Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:18:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525153.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_SRR10525153 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525153.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:18:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	852,154
Mapped reads	762,458 / 89.47%
Unmapped reads	89,696 / 10.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,588 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,791 / 1.74%
Duplication rate	1.39%
Clipped reads	761,206 / 89.33%

2.2. ACGT Content

Number/percentage of A's	12,136,351 / 26.08%
Number/percentage of C's	9,183,361 / 19.73%
Number/percentage of T's	14,155,091 / 30.41%
Number/percentage of G's	11,067,711 / 23.78%
Number/percentage of N's	1,164 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1701

2.4. Mapping Quality

Mean Mapping Quality	45.55

2.5. Mismatches and indels

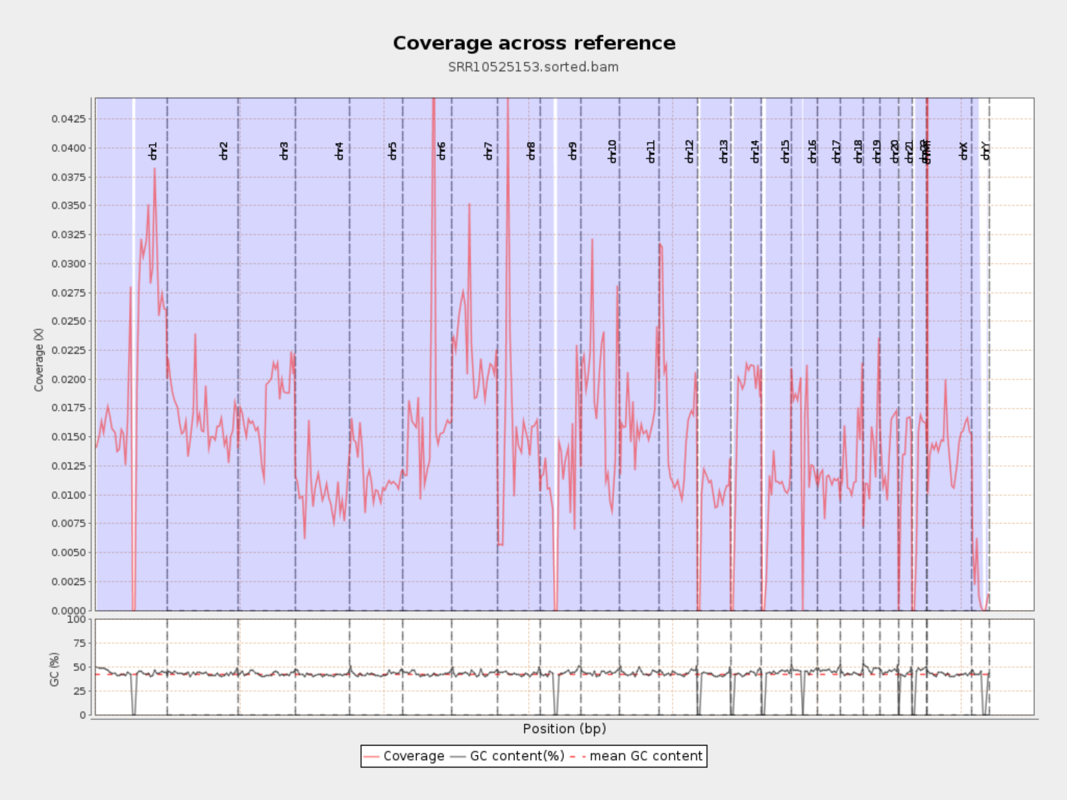
General error rate	0.5%
Mismatches	224,983
Insertions	4,044
Mapped reads with at least one insertion	0.53%
Deletions	9,419
Mapped reads with at least one deletion	1.23%
Homopolymer indels	40.25%

2.6. Chromosome stats

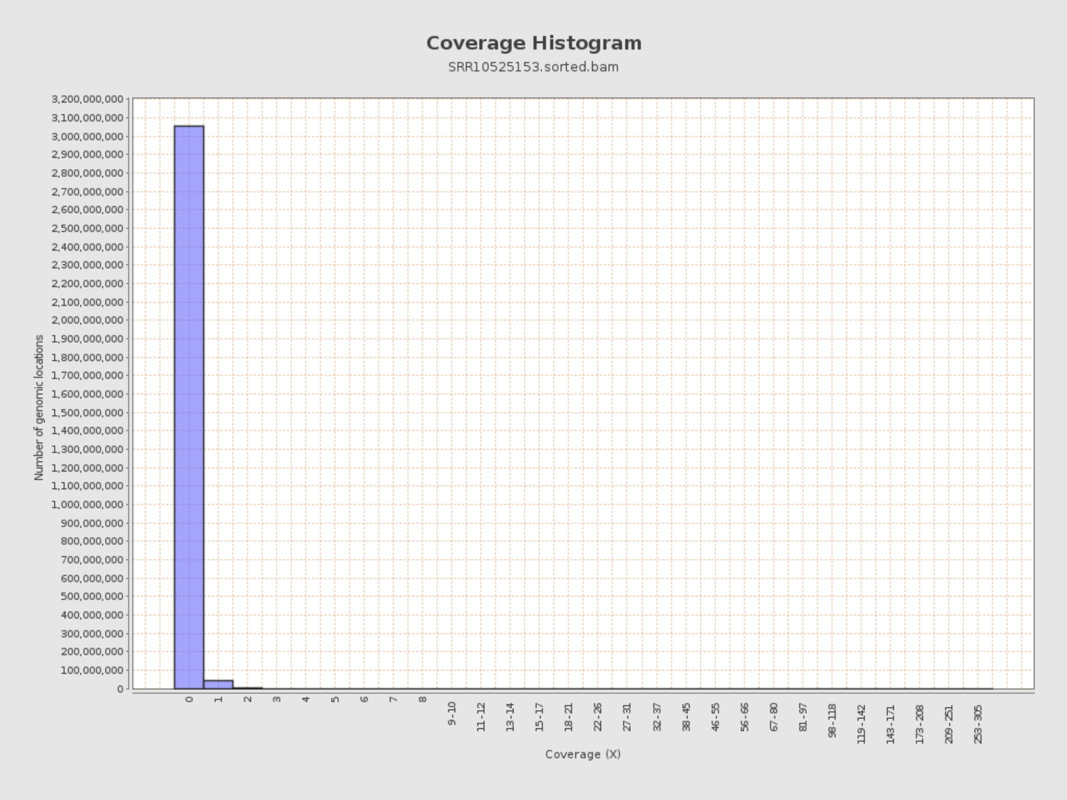
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5215066	0.0209	0.2958
chr2	243199373	3999831	0.0164	0.1844
chr3	198022430	3522661	0.0178	0.1396
chr4	191154276	1950757	0.0102	0.1086
chr5	180915260	2130336	0.0118	0.1133
chr6	171115067	2944021	0.0172	0.1434
chr7	159138663	3605571	0.0227	0.2899

chr8	146364022	2295418	0.0157	0.1436
chr9	141213431	1618755	0.0115	0.1284
chr10	135534747	2560969	0.0189	0.1837
chr11	135006516	2210357	0.0164	0.1492
chr12	133851895	2195251	0.0164	0.1343
chr13	115169878	1074989	0.0093	0.1007
chr14	107349540	1802716	0.0168	0.1381
chr15	102531392	915652	0.0089	0.0991
chr16	90354753	1344910	0.0149	0.1348
chr17	81195210	896014	0.011	0.1118
chr18	78077248	1020407	0.0131	0.2264
chr19	59128983	805981	0.0136	0.2057
chr20	63025520	865696	0.0137	0.1232
chr21	48129895	612668	0.0127	0.1198
chr22	51304566	570169	0.0111	0.1095
chrMT	16571	52312	3.1568	2.3372
chrX	155270560	2230045	0.0144	0.1295
chrY	59373566	118354	0.002	0.0621

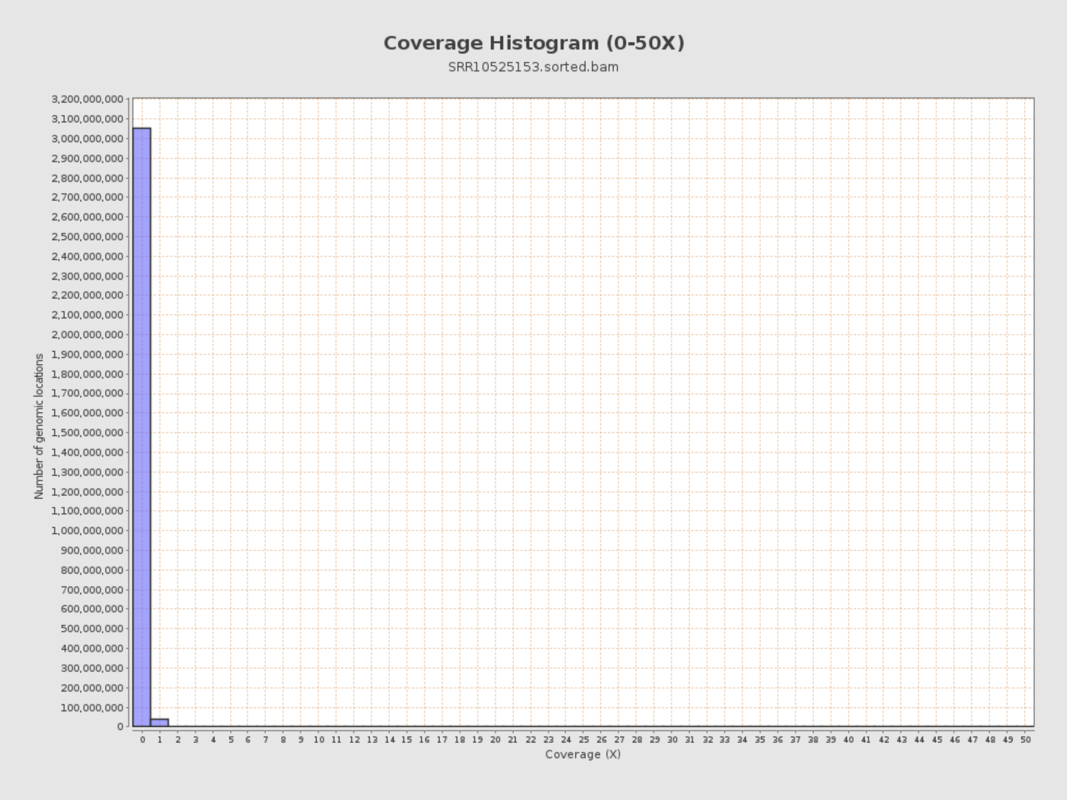
3. Results : Coverage across reference



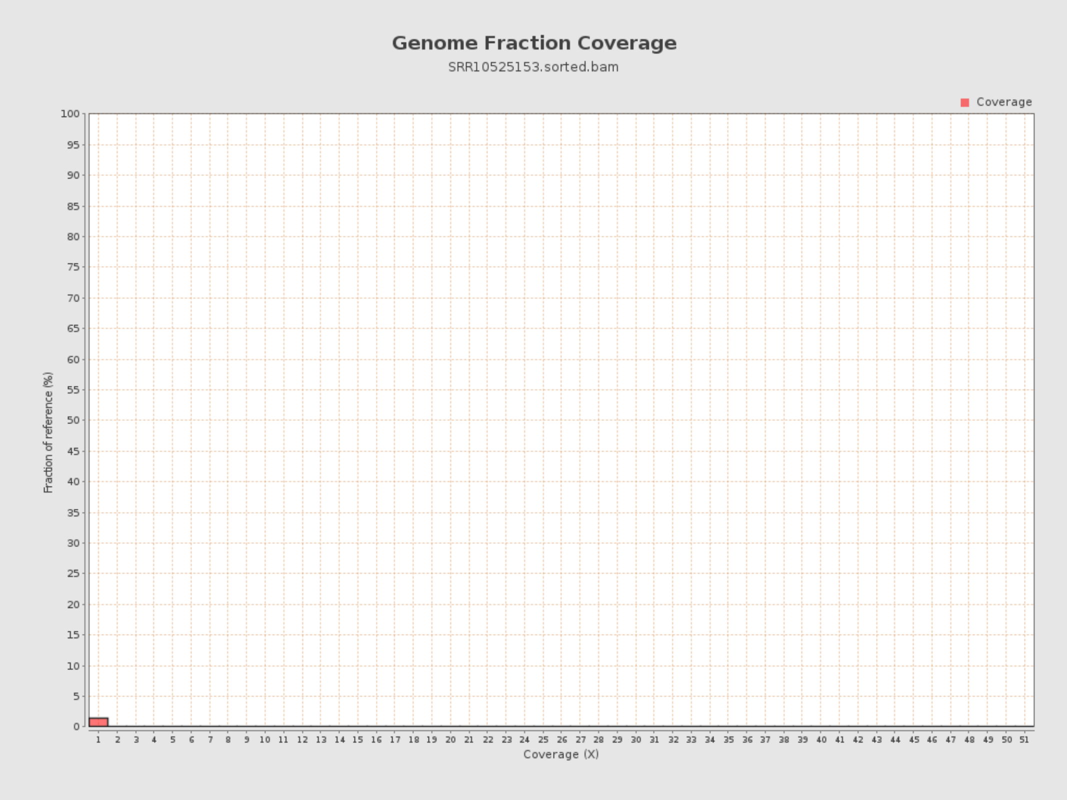
4. Results : Coverage Histogram



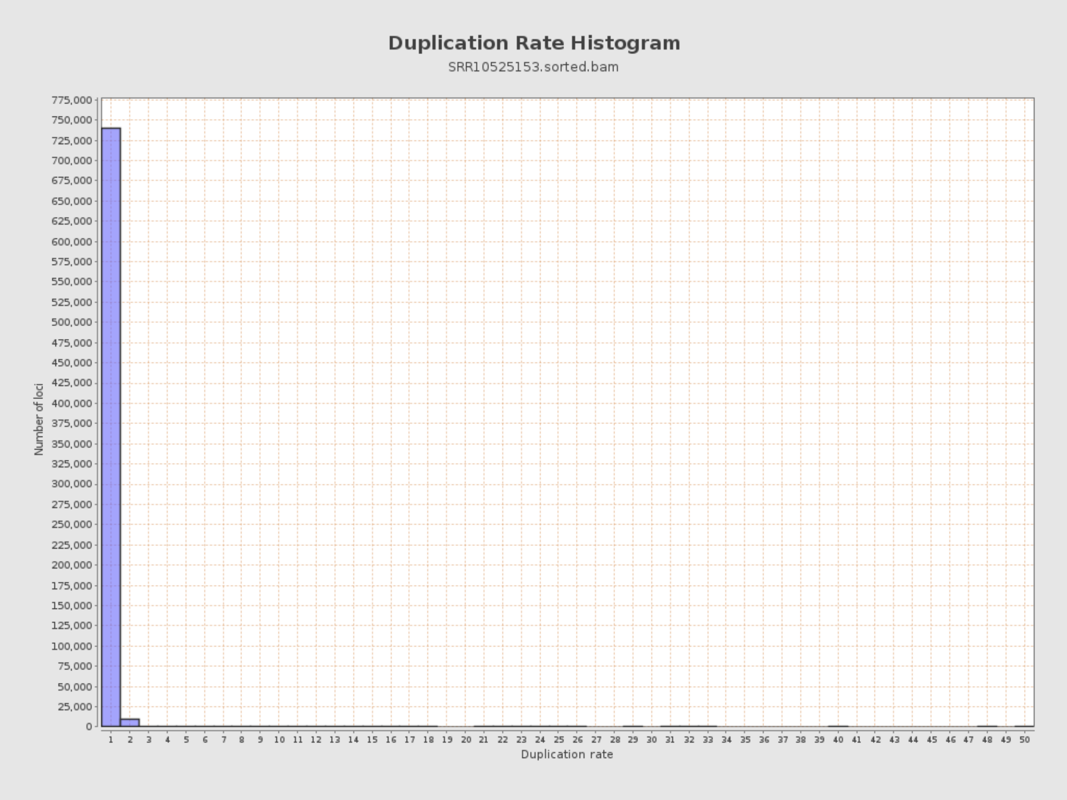
5. Results : Coverage Histogram (0-50X)



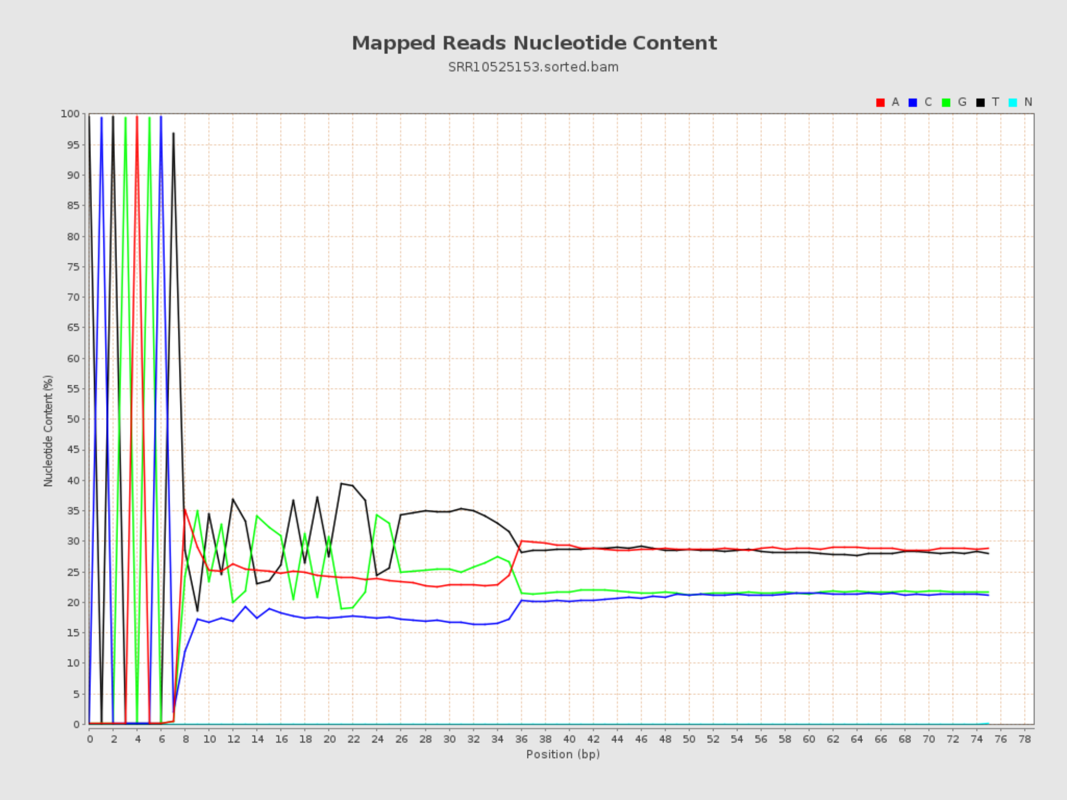
6. Results : Genome Fraction Coverage



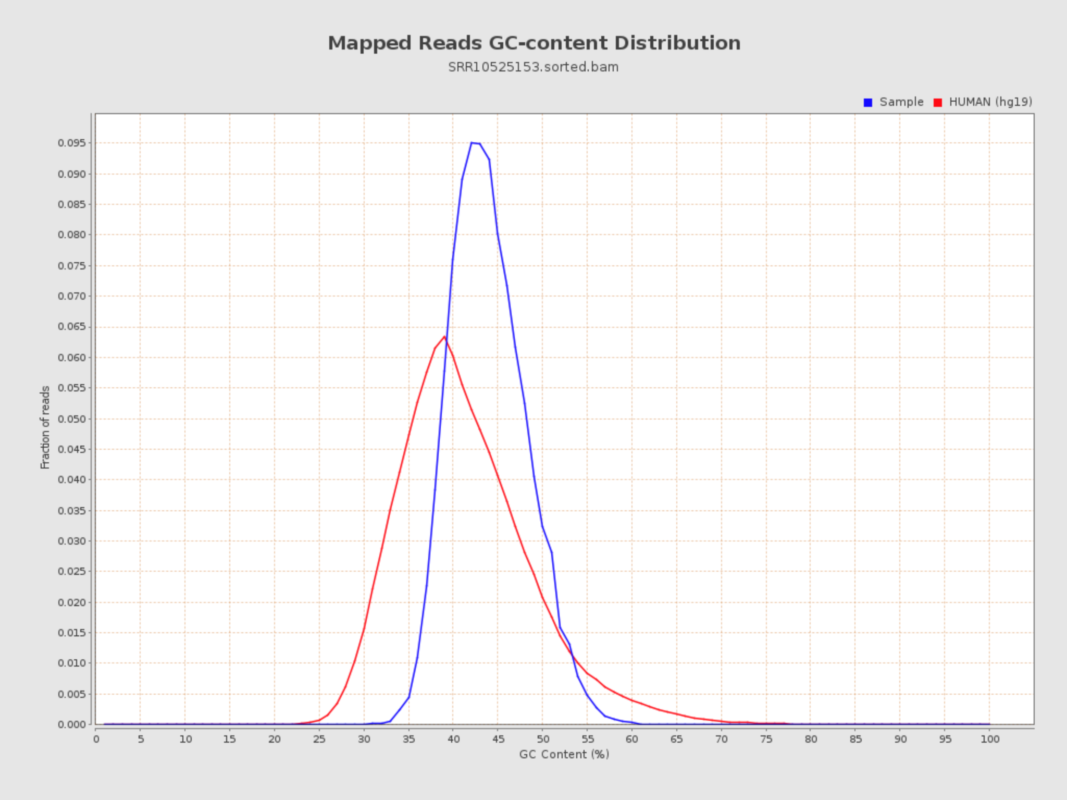
7. Results : Duplication Rate Histogram



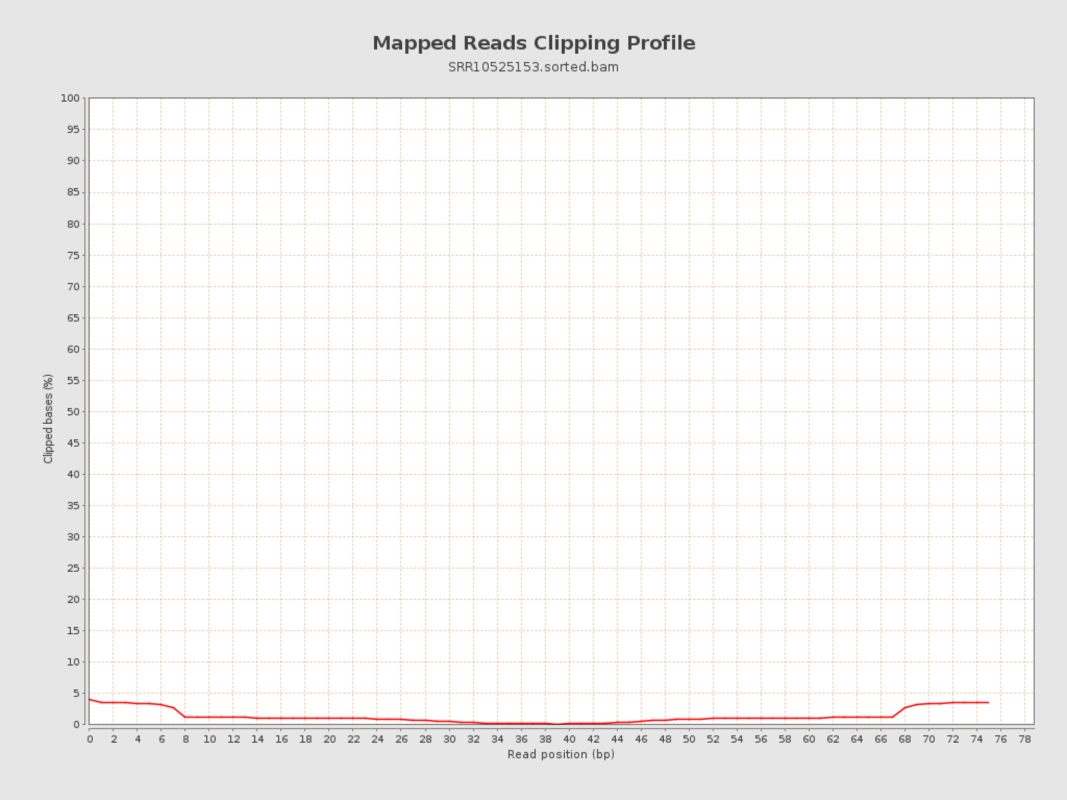
8. Results : Mapped Reads Nucleotide Content



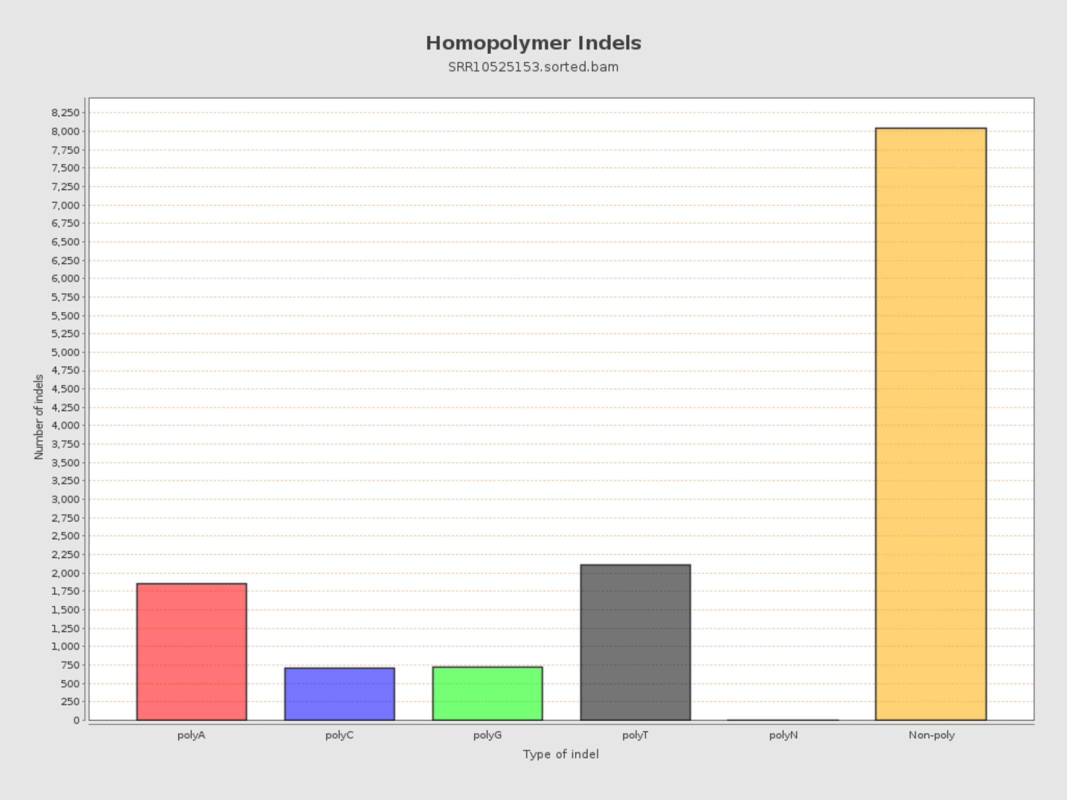
9. Results : Mapped Reads GC-content Distribution



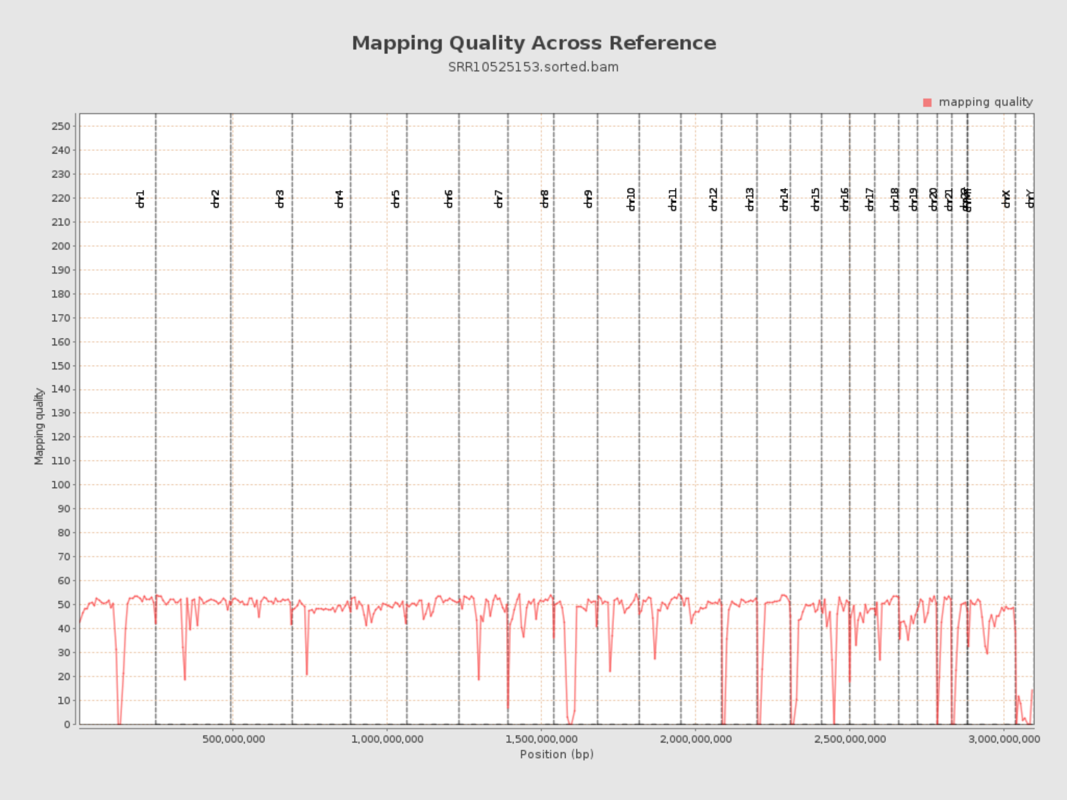
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram