

#133239 ESOPHAGEAL CANCER

OMIM Gene ID	HGNC	UniProtAC
120470	DCC	P43146
190182	TGFBR2	P37173
604050	DLEC1	Q9Y238
604242	RNF6	Q9Y252
604767	DEC1	Q9P2X7
605131	WWOX	Q9NZC7
606551	LZTS1	Q9Y250

Table 1: OMIM - UniProtAC mapping

Legend

- N1: #input proteins associated to the significant GO term
- N2: #proteins associated to the significant GO term
- P-value: Bonferroni-corrected p-value of Fisher's exact test
- *red*: go terms not related to the input proteins
- *blue*: go terms related to the input proteins (enriched uniquely by network-based method)
- *green*: go terms ancestors of terms enriched with the standard method (enriched uniquely by network-based method)

1 Standard enrichment

GO Term	N1	N2	P-value	Description
GO:0048523	7	5279	0.000483173	negative regulation of cellular process
GO:0048519	7	5756	0.00088558	negative regulation of biological process
GO:0048638	3	207	0.00259246	regulation of developmental growth
GO:0022603	4	1116	0.0114721	regulation of anatomical structure morphogenesis
GO:0048640	2	44	0.0128662	negative regulation of developmental growth
GO:0010769	3	381	0.0160485	regulation of cell morphogenesis involved in differentiation
GO:0010975	3	488	0.0334927	regulation of neuron projection development
GO:0050771	2	79	0.041774	negative regulation of axonogenesis

Table 2: Overrepresented GO terms with the standard enrichment

2 Network-based enrichment

GO Term	N1	N2	P-value	Description
GO:0030308	4	575	0.00224156	negative regulation of cell growth
GO:0045926	4	891	0.0126752	negative regulation of growth

Table 3: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.