Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053636.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_SRR053636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:43:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,181,145
Mapped reads	7,439,182 / 66.53%
Unmapped reads	3,741,963 / 33.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	188 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,864,700 / 16.68%
Duplication rate	17.5%
Clipped reads	782,718 / 7%

2.2. ACGT Content

Number/percentage of A's	104,458,144 / 29.82%
Number/percentage of C's	70,079,391 / 20.01%
Number/percentage of T's	103,484,050 / 29.54%
Number/percentage of G's	72,264,341 / 20.63%
Number/percentage of N's	463 / 0%
GC Percentage	40.64%

2.3. Coverage

Mean	0.1132

Standard Deviation	1.1746

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

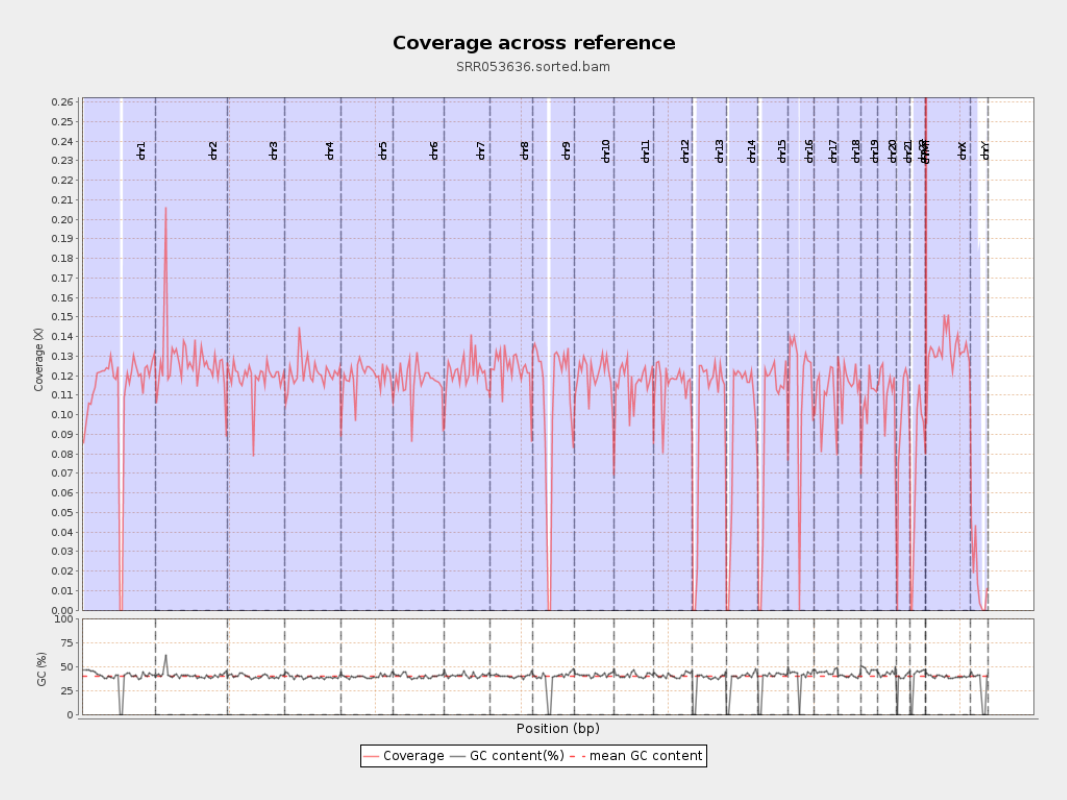
General error rate	0.74%
Mismatches	2,568,737
Insertions	15,022
Mapped reads with at least one insertion	0.2%
Deletions	48,102
Mapped reads with at least one deletion	0.65%
Homopolymer indels	46.83%

2.6. Chromosome stats

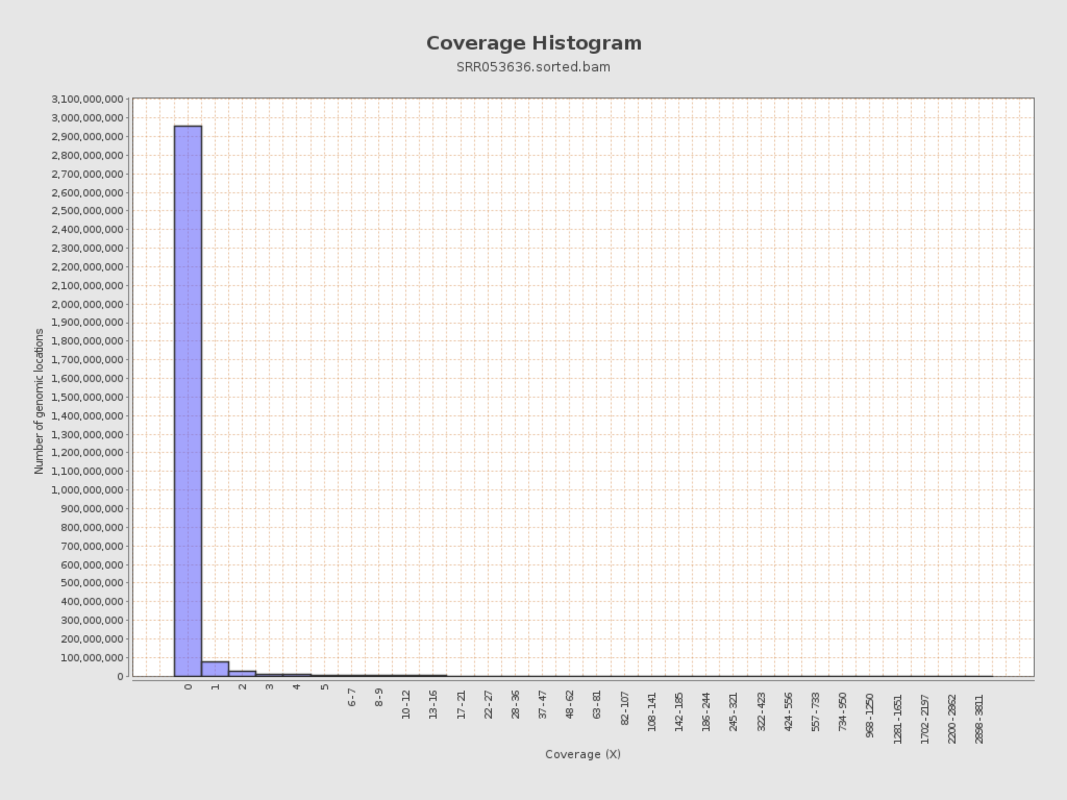
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27697149	0.1111	1.0114
chr2	243199373	30904496	0.1271	2.6874
chr3	198022430	23602929	0.1192	0.9012
chr4	191154276	23270436	0.1217	0.9438
chr5	180915260	21560738	0.1192	0.8967
chr6	171115067	20035377	0.1171	0.96
chr7	159138663	19335446	0.1215	1.0595

chr8	146364022	18049206	0.1233	1.0463
chr9	141213431	15095900	0.1069	0.89
chr10	135534747	16365689	0.1207	0.9806
chr11	135006516	15686570	0.1162	1.0023
chr12	133851895	15527538	0.116	0.8798
chr13	115169878	11500569	0.0999	0.8264
chr14	107349540	10450090	0.0973	1.0953
chr15	102531392	9857118	0.0961	0.7991
chr16	90354753	10122731	0.112	0.892
chr17	81195210	8883472	0.1094	0.8361
chr18	78077248	9177135	0.1175	0.9877
chr19	59128983	6397302	0.1082	0.9951
chr20	63025520	7065326	0.1121	0.9137
chr21	48129895	4521944	0.094	0.8394
chr22	51304566	3660698	0.0714	0.6478
chrMT	16571	57928	3.4957	5.9885
chrX	155270560	20592897	0.1326	0.9934
chrY	59373566	939160	0.0158	0.3122

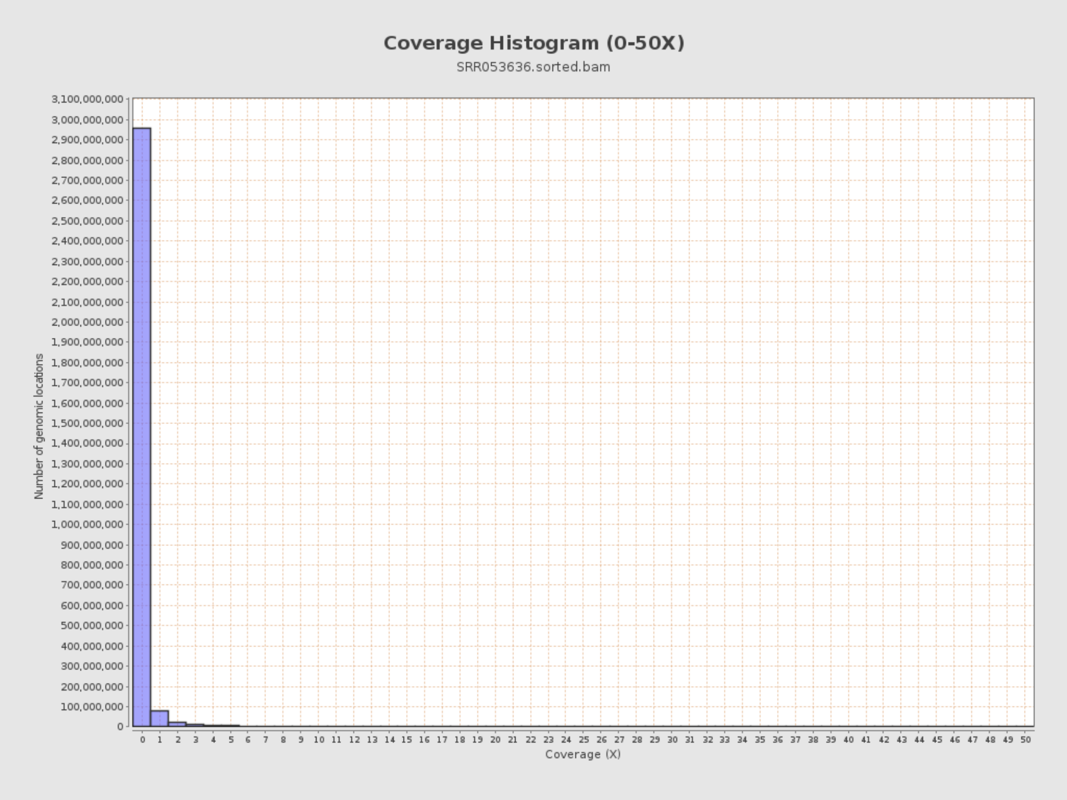
3. Results : Coverage across reference



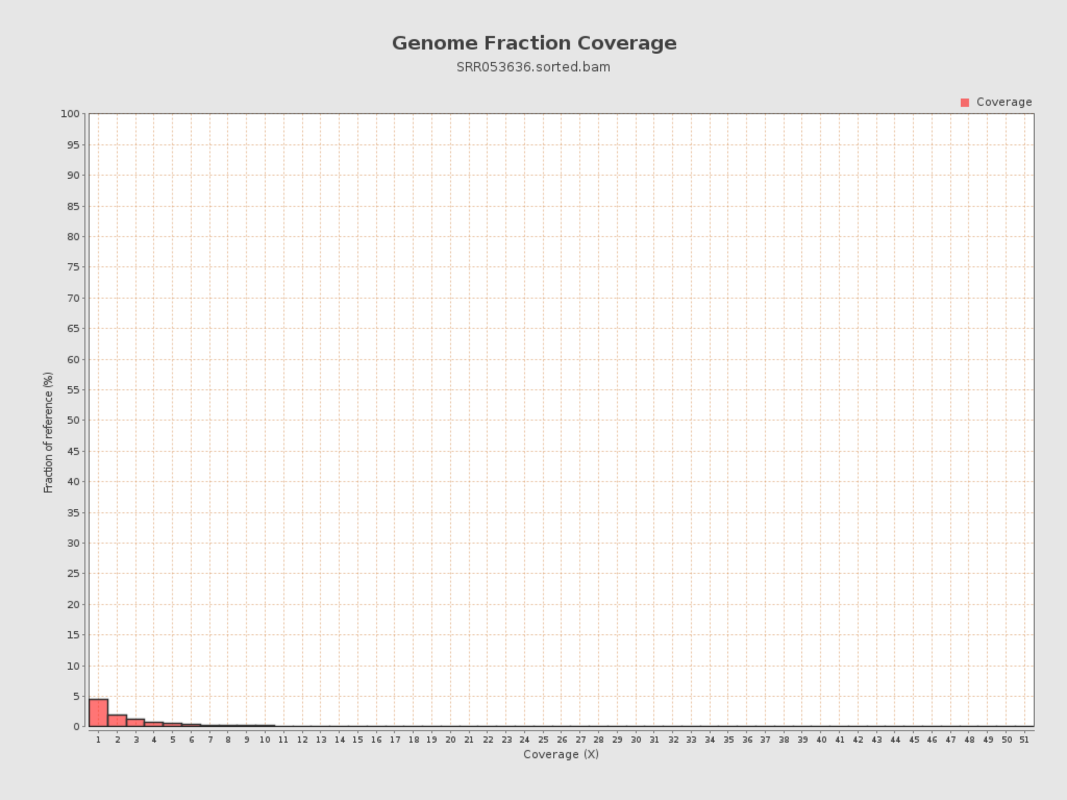
4. Results : Coverage Histogram



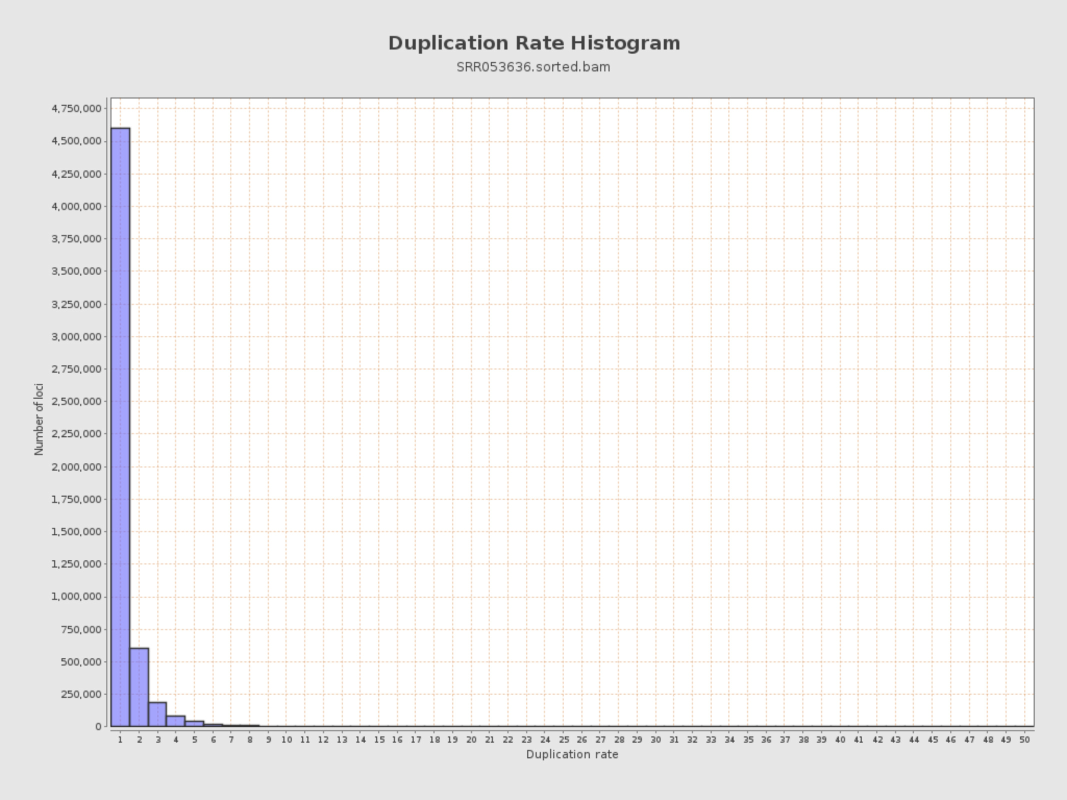
5. Results : Coverage Histogram (0-50X)



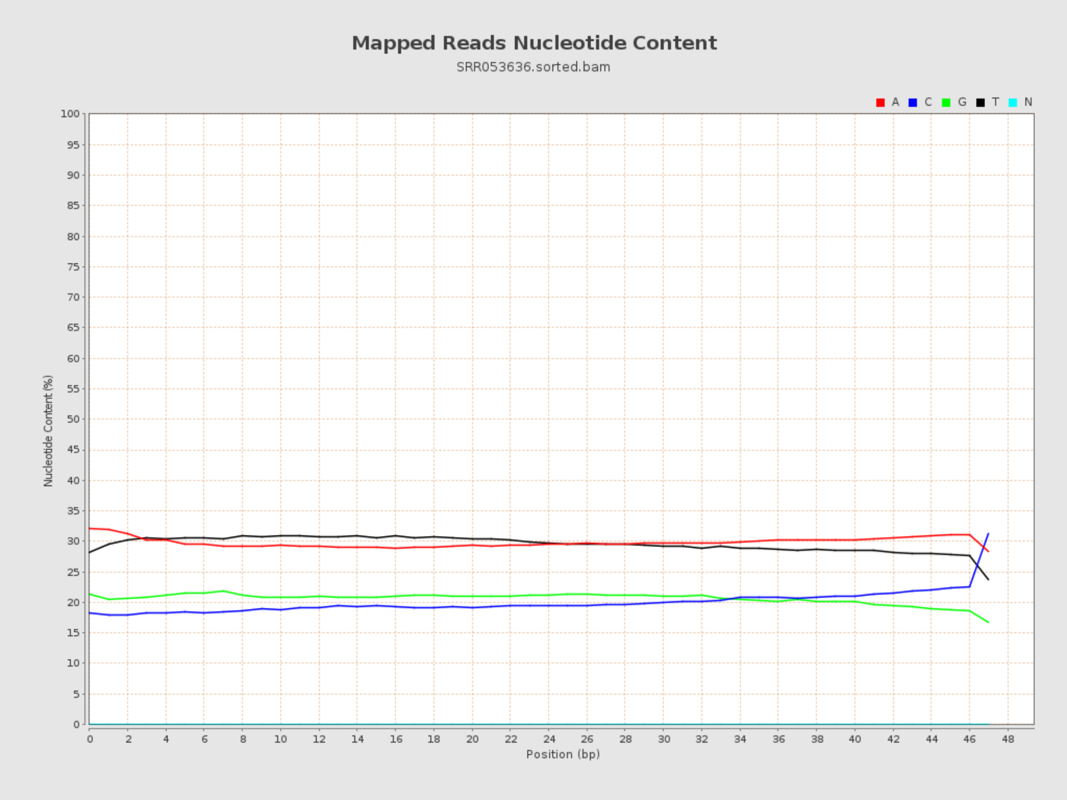
6. Results : Genome Fraction Coverage



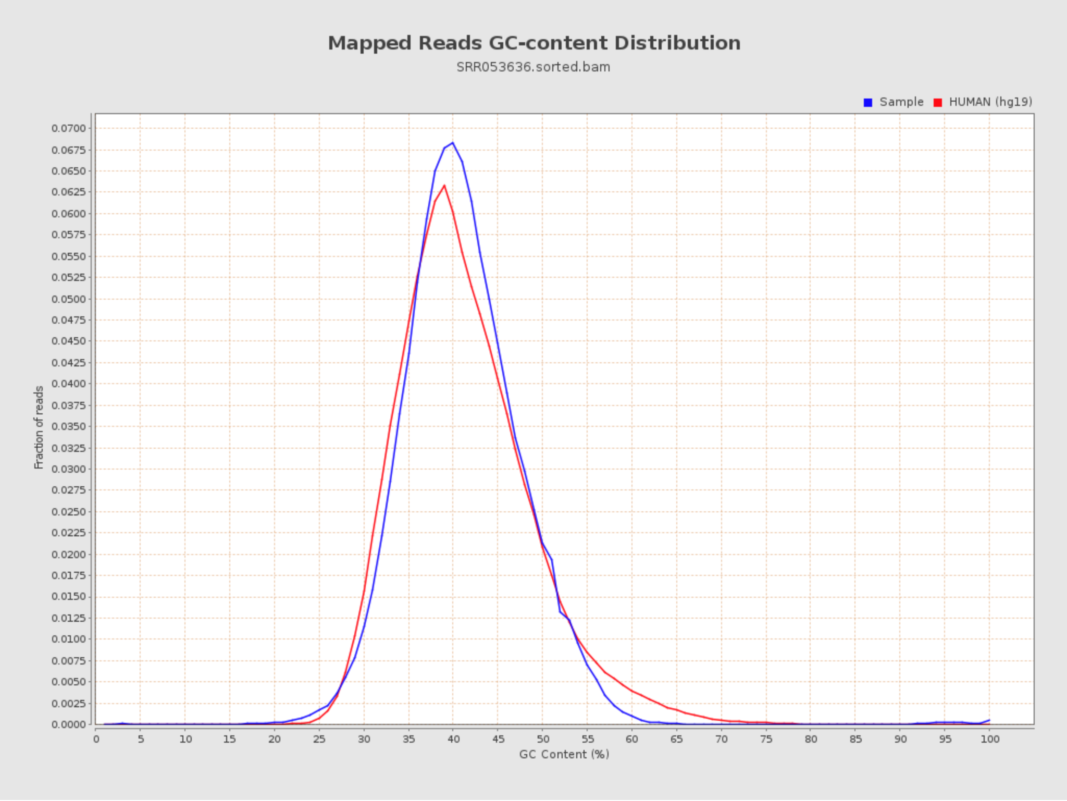
7. Results : Duplication Rate Histogram



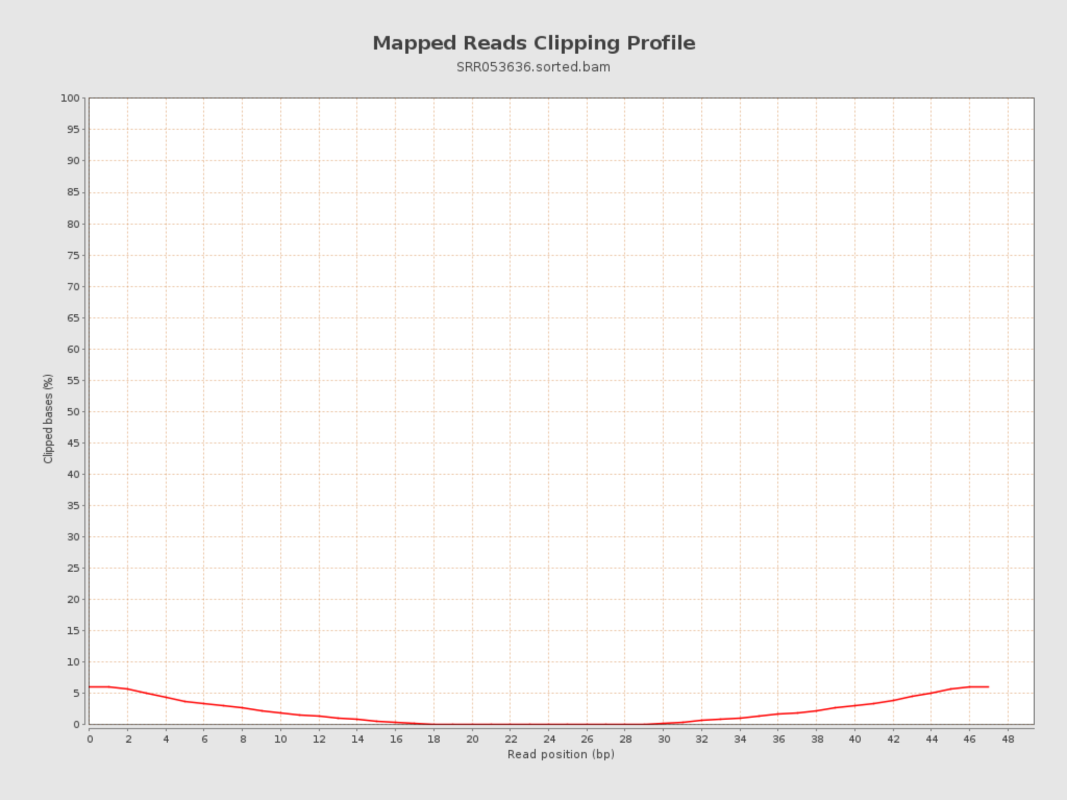
8. Results : Mapped Reads Nucleotide Content



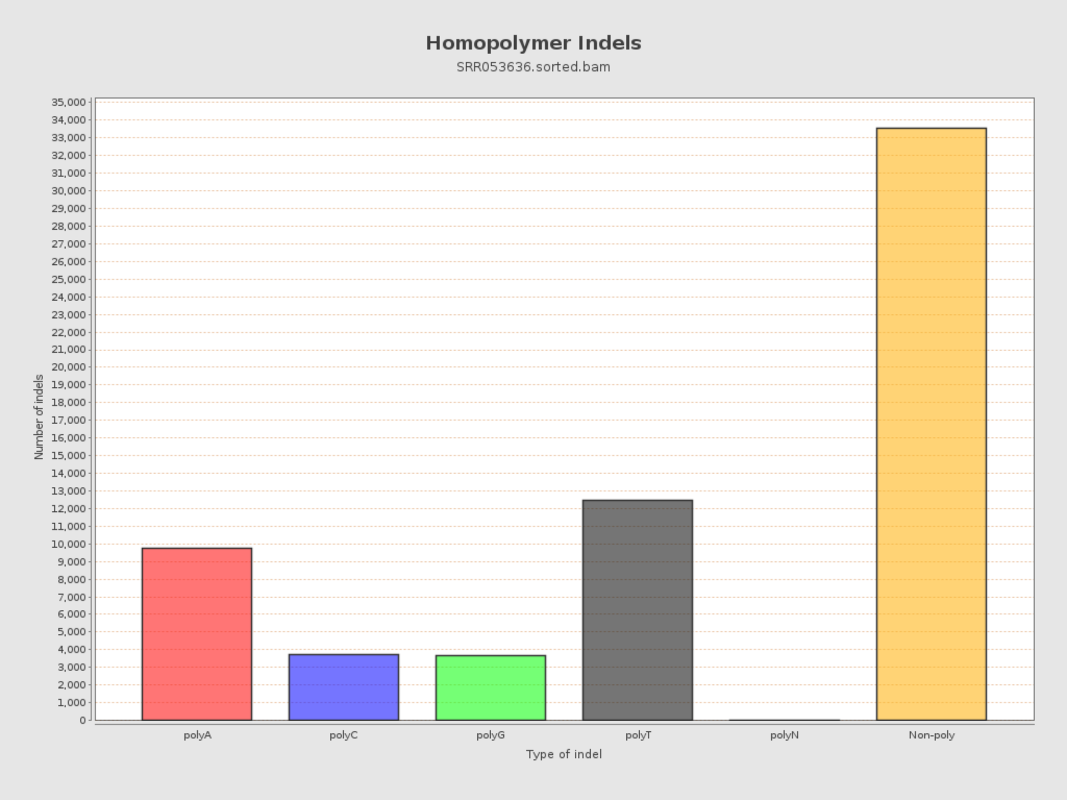
9. Results : Mapped Reads GC-content Distribution



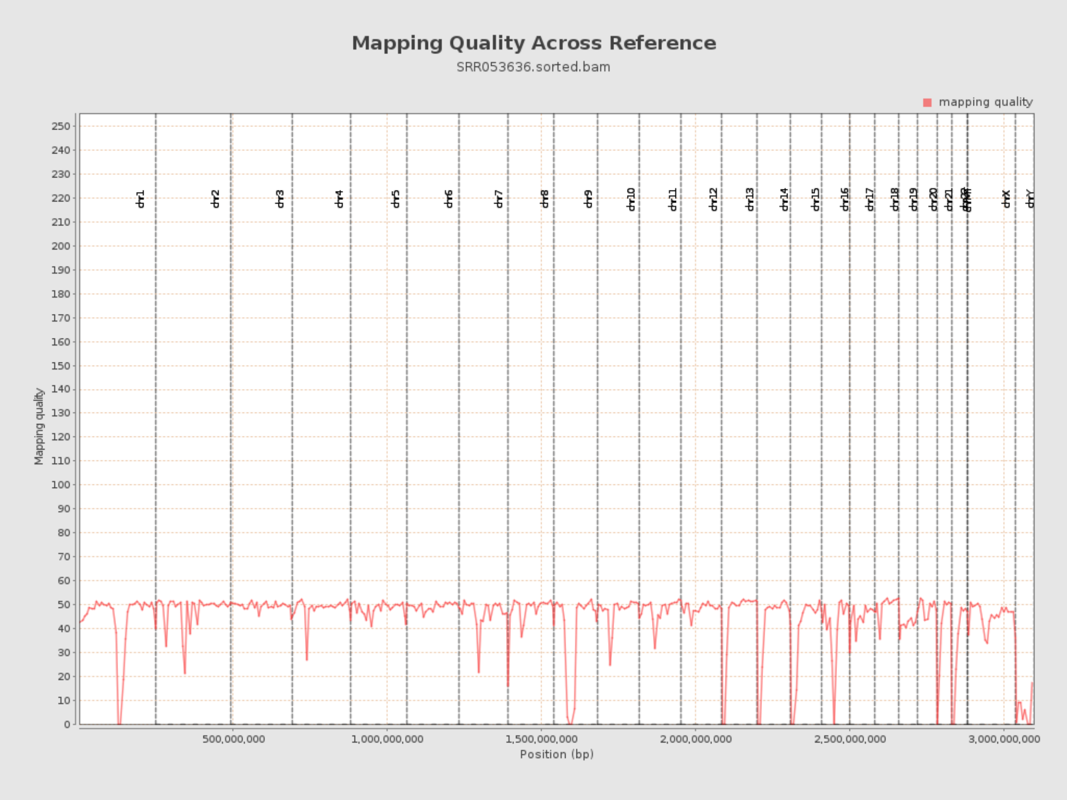
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram