Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:20:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053667.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_SRR053667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053667.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:19:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,912,281
Mapped reads	10,214,711 / 73.42%
Unmapped reads	3,697,570 / 26.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	298 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,556,031 / 25.56%
Duplication rate	23.8%
Clipped reads	831,789 / 5.98%

2.2. ACGT Content

Number/percentage of A's	141,930,336 / 29.39%
Number/percentage of C's	94,373,924 / 19.54%
Number/percentage of T's	142,559,723 / 29.52%
Number/percentage of G's	103,760,396 / 21.49%
Number/percentage of N's	314,400 / 0.07%
GC Percentage	41.03%

2.3. Coverage

Mean	0.156

Standard Deviation	1.3935

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

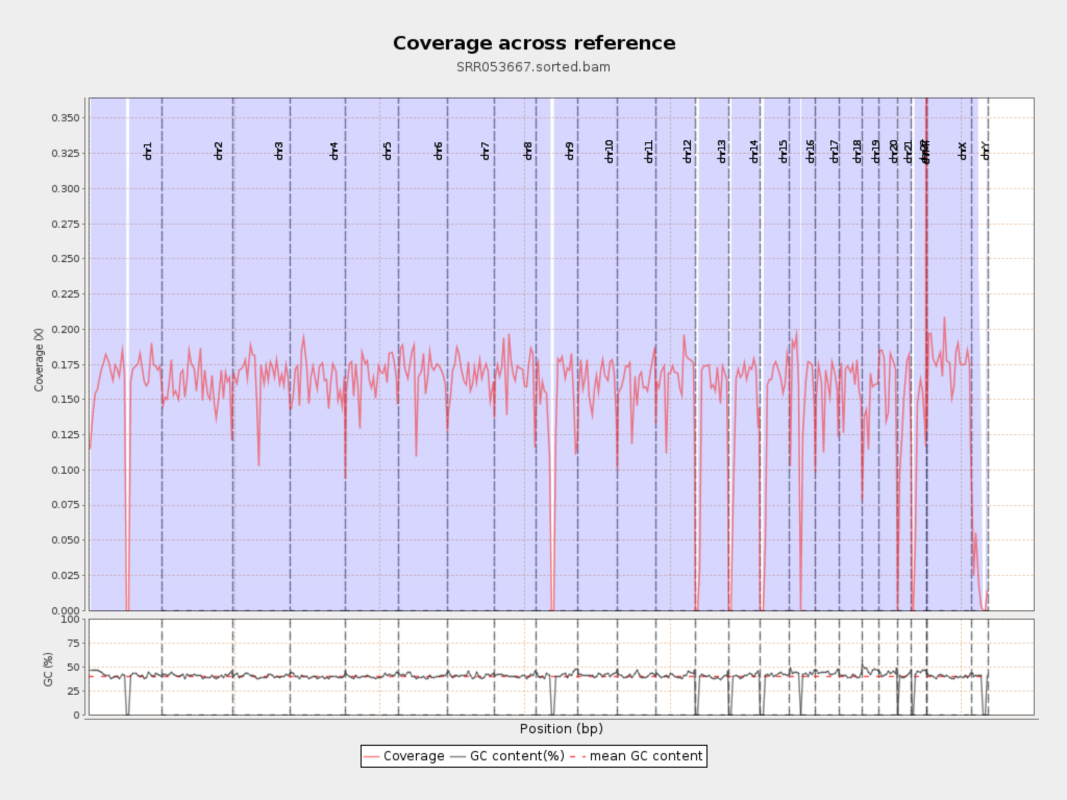
General error rate	0.58%
Mismatches	2,777,132
Insertions	19,320
Mapped reads with at least one insertion	0.19%
Deletions	59,350
Mapped reads with at least one deletion	0.58%
Homopolymer indels	46.11%

2.6. Chromosome stats

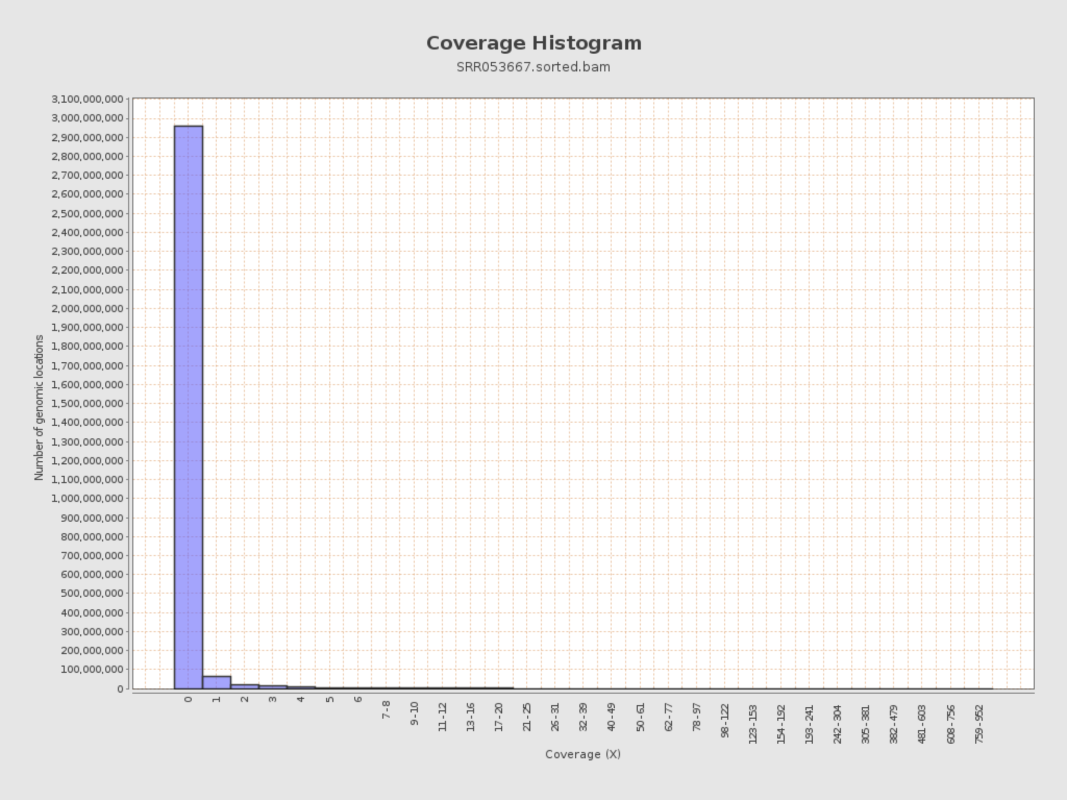
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39314654	0.1577	1.5135
chr2	243199373	39035811	0.1605	1.467
chr3	198022430	33139420	0.1674	1.3655
chr4	191154276	31366118	0.1641	1.4339
chr5	180915260	30245933	0.1672	1.3499
chr6	171115067	29041239	0.1697	1.5038
chr7	159138663	26639750	0.1674	1.4591

chr8	146364022	24831043	0.1697	1.4683
chr9	141213431	19812813	0.1403	1.2602
chr10	135534747	22290140	0.1645	1.4309
chr11	135006516	21876674	0.162	1.4843
chr12	133851895	22316097	0.1667	1.3603
chr13	115169878	15888564	0.138	1.2379
chr14	107349540	14930905	0.1391	1.342
chr15	102531392	13818784	0.1348	1.2142
chr16	90354753	13672559	0.1513	1.3098
chr17	81195210	12748251	0.157	1.2963
chr18	78077248	12811916	0.1641	1.5405
chr19	59128983	8678269	0.1468	1.4661
chr20	63025520	10456514	0.1659	1.4198
chr21	48129895	6224803	0.1293	1.2924
chr22	51304566	5258074	0.1025	1.0137
chrMT	16571	17817	1.0752	2.9344
chrX	155270560	27411634	0.1765	1.4762
chrY	59373566	1199432	0.0202	0.4463

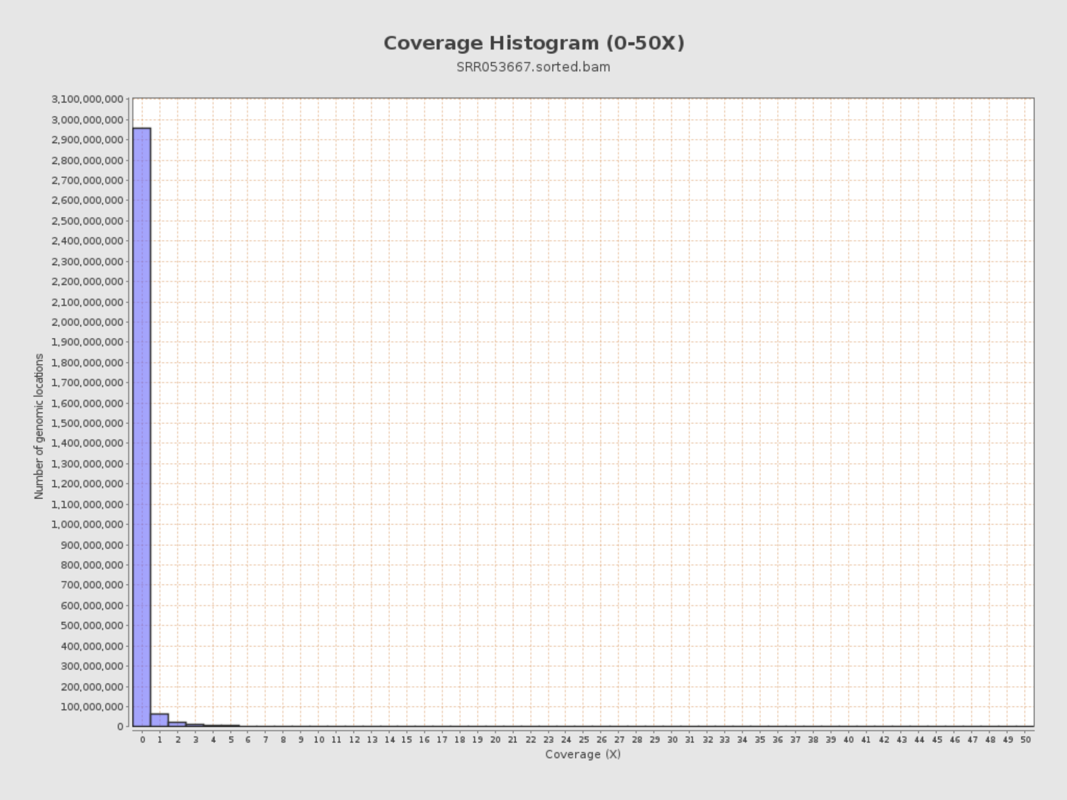
3. Results : Coverage across reference



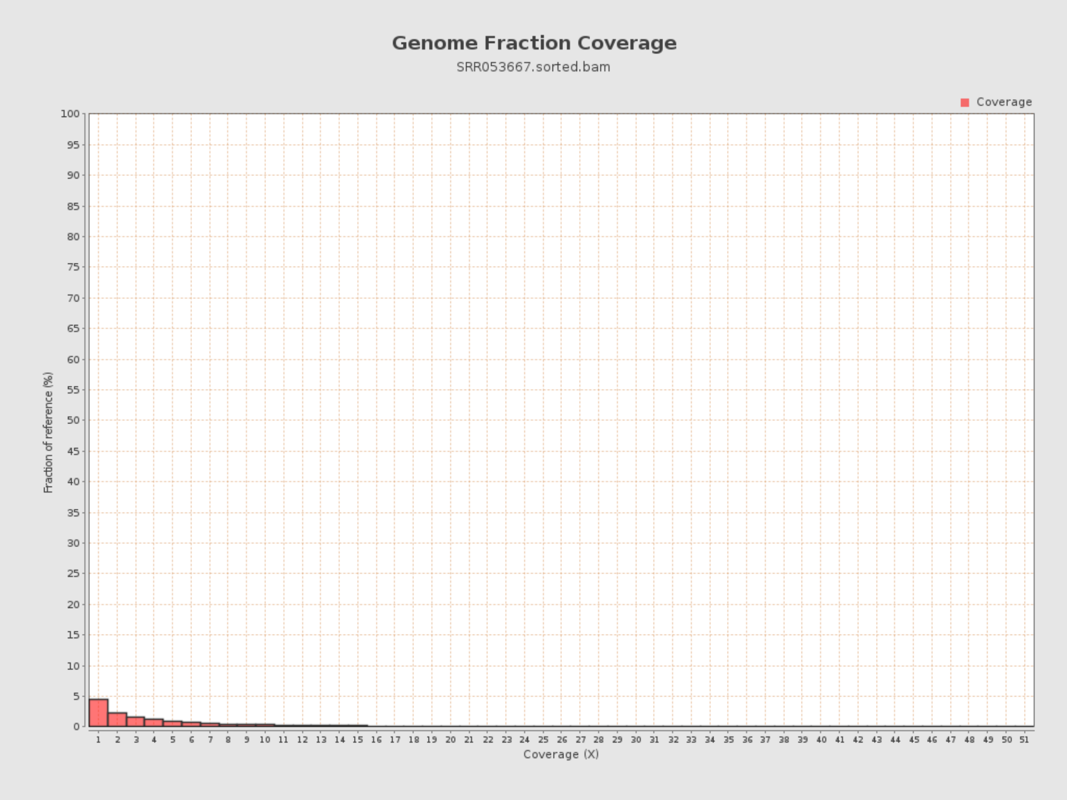
4. Results : Coverage Histogram



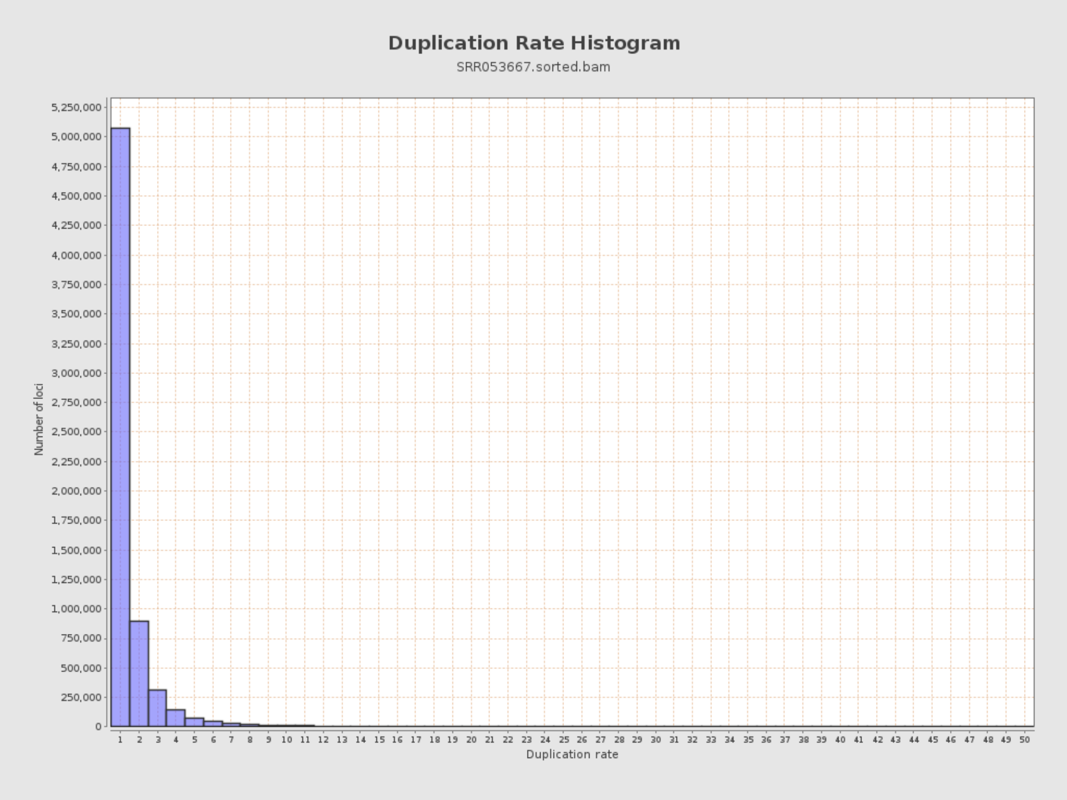
5. Results : Coverage Histogram (0-50X)



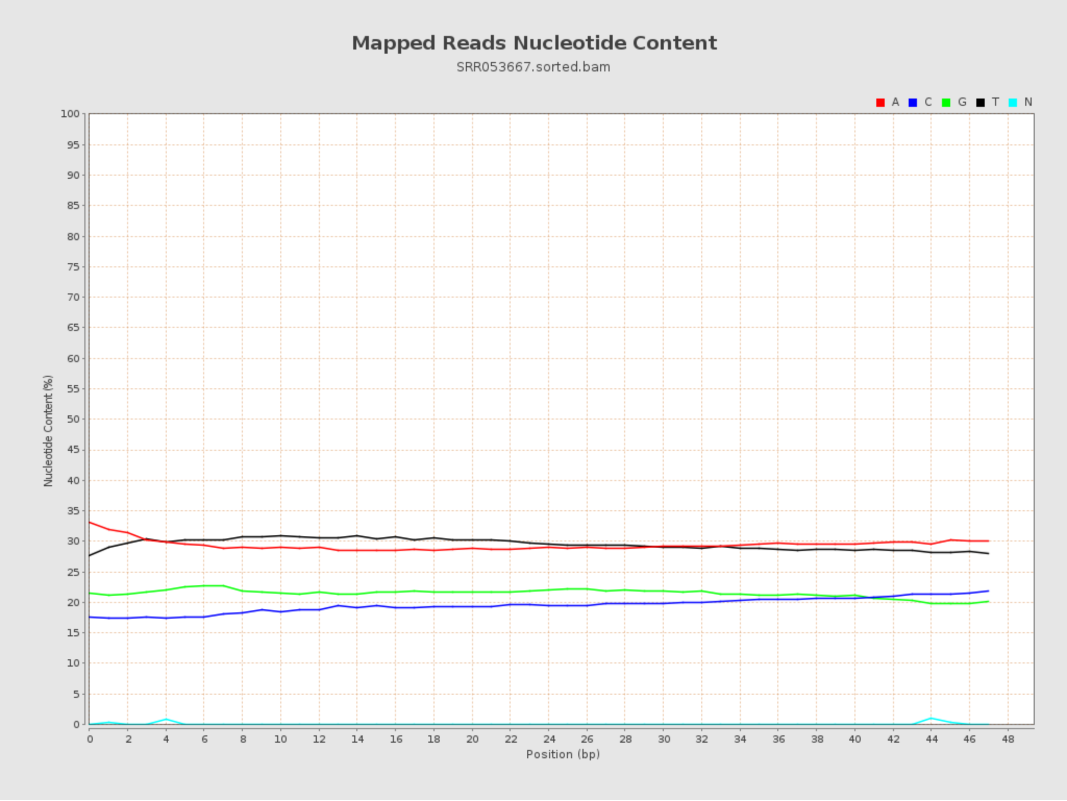
6. Results : Genome Fraction Coverage



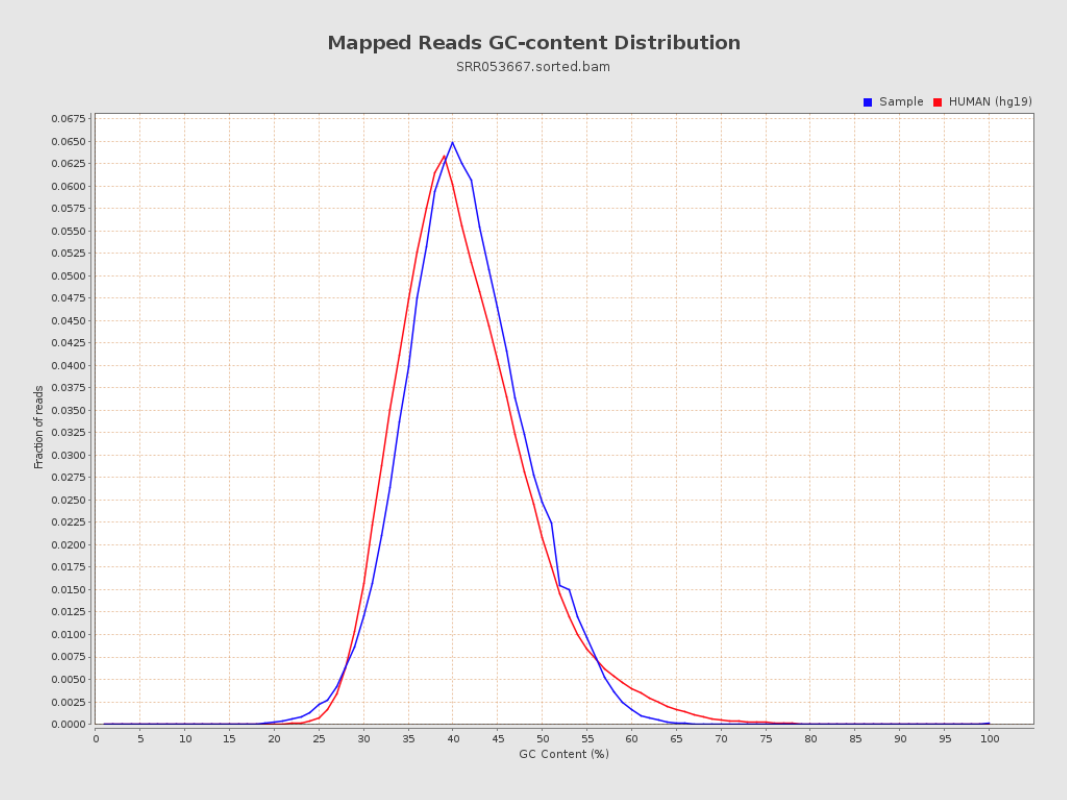
7. Results : Duplication Rate Histogram



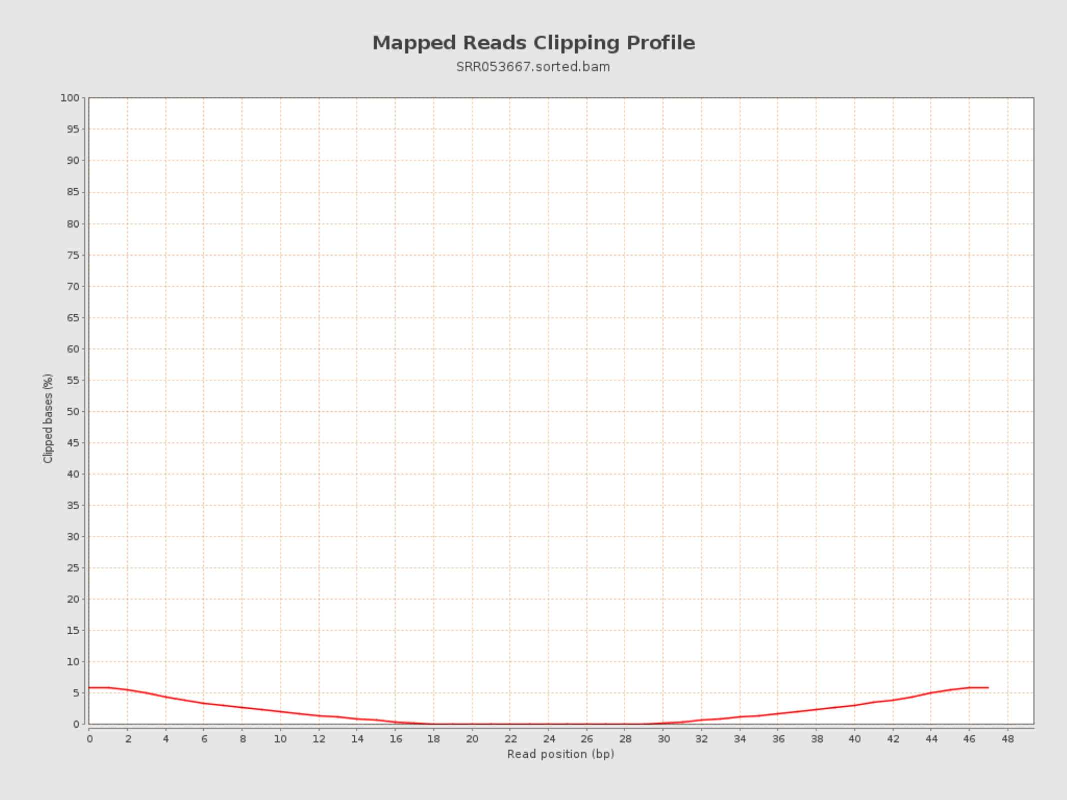
8. Results : Mapped Reads Nucleotide Content



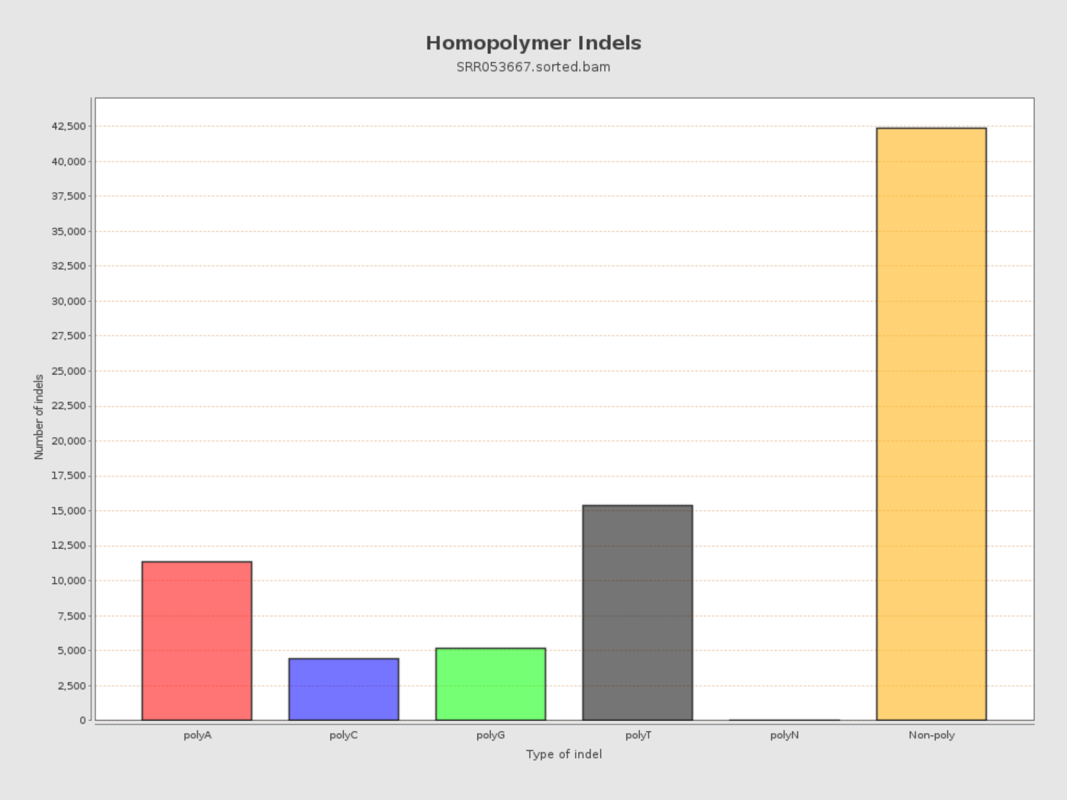
9. Results : Mapped Reads GC-content Distribution



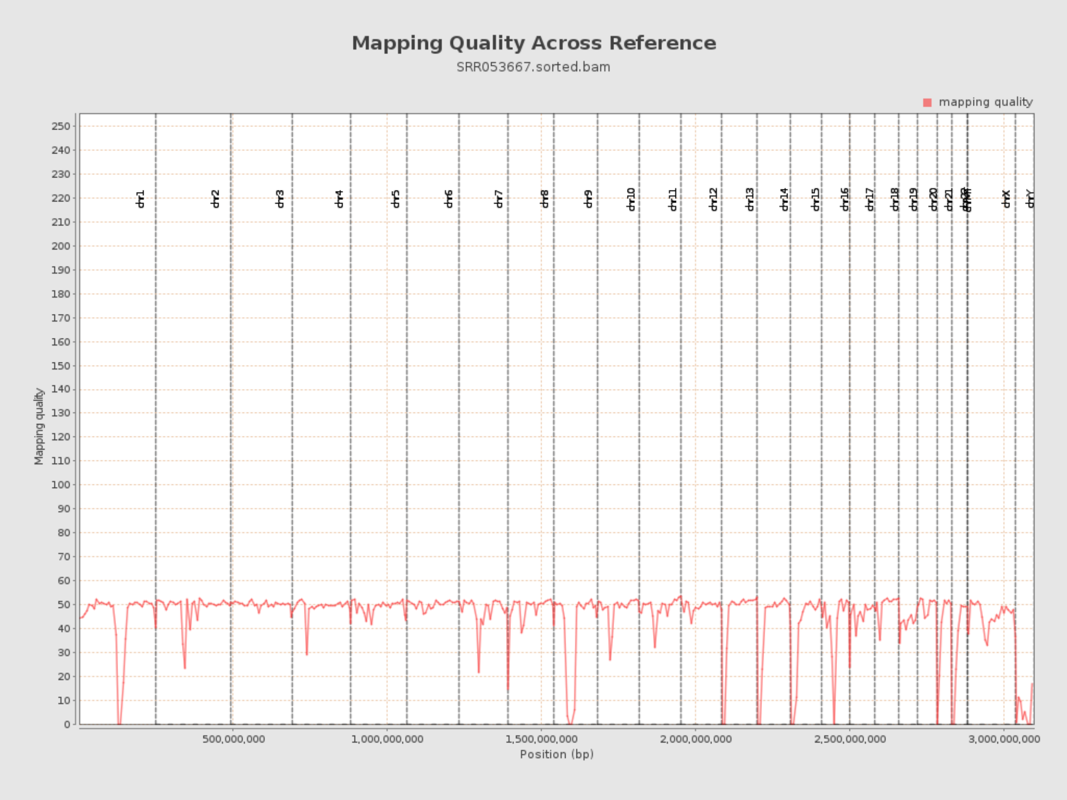
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram