

Sample name	Raw reads	Clean reads	Raw bases	Clean bases	Error rate (%)	Q20(%)	Q30(%)	GC content(%)
Aged FHV24-1	43181358	41531914	6.5G	6.2G	0.03	97.62	93.32	48.55
Aged FHV24-2	43835068	42879432	6.6G	6.4G	0.03	97.41	92.77	46.78
Aged FHV24-3	41306752	40294296	6.2G	6G	0.03	97.52	93.01	47.27
Aged FHV48-1	43643790	42993982	6.5G	6.4G	0.03	97.35	92.7	47.85
Aged FHV48-2	47676076	46626088	7.2G	7G	0.03	97.93	94.02	47.78
Aged FHV48-3	48076860	46938414	7.2G	7G	0.03	97.9	93.99	48.51
Aged Non-inf-1	42640642	41754964	6.4G	6.3G	0.03	97.59	93.26	48.79
Aged Non-inf-2	45245250	44009154	6.8G	6.6G	0.03	97.58	93.3	48.24
Aged Non-inf-3	48714724	47447696	7.3G	7.1G	0.03	97.77	93.72	47.81
Aged Tris24-1	47657110	46618452	7.1G	7G	0.03	97.76	93.66	48.95
Aged Tris24-2	52770316	51865854	7.9G	7.8G	0.03	97.69	93.52	48.71
Aged Tris24-3	44515816	43390554	6.7G	6.5G	0.03	97.58	93.25	48.49
Aged Tris48-1	42122914	41067454	6.3G	6.2G	0.03	97.55	93.18	49.19
Aged Tris48-2	38879250	38104700	5.8G	5.7G	0.03	97.84	93.74	48.85
Aged Tris48-3	44595486	43635216	6.7G	6.5G	0.03	97.57	93.15	47.16
Young FHV24-1	46225316	45062656	6.9G	6.8G	0.03	97.62	93.25	47.3
Young FHV24-2	38577182	37691062	5.8G	5.7G	0.03	97.62	93.32	48.45
Young FHV24-3	43430650	42233746	6.5G	6.3G	0.03	97.39	92.85	48.08
Young FHV48-1	41222318	39901114	6.2G	6G	0.03	97.41	92.89	49.47
Young FHV48-2	39984078	39169108	6G	5.9G	0.03	97.63	93.31	49.28
Young FHV48-3	42843394	41931260	6.4G	6.3G	0.03	97.58	93.2	49.07
Young Non-inf-1	43123072	41715218	6.5G	6.3G	0.03	97.27	92.61	48.95
Young Non-inf-2	43597424	42037394	6.5G	6.3G	0.03	97.7	93.49	48.98
Young Non-inf-3	43279546	42197994	6.5G	6.3G	0.03	97.59	93.28	48.81
Young Tris24-1	58677044	56381882	8.8G	8.5G	0.03	97.42	92.9	48.78
Young Tris24-2	41739006	40412126	6.3G	6.1G	0.03	97.52	93.13	48.32
Young Tris24-3	47251712	45596772	7.1G	6.8G	0.03	97.45	92.99	48.03
Young Tris48-1	39189084	38102524	5.9G	5.7G	0.03	97.44	92.96	48.16
Young Tris48-2	42894488	41332648	6.4G	6.2G	0.03	97.41	92.86	47.9
Young Tris48-3	41444186	40134822	6.2G	6G	0.03	97.48	92.99	48.31

Table S4. RNA seq samples quality control.

Raw Reads: the original sequencing reads counts

Clean Reads: number of reads after filtering

Raw Bases: raw reads number multiply read length, saved in G unit

Clean Bases: clean reads number multiply read length, saved in G unit

Error Rate: average sequencing error rate, which is calculated by $Q_{phred} = -10\log_{10}(e)$

Q20: percentages of bases whose correct base recognition rates are greater than 99% in total bases

Q30: percentages of bases whose correct base recognition rates are greater than 99.9% in total bases

GC content: percentages of G and C in total bases