

Fusion Transcripts generated by vector gene trapping of targeted genes in iPS clones. VIS that are in the same orientation of gene and within introns are highlighted, and premature termination expected.

iPS clones subjected to RNAseq	VIS	OUT/Intron/Exon	Proviral Orientation / Gene Orientation	same orientation	RNAseq Identified GeneTrap	observed fusion transcripts upstream exons	observed fusion transcripts downstream ch54 Vector-bp224
10/11/21/26	HMGA2(chr12+66327484)	intron	+/+	Same	HMGA2 Exon3	AAACGGCCAAGAGGCAGACCTAGGAAATGG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	CDC101(chr16-28588950)	intron	-/+	reverse			
	CDKAL1(chr6+21048330)	intron	+/+	Same	CDKAL1	CAAAAGAGTAGTGGATTTCTGAAAGAGAA	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	DIP2A(chr21+47931106)	intron	+/+	Same	DIP2A Exon7	TTGTGGATGATTTTGAGGAATTGTTGGAAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	MARK3(chr14+103866754)	intron	+/+	Same	MARK3, Exon1, and also hidden Exon in intron 1	CCAACGGTGAATGAACGAGACACTGAAAC	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	NRTN(chr19+5812281)	intron	+/+	Same	NRTN Exon1	CTTGTAACCTGATTCTTCTCATGTGGGAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	PARN(chr16+14652221)	intron	+/-	reverse		CACGTGACGGGTAGTCCGGCGCCACAGCAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	SPPL3(chr12+121246774)	intron	+/-	reverse			
	STAG3(chr7+99783923)	intron	+/+	Same	STAG3 Exon5	ACTTTTTCATCCAATCTTGCGGATGTAAAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	ZNF586(chr19-58292195)	out	-/+	reverse	Not expected since it is outside this gene: Vector trapped another gene ZNF552 Exon2 chr19-58324661, skip exon3, 32,466bp upstream of IS, also another hidden Exon 3' to ZNF552	TGGAGAACCTGGCACTTATGTCTCCCTGG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
10/11/	TALDO1(chr11-758954)	exon	-/+	reverse		CAGCAAGCGCAGAGCCAAACAGCCAGGCAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
17	HMGA2(chr12+66249148)	intron	+/+	Same	HMGA2 Exon3	AAACGGCCAAGAGGCAGACCTAGGAAATGG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	ACACA(chr17+35624498)	intron	+/-	reverse			
	CHSY1(chr15-101690556)	out	-/-	Same			
	CTSS(chr1-150731112)	intron	-/-	Same	not detected due to low expression in iPS cells		
	DEDD2(chr19-42711507)	intron	-/-	Same	DEDD2 Exon4	GACCTTCTCTGAAGGCAAAGTGACCTGTG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	INPP5B(chr1-38352834)	intron	+/-	reverse			
	SLC7A5(chr16-87899252)	intron	-/-	Same	SLC7A5 Exon1	CAGCCAAGCTCTGTGCCCTGCCCTGTGCTGC	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	TEP1(chr14+20872943)	intron	+/-	reverse			
	TMEM187(chrX+153254921)	out	+/+	Same			
	TUBA1A(chr12-49598267)	out	-/-	Same			
18	HMGA2(chr12+66308146)	intron	+/+	Same	HMGA2 Exon3	AGCGAGAAGCGTTGGCAGACCTAGGAAATGG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	BAIAP2L2(chr22-38487560)	intron	-/-	Same	BAIAP2L2 Exon7	TCCAACACCTTCTCGAGTTCTTCGGCCGG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	LOC554223(chr6-29754777)	out	-/+	reverse			
20	USP28(chr11+113712165)	intron	+/-	reverse			
	UBE2G1(chr17-4246338)	intron	-/-	Same	UBE2G1 Exon1, also another hidden Exon in intron1	CGGCACCTGCTACTGCGAAGACAGCTGGCAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	MPHOSPH9(chr12+123645319)	intron	+/-	reverse		GGGCGGAAGGACCGGCCCTGGCGGGATAG	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
	GOSR1(chr17+28827327)	intron	+/+	Same	GOSR1 Exon5, and also Exon6+13bp intron, another SA	ATTTTGAAGAACATGACCACCTTCGAAA	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
						CATGACCACCTTCGAAAGTAGGTATTGAAT	GTGCTGCAGGCTCAAAGAGCAGCGAGAAGCGTT
22/23	no VIS						