Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:36:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506332.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_SRR1506332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506332.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:36:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506332.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,355,571
Mapped reads	3,875,841 / 72.37%
Unmapped reads	1,479,730 / 27.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,756 / 1.21%
Read min/max/mean length	30 / 94 / 94.43
Duplicated reads (estimated)	383,852 / 7.17%
Duplication rate	7.76%
Clipped reads	2,559,000 / 47.78%

2.2. ACGT Content

Number/percentage of A's	81,336,920 / 27.09%
Number/percentage of C's	56,547,877 / 18.84%
Number/percentage of T's	88,628,685 / 29.52%
Number/percentage of G's	73,609,028 / 24.52%
Number/percentage of N's	72,410 / 0.02%
GC Percentage	43.36%

2.3. Coverage

Mean	0.097

Standard Deviation	0.6894

2.4. Mapping Quality

Mean Mapping Quality	47.46

2.5. Mismatches and indels

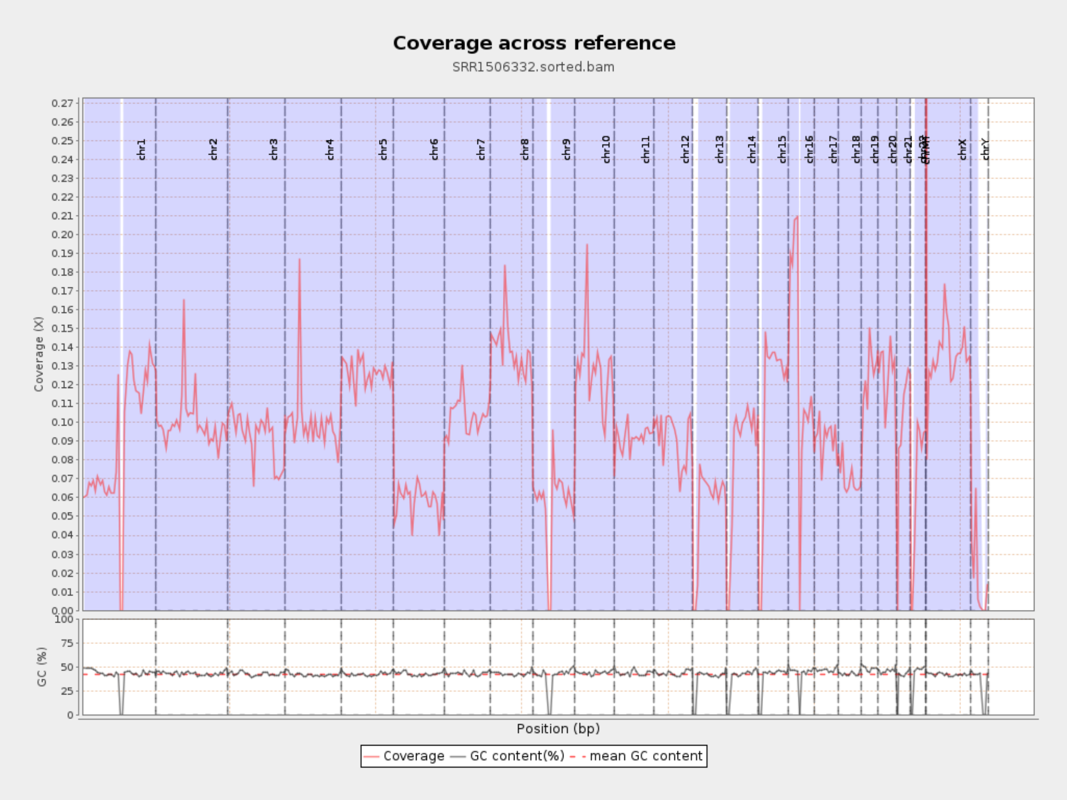
General error rate	0.76%
Mismatches	2,223,973
Insertions	24,399
Mapped reads with at least one insertion	0.62%
Deletions	63,489
Mapped reads with at least one deletion	1.61%
Homopolymer indels	43.63%

2.6. Chromosome stats

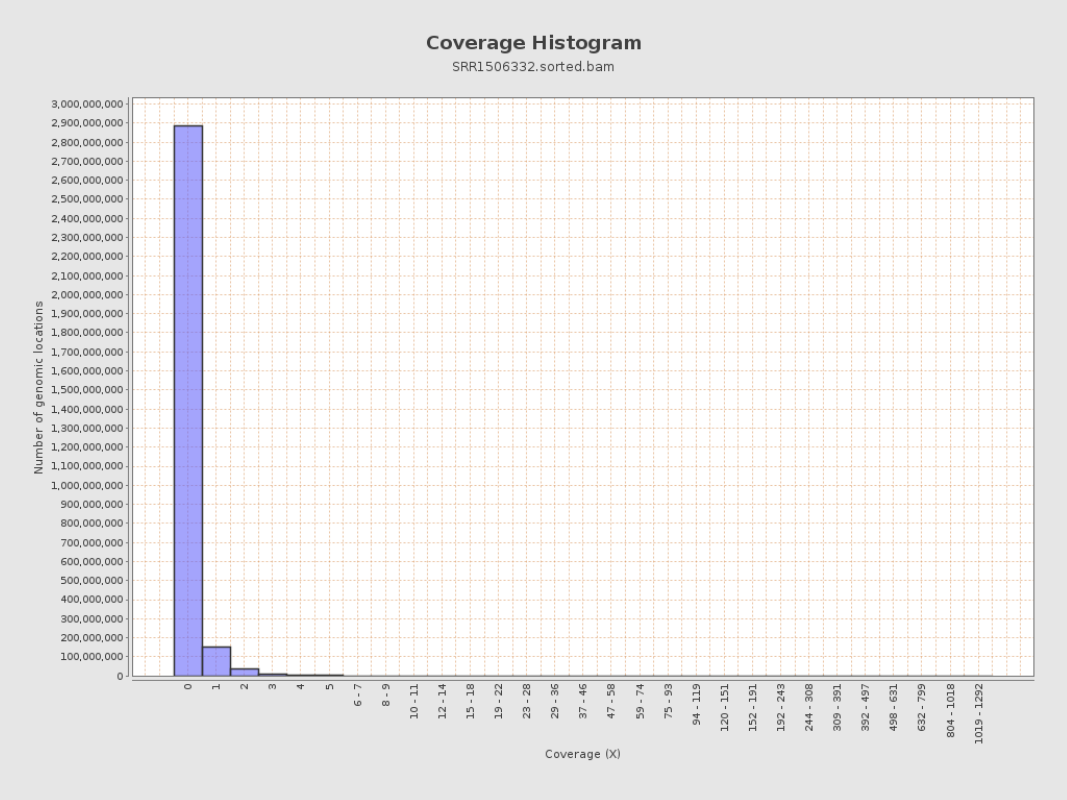
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22244762	0.0892	1.1755
chr2	243199373	24400899	0.1003	0.7874
chr3	198022430	18311003	0.0925	0.4078
chr4	191154276	19264019	0.1008	0.5729
chr5	180915260	22917727	0.1267	0.4922
chr6	171115067	10049229	0.0587	0.357
chr7	159138663	16542703	0.104	0.845

chr8	146364022	20261115	0.1384	0.8612
chr9	141213431	7991728	0.0566	0.6321
chr10	135534747	17293796	0.1276	0.8121
chr11	135006516	12399152	0.0918	0.6529
chr12	133851895	12233072	0.0914	0.4215
chr13	115169878	6402630	0.0556	0.3103
chr14	107349540	8927536	0.0832	0.4499
chr15	102531392	11156997	0.1088	0.4631
chr16	90354753	11503240	0.1273	0.5861
chr17	81195210	7476868	0.0921	0.5061
chr18	78077248	5462339	0.07	1.074
chr19	59128983	7340942	0.1242	0.9608
chr20	63025520	7935028	0.1259	0.5201
chr21	48129895	4783632	0.0994	0.5548
chr22	51304566	3354118	0.0654	0.3555
chrMT	16571	31763	1.9168	2.5924
chrX	155270560	21043083	0.1355	0.5856
chrY	59373566	993728	0.0167	0.5827

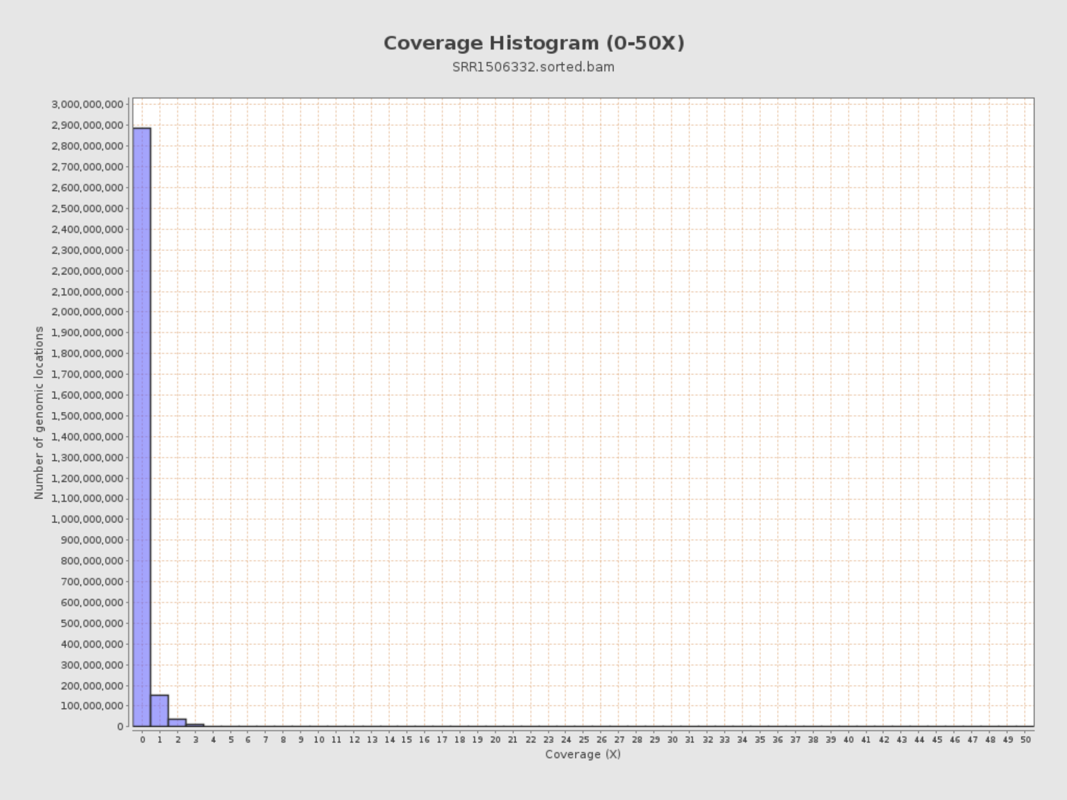
3. Results : Coverage across reference



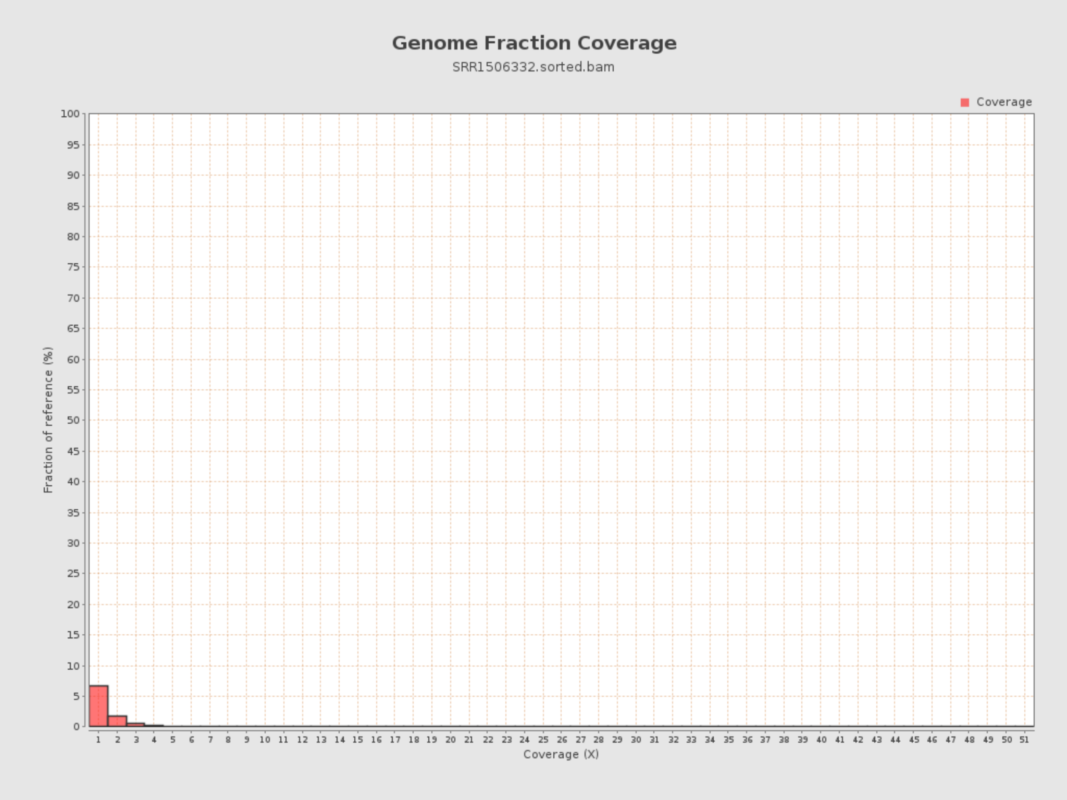
4. Results : Coverage Histogram



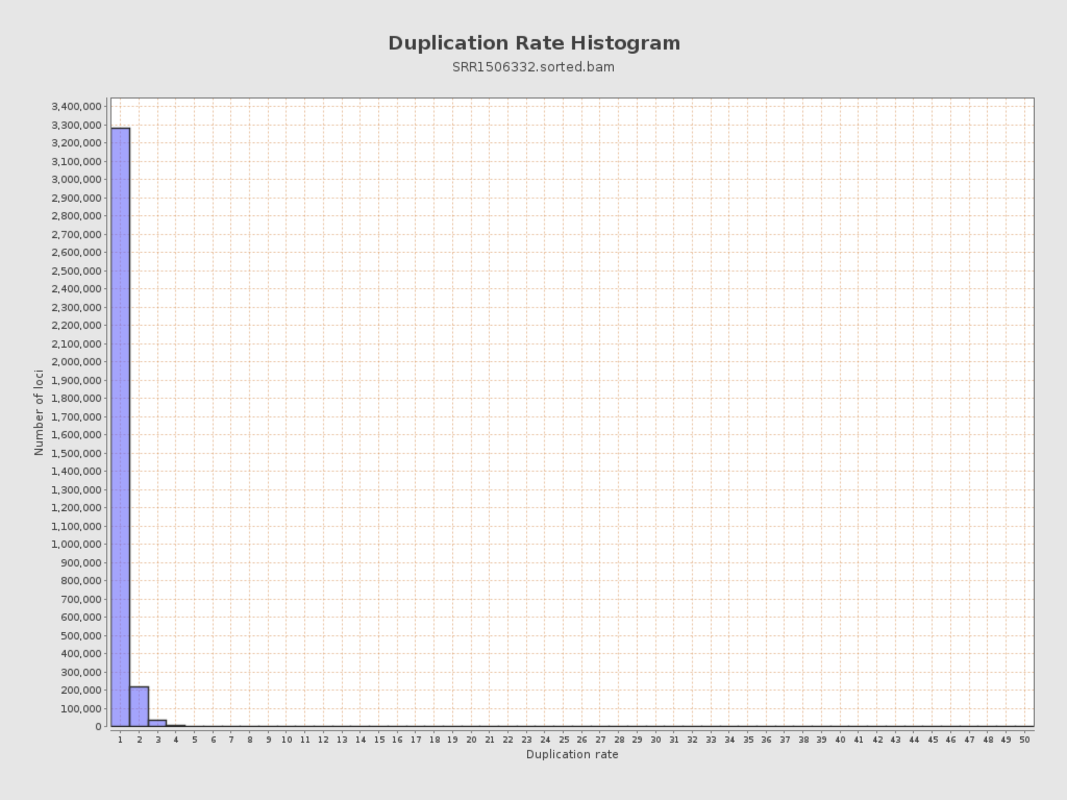
5. Results : Coverage Histogram (0-50X)



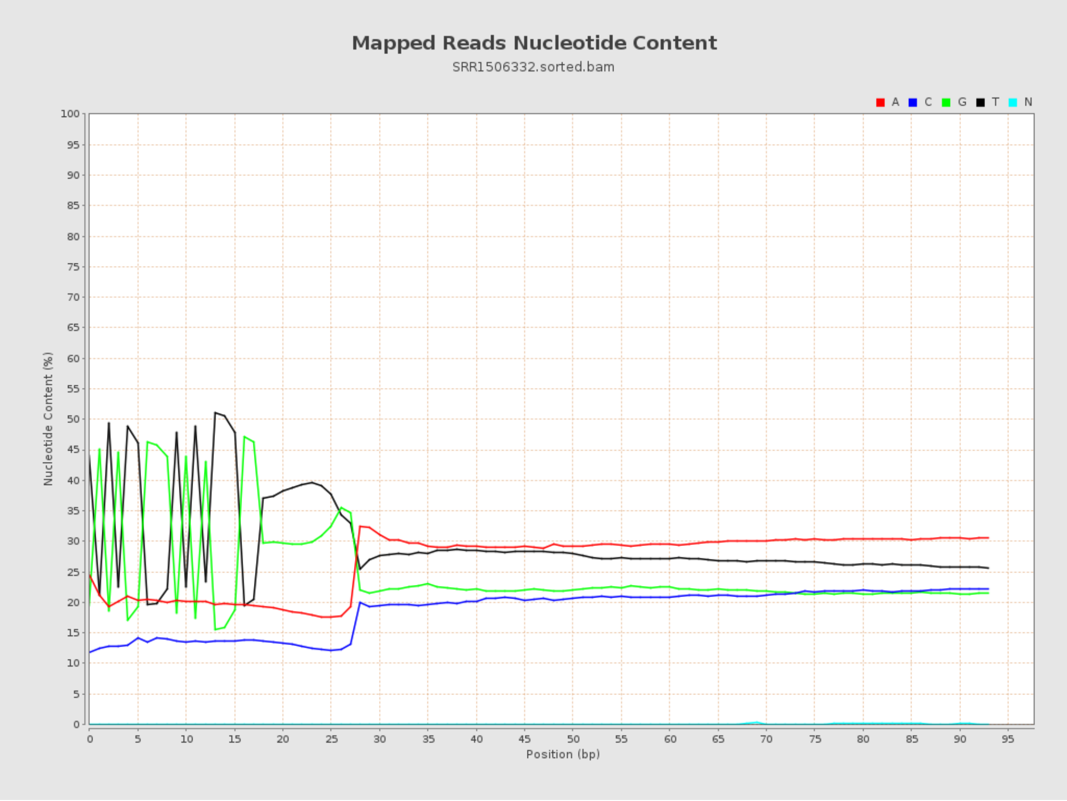
6. Results : Genome Fraction Coverage



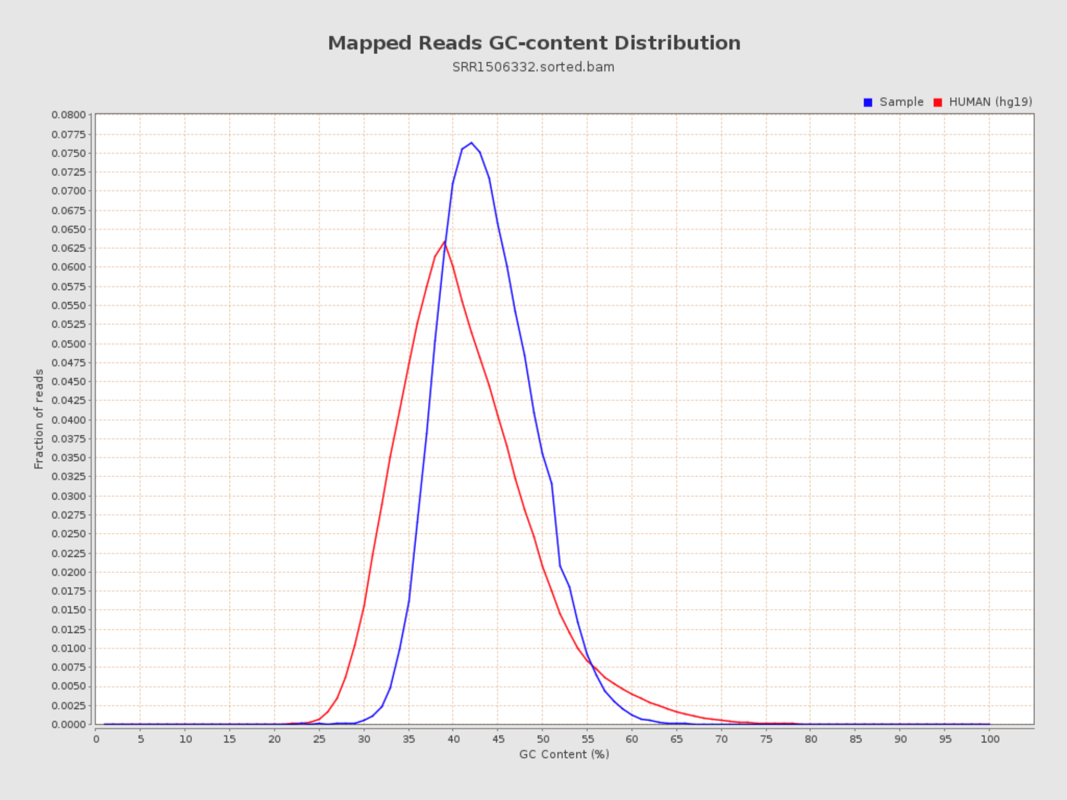
7. Results : Duplication Rate Histogram



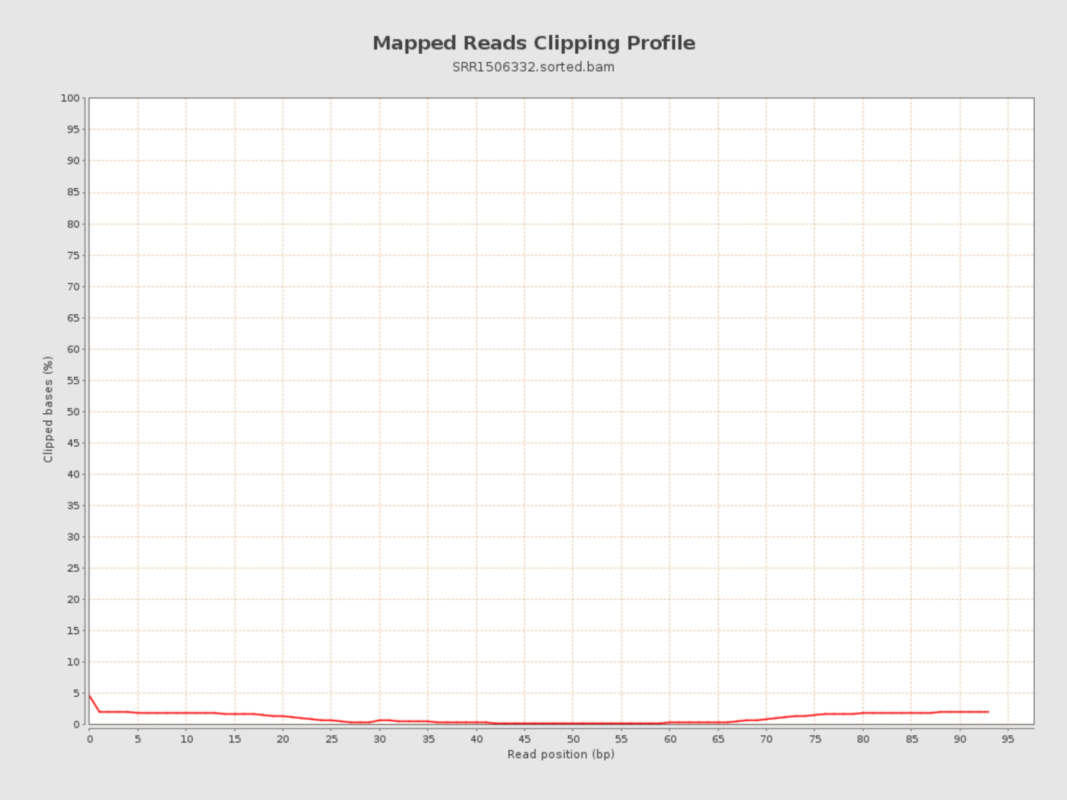
8. Results : Mapped Reads Nucleotide Content



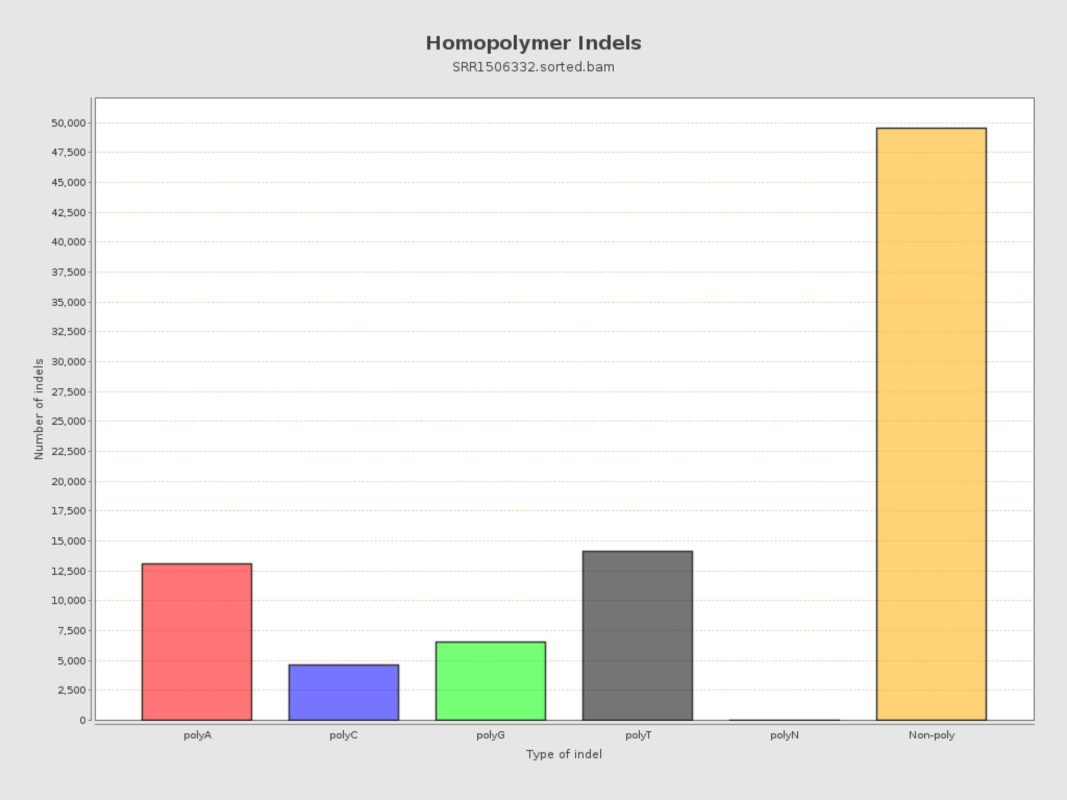
9. Results : Mapped Reads GC-content Distribution



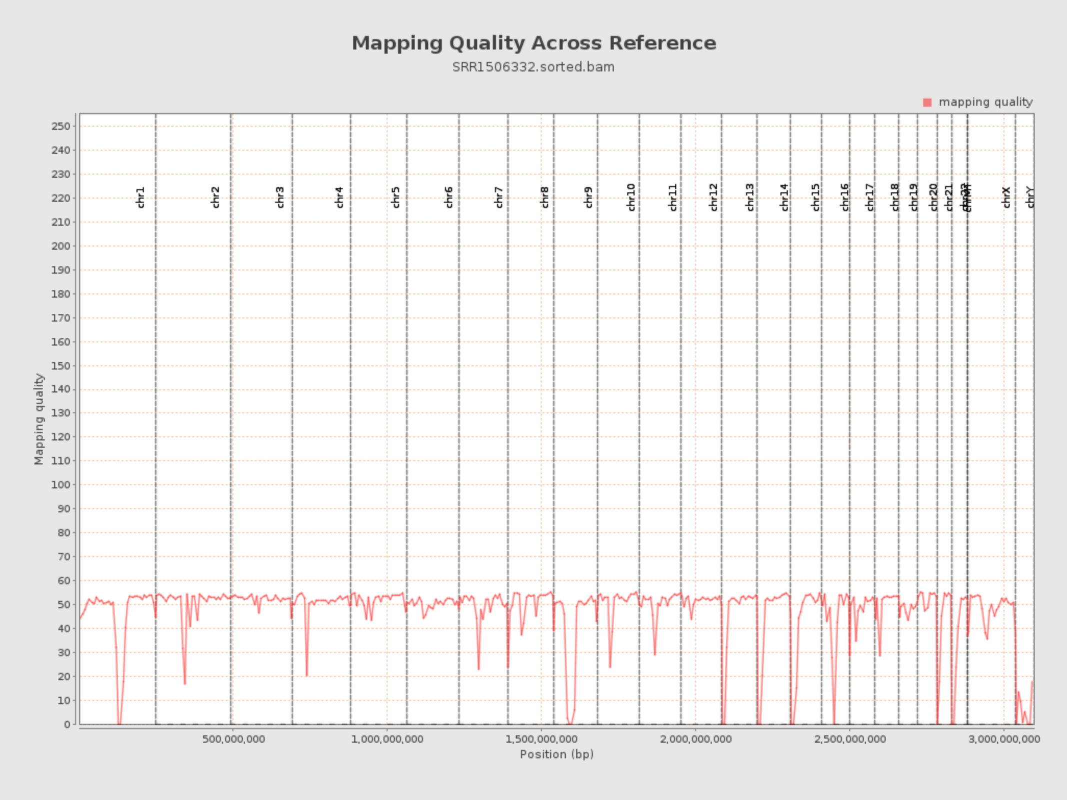
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram