中華民國 107 年 4 月 12 日

國立臺灣大學系統生物學研究中心
生物資訊核心實驗室
生物資訊服務收費標準

分析服務名稱	收費標準 **(NTD)**		分析服務說明
	校內	校外	
SNV/indel variant calling			**Output:** BAM + vcf
✧ Gene panel	1,000/sample	2,000/sample	Read mapping + variant calling + ANNOVAR
✧ Whole exome	2,000/sample	4,000/sample	Read mapping + variant calling + ANNOVAR
✧ Whole genome	5,000/sample	10,000/sample	Read mapping + variant calling + ANNOVAR
✧ Case/control analysis	2,000	4,000	
RNA-seq analysis			
✧ Quantification	2,000/sample	4,000/sample	Read mapping + quantification **Output:** mapping rate + pair-wise correlation
✧ Differential analysis	2,000	4,000	List of differential genes + GO analysis (if available) **Output:** list of DEG with GO terms
Non-coding RNA analysis			(with reference genomes)
✧ LncRNA quantification	2,000/sample	4,000/sample	Read mapping + quantification
✧ microRNA quantification	2,000/sample	4,000/sample	Read mapping + quantification
✧ piRNA analysis	2,000/sample	4,000/sample	piRNA candidacy filtering ping-pong cycle feature analysis piRNA annotation piRNA clustering
Transcriptome assembly			
✧ *De novo* assembly	5,000	10,000	Assembly by Trinity **Output:** FASTA sequences + summary + mapping rate
✧ Annotation	2,000 (single-species database)	4,000 (single-species database)	BLASTx against protein databases
ChIP-seq analysis			
✧ Peak calling	2,000/sample	4,000/sample	Read mapping + peak calling
✧ Peak annotation	2,000/sample	4,000/sample	Finding the nearest gene

✧ Case/control analysis	2,000	4,000	
✧ Motif analysis	2,000/sample	4,000/sample	Motif discovery + scanning
Metagenomics			
✧ Metagenomics	1,000/sample	2,000/sample	
Customized services			
✧ Pipeline design	1,000/hour	2,000/hour	
✧ Machine learning	1,000/hour	2,000/hour	
✧ NTU Galaxy tools	1,000/hour	2,000/hour	
✧ Script programming	1,000/hour	2,000/hour	

[Note] 20% off if the number of samples ≥20