Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:27:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751225.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_SRR8751225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:27:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,222,297
Mapped reads	4,908,410 / 93.99%
Unmapped reads	313,887 / 6.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	188,410 / 3.61%
Read min/max/mean length	30 / 101 / 102.49
Duplicated reads (estimated)	157,506 / 3.02%
Duplication rate	1.79%
Clipped reads	1,049,642 / 20.1%

2.2. ACGT Content

Number/percentage of A's	140,658,444 / 29.26%
Number/percentage of C's	99,790,726 / 20.76%
Number/percentage of T's	141,335,571 / 29.4%
Number/percentage of G's	98,912,419 / 20.58%
Number/percentage of N's	2,582 / 0%
GC Percentage	41.34%

2.3. Coverage

Mean	0.1553

Standard Deviation	1.4563

2.4. Mapping Quality

Mean Mapping Quality	51.16

2.5. Mismatches and indels

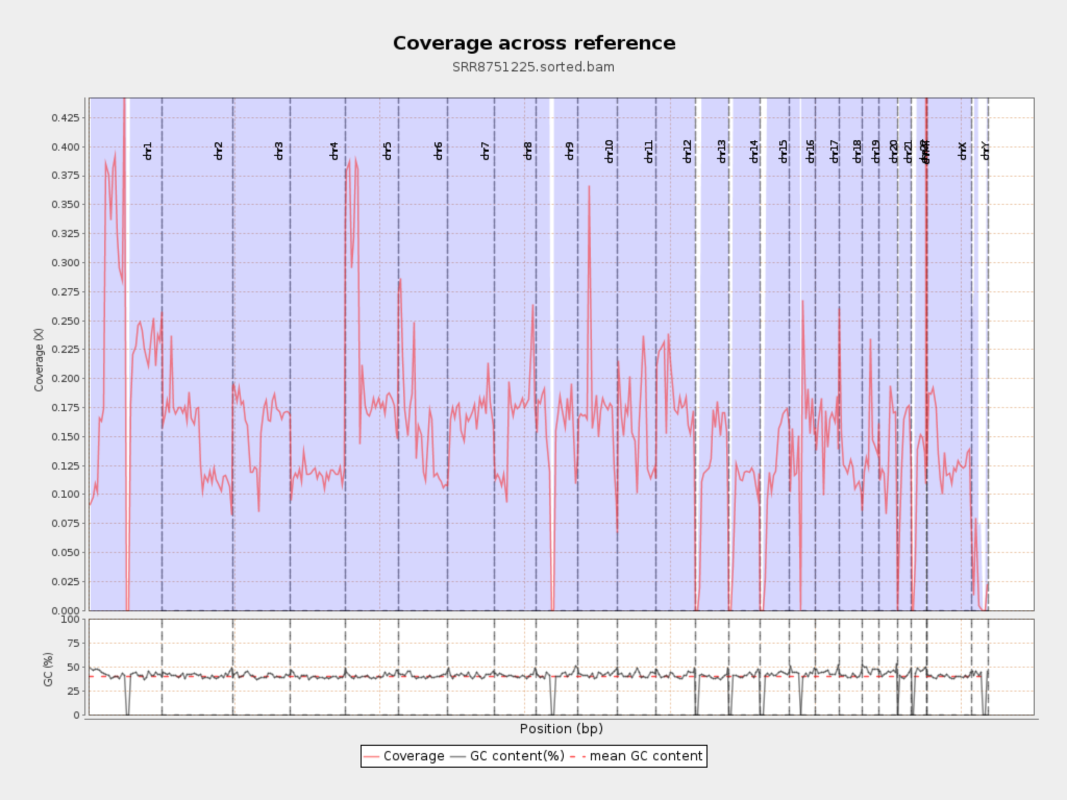
General error rate	0.42%
Mismatches	1,795,722
Insertions	138,088
Mapped reads with at least one insertion	2.75%
Deletions	64,451
Mapped reads with at least one deletion	1.29%
Homopolymer indels	49.1%

2.6. Chromosome stats

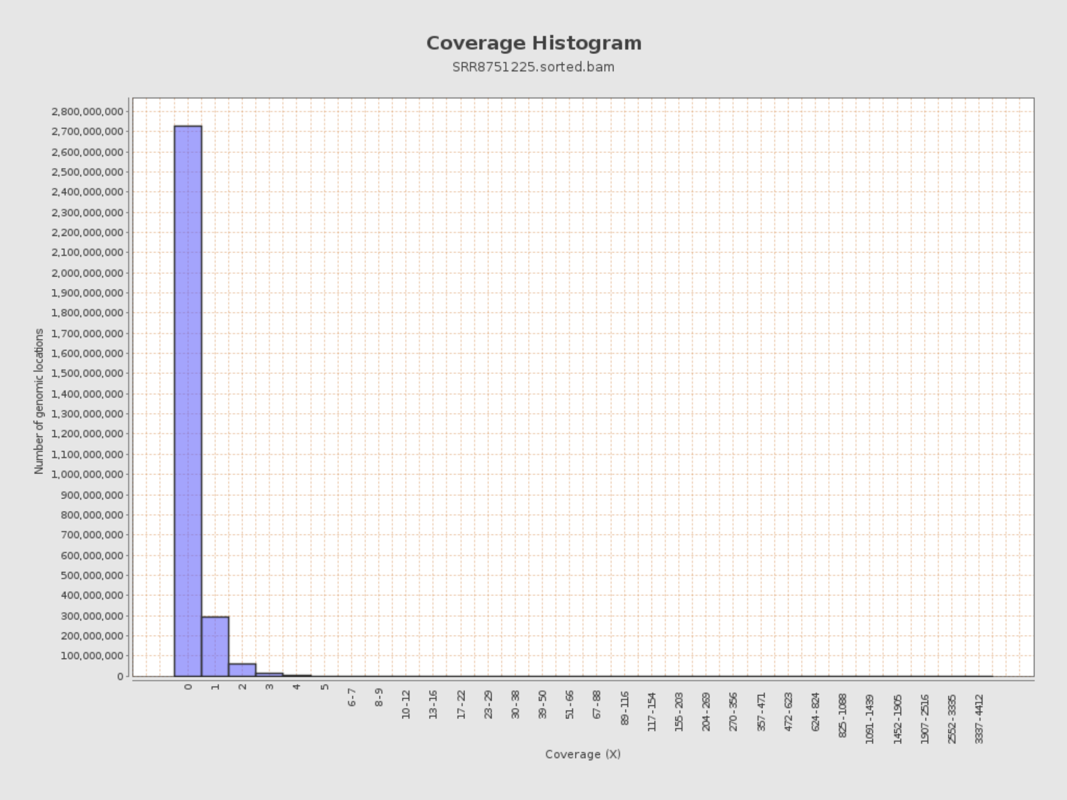
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57214909	0.2295	4.1287
chr2	243199373	35533289	0.1461	0.606
chr3	198022430	32167868	0.1624	0.5305
chr4	191154276	22389779	0.1171	0.4893
chr5	180915260	40380140	0.2232	0.5749
chr6	171115067	27143987	0.1586	0.9842
chr7	159138663	27085087	0.1702	0.8317

chr8	146364022	23941949	0.1636	0.5744
chr9	141213431	20813689	0.1474	0.7111
chr10	135534747	23916479	0.1765	1.9523
chr11	135006516	21671331	0.1605	0.7228
chr12	133851895	25291070	0.1889	0.526
chr13	115169878	13983551	0.1214	0.4155
chr14	107349540	10294350	0.0959	0.3822
chr15	102531392	11423792	0.1114	0.395
chr16	90354753	13353261	0.1478	1.0341
chr17	81195210	12763946	0.1572	0.7251
chr18	78077248	9932092	0.1272	1.3964
chr19	59128983	8583798	0.1452	2.9328
chr20	63025520	8541826	0.1355	0.4526
chr21	48129895	6137230	0.1275	0.4686
chr22	51304566	5015503	0.0978	0.3772
chrMT	16571	1120372	67.6104	27.826
chrX	155270560	21013858	0.1353	0.4962
chrY	59373566	1129023	0.019	0.735

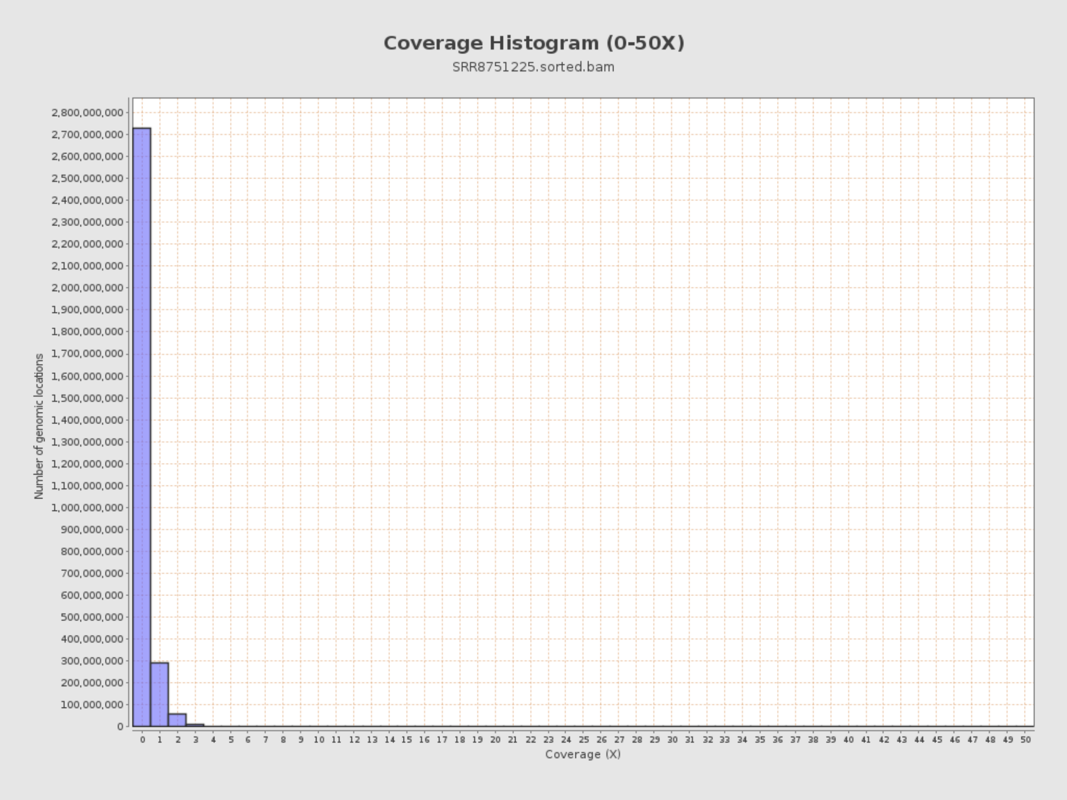
3. Results : Coverage across reference



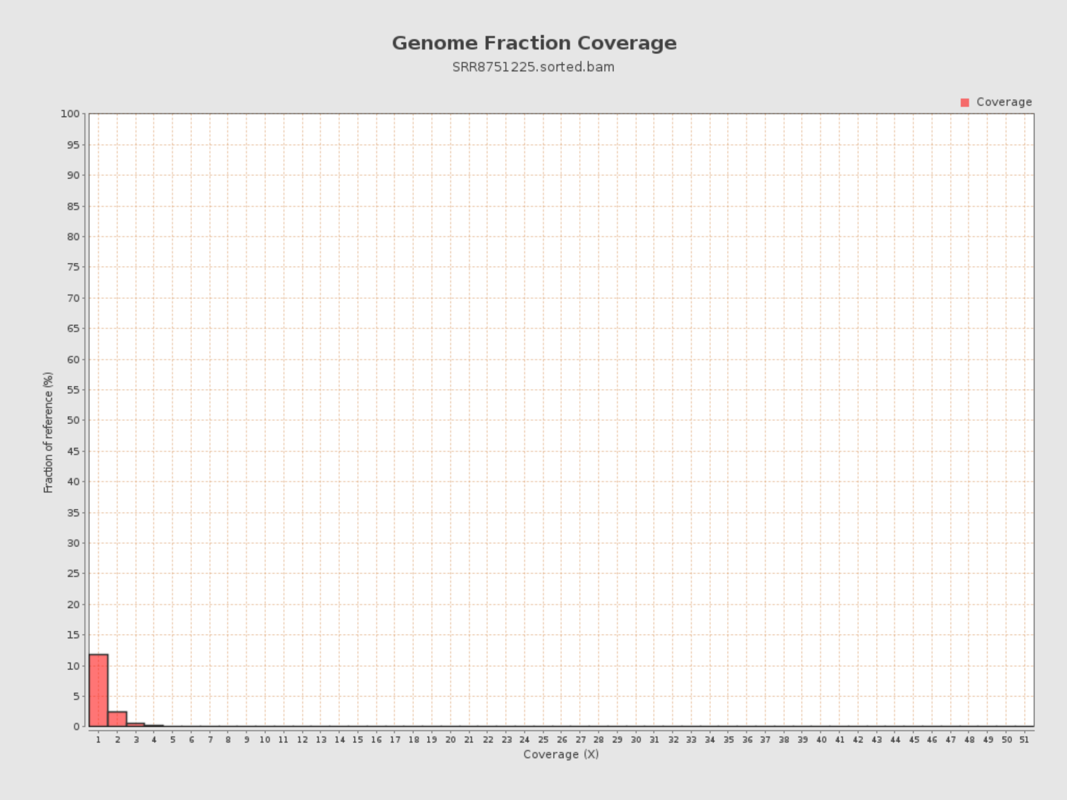
4. Results : Coverage Histogram



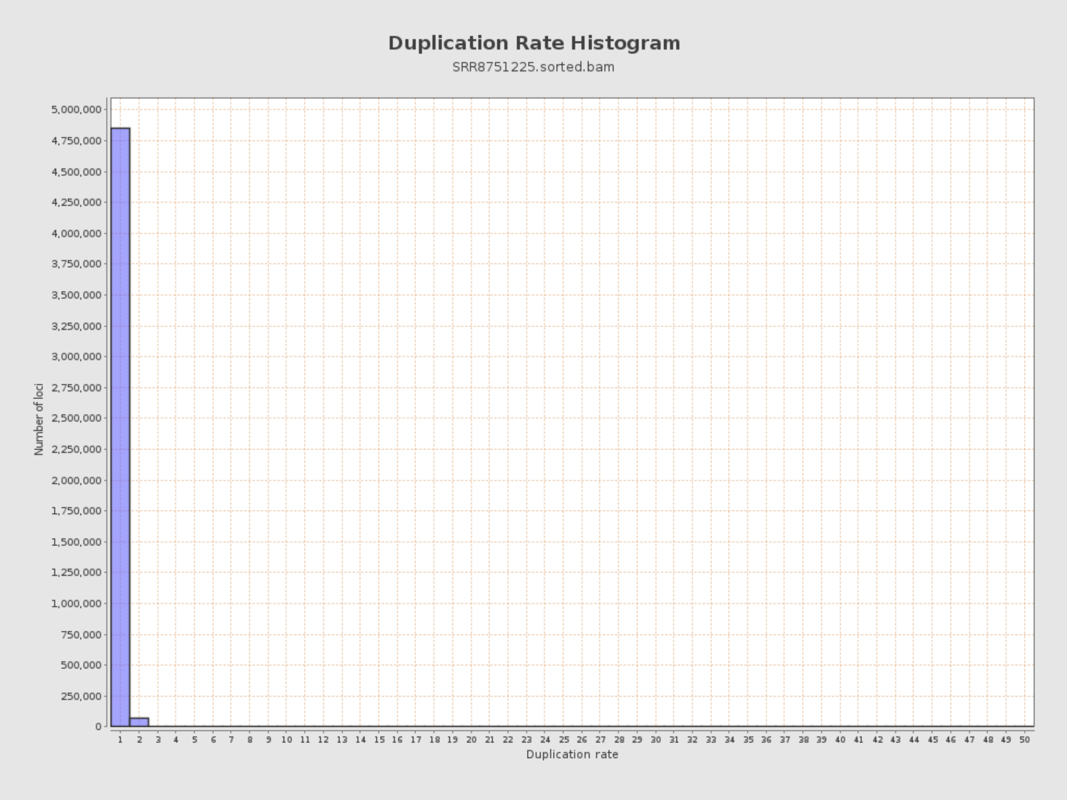
5. Results : Coverage Histogram (0-50X)



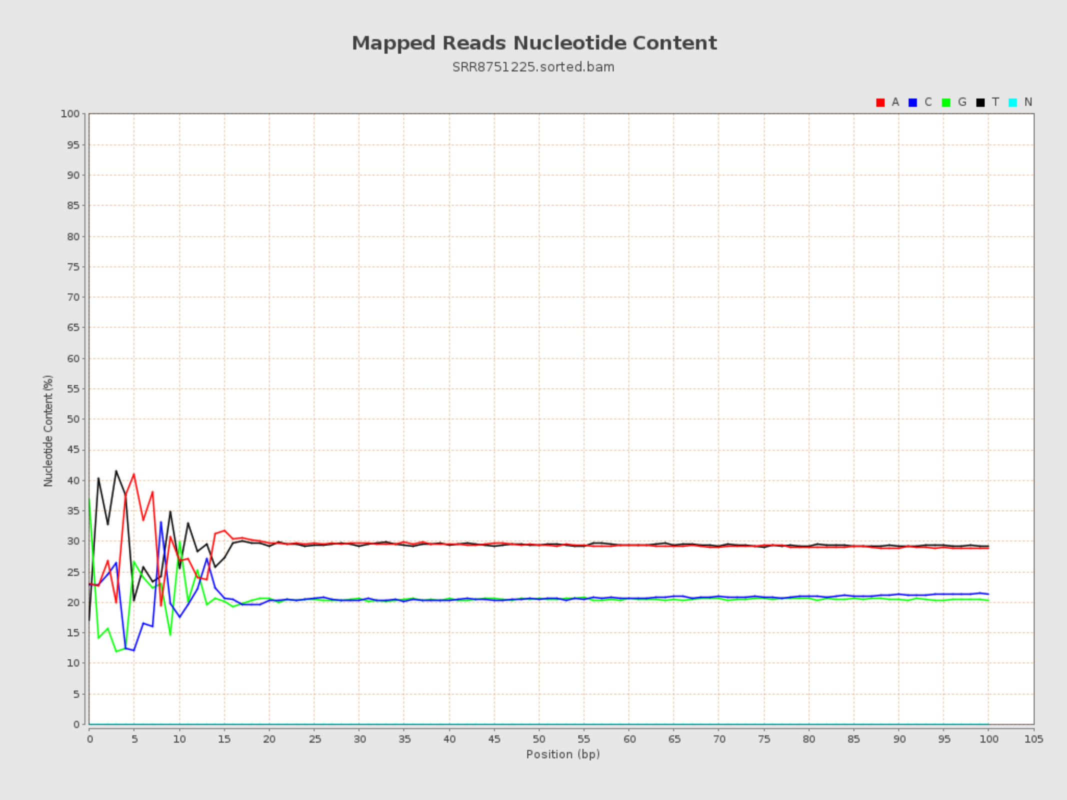
6. Results : Genome Fraction Coverage



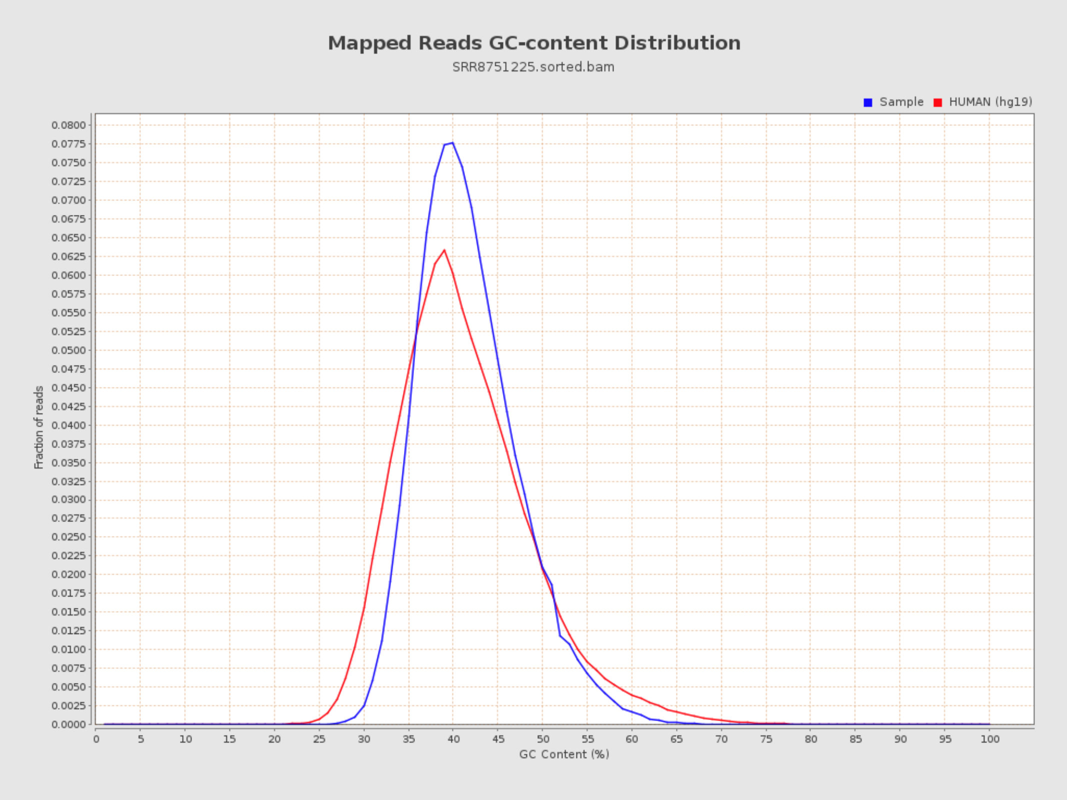
7. Results : Duplication Rate Histogram



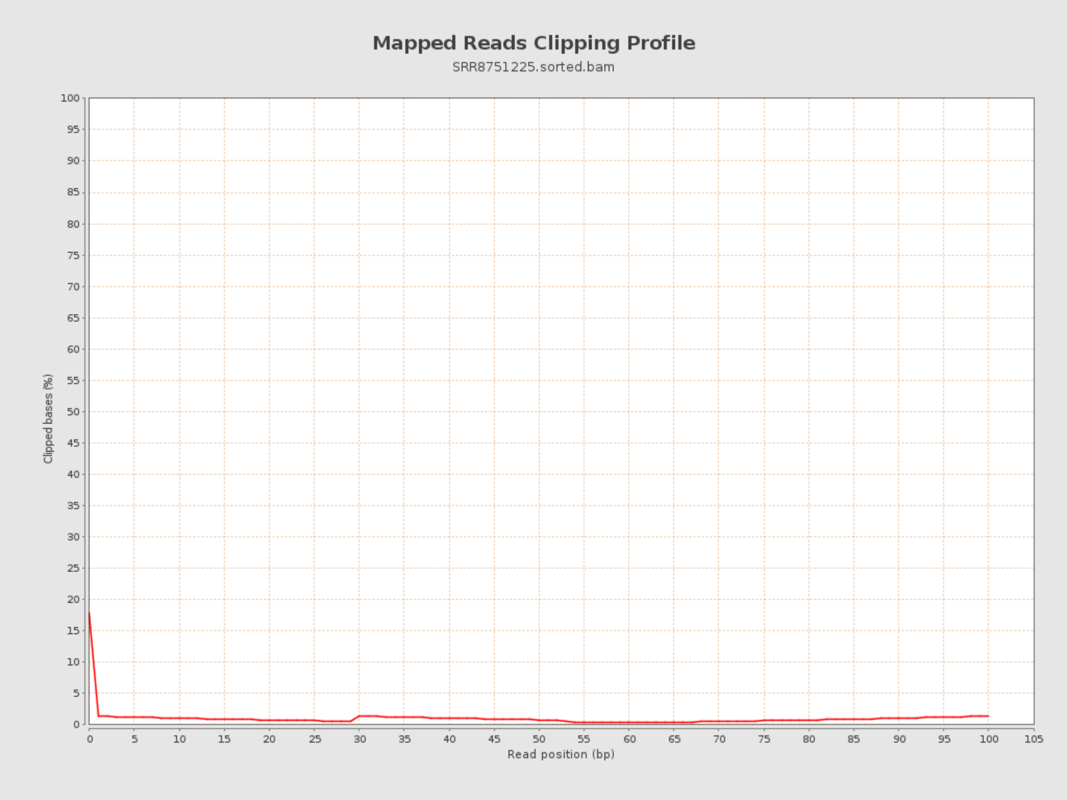
8. Results : Mapped Reads Nucleotide Content



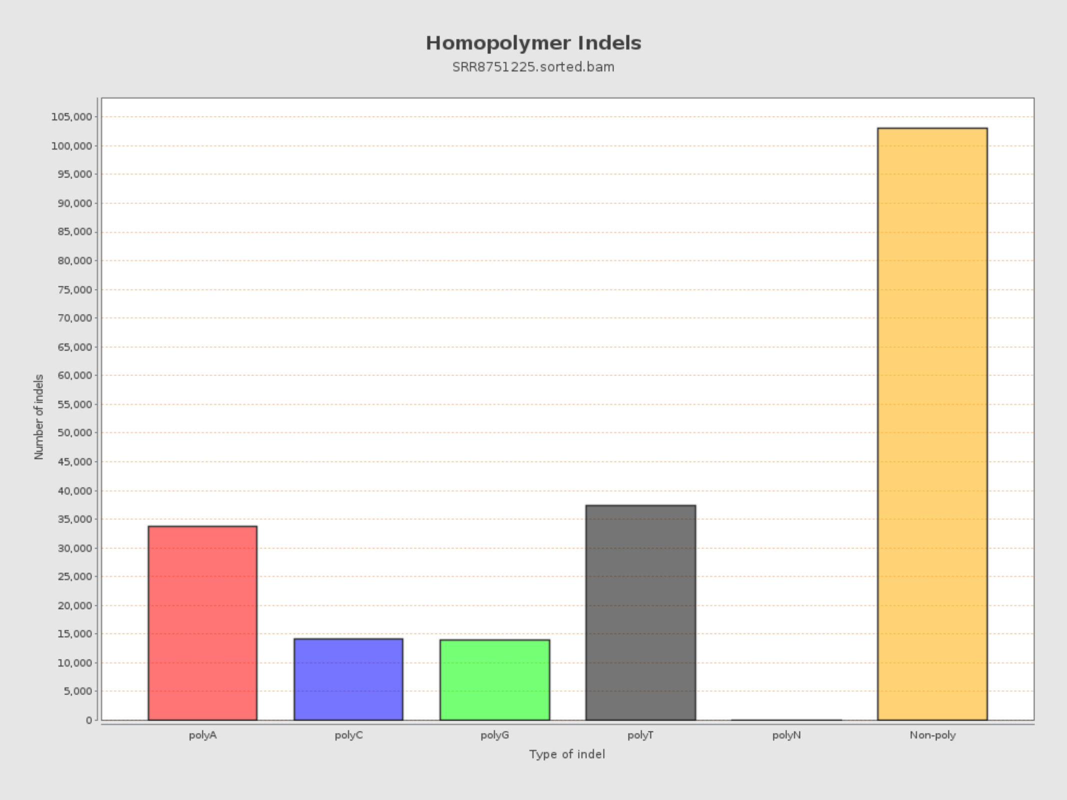
9. Results : Mapped Reads GC-content Distribution



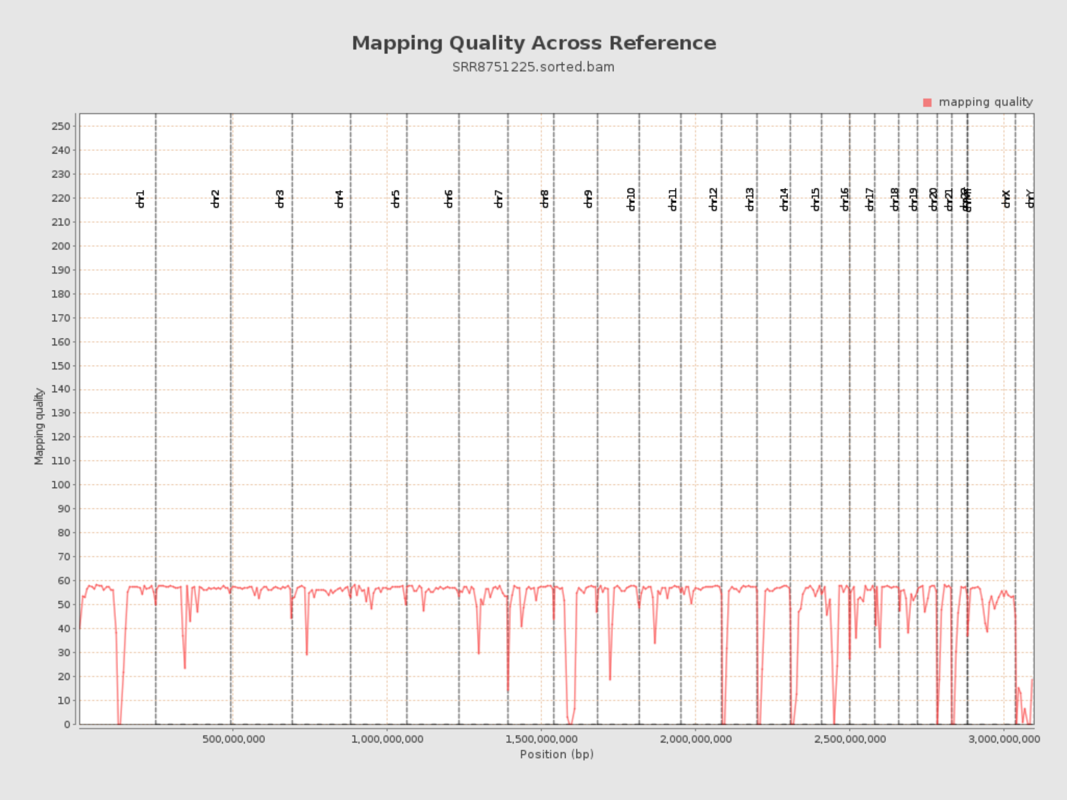
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram