High throughput trapping of secretory pathway genes in mouse embryonic stem cells

Suppementary Information

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Running title: Secretory gene trap resource

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Figure 1: Quantitative RT-PCR of wild type transcripts expressed in embryoid bodies derived from trapped ES cell lines. Transcript levels are normalized to corresponding wild type levels expressed in the parental cells after feeder cell removal (ES) (see Methods) or in the embryoid bodies (EB) derived from them. Gene specific primers were chosen in exons flanking the insertion sites (Suppl. Table 1 & Suppl. Figure 2). Results are means from triplicate reactions ± SD.

Figure 2: Analysis of gene expression in trapped ES cell lines. Genes are shown as annotated in ENSEMBL. Gene trap insertions are indicated by vertical arrows. The positions of the primers in the exons flanking the insertion sites are marked by horizontal arrows. Since the mapping was based on GTSTs obtained by 5'RACE, the exact position of the insertion sites within introns could not be determined.

Table 1: Gene specific primers used for the analysis of gene expression in trapped ES cell lines.

Clone	Gene Symbol	Primer pair	Sense (s)	Antisense (as)
G024D09	Idh3g	RT01	AAAGGCAATGCTCAAGCCAAC	CCGCCCACCATACTTAGCAGA'
G047F01	Tmem32	RT02	CCGTCTACCTGGCCGACTTG	AATCACGCCAAACACCATTCC'
G049B05	Ndufa1	RT03	GGCTTGTAGGTGTCGGGCTTT	AACTGCAAAGGCCAGAAGTGTC'
G067H01 P086B06	2610529C09 Rik	RT04	GCCAAGGTGGTTCTGGTCTGT	CGACGGAACTTGTCTCCATTCA
P071A12	Pdha1	RT05	CACAGCATGAGTGACCCTGGA	GGGCAGCATCCTCGATTTCTT
P071D05	Prdx4	RT06	GTGGACGAGACACTGCGTTTG'	GCTGGATCTGGGATTATTGTTT
P071F11	Ndufb11	RT07	AGTGGCAGGAGGACCCAGAAC	CACGAAGGTGGTCCCAAAGAC
P072A05	Atp6ap2	RT08	ATGGTGGGAACGCAGTGGTAG'	GGGACTTTGGGTGTTCTCTTG
P076F03	Gla	RT09	GGAGATTGTTGAAGTCGCTGGA	CGCAGATCGTTGGACATGAGT