

Table S1. Primers list

Primer name	Primer sequences	Restriction enzyme sites
OsNAC78-HA-F	CAGGATATCCAGATCCAGTGGGATCC ATGAGCCAATCGCCGCCGGA	<i>Bam</i> HI
OsNAC78-HA-R	ACTAGTAAGCTTGGTACCGAGCTCCC TGCTGTAGATACACAGCC	<i>Sac</i> I
OsNAC78-Q-F	AACTGGGTCATGCACGAGTA	/
OsNAC78-Q-R	TCCTCAGTCGACTCATCTGC	/
Os01g0934800-Q-F	AGGGCTCAGGAGTTGCAAT	/
Os01g0934800-Q-R	ACACCTTCTTCACCGATCCA	/
Os01g0949900-Q-F	GCTCGTTTCTGGGCTCAATT	/
Os01g0949900-Q-R	CGATGTTGGCGTACTCCTTG	/
Ubiquitin-Q-F	AACCAGCTGAGGCCCAAGA	/
Ubiquitin-Q-R	ACGATTGATTTAACCAGTCCATGA	/
Os01g0934800-F1-LacZ-F	CCGGAATTCGAAAACATCTCAATCTT CTACCT	<i>Eco</i> RI
Os01g0934800-F1-LacZ-R	CGGGGTACCCATTGCCATGTGATCCG CTC	<i>Kpn</i> I
Os01g0934800-F2-LacZ-F	CCGGAATTCGATCAATTTTATCCCGAT CT	<i>Eco</i> RI
Os01g0934800-F2-LacZ-R	CGGGGTACCCTAGATGAAAAGTTATA TTGTTT	<i>Kpn</i> I
Os01g0934800-F3-LacZ-F	CCGGAATTCTTGTCCTCTAACGTATGT CACTA	<i>Eco</i> RI
Os01g0934800-F3-LacZ-R	CGGGGTACCAGTGGGCCCAAATCTCG TGA	<i>Kpn</i> I
Os01g0934800-F4-LacZ-F	CCGGAATTCACTGTGTGTCCGTGGTGT CA	<i>Eco</i> RI
Os01g0934800-F4-LacZ-R	CGGGGTACCTTAGTGAAGATAACACG ATGTCG	<i>Kpn</i> I
Os01g0949900-F1-LacZ-F	CCGGAATTCGCTTCTCGCCAAAAACC CCA	<i>Eco</i> RI
Os01g0949900-F1-LacZ-R	CGGGGTACCGAACTAAACAGCCCCTC ATT	<i>Kpn</i> I
Os01g0949900-F2-LacZ-F	CCGGAATTCCATGAACATGTACAGTG CTC	<i>Eco</i> RI
Os01g0949900-F2-LacZ-R	CGGGGTACCCTCGCCGTCCAACCACA ATG	<i>Kpn</i> I
Os01g0949900-F3-LacZ-F	CCGGAATTCCAAGGAGTACACCTCT GAT	<i>Eco</i> RI
Os01g0949900-F3-LacZ-R	CGGGGTACCAATAATGGTCAAAGTTG TTTTTG	<i>Kpn</i> I

Os01g0934800-LUC-F	CGGTATCGATAAGCTTAGCCCACCAG AGGTAACAA	<i>HindIII</i>
Os01g0934800-LUC-R	TTGGCGTCTTCCATGGTTTTAGCTCAG CTGCTTCGA	<i>NcoI</i>
Os01g0949900-LUC-F	CGGTATCGATAAGCTTTGGCGACCGT GCCATCTG	<i>HindIII</i>
Os01g0949900-LUC-R	TTGGCGTCTTCCATGGATTCCTGTATT CTTGGCTAAACC	<i>NcoI</i>
OsNAC78-MBP-F	GGATTTACATATGTCCATGAGCCAA TCGCCGCCGA	<i>NcoI</i>
OsNAC78-MBP-R	ACCTGCAGGGAATTCGGATCCTCACC TGCTGTAGATACACAGCC	<i>BamHI</i>
Os01g0934800-Cy5.5-Probe1	GTGGATTTAGAGCGTGTTTCGGGGGAG TT	/
Os01g0949900-Cy5.5-Probe1	GAAGGTCCCCGTGCTCCTCCATGGCG ACCGTGCCATCTGC	/
Os01g0949900-Cy5.5-Probe2	GTGCTCGAGGTCATCGTGGCTGGCAT TGTG	/

Table S2. The index of samples used for 10× Genomics' scRNA-seq

Sample	Cell concentration	Cell viability
Control	2080/μl	93%
TOE	1840/μl	92%

Table S3. The statistical quality results of sequencing date

Reads parameters	Reads number	
	Control	TOE
Estimated number of cells	12,891	13,639
Fraction reads in cells	89.9%	90.6%
Mean reads per cell	42,915	37,675
Median genes per cell	1,913	1,765
Median UMI counts per cell	5,116	4,696
Total genes detected	24,715	24,801

