Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:00:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089526.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_SRR089526 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089526.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:00:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089526.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,892,841
Mapped reads	19,221,640 / 80.45%
Unmapped reads	4,671,201 / 19.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	753 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,071,005 / 8.67%
Duplication rate	8.23%
Clipped reads	3,348,835 / 14.02%

2.2. ACGT Content

Number/percentage of A's	269,764,702 / 30.29%
Number/percentage of C's	188,059,794 / 21.12%
Number/percentage of T's	239,098,662 / 26.85%
Number/percentage of G's	193,587,013 / 21.74%
Number/percentage of N's	83,925 / 0.01%
GC Percentage	42.85%

2.3. Coverage

Mean	0.2877

Standard Deviation	1.3452

2.4. Mapping Quality

Mean Mapping Quality	42.59

2.5. Mismatches and indels

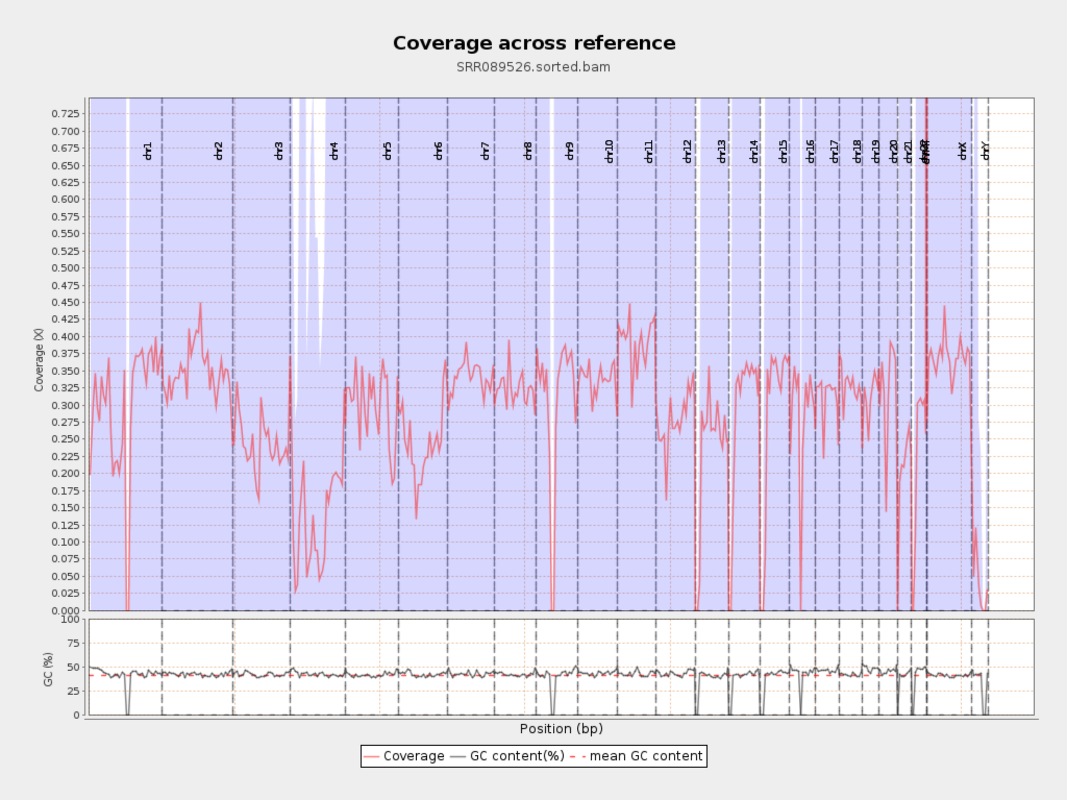
General error rate	0.43%
Mismatches	3,764,652
Insertions	37,889
Mapped reads with at least one insertion	0.2%
Deletions	115,110
Mapped reads with at least one deletion	0.6%
Homopolymer indels	42.57%

2.6. Chromosome stats

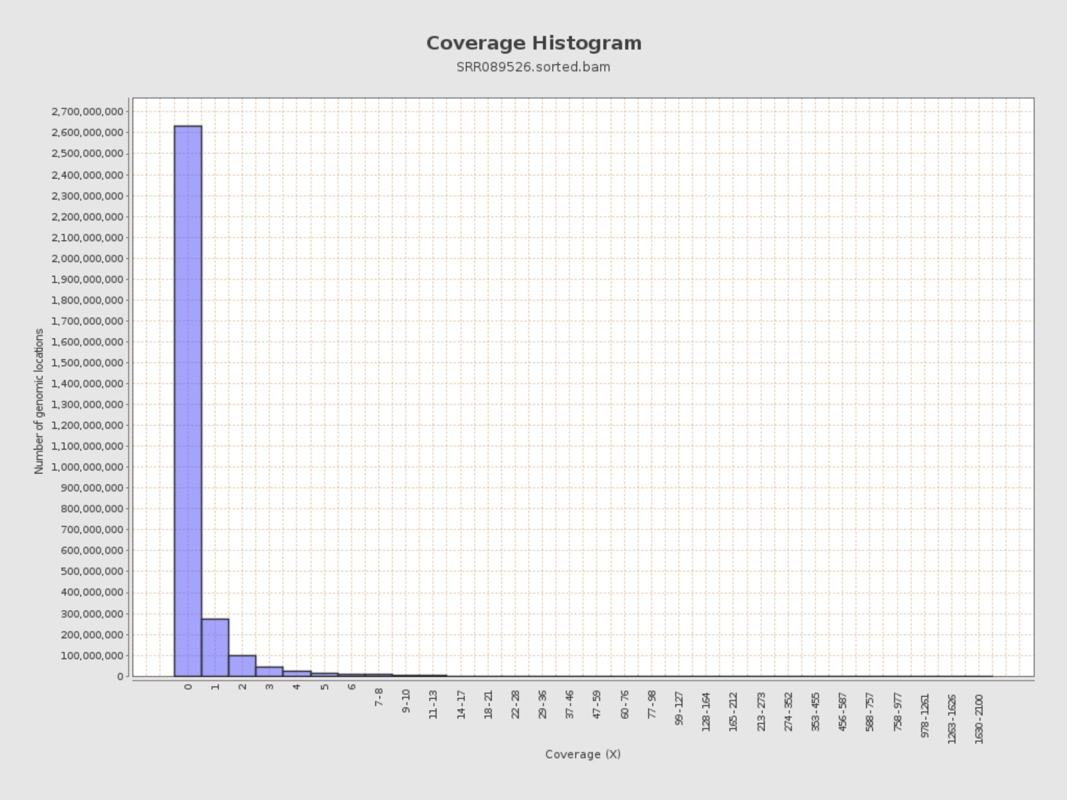
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	73788825	0.296	1.8622
chr2	243199373	85138090	0.3501	1.7028
chr3	198022430	47892936	0.2419	0.8468
chr4	191154276	26465917	0.1385	0.7523
chr5	180915260	54285014	0.3001	0.9703
chr6	171115067	42134946	0.2462	0.9264
chr7	159138663	54336284	0.3414	1.9782

chr8	146364022	47263564	0.3229	1.4908
chr9	141213431	42526354	0.3011	1.3751
chr10	135534747	45859903	0.3384	1.4036
chr11	135006516	52762990	0.3908	1.6152
chr12	133851895	37156625	0.2776	0.9635
chr13	115169878	26403895	0.2293	0.8381
chr14	107349540	30612091	0.2852	1.1232
chr15	102531392	28929112	0.2821	0.9561
chr16	90354753	25679171	0.2842	1.0565
chr17	81195210	25170788	0.31	1.1374
chr18	78077248	25596827	0.3278	2.0882
chr19	59128983	18379120	0.3108	1.7847
chr20	63025520	20128764	0.3194	1.0673
chr21	48129895	9837323	0.2044	1.0165
chr22	51304566	10777436	0.2101	0.8268
chrMT	16571	86578	5.2247	5.6223
chrX	155270560	56974784	0.3669	1.3144
chrY	59373566	2578767	0.0434	0.6067

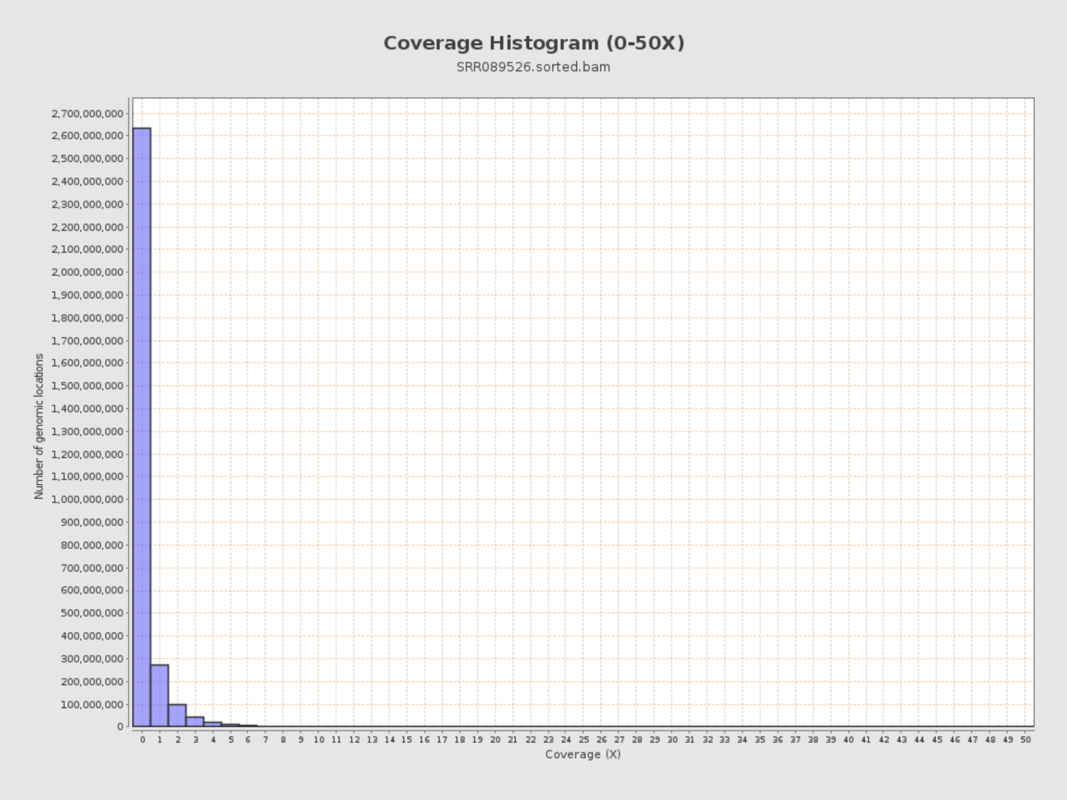
3. Results : Coverage across reference



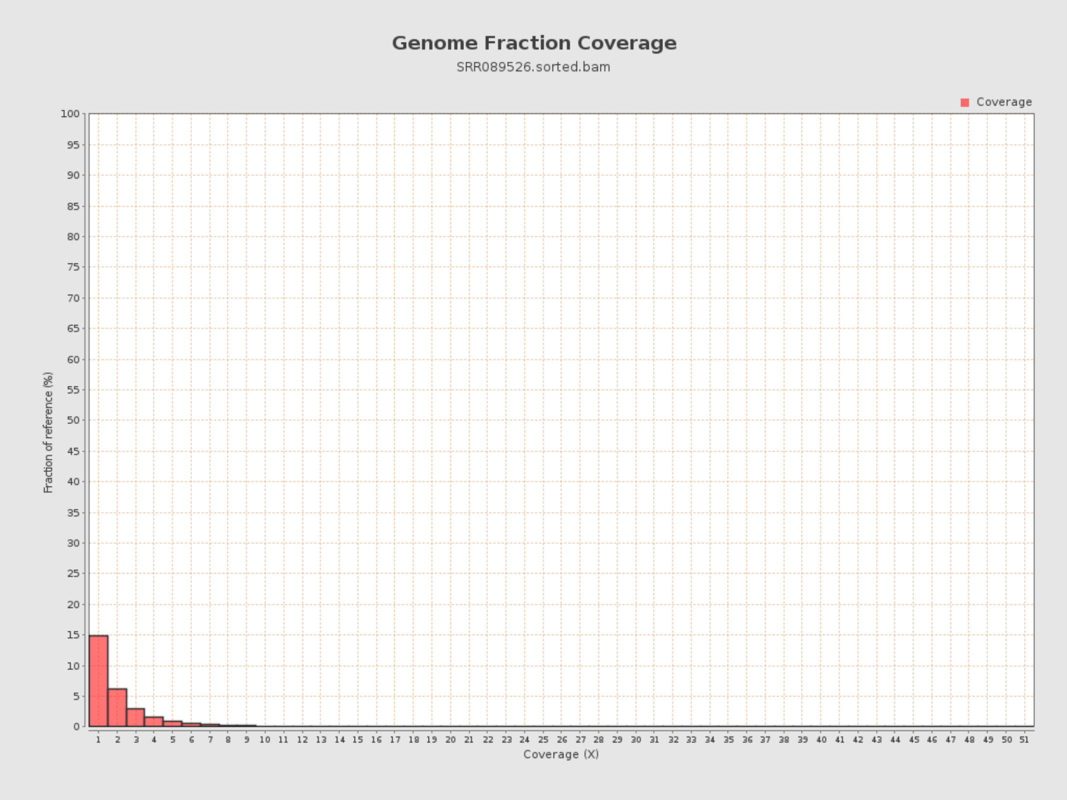
4. Results : Coverage Histogram



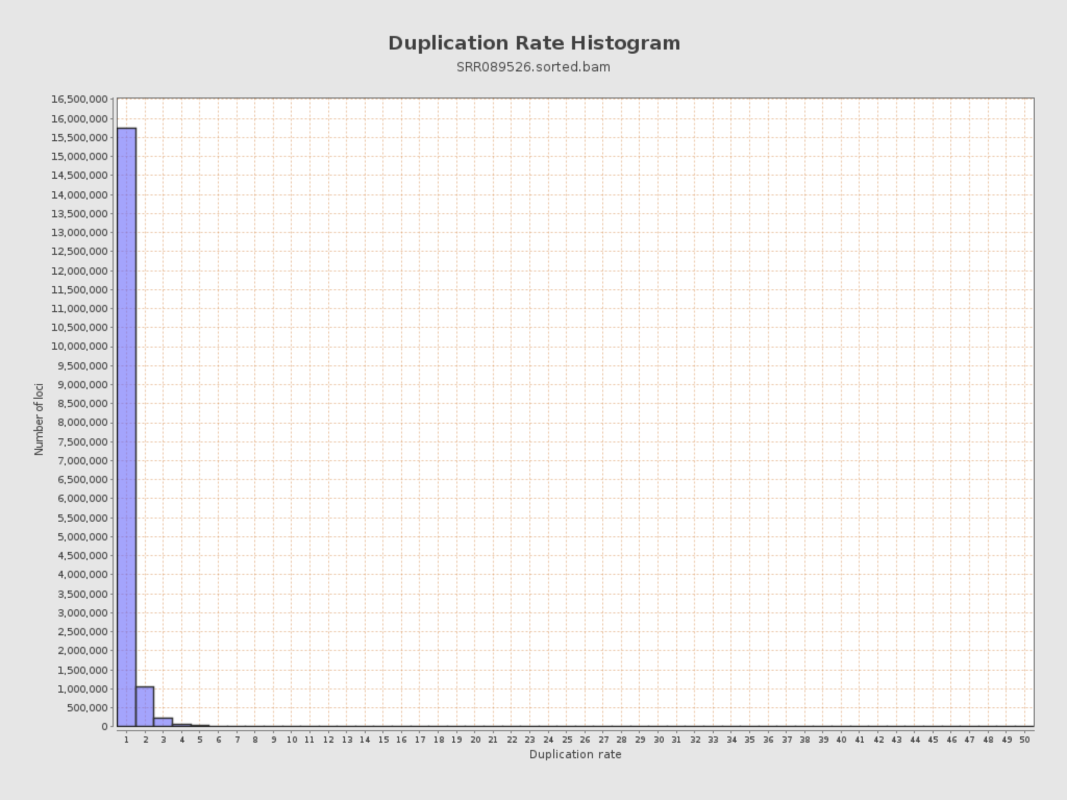
5. Results : Coverage Histogram (0-50X)



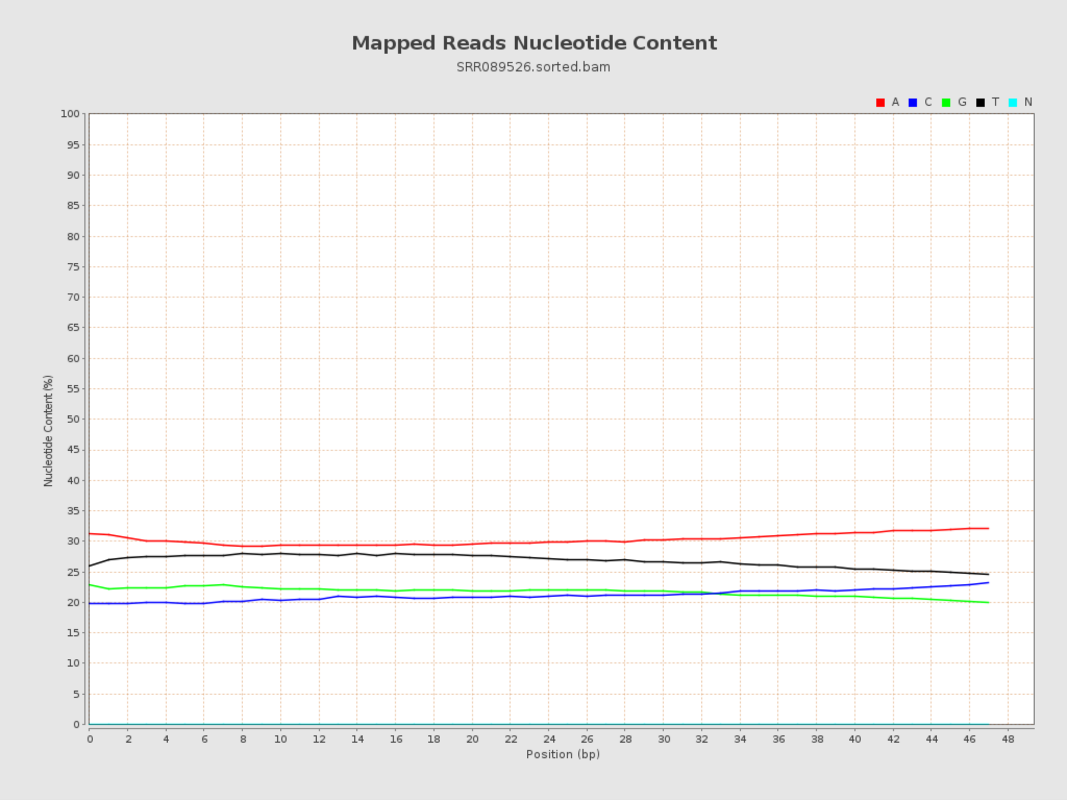
6. Results : Genome Fraction Coverage



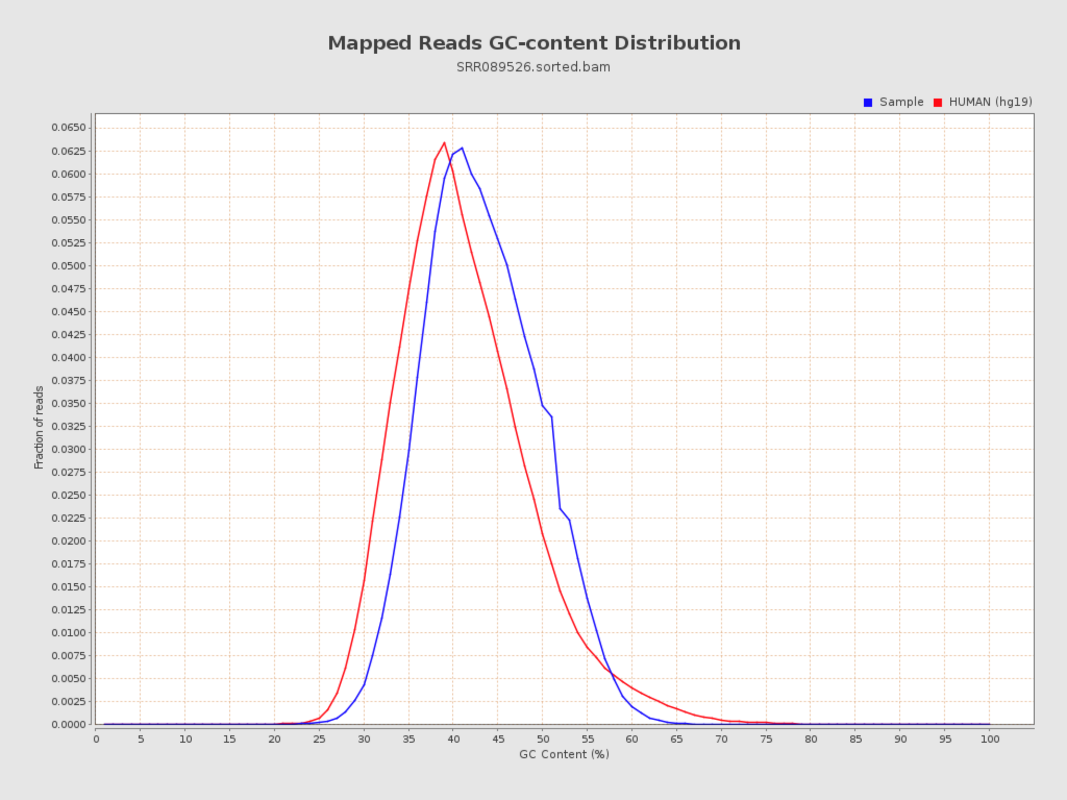
7. Results : Duplication Rate Histogram



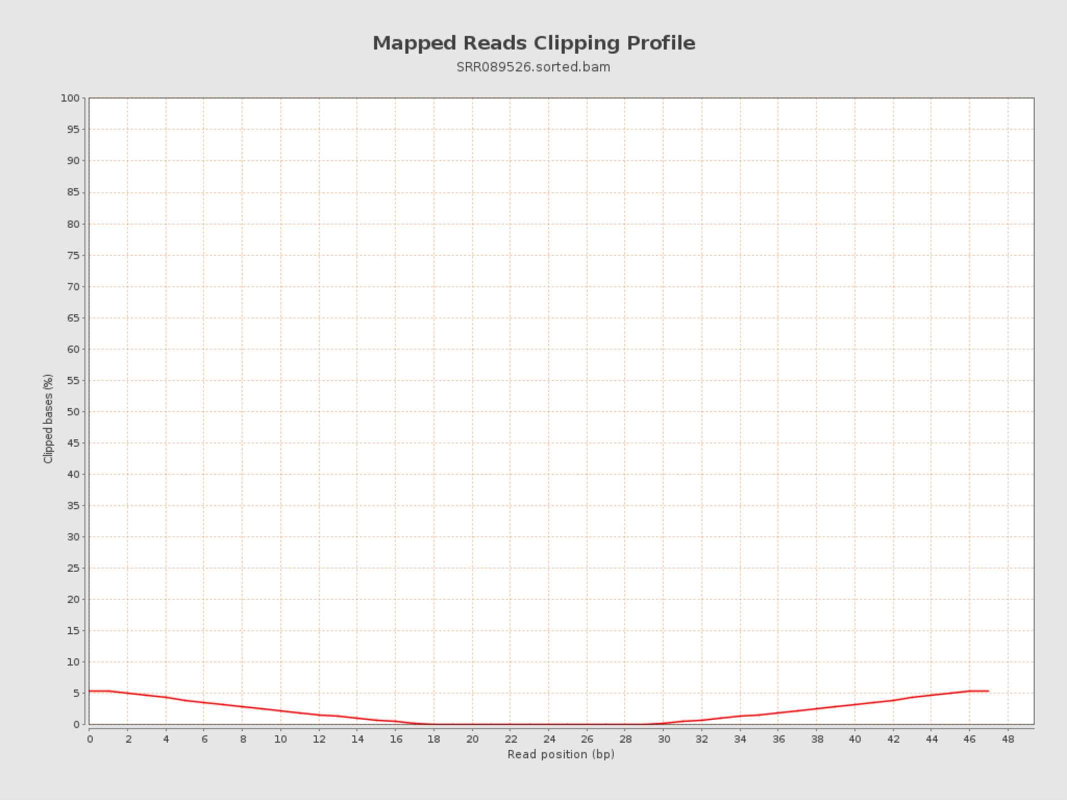
8. Results : Mapped Reads Nucleotide Content



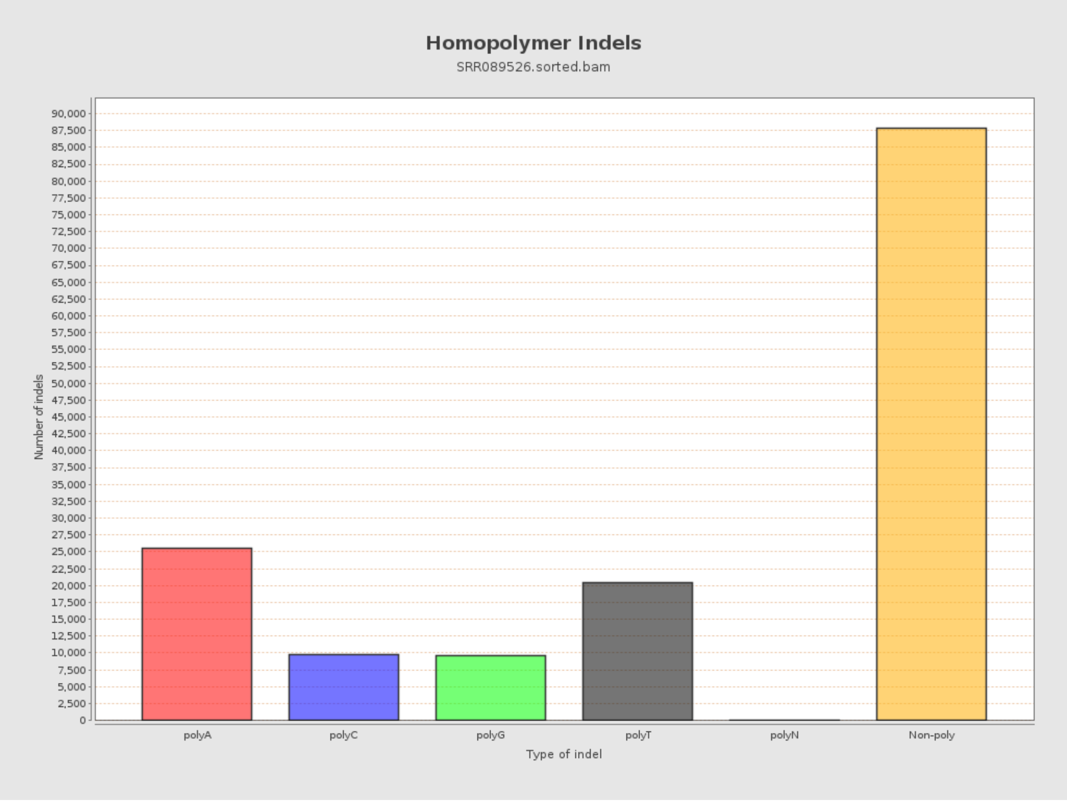
9. Results : Mapped Reads GC-content Distribution



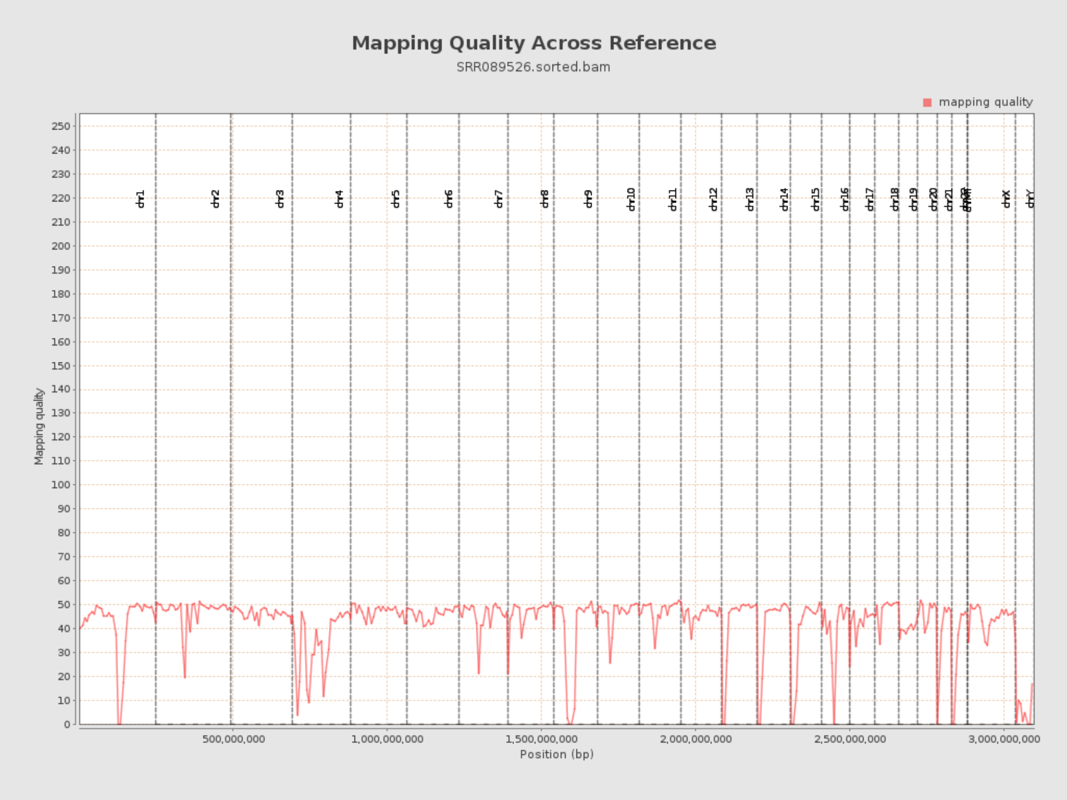
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram