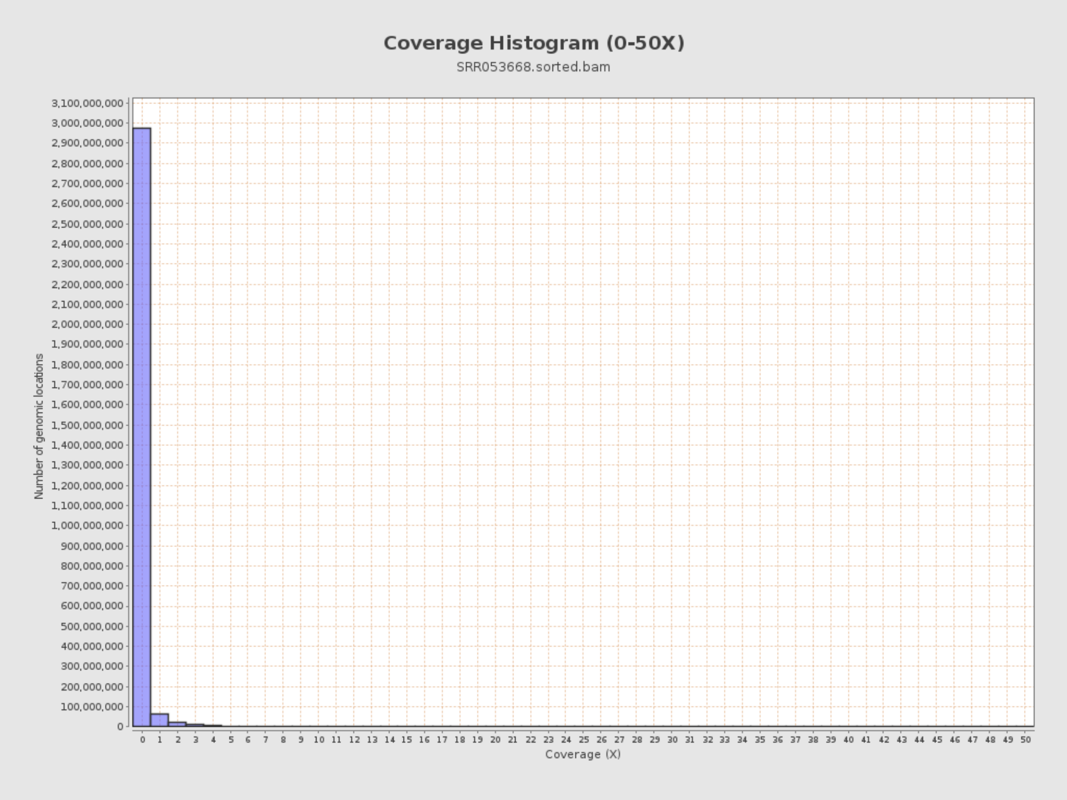
3. Results : Coverage across reference



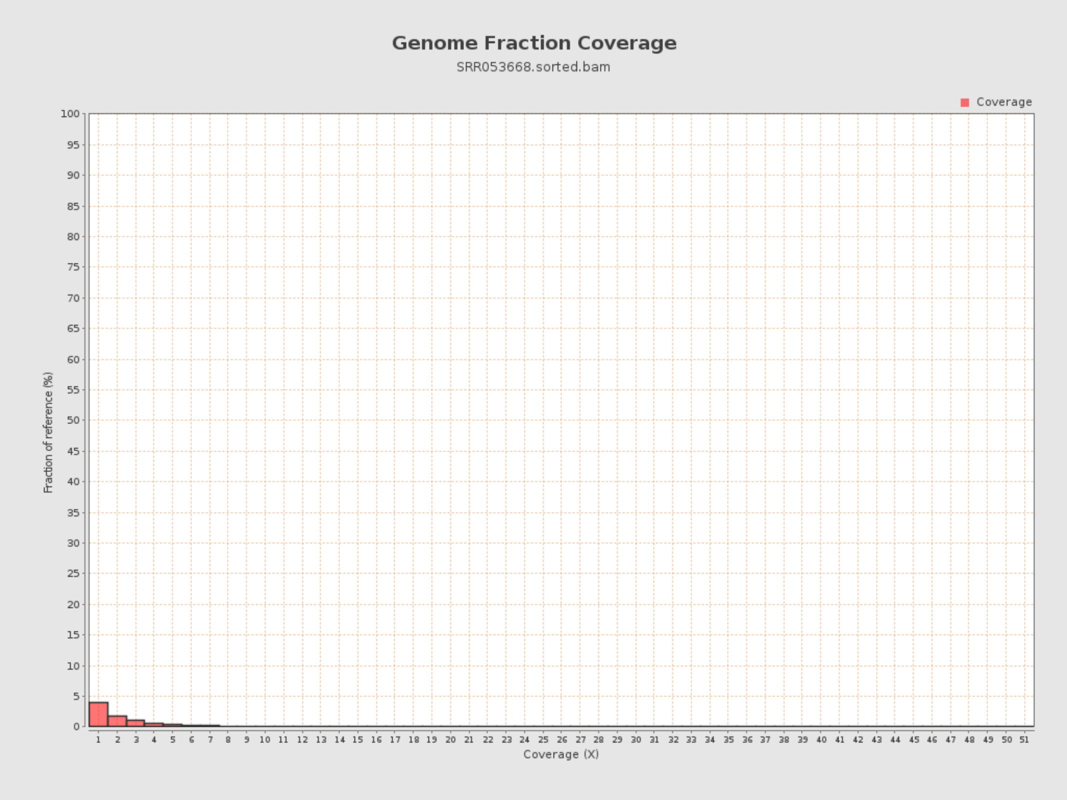
4. Results : Coverage Histogram



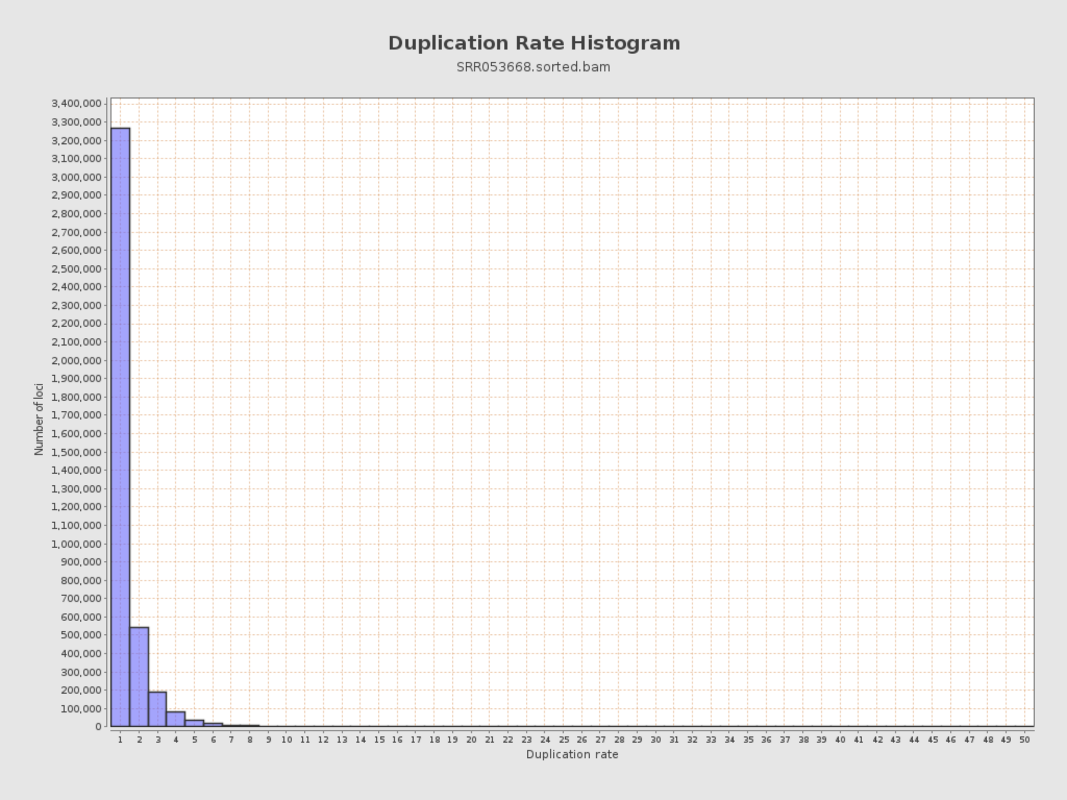
5. Results : Coverage Histogram (0-50X)



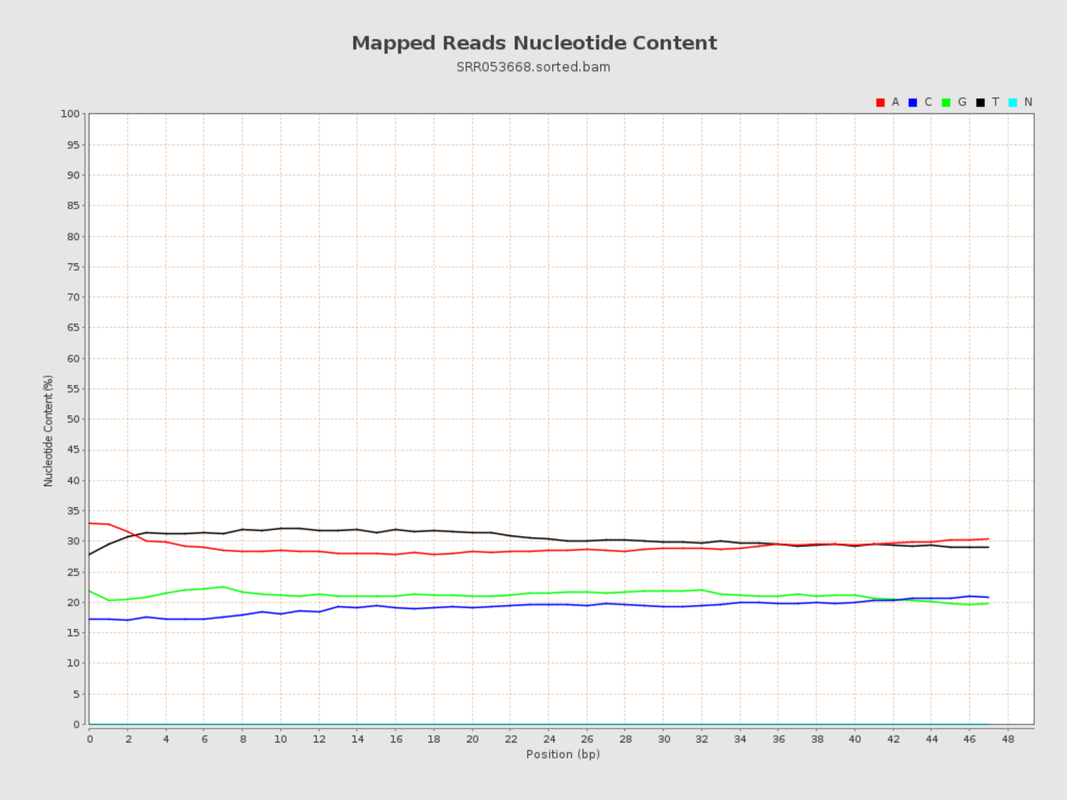
6. Results : Genome Fraction Coverage



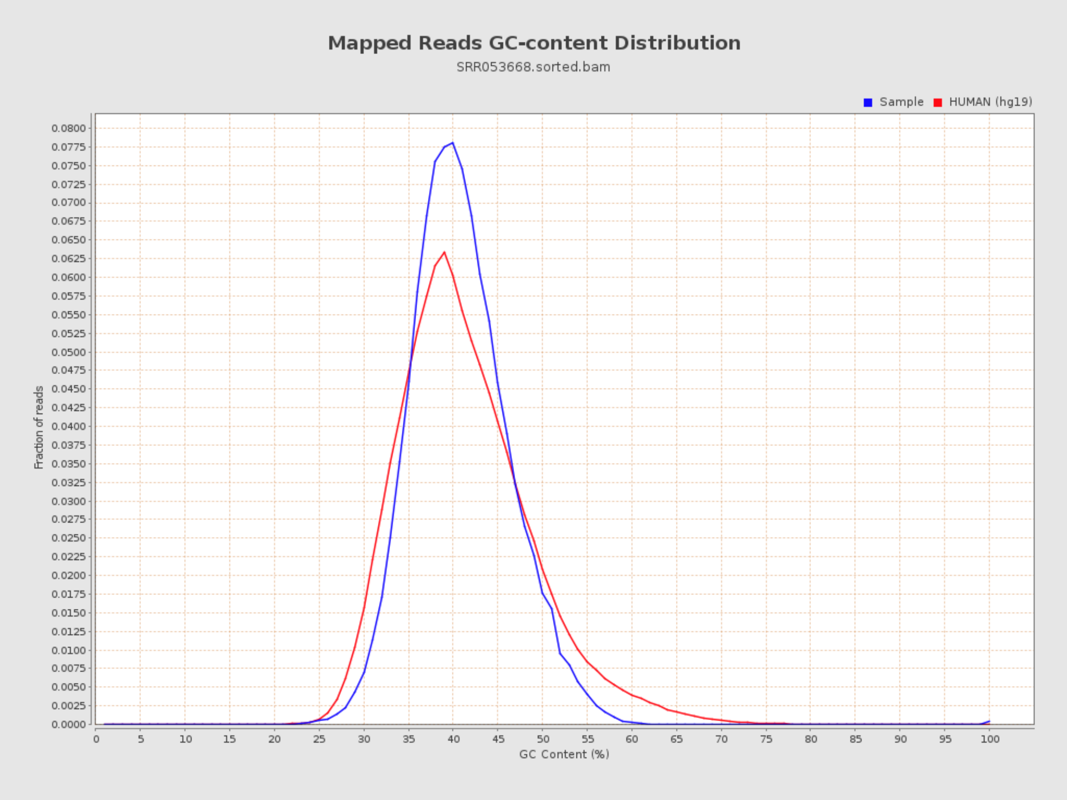
7. Results : Duplication Rate Histogram



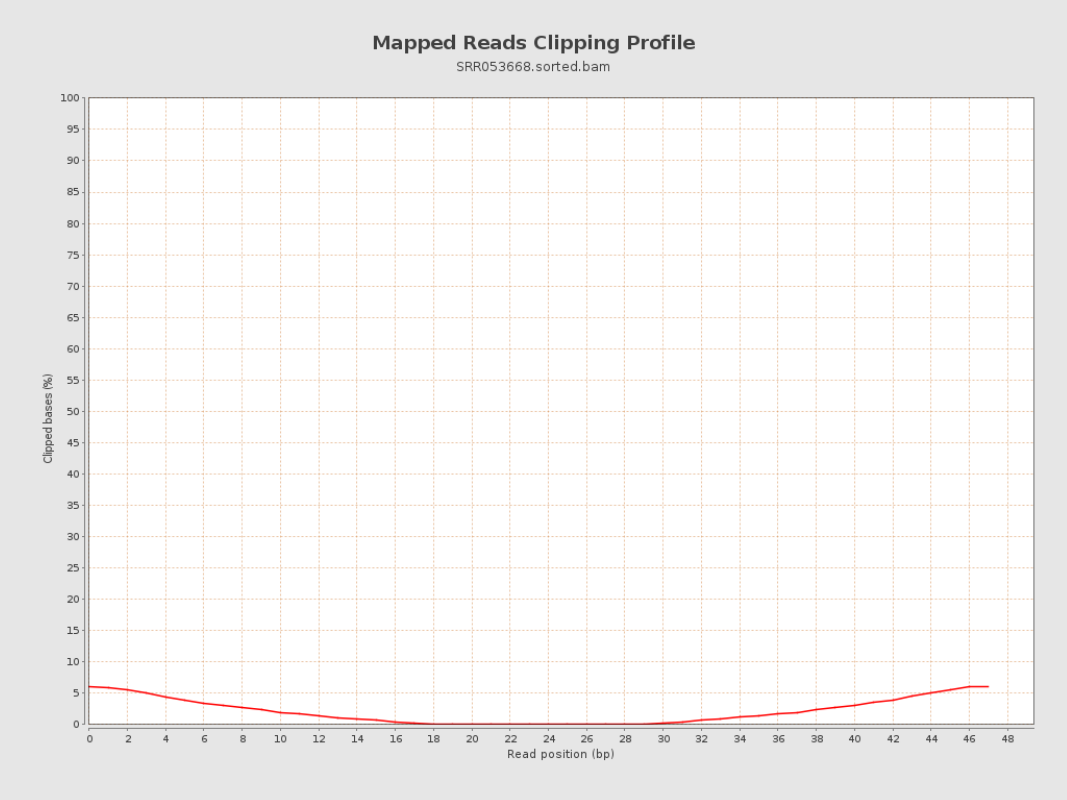
8. Results : Mapped Reads Nucleotide Content



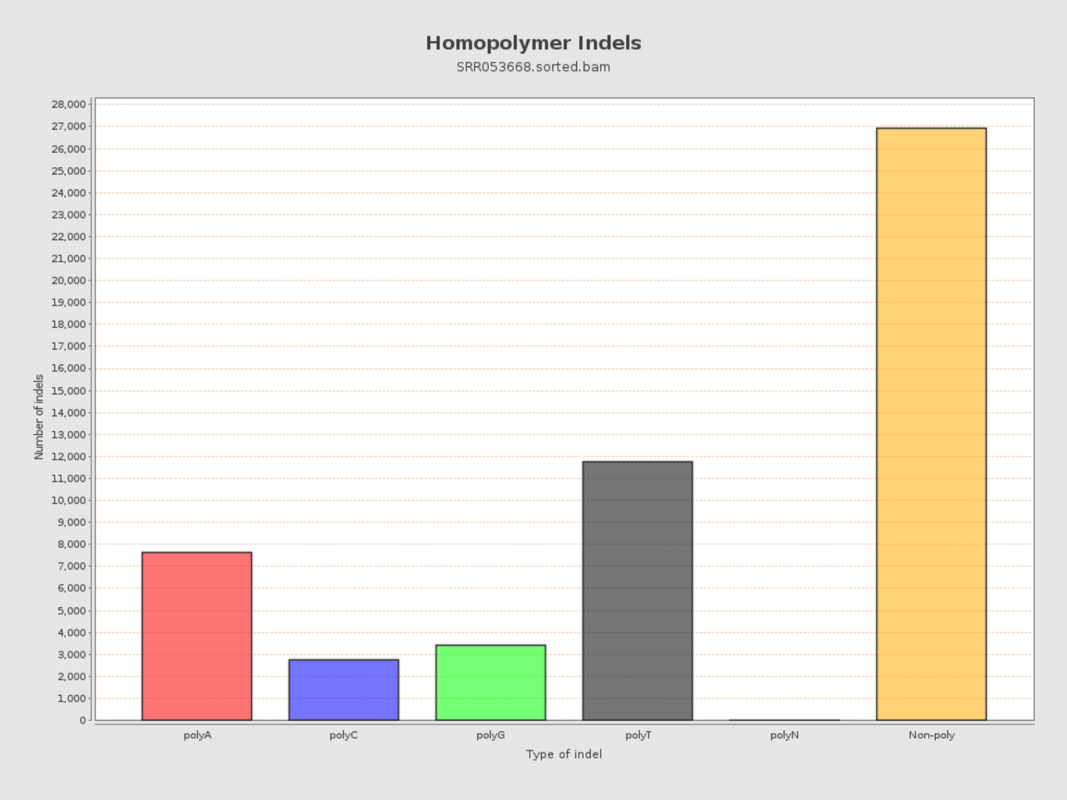
9. Results : Mapped Reads GC-content Distribution



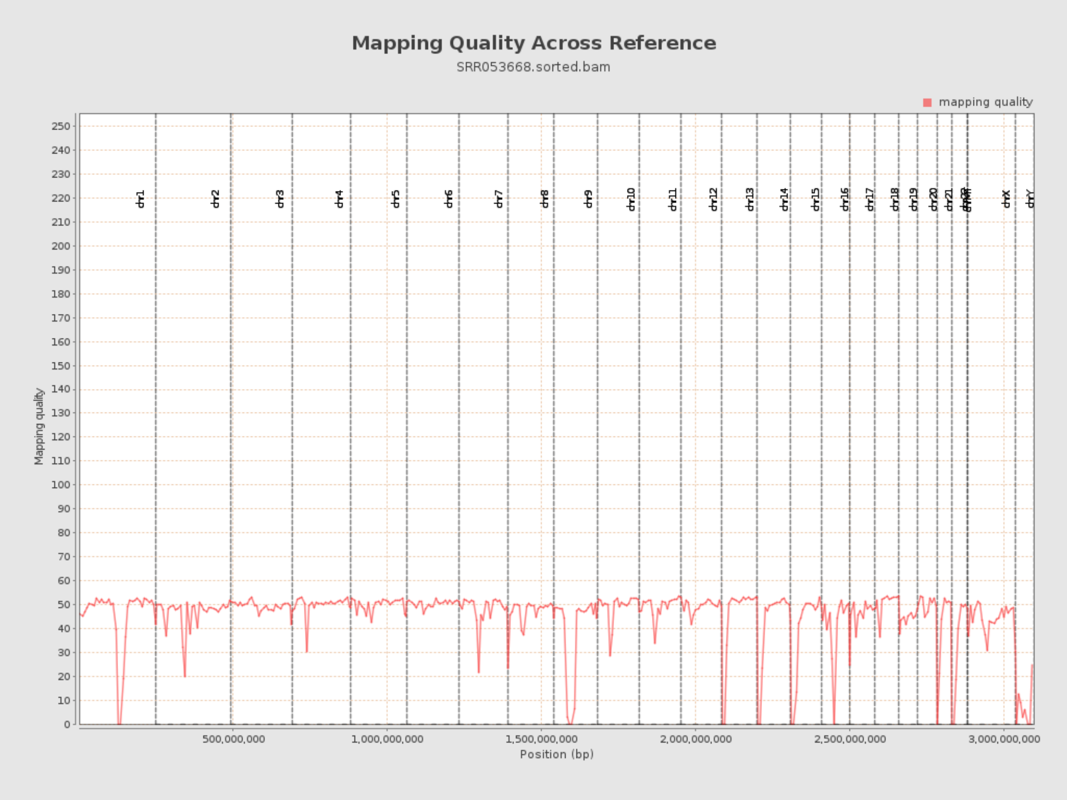
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram