

Table S2 Cassava transcriptome sequencing data and alignment results

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Clean Bases (Gb)	Clean Reads Q30 (%)	Total Mapping(%)	Uniquely Mapping(%)
CKKU1	45.44	44.26	6.64	93.75	55.58	53.33
CKKU2	45.44	44.14	6.62	94.44	87.21	84.73
CKKU3	45.44	44.11	6.62	93.83	62.65	60.3
CKSC1	45.44	43.85	6.58	94.01	52.45	51.04
CKSC2	45.44	44.27	6.64	94.18	75.01	72.47
CKSC3	45.44	44.5	6.67	93.75	67.69	65.76
PG10hKU1	45.44	44.27	6.64	93.77	63.82	62.05
PG10hKU2	45.44	44.12	6.62	94.29	77.31	75.17
PG10hKU3	45.44	44.15	6.62	94.47	78.06	75.9
PG10hSC1	47.19	45.48	6.82	94.6	36.12	35.09
PG10hSC2	45.44	44.17	6.62	93.88	65.98	63.93
PG10hSC3	45.44	44.15	6.62	94.05	27.21	26.43
PG24hKU1	45.44	43.91	6.59	93.94	72.87	70.57
PG24hKU2	45.44	43.93	6.59	94.25	39.42	38.34
PG24hKU3	45.44	43.99	6.6	94.02	49.2	47.84
PG24hSC1	47.19	45	6.75	94.28	34.95	33.95
PG24hSC2	45.44	44.15	6.62	93.69	46.37	45.01
PG24hSC3	47.19	45.37	6.81	94.08	35.08	34
PG2hKU1	47.19	45.43	6.81	94.1	40.4	39.31
PG2hKU2	45.44	44.28	6.64	94.06	82.68	80.35
PG2hKU3	45.44	44.3	6.65	94.25	86.35	83.92
PG2hSC1	47.19	45.39	6.81	93.8	43.32	42.09
PG2hSC2	45.44	43.9	6.58	93.61	65.96	64.02
PG2hSC3	45.44	43.9	6.59	93.91	54.13	52.59
PG48hKU1	47.19	45.18	6.78	94.52	62.02	60.08
PG48hKU2	45.44	43.96	6.59	94.26	79.96	77.62
PG48hKU3	47.19	45.46	6.82	93.84	34.11	33.23
PG48hSC1	45.44	43.91	6.59	93.5	31.34	30.48
PG48hSC2	45.44	43.99	6.6	93.77	48.79	47.27
PG48hSC3	45.44	44.32	6.65	93.44	67.42	65.37
PG6hKU1	45.44	44.08	6.61	94.36	77.98	75.59
PG6hKU2	47.19	45.35	6.8	94.19	40.89	39.77
PG6hKU3	47.19	45.5	6.83	93.79	42.88	41.63
PG6hSC1	45.44	43.9	6.59	94.33	24.75	24.03
PG6hSC2	45.44	44.03	6.6	94.28	44.52	43.09
PG6hSC3	45.44	43.99	6.6	94.16	29.38	28.57