

Table S1. Read quality statistics

Sample	Total	Raw	Total	Clean	Total	Clean	Clean Reads	Clean Reads	Clean Reads
	Reads (M)		Reads (M)		Bases(Gb)		Q20(%)	Q30(%)	Ratio(%)
C1	45.44		43.16		6.47		97.53	92.69	94.99
C2	45.44		43.53		6.53		97.63	92.89	95.80
C3	43.69		42.02		6.30		97.63	92.92	96.19
T11	45.44		43.44		6.52		97.78	93.31	95.61
T12	45.44		43.37		6.51		97.73	93.19	95.44
T13	45.44		43.23		6.48		97.97	93.70	95.14
T21	45.44		43.24		6.49		97.98	93.69	95.16
T22	45.44		42.40		6.36		97.91	93.62	93.31
T23	43.69		42.34		6.35		97.81	93.24	96.90
T31	43.69		42.09		6.31		97.77	93.15	96.35
T32	43.69		42.14		6.32		97.92	93.55	96.45
T33	43.69		42.02		6.30		98.03	93.84	96.18
T41	45.44		43.58		6.54		97.91	93.50	95.90
T42	45.44		43.28		6.49		97.90	93.52	95.25
T43	45.44		43.47		6.52		97.91	93.58	95.68

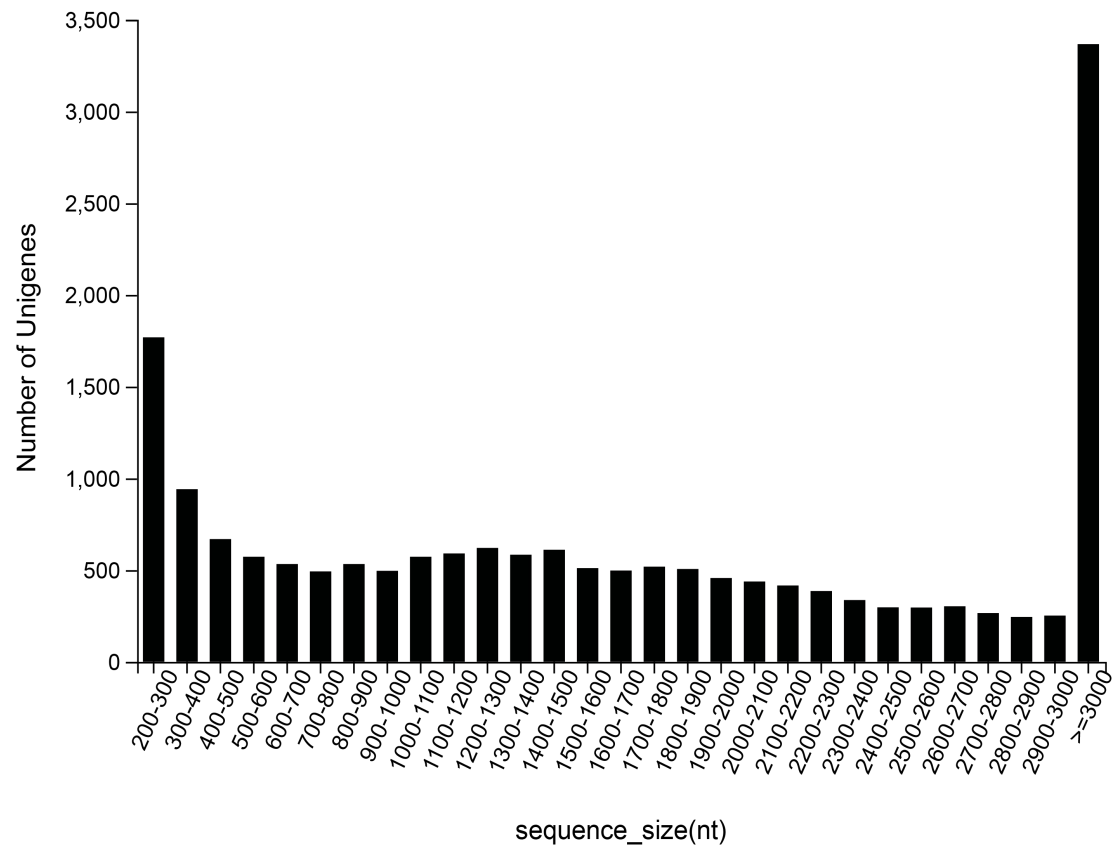


Fig. S1 Unigene length distribution

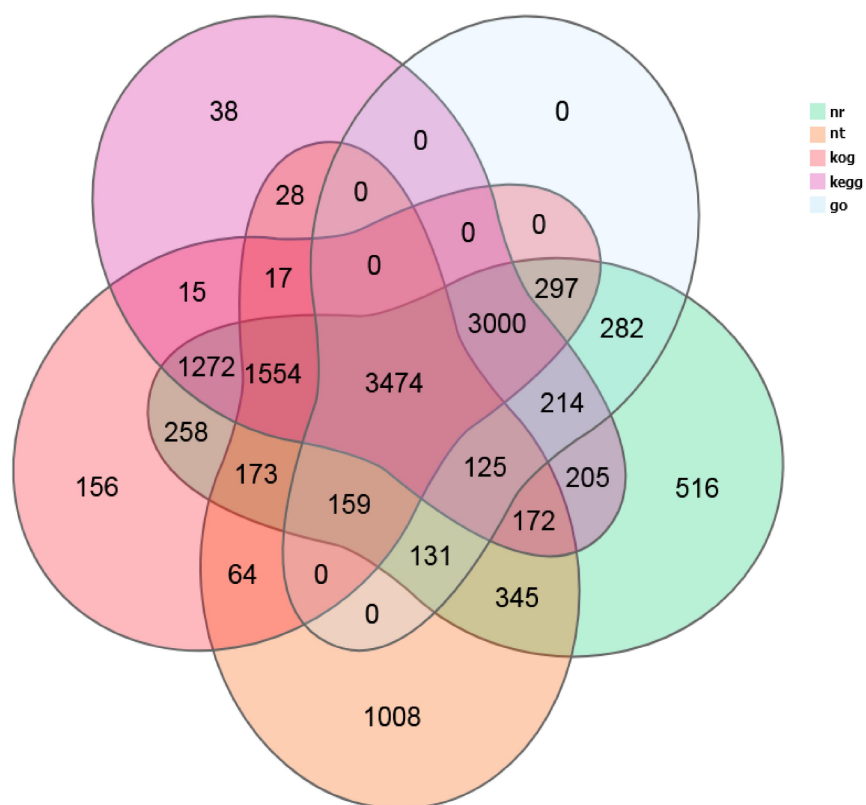


Fig. S2. Venn diagram of the gene function annotation results.