Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:49:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083754.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_SRR3083754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:48:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,399,251
Mapped reads	1,056,655 / 75.52%
Unmapped reads	342,596 / 24.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,076 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	17,881 / 1.28%
Duplication rate	1.24%
Clipped reads	397,754 / 28.43%

2.2. ACGT Content

Number/percentage of A's	22,674,258 / 31.45%
Number/percentage of C's	13,097,547 / 18.17%
Number/percentage of T's	20,622,926 / 28.6%
Number/percentage of G's	15,690,869 / 21.76%
Number/percentage of N's	10,764 / 0.01%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2307

2.4. Mapping Quality

Mean Mapping Quality	47.84

2.5. Mismatches and indels

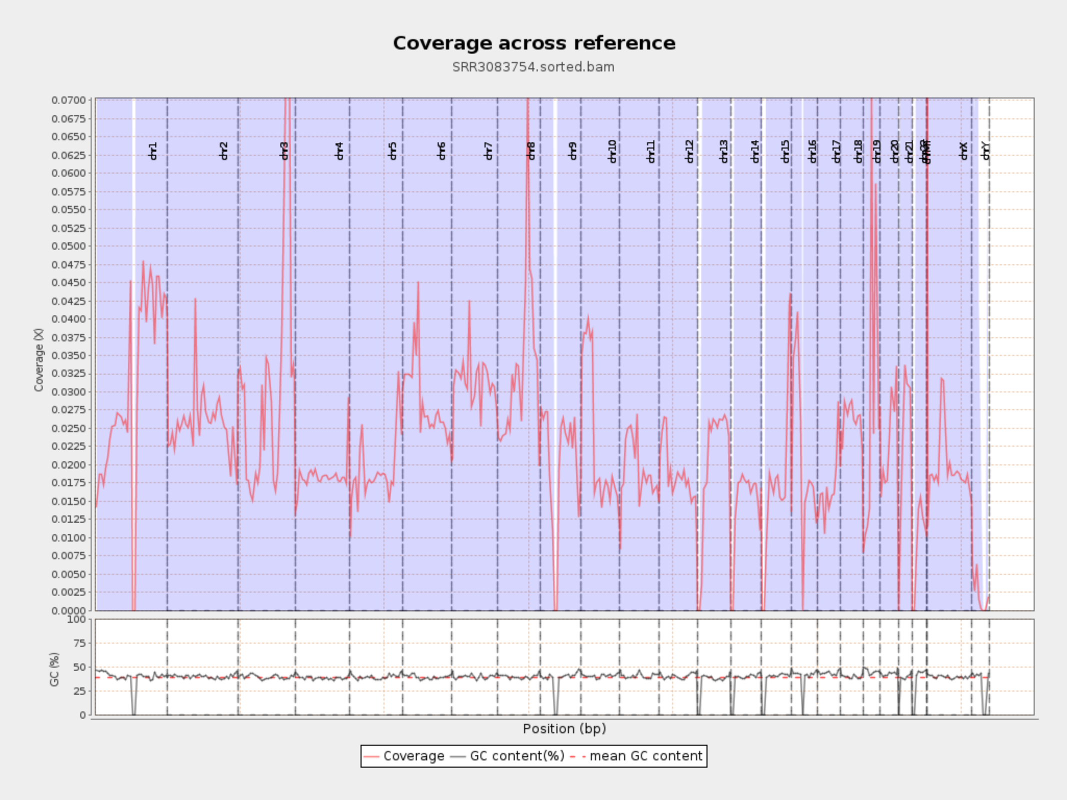
General error rate	0.85%
Mismatches	601,290
Insertions	4,827
Mapped reads with at least one insertion	0.45%
Deletions	12,585
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.72%

2.6. Chromosome stats

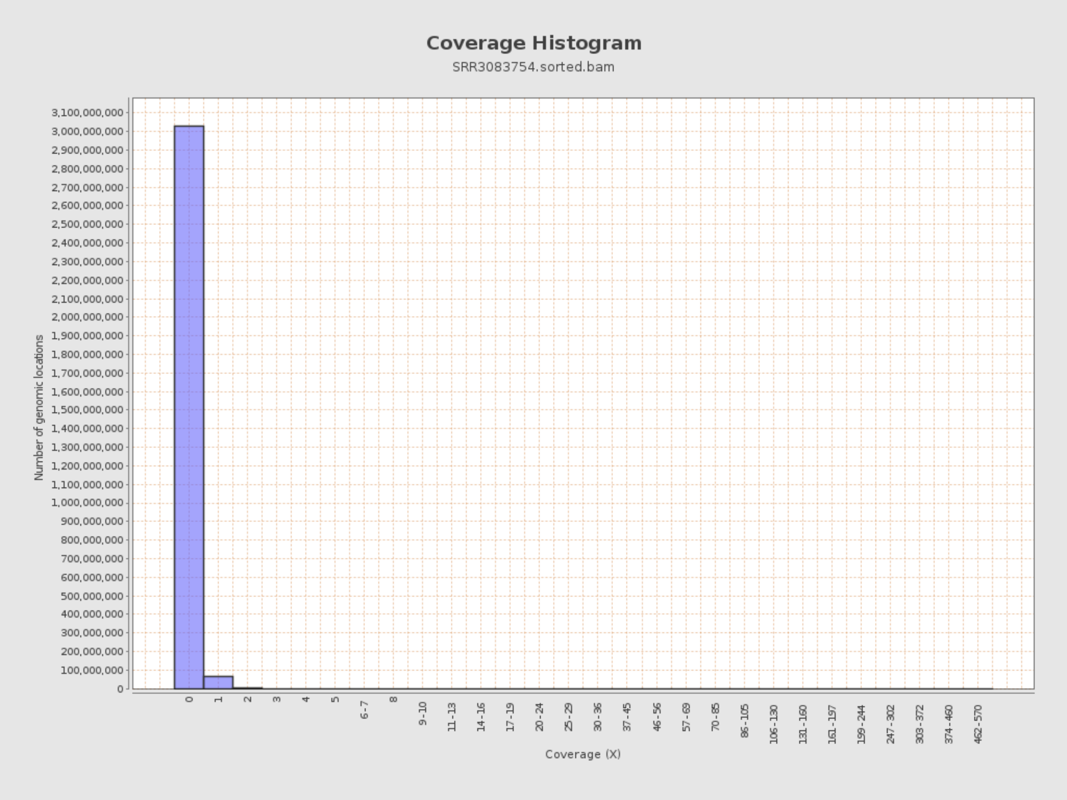
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7606424	0.0305	0.5007
chr2	243199373	6265704	0.0258	0.2098
chr3	198022430	6157469	0.0311	0.1817
chr4	191154276	3516701	0.0184	0.139
chr5	180915260	3517047	0.0194	0.1428
chr6	171115067	4947322	0.0289	0.2077
chr7	159138663	5012104	0.0315	0.3056

chr8	146364022	4920246	0.0336	0.2664
chr9	141213431	2856037	0.0202	0.168
chr10	135534747	3201992	0.0236	0.2083
chr11	135006516	2624906	0.0194	0.1645
chr12	133851895	2531761	0.0189	0.1414
chr13	115169878	2311691	0.0201	0.1442
chr14	107349540	1539804	0.0143	0.1255
chr15	102531392	1785833	0.0174	0.1354
chr16	90354753	1883440	0.0208	0.1576
chr17	81195210	1369843	0.0169	0.1383
chr18	78077248	2053824	0.0263	0.2888
chr19	59128983	1745834	0.0295	0.3014
chr20	63025520	1456000	0.0231	0.1565
chr21	48129895	1129368	0.0235	0.1592
chr22	51304566	492198	0.0096	0.1002
chrMT	16571	4629	0.2793	0.554
chrX	155270560	3059541	0.0197	0.1499
chrY	59373566	127311	0.0021	0.0661

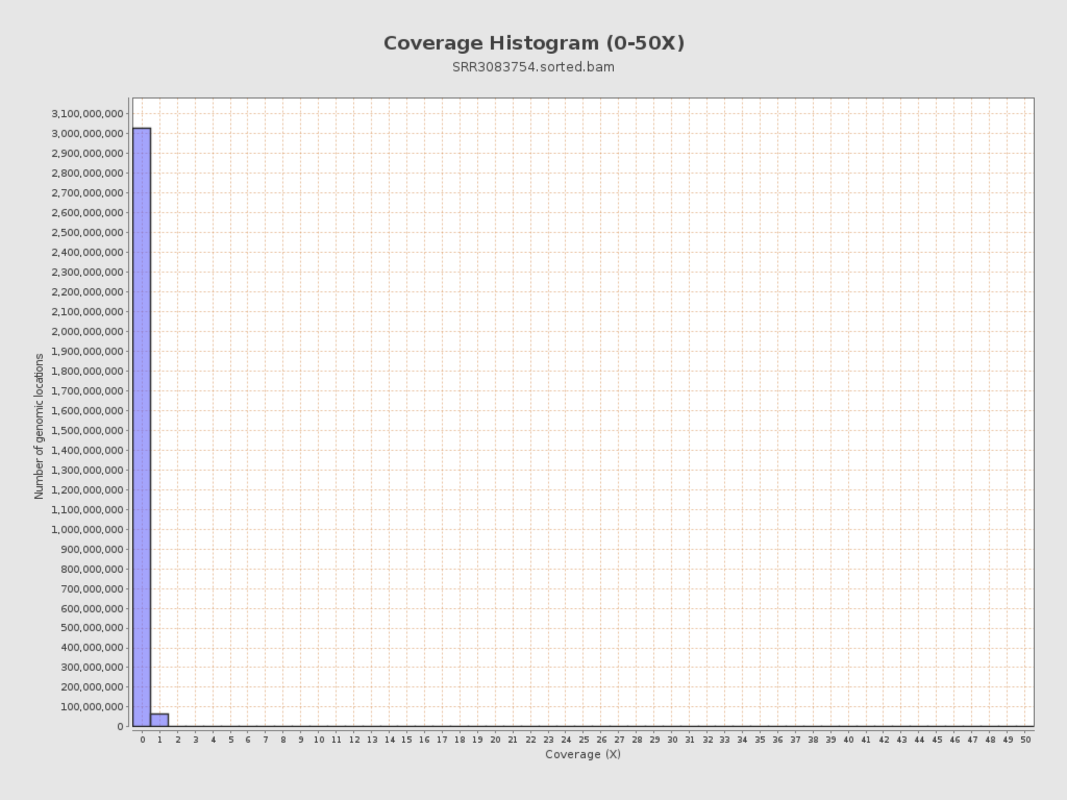
3. Results : Coverage across reference



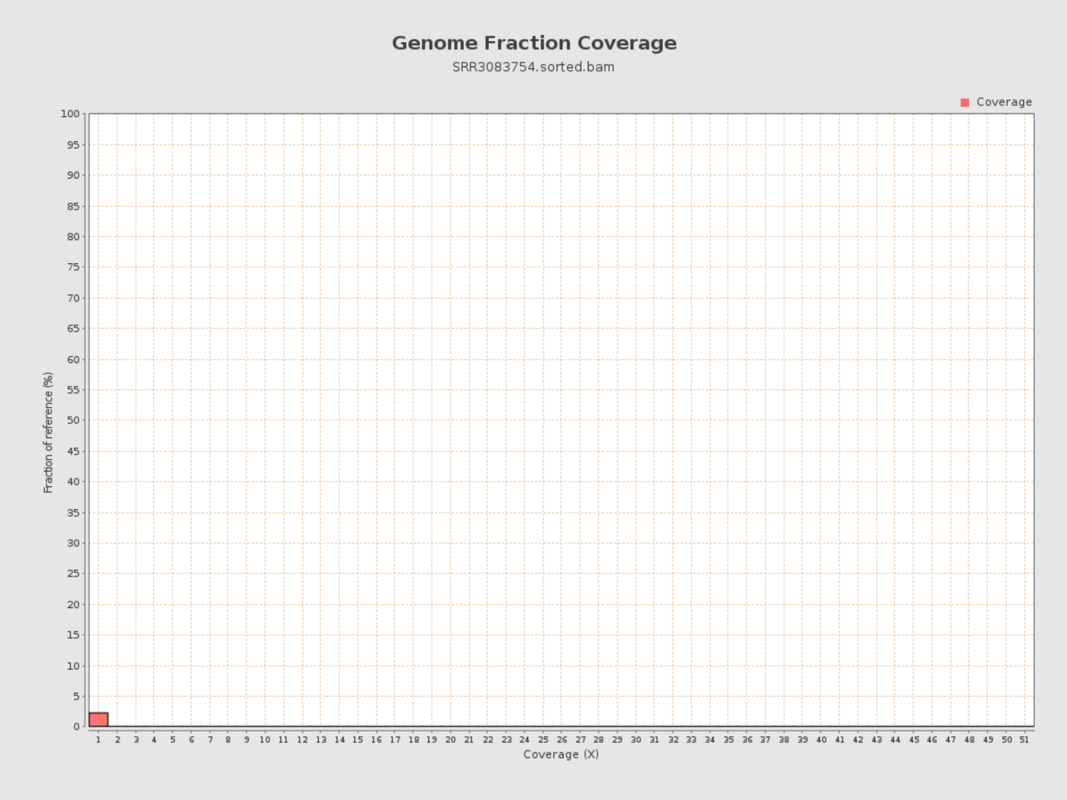
4. Results : Coverage Histogram



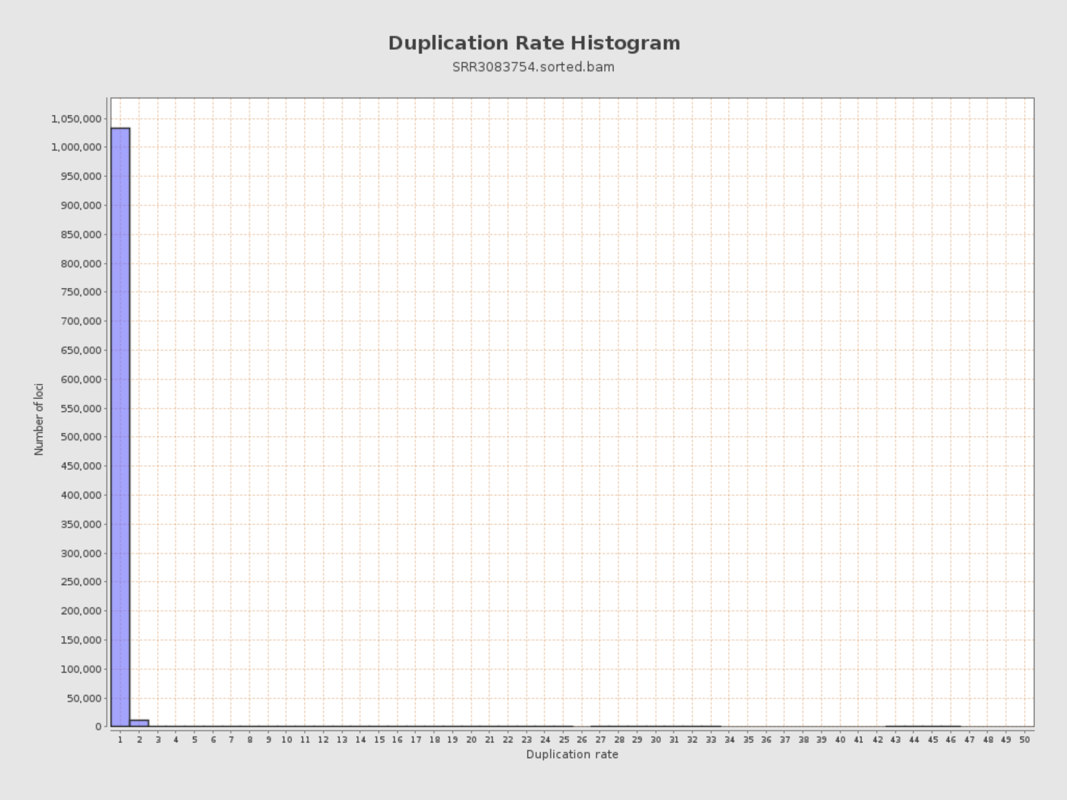
5. Results : Coverage Histogram (0-50X)



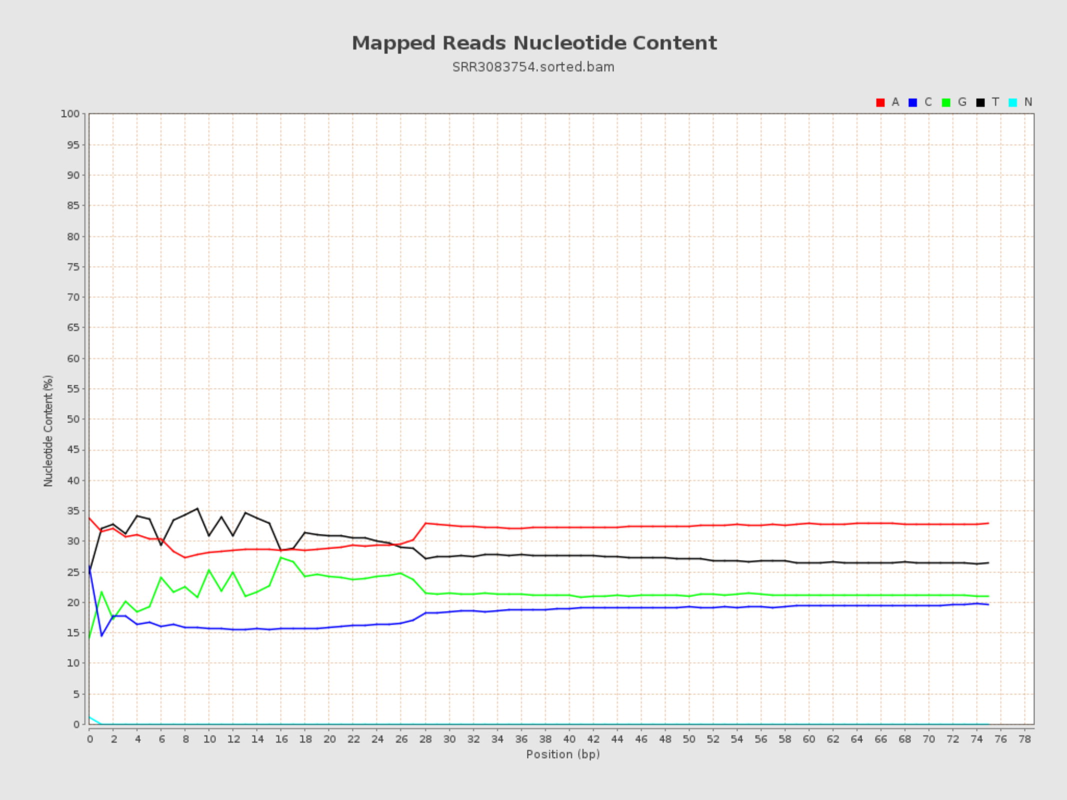
6. Results : Genome Fraction Coverage



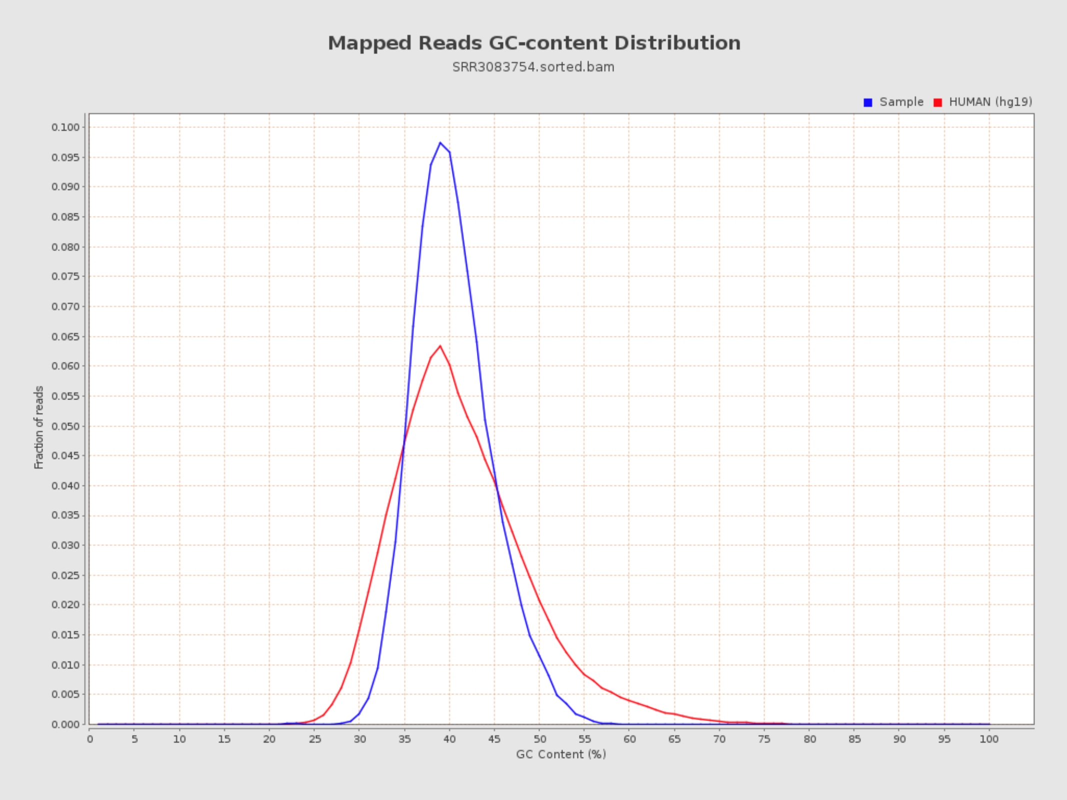
7. Results : Duplication Rate Histogram



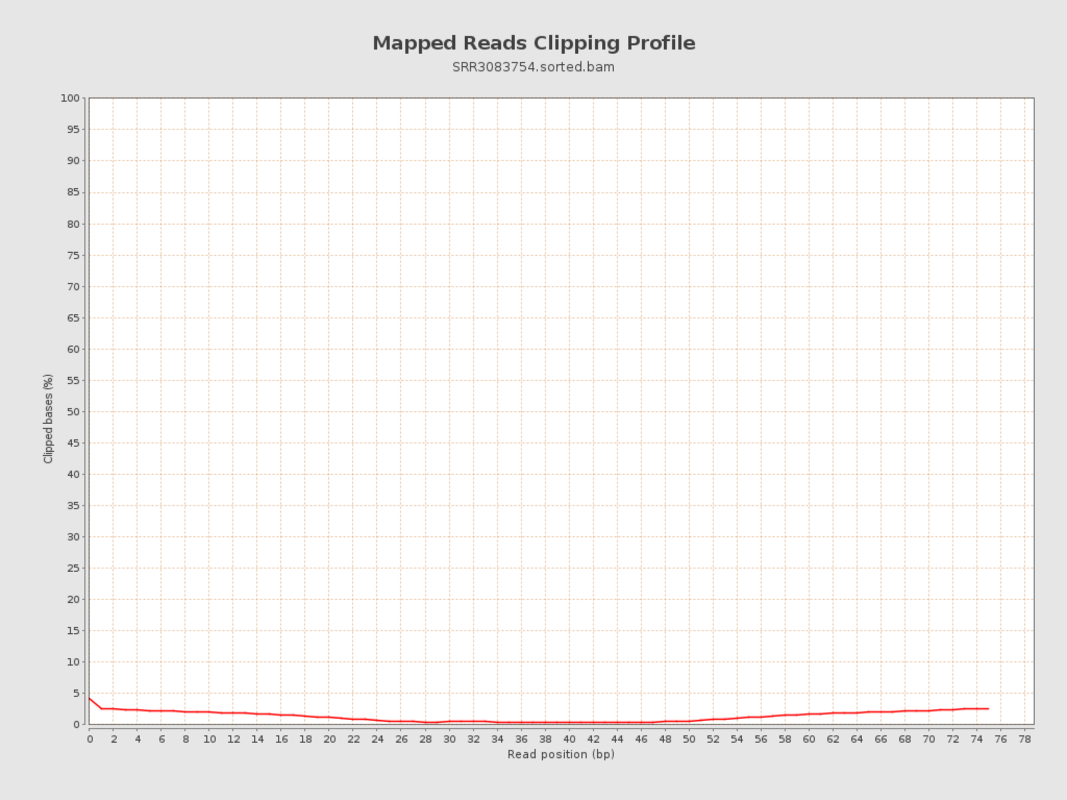
8. Results : Mapped Reads Nucleotide Content



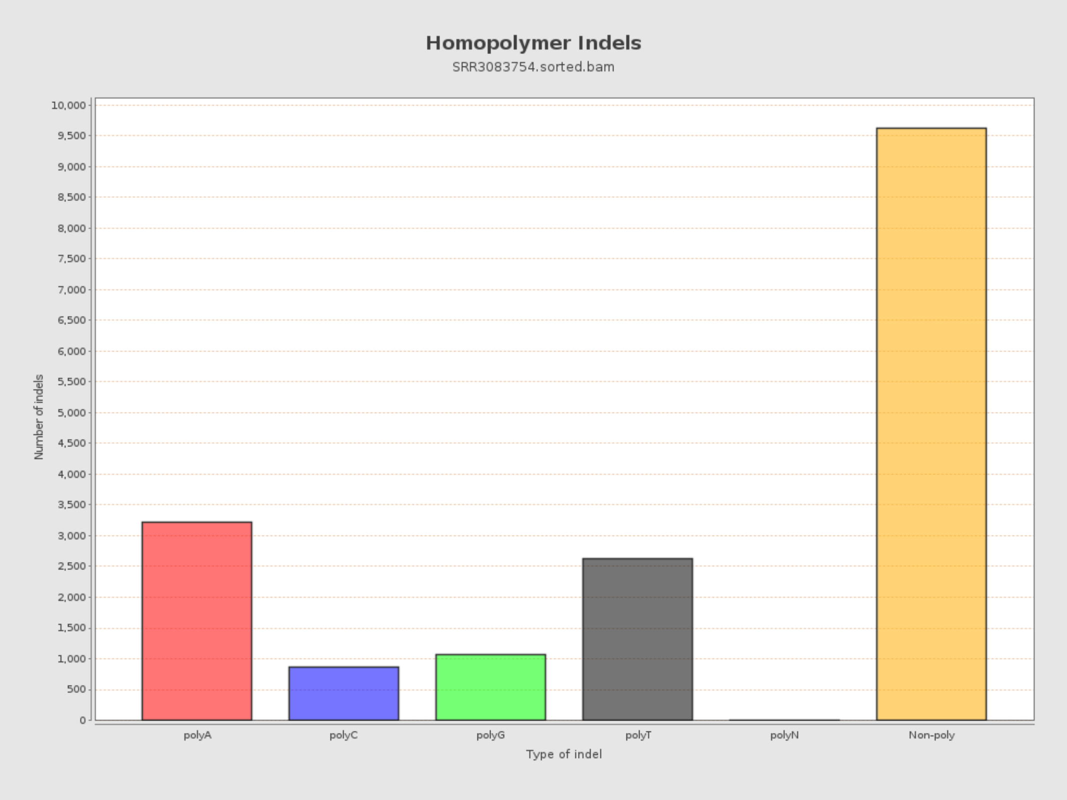
9. Results : Mapped Reads GC-content Distribution



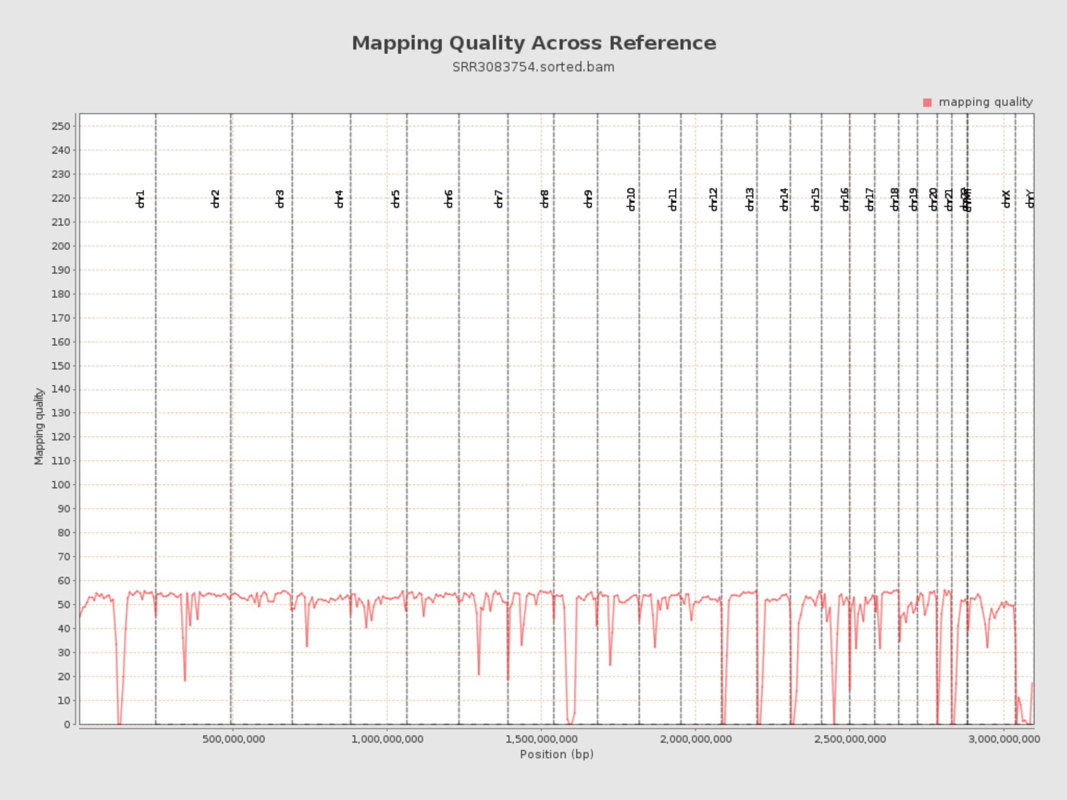
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram