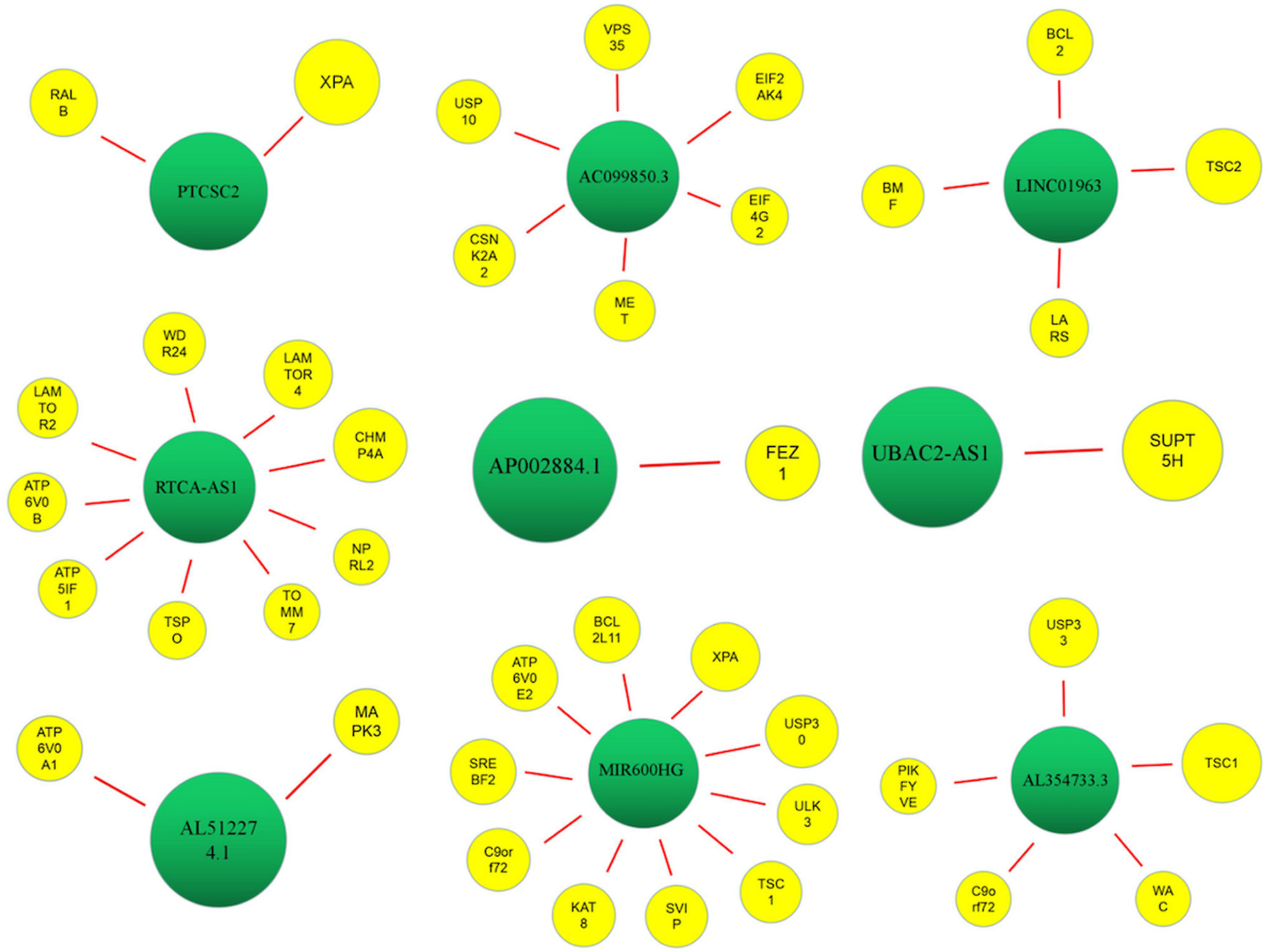

Figure S1. Autophagy genes co-expressed with the nine lncRNAs. The green circles represent lncRNAs, and the yellow circles represent autophagy genes. Red lines indicate a positive correlation. The area of the yellow circle was positively associated with the co-expression coefficient of the lncRNAs. lncRNA, long non-coding RNA.

Table SI. Autophagy-related genes positively co-expressed with the nine lncRNAs.

LncRNA	Autophagy-related gene	Cor	P-value
PTCSC2	XPA	0.614	1.64x10^{-33}
	RALB	0.483	1.32x10^{-19}
AC099850.3	EIF2AK4	0.482	1.88x10^{-19}
	VPS35	0.470	1.83x10^{-18}
	USP10	0.459	1.44x10^{-17}
	CSNK2A2	0.443	2.48x10^{-16}
	MET	0.436	8.06x10^{-16}
	EIF4G2	0.409	6.47x10^{-14}
LINC01963	TSC2	0.533	3.81x10^{-24}
	BCL2	0.462	8.94x10^{-18}
	BMF	0.439	4.95x10^{-16}
	LARS	0.410	4.98x10^{-14}
RTCA-AS1	CHMP4A	0.531	6.20x10^{-24}
	LAMTOR4	0.495	1.51x10^{-20}
	WDR24	0.447	1.25x10^{-16}
	LAMTOR2	0.433	1.45x10^{-15}
	ATP6V0B	0.423	6.99x10^{-15}
	ATP5IF1	0.418	1.51x10^{-14}
	TSPO	0.417	1.92x10^{-14}
	TOMM7	0.405	1.09x10^{-13}
	NPRL2	0.402	1.72x10^{-13}
AP002884.1	FEZ1	0.415	2.43x10^{-14}
UBAC2-AS1	SUPT5H	0.576	7.88x10^{-29}
AL512274.1	MAPK3	0.409	6.14x10^{-14}
	ATP6V0A1	0.408	6.92x10^{-14}
MIR600HG	USP30	0.532	3.36x10^{-29}
	XPA	0.502	9.63x10^{-26}
	BCL2L11	0.485	7.40x10^{-24}
	ATP6V0E2	0.484	9.74x10^{-24}
	SREBF2	0.481	1.84x10^{-23}
	C9orf72	0.461	1.75x10^{-21}
	KAT8	0.461	1.78x10^{-21}
	SVIP	0.456	5.98x10^{-21}
	TSC1	0.451	1.70x10^{-20}
	ULK3	0.443	9.92x10^{-20}
	ZKSCAN3	0.436	3.83x10^{-19}
	BMF	0.424	4.75x10^{-18}
	TSC2	0.416	2.27x10^{-17}
	TP53INP1	0.412	5.27x10^{-17}
	HDAC6	0.411	5.63x10^{-17}
	WDR6	0.411	5.94x10^{-17}
	KIAA1324	0.409	7.96x10^{-17}
	SREBF1	0.403	2.50x10^{-16}
	MTMR3	0.402	3.31x10^{-16}
	BCL2	0.400	4.43x10^{-16}
AL354733.3	TSC1	0.592	2.11x10^{-37}
	USP33	0.518	1.66x10^{-27}
	PIKFYVE	0.417	1.98x10^{-17}
	C9orf72	0.412	4.82x10^{-17}
	WAC	0.411	5.92x10^{-17}

lncRNA, long non-coding RNA; Cor, correlation coefficient.