HTSF Recommended Submission DNA and RNA and QAQC Values

Welcome! Below are guidelines on sample requirements when submitting to the HTSF.

You will find library input requirements for both RNA and DNA. Please follow the key below for information on our material type abbreviations.

Material Type Abbreviation Key

Input material Types:	Abbreviation
TRN	Total RNA
RN PE	Total RNA made from Formalin fixed Paraffin Embedded tissues
RN FF	Total RNA made from Fresh Frozen Tosses
RN LMD	Total RNA from Laser Microdissection
WG_DN	Whole Genomic DNA

RNA Library Preparation Input

Total RNA Seq Protocols	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Ribosomal Depletion for: Organisms Compatible	Special notes
Truseq Total RNA Seq with RZG	TRN	60	1750	29	RIN > 3, DV200 > 30%	HMR	Stranded
	RN PE						
	RN FF						
	RN LMD						
Roche Seq (Kapa) Total RNA Seq with RiboErase	TRN	60	1750	29	RIN > 3, DV200 > 30%	HMR	Stranded
	RN PE						
	RN FF						
Tecan Genomics Universal RNA Seq with NuQuant	TRN	20	700	35	RIN > 3, DV200 > 30%	**Inquire (Human, Mouse, arabidopsis thaliana, drosophila melanogaster)	Total RNA Assay, Non-Stranded, must be DNase Treated prior to prep (we can do this for an additional fee -- concentration will be lost).

		Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Ribosomal Depletion for: Organisms Compatible	Special notes
RNA Seq with NuQuant	RN PE				30%		
	RN FF						
Tecan Genomics Solo	TRN	25	10	0.40	RIN > 3, DV200 > 30%	**Inquire (Human, Mouse, arabidopsis thaliana, drosophila melanogaster)	**not able to be automated Works down to 0.01ng Must be DNase Treated
	RN PE						
	RN FF						
Tecan Genomics Trio	TRN	25	500	20	RIN > 3, DV200 > 30%	**Inquire (Human, Mouse, arabidopsis thaliana, drosophila melanogaster)	**preferred low-input option for large number of samples Works down to 0.5 ng input Must be DNase Treated
	RN PE						
	RN FF						

mRNA Seq Protocols	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Ribosomal Depletion for: Organisms Compatible	Special notes
Kapa mRNA	TRN	60	1750	29	RIN > 7		Stranded
	RN FF						
Kapa Hyper mRNA	TRN	25	250	10	RIN > 7		Non-Stranded
	RN FF						
SMART-HT + NexteraXT	TRN	7	5	1	RIN > 7		Non-Stranded
Tecan Genomics Universal mRNA Seq with NuQuant	TRN	60	1750	29	RIN > 7		Non-Stranded **not recommended** Many clients complain about results
Lexogen QuantSeq 3' mRNA-Seq Library Prep Kit FWD for Illumina	TRN	15	500	33	RIN >4		3' bias **not recommended due to high failure rate Works down to 0.1 ng
	RN PE		10	0.7			

RNA Exome Protocols	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Ribosomal Depletion for: Organisms Compatible	Special notes
Truseq RNA Exome	TRN						
	RN PE	25	250	10	RIN > 3, DV200 >		

	Input Material Type				Quality		
TruSeq RNA Exome		25	250	10	30%		
	RN FF						
	RN LMD						
SureSelect XT	TRN	25	600	24	RIN > 3, DV200 > 30%		special request
	RN PE						
	RN FF						

miRNA/small RNA Protocols	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Ribosomal Depletion for: Organisms Compatible	Special notes
BioO Scientific Nextflex small RNA	TRN	30	2000	67	NA		** works down to 1 ng, so submission concentration can be very low.
	RN PE			0.0			
	RN FF						
	RN LMD						
HTG miRNA	TRN	60	88	1.5	NA		**only detects KNOWN miRNA's
	RN PE						
	RN FF						

Two Library Preps with Single Aliquot Submission	Input Material Type	Min Submission Vol (ul) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Special notes
Total RNA (TruSeq Ribo Zero Gold) + Small RNA (BioO Next Flex)	TRN	25	1.5ng	2ug	RIN > 3, DV200 > 30%	
mRNA (Kapa) + Small RNA (BioO Next Flex)	TRN	25	1.5ng	2ug	RIN > 3, DV200 > 30%	

DNA Library Preparation Input						
DNA Protocols	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Special notes
Kapa Hyper (DNA)	Whole Genome DNA	60	2000	33.33	Optimal with full sized genome fragments	*Covaris Sonication Preferred prep for most applications

	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Special notes
Tecan Genomics (NUGEN) Celero	Whole Genome DNA	30	1500	50.00	Optimal with full sized genome fragments	*Enzymatic Fragmentation Preferred for PCR-Free Assays
Thruplex DNA Seq	Whole Genome DNA	25	30	1.20	Optimal with full sized genome fragments	*Optimal for low-input for materials such as PCR Products, ChIP DNA, FAIRE-Seq DNA, Cut-and-Run, etc *works down to 0.050ng
Nextera XT	Whole Genome DNA	15	3	0.20	Optimal for small genomes, plasmids, cDNA	*fragmenting via tagmentation
NexteraFlex	Whole Genome DNA	90	1500	16.67	Optimal with full sized genome fragments	*fragmenting via tagmentation

DNA Exome	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Special notes
Kapa Hyper + IDT xGEN Lockdown Probes	Whole Genome DNA	60	2000	33.33	Optimal with full sized genome fragments	Human and Mouse
Kapa Target Enrichment **replaces Roche SeqCap	Whole Genome DNA	60	1500	25.00	>3 DIN	Human and Mouse
SureSelectXT Low Input (enzymatic fragmentation)	Whole Genome DNA	20	500	25.00	>3 DIN	Custom Human, Human, and Mouse
SureSelectXT Low Input (sonication fragmentation)	Whole Genome DNA	60	500	8.33	>3 DIN	Custom Human, Human, and Mouse
SureSelectXT v10	Whole Genome DNA	30	850	28.33	na	Custom Human, can work with as little as 75ng in 25ul

16S, 18S, ITS	Input Material Type	Min Submission Vol (uL) required	Optimal Submission ng (total ng)	Optimal Submission ng/uL (Optimal Conc)	Quality	Special notes
16S	Whole Genome DNA	15	30	2.00	>3 DIN	In-house custom primers for amplicon sequencing

18S	Whole Genome DNA	15	30	2.00	>3 DIN	Customer Supplied custom primers for amplicon sequencing
ITS	Whole Genome DNA	15	30	2.00	>3 DIN	In-house custom primers for amplicon sequencing