Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:39:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053681.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_SRR053681 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053681.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:39:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053681.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,414,639
Mapped reads	7,029,007 / 83.53%
Unmapped reads	1,385,632 / 16.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	205 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,615,206 / 19.2%
Duplication rate	16.57%
Clipped reads	590,560 / 7.02%

2.2. ACGT Content

Number/percentage of A's	95,734,303 / 28.84%
Number/percentage of C's	66,305,920 / 19.98%
Number/percentage of T's	96,855,193 / 29.18%
Number/percentage of G's	72,958,021 / 21.98%
Number/percentage of N's	83,425 / 0.03%
GC Percentage	41.95%

2.3. Coverage

Mean	0.1072

Standard Deviation	0.9197

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

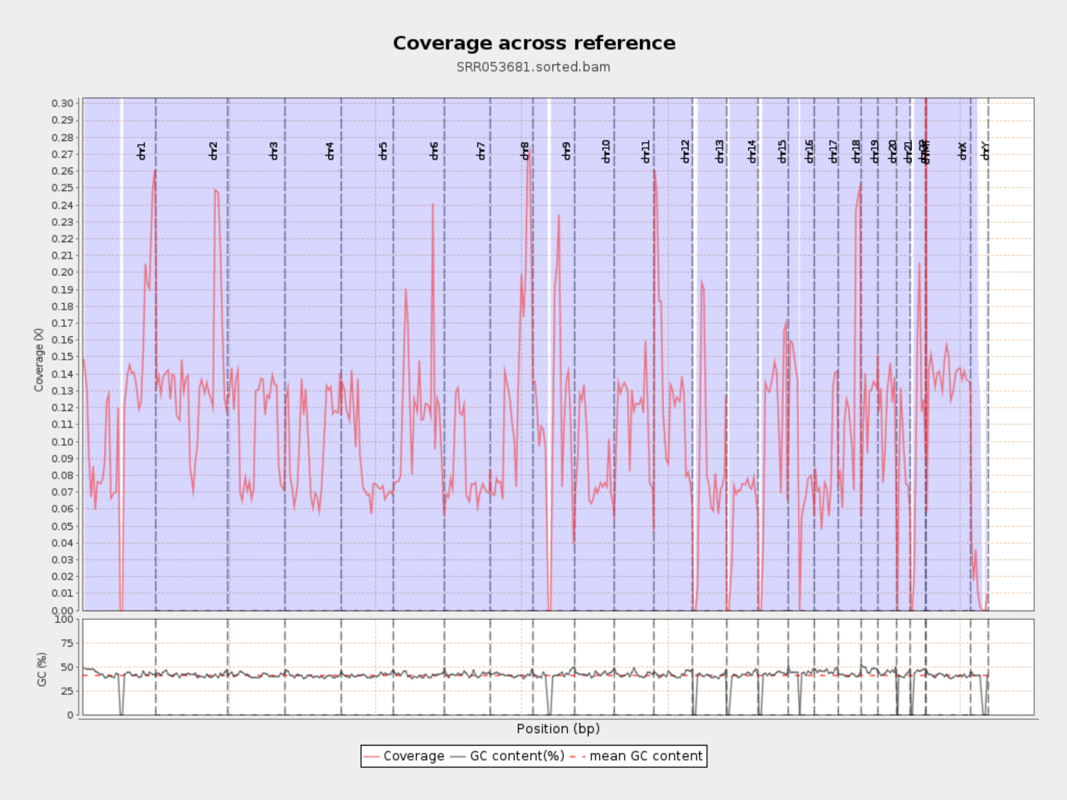
General error rate	0.47%
Mismatches	1,556,075
Insertions	12,582
Mapped reads with at least one insertion	0.18%
Deletions	42,855
Mapped reads with at least one deletion	0.61%
Homopolymer indels	46.11%

2.6. Chromosome stats

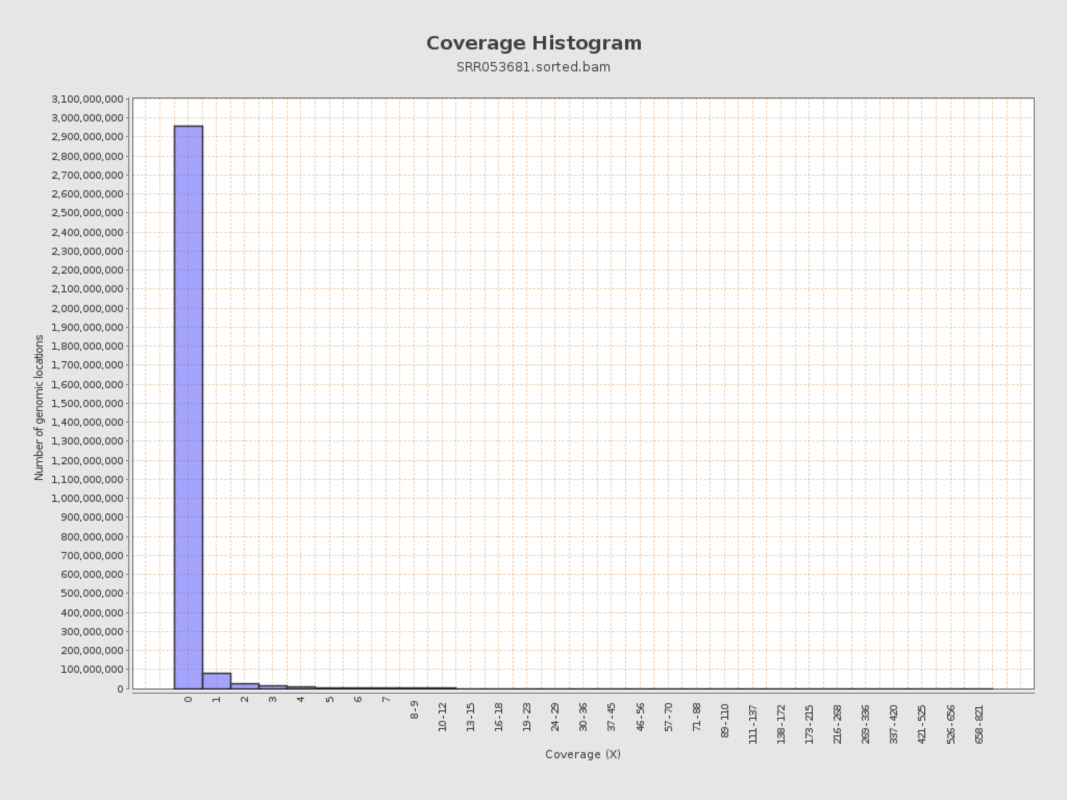
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29752157	0.1194	1.0121
chr2	243199373	33336347	0.1371	1.149
chr3	198022430	21470886	0.1084	0.9271
chr4	191154276	19247979	0.1007	0.8937
chr5	180915260	16204713	0.0896	0.7166
chr6	171115067	20606293	0.1204	1.1084
chr7	159138663	13221978	0.0831	0.744

chr8	146364022	19626590	0.1341	1.0782
chr9	141213431	15732076	0.1114	0.8895
chr10	135534747	11524355	0.085	0.8047
chr11	135006516	15757885	0.1167	0.914
chr12	133851895	17846138	0.1333	0.9299
chr13	115169878	9014257	0.0783	0.7469
chr14	107349540	6491986	0.0605	0.7077
chr15	102531392	10829309	0.1056	0.8521
chr16	90354753	8311047	0.092	0.7962
chr17	81195210	6958585	0.0857	0.7526
chr18	78077248	10400388	0.1332	1.1013
chr19	59128983	7219292	0.1221	0.918
chr20	63025520	7465773	0.1185	0.988
chr21	48129895	3753570	0.078	0.8431
chr22	51304566	5086053	0.0991	0.8649
chrMT	16571	20037	1.2092	2.6018
chrX	155270560	21316419	0.1373	0.9761
chrY	59373566	807844	0.0136	0.3111

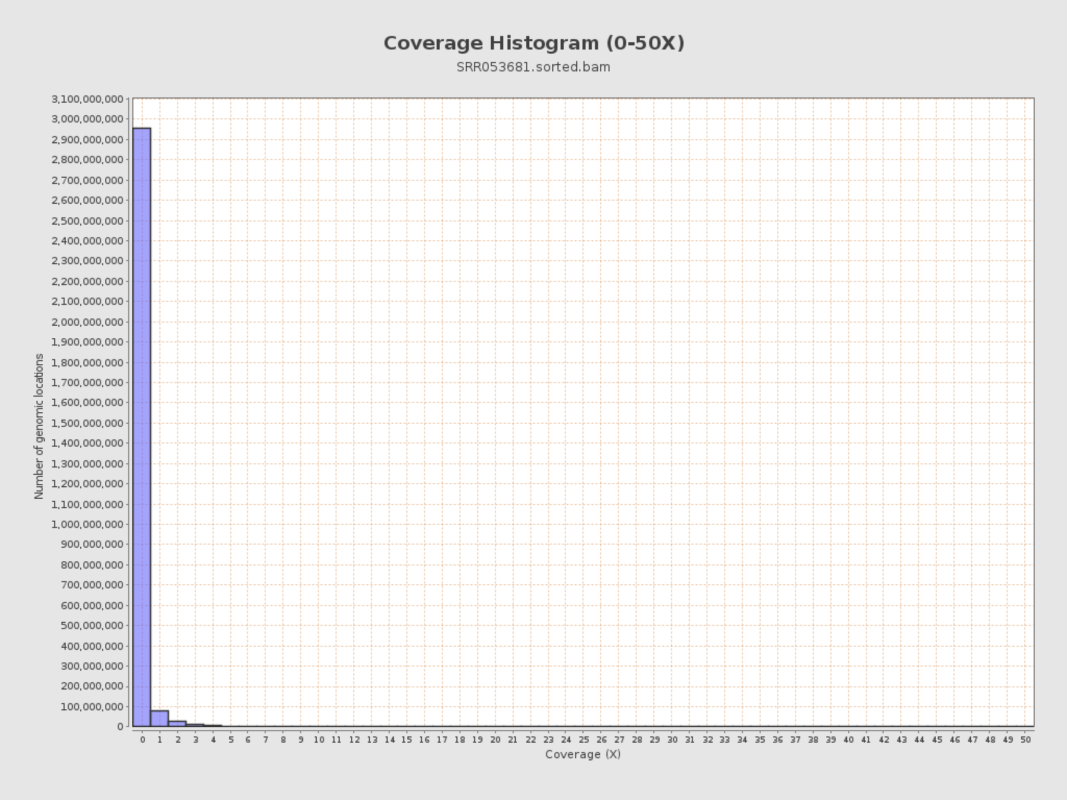
3. Results : Coverage across reference



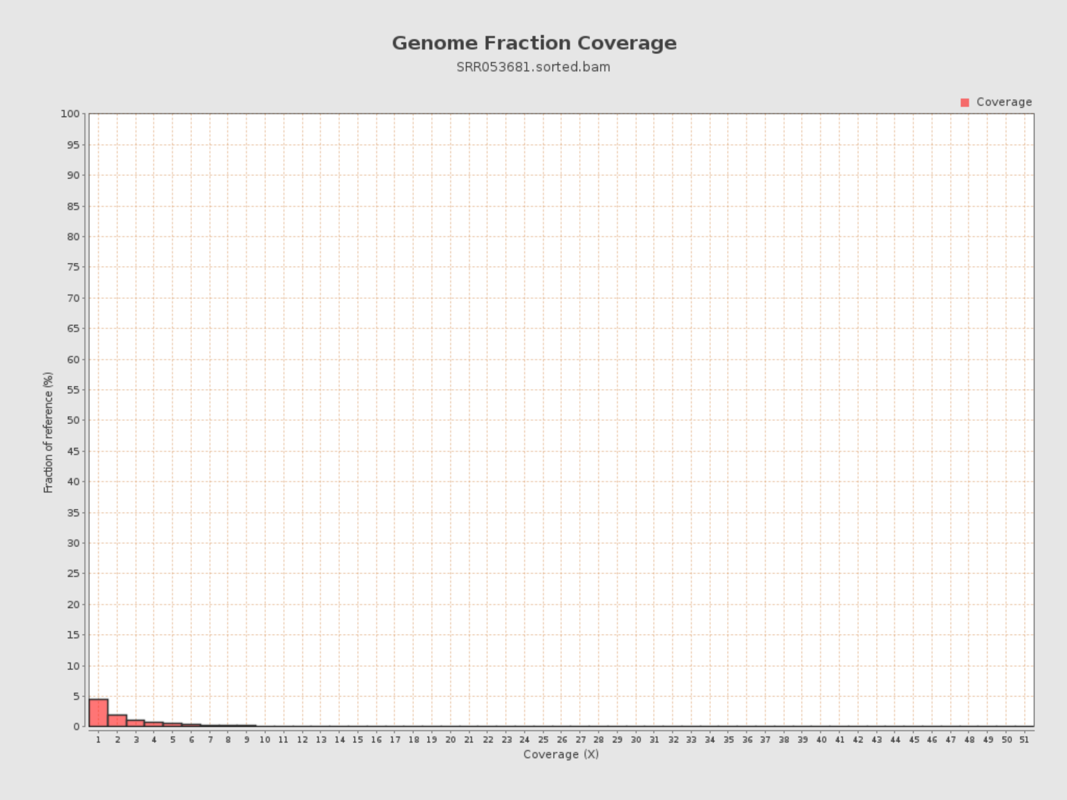
4. Results : Coverage Histogram



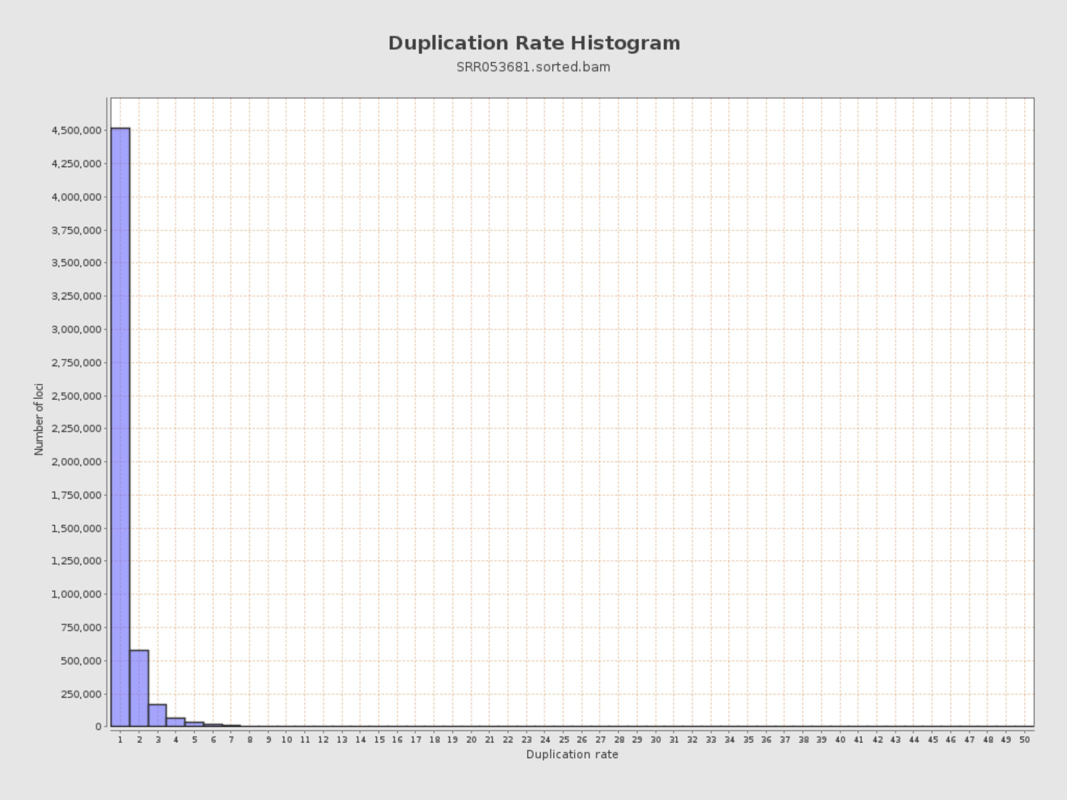
5. Results : Coverage Histogram (0-50X)



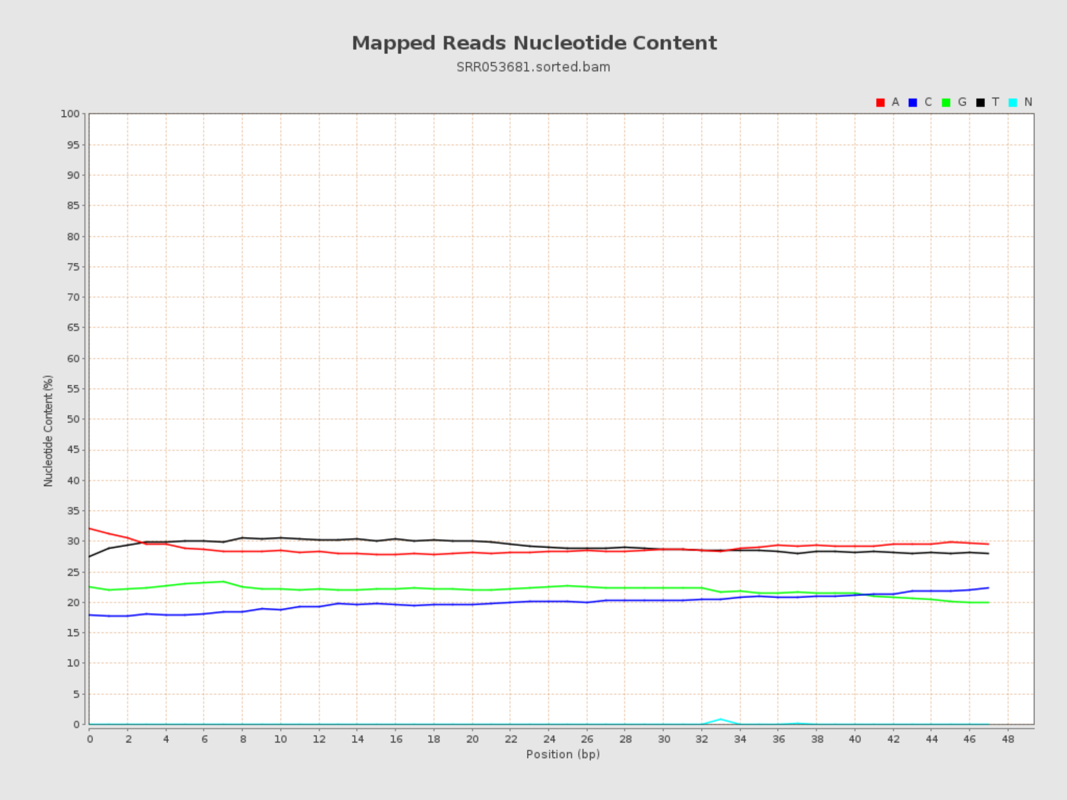
6. Results : Genome Fraction Coverage



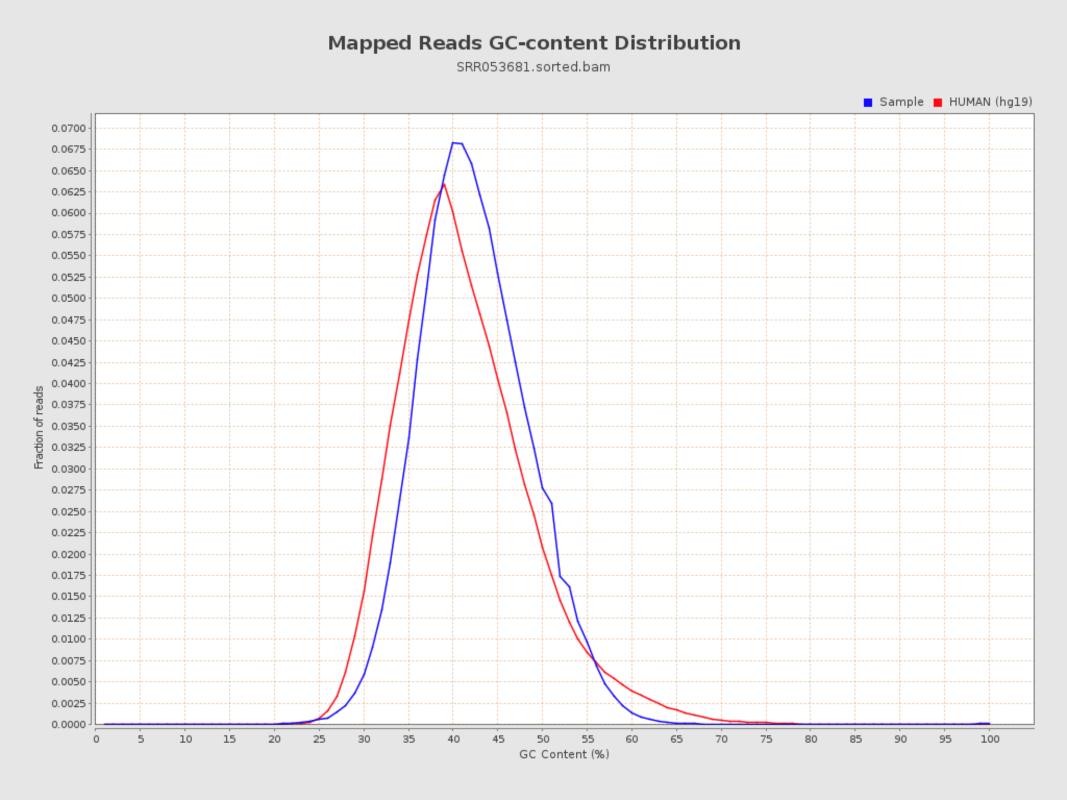
7. Results : Duplication Rate Histogram



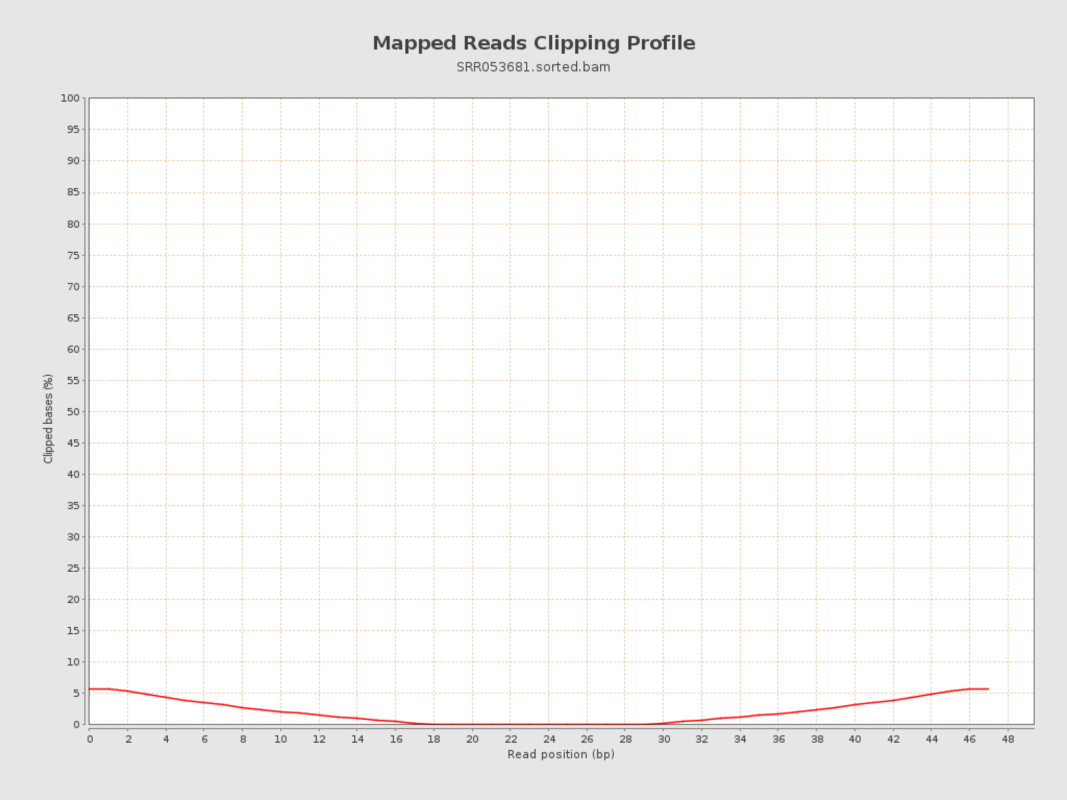
8. Results : Mapped Reads Nucleotide Content



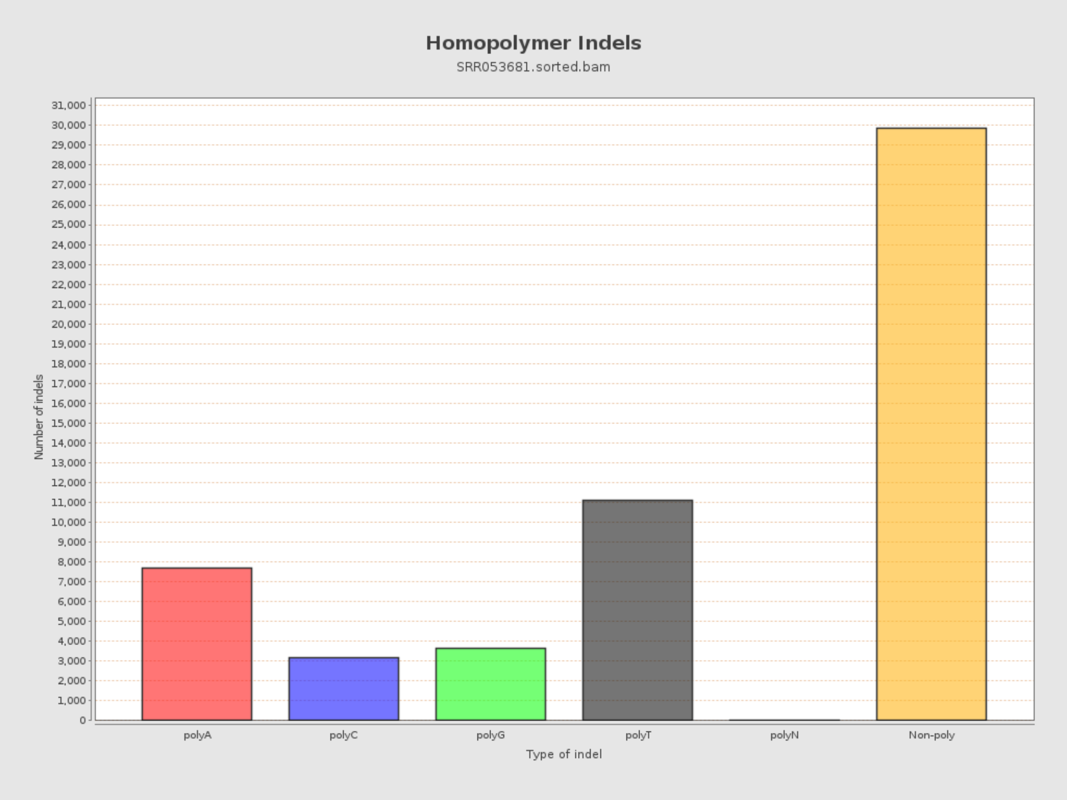
9. Results : Mapped Reads GC-content Distribution



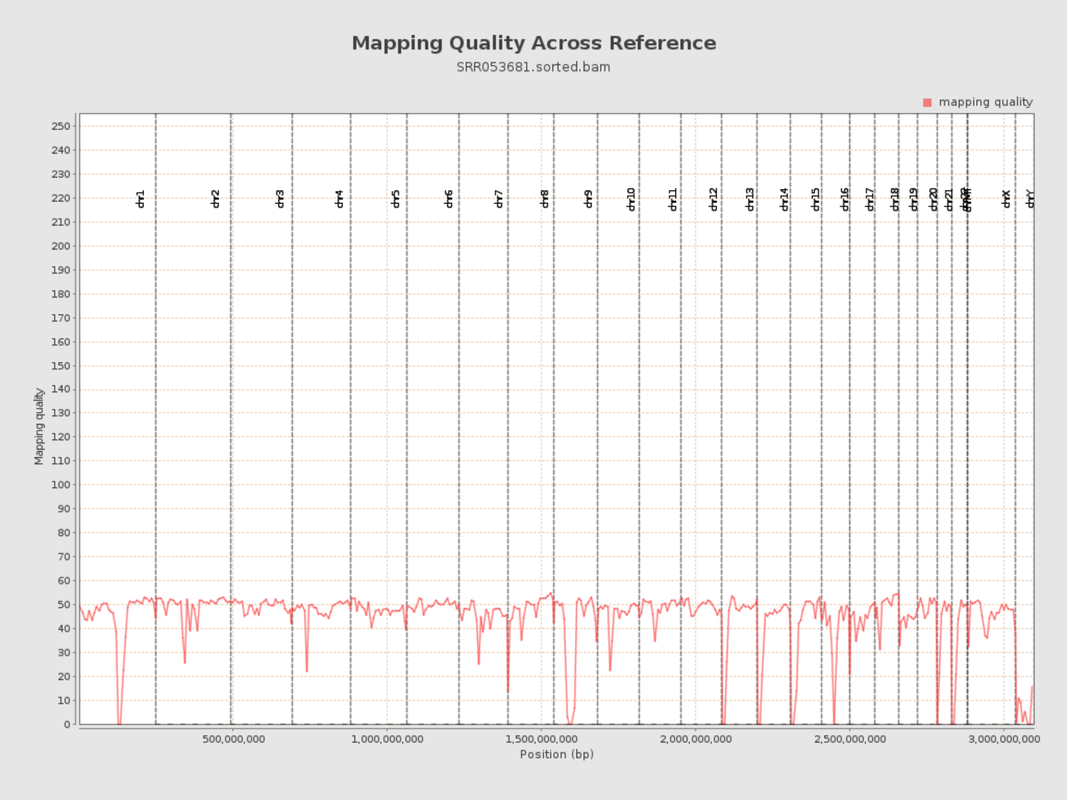
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram