

Supplementary Table S1 Sample sequencing data quality summary

sample	library	raw_reads	raw_bases	clean_reads	clean_bases	error_rate	Q20	Q30	GC_pct
C_1	FRAS210258659-1r	49097042	7.36G	47650494	7.15G	0.03	97.88	93.88	41.05
C_2	FRAS210258660-1r	42127470	6.32G	40544014	6.08G	0.03	97.7	93.57	41.01
C_3	FRAS210258661-1r	46371834	6.96G	44471790	6.67G	0.03	97.97	94.13	41.18
AL_1	FRAS210258662-1r	41323968	6.2G	39800440	5.97G	0.03	97.87	93.9	42.58
AL_2	FRAS210258663-1r	40454688	6.07G	38052958	5.71G	0.03	97.84	93.88	41.02
AL_3	FRAS210258664-1r	46349704	6.95G	44197066	6.63G	0.03	97.77	93.66	40.97
AH_1	FRAS210258665-1r	45810688	6.87G	44109468	6.62G	0.03	97.87	93.92	41.35
AH_2	FRAS210258666-1r	45386156	6.81G	43704576	6.56G	0.03	97.84	93.84	41.31
AH_3	FRAS210258667-1r	46681954	7G	44892200	6.73G	0.03	97.81	93.75	41.27
LL_1	FRAS210258668-1r	43477412	6.52G	41949060	6.29G	0.03	97.82	93.78	41.36
LL_2	FRAS210258669-1r	47259564	7.09G	45180382	6.78G	0.03	97.85	93.89	41.33
LL_3	FRAS210258670-1r	42716292	6.41G	41326010	6.2G	0.03	97.82	93.78	41.29
LH_1	FRAS210258671-1r	44999236	6.75G	43251306	6.49G	0.03	97.76	93.69	41
LH_2	FRAS210258672-1r	46979878	7.05G	45059198	6.76G	0.03	97.82	93.81	40.95
LH_3	FRAS210258673-1r	45758748	6.86G	43979916	6.6G	0.03	97.77	93.69	40.93

Note: raw_Reads: the number of reads in the raw data, clean_Reads: the number of filtered reads of the raw data, clean_Bases: base number of filtered raw data

(clean base = clean reads * 150bp), error_Rate: overall sequencing error rate of data, Q20: percentage of bases with phred value greater than 20 in total bases,

Q30: percentage of bases with phred value greater than 30 in total bases, GC_PCT: percentage of G and C in four bases of clean reads.