Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:50:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525069.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_SRR10525069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:50:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	708,394
Mapped reads	600,593 / 84.78%
Unmapped reads	107,801 / 15.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,835 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	21,576 / 3.05%
Duplication rate	3.04%
Clipped reads	600,809 / 84.81%

2.2. ACGT Content

Number/percentage of A's	9,139,274 / 25.98%
Number/percentage of C's	6,213,065 / 17.66%
Number/percentage of T's	11,122,143 / 31.62%
Number/percentage of G's	8,702,106 / 24.74%
Number/percentage of N's	3,239 / 0.01%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0114

Standard Deviation	0.1369

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

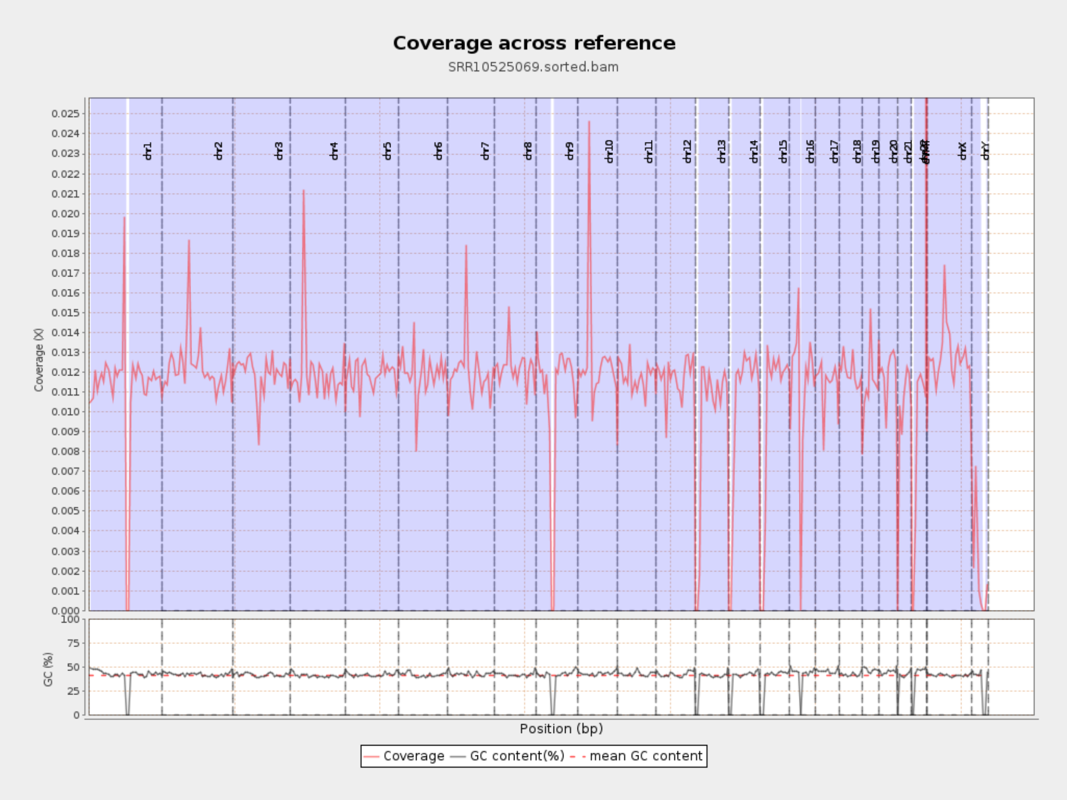
General error rate	0.49%
Mismatches	168,873
Insertions	2,587
Mapped reads with at least one insertion	0.43%
Deletions	7,110
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.09%

2.6. Chromosome stats

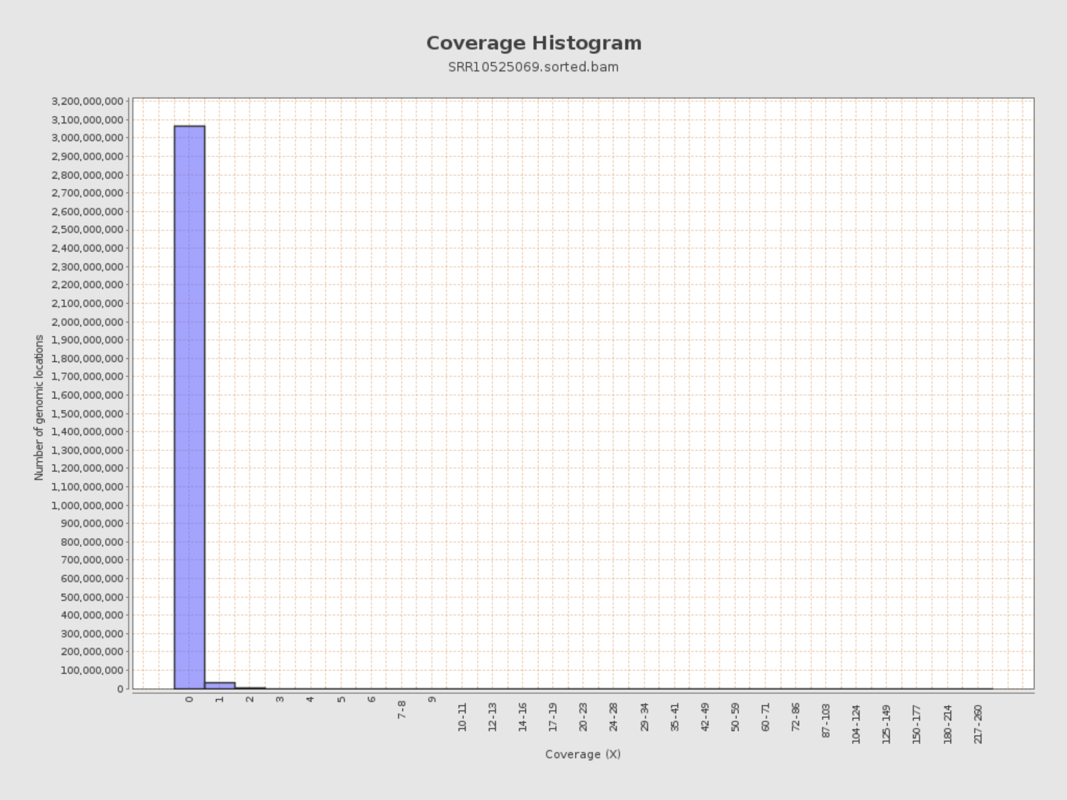
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2784693	0.0112	0.2165
chr2	243199373	2995717	0.0123	0.1542
chr3	198022430	2363379	0.0119	0.1157
chr4	191154276	2292774	0.012	0.1231
chr5	180915260	2141447	0.0118	0.1147
chr6	171115067	2046243	0.012	0.1212
chr7	159138663	1911203	0.012	0.1509

chr8	146364022	1786970	0.0122	0.1453
chr9	141213431	1491162	0.0106	0.1221
chr10	135534747	1709502	0.0126	0.1463
chr11	135006516	1583631	0.0117	0.1252
chr12	133851895	1572069	0.0117	0.1165
chr13	115169878	1088069	0.0094	0.1029
chr14	107349540	1091398	0.0102	0.1073
chr15	102531392	1021113	0.01	0.105
chr16	90354753	1019453	0.0113	0.1157
chr17	81195210	922649	0.0114	0.1164
chr18	78077248	939440	0.012	0.1659
chr19	59128983	684155	0.0116	0.1687
chr20	63025520	748583	0.0119	0.1174
chr21	48129895	470130	0.0098	0.1125
chr22	51304566	410742	0.008	0.0949
chrMT	16571	19957	1.2043	1.3443
chrX	155270560	1978701	0.0127	0.1251
chrY	59373566	118088	0.002	0.0749

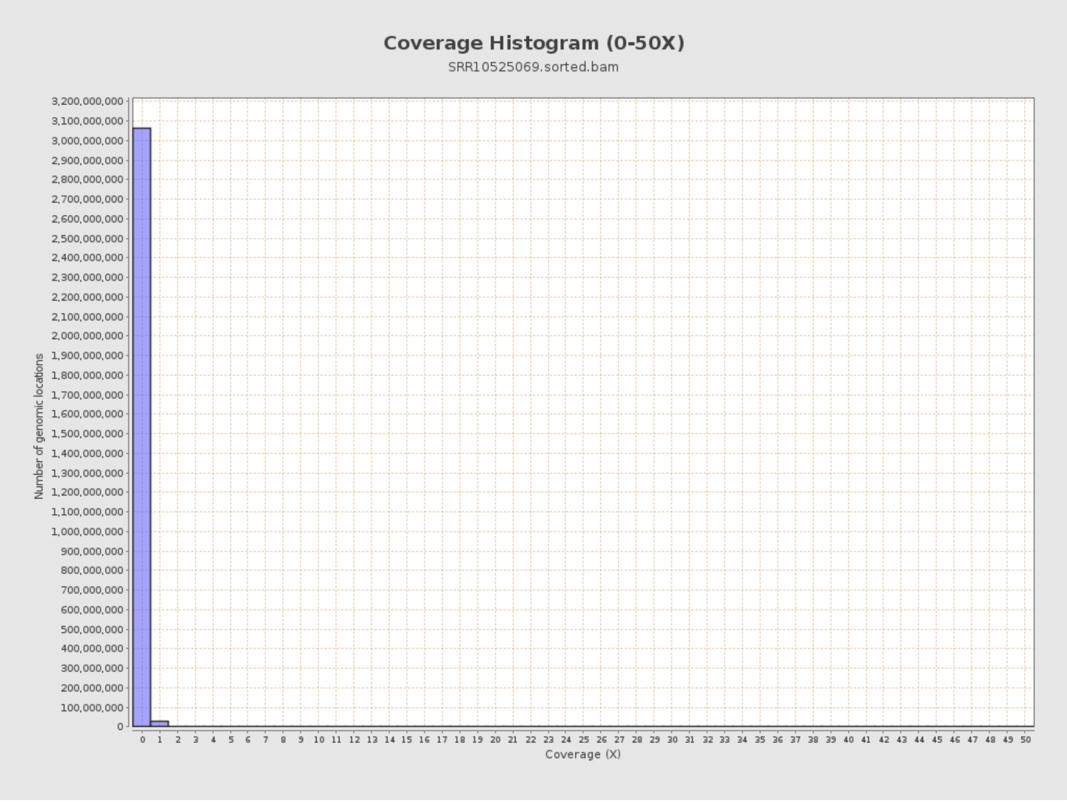
3. Results : Coverage across reference



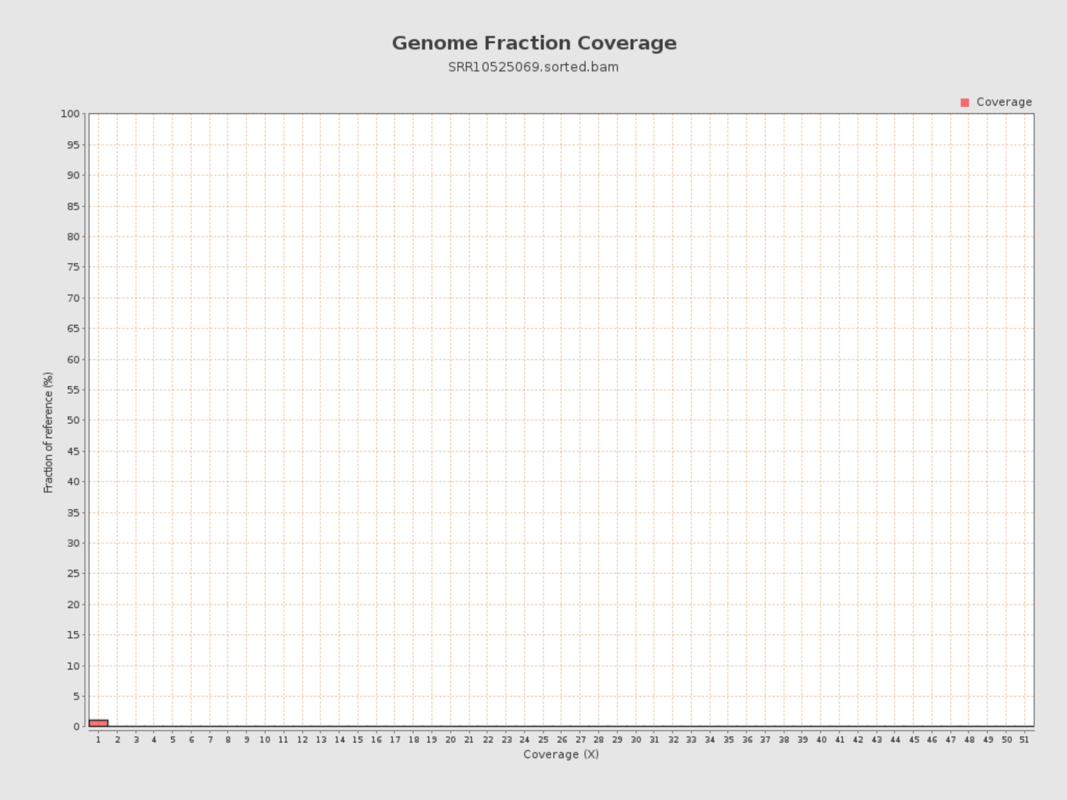
4. Results : Coverage Histogram



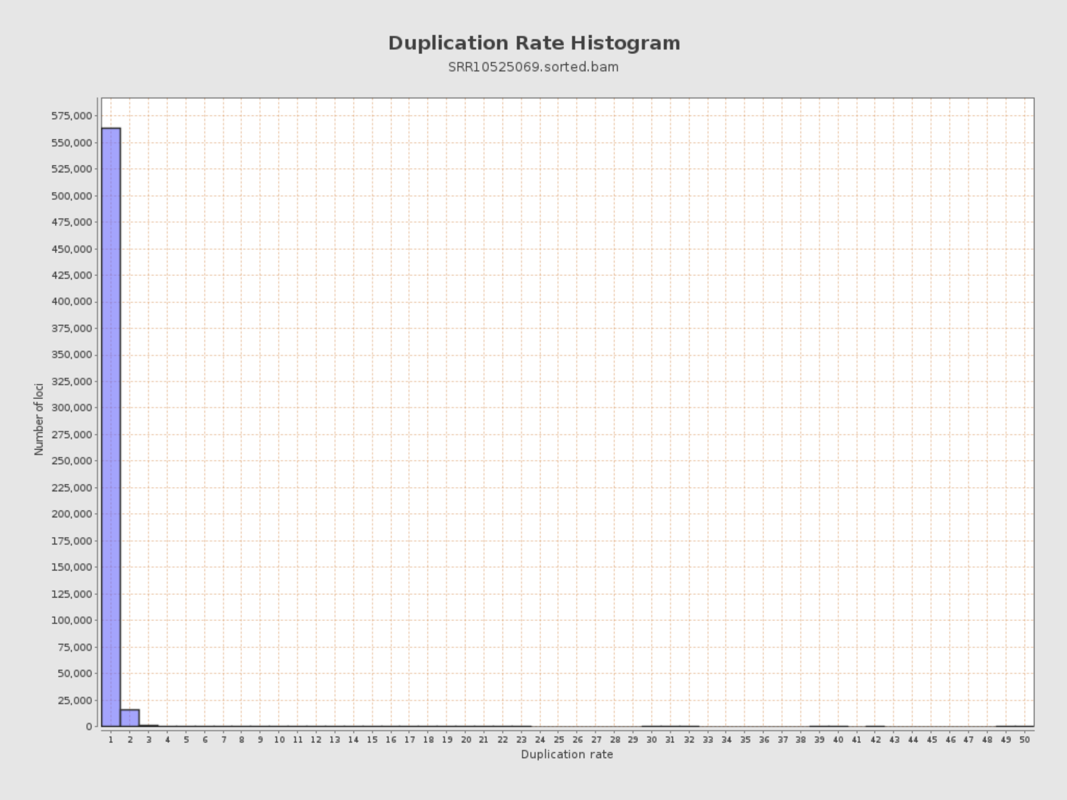
5. Results : Coverage Histogram (0-50X)



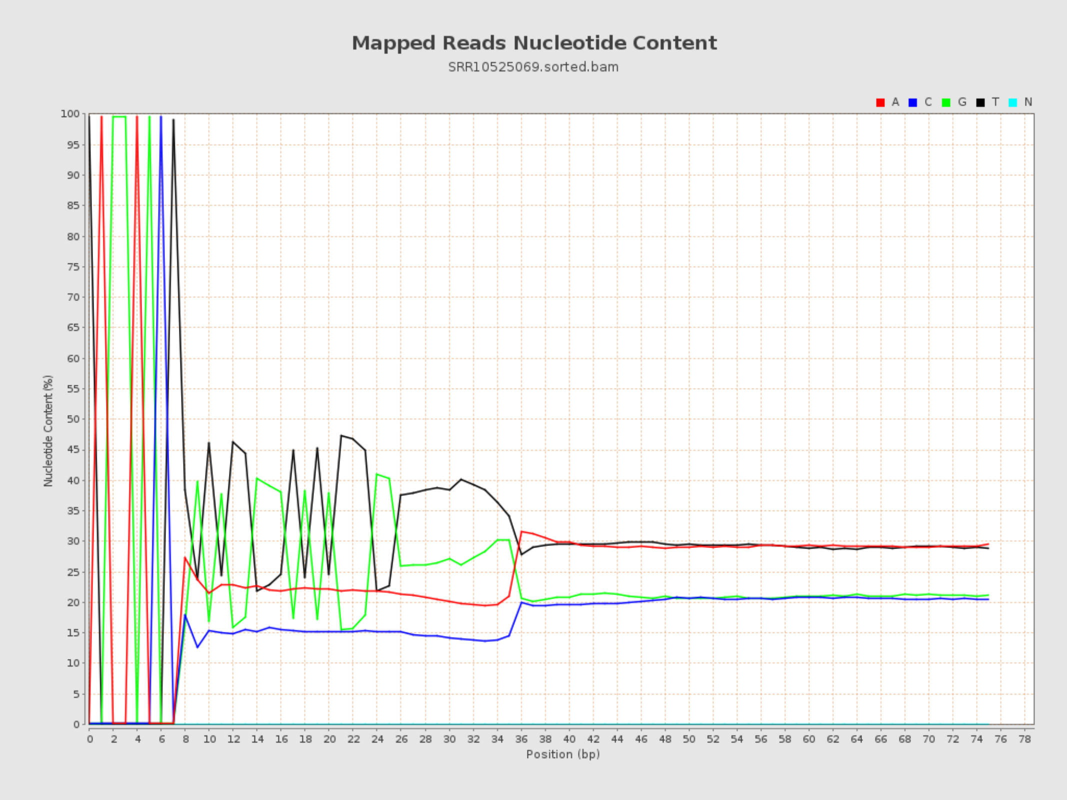
6. Results : Genome Fraction Coverage



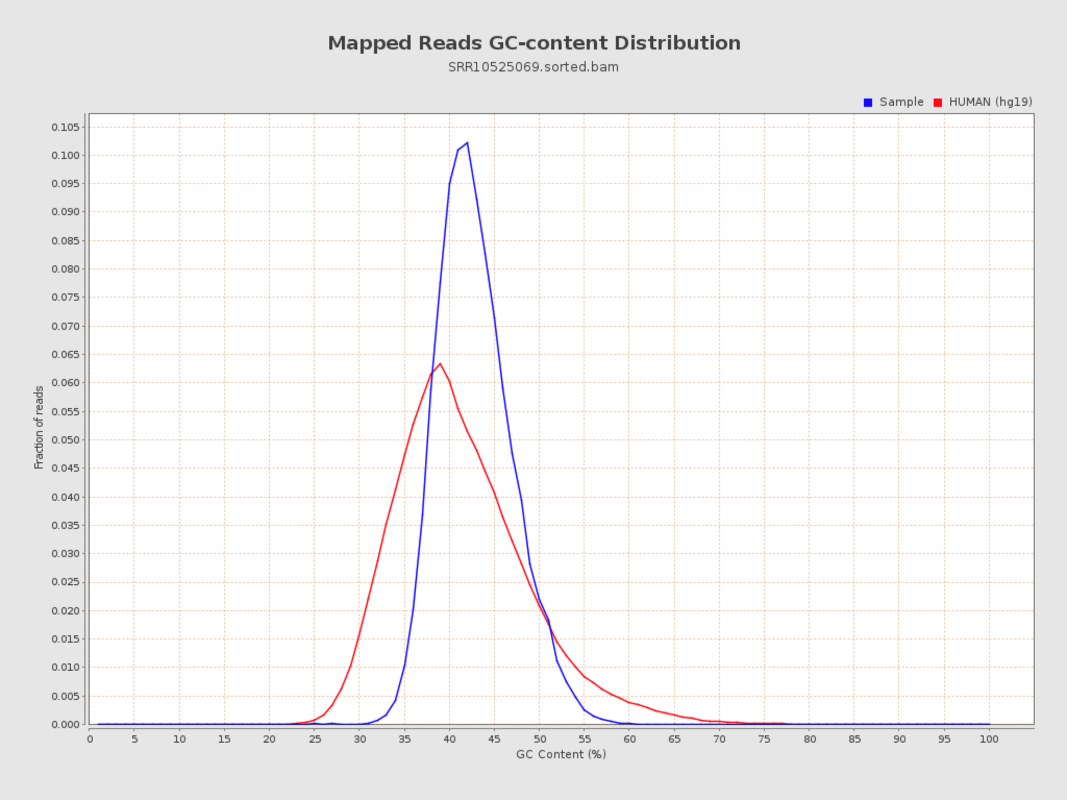
7. Results : Duplication Rate Histogram



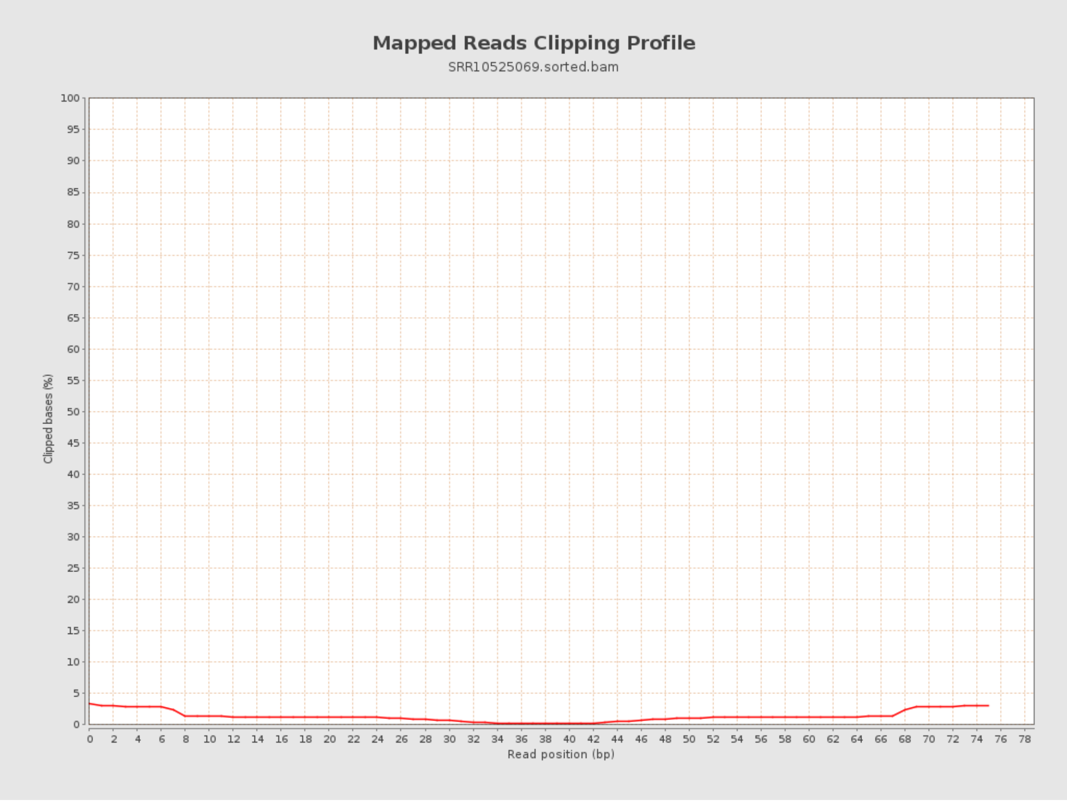
8. Results : Mapped Reads Nucleotide Content



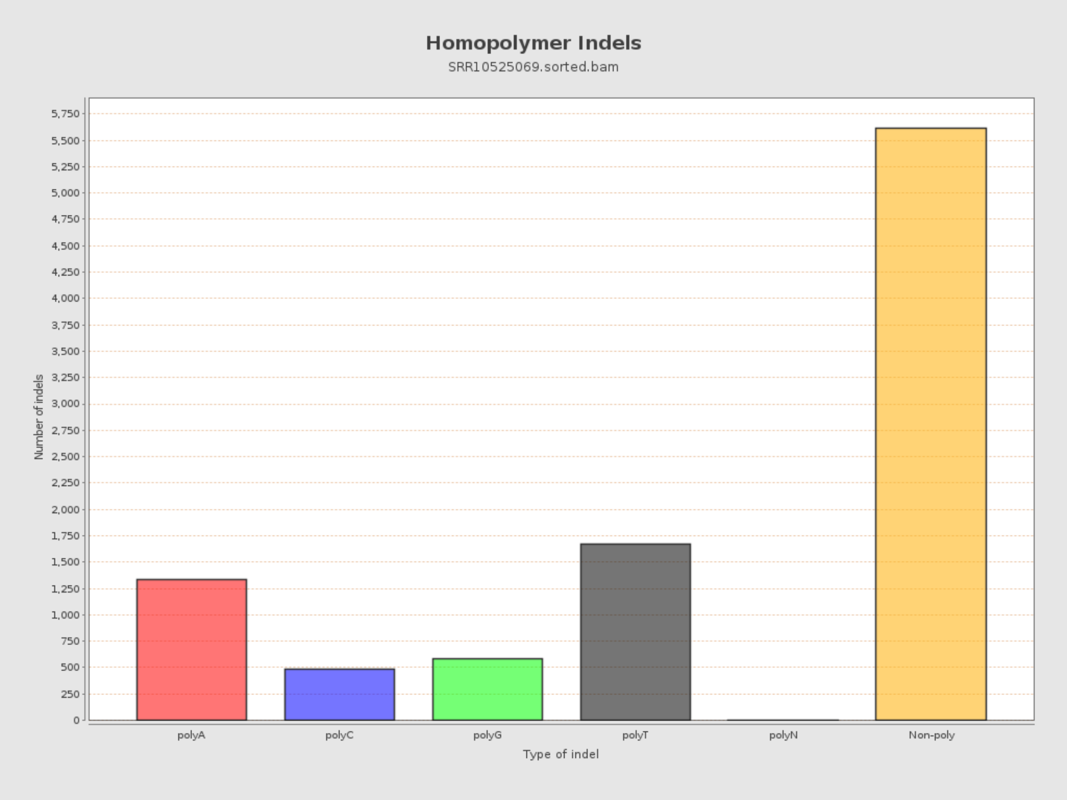
9. Results : Mapped Reads GC-content Distribution



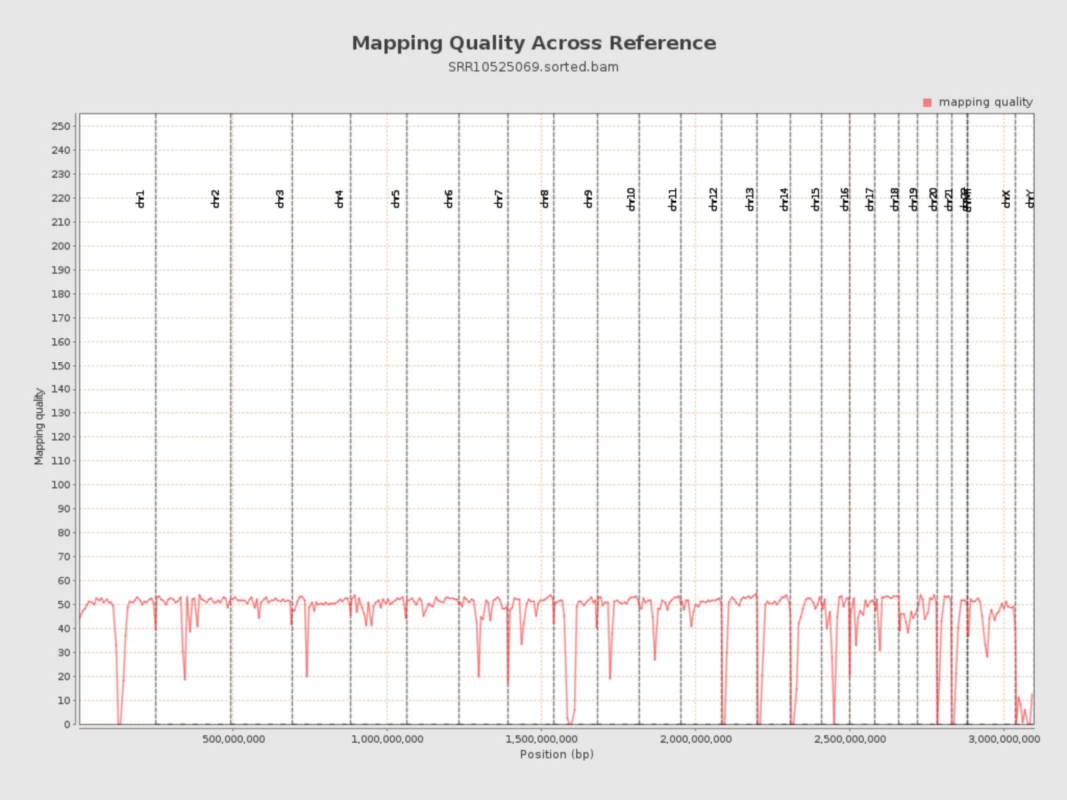
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram