Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:38:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525197.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_SRR10525197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525197.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:38:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	979,060
Mapped reads	891,958 / 91.1%
Unmapped reads	87,102 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,081 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	23,793 / 2.43%
Duplication rate	1.87%
Clipped reads	891,723 / 91.08%

2.2. ACGT Content

Number/percentage of A's	12,885,620 / 25.3%
Number/percentage of C's	9,522,147 / 18.7%
Number/percentage of T's	16,330,028 / 32.07%
Number/percentage of G's	12,187,612 / 23.93%
Number/percentage of N's	1,164 / 0%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0165

Standard Deviation	0.1892

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

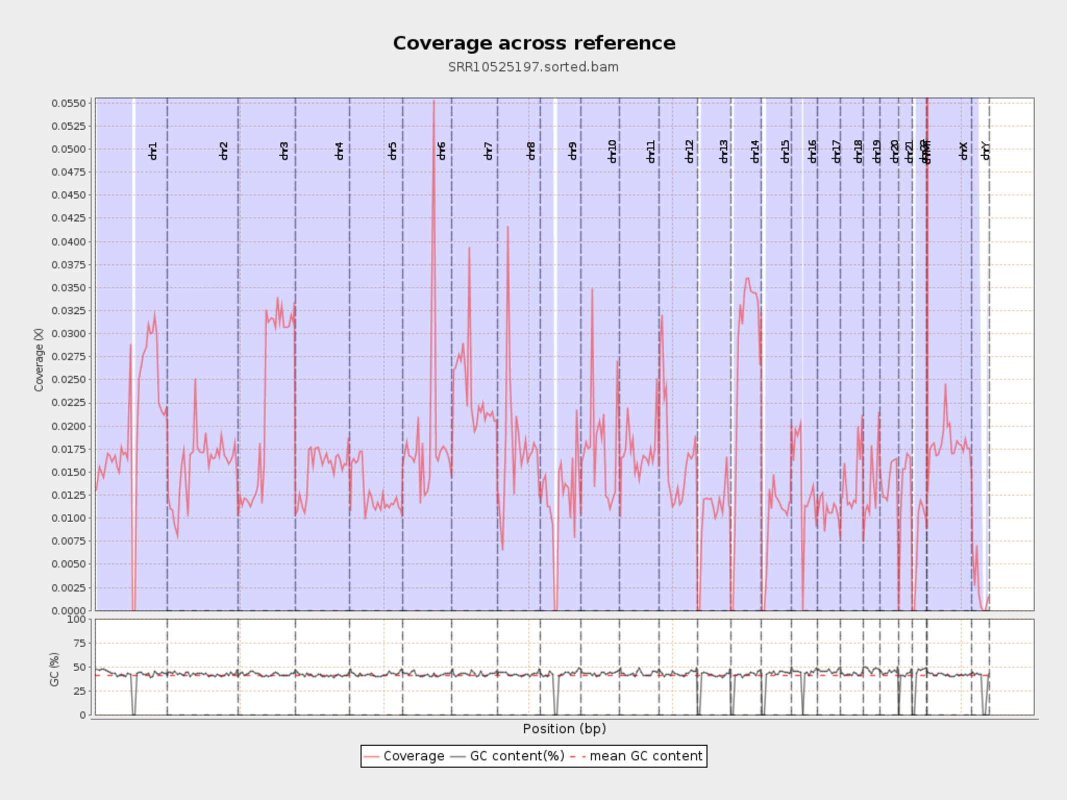
General error rate	0.53%
Mismatches	264,937
Insertions	3,753
Mapped reads with at least one insertion	0.42%
Deletions	9,941
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.23%

2.6. Chromosome stats

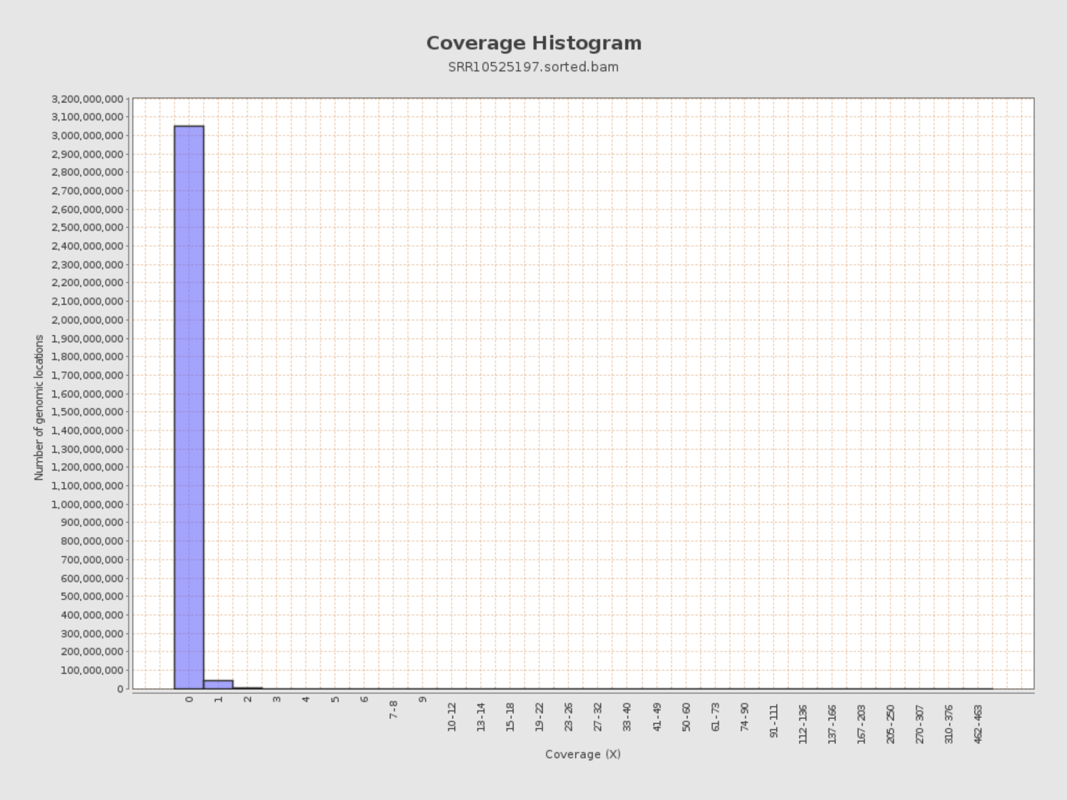
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4944647	0.0198	0.2958
chr2	243199373	3835314	0.0158	0.2344
chr3	198022430	4465677	0.0226	0.1596
chr4	191154276	2931345	0.0153	0.1337
chr5	180915260	2313668	0.0128	0.1193
chr6	171115067	3240903	0.0189	0.1582
chr7	159138663	3779311	0.0237	0.3348

chr8	146364022	2592715	0.0177	0.1643
chr9	141213431	1690719	0.012	0.1386
chr10	135534747	2409679	0.0178	0.2082
chr11	135006516	2318995	0.0172	0.168
chr12	133851895	2292343	0.0171	0.1386
chr13	115169878	1208231	0.0105	0.1092
chr14	107349540	2925792	0.0273	0.1749
chr15	102531392	981349	0.0096	0.1068
chr16	90354753	1223900	0.0135	0.1342
chr17	81195210	881639	0.0109	0.1127
chr18	78077248	1094701	0.014	0.2337
chr19	59128983	806899	0.0136	0.2204
chr20	63025520	881617	0.014	0.126
chr21	48129895	637249	0.0132	0.123
chr22	51304566	395028	0.0077	0.0918
chrMT	16571	143465	8.6576	5.6225
chrX	155270560	2809709	0.0181	0.1537
chrY	59373566	137251	0.0023	0.0666

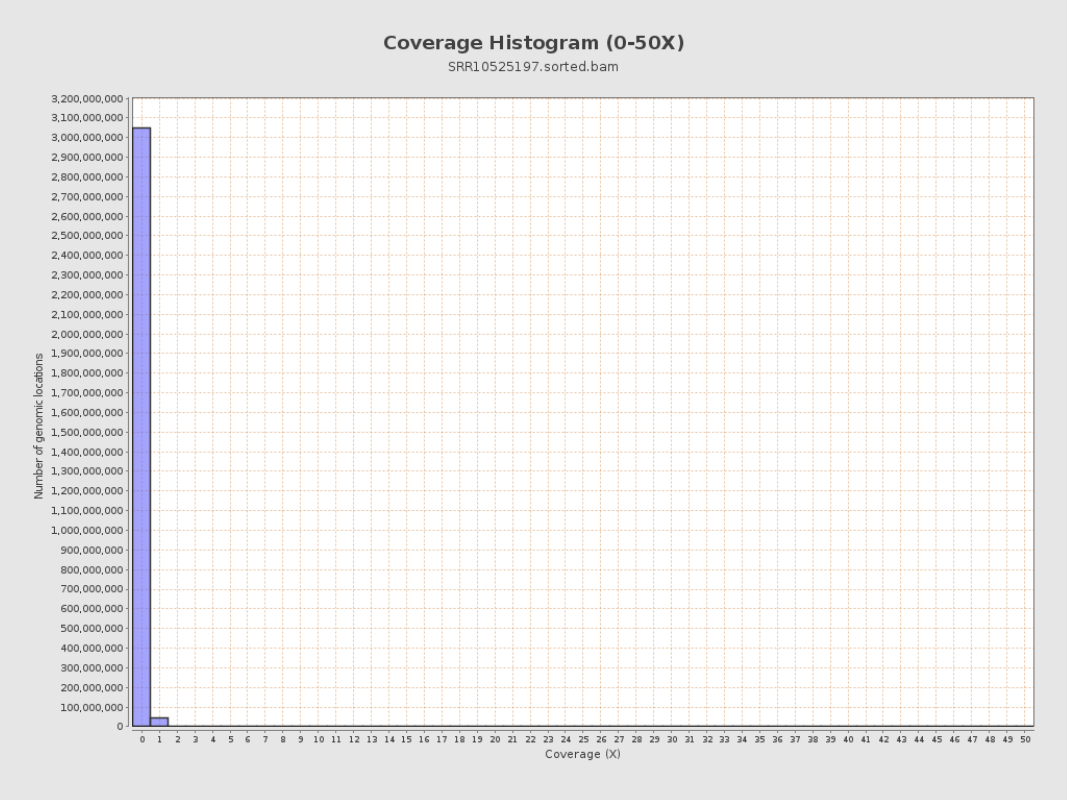
3. Results : Coverage across reference



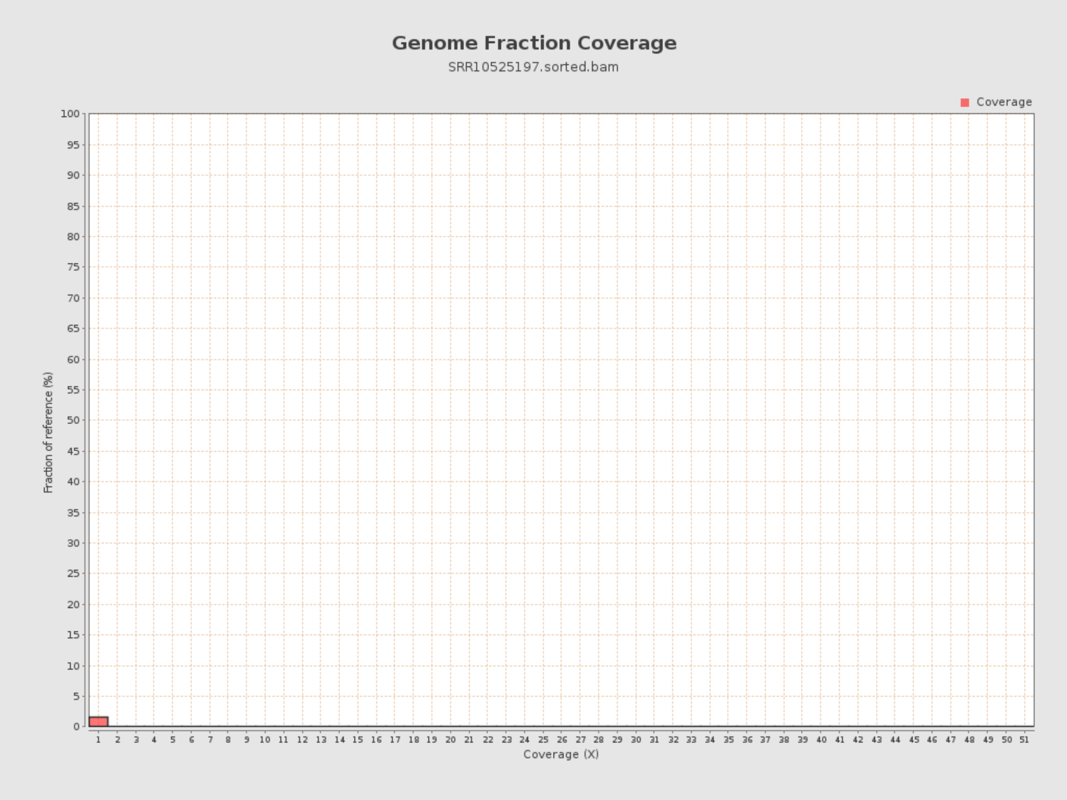
4. Results : Coverage Histogram



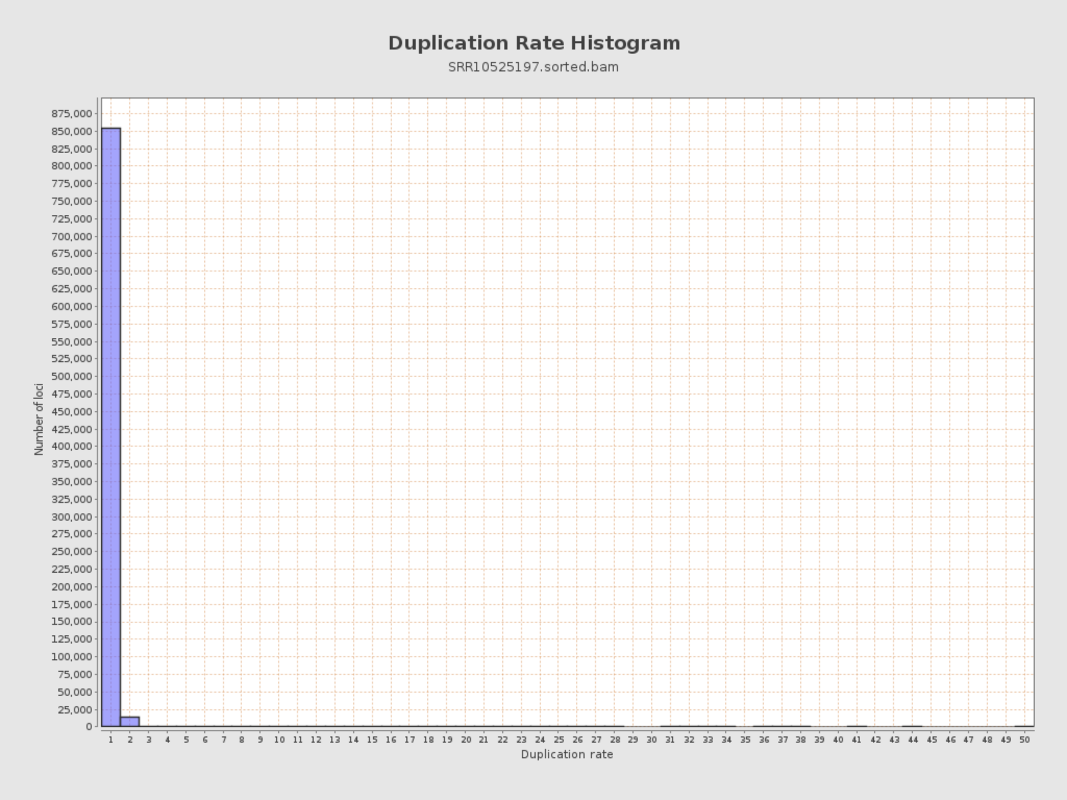
5. Results : Coverage Histogram (0-50X)



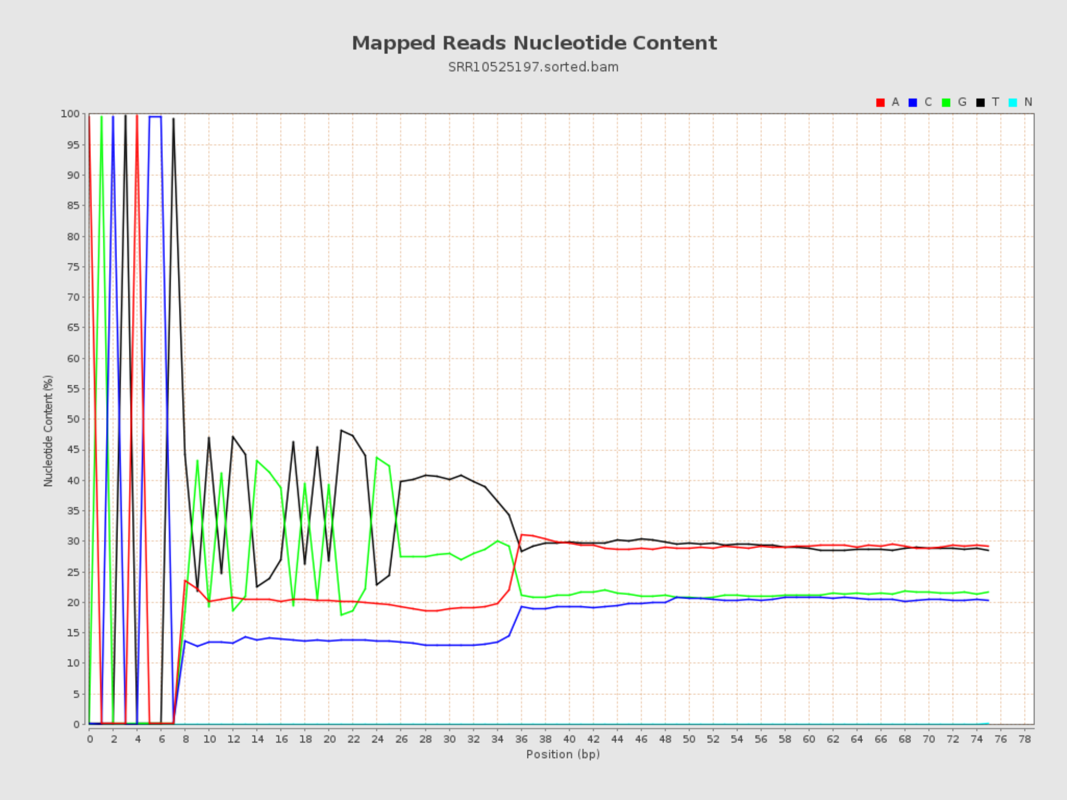
6. Results : Genome Fraction Coverage



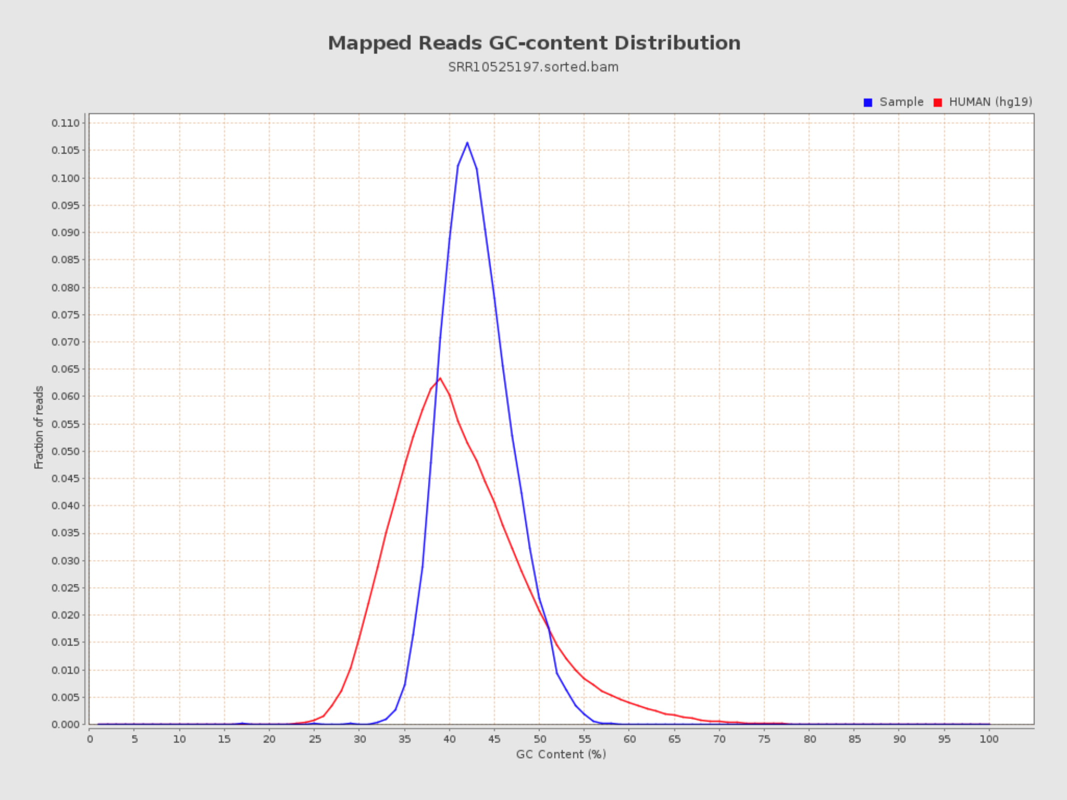
7. Results : Duplication Rate Histogram



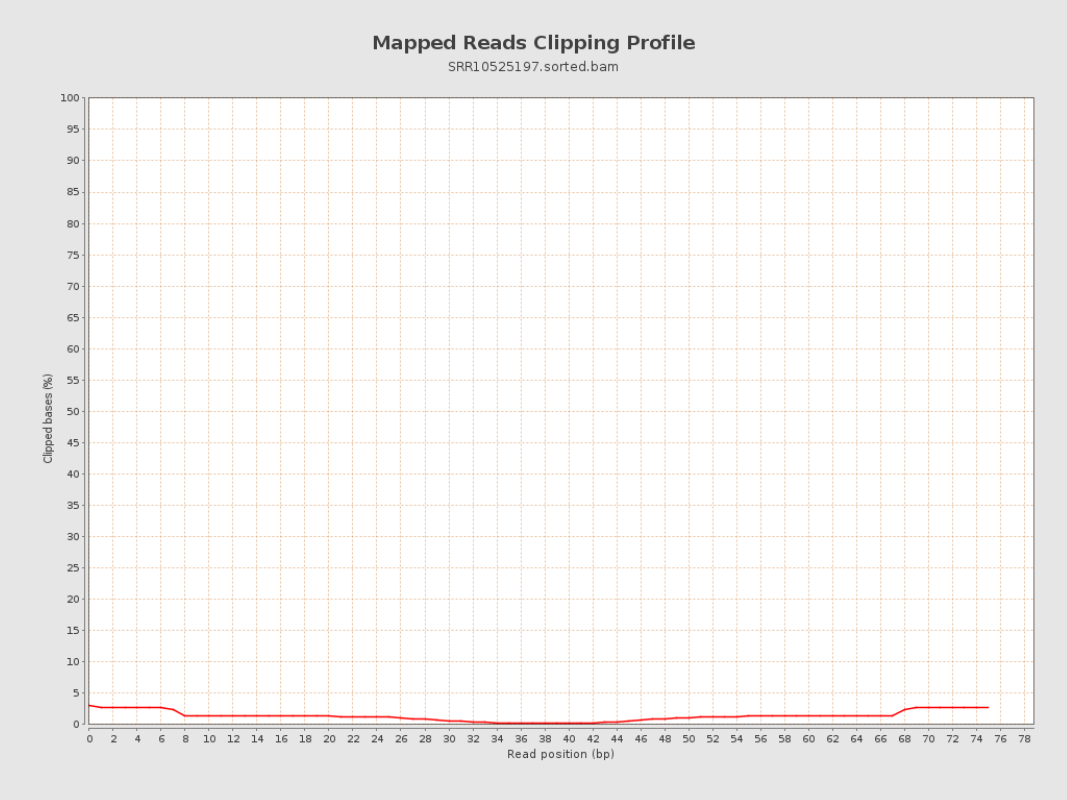
8. Results : Mapped Reads Nucleotide Content



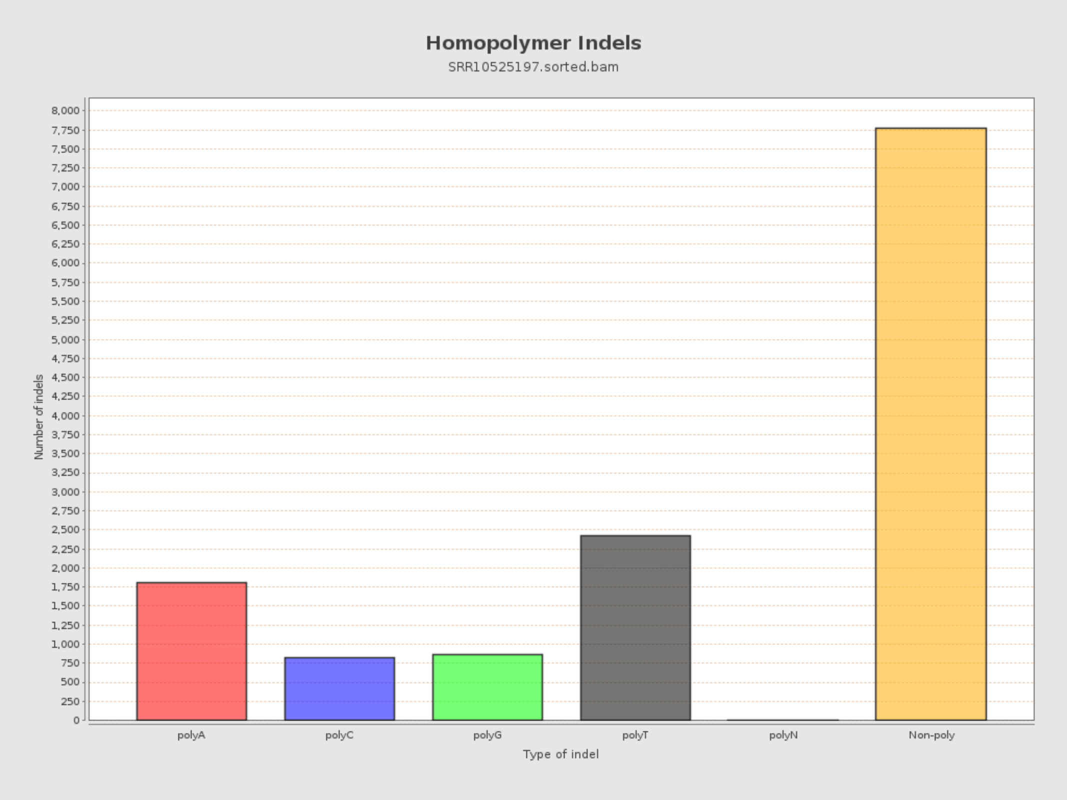
9. Results : Mapped Reads GC-content Distribution



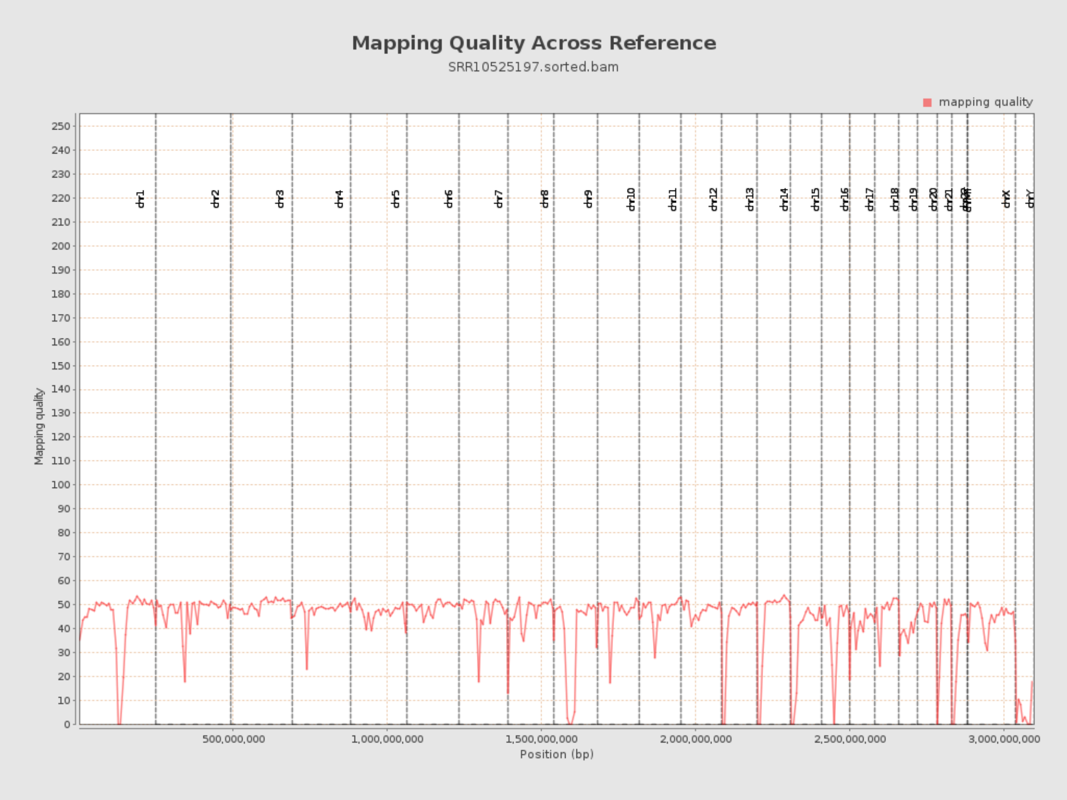
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram