H19

HSC 383 AAGAAA SC 819 AGTGCC SC 819 AGTGCC SC 819 AGTGCC SC 879 GGTATTGC HISC 283 GGTATTGC SC 879 GGTATTGC HISC 283 GGTATTGC HISC 283 GAGCTC SC 905 GAGCTCC HISC 173 GAGCCC SC 965 GAGCCCC SC 965 GAGCCCC SC 1025 TGTGGT HISC 113 IGTGGT	2e-85 ACCATEGECCTATECT TCCATEGECCTATECT CCATEGECTATECT CCCATEGECTATECT CCCATEGECTATECT CCCATEGECTATECTA CCCATEGECTATECTA CCCATEGECATECTA CCCATEGECATECTATECTATECTATECTATECTATECTA	AATCOATTECCECAAACCTAAAC AATCOATTECCECAAACCTAAAG AATCOTETEGEGCCACACCTAAAG AATGCTETEGEGCCACCCAGTTC AATGCTETEGEGCCACCCAGTTC ISJ/183(100%) GCCAAACGTCATCOTCAC GCCAAACGTCATCOTCCACTAC ACCTTCGGGAQTGTCACCCCCCAGA	Gaps 0/183(0%) 0/183(0%) 0/183(0%) Control of the control	Strand Plus/Minus 818 324 878 264 Strand Plus/Minus 964 174 1024 114 1084 54	Score 298 bits pESC 76 NSC 14 pESC 82 NSC 20 pESC 83 NSC 20 pESC 80 NSC 21 pESC 80 NSC 21 331 bits pESC 40 NSC 11 pESC 10 NSC 11 pESC 10 NSC 11 pESC 10 NSC 11	0 AAGG 0 AAGG 0 AAGT 0 AGT 0 AGT 0 AGT 0 GGTA 50 to 2 (366) 12 GAGC 12 TGTG 13 GACC 14 GACC 15 GACC 16 GACC 17 GACC	ATTGOLATTCACAAATGG TTGOLATTCACAAATGG 232 Graphics Expect 4e-95 CTCAAAGAGTCCAGAGAG CTCAAGAGTCCAGAGAG CTCAAGAGTCCAGAGAGAGC CTCCAAGAGTCCAGAGAGAGC CTCCAGTCCAGAGAGAGC CTCCAGTCCAGAGAGAGC CTCCAGTCCAGAGAGAGC CTCCAGTCCAGAGGAGCC CT	AMATCAN TROCCOMACT MAN MATCAN TROCCOMACT MAN CANTECT GIGGGTCACCOMAGT CANTECT GIGGGTCACCOMAGT Identities 183/183(100%) SECRAMONTCAT CENTERCE (CENTER)	99991114 1A ACSCO399 GAGCCCCCCACCCCT GAGCCCCCCACCCCT C 924 C 304 Gages 0/183(0%) CCTGTTACCACCCAAA CCAGTGAATCAAATTA TCAGTGAATCAAATTA TTCAGTGAATCAAATTA	St	atch ▲ Previous Ma rand s/Minus
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mge 1: 51 to 233 g core 31 bits(366) SC 905 GACT/A SC 905 GACT/A NSC 233 GABCT/A SC 905 GACC/A NSC 173 GACCOCC NSC 173 GACCOCC SC 1025 TGTGGT/A SC 1025 TGTGGT/A SC 1025 TGTGGT/A SC 1025 CA 10 NSC 53 CCA 51 mge 1: 119 to 315 core	Graphics Expect 3e-95 CAAAGAGTTCAGAGAG COCCACGREGGAGACC COCCACGREGGAGACC CAATCTGCAATGTAG AATTCTGCAATGTAG AATTCTGCAATGTAG CAATCTGCAATGTAG	Identities 183/183(100%) 60CAAAGTCATGSTCOCTEAT TCTTCG6640FSTCATGSTCOCTEAT TCTTCG6640FSTCATGSTCATGSTCATG TCTTCG6640FSTCATGCATGCATGCA	Gaps 0/183(0%) ICETETTACCACCCAAA ICCAETEAATCAACTAA ATCAETEAATCAAATTA ITCAETEAATCAAATTA	Strand Plus/Minus 964 174 1024 114 1084	NSC 26	50 to 2 (366) 3 GAGC 32 GAGC 1111 32 GAGC 18 GAGC 18 GAGC 1111 2 GACC 1111 2 TGTG 21 TGTG 21 TGTG 21 TGTG	232 Graphics Expect 4e-95 TCAAAAGIGT CABAGAG TCAAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIG TCAAAGIG TCAAGIGT CABAGAG TCAAGIG TCAAGIGT CABAGAG TCAAGIGT CABAGAG TCAAGIG TCAAAGIG TCAAGIG	Identities 183/183(100%) SCRAMGERCATOSTOCOTAN SCRAMGERCATOSTOCOTAN TETEGORANTETICAGEACCA TETEGORANTETISTACCTOCTO	Gape 0/183(0%) CGTGTTACCACCCAAA TCAGTGAATCAAATTA TCAGTGAATCAAATTA TCAGTGAATCAAATTA TCAGTGAATCAAATTA TTGAGCGGGACCAGTT	St Pli 107 173 167 113 227	rand
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50 5100(054)	5 <u>Graphics</u> Expect 9e-103	Identities 197/197(100%)	Gaps 0/197(0%)	Next Match 🛦 Previou Strand Plus/Plus	us Match Range 1: Score 356 blts(315 <u>Graphics</u> Expect 1e-102	Identities 197/197(100%)	Gaps 0/197(0%)	Next N	latch 🔺 Previous M Strand Plus/Plus
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SC 178 CCCTCATT		GTGCATCGCCTGCGGAGGCTCCA		237 238	pESC 83 NSC 17			TGTGCATCGCCTGCGGAGGCTCC		898 238	
	TCOCCGAAGAAGTAT			297	pESC 89		CGGTCCCCGAAGAAGTA	TACCCT6GACCGCATTACGTGTT TACCCT6GACCGCATTACGTGTT		958	
	GECATTITCA 314		CTGATGACCCTCTCTC	298	NSC 23 pESC 95		GCGGTCCCCGAAGAAGTA		CTGATGACCCTCTCTC	298	
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nge 1: 236 to 395		Identities		Next Match 🔺 Previou	Match Range 1:	236 to	395 Graphics	Identities			latch 🛕 Previous M
ore 39 bits(320)		160/160(100%)	Gaps 0/160(0%)	Plus/Minus	289 bits		Expect 9e-83	160/160(100%)	Gaps 0/160(0%)	Pl	rand us/Minus
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C 900 CGCCGCCG	JOGOHOUAUUAUUAIU	GGAGGAGAAGCGGAGAGATGTCC TGTGGGTGCACTAGACTG 939	CACCCTGGGCTGGTGG		pESC 88	0 0.1011	CGCGGGAGGACGAGCAT	CGGAGGAGAAGCGGAGAGATGTC GTGTGGGTGCACTAGACTG 92			

Fig. S3. Comparison of DNA sequences between fusion partner cells in H19, Ifg2, Peg1, and Peg3 genes.

The sequences between ESCs and pNSCs and between pESCs and NSCs were 100% identical in H19, Ifg2, Peg1, and Peg3 genes. Thus, there was no SNP in these genes between fusion partner cells (between ESCs and pNSCs, and pESCs and NSCs). These analyses were performed using BLAST® program of National Library of Medicine.