Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 06:19:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090126.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_SRR090126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 06:19:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,890,336
Mapped reads	20,266,663 / 84.83%
Unmapped reads	3,623,673 / 15.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,021 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,085,218 / 12.91%
Duplication rate	10.64%
Clipped reads	1,541,880 / 6.45%

2.2. ACGT Content

Number/percentage of A's	280,615,345 / 29.28%
Number/percentage of C's	195,402,285 / 20.39%
Number/percentage of T's	275,981,709 / 28.79%
Number/percentage of G's	206,371,618 / 21.53%
Number/percentage of N's	117,859 / 0.01%
GC Percentage	41.92%

2.3. Coverage

Mean	0.3097

Standard Deviation	1.5368

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

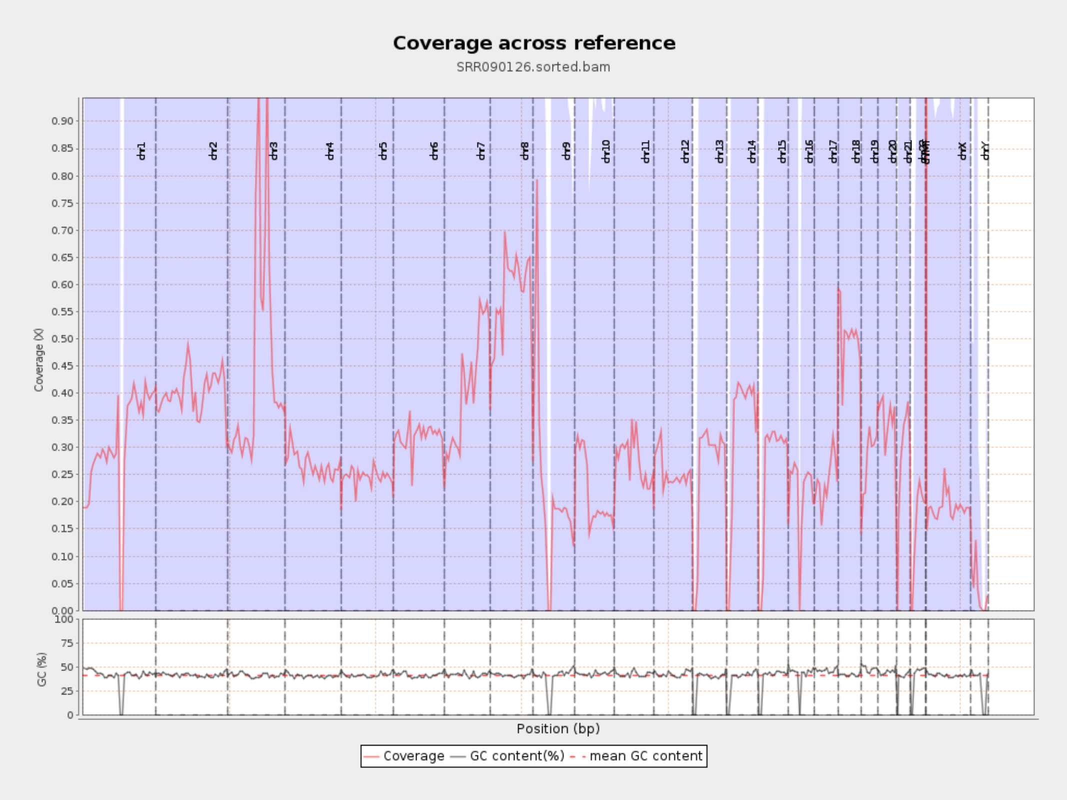
General error rate	0.49%
Mismatches	4,619,363
Insertions	35,285
Mapped reads with at least one insertion	0.17%
Deletions	115,453
Mapped reads with at least one deletion	0.57%
Homopolymer indels	46.64%

2.6. Chromosome stats

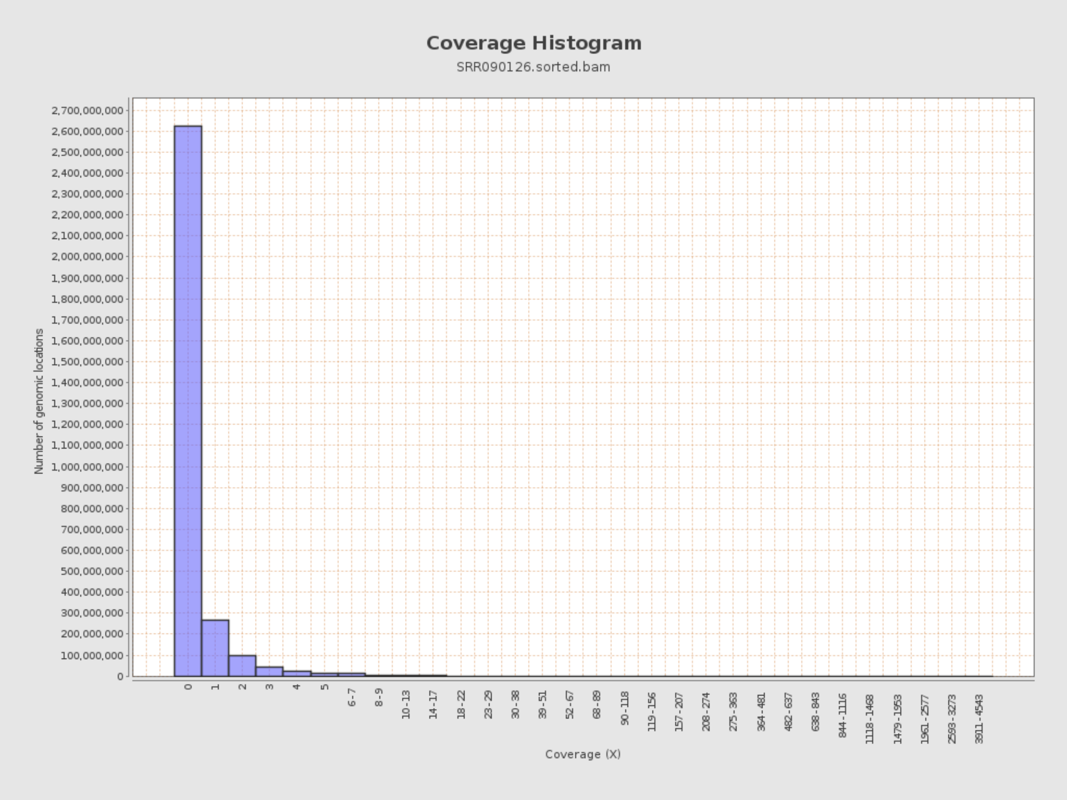
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	76022138	0.305	2.3373
chr2	243199373	98384785	0.4045	1.6142
chr3	198022430	88428986	0.4466	1.3711
chr4	191154276	51219639	0.2679	0.9885
chr5	180915260	44516890	0.2461	0.9252
chr6	171115067	54938021	0.3211	1.179
chr7	159138663	65210014	0.4098	2.3525

chr8	146364022	85232164	0.5823	2.9112
chr9	141213431	31775654	0.225	1.2702
chr10	135534747	29207400	0.2155	1.1281
chr11	135006516	37222536	0.2757	1.2433
chr12	133851895	34104249	0.2548	0.9597
chr13	115169878	29652940	0.2575	0.974
chr14	107349540	35558927	0.3312	1.1307
chr15	102531392	25999056	0.2536	0.9521
chr16	90354753	19305830	0.2137	0.878
chr17	81195210	19610507	0.2415	0.9905
chr18	78077248	39407862	0.5047	2.1523
chr19	59128983	16659837	0.2818	1.6087
chr20	63025520	22117224	0.3509	1.1895
chr21	48129895	13337797	0.2771	1.1109
chr22	51304566	7873392	0.1535	0.7129
chrMT	16571	1075682	64.9135	42.7107
chrX	155270560	29493703	0.19	0.8614
chrY	59373566	2309671	0.0389	1.1836

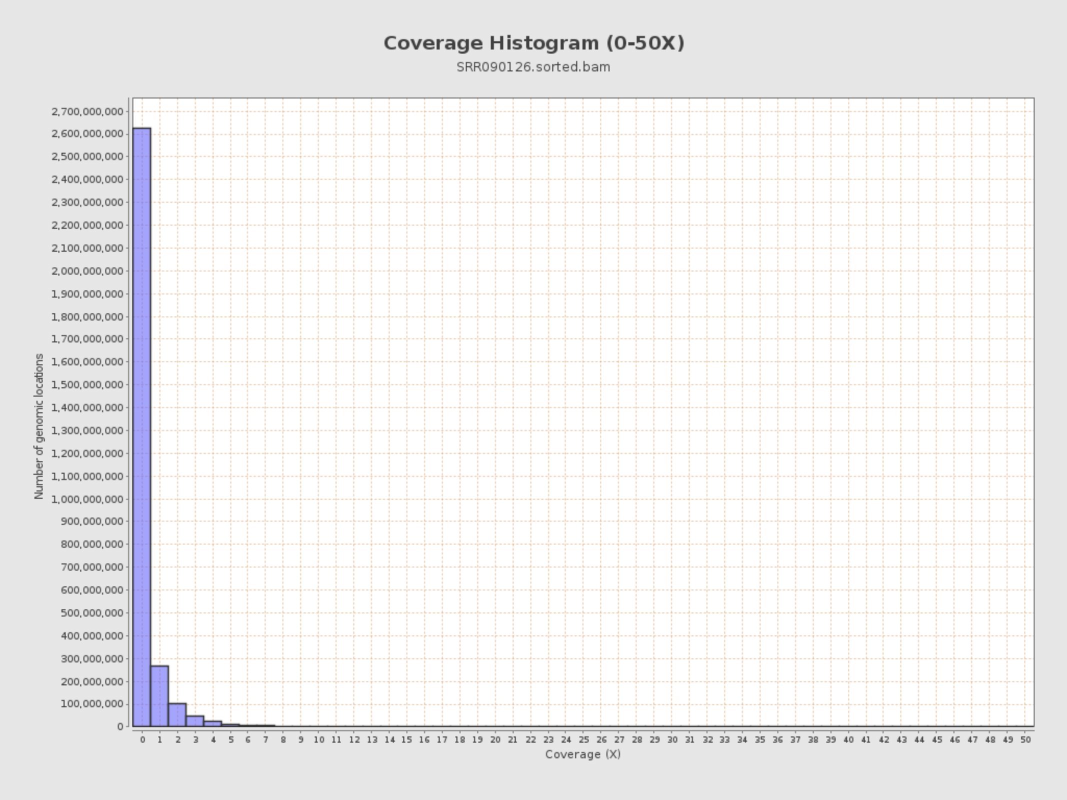
3. Results : Coverage across reference



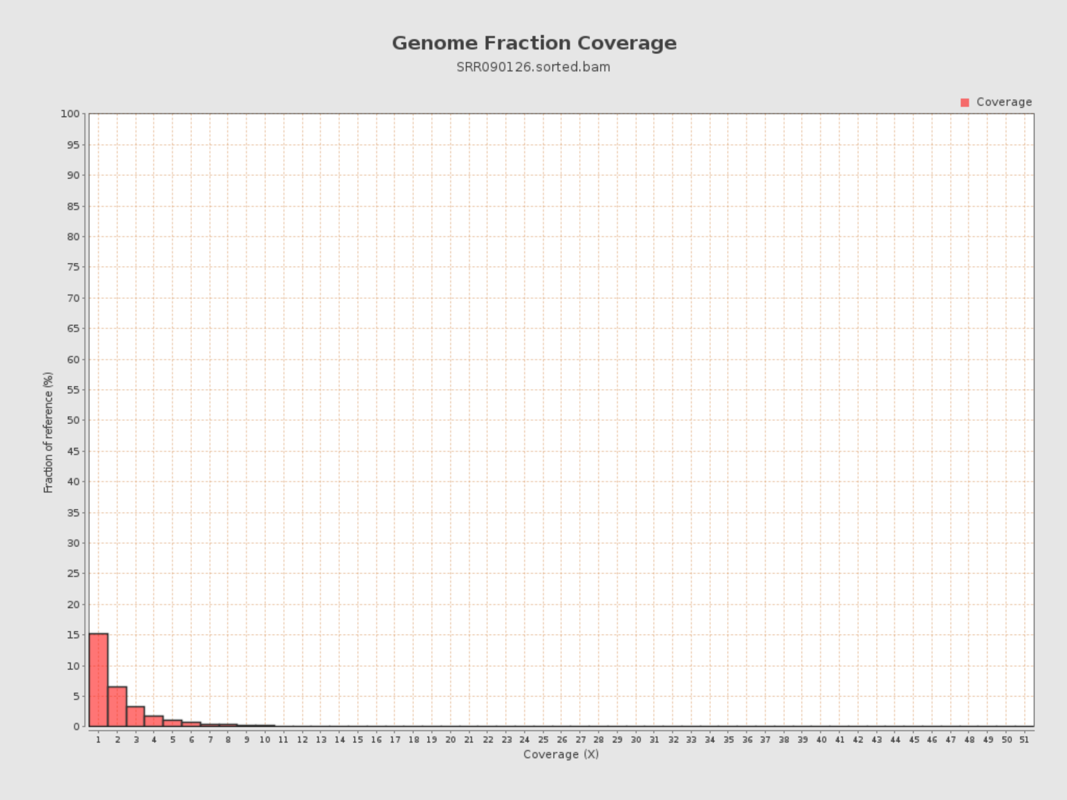
4. Results : Coverage Histogram



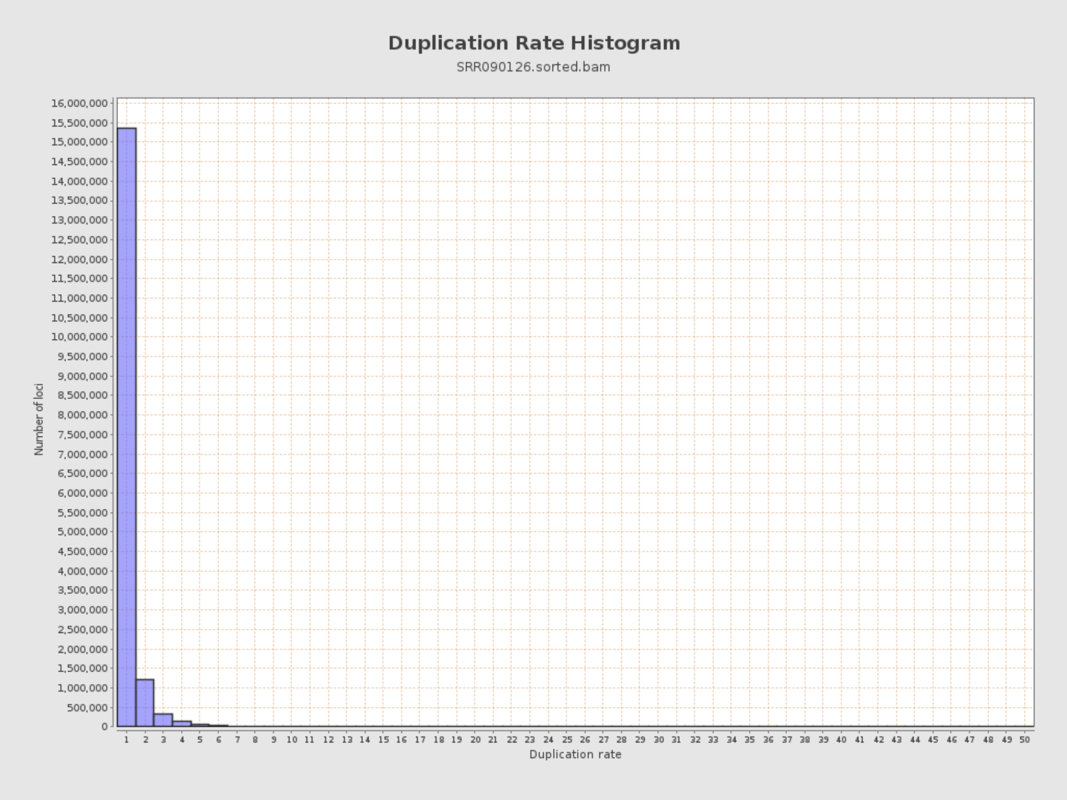
5. Results : Coverage Histogram (0-50X)



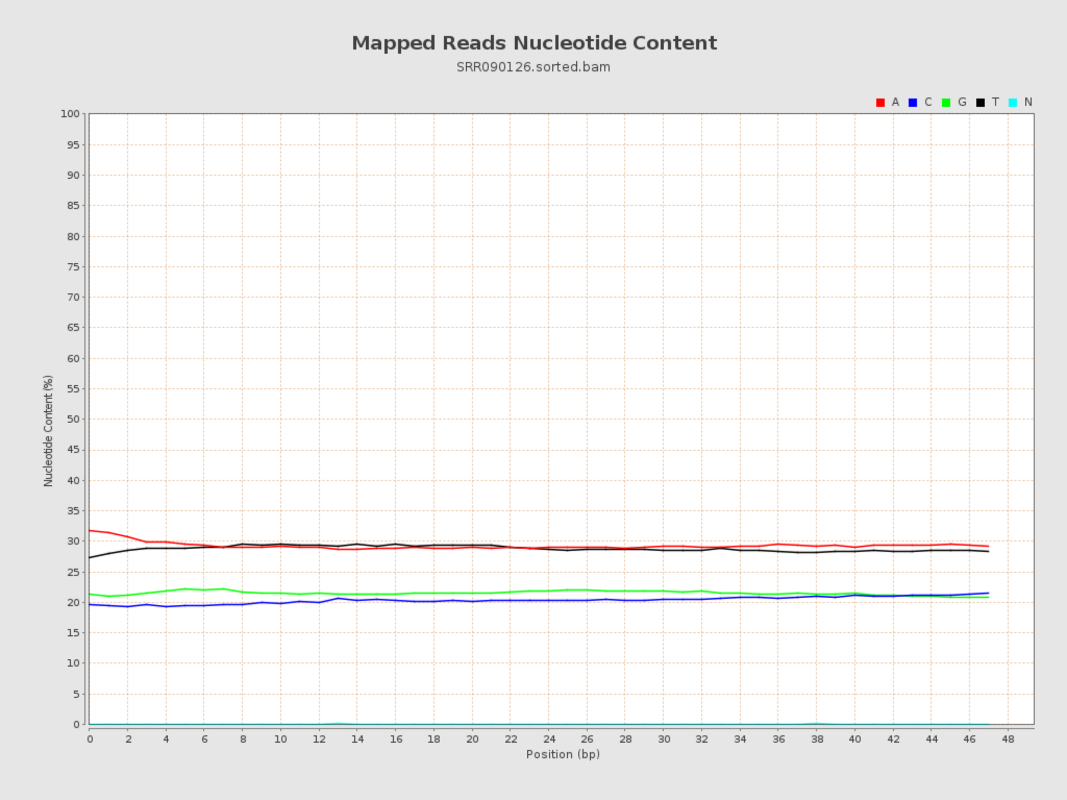
6. Results : Genome Fraction Coverage



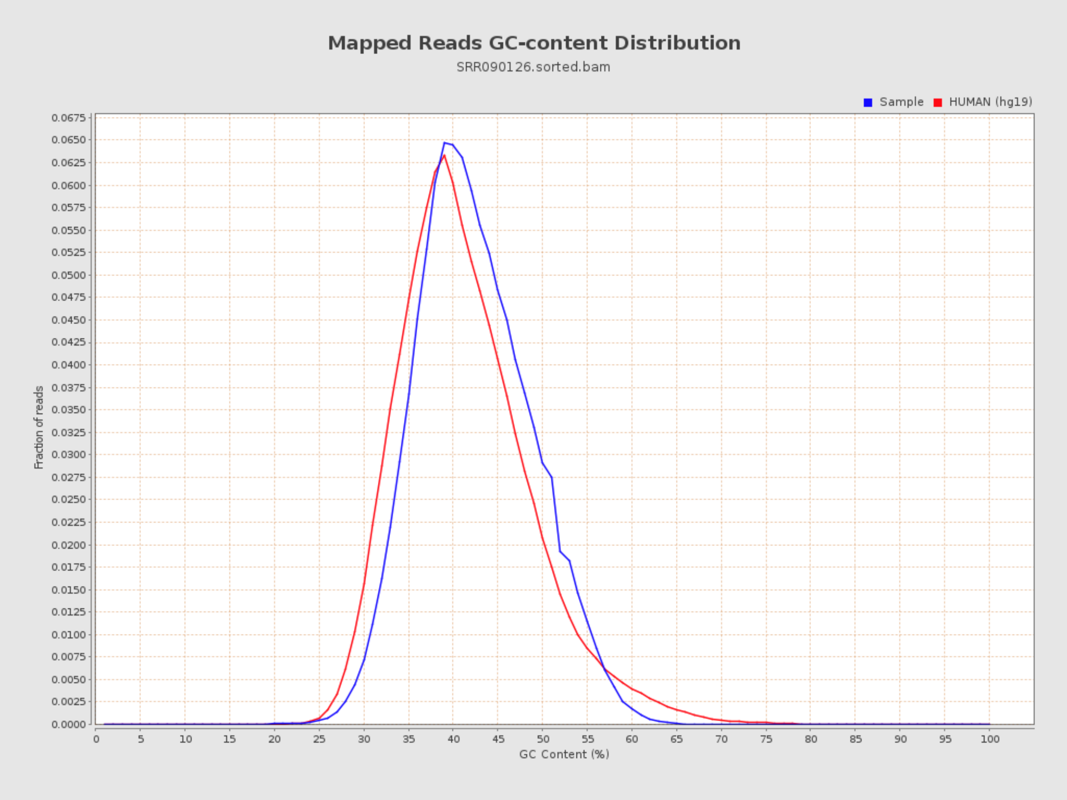
7. Results : Duplication Rate Histogram



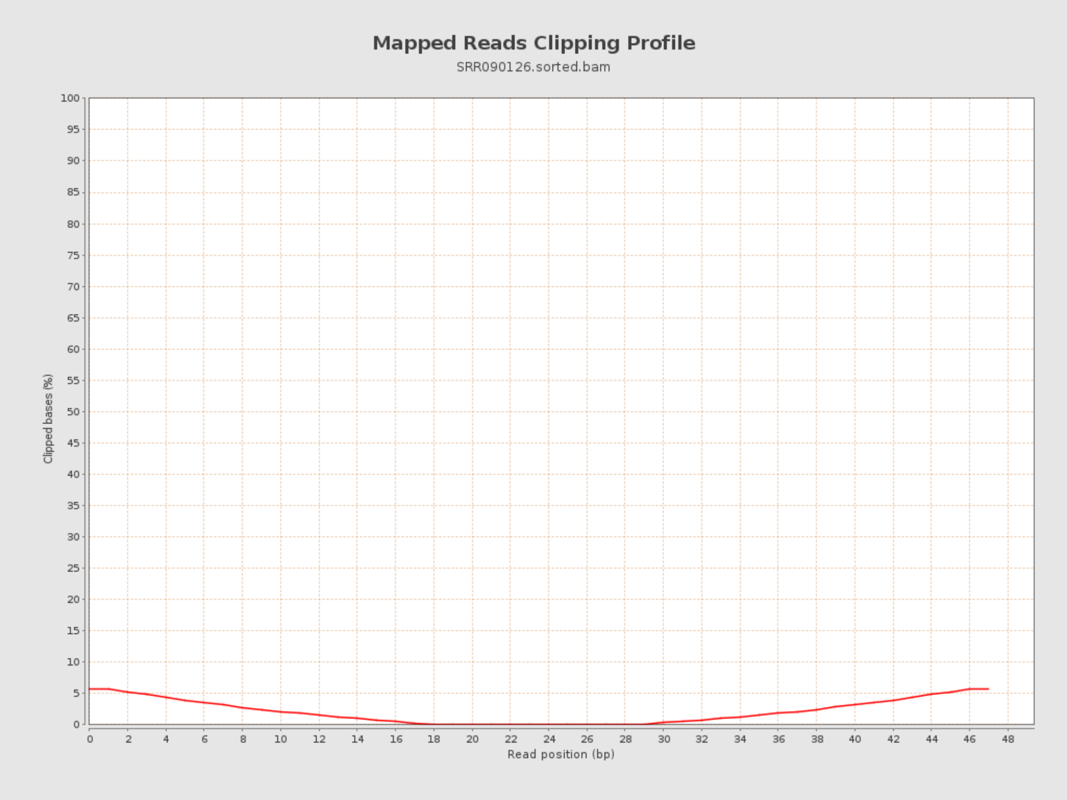
8. Results : Mapped Reads Nucleotide Content



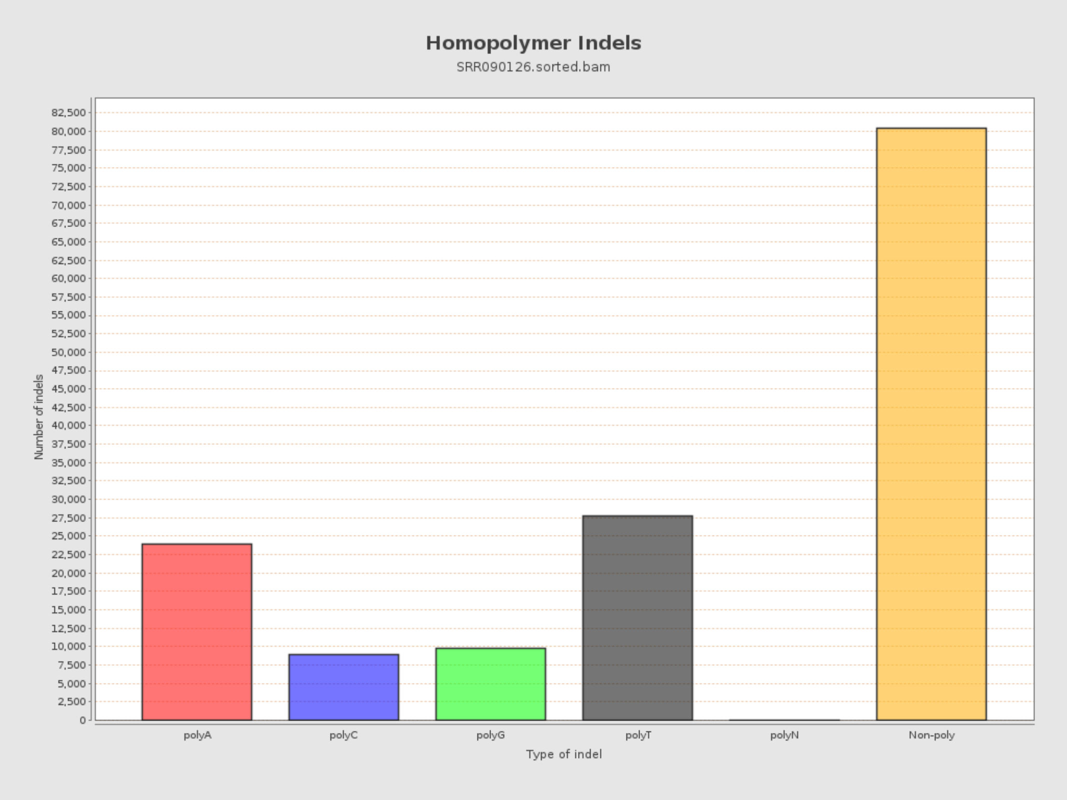
9. Results : Mapped Reads GC-content Distribution



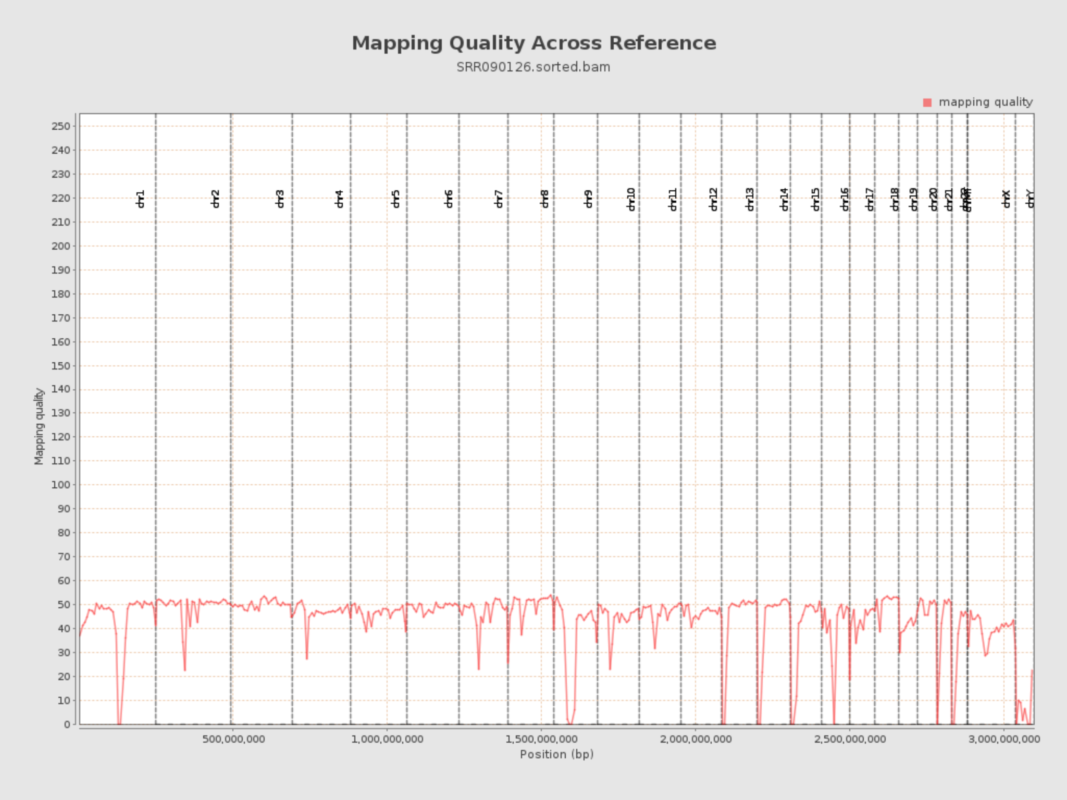
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram