Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 04:23:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506338.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_SRR1506338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506338.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 04:23:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,568,509
Mapped reads	5,461,398 / 83.15%
Unmapped reads	1,107,111 / 16.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	126,554 / 1.93%
Read min/max/mean length	30 / 94 / 94.69
Duplicated reads (estimated)	993,095 / 15.12%
Duplication rate	13.3%
Clipped reads	3,417,502 / 52.03%

2.2. ACGT Content

Number/percentage of A's	121,185,694 / 28.15%
Number/percentage of C's	77,821,573 / 18.08%
Number/percentage of T's	130,050,224 / 30.21%
Number/percentage of G's	101,286,821 / 23.53%
Number/percentage of N's	105,671 / 0.02%
GC Percentage	41.61%

2.3. Coverage

Mean	0.1391

Standard Deviation	1.1305

2.4. Mapping Quality

Mean Mapping Quality	47.93

2.5. Mismatches and indels

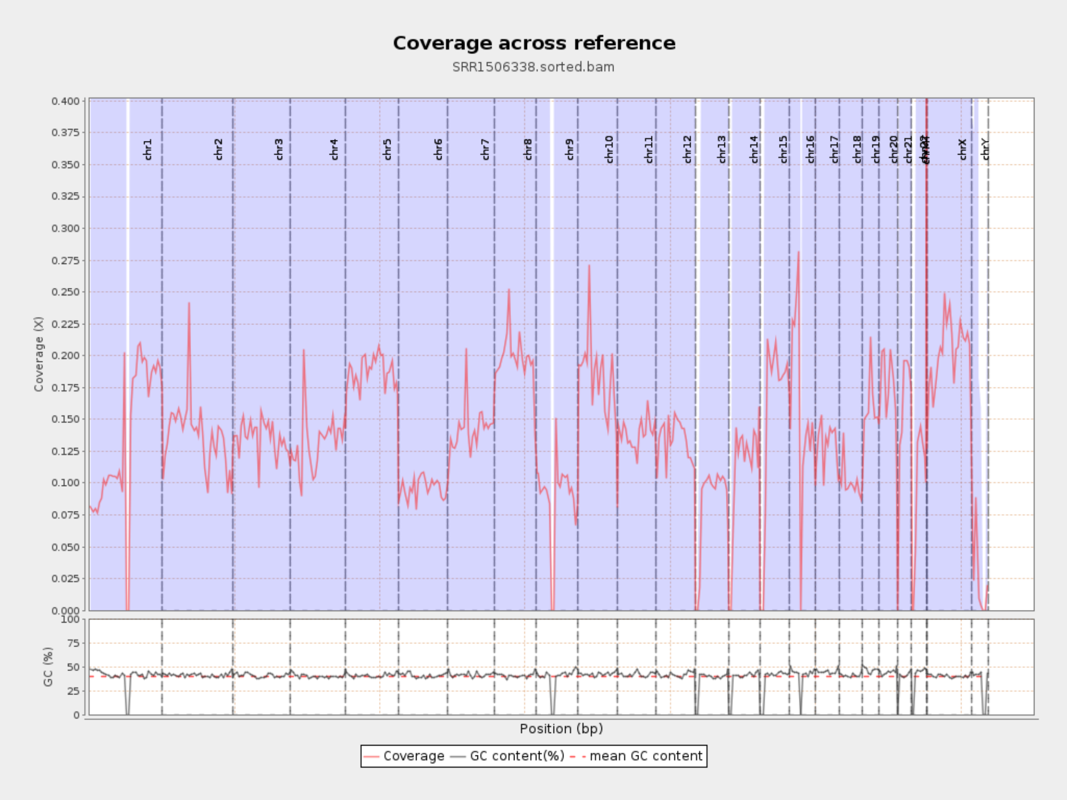
General error rate	0.74%
Mismatches	3,114,589
Insertions	34,802
Mapped reads with at least one insertion	0.63%
Deletions	97,894
Mapped reads with at least one deletion	1.76%
Homopolymer indels	45.67%

2.6. Chromosome stats

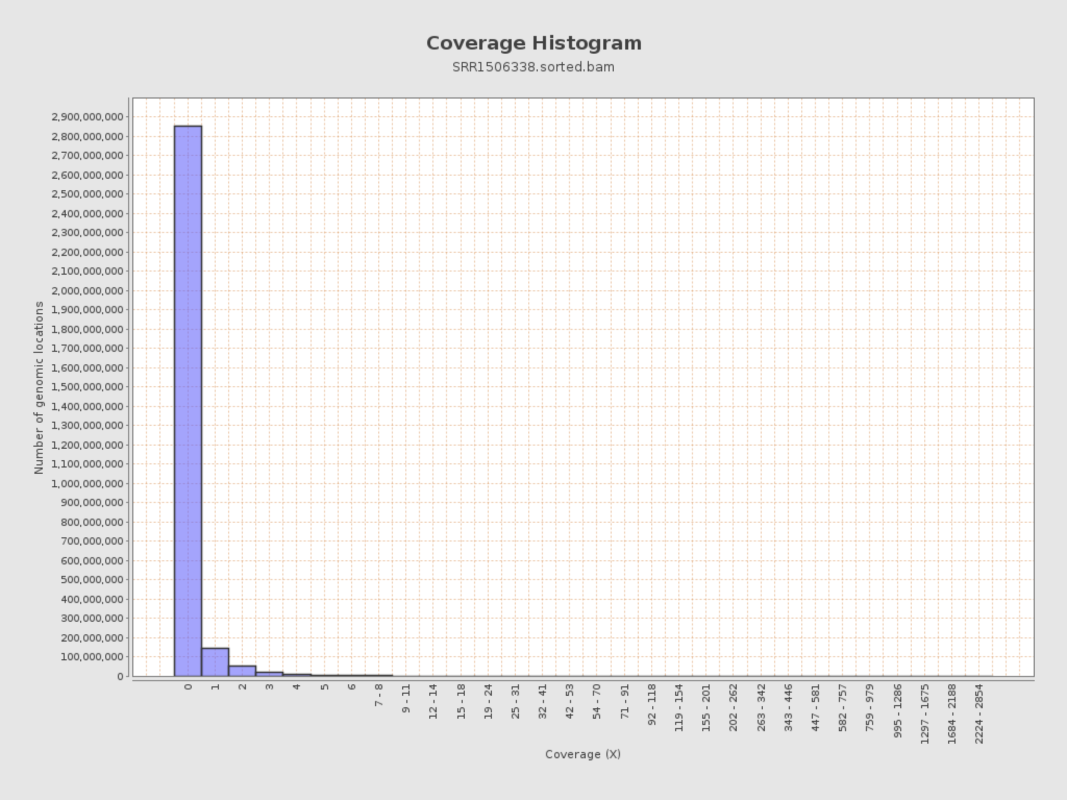
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33330873	0.1337	2.187
chr2	243199373	33502943	0.1378	1.0437
chr3	198022430	26920877	0.1359	0.5812
chr4	191154276	25067111	0.1311	0.7303
chr5	180915260	33915618	0.1875	0.6988
chr6	171115067	16420667	0.096	0.5831
chr7	159138663	22640505	0.1423	1.2958

chr8	146364022	28960033	0.1979	2.0945
chr9	141213431	12409416	0.0879	0.9448
chr10	135534747	25265743	0.1864	1.2017
chr11	135006516	18615927	0.1379	0.9475
chr12	133851895	17857752	0.1334	0.5914
chr13	115169878	9620539	0.0835	0.4508
chr14	107349540	11552291	0.1076	0.6011
chr15	102531392	16073044	0.1568	0.6387
chr16	90354753	14488269	0.1603	0.73
chr17	81195210	10546801	0.1299	0.6668
chr18	78077248	7879924	0.1009	1.7466
chr19	59128983	9453951	0.1599	1.5542
chr20	63025520	11129878	0.1766	0.7074
chr21	48129895	7452459	0.1548	0.7557
chr22	51304566	4656320	0.0908	0.4842
chrMT	16571	13835	0.8349	1.2847
chrX	155270560	31439236	0.2025	0.8212
chrY	59373566	1421939	0.0239	0.7753

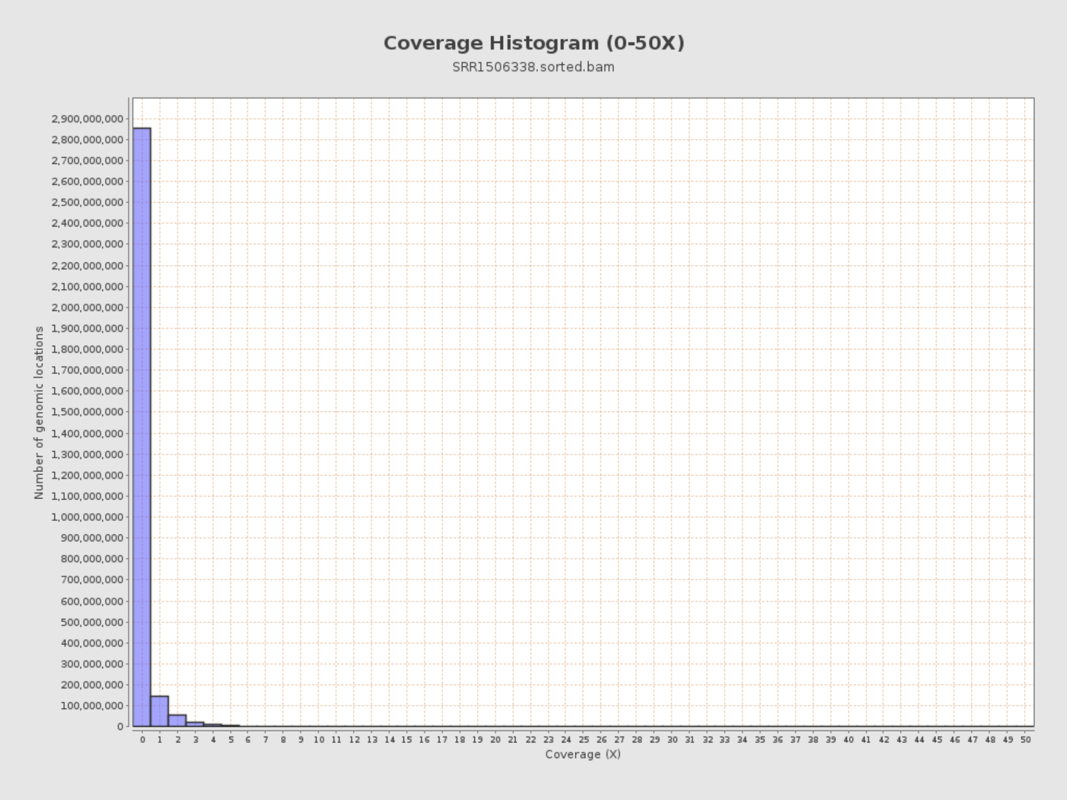
3. Results : Coverage across reference



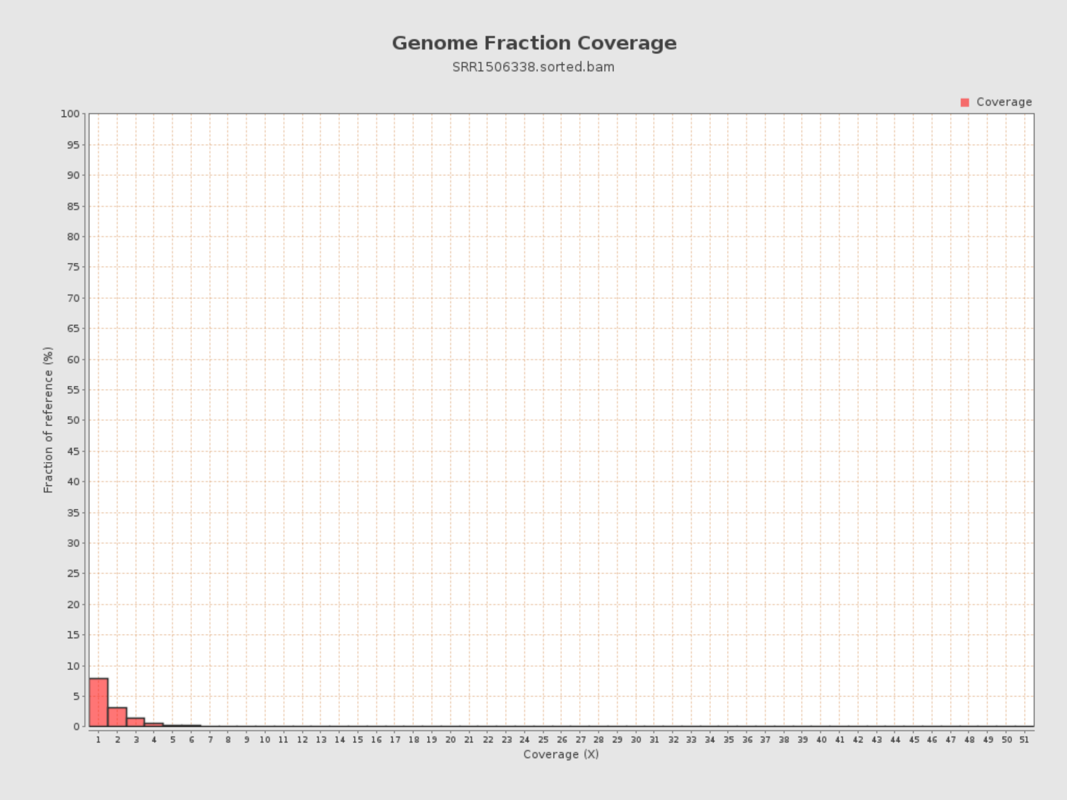
4. Results : Coverage Histogram



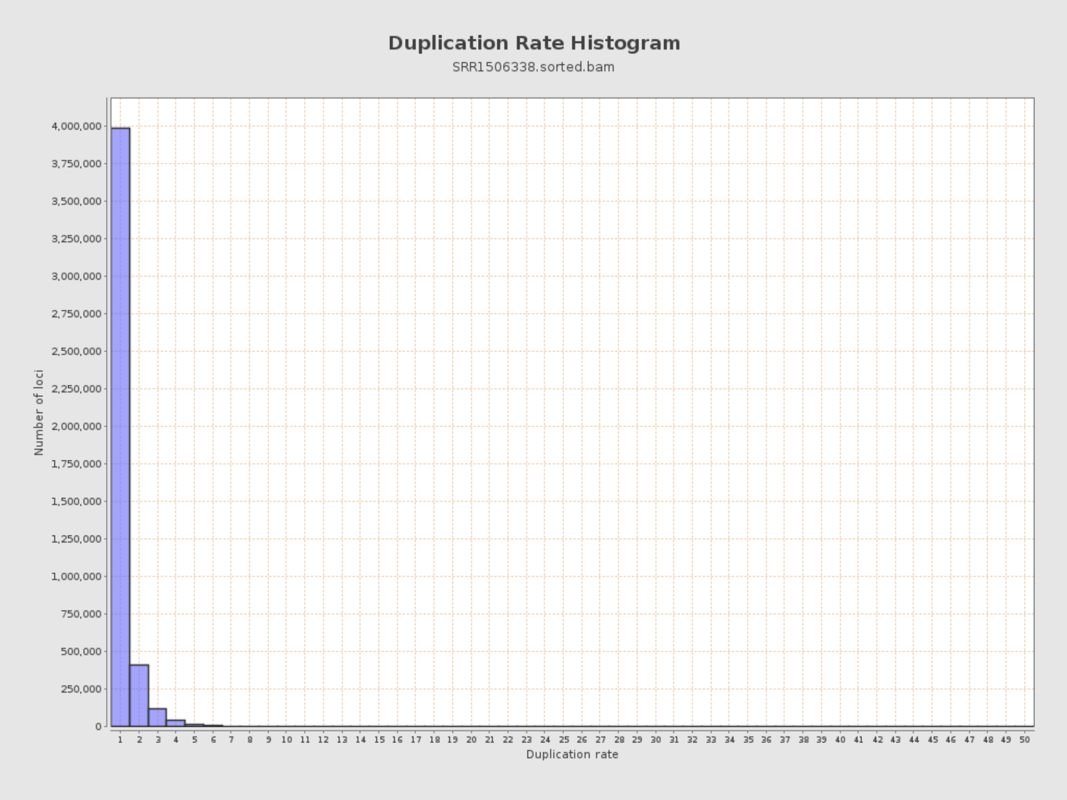
5. Results : Coverage Histogram (0-50X)



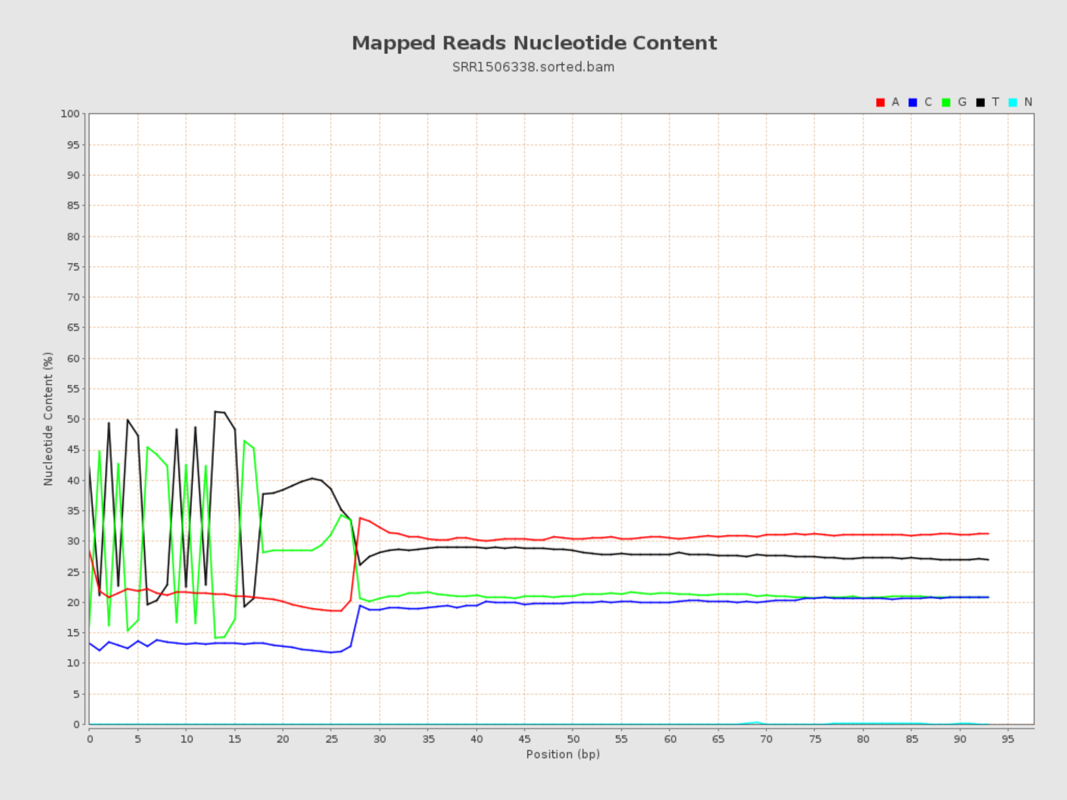
6. Results : Genome Fraction Coverage



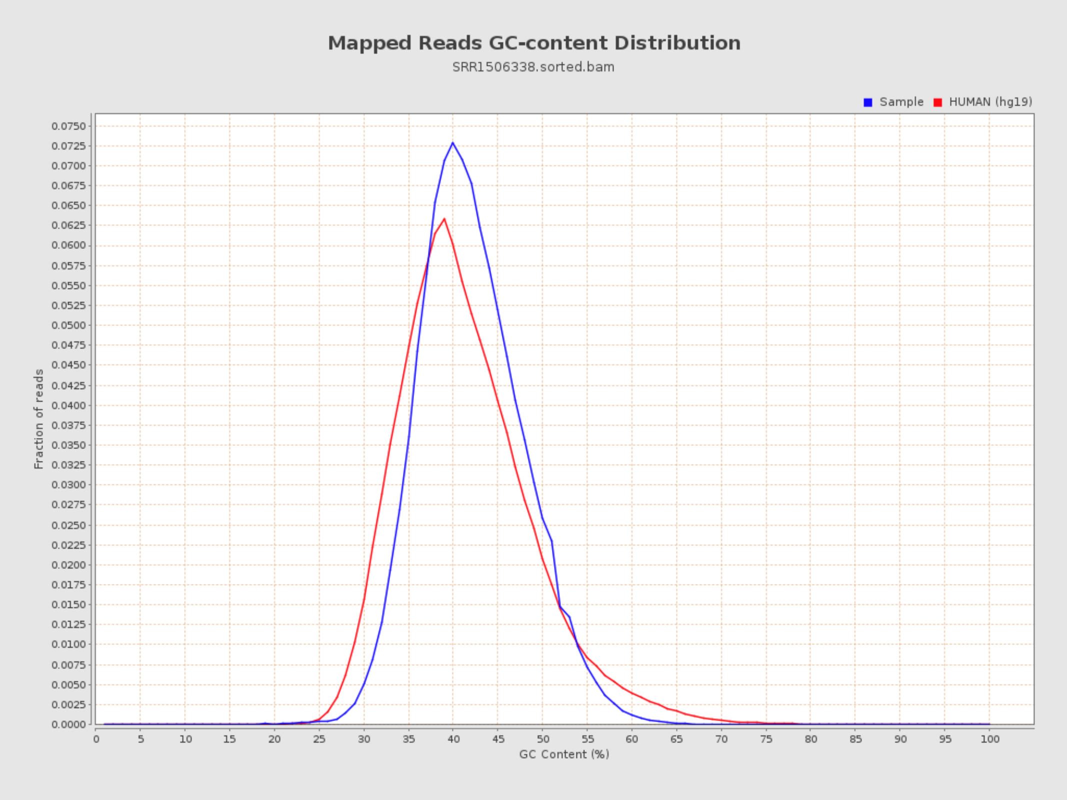
7. Results : Duplication Rate Histogram



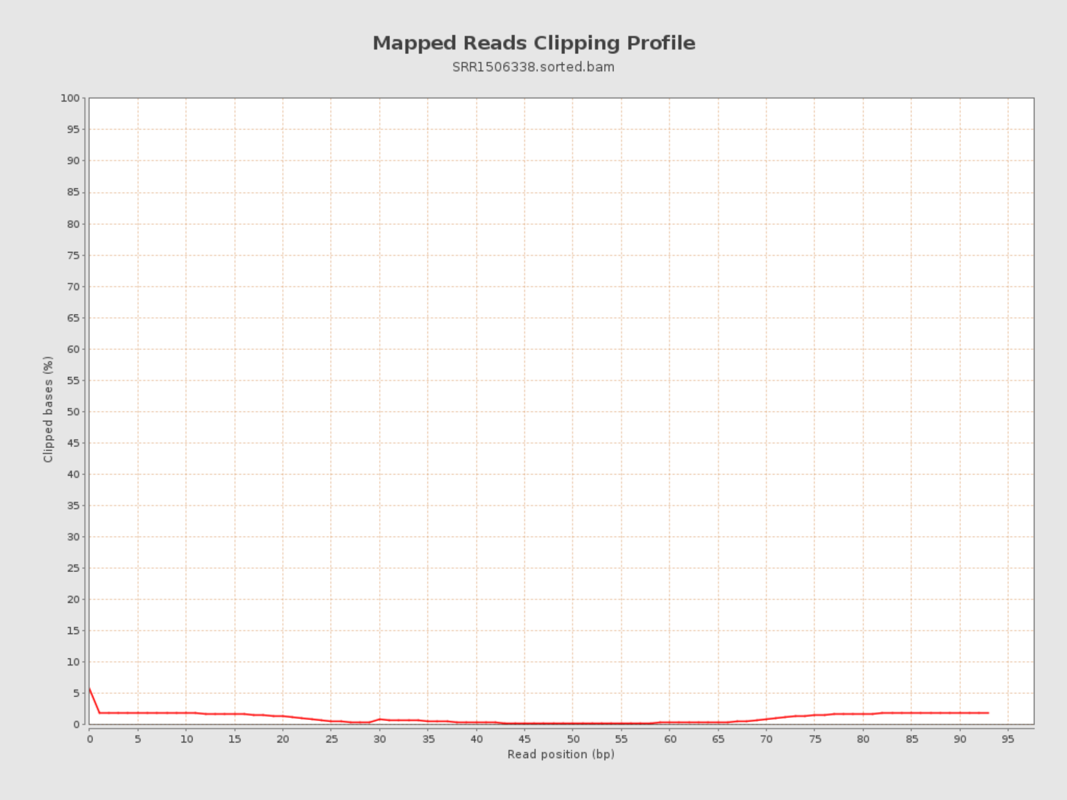
8. Results : Mapped Reads Nucleotide Content



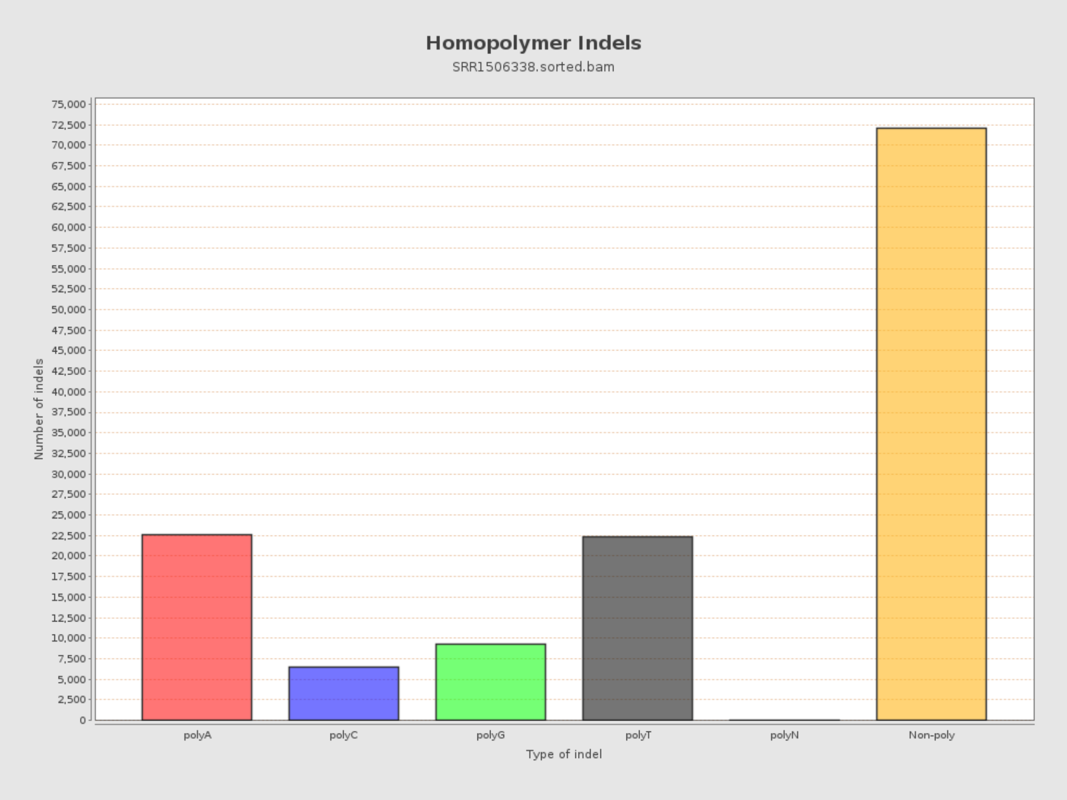
9. Results : Mapped Reads GC-content Distribution



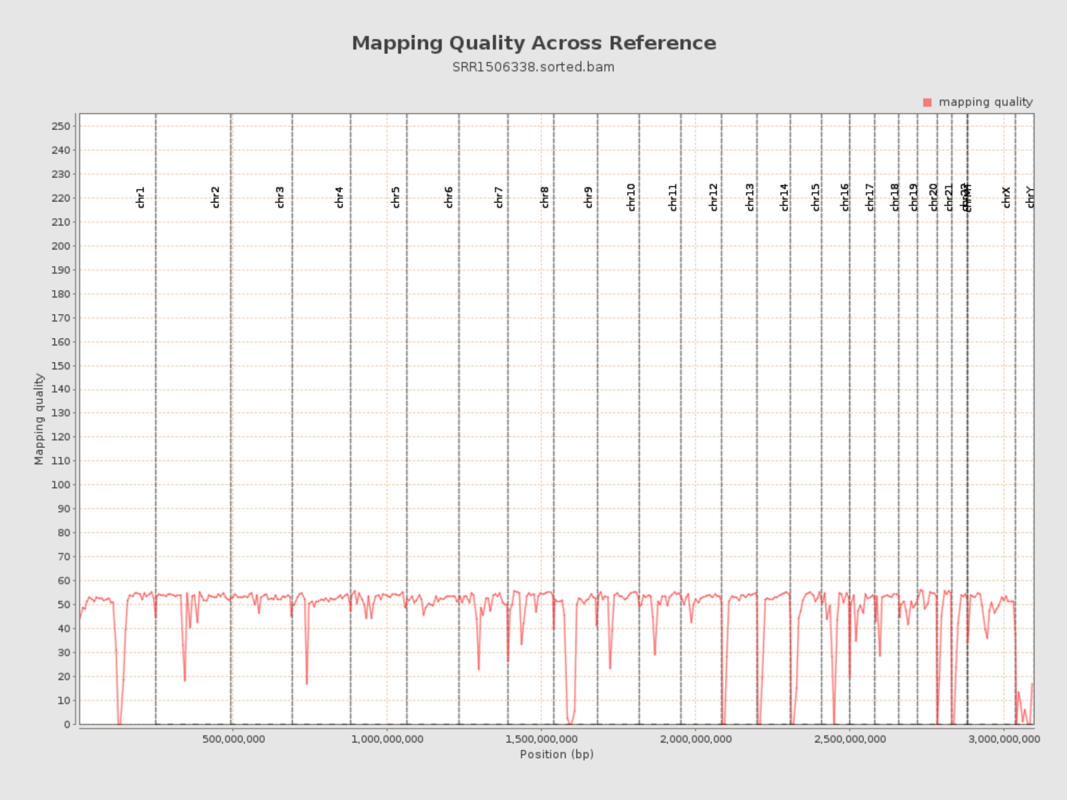
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram