

Table 9. PLA result for TP53, TP53INP1, TPBP1, TPBP2

Gene Name	LA Score	Gene Information										
TBL3	0.697	transducin (beta)-like 3 [3':AA021146,5':AA021145]										
CCNL1	0.685	cyclin L 1 [3':AA016305,5':AA017675]										
SEPW1	0.658	selenoprotein W, 1 [3':AA046261,5':AA046220]										
AP1GBP1	0.657	AP1 gamma subunit binding protein 1 [3':H18954,5':H19398*]										
NA-2444	0.653	ESTs [3':H40688*,5':NA]										
NA-1189	0.638	ESTs [3':R60021,5':R60081]										
HDLBP	0.638	high density lipoprotein binding protein (vigilin) [3':AA057676,5':AA057691]										
SEC14L2	0.637	SEC14-like 2 (S. cerevisiae) [3':AA028050,5':AA028049]										
GNAT1	0.634	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1 [3':AA056970,5':AA057020]										
NA-391	0.631	NA [3':T72633*,5':T72702]										
PRKCQ	0.631	protein kinase C, theta [3':R16896,5':R16950*]										
A2M	0.620	alpha-2-macroglobulin [3':T59946,5':T60017*]										
NA-3866	0.618	Homo sapiens, clone MGC:10120 IMAGE:3900723, mRNA, complete cds [3':N48606,5':N47289]										
SIAT1	0.618	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) [3':T87101,5':T87100]										
ZNF278	0.616	zinc finger protein 278 [3':AA020865,5':AA020915]										
HIRIP3	0.616	HIRA interacting protein 3 [3':H09174,5':H09232]										
KIAA0774	0.614	KIAA0774 protein [3':H04808,5':H04911]										
PMS2L2	0.614	postmeiotic segregation increased 2-like 2 [3':H25510,5':H25509*]										
NA-2884	0.613	ESTs [3':H92021,5':H92020*]										
HNRPA2B1	0.613	heterogeneous nuclear ribonucleoprotein A2/B1 [3':AA036731,5':AA036938]										
LPIN2	-0.687	lipin 2 [3':AA031651*,5':AA031742]										
<b>CAV1</b>	-0.674	caveolin 1, caveolae protein, 22 kDa [3':AA047243,5':AA047106]										
<b>NRG1</b>	-0.670	neuregulin 1 [3':H24357,5':H25173]										
<b>SMARCA4</b>	-0.658	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 [3':AA054955,5':AA055417]										
NA-1487	-0.649	ESTs [3':R81328,5':R81579]										
<b>PDCD2</b>	-0.641	programmed cell death 2 [3':W73377*,5':W73438]										
NA-3802	-0.639	ESTs [3':N63566,5':N94730]										
INSL4	-0.638	insulin-like 4 (placenta) [3':H59825,5':H60640*]										
ALS2CR9	-0.636	reserved [3':W74616,5':W94188]										
FOSL1	-0.635	FOS-like antigen 1 [3':T89996,5':T82817]										
NA-8094	-0.630	ESTs, Weakly similar to T08599 probable transcription factor CA150 - human [H. sapiens] [3':AA035263*,5':AA035262]										
EVA1	-0.625	epithelial V-like antigen 1 [3':N70439*,5':NA]										
SNTB2	-0.621	syntrophin, beta 2 (dystrophin-associated protein A1, 59 kDa, basic component 2) [3':AA035253,5':AA035252]										
<b>CITED2</b>	-0.621	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 [3':AA040200,5':AA040844]										
VRP	-0.616	vascular Rab-GAP/TBC-containing [3':W69438,5':W69521]										
LOC51035	-0.611	ORF [3':AA010706,5':AA010705]										
CXX1	-0.609	CAAX box 1 [3':W95708*,5':W95707]										
FLJ10830	-0.607	hypothetical protein FLJ10830 [3':AA031267*,5':AA031392]										
PDE1A	-0.597	phosphodiesterase 1A, calmodulin-dependent [3':AA037493,5':AA037435]										
<b>CAV1</b>	-0.594	caveolin 1, caveolae protein, 22 kDa [3':AA054588,5':AA054776]										
Permutation Test												
Percent	0.100	0.5	1	2.5	5	10	90	95	97.5	99	99.5	99.9
threshold	-0.570	-0.506	-0.473	-0.433	-0.396	-0.356	0.355	0.394	0.436	0.468	0.503	0.580