Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:06:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054615.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_SRR054615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:06:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,021,568
Mapped reads	15,364,061 / 80.77%
Unmapped reads	3,657,507 / 19.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,717 / 0.01%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,486,163 / 13.07%
Duplication rate	11.73%
Clipped reads	2,446,688 / 12.86%

2.2. ACGT Content

Number/percentage of A's	213,381,145 / 29.87%
Number/percentage of C's	145,754,767 / 20.4%
Number/percentage of T's	205,535,766 / 28.77%
Number/percentage of G's	149,512,923 / 20.93%
Number/percentage of N's	166,115 / 0.02%
GC Percentage	41.33%

2.3. Coverage

Mean	0.2308

Standard Deviation	1.2513

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

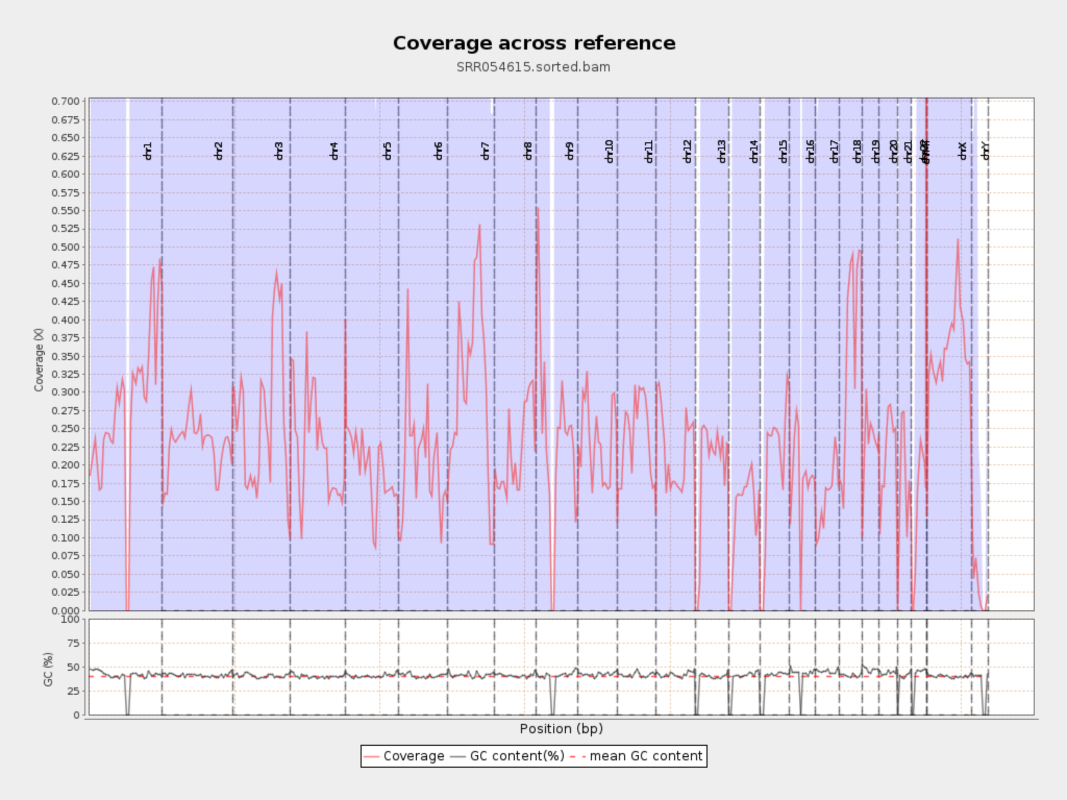
General error rate	0.52%
Mismatches	3,647,364
Insertions	38,846
Mapped reads with at least one insertion	0.25%
Deletions	109,045
Mapped reads with at least one deletion	0.71%
Homopolymer indels	42.88%

2.6. Chromosome stats

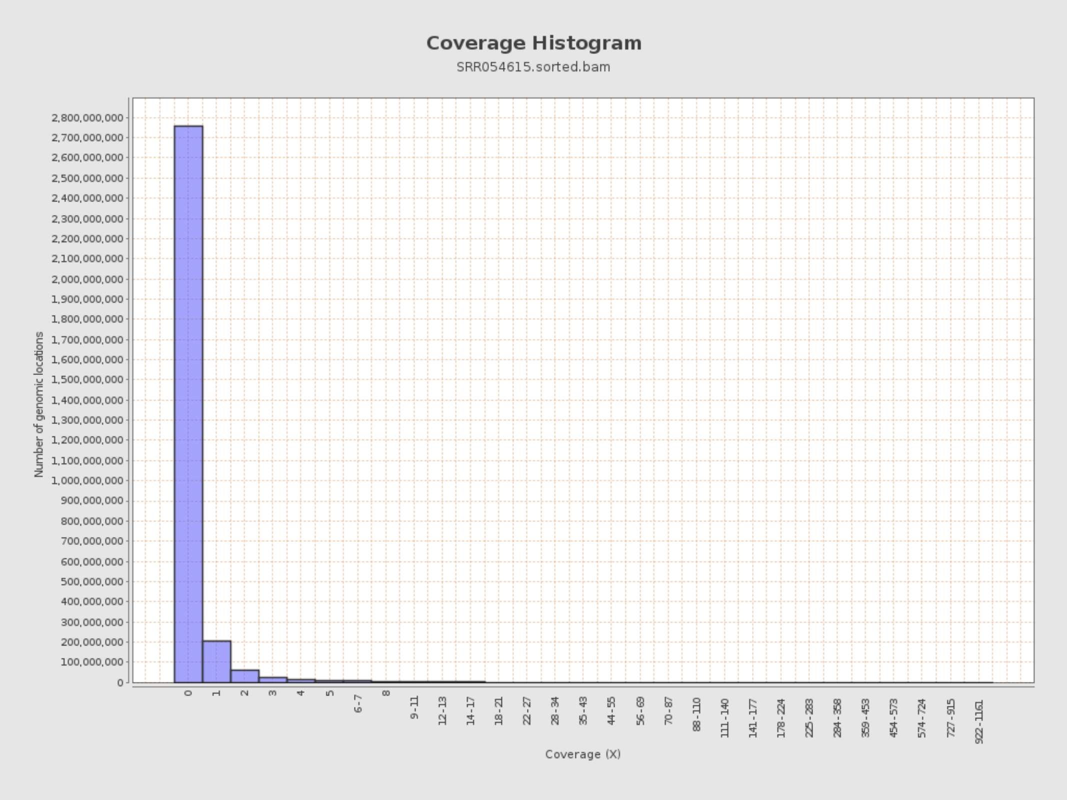
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68909941	0.2765	1.6443
chr2	243199373	55731101	0.2292	1.3228
chr3	198022430	53228187	0.2688	1.2047
chr4	191154276	42855691	0.2242	1.1083
chr5	180915260	35213831	0.1946	0.9605
chr6	171115067	34631120	0.2024	1.1744
chr7	159138663	50123748	0.315	1.6414

chr8	146364022	32376885	0.2212	1.204
chr9	141213431	33501025	0.2372	1.2433
chr10	135534747	31863619	0.2351	1.3776
chr11	135006516	32365395	0.2397	1.2317
chr12	133851895	29393768	0.2196	1.0576
chr13	115169878	21883059	0.19	0.9699
chr14	107349540	14246639	0.1327	0.8784
chr15	102531392	20236852	0.1974	0.9839
chr16	90354753	16432011	0.1819	1.0594
chr17	81195210	12814910	0.1578	0.8615
chr18	78077248	28260015	0.3619	1.6898
chr19	59128983	14039921	0.2374	1.381
chr20	63025520	13725563	0.2178	1.0688
chr21	48129895	8150488	0.1693	1.1162
chr22	51304566	7076801	0.1379	0.7979
chrMT	16571	49553	2.9903	4.7684
chrX	155270560	55636978	0.3583	1.554
chrY	59373566	1766974	0.0298	0.4616

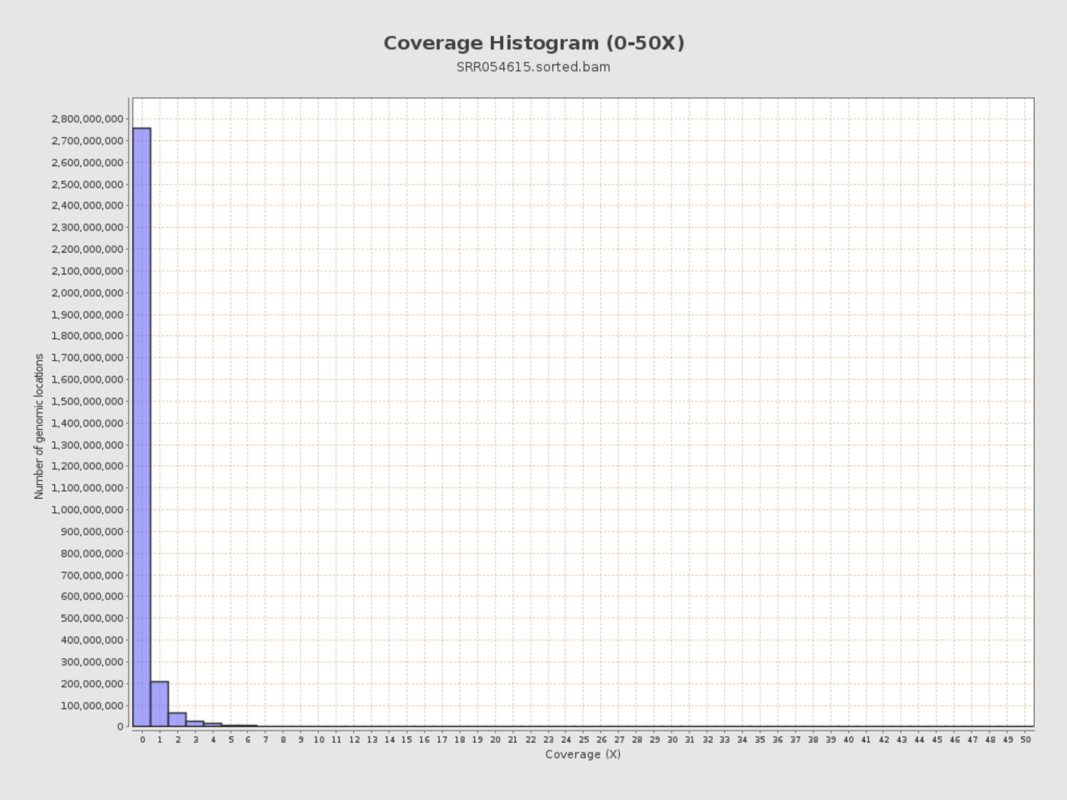
3. Results : Coverage across reference



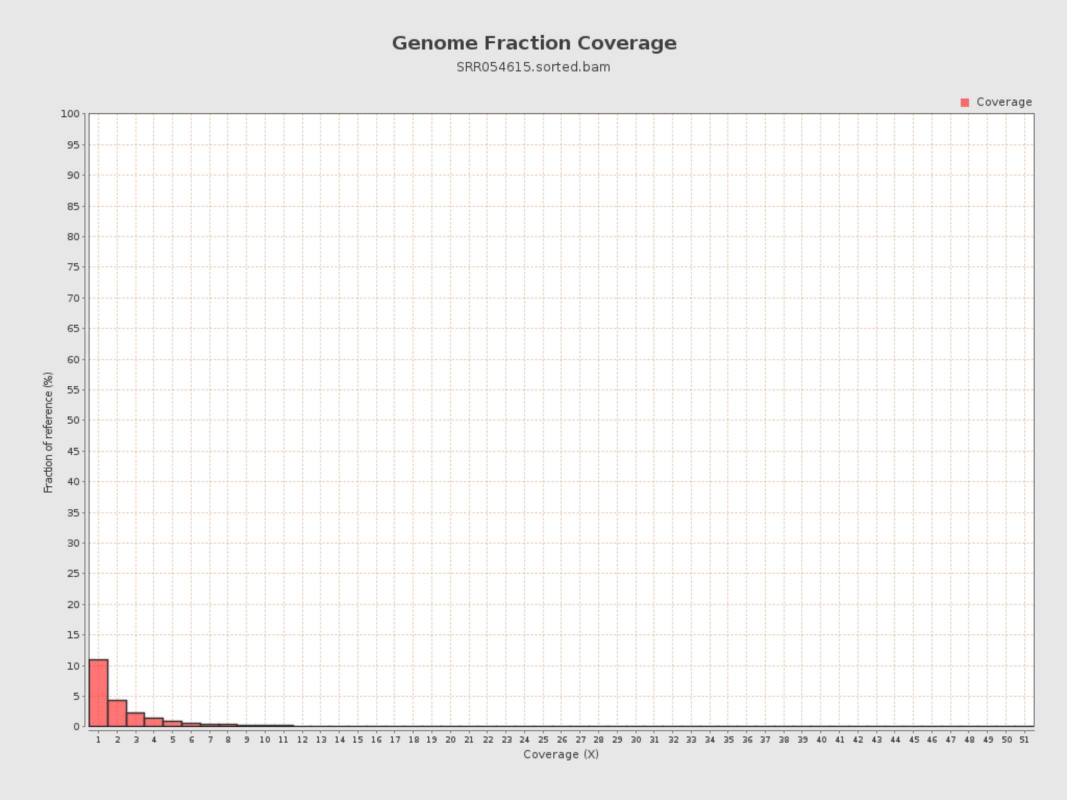
4. Results : Coverage Histogram



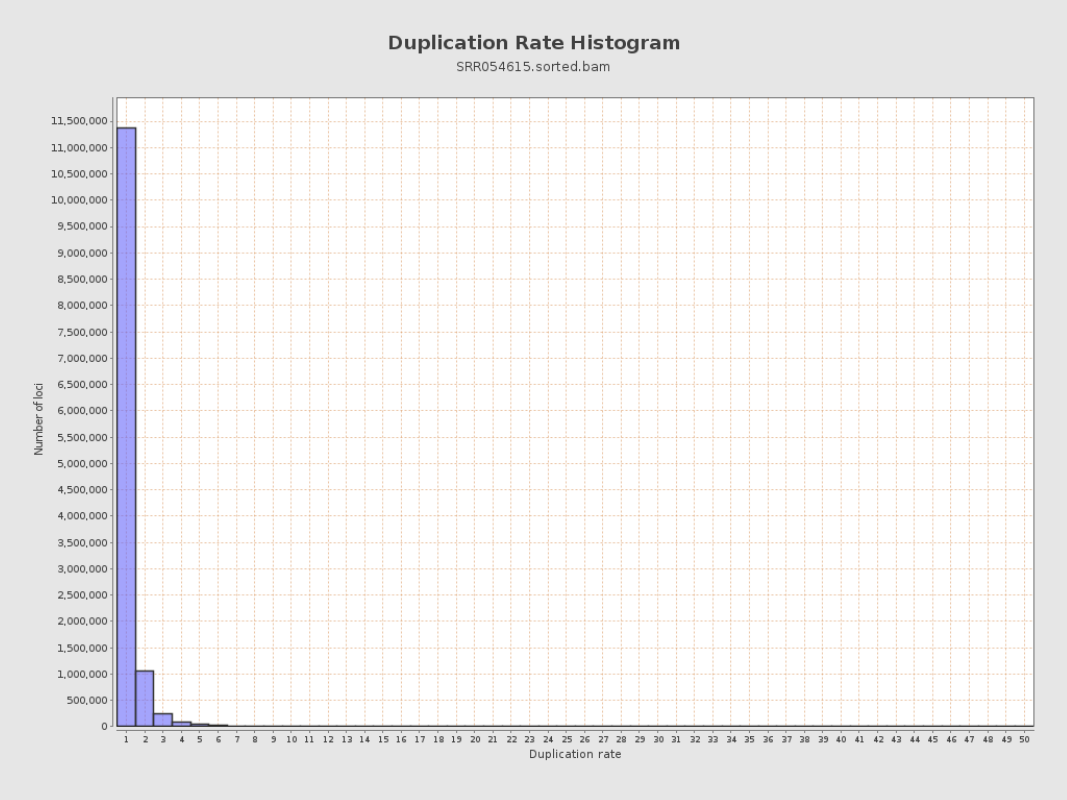
5. Results : Coverage Histogram (0-50X)



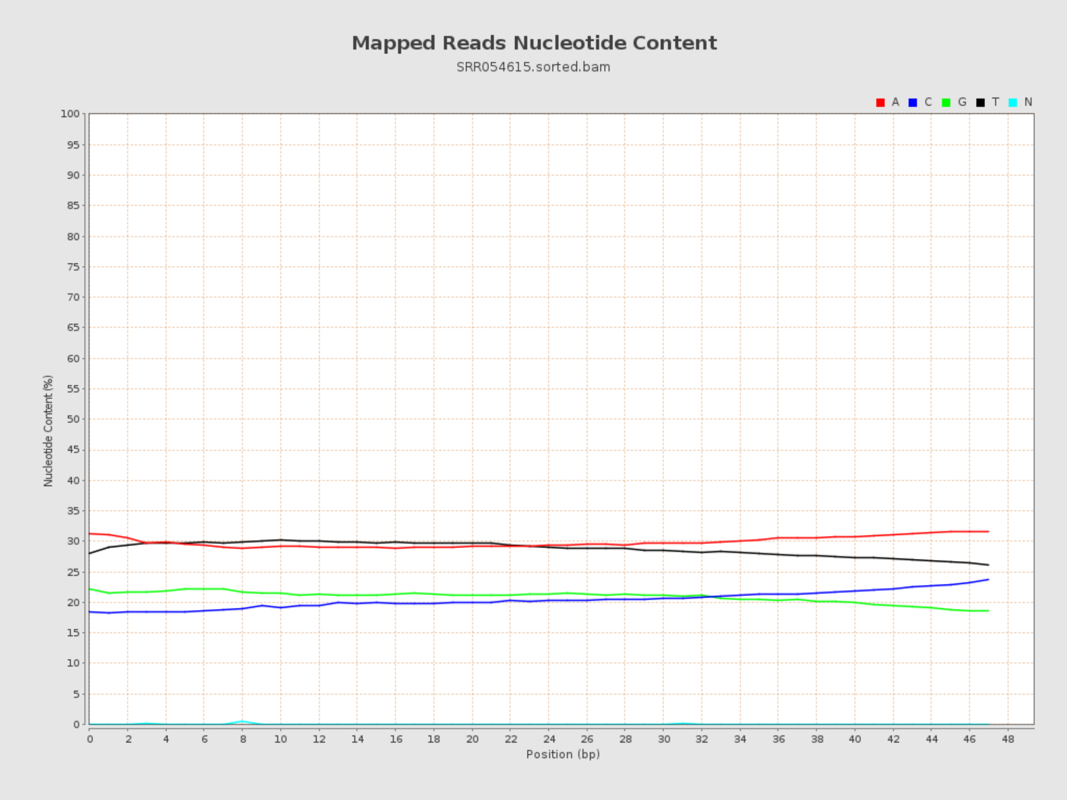
6. Results : Genome Fraction Coverage



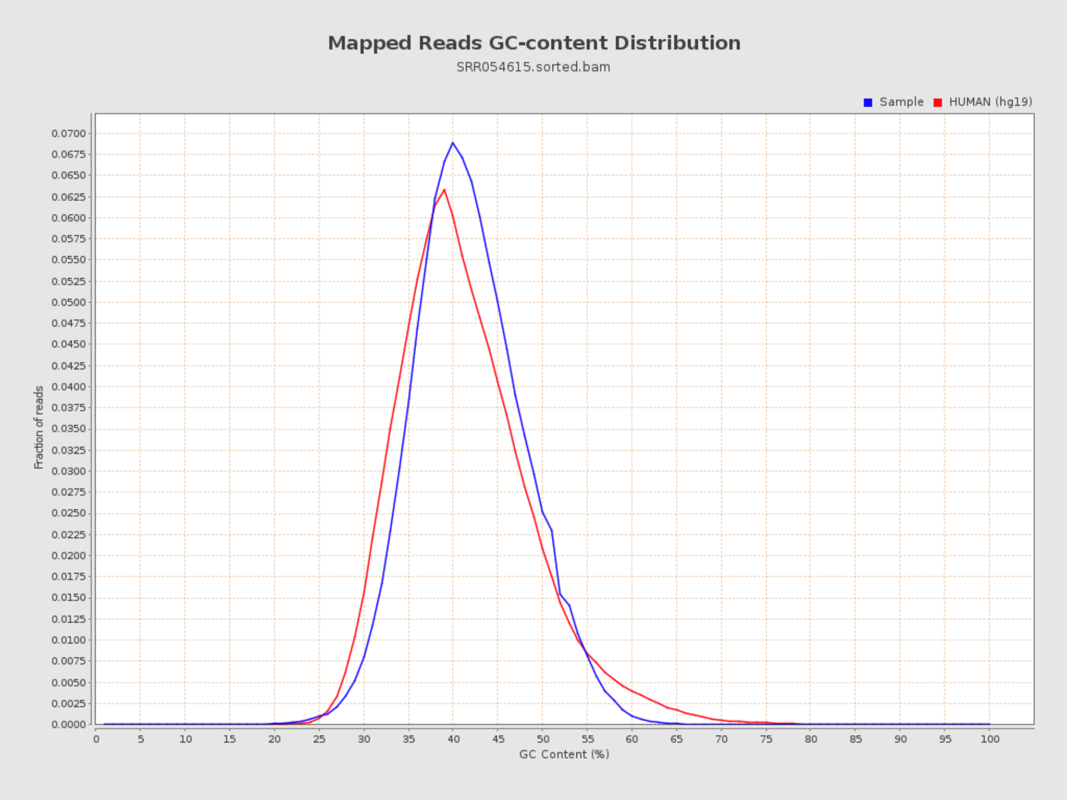
7. Results : Duplication Rate Histogram



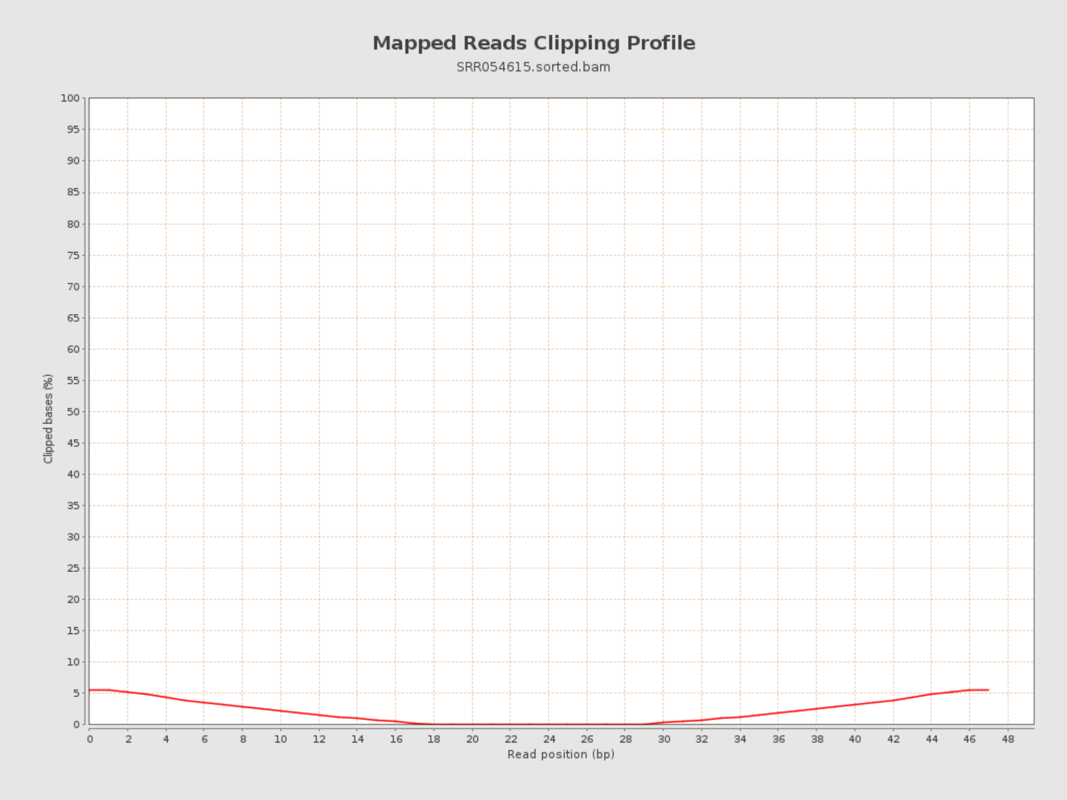
8. Results : Mapped Reads Nucleotide Content



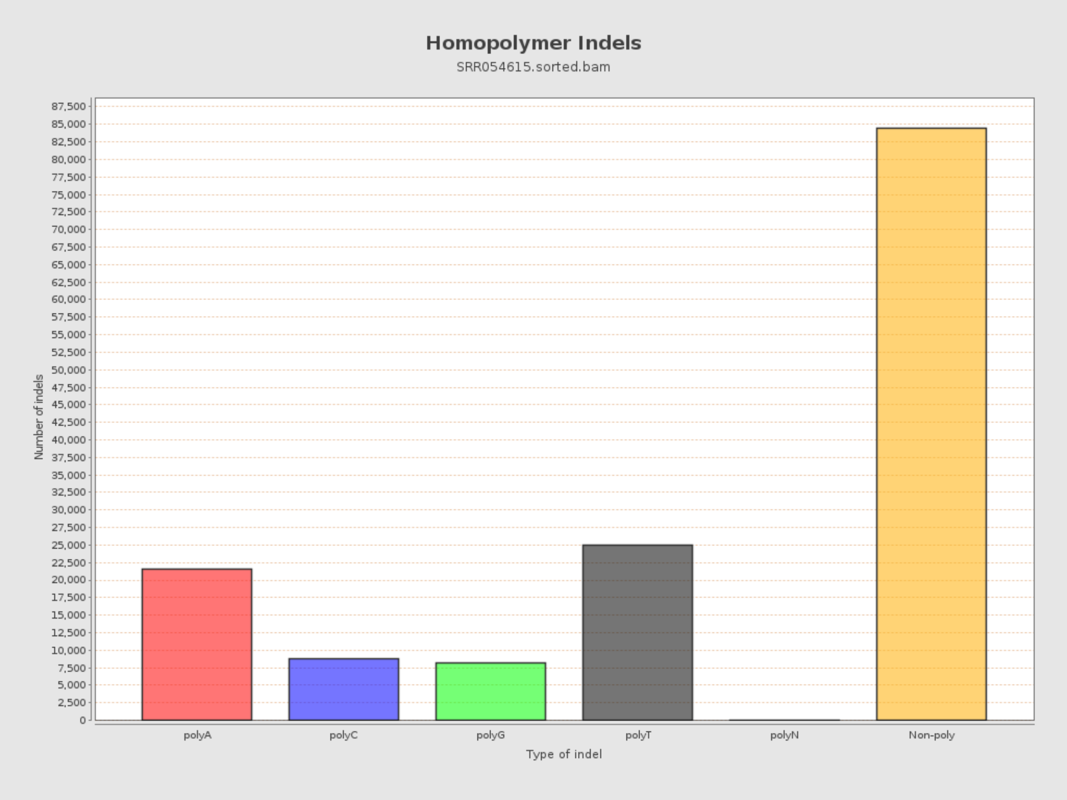
9. Results : Mapped Reads GC-content Distribution



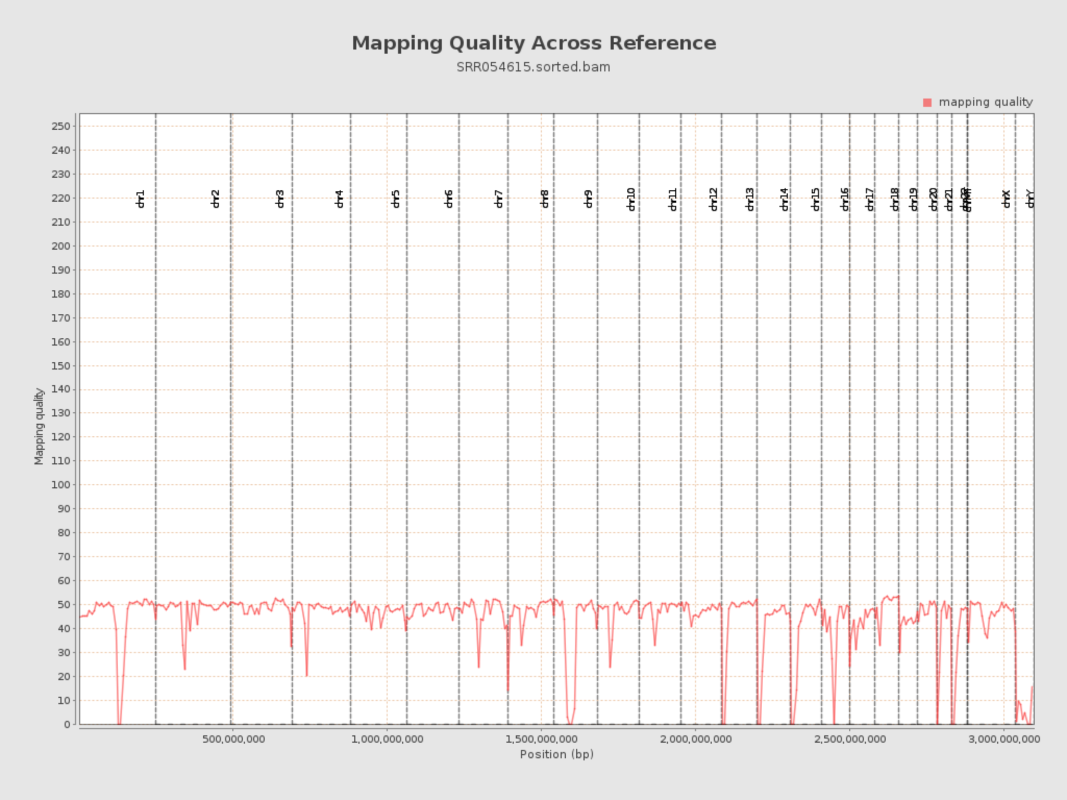
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram