Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:14:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525188.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_SRR10525188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:14:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,957,159
Mapped reads	2,717,324 / 91.89%
Unmapped reads	239,835 / 8.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,606 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	139,958 / 4.73%
Duplication rate	3.75%
Clipped reads	2,719,753 / 91.97%

2.2. ACGT Content

Number/percentage of A's	40,022,207 / 25.41%
Number/percentage of C's	30,283,036 / 19.23%
Number/percentage of T's	49,765,643 / 31.6%
Number/percentage of G's	37,429,839 / 23.76%
Number/percentage of N's	3,795 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.458

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

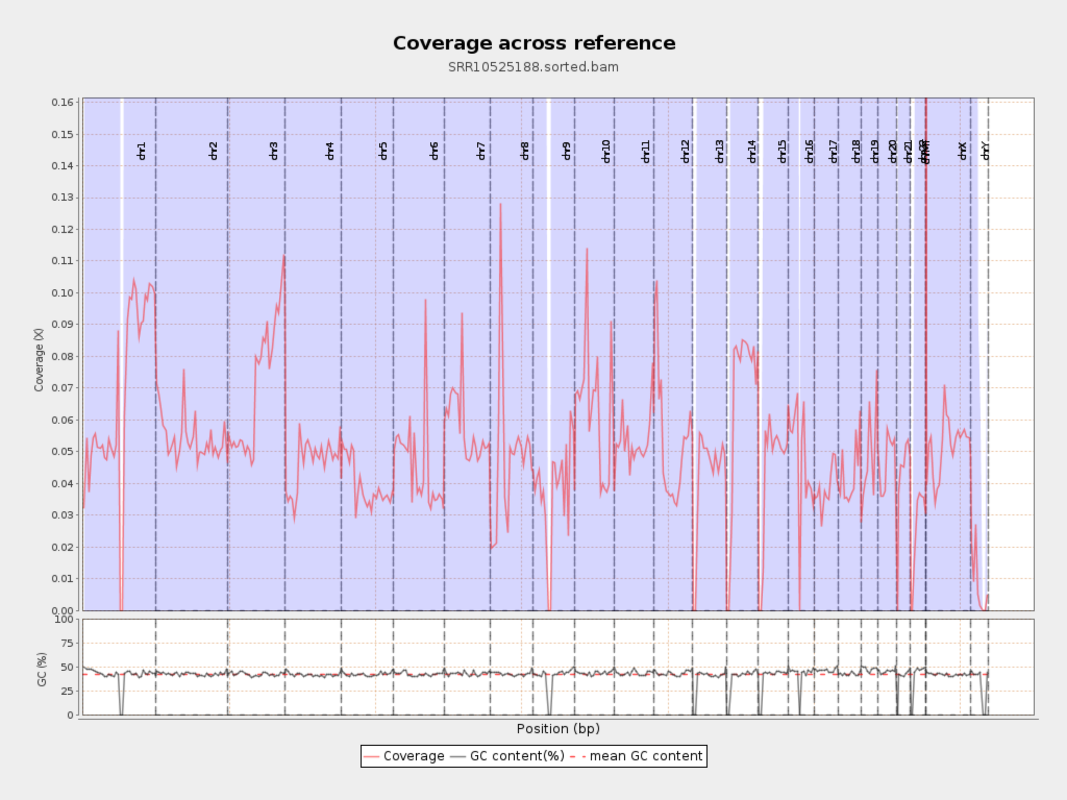
General error rate	0.53%
Mismatches	806,894
Insertions	11,255
Mapped reads with at least one insertion	0.41%
Deletions	32,602
Mapped reads with at least one deletion	1.19%
Homopolymer indels	43.54%

2.6. Chromosome stats

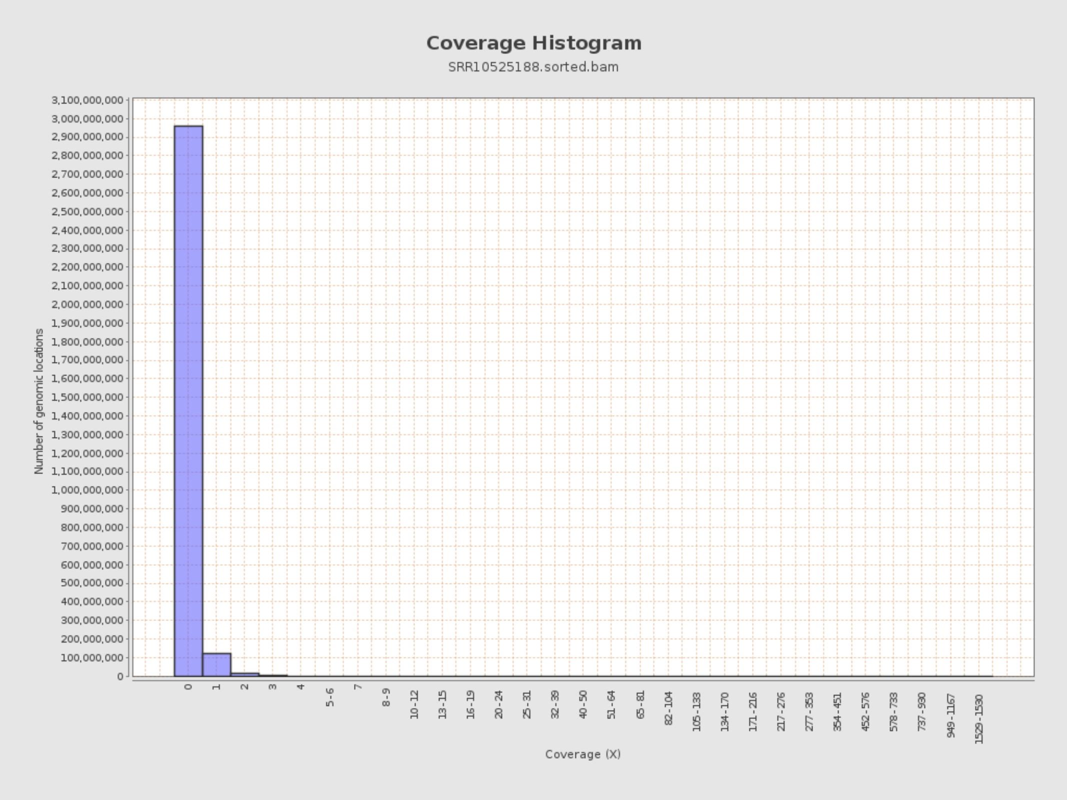
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16785615	0.0673	0.8757
chr2	243199373	13253834	0.0545	0.6721
chr3	198022430	13957969	0.0705	0.3072
chr4	191154276	8951224	0.0468	0.2707
chr5	180915260	7114422	0.0393	0.2278
chr6	171115067	7815641	0.0457	0.2969
chr7	159138663	9218165	0.0579	0.6809

chr8	146364022	7284182	0.0498	0.3758
chr9	141213431	5270983	0.0373	0.3164
chr10	135534747	8599194	0.0634	0.492
chr11	135006516	7201770	0.0533	0.3857
chr12	133851895	7155374	0.0535	0.2694
chr13	115169878	4907656	0.0426	0.2415
chr14	107349540	7214609	0.0672	0.3059
chr15	102531392	4390061	0.0428	0.2435
chr16	90354753	4269433	0.0473	0.2911
chr17	81195210	3156206	0.0389	0.2382
chr18	78077248	3313722	0.0424	0.6972
chr19	59128983	2894318	0.0489	0.5945
chr20	63025520	2917617	0.0463	0.2548
chr21	48129895	2048386	0.0426	0.2569
chr22	51304566	1291768	0.0252	0.1807
chrMT	16571	8101	0.4889	0.7698
chrX	155270560	8057021	0.0519	0.2988
chrY	59373566	479166	0.0081	0.2209

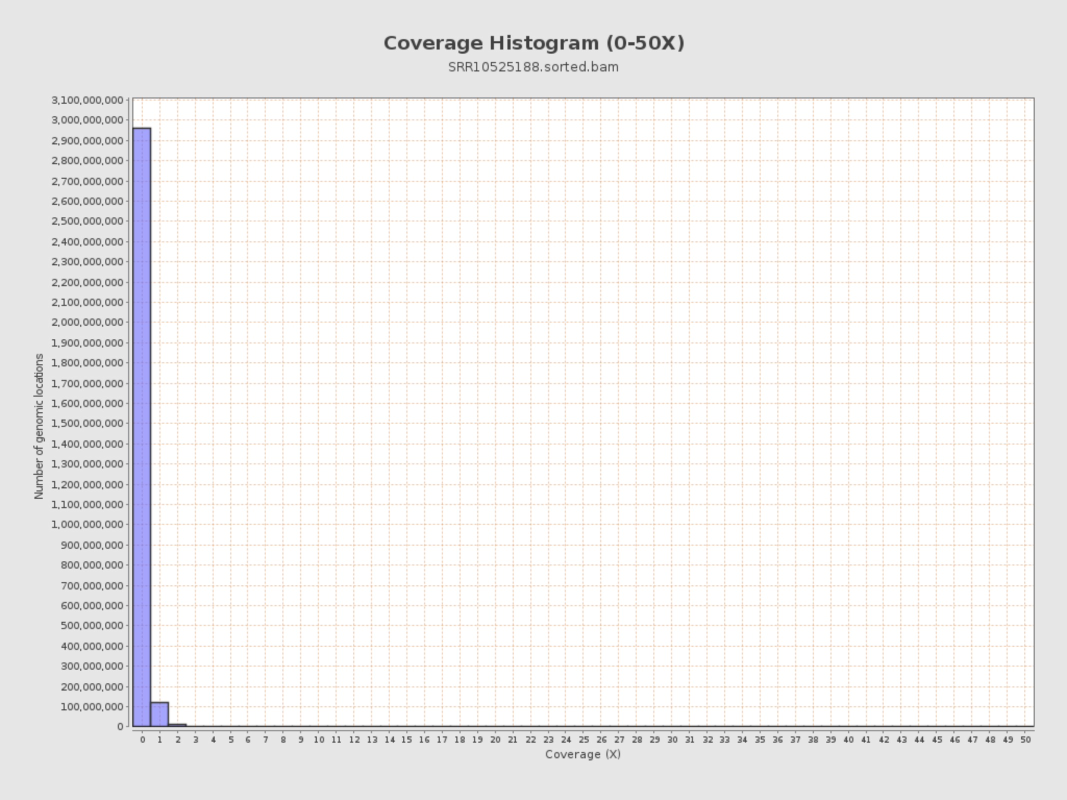
3. Results : Coverage across reference



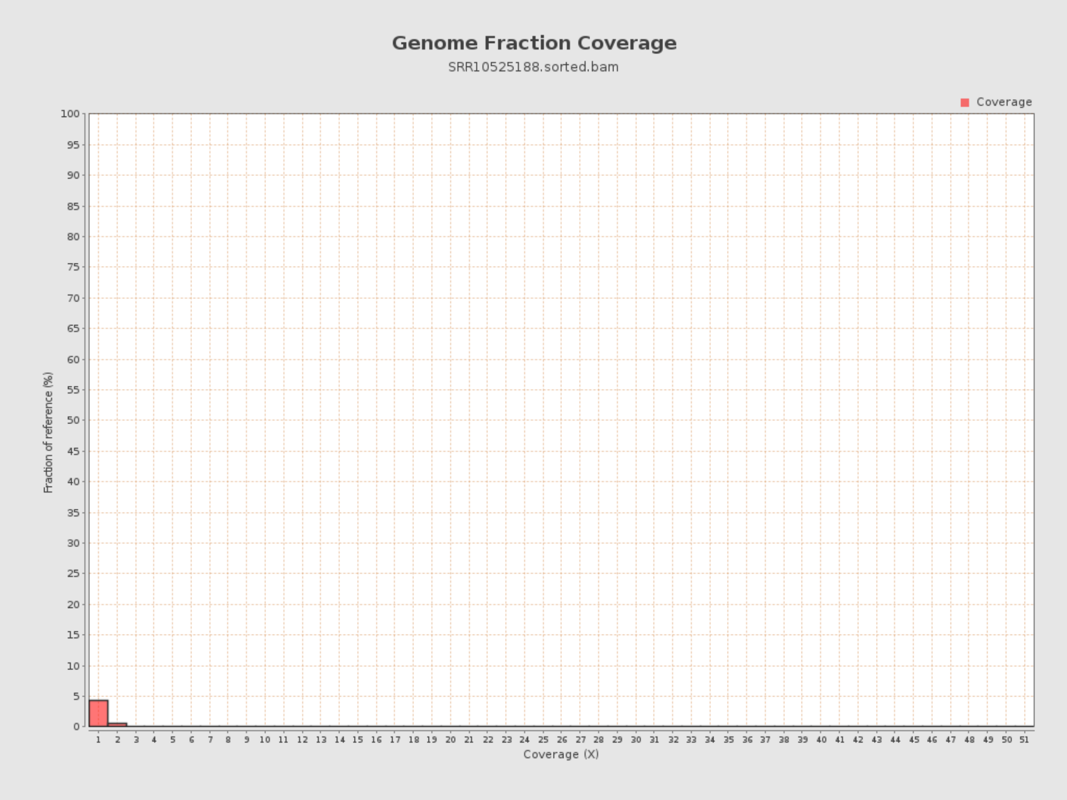
4. Results : Coverage Histogram



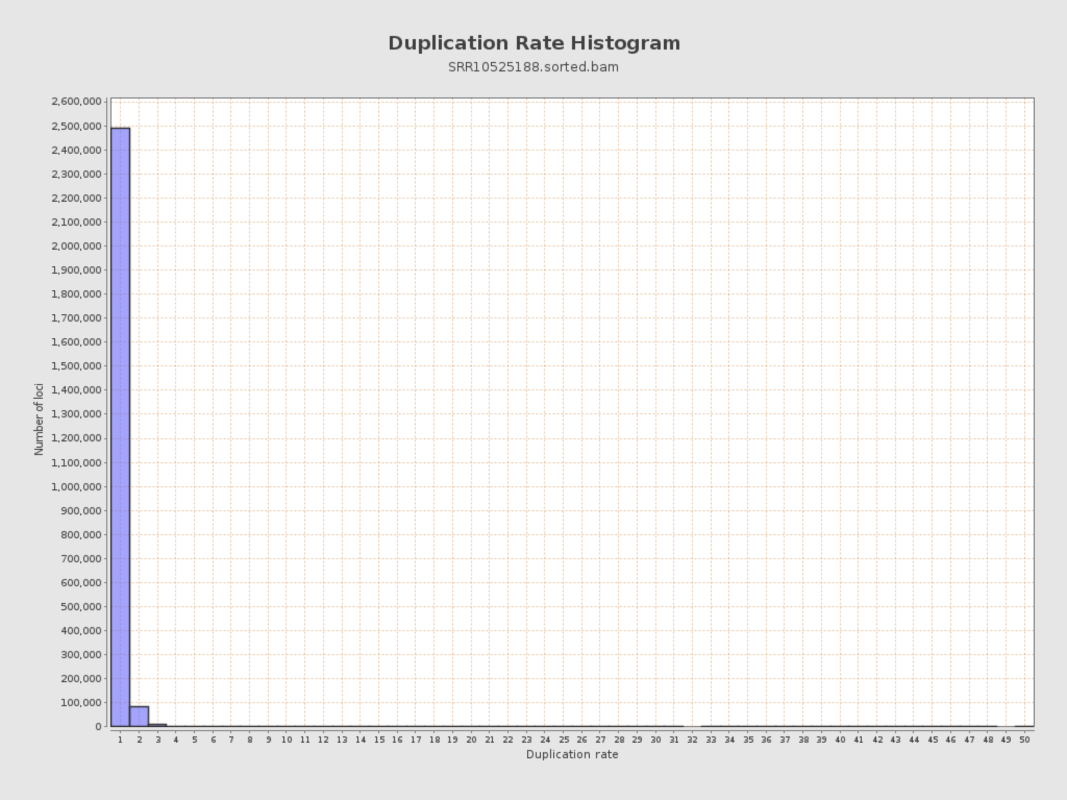
5. Results : Coverage Histogram (0-50X)



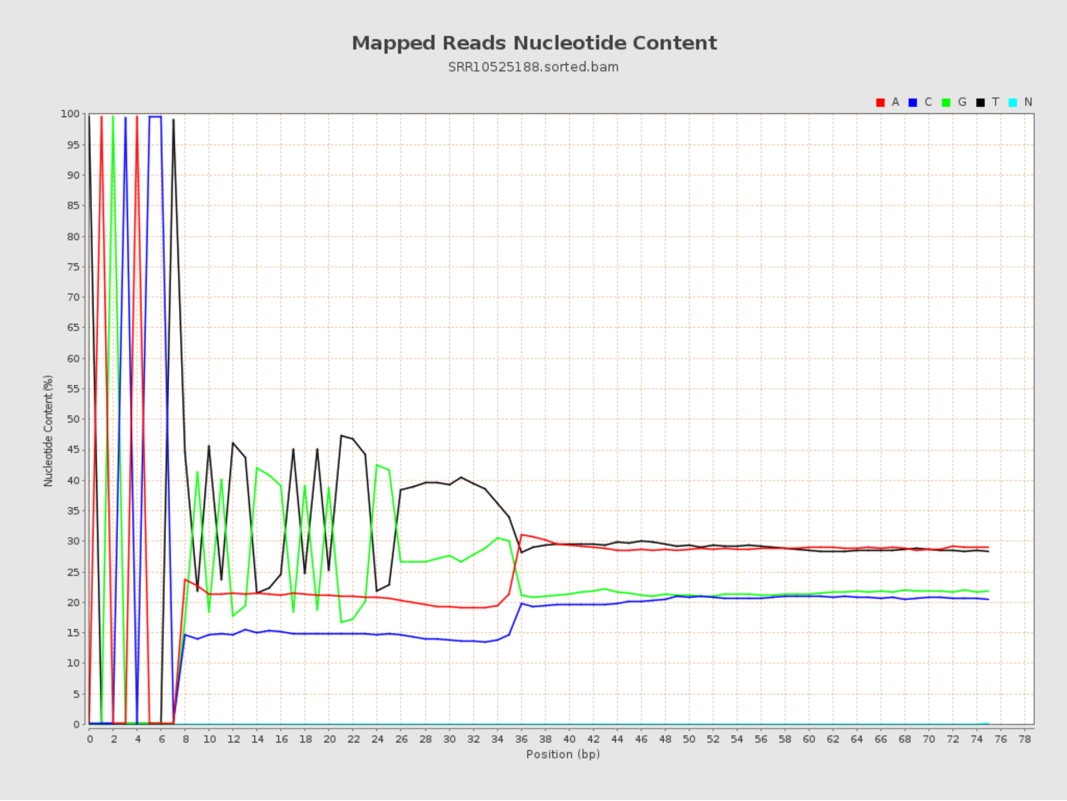
6. Results : Genome Fraction Coverage



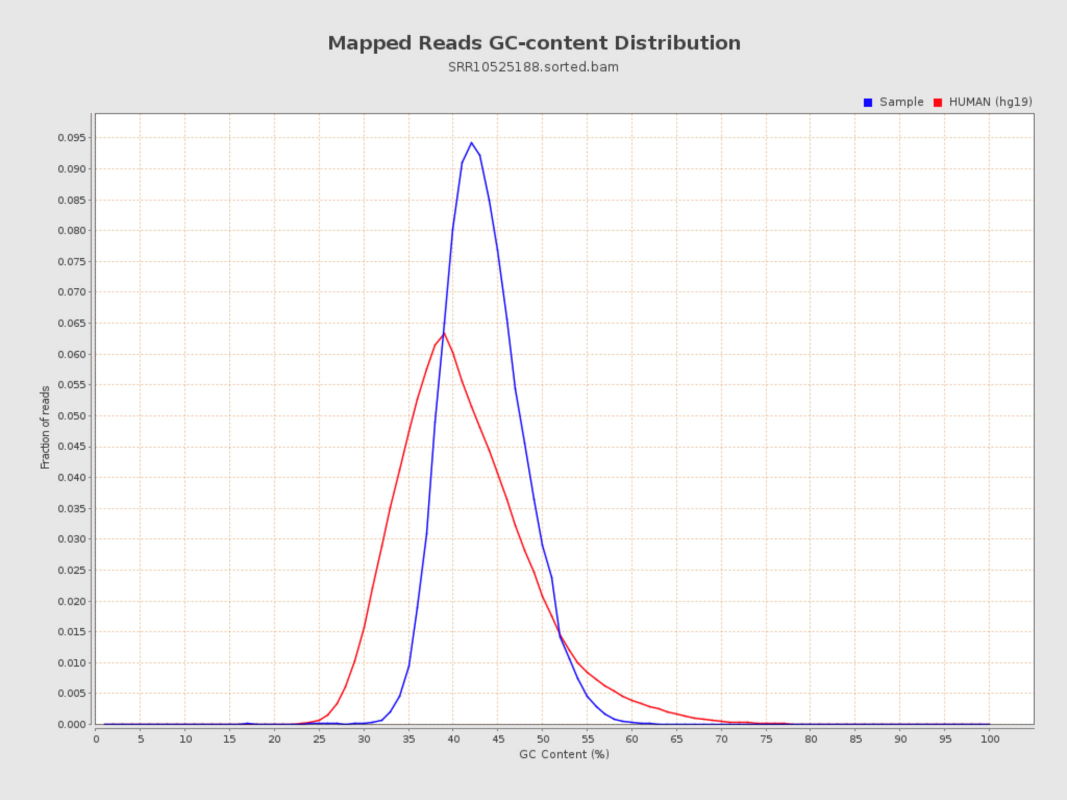
7. Results : Duplication Rate Histogram



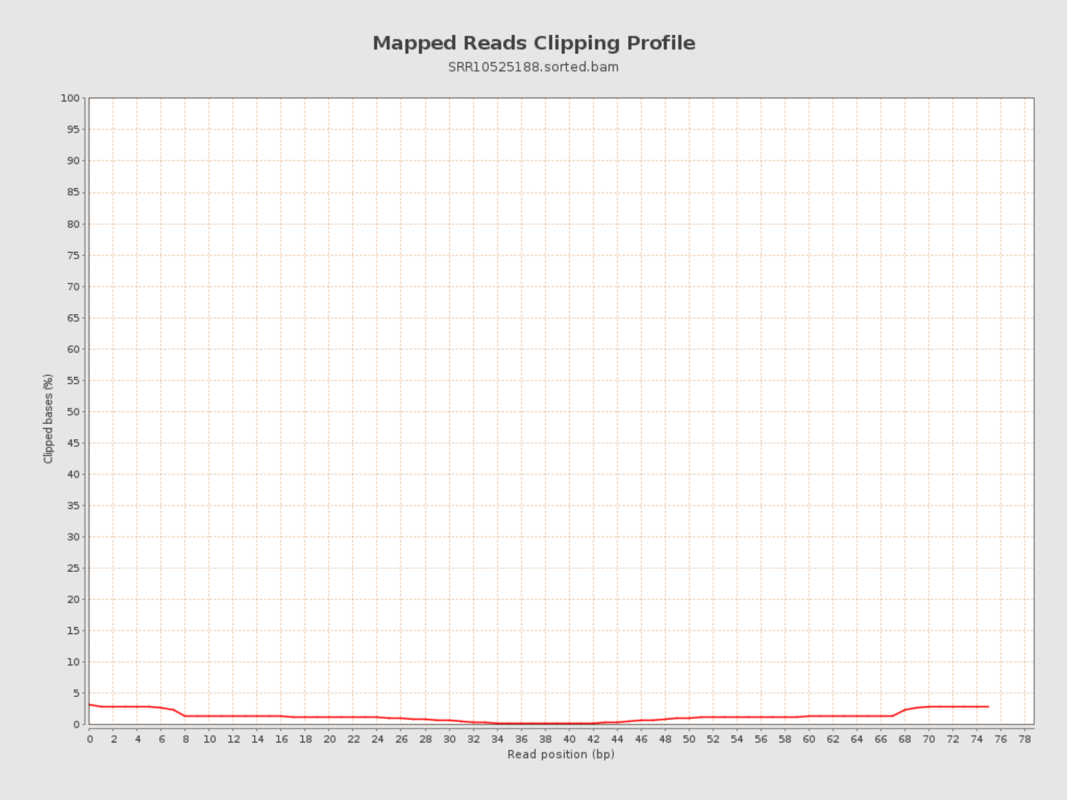
8. Results : Mapped Reads Nucleotide Content



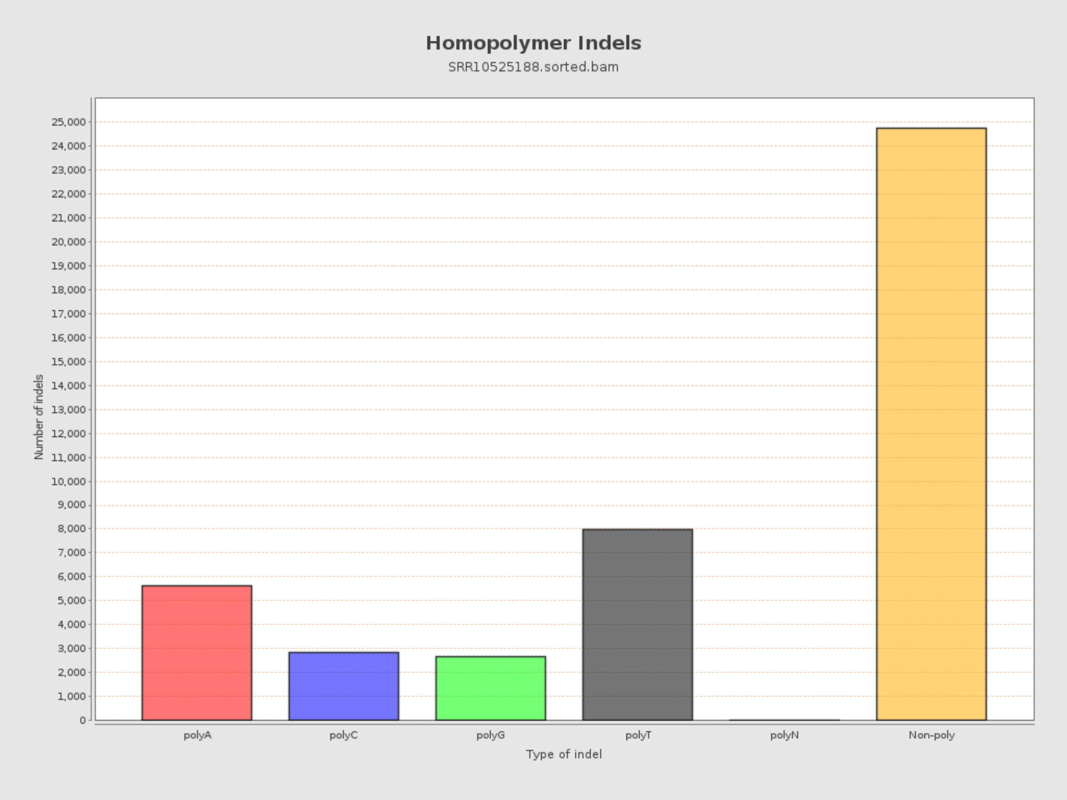
9. Results : Mapped Reads GC-content Distribution



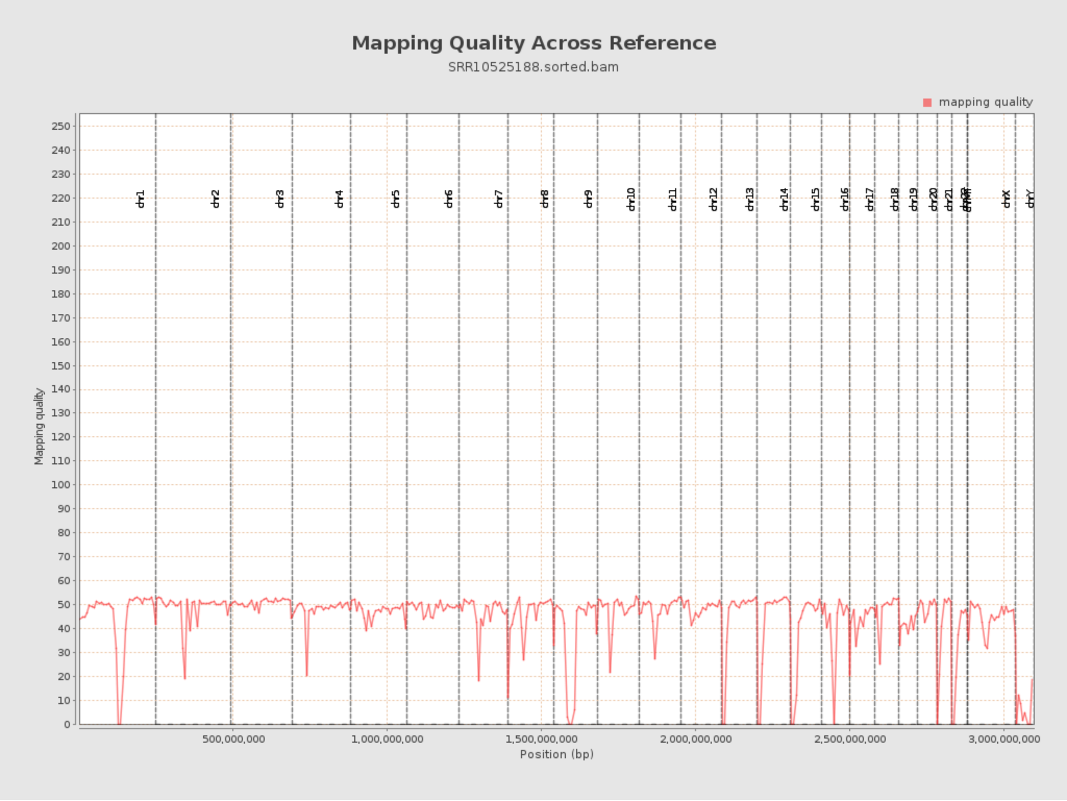
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram