Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:08:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525149.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_SRR10525149 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525149.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:08:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525149.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,422,228
Mapped reads	1,345,935 / 94.64%
Unmapped reads	76,293 / 5.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,976 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	34,155 / 2.4%
Duplication rate	1.81%
Clipped reads	1,349,379 / 94.88%

2.2. ACGT Content

Number/percentage of A's	22,893,803 / 27.26%
Number/percentage of C's	18,421,277 / 21.93%
Number/percentage of T's	23,820,349 / 28.36%
Number/percentage of G's	18,850,116 / 22.44%
Number/percentage of N's	2,187 / 0%
GC Percentage	44.38%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2582

2.4. Mapping Quality

Mean Mapping Quality	46.15

2.5. Mismatches and indels

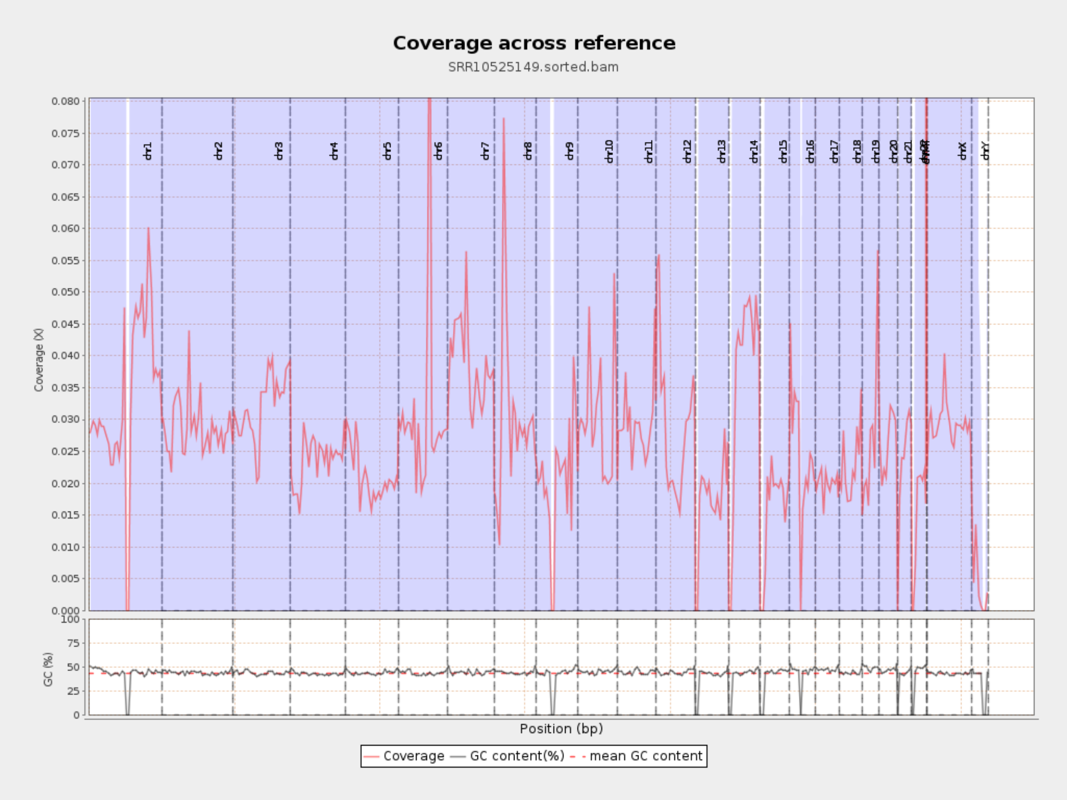
General error rate	0.47%
Mismatches	383,333
Insertions	5,450
Mapped reads with at least one insertion	0.4%
Deletions	15,932
Mapped reads with at least one deletion	1.17%
Homopolymer indels	44.17%

2.6. Chromosome stats

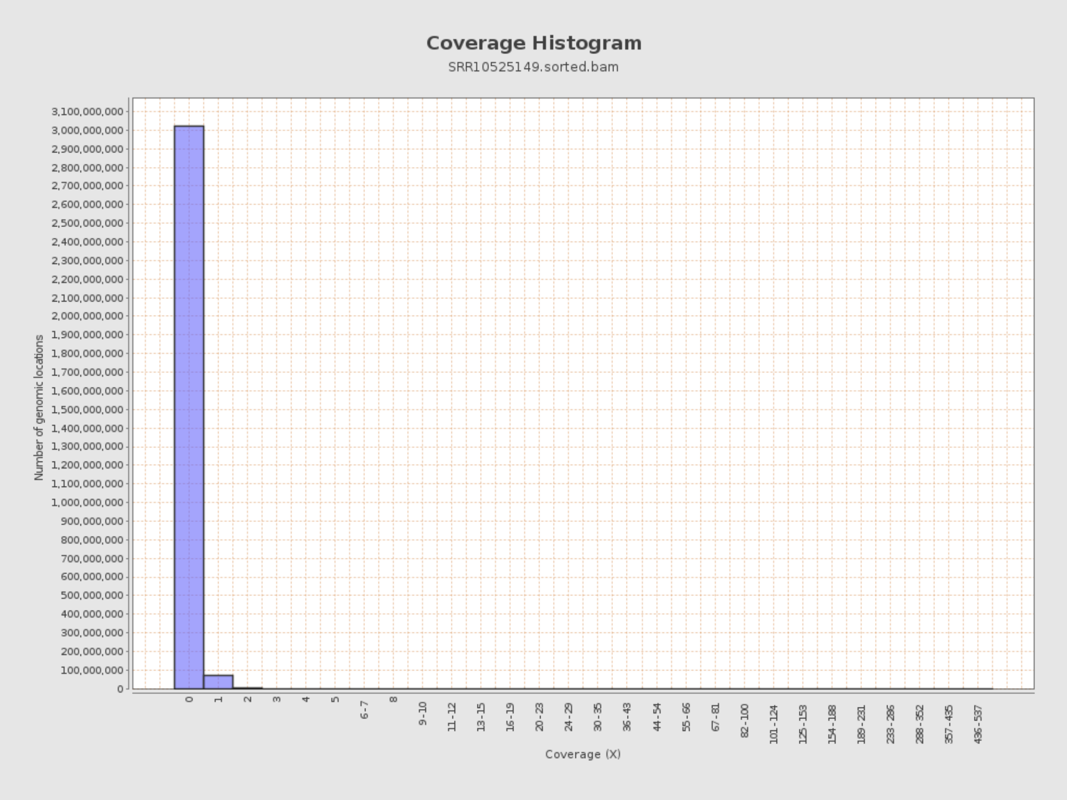
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8329743	0.0334	0.4767
chr2	243199373	6992380	0.0288	0.2789
chr3	198022430	6327482	0.032	0.1909
chr4	191154276	4502868	0.0236	0.1733
chr5	180915260	3811289	0.0211	0.1553
chr6	171115067	5421571	0.0317	0.2078
chr7	159138663	6211345	0.039	0.4103

chr8	146364022	4380261	0.0299	0.2264
chr9	141213431	2867307	0.0203	0.2013
chr10	135534747	4090761	0.0302	0.2494
chr11	135006516	3958677	0.0293	0.2144
chr12	133851895	3851554	0.0288	0.1841
chr13	115169878	1977173	0.0172	0.1404
chr14	107349540	3963830	0.0369	0.2155
chr15	102531392	1603929	0.0156	0.1348
chr16	90354753	2179248	0.0241	0.1824
chr17	81195210	1611290	0.0198	0.1591
chr18	78077248	1775163	0.0227	0.3679
chr19	59128983	1607774	0.0272	0.3379
chr20	63025520	1642020	0.0261	0.1747
chr21	48129895	1125716	0.0234	0.1752
chr22	51304566	745261	0.0145	0.1283
chrMT	16571	232638	14.0389	7.498
chrX	155270560	4569207	0.0294	0.195
chrY	59373566	235221	0.004	0.1239

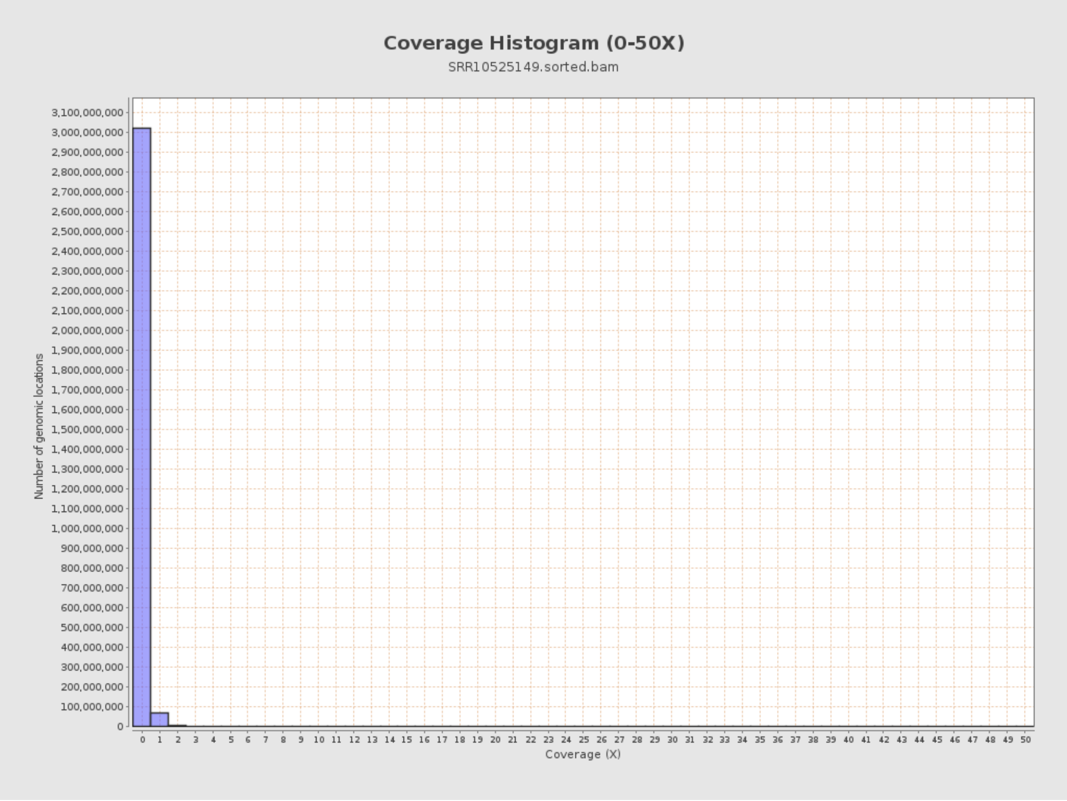
3. Results : Coverage across reference



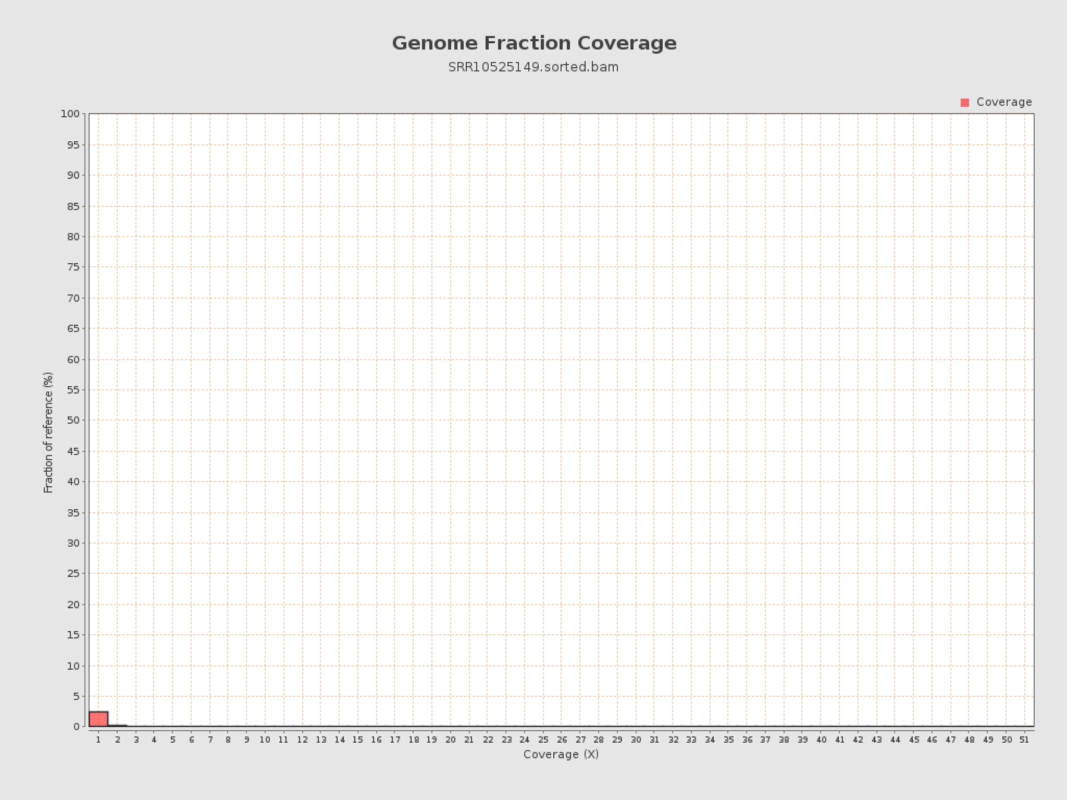
4. Results : Coverage Histogram



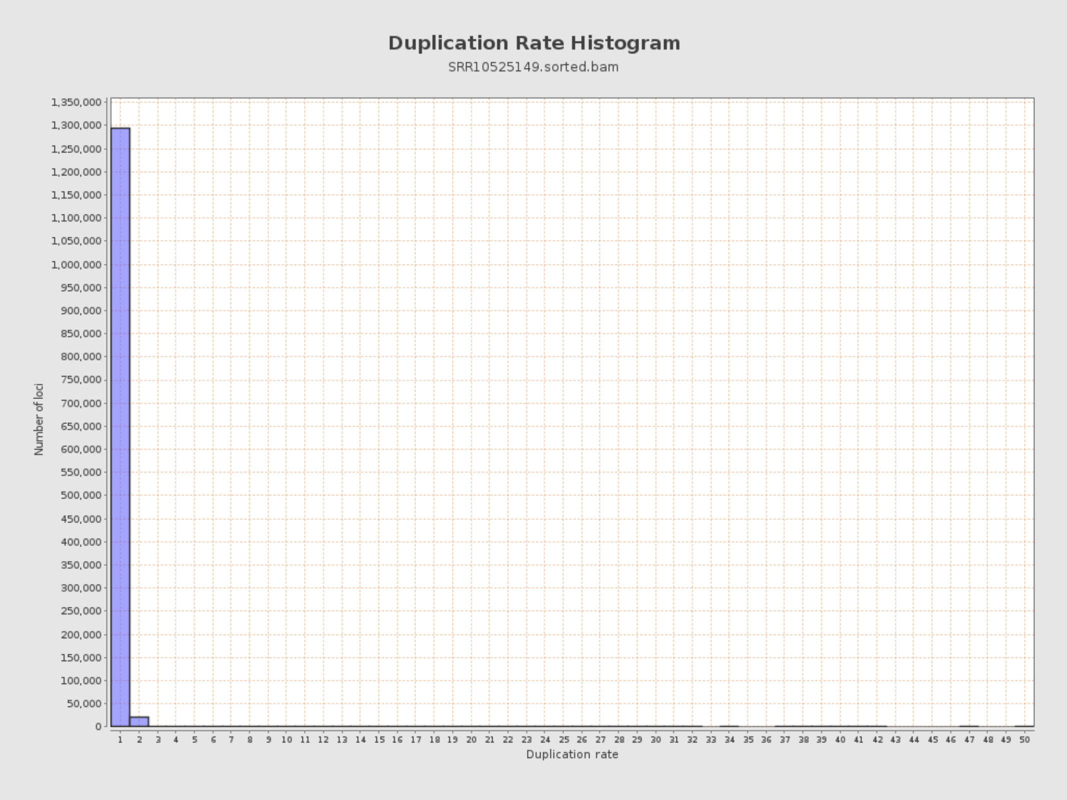
5. Results : Coverage Histogram (0-50X)



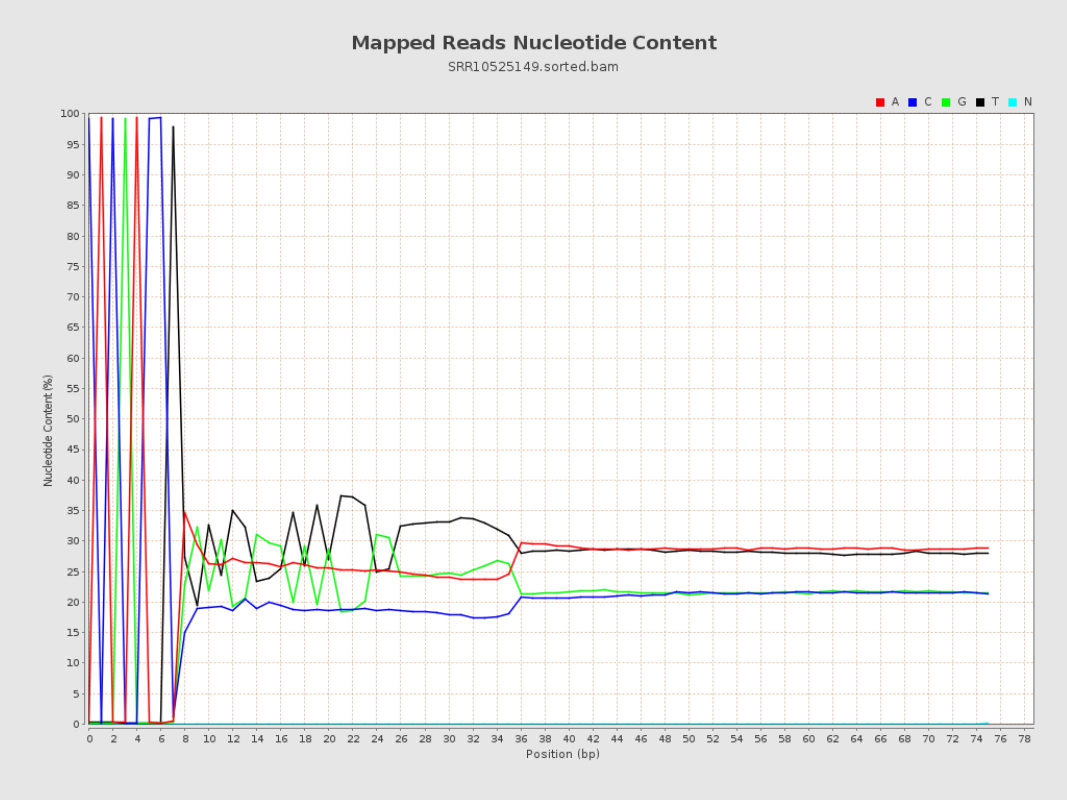
6. Results : Genome Fraction Coverage



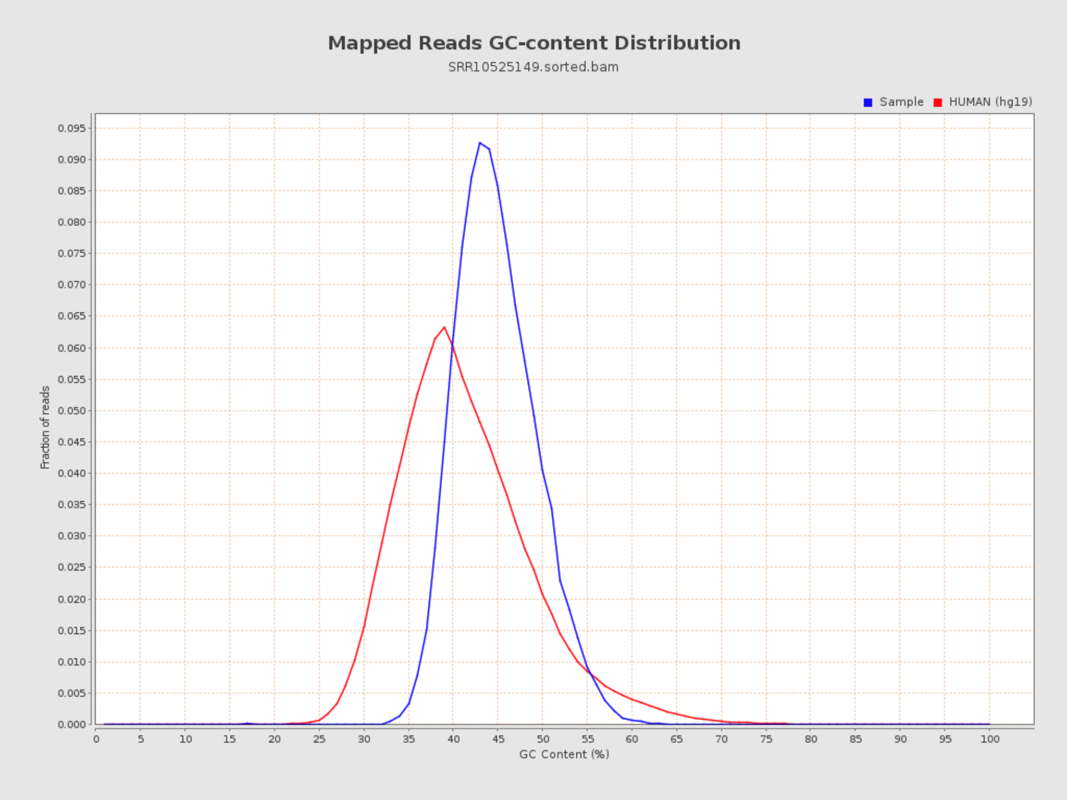
7. Results : Duplication Rate Histogram



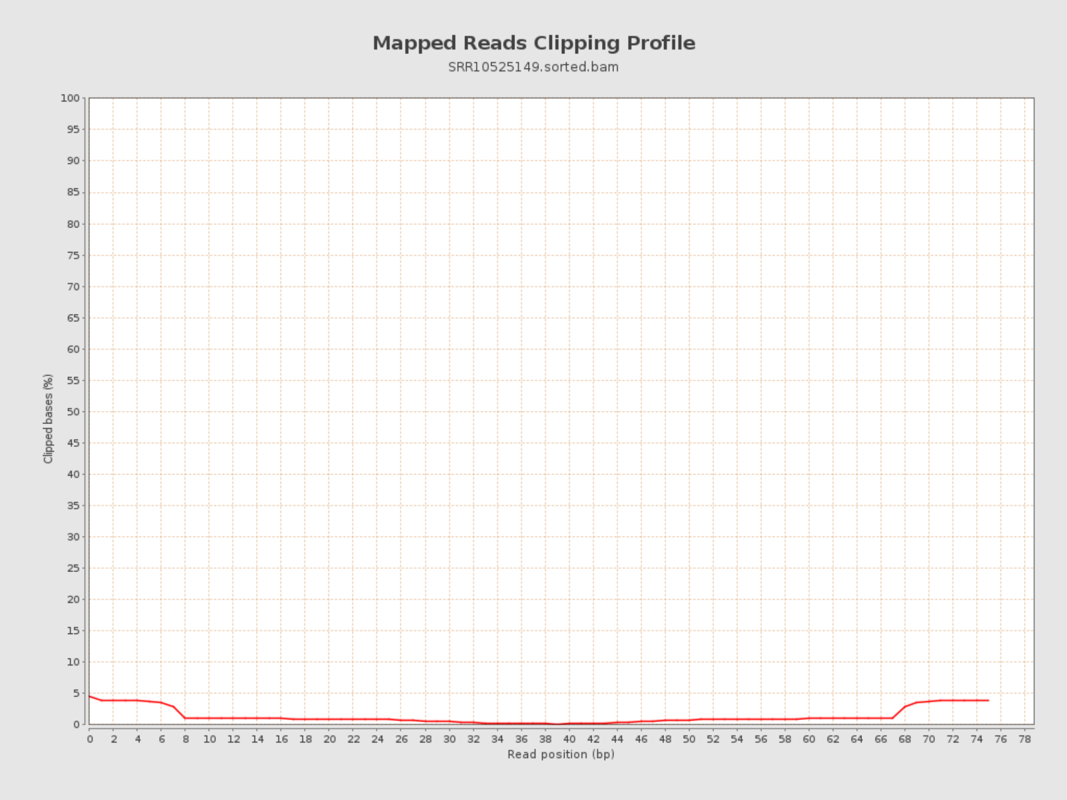
8. Results : Mapped Reads Nucleotide Content



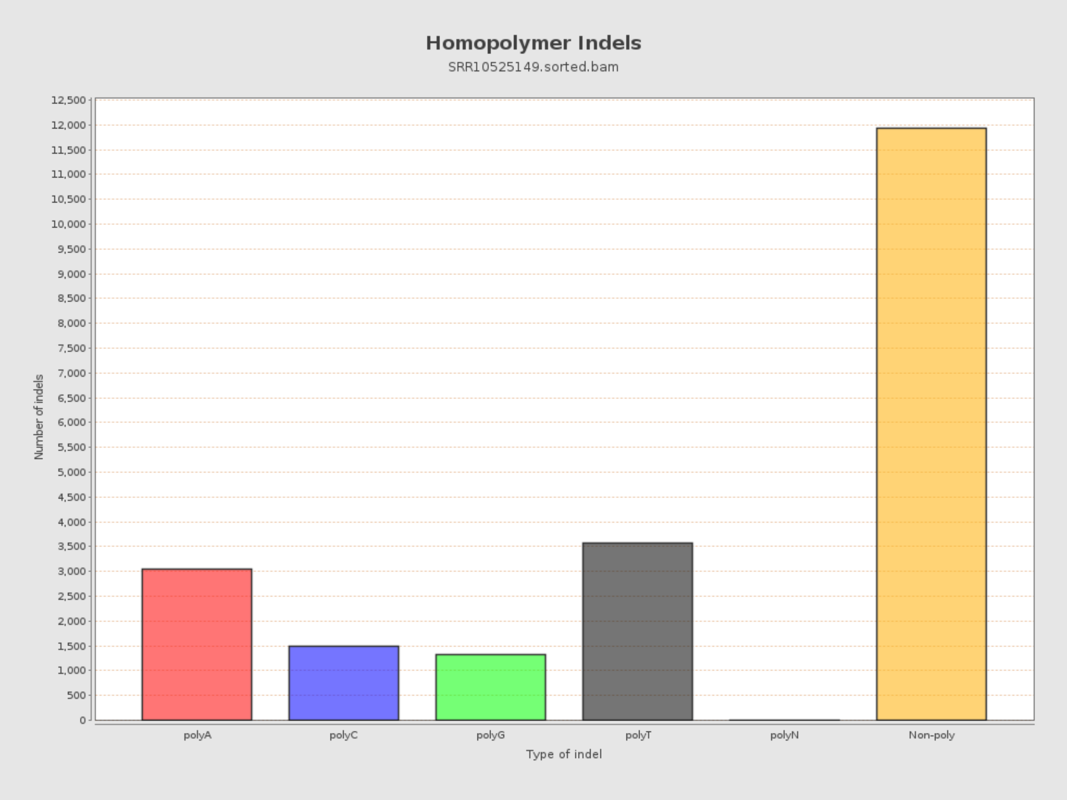
9. Results : Mapped Reads GC-content Distribution



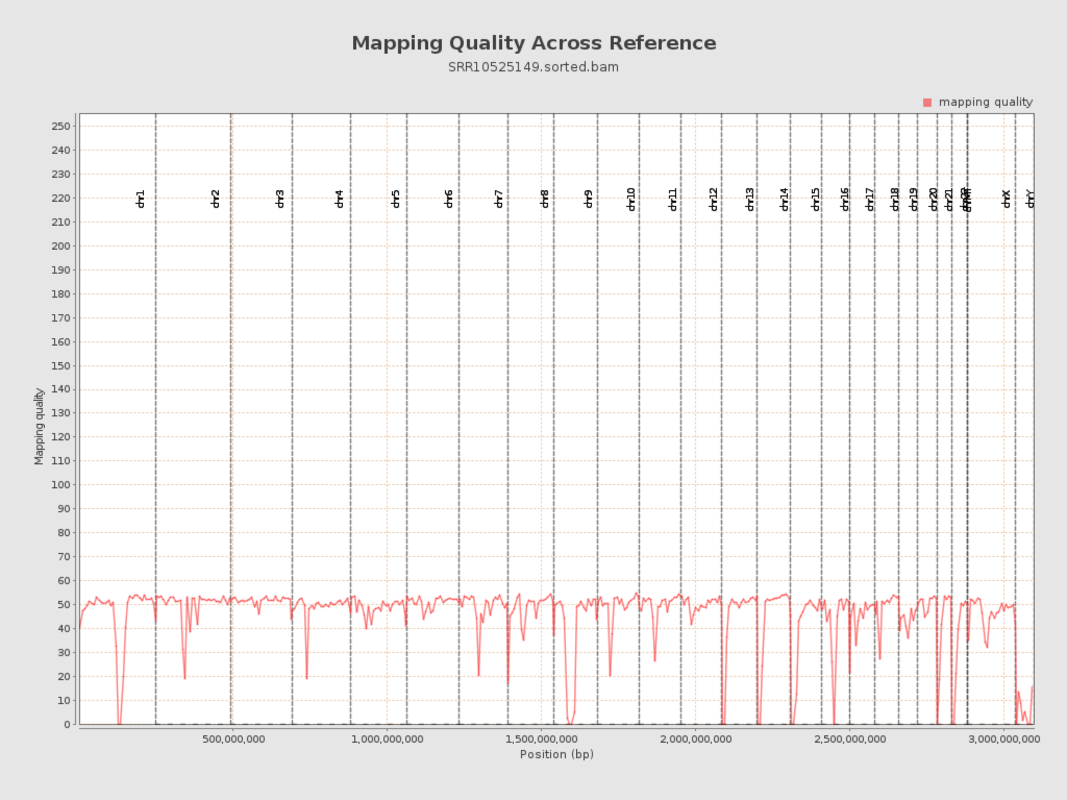
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram