

Table 1 The overrepresented GO terms for the 5% highly codon biased genes of the pig genome

GO ACCESSION	CHI-SQUARED	P-VALUE	GO TERM
GO:0003779	14.8161	0.0001185	actin binding
GO:0009986	21.3826	3.76E-006	cell surface
GO:0006281	12.9777	0.0003152	DNA repair
GO:0020037	23.3437	1.36E-006	Heme binding
GO:0060749	0.019	0.00003	mammary gland alveolus development
GO:0005624	20.806	5.08E-006	membrane fraction
GO:0003676	113.4532	2.20E-016	nucleic acid binding
GO:0005730	41.2299	1.35E-010	nucleolus
GO:0005654	8.1772	0.004242	nucleoplasm
GO:0000166	131.9434	2.20E-016	nucleotide binding
GO:0005634	352.4049	2.20E-016	nucleus
GO:0055114	63.8083	1.37E-015	oxidation-reduction process
GO:0016491	48.2633	3.73E-012	oxidoreductase activity
GO:0008233	26.921	2.12E-007	peptidase activity
GO:0016310	26.921	2.12E-007	phosphorylation
GO:0005886	127.9523	2.20E-016	plasma membrane
GO:0004672	61.0469	5.57E-015	protein kinase activity
GO:0019901	18.1546	2.04E-005	protein kinase binding
GO:0030529	15.2761	9.29E-005	ribonucleoprotein complex
GO:0005840	20.5753	5.73E-006	ribosome
GO:0003735	21.0366	4.51E-006	structural constituent of ribosome
GO:0005198	14.8161	0.0001185	structural molecule activity
GO:0055085	53.909	2.10E-013	transmembrane transport
GO:0006511	12.5187	0.0004029	ubiquitin-dependent protein catabolic process
GO:0004842	14.7011	0.000126	ubiquitin-protein ligase activity