Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:35:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083637.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_SRR3083637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083637.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:35:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,809,054
Mapped reads	1,414,364 / 78.18%
Unmapped reads	394,690 / 21.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,074 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	40,598 / 2.24%
Duplication rate	2.33%
Clipped reads	889,670 / 49.18%

2.2. ACGT Content

Number/percentage of A's	25,906,669 / 29.62%
Number/percentage of C's	16,416,939 / 18.77%
Number/percentage of T's	26,074,136 / 29.82%
Number/percentage of G's	19,041,031 / 21.77%
Number/percentage of N's	11,941 / 0.01%
GC Percentage	40.55%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.2412

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

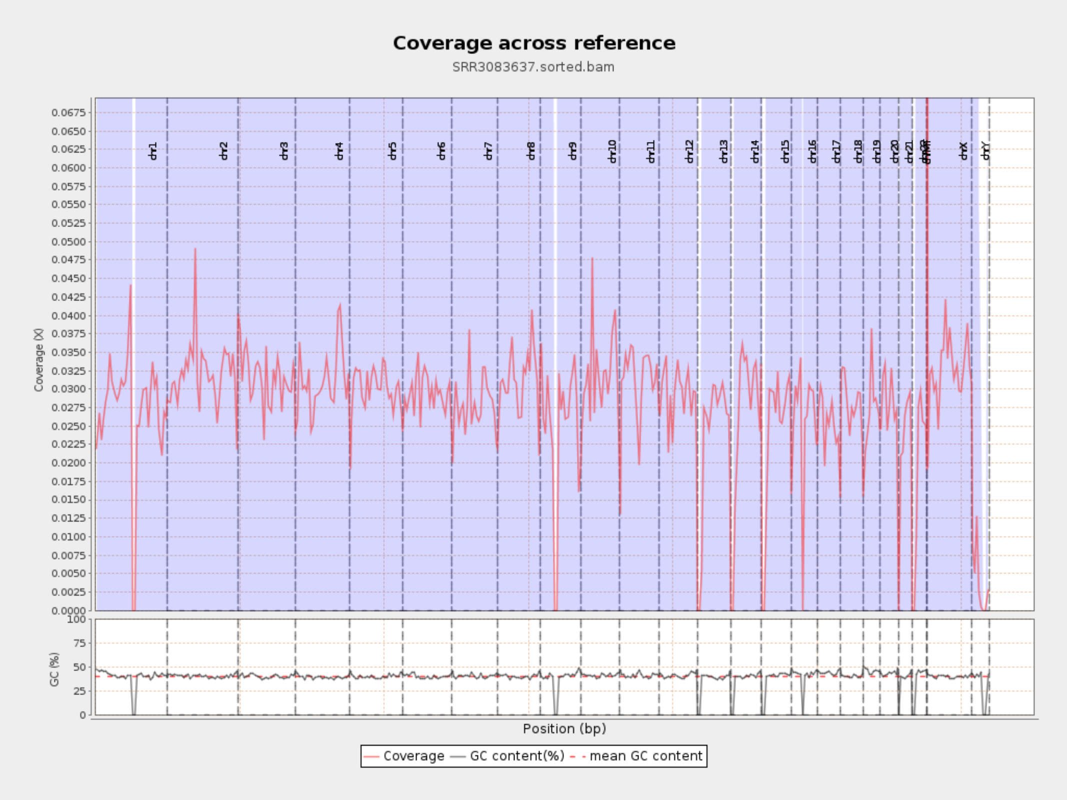
General error rate	0.9%
Mismatches	771,302
Insertions	6,566
Mapped reads with at least one insertion	0.46%
Deletions	18,429
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.66%

2.6. Chromosome stats

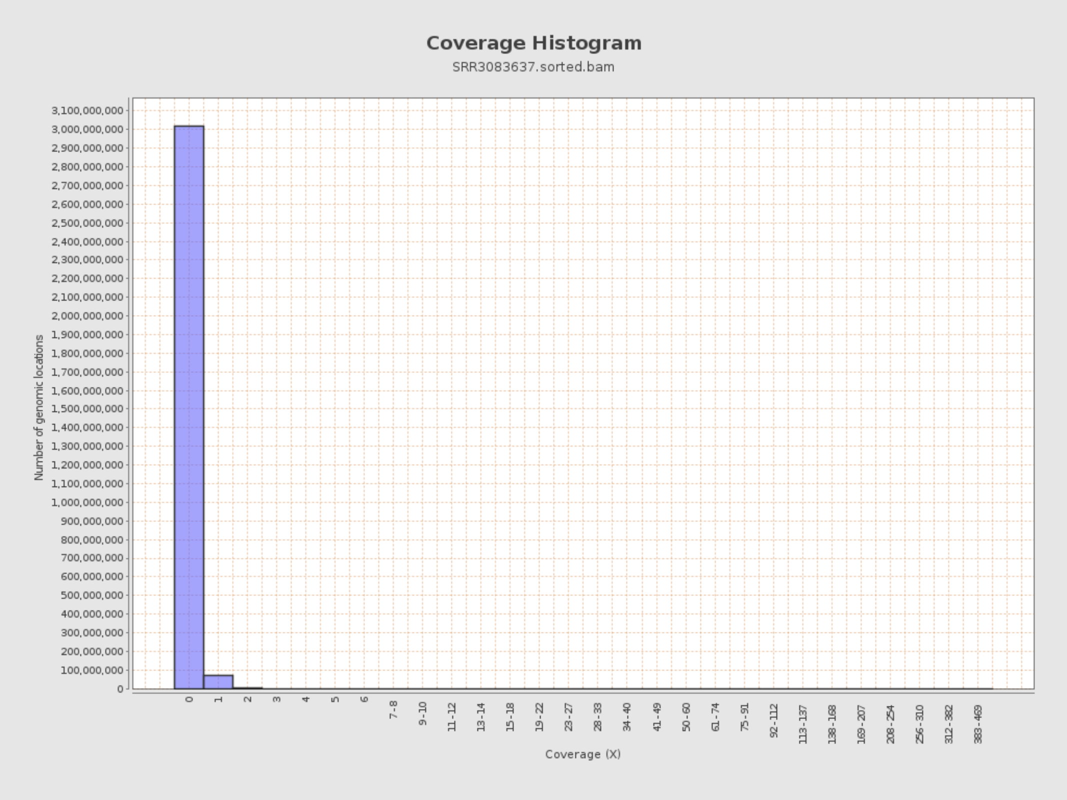
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6758775	0.0271	0.408
chr2	243199373	7816673	0.0321	0.2477
chr3	198022430	6271645	0.0317	0.1911
chr4	191154276	5944522	0.0311	0.1967
chr5	180915260	5503349	0.0304	0.1877
chr6	171115067	5018724	0.0293	0.196
chr7	159138663	4432780	0.0279	0.2449

chr8	146364022	4577015	0.0313	0.3424
chr9	141213431	3541095	0.0251	0.2258
chr10	135534747	4318205	0.0319	0.2579
chr11	135006516	4213709	0.0312	0.2175
chr12	133851895	3913650	0.0292	0.1855
chr13	115169878	2683609	0.0233	0.1636
chr14	107349540	2778434	0.0259	0.1802
chr15	102531392	2432142	0.0237	0.1652
chr16	90354753	2278672	0.0252	0.1844
chr17	81195210	2044246	0.0252	0.1856
chr18	78077248	2219416	0.0284	0.3598
chr19	59128983	1597595	0.027	0.2917
chr20	63025520	1757890	0.0279	0.1827
chr21	48129895	1089923	0.0226	0.1714
chr22	51304566	954761	0.0186	0.1466
chrMT	16571	7431	0.4484	0.6866
chrX	155270560	5096418	0.0328	0.2053
chrY	59373566	229470	0.0039	0.0999

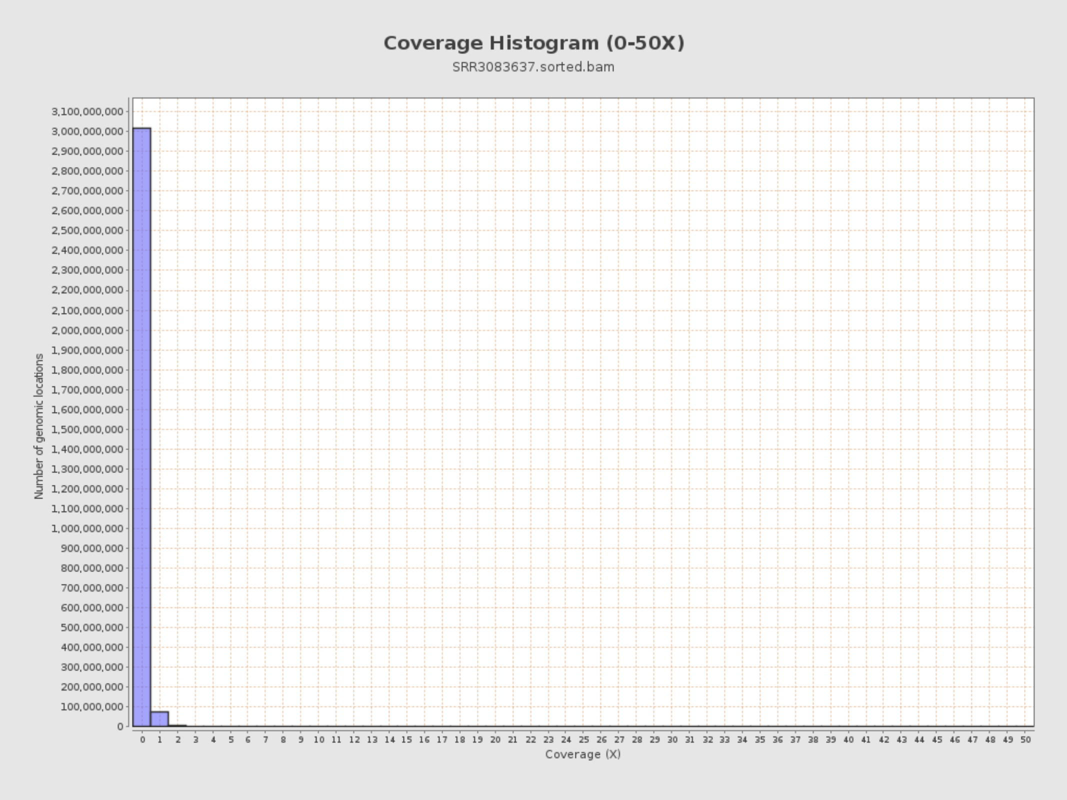
3. Results : Coverage across reference



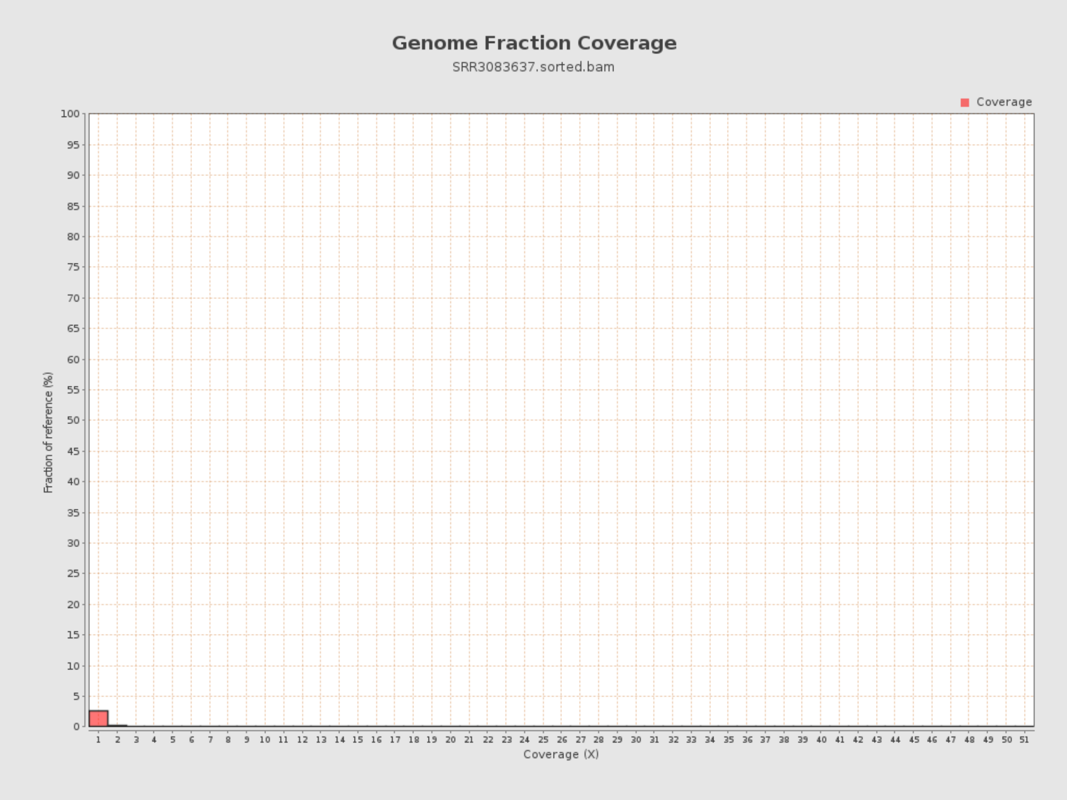
4. Results : Coverage Histogram



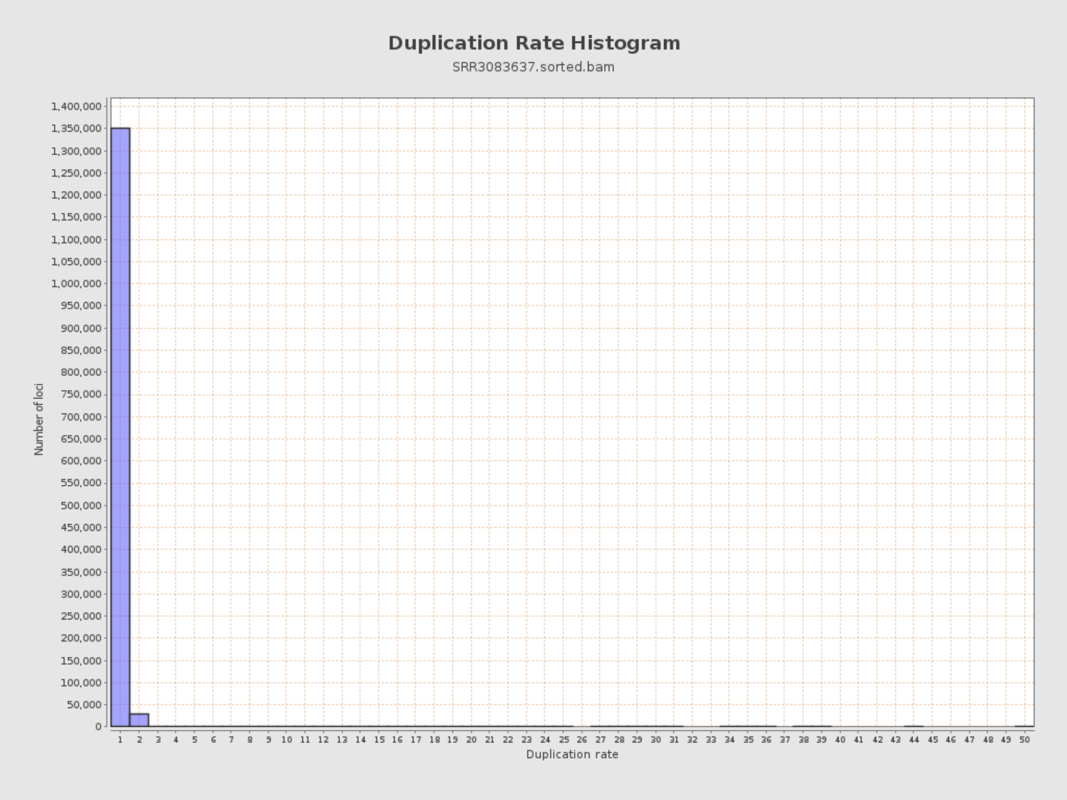
5. Results : Coverage Histogram (0-50X)



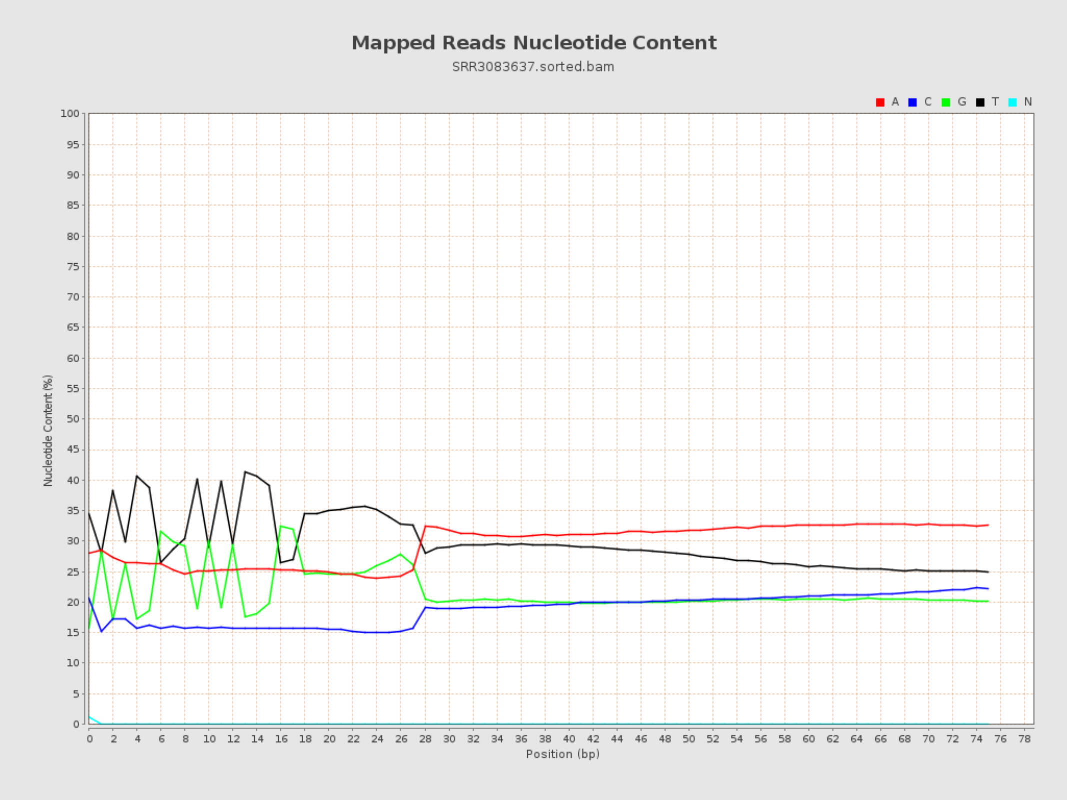
6. Results : Genome Fraction Coverage



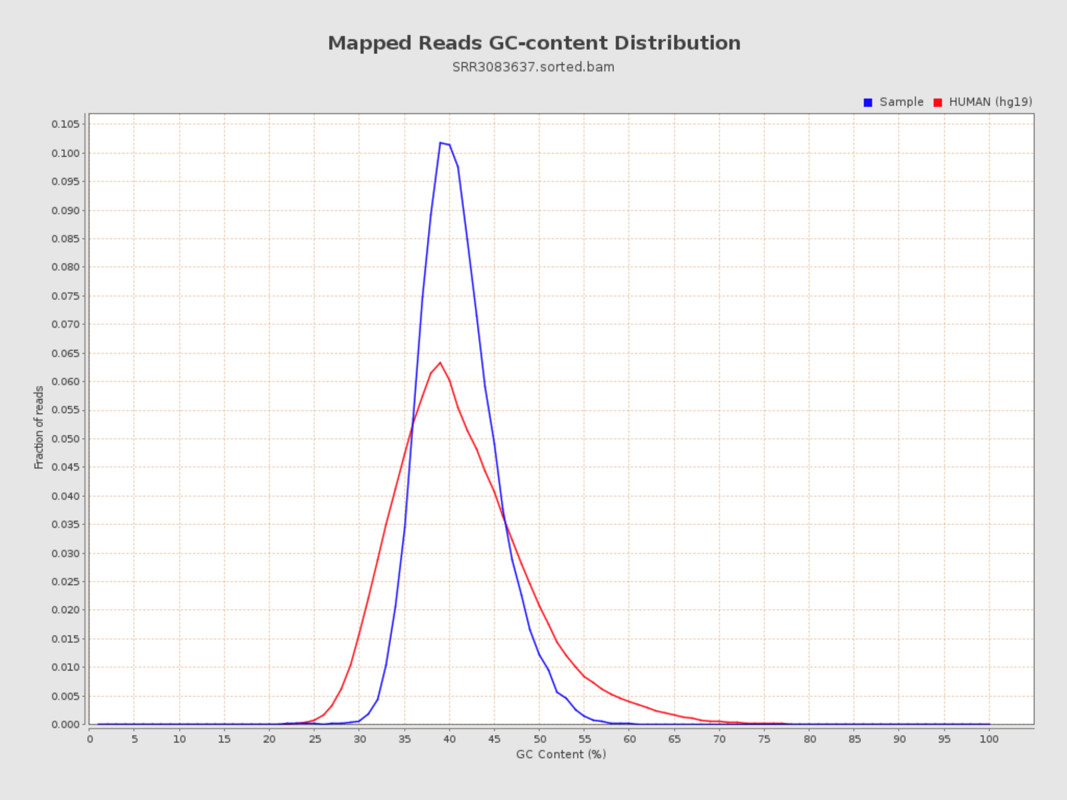
7. Results : Duplication Rate Histogram



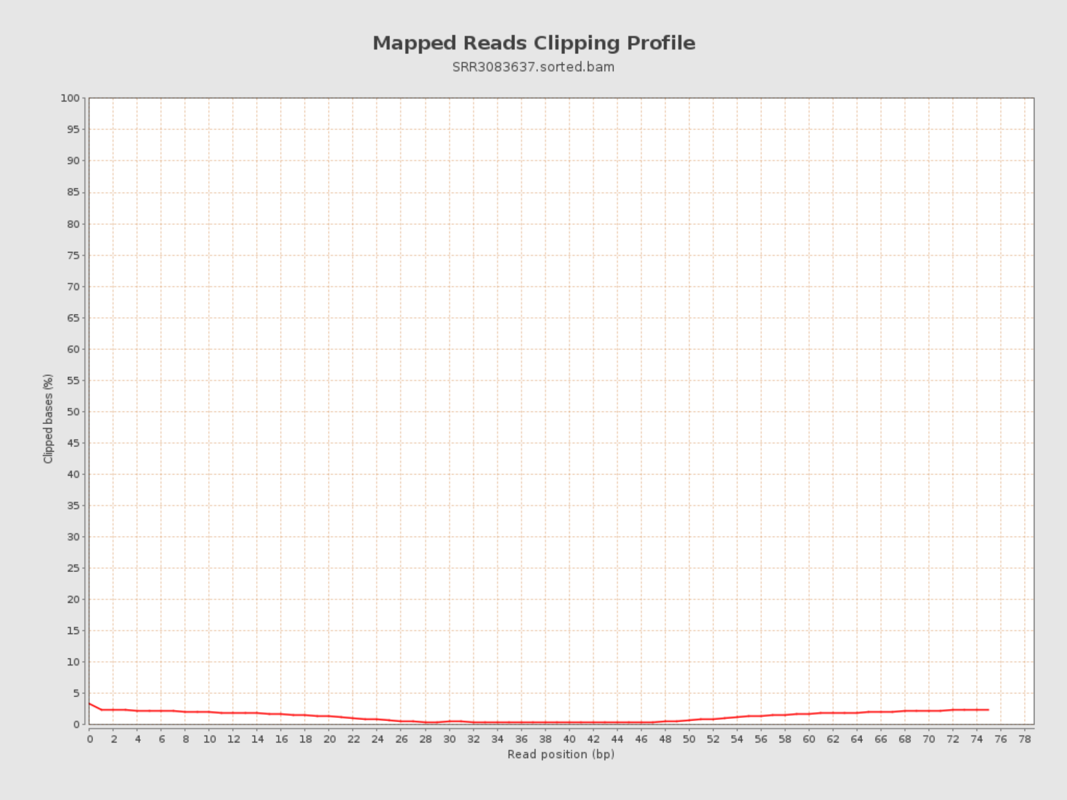
8. Results : Mapped Reads Nucleotide Content



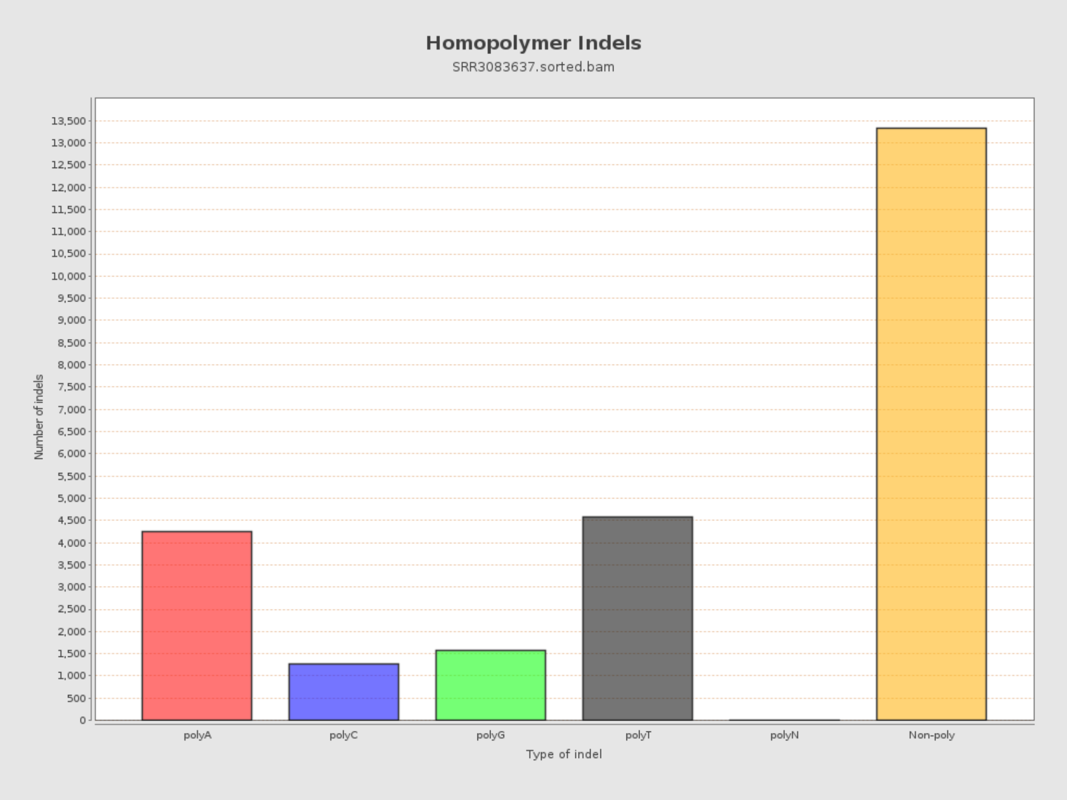
9. Results : Mapped Reads GC-content Distribution



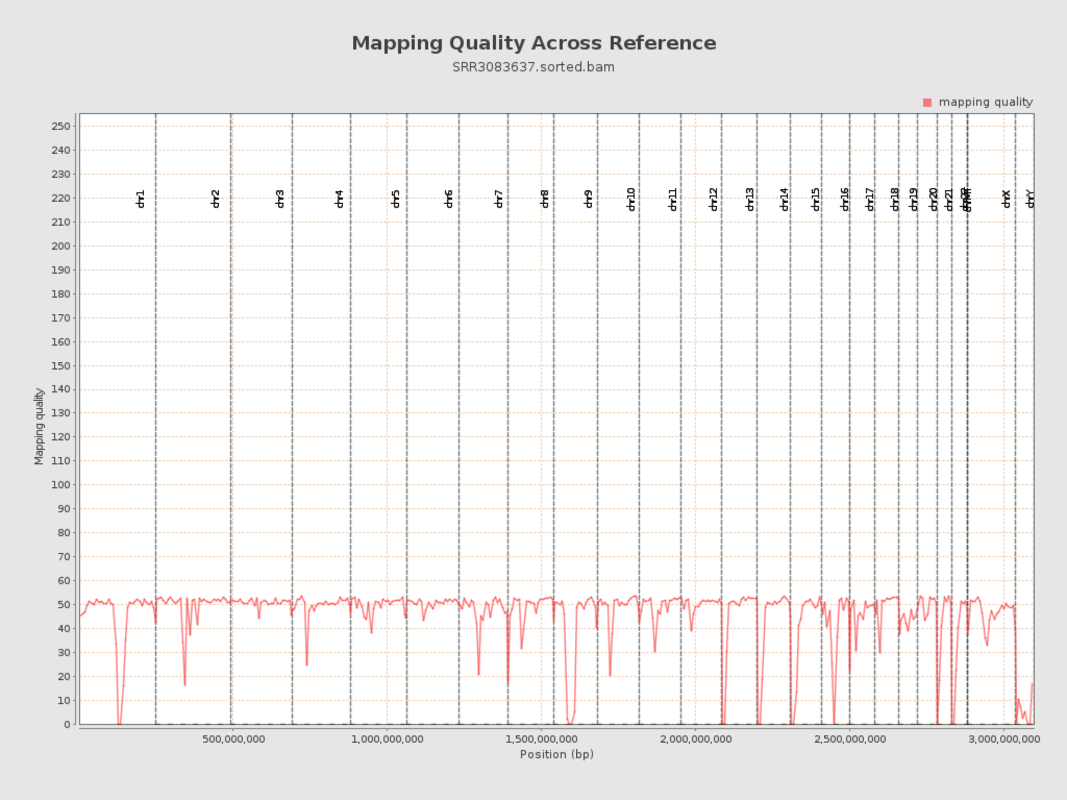
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram