Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:17:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525189.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_SRR10525189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:17:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,098,522
Mapped reads	1,909,425 / 90.99%
Unmapped reads	189,097 / 9.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,039 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	82,210 / 3.92%
Duplication rate	3.09%
Clipped reads	1,909,710 / 91%

2.2. ACGT Content

Number/percentage of A's	26,313,008 / 24.2%
Number/percentage of C's	18,490,530 / 17.01%
Number/percentage of T's	36,803,067 / 33.85%
Number/percentage of G's	27,123,898 / 24.95%
Number/percentage of N's	2,541 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.3455

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

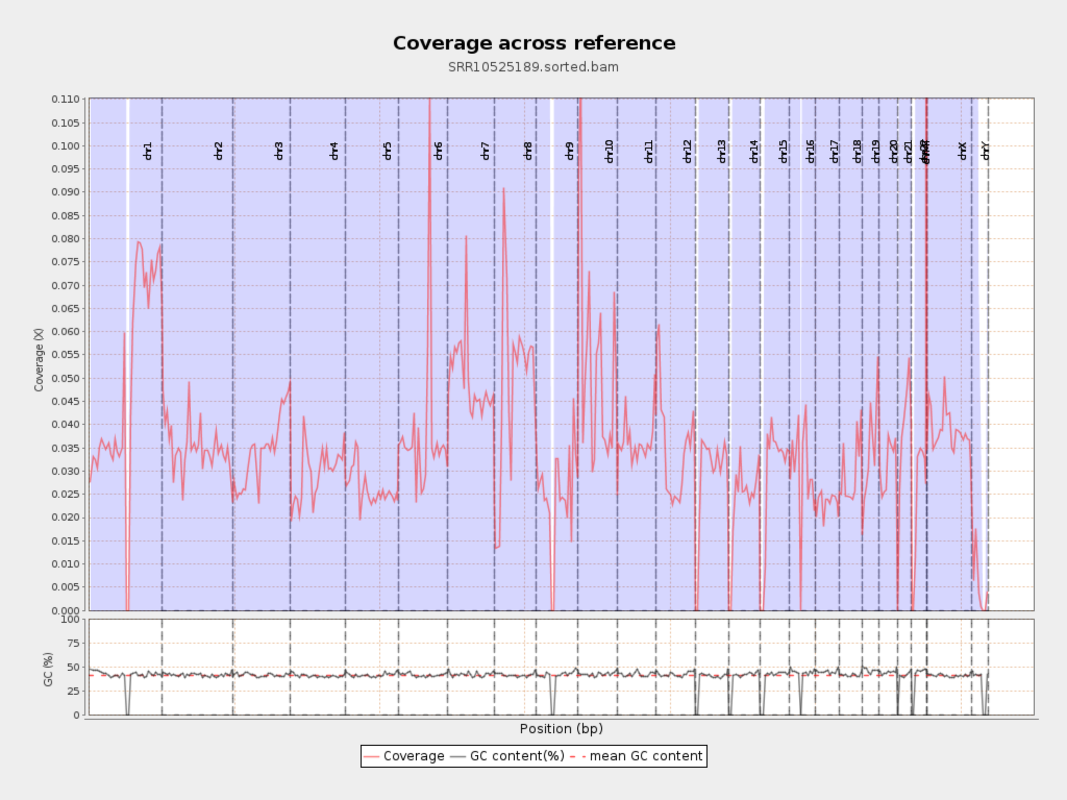
General error rate	0.54%
Mismatches	573,929
Insertions	7,572
Mapped reads with at least one insertion	0.39%
Deletions	21,396
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.99%

2.6. Chromosome stats

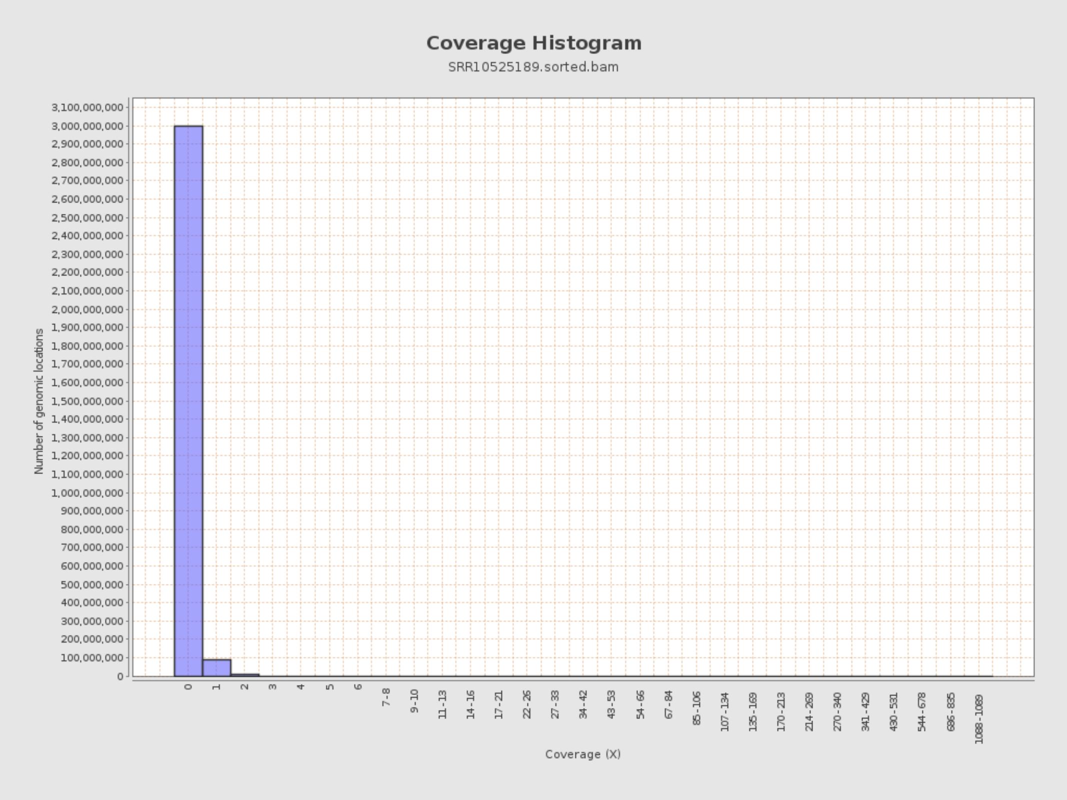
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12216798	0.049	0.6081
chr2	243199373	8566975	0.0352	0.4818
chr3	198022430	6744350	0.0341	0.2082
chr4	191154276	5651418	0.0296	0.2027
chr5	180915260	4751193	0.0263	0.1813
chr6	171115067	6557626	0.0383	0.2489
chr7	159138663	7974016	0.0501	0.6315

chr8	146364022	7047817	0.0482	0.3272
chr9	141213431	3456569	0.0245	0.2379
chr10	135534747	7242577	0.0534	0.3852
chr11	135006516	4926809	0.0365	0.2831
chr12	133851895	4636250	0.0346	0.2087
chr13	115169878	3325413	0.0289	0.1902
chr14	107349540	2485693	0.0232	0.175
chr15	102531392	2935064	0.0286	0.1936
chr16	90354753	2670327	0.0296	0.2184
chr17	81195210	1870139	0.023	0.1758
chr18	78077248	2303071	0.0295	0.4776
chr19	59128983	2071088	0.035	0.432
chr20	63025520	1957843	0.0311	0.1997
chr21	48129895	1798782	0.0374	0.2255
chr22	51304566	1186246	0.0231	0.1672
chrMT	16571	9459	0.5708	0.8446
chrX	155270560	6043726	0.0389	0.2425
chrY	59373566	337775	0.0057	0.1421

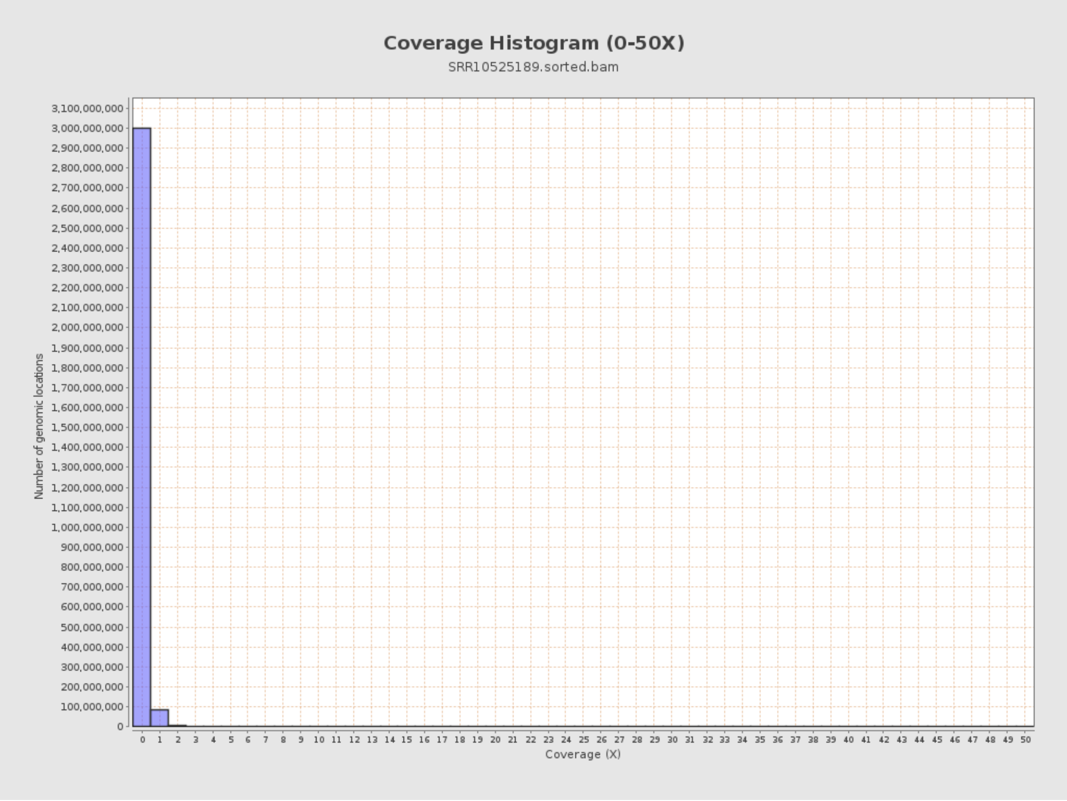
3. Results : Coverage across reference



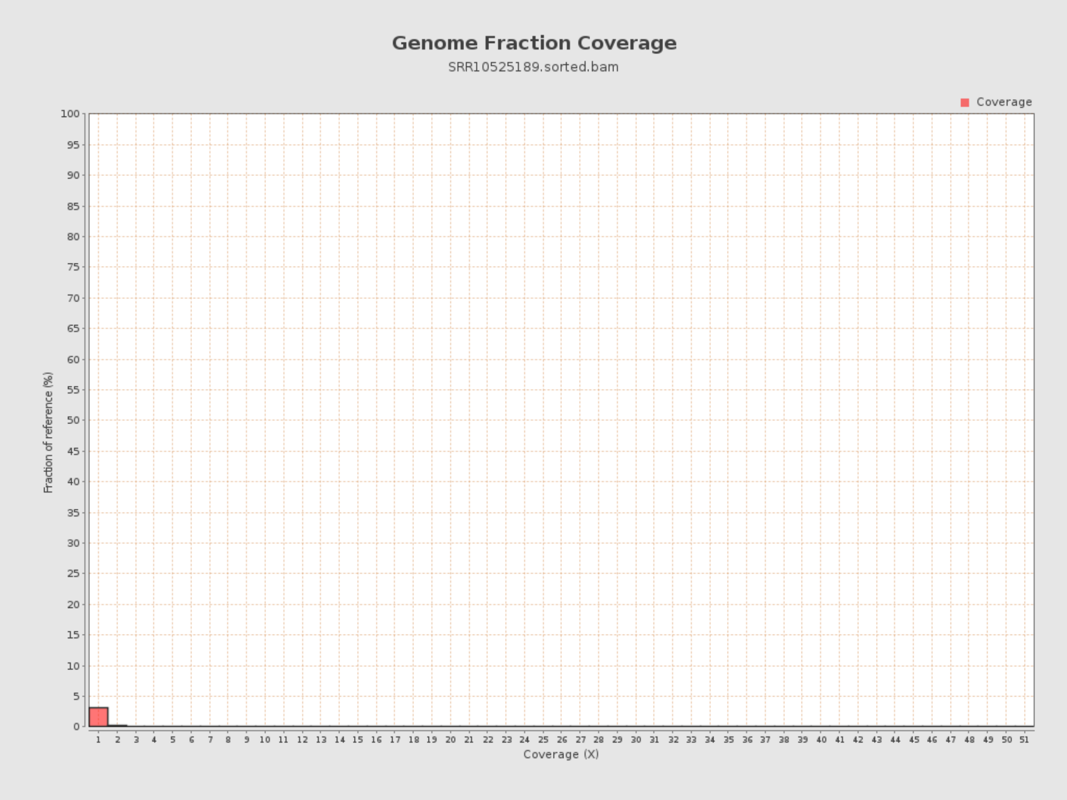
4. Results : Coverage Histogram



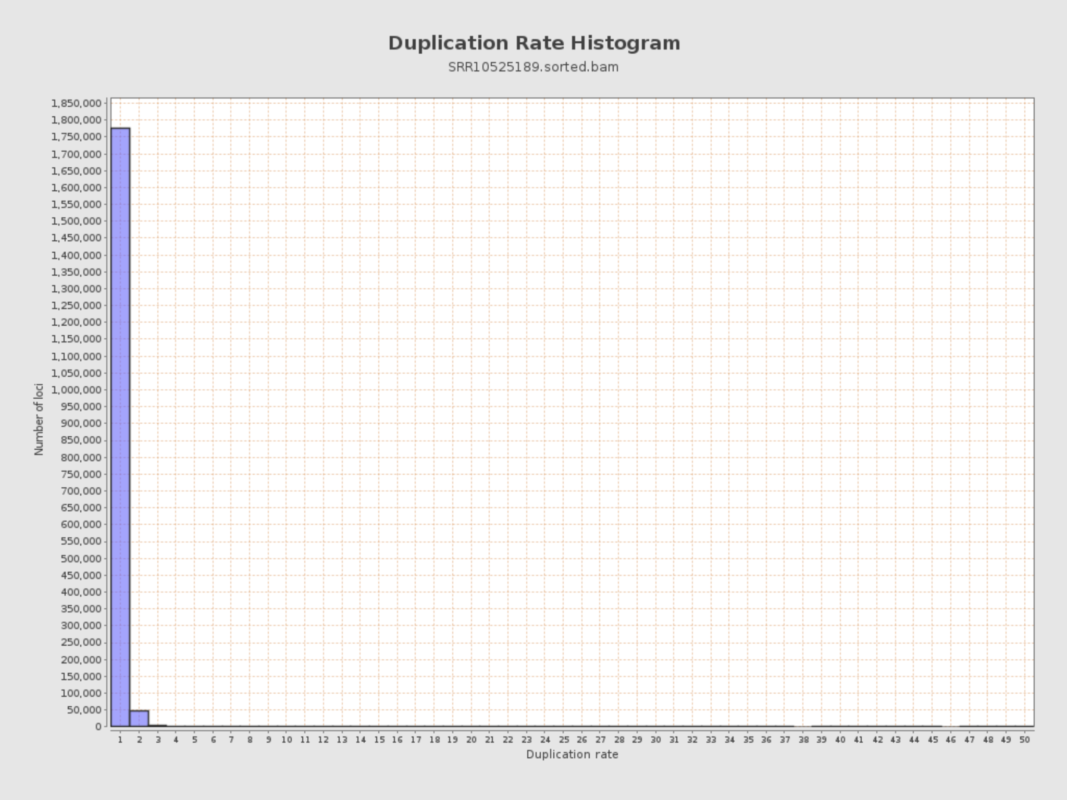
5. Results : Coverage Histogram (0-50X)



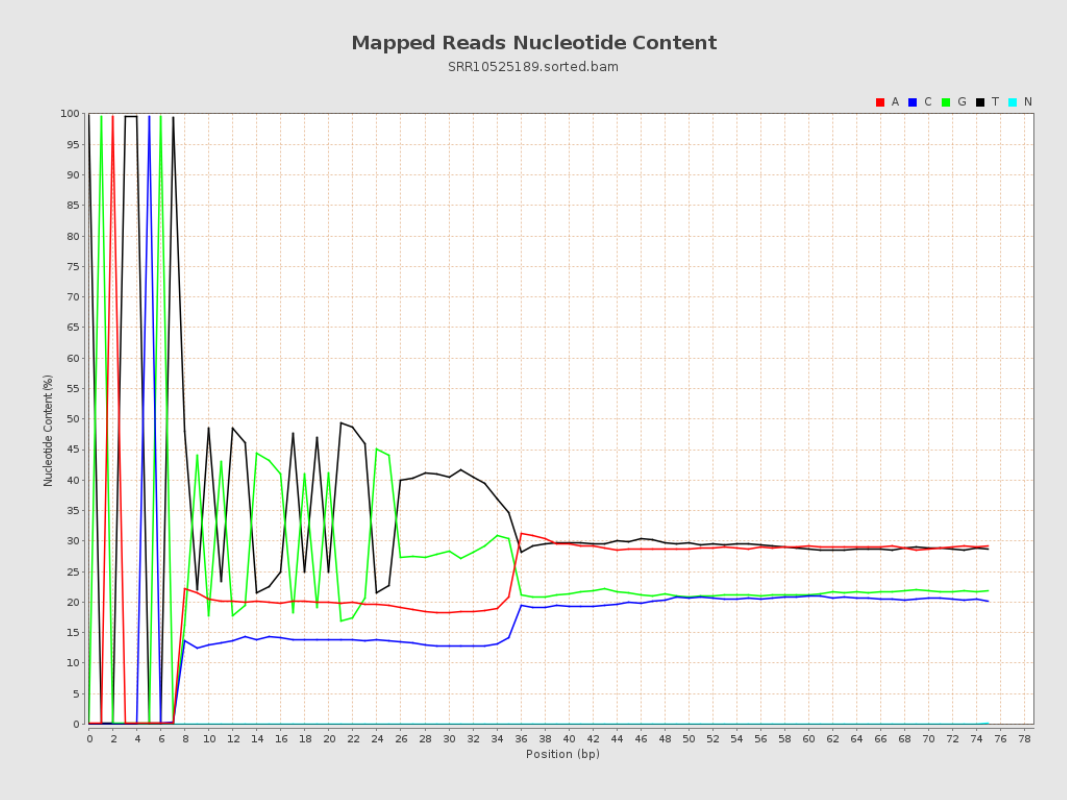
6. Results : Genome Fraction Coverage



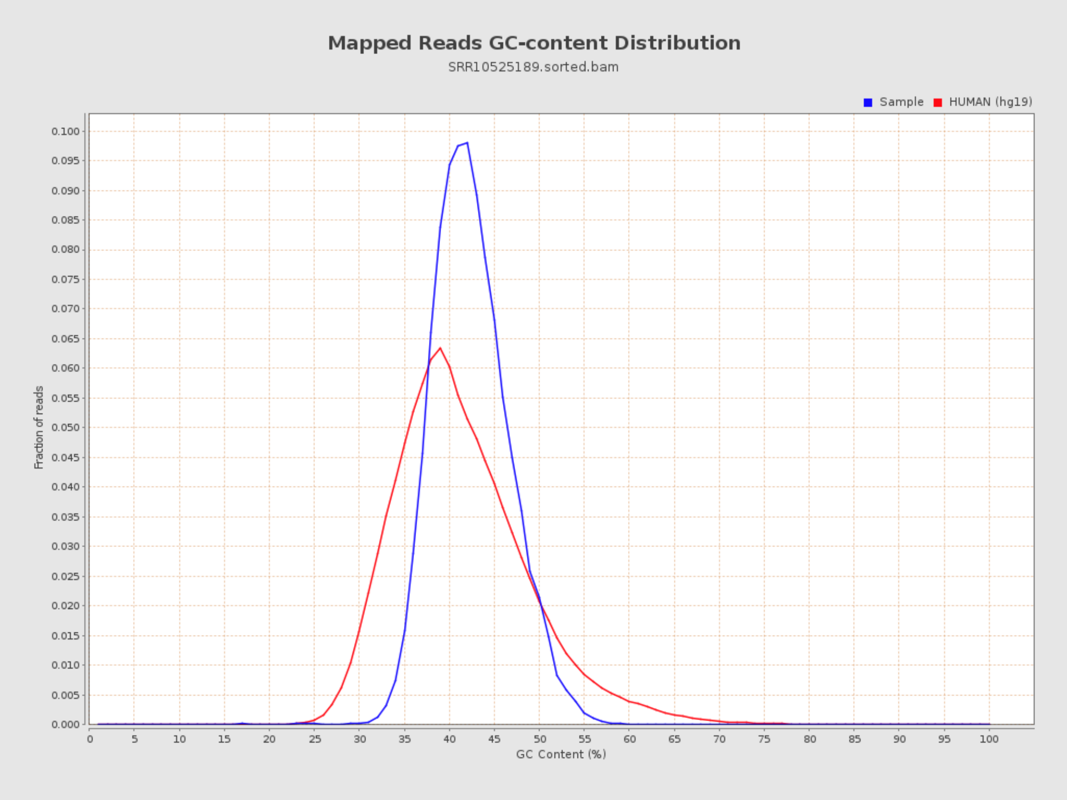
7. Results : Duplication Rate Histogram



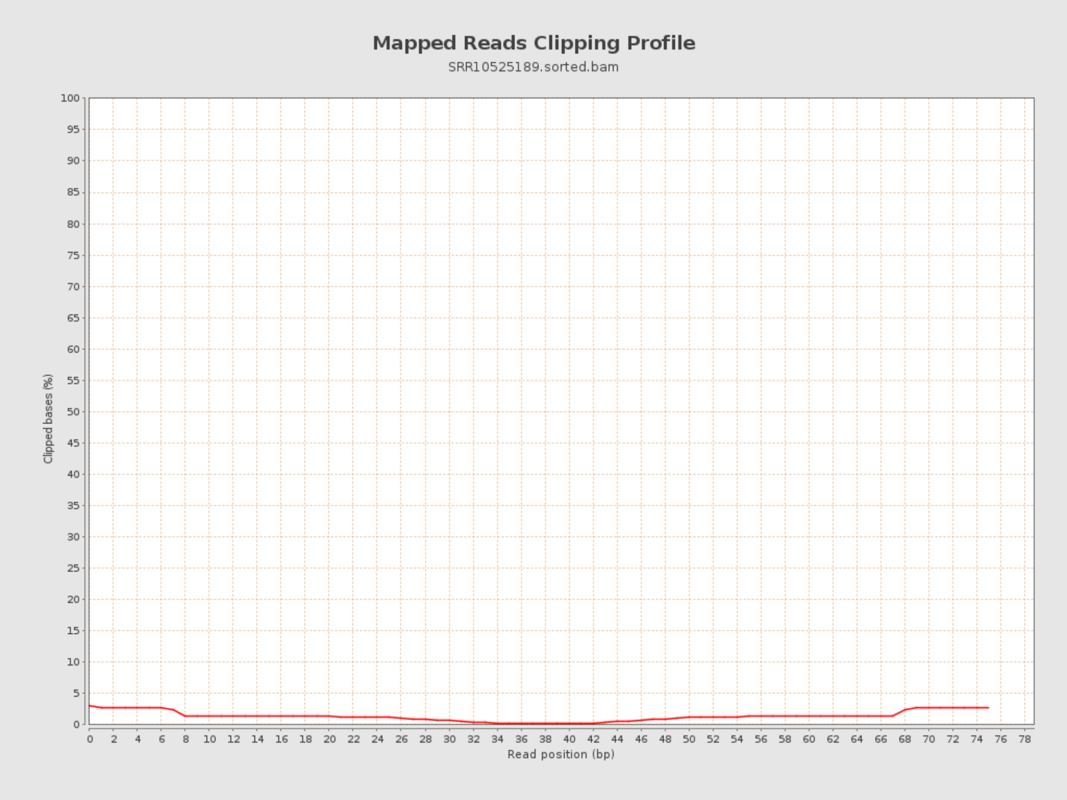
8. Results : Mapped Reads Nucleotide Content



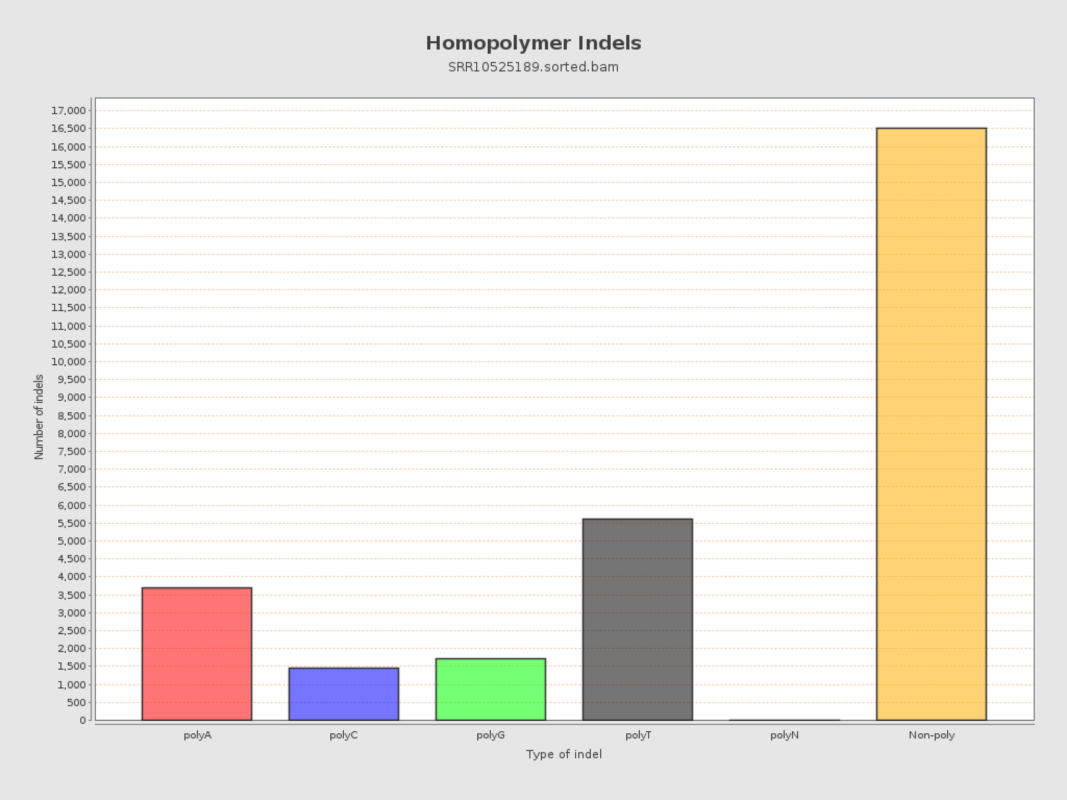
9. Results : Mapped Reads GC-content Distribution



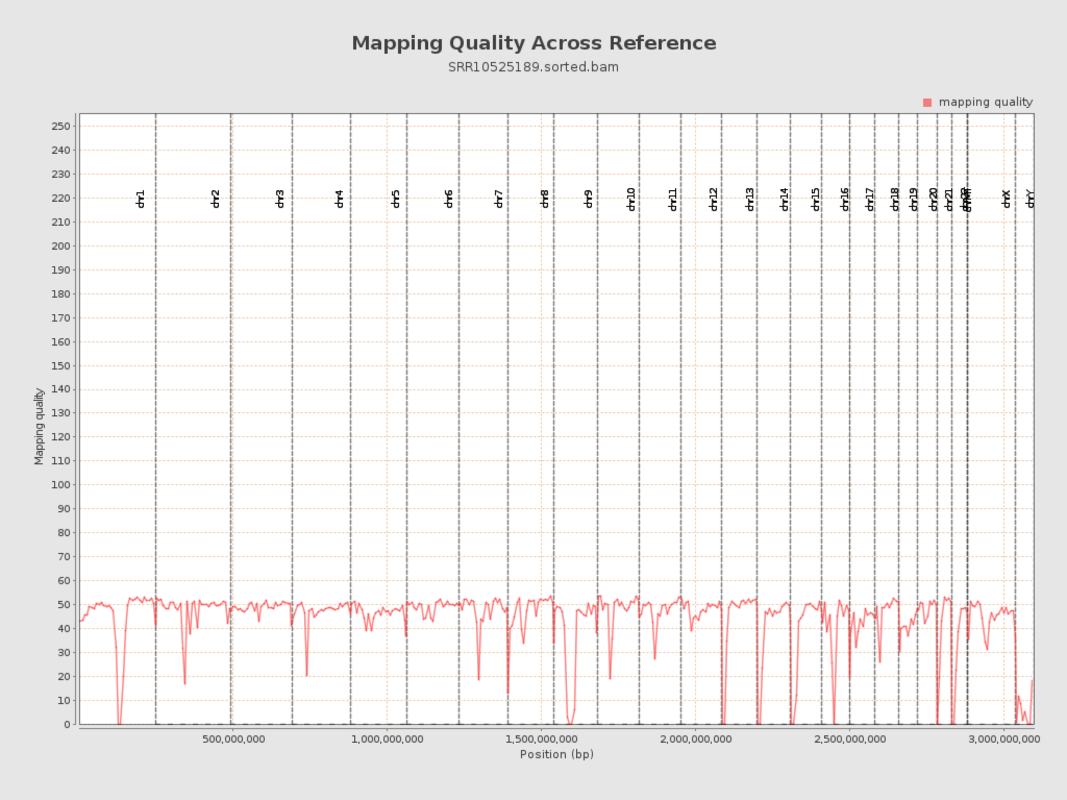
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram