S4 Table. Canonical cheRNAs can be better identified by Tuxedo and Concatenating methods. Colored cells are validated in tissue-specific experiments and used as gold standards.

16 alidations				HEK293				K562			
result	**cell**	**method**	**RNA Symbol**	Werner	Tuxedo	Concat.	Taco	Werner	Tuxedo	Concat.	Taco
CPE	HEK293	RT-PCR	KCNQ1OT1	CPE	CPE	CPE	None				
	HEK293	RT-PCR	XIST	HIDATA	CPE	CPE	CPE				
	HEK293 /K562	RT-PCR	PVT1	-	CPE	CPE	-	CPE	CPE	CPE	CPE
	K562	function	BONIFACIO					CPE	CPE	CPE	CPE
	K562	function	ILYICH					CPE	CPE	CPE	CPE
	K562	function	HIDALGO					-	CPE	CPE	CPE
SNE	HEK293	RT-PCR	GAPDH	SNE	SNE	SNE	SNE				
	HEK293	RT-PCR	ACTB	SNE	SNE	SNE	SNE				
	HEK293 /K562	RT-PCR	MYC	SNE	SNE	SNE	SNE	SNE	SNE	SNE	SNE
	K562	RNA-seq reads	B3GNT2					SNE	SNE	SNE	SNE
	K562	RNA-seq reads	IL6					-	-	-	NA
	K562	RNA-seq reads	PDCD6IP					-	SNE	SNE	SNE
intermediate	HEK293	RT-PCR	HOTAIR	SNE	-	-	NonA				
	HEK293	RT-PCR	DLX6-AS1, Evf-2_5p	-	CPE	CPE	NonA				
correct prediction:				5	7	7	4	5	7	7	7
number of gold standarad:				8	8	8	8	8	8	8	8
PPV				0.63	0.88	0.88	0.50	0.63	0.88	0.88	0.88

NonA:	not assembled
NA:	not tested because of low expression level
HIDATA:	not tested by Cuffdiff because of high expression level
"-":	tested but not significantly differentially expressed
PPV:	number of correct predictions /number of gold standard in each cell line (8 gold standard in HEK293 while 8 gold standard in K562)