Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 16:40:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089600.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_SRR089600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 16:40:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,620,644
Mapped reads	8,896,905 / 83.77%
Unmapped reads	1,723,739 / 16.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	393 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,491,566 / 23.46%
Duplication rate	20.76%
Clipped reads	936,713 / 8.82%

2.2. ACGT Content

Number/percentage of A's	131,896,049 / 31.52%
Number/percentage of C's	79,277,277 / 18.94%
Number/percentage of T's	116,081,601 / 27.74%
Number/percentage of G's	90,793,526 / 21.7%
Number/percentage of N's	428,444 / 0.1%
GC Percentage	40.64%

2.3. Coverage

Mean	0.1352

Standard Deviation	1.0277

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

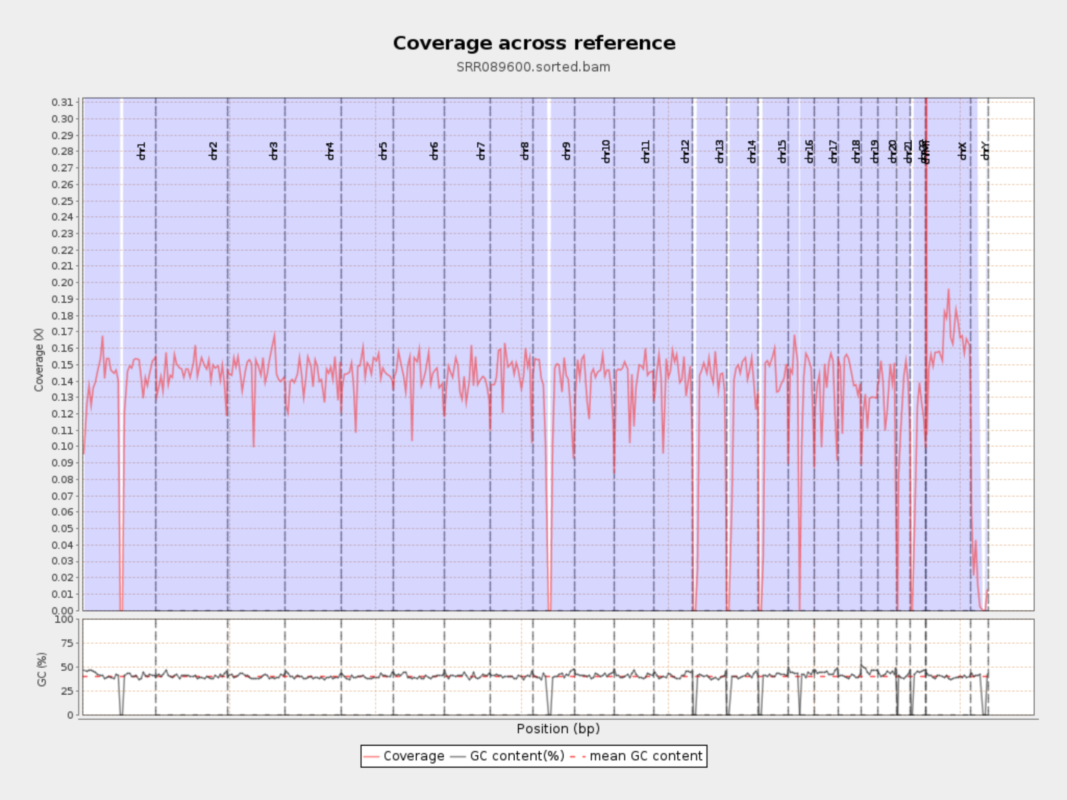
General error rate	0.58%
Mismatches	2,389,386
Insertions	17,978
Mapped reads with at least one insertion	0.2%
Deletions	56,261
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.95%

2.6. Chromosome stats

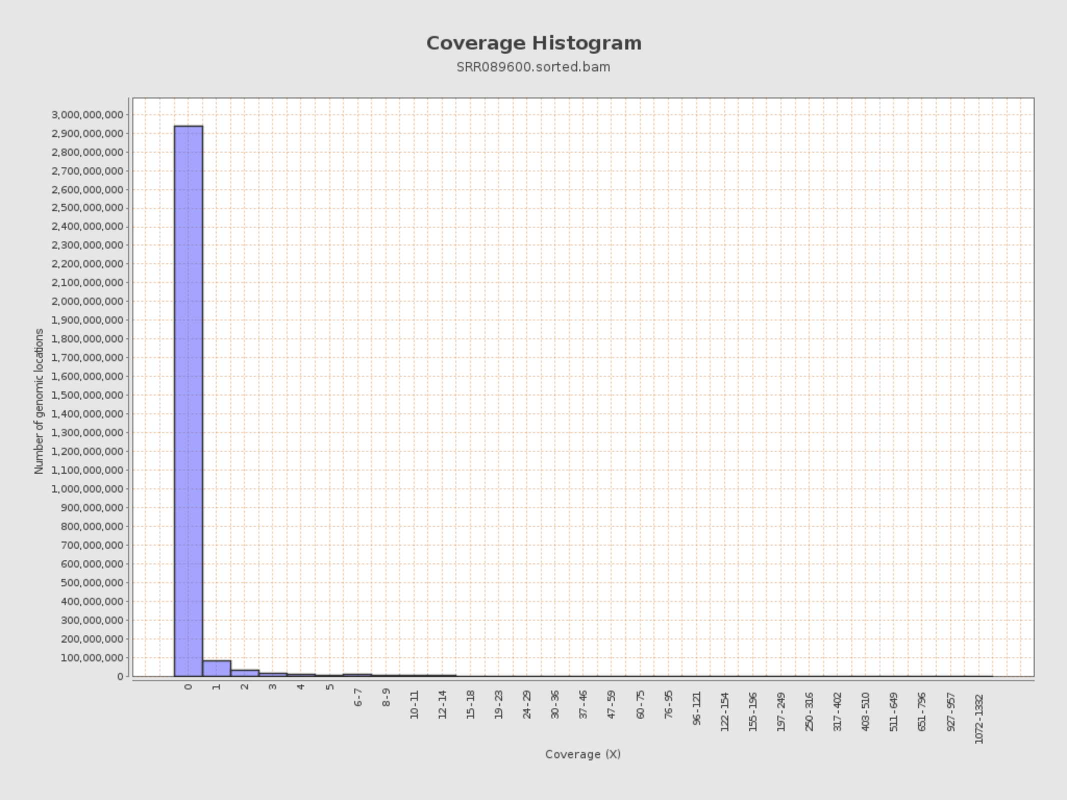
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33365579	0.1339	1.1016
chr2	243199373	35427842	0.1457	1.2065
chr3	198022430	28964801	0.1463	0.9987
chr4	191154276	27150777	0.142	1.011
chr5	180915260	26216867	0.1449	0.9984
chr6	171115067	24694929	0.1443	1.0316
chr7	159138663	22431118	0.141	1.0697

chr8	146364022	21259163	0.1452	1.2453
chr9	141213431	17133856	0.1213	0.9215
chr10	135534747	19299453	0.1424	1.0385
chr11	135006516	19076811	0.1413	1.0487
chr12	133851895	19073755	0.1425	0.9909
chr13	115169878	13811640	0.1199	0.9019
chr14	107349540	12965997	0.1208	0.9698
chr15	102531392	12019296	0.1172	0.8726
chr16	90354753	11522037	0.1275	0.9374
chr17	81195210	10952977	0.1349	0.9583
chr18	78077248	11062190	0.1417	1.0696
chr19	59128983	7383680	0.1249	0.9705
chr20	63025520	8498861	0.1348	0.9743
chr21	48129895	5398739	0.1122	0.9539
chr22	51304566	4489888	0.0875	0.7464
chrMT	16571	43856	2.6466	5.4615
chrX	155270560	25277663	0.1628	1.1087
chrY	59373566	1039557	0.0175	0.3274

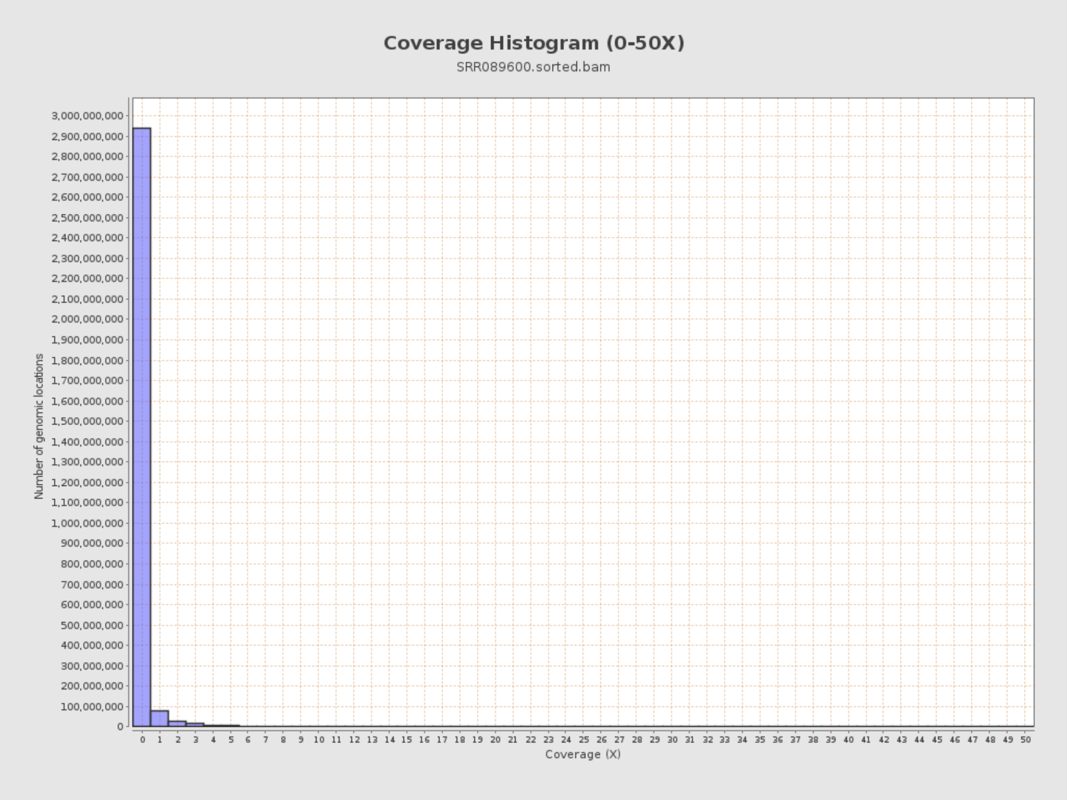
3. Results : Coverage across reference



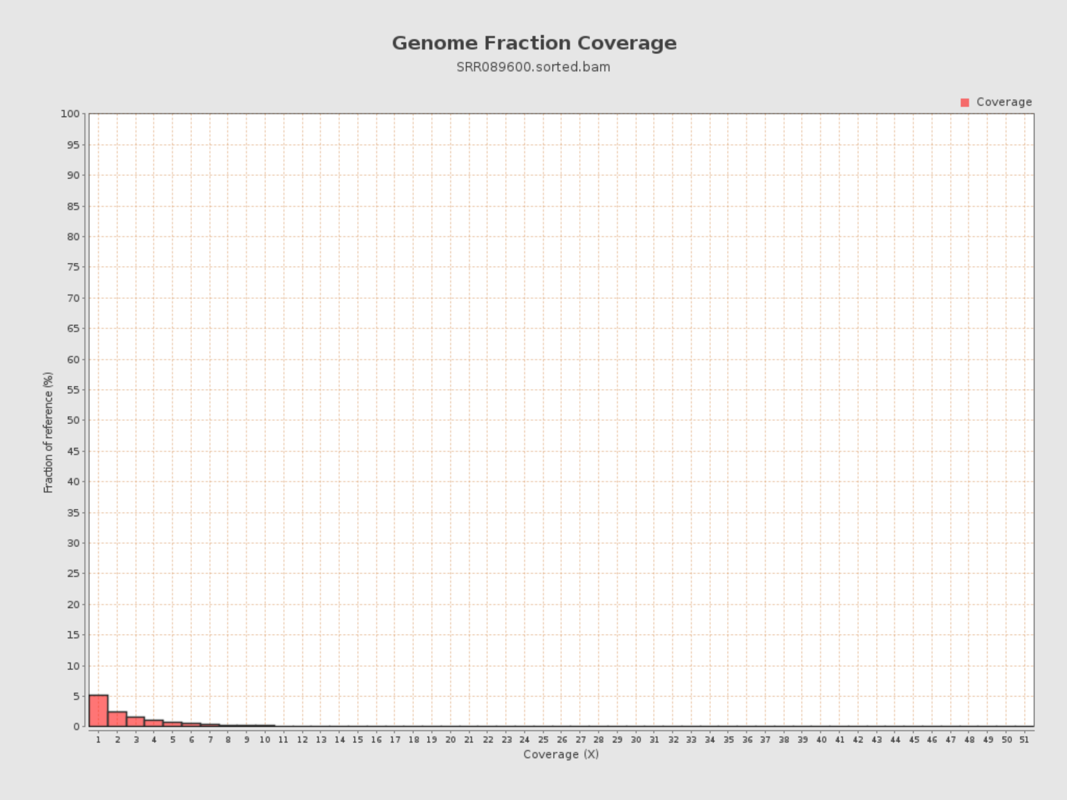
4. Results : Coverage Histogram



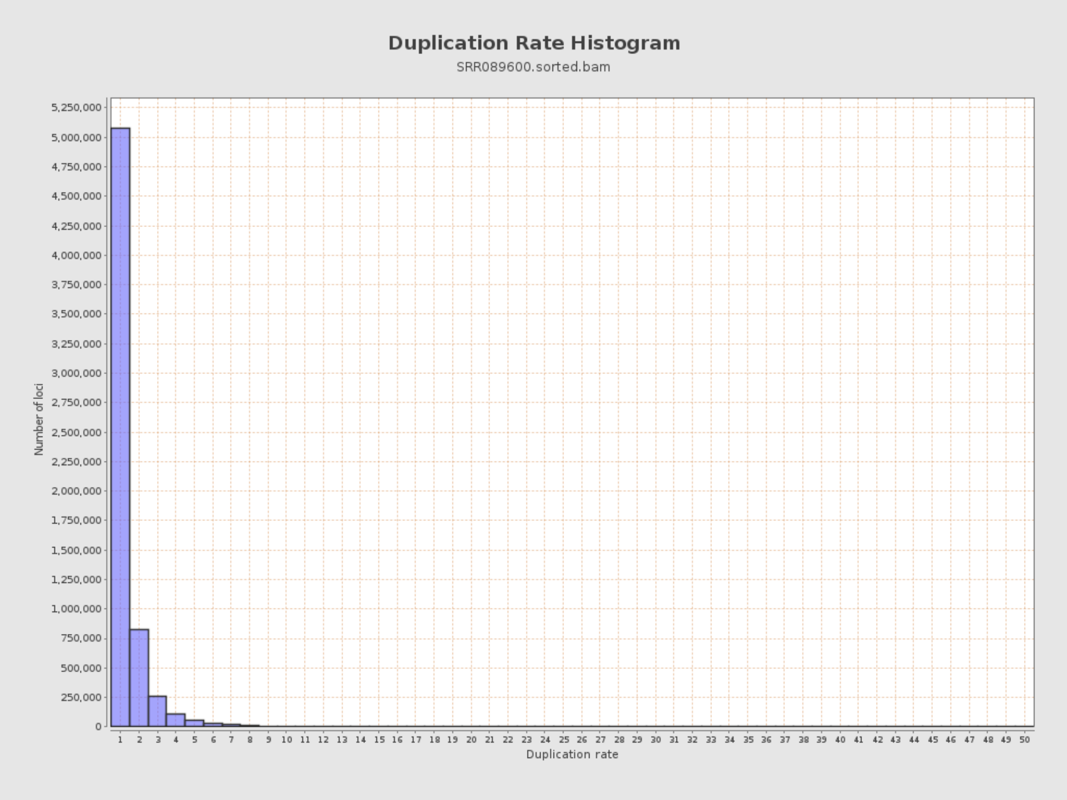
5. Results : Coverage Histogram (0-50X)



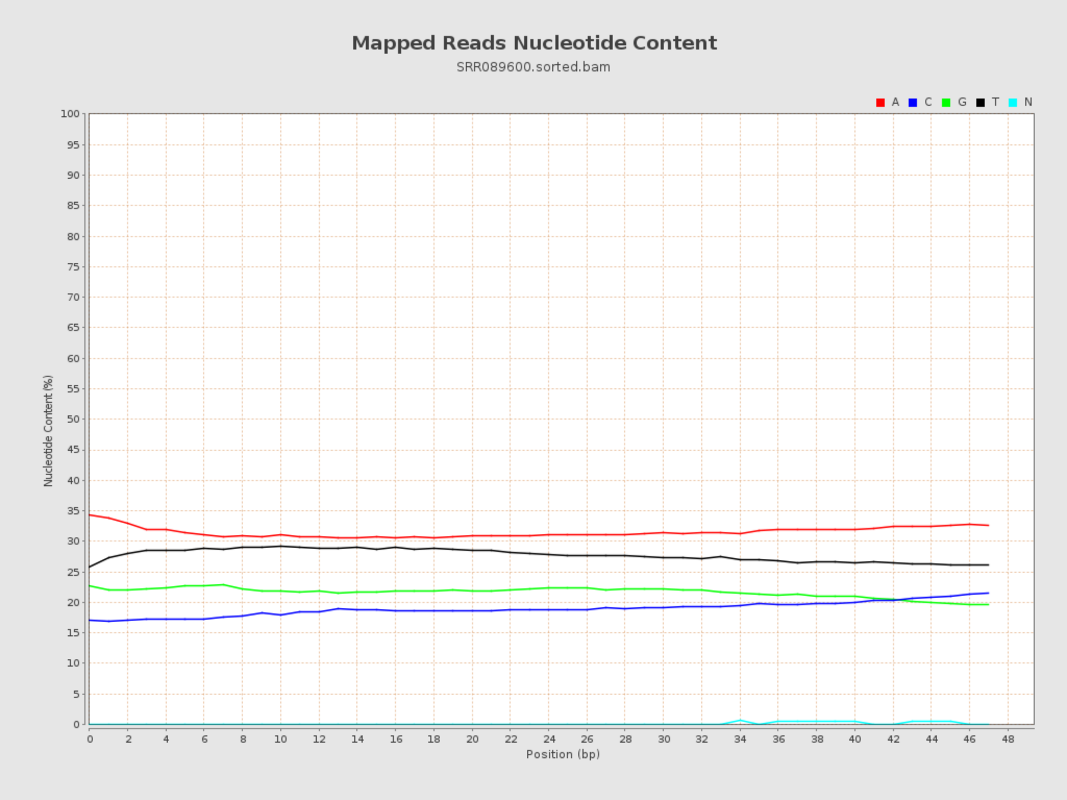
6. Results : Genome Fraction Coverage



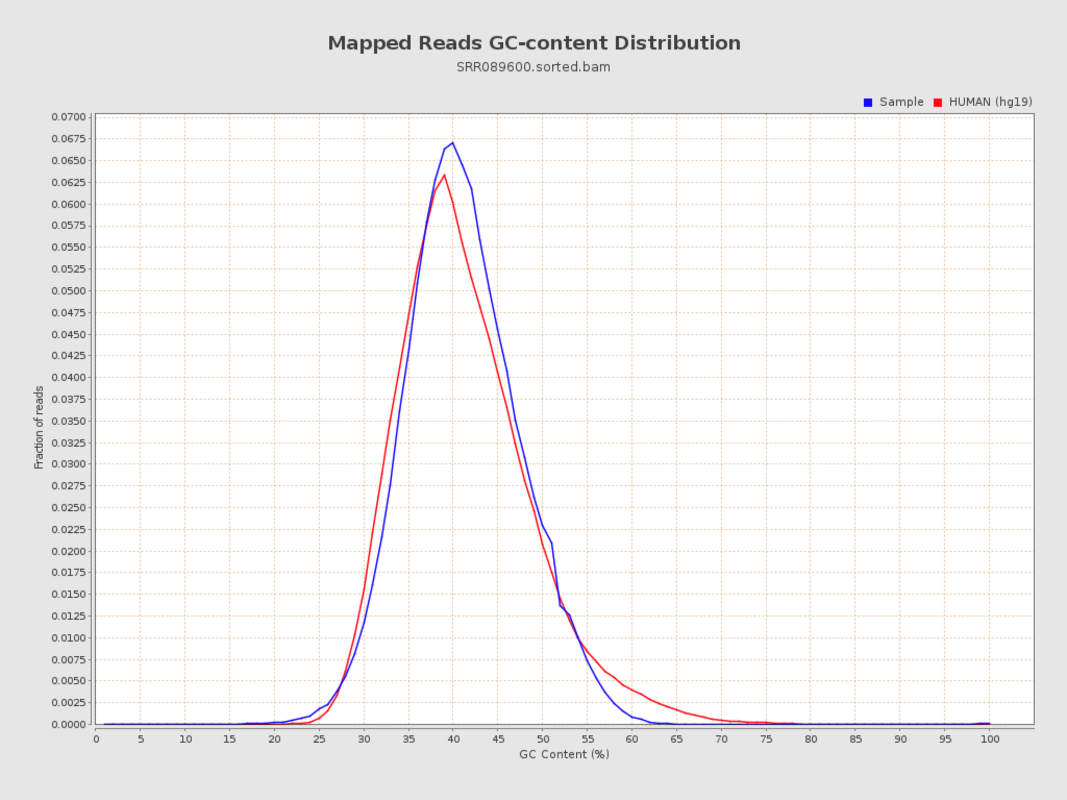
7. Results : Duplication Rate Histogram



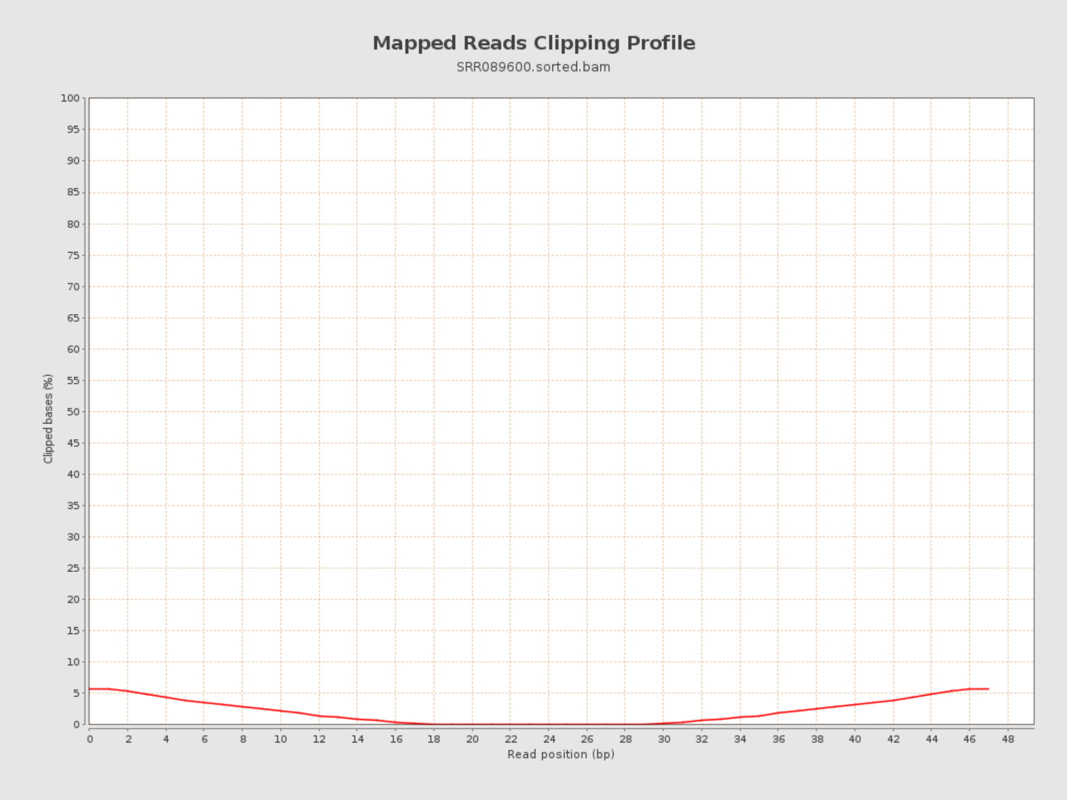
8. Results : Mapped Reads Nucleotide Content



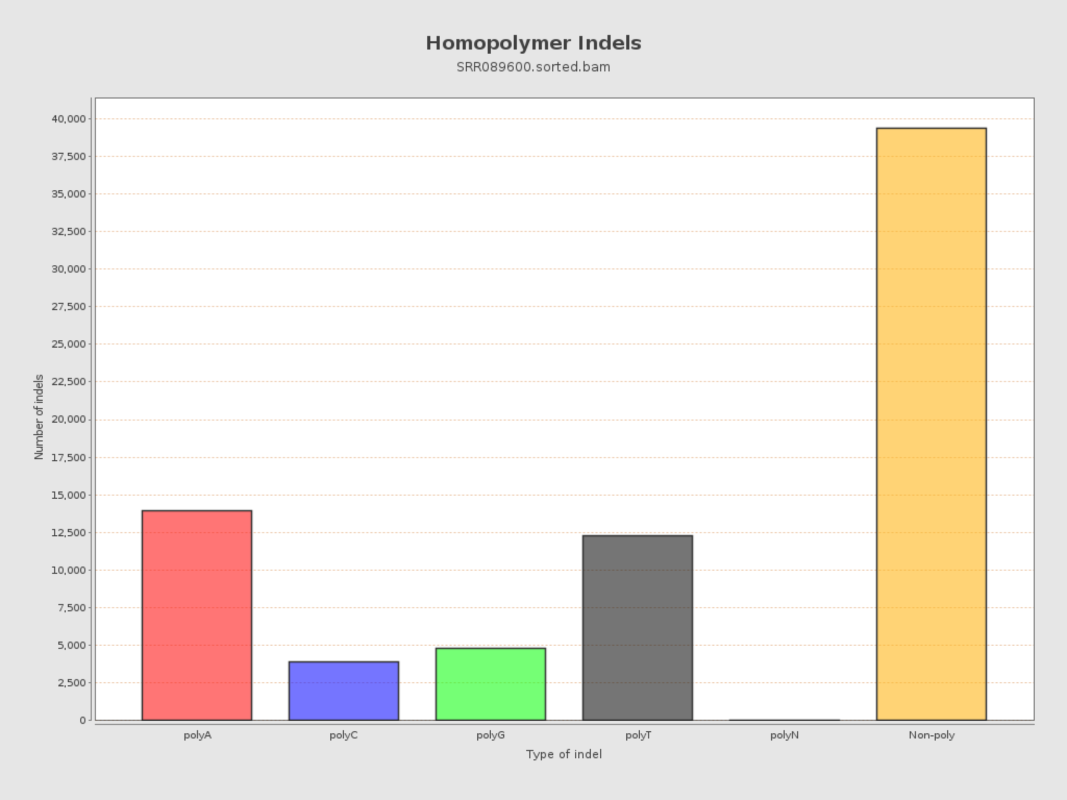
9. Results : Mapped Reads GC-content Distribution



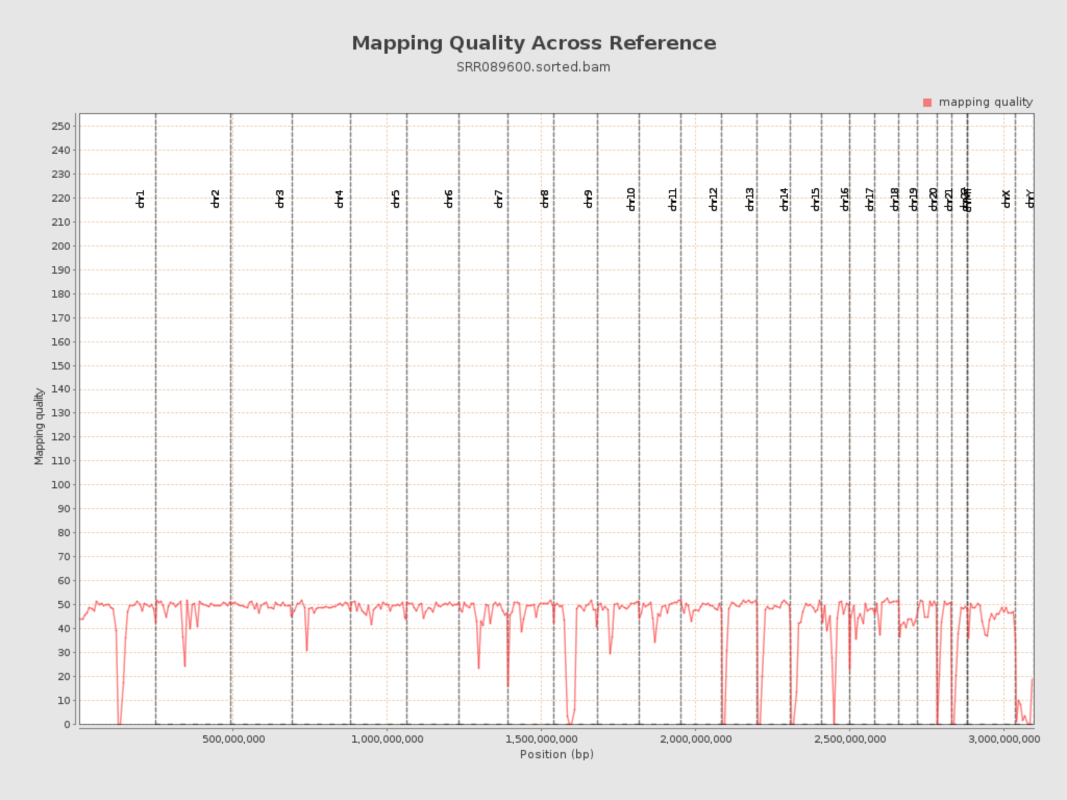
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram