

H19

Range 1: 219 to 383 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
298 bits(330)	2e-85	165/165(100%)	0/165(0%)	Plus/Minus
ESC 759	AAGBAGACATGCCCTATTCTTGGAGCTCTGCTGAATCAGTTGTGGGGTTTATACGGGG	818		
pNSC 383	AAGBAGACATGCCCTATTCTTGGAGCTCTGCTGAATCAGTTGTGGGGTTTATACGGGG	324		
ESC 819	AGTTGCCCGGTGGTGGCAGAAAATCGATTGGCCAAACCTAAAGAGCCCGCCACCCCT	878		
pNSC 323	AGTTGCCCGGTGGTGGCAGAAAATCGATTGGCCAAACCTAAAGAGCCCGCCACCCCT	264		
ESC 879	BGTTATTGGAATTCACAAATGGCAATGCTGTGGGTCCACCAAGTTC	923		
pNSC 263	BGTTATTGGAATTCACAAATGGCAATGCTGTGGGTCCACCAAGTTC	219		

Range 1: 140 to 304 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
298 bits(330)	2e-85	165/165(100%)	0/165(0%)	Plus/Plus
pESC 760	AAGBAGACATGCCCTATTCTTGGAGCTCTGCTGAATCAGTTGTGGGGTTTATACGGGG	819		
NSC 140	AAGBAGACATGCCCTATTCTTGGAGCTCTGCTGAATCAGTTGTGGGGTTTATACGGGG	199		
pESC 820	AGTTGCCCGGTGGTGGCAGAAAATCGATTGGCCAAACCTAAAGAGCCCGCCACCCCT	879		
NSC 200	AGTTGCCCGGTGGTGGCAGAAAATCGATTGGCCAAACCTAAAGAGCCCGCCACCCCT	269		
pESC 880	BGTTATTGGAATTCACAAATGGCAATGCTGTGGGTCCACCAAGTTC	924		
NSC 260	BGTTATTGGAATTCACAAATGGCAATGCTGTGGGTCCACCAAGTTC	304		

Igf2

Range 1: 51 to 233 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
331 bits(366)	3e-95	183/183(100%)	0/183(0%)	Plus/Minus
ESC 905	GAGCTCAAGAGTTCAGAGAGGCAAAAGCTCATGTCCTGATGATGTTTACCACCCAAA	964		
pNSC 233	GAGCTCAAGAGTTCAGAGAGGCAAAAGCTCATGTCCTGATGATGTTTACCACCCAAA	174		
ESC 965	GACCCCGCCACGAGGAGGCTCTTCCAGCAACCATCAGTGAATCAAAATTA	1024		
pNSC 173	GACCCCGCCACGAGGAGGCTCTTCCAGCAACCATCAGTGAATCAAAATTA	114		
ESC 1025	TGTGGTAATTCGCAATGATGATACCATCACTGTGACCTCCTCTGAGCAGGACAGTT	1084		
pNSC 113	TGTGGTAATTCGCAATGATGATACCATCACTGTGACCTCCTCTGAGCAGGACAGTT	54		
ESC 1085	CCA 1087			
pNSC 53	CCA 51			

Range 1: 50 to 232 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
331 bits(366)	4e-95	183/183(100%)	0/183(0%)	Plus/Plus
pESC 48	GAGCTCAAGAGTTCAGAGAGGCAAAAGCTCATGTCCTGATGATGTTTACCACCCAAA	107		
NSC 232	GAGCTCAAGAGTTCAGAGAGGCAAAAGCTCATGTCCTGATGATGTTTACCACCCAAA	173		
pESC 108	GACCCCGCCACGAGGAGGCTCTTCCAGCAACCATCAGTGAATCAAAATTA	167		
NSC 172	GACCCCGCCACGAGGAGGCTCTTCCAGCAACCATCAGTGAATCAAAATTA	113		
pESC 168	TGTGGTAATTCGCAATGATGATACCATCACTGTGACCTCCTCTGAGCAGGACAGTT	227		
NSC 112	TGTGGTAATTCGCAATGATGATACCATCACTGTGACCTCCTCTGAGCAGGACAGTT	53		
pESC 228	CCA 230			
NSC 52	CCA 50			

Peg1

Range 1: 119 to 315 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
356 bits(394)	9e-103	197/197(100%)	0/197(0%)	Plus/Plus
ESC 118	GACATGACAGAAAATTTCTGAAATCAAAAAGAAAATGTAAAAAGTGCACCCCTCGAT	177		
pNSC 119	GACATGACAGAAAATTTCTGAAATCAAAAAGAAAATGTAAAAAGTGCACCCCTCGAT	178		
ESC 178	CCCTCAATCACTTCAAACTCTGTGCATGCGCTGCGAGAGGCTCCACACAAGCATTTGTT	237		
pNSC 179	CCCTCAATCACTTCAAACTCTGTGCATGCGCTGCGAGAGGCTCCACACAAGCATTTGTT	238		
ESC 238	CCTGCGGTCCCGAAGAGTATACCCGAGAGGCAATACGTTTCTGATGACCCCTCTCTC	287		
pNSC 239	CCTGCGGTCCCGAAGAGTATACCCGAGAGGCAATACGTTTCTGATGACCCCTCTCTC	298		
ESC 298	AGGTGCTGGCAATTTCA 314			
pNSC 299	AGGTGCTGGCAATTTCA 315			

Range 1: 119 to 315 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
356 bits(394)	1e-102	197/197(100%)	0/197(0%)	Plus/Plus
pESC 779	GACATGACAGAAAATTTCTGAAATCAAAAAGAAAATGTAAAAAGTGCACCCCTCGAT	838		
NSC 119	GACATGACAGAAAATTTCTGAAATCAAAAAGAAAATGTAAAAAGTGCACCCCTCGAT	178		
pESC 839	CCCTCAATCACTTCAAACTCTGTGCATGCGCTGCGAGAGGCTCCACACAAGCATTTGTT	898		
NSC 179	CCCTCAATCACTTCAAACTCTGTGCATGCGCTGCGAGAGGCTCCACACAAGCATTTGTT	238		
pESC 899	CCTGCGGTCCCGAAGAGTATACCCGAGAGGCAATACGTTTCTGATGACCCCTCTCTC	958		
NSC 239	CCTGCGGTCCCGAAGAGTATACCCGAGAGGCAATACGTTTCTGATGACCCCTCTCTC	298		
pESC 959	AGGTGCTGGCAATTTCA 975			
NSC 299	AGGTGCTGGCAATTTCA 315			

Peg3

Range 1: 236 to 395 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
289 bits(320)	9e-83	160/160(100%)	0/160(0%)	Plus/Minus
ESC 780	TGCAGAGACCCCTGACAAAGAGGTTGCCCGAGCCCTTGTCTGACAGCGTGGGAGTCA	839		
pNSC 395	TGCAGAGACCCCTGACAAAGAGGTTGCCCGAGCCCTTGTCTGACAGCGTGGGAGTCA	336		
ESC 840	GAGTCCGAGGAGACGAGCATCGAGAGGAGAGCGAGAGATGTCCACCCCTGGGCTGGT	899		
pNSC 335	GAGTCCGAGGAGACGAGCATCGAGAGGAGAGCGAGAGATGTCCACCCCTGGGCTGGT	276		
ESC 900	CGCCCGCGGCGCCCGGTTTCAAGTGTGGGTGCACTAGACTG 939			
pNSC 275	CGCCCGCGGCGCCCGGTTTCAAGTGTGGGTGCACTAGACTG 236			

Range 1: 236 to 395 Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
289 bits(320)	9e-83	160/160(100%)	0/160(0%)	Plus/Plus
pESC 769	TGCAGAGACCCCTGACAAAGAGGTTGCCCGAGCCCTTGTCTGACAGCGTGGGAGTCA	820		
NSC 395	TGCAGAGACCCCTGACAAAGAGGTTGCCCGAGCCCTTGTCTGACAGCGTGGGAGTCA	336		
pESC 829	GAGTCCGAGGAGACGAGCATCGAGAGGAGAGCGAGAGATGTCCACCCCTGGGCTGGT	888		
NSC 335	GAGTCCGAGGAGACGAGCATCGAGAGGAGAGCGAGAGATGTCCACCCCTGGGCTGGT	276		
pESC 889	CGCCCGCGGCGCCCGGTTTCAAGTGTGGGTGCACTAGACTG 928			
NSC 275	CGCCCGCGGCGCCCGGTTTCAAGTGTGGGTGCACTAGACTG 236			

Fig. S3. Comparison of DNA sequences between fusion partner cells in H19, Igf2, Peg1, and Peg3 genes.

The sequences between ESCs and pNSCs and between pESCs and NSCs were 100% identical in H19, Igf2, 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.