Class	S. tuberosum	S. lycopersicum	E. salsugineum	A. thaliana	Z. mays	O. sativa	A. trichopoda	S. moellendorffi	P. patens	C. reinhartdtii	B. hygrometrica	Averages
=	na	na	na	0.30%	0.70%	0.10%	na	na	5.00%	0.80%	na	0.90%
c	na	0.10%	na	0.30%	1.30%	na	na	na	1.20%	0.40%	na	0.40%
e	2.20%	29.40%	28.90%	5.10%	10.90%	26.00%	18.10%	20.70%	5.90%	24.20%	9.00%	16.40%
i	2.00%	4.70%	1.10%	1.00%	2.30%	18.70%	3.40%	0.40%	0.60%	0.50%	5.10%	4.40%
j	na	na	0.20%	8.60%	7.70%	4.00%	na	na	12.20%	3.20%	na	3.90%
k	na	0.10%	na	3.10%	0.50%	na	na	na	14.60%	0.10%	na	2.20%
o	na	0.20%	0.10%	4.80%	5.30%	0.50%	na	0.30%	4.40%	2.10%	na	1.80%
p	15.80%	18.10%	20.90%	13.90%	8.70%	12.20%	13.40%	15.30%	4.60%	11.00%	30.00%	13.60%
s	na	0.10%	na	0.10%	0.50%	na	na	na	na	na	na	0.10%
u	79.90%	46.10%	46.30%	34.90%	45.50%	36.90%	65.00%	62.40%	44.40%	56.20%	55.90%	52.30%
x	na	1.20%	2.50%	27.70%	16.60%	1.40%	na	0.90%	6.80%	1.60%	na	3.90%
y	na	na	na	0.20%	na	0.20%	na	na	0.20%	na	na	0.1%

Table S1: Transcript classes of predicted lncRNAs as identified by gffcompare. Classes are: '=': complete match of intron chain, 'c': contained in reference (intron compatible), 'k': containment of reference (reverse containment), 'm': retained intron(s), full intron chain overlap/match, 'n': retained intron(s), partial or no intron chain match, 'j': multi-exon with at least one junction match, 'e': single exon transfrag partially covering an intron, 'o': other same strand overlap with reference exons, 's': intron match on the opposite strand, 'x': exonic overlap on the opposite strand, 'i': fulling contained within a reference intron, 'y': contains a reference with its intron(s), 'p': possible polymerase run-on (no actual overlap), 'u': none of the above (unknown, intergenic).