

Supplemental Table 1. Top Genes Dysregulated by miR-290				
	Gene Symbol	Gene	p-value	FC
Down	Gpnmb	Transmembrane glycoprotein NMB precursor	3.58E-03	-6.22
	Plekhh2	Pleckstrin homology domain containing, family H	5.89E-04	-5.25
	Car12	Carbonic anhydrase 12	8.63E-03	-4.84
	Gzme	Granzyme E precursor	6.95E-03	-4.64
	Mcpt1	Mast cell protease 1 precursor	1.22E-02	-4.57
	Sdr39u1	Short chain dehydrogenase/reductase family 39U, member 1	1.38E-04	-4.51
	Baiap2l1	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	1.88E-03	-4.24
	Prr9	Proline rich 9	2.98E-03	-3.97
	Gzmd	Granzyme D	4.02E-02	-3.91
	Slc25a43	Solute carrier family 25, member 43	2.06E-05	-3.69
Up	Cyp2e1	Cytochrome P450, family 2, subfamily e, polypeptide 1	9.48E-05	74.86
	Car3	Carbonic anhydrase 3	4.78E-03	34.30
	Retn	Adipose tissue-specific secretory factor	6.16E-05	33.89
	Cfd	Complement factor D	1.58E-04	25.87
	Adipoq	Adiponectin, C1Q and collagen domain containing	1.11E-03	24.23
	Retnla	Resistin like alpha	5.49E-04	20.68
	Hp	Haptoglobin	5.63E-04	20.35
	Cidec	Cell death-inducing DFFA-like effector c	4.19E-04	20.27
	Lgals12	Lectin, galactose binding, soluble 12	8.09E-04	19.65
	Ces1d	Carboxylesterase 1D	2.59E-03	19.57

The top differentially expressed genes based on fold change (FC) in the miR-290 tumors. Major urinary proteins 1, 2, 7, 11 and 19 displayed significant fold changes between the fold changes displayed by Cyp2e1 and Car3, but were not listed so more biologically relevant genes could be listed.