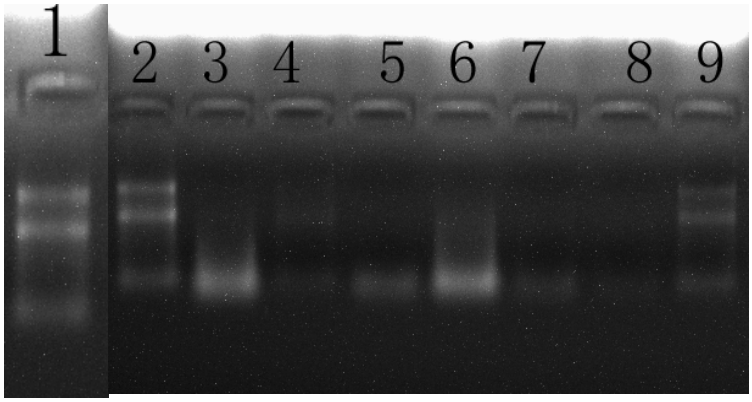
RNA QC

1. RNA Quantification and Quality Assurance by NanoDrop ND-1000

Sample ID	OD260/280 Ratio	OD260/230 Ratio	Conc. (ng/µl)	Volume (µl)	Quantity (ng)	QC Purity Pass or Fail
IR1	2.00	1.89	799.02	30	23970.60	Pass
IR2	2.00	1.93	848.80	30	25464.00	Pass
IR3	1.94	1.84	277.20	20	5544.00	Pass
IN1	1.70	1.87	87.16	20	1743.20	Pass
IN2	1.89	1.84	113.93	15	1708.95	Pass
IN3	2.03	1.97	804.81	40	32192.40	Pass
NI1	1.82	1.82	112.32	15	1684.80	Pass
NI2	1.77	1.38	70.87	15	1063.05	Pass
NI3	2.01	1.99	522.39	20	10447.80	Pass

*For spectrophotometer, the O.D. A260 /A280 ratio should be close to 2.0 for pure RNA (ratios between 1.8 and 2.1 are acceptable). The O.D. A260/A230 ratio should be more than 1.8.

2. RNA Integrity and gDNA contamination test by Denaturing Agarose Gel Electrophoresis



Lane 1: Total RNA of sample IR1
Lane 2: Total RNA of sample IR2
Lane 3: Total RNA of sample IR3
Lane 4: Total RNA of sample IN1
Lane 5: Total RNA of sample IN2
Lane 6: Total RNA of sample IN3
Lane 7: Total RNA of sample NI1
Lane 8: Total RNA of sample NI2
Lane 9: Total RNA of sample NI3

*The 28S and 18S ribosomal RNA bands should be fairly sharp, intense bands. The intensity of the upper band should be about twice that of the lower band. Smaller, more diffuse bands representing low molecular weight RNAs (tRNA and 5S ribosomal RNA) may be present. It is normal to see a diffuse smear of ethidium bromide staining material migrating between the 18S and 28S ribosomal bands, probably comprised of mRNAand other heterogeneous RNA species. DNA contamination of the RNA preparation will be evident as a high molecular weight smear or band migrating above the 28S ribosomal RNA band. Degradation of the RNA will be reflected by smearing of ribosomal RNA bands.

3.Quality Assessment of Sequencing Library

Sequencing library was determined by Agilent 2100 Bioanalyzer using the Agilent DNA 1000 chip kit (Agilent, part # 5067-1504)

Sample Name	Size (bp)	Conc. (ng/μl)	Conc. (nmol/L)	Volume (μl)**	Total Amount (ng)
IR1	376	6.03	24.3	10	60.3
IR2	473	6.33	20.3	10	63.3
IR3	286	6.6	35	10	66
IN1	313	6.06	29.4	10	60.6
IN2	283	5.86	31.4	10	58.6
IN3	382	8.82	34.9	10	88.2
NI1	339	6.41	28.6	10	64.1
NI2	374	11.7	47.4	10	117
NI3	390	7.01	27.2	10	70.1

**The libraries were adjusted to 10nM before cluster generatio