Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 16:53:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089601.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_SRR089601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 16:53:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,712,347
Mapped reads	20,076,263 / 78.08%
Unmapped reads	5,636,084 / 21.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	843 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,891,813 / 7.36%
Duplication rate	7.1%
Clipped reads	4,117,096 / 16.01%

2.2. ACGT Content

Number/percentage of A's	282,990,178 / 30.63%
Number/percentage of C's	193,638,805 / 20.96%
Number/percentage of T's	251,579,440 / 27.23%
Number/percentage of G's	195,581,669 / 21.17%
Number/percentage of N's	106,803 / 0.01%
GC Percentage	42.13%

2.3. Coverage

Mean	0.2985

Standard Deviation	1.5692

2.4. Mapping Quality

Mean Mapping Quality	42.53

2.5. Mismatches and indels

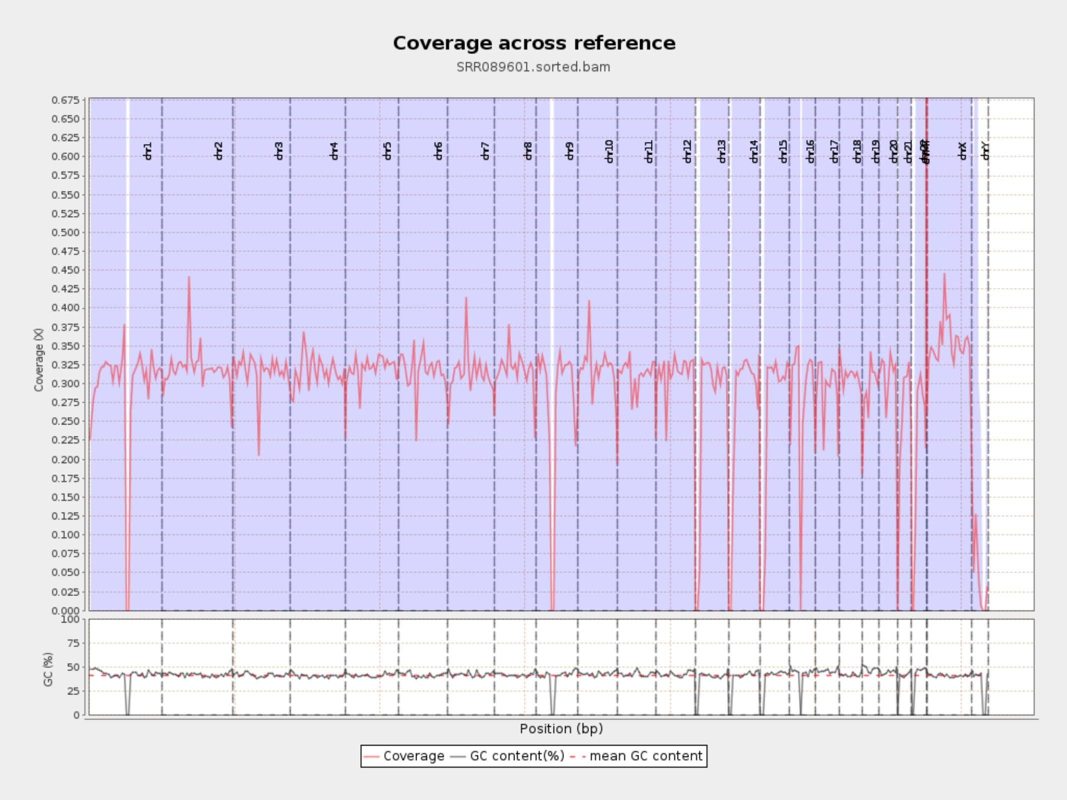
General error rate	0.45%
Mismatches	4,075,494
Insertions	41,583
Mapped reads with at least one insertion	0.21%
Deletions	121,699
Mapped reads with at least one deletion	0.6%
Homopolymer indels	42.29%

2.6. Chromosome stats

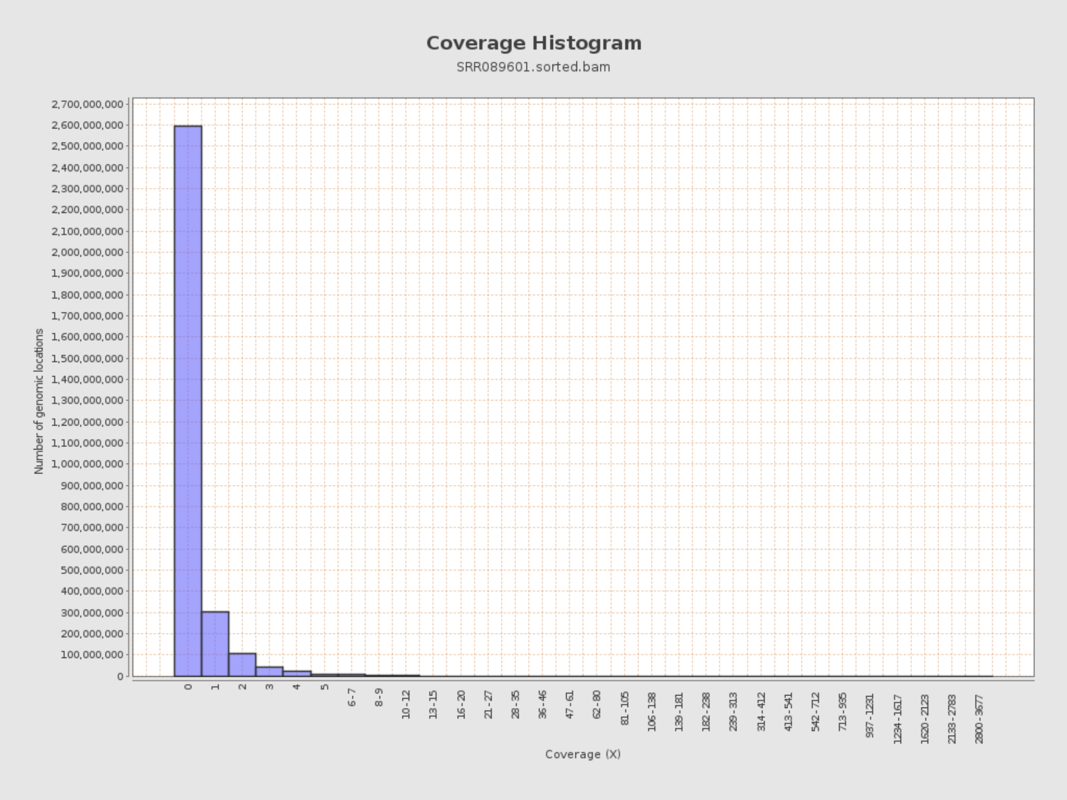
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	73265233	0.2939	2.4361
chr2	243199373	78116378	0.3212	1.9605
chr3	198022430	62787651	0.3171	0.968
chr4	191154276	60317524	0.3155	1.0565
chr5	180915260	58006300	0.3206	0.993
chr6	171115067	54368460	0.3177	1.1971
chr7	159138663	50291399	0.316	2.1787

chr8	146364022	46581950	0.3183	2.2878
chr9	141213431	38667328	0.2738	1.4846
chr10	135534747	43640644	0.322	1.5433
chr11	135006516	41930826	0.3106	1.5274
chr12	133851895	41880388	0.3129	1.0374
chr13	115169878	30175657	0.262	0.8863
chr14	107349540	28154571	0.2623	1.1683
chr15	102531392	25941264	0.253	0.8727
chr16	90354753	25578176	0.2831	1.0984
chr17	81195210	23680194	0.2916	1.1541
chr18	78077248	24290249	0.3111	2.432
chr19	59128983	17398606	0.2942	2.2024
chr20	63025520	19406818	0.3079	1.0771
chr21	48129895	11909816	0.2475	1.0739
chr22	51304566	10244963	0.1997	0.7835
chrMT	16571	27817	1.6787	2.5034
chrX	155270560	54751307	0.3526	1.3874
chrY	59373566	2664350	0.0449	0.6573

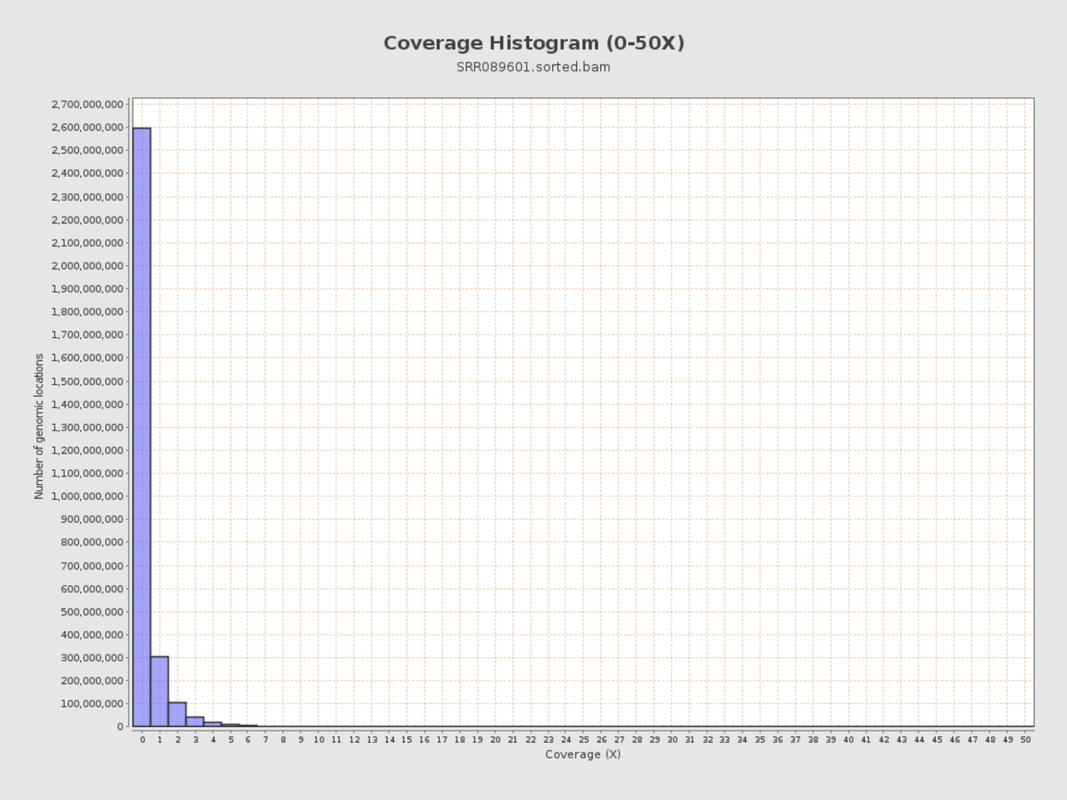
3. Results : Coverage across reference



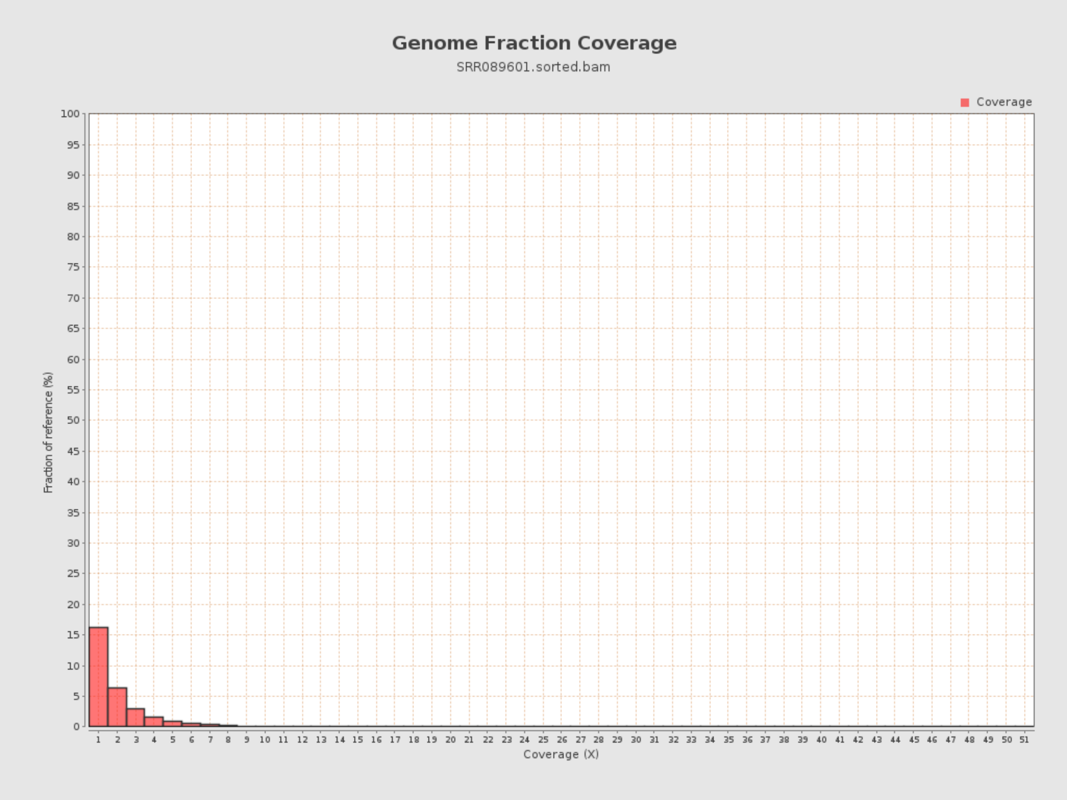
4. Results : Coverage Histogram



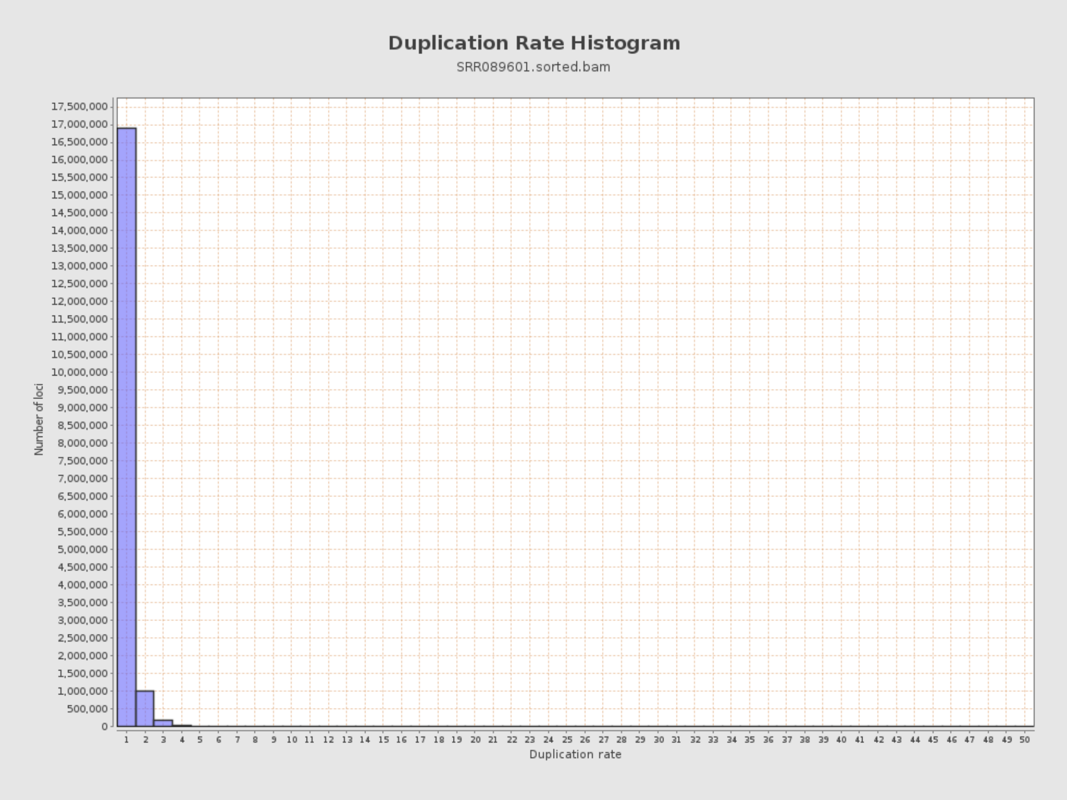
5. Results : Coverage Histogram (0-50X)



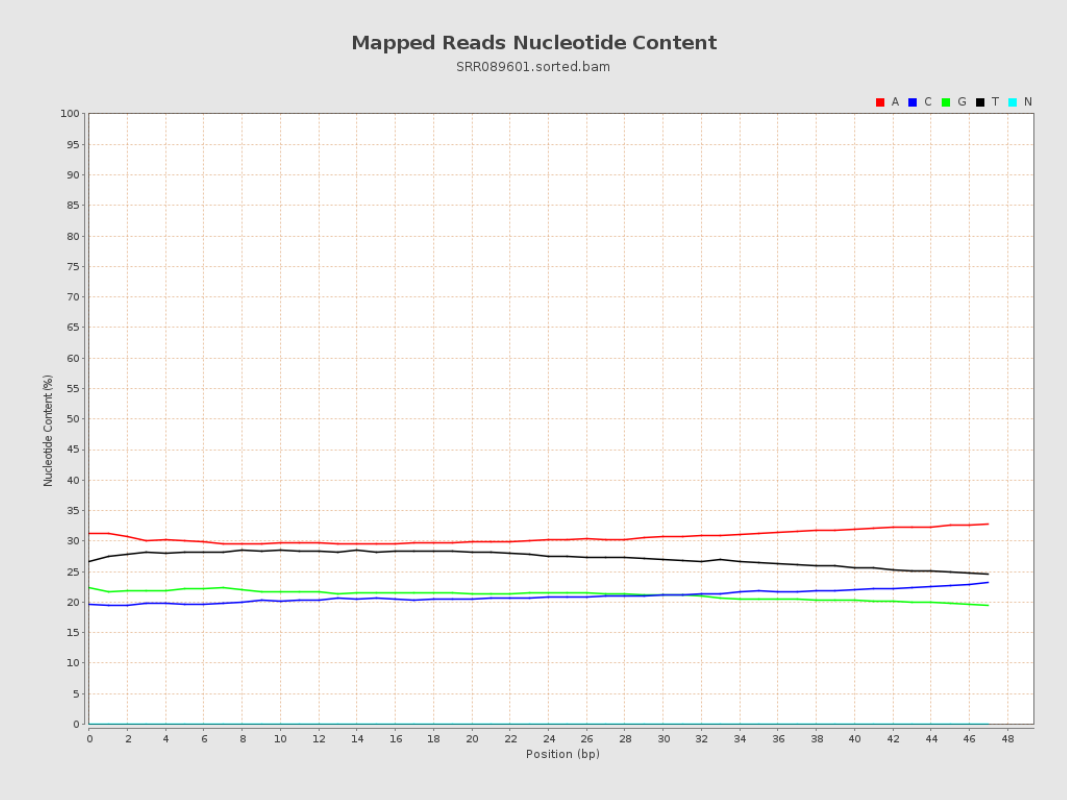
6. Results : Genome Fraction Coverage



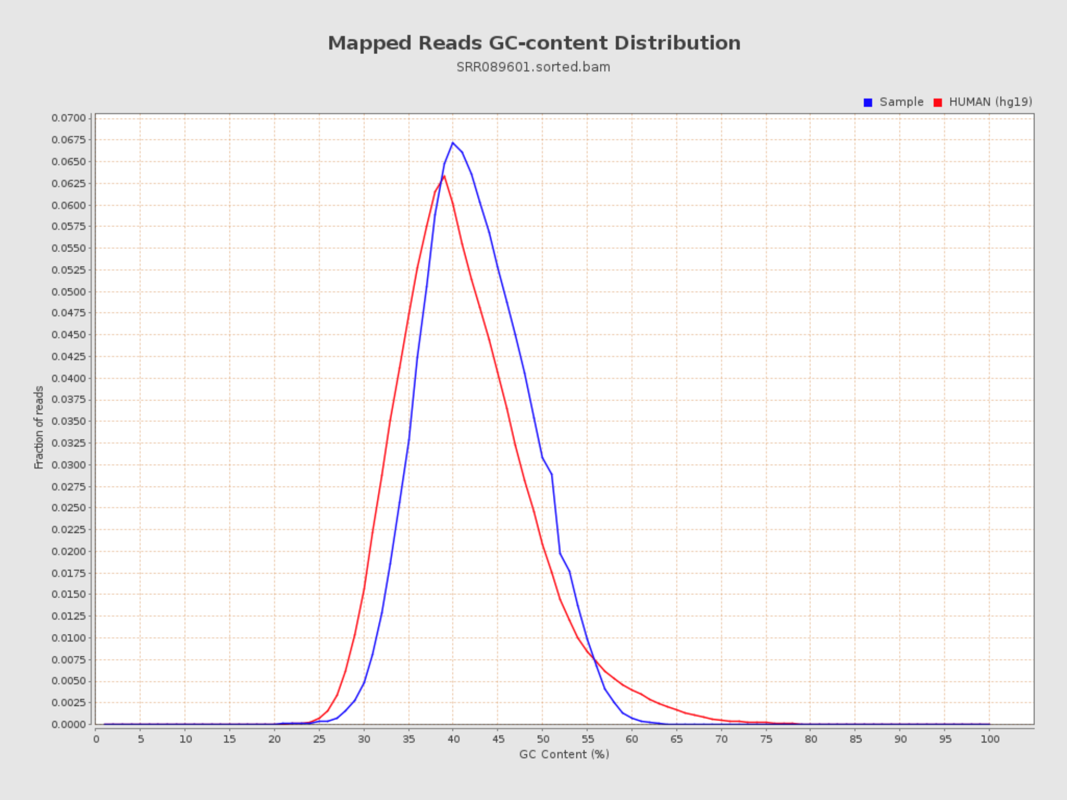
7. Results : Duplication Rate Histogram



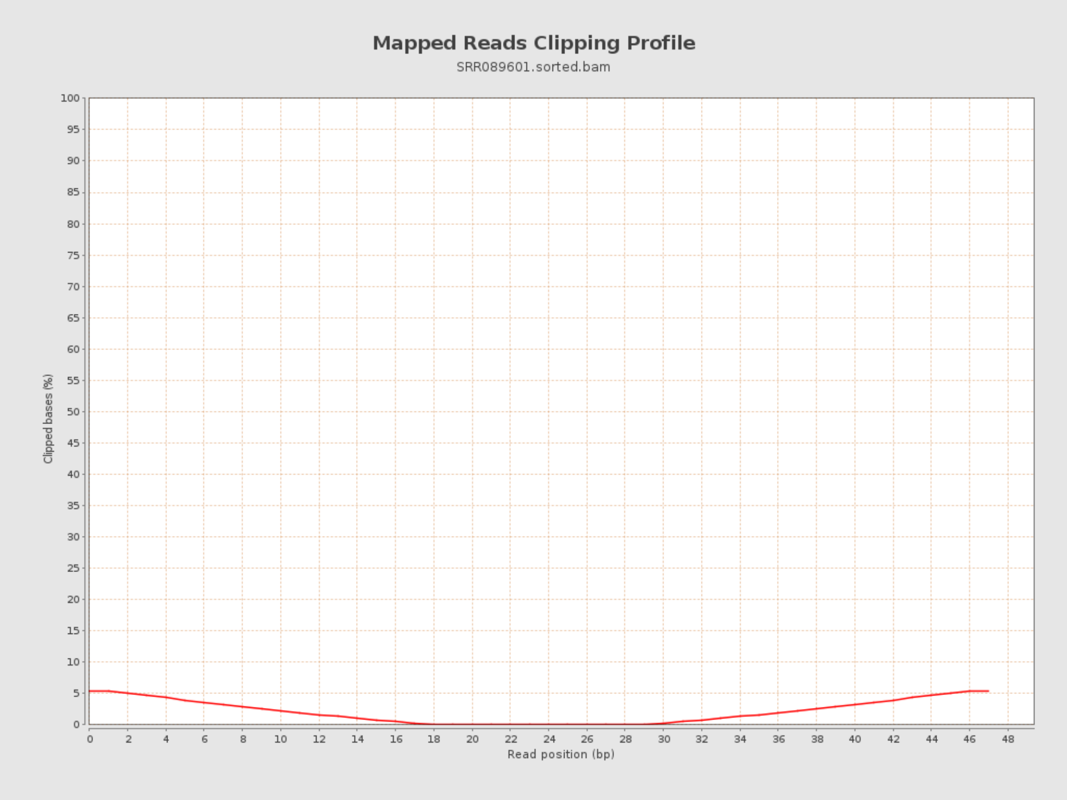
8. Results : Mapped Reads Nucleotide Content



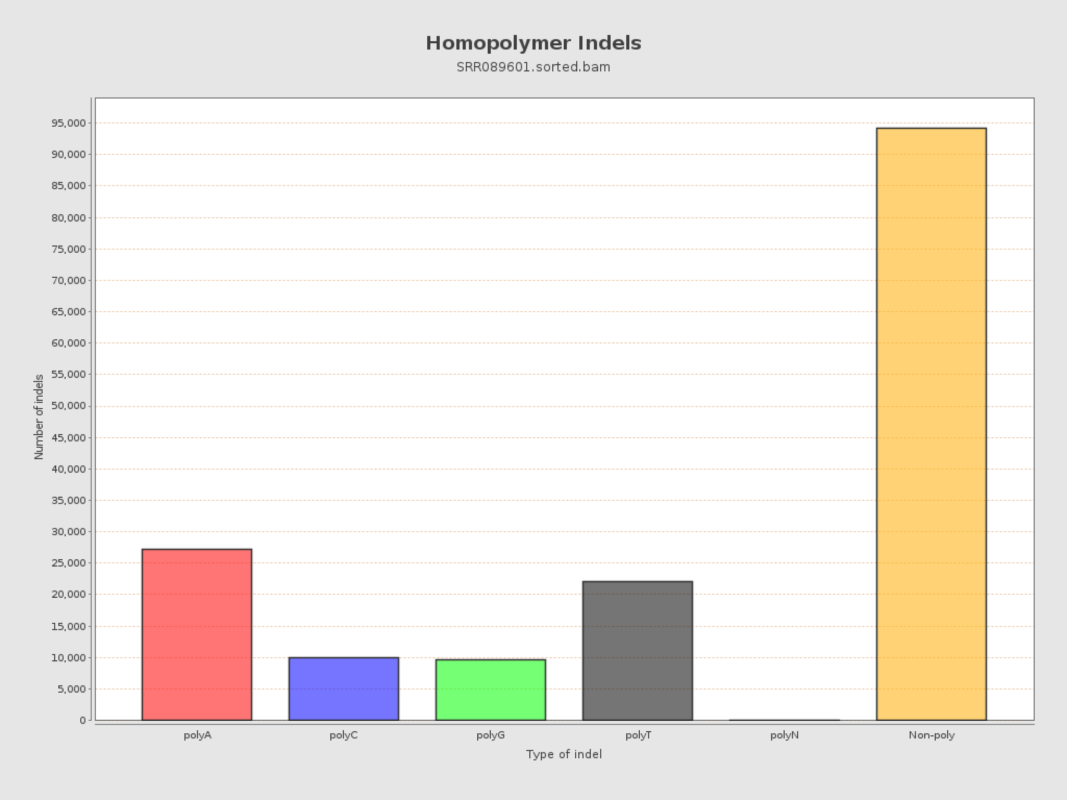
9. Results : Mapped Reads GC-content Distribution



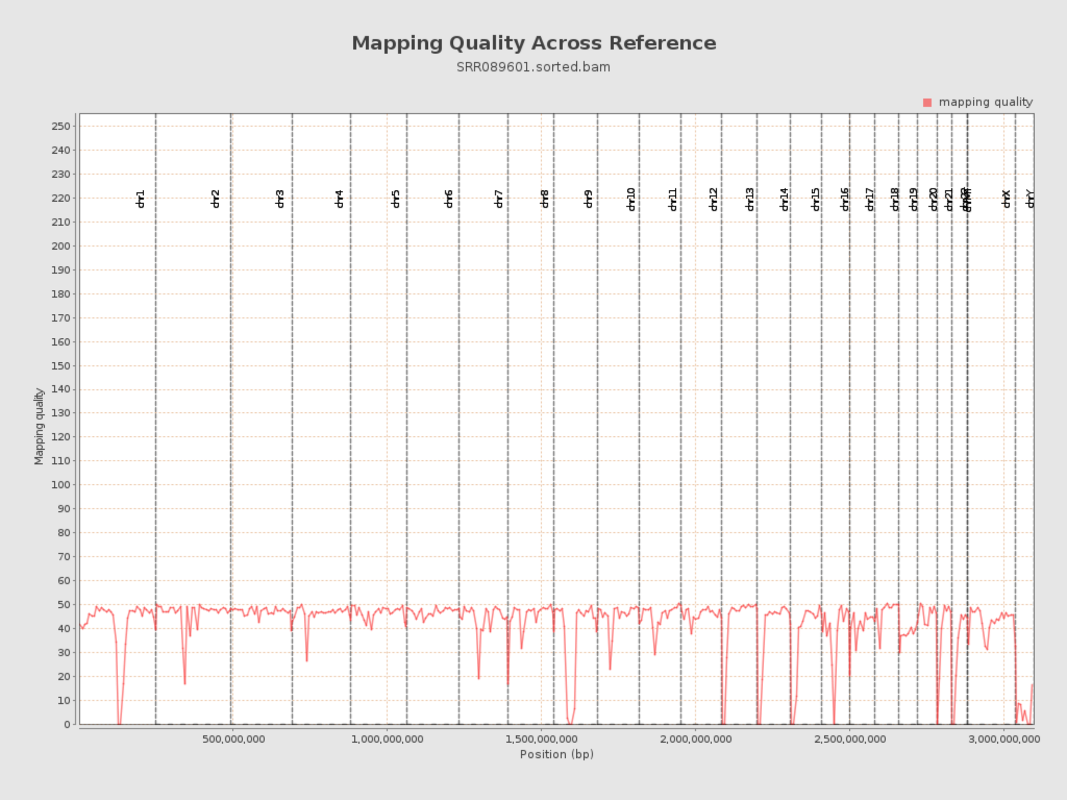
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram