Supplementary Table 2. Genome-wide expression analysis of sh-Control cells treated with vehicle vs. sh-Control cells treated with TMZ

ID	logFC	t	P.Value	adj.P.Val	Gene Symbol	Gene Title	Entrez Gene ID	Cytoband	Overlapped in "sh-p105 vs. sh-p105 TMZ"
221577_x_at	1.135132792	14.537524	4.94E-09	0.000144655	DF15 /// LOC10029246	growth differentiation factor 15 /// similar to growth differentiation factor 15	100292463 /// 9518	19p13.11	YES
237737_at	0.970811682	14.4496941	5.29E-09	0.000144655	LOC100289026	similar to hCG1744891	100289026	---	YES
202284_s_at	0.884328952	13.7553241	9.31E-09	0.00016964	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1026	6p21.2	YES
201236_s_at	1.121974278	12.7752204	2.16E-08	0.000295256	BTG2	BTG family, member 2	7832	1q32	YES
207813_s_at	0.808946167	11.7750365	5.42E-08	0.000584067	FDXR	ferredoxin reductase	2232	17q24-q25	YES
238733_at	1.083525578	11.4976142	7.07E-08	0.000584067	---	---	---	---	YES
1559462_at	0.870868989	11.4403532	7.48E-08	0.000584067	---	---	---	---	YES
209806_at	-0.68871326	-10.8872631	1.30E-07	0.000886566	HIST1H2BK	histone cluster 1, H2bk	85236	6p21.33	YES
203409_at	0.683286021	10.6893251	1.59E-07	0.000965243	DDB2	damage-specific DNA binding protein 2, 48kDa	1643	11p12-p11	YES
201939_at	0.542588502	9.73561734	4.42E-07	0.00227022	PLK2	polo-like kinase 2 (Drosophila)	10769	5q12.1-q13.2	
225160_x_at	0.832972337	9.70549739	4.57E-07	0.00227022	MDM2	Mdm2 p53 binding protein homolog (mouse)	4193	12q14.3-q15	
204781_s_at	0.558055219	9.16730379	8.44E-07	0.003845779	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
208490_x_at	-0.66821344	-9.08980419	9.24E-07	0.003887041	HIST1H2BF	histone cluster 1, H2bf	8343	6p21.3	
204780_s_at	0.577162016	8.83220463	1.25E-06	0.004900615	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	
244117_at	0.940702451	8.73309606	1.41E-06	0.005154257	---	---	---	---	
205543_at	0.552391245	8.55495964	1.76E-06	0.005688746	HSPA4L	heat shock 70kDa protein 4-like	22824	4q28	YES
218346_s_at	0.587130562	8.54292212	1.78E-06	0.005688746	SESN1	sestrin 1	27244	6q21	YES
236640_at	-0.59668149	-8.50323587	1.87E-06	0.005688746	LOC399959	Hypothetical LOC399959	399959	11q24.1	YES
215719_x_at	0.6823407	8.23071828	2.63E-06	0.007063346	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
200974_at	0.549493843	8.20661423	2.71E-06	0.007063346	ACTA2	actin, alpha 2, smooth muscle, aorta	59	10q23.3	YES
201060_x_at	0.53978797	8.19617736	2.75E-06	0.007063346	STOM	stomatin	2040	9q34.1	YES
242134_at	0.618378387	8.17025563	2.84E-06	0.007063346	---	---	---	---	
231534_at	0.554439703	8.10335853	3.10E-06	0.007357641	CDK1	Cyclin-dependent kinase 1	983	10q21.1	
1566147_a_at	0.728594773	8.03176513	3.39E-06	0.007729129	LOC375010	ankyrin repeat domain 20 family, member A pseudogene	375010	1q21.1	YES
208579_x_at	-0.62627162	-7.85369249	4.27E-06	0.009347256	H2BFS	H2B histone family, member S	54145	21q22.3	
228582_x_at	0.787458567	7.77673727	4.73E-06	0.009369709	MALAT1	Metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	378938	11q13.1	
210609_s_at	0.586057234	7.75678018	4.85E-06	0.009369709	TP53I3	tumor protein p53 inducible protein 3	9540	2p23.3	
235456_at	-1.10645703	-7.75393722	4.87E-06	0.009369709	---	---	---	---	
229711_s_at	0.607335871	7.7388853	4.97E-06	0.009369709	MDM2	Mdm2 p53 binding protein homolog (mouse)	4193	12q14.3-q15	YES
229795_at	-0.54843367	-7.59569238	6.01E-06	0.010895418	---	---	---	---	
208890_s_at	0.593964757	7.57532558	6.18E-06	0.010895418	PLXNB2	plexin B2	23654	22q13.33	YES
229868_s_at	1.052165298	7.44897527	7.32E-06	0.012514035	LOC100287132	hypothetical protein LOC100287132	100287132	19p13.11	YES
234689_at	0.953982594	7.3123553	8.82E-06	0.014619659	C6orf138	chromosome 6 open reading frame 138	442213	6p12.3	
225912_at	0.716295931	7.28046319	9.22E-06	0.014825257	TP53INP1	tumor protein p53 inducible nuclear protein 1	94241	8q22	YES
220623_s_at	0.598129995	7.12326061	1.15E-05	0.017906987	TSGA10	testis specific, 10	80705	2q11.2	YES
1561754_at	0.752863772	7.07149035	1.23E-05	0.018227574	---	---	---	---	
209375_at	0.433008665	7.07085513	1.23E-05	0.018227574	XPC	xeroderma pigmentosum, complementation group C	7508	3p25	YES
217373_x_at	0.668641399	7.00726412	1.35E-05	0.01940828	MDM2	Mdm2 p53 binding protein homolog (mouse)	4193	12q14.3-q15	
228176_at	0.63576854	6.89245445	1.59E-05	0.022253606	S1PR3	sphingosine-1-phosphate receptor 3	1903	9q22.1-q22.2	YES
209693_at	0.841187944	6.82104892	1.76E-05	0.023282887	ASTN2	astrotactin 2	23245	9q33.1	
201392_s_at	0.513431286	6.82209671	1.76E-05	0.023282887	IGF2R	insulin-like growth factor 2 receptor	3482	6q26	
237241_at	0.609194314	6.80738014	1.79E-05	0.023282887	ECT2	Epithelial cell transforming sequence 2 oncogene	1894	3q26.1-q26.2	
218192_at	0.404185932	6.79267799	1.83E-05	0.023282887	IP6K2	inositol hexakisphosphate kinase 2	51447	3p21.31	
211767_at	0.492003221	6.72845486	2.01E-05	0.024962339	GINS4	GINS complex subunit 4 (Sld5 homolog)	84296	8p11.21	
235102_x_at	0.463216647	6.71244826	2.06E-05	0.024979831	---	---	---	---	
216252_x_at	0.551150618	6.65313722	2.24E-05	0.026635682	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
235681_at	-0.70819464	-6.53068985	2.68E-05	0.030442341	---	---	---	---	
230090_at	0.495712416	6.52839339	2.69E-05	0.030442341	LOC100287032	similar to hCG2006445	100287032	5p13.2	
219361_s_at	0.415127106	6.50680056	2.78E-05	0.030442341	AEN	apoptosis enhancing nuclease	64782	15q26.1	
209709_s_at	0.366780512	6.49853714	2.81E-05	0.030442341	HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	5q33.2-qter	YES
226093_at	0.404489532	6.49178567	2.84E-05	0.030442341	DCP1B	DCP1 decapping enzyme homolog B (S. cerevisiae)	196513	12p13.33	YES
219928_s_at	0.596810459	6.46447512	2.96E-05	0.031088475	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	26256	18q11.2	
229442_at	0.376682736	6.32579134	3.64E-05	0.037509865	C18orf54	chromosome 18 open reading frame 54	162681	18q21.2	
211163_s_at	0.796459467	6.26260955	4.00E-05	0.040487794	TNFRSF10C	or necrosis factor receptor superfamily, member 10c, decoy without an intracellular dom	8794	8p22-p21	
240574_at	-0.73005206	-6.24891982	4.08E-05	0.040582074	---	---	---	---	
241014_at	0.88013434	6.21756295	4.28E-05	0.041794375	LOC339400	hypothetical protein LOC339400	339400	1q21.3	
219655_at	0.585624754	6.17501992	4.57E-05	0.043801166	C7orf10	chromosome 7 open reading frame 10	79783	7p14.1	YES
235217_at	-0.50448754	-6.15228329	4.73E-05	0.044562587	LOC100216546	hypothetical LOC100216546	100216546	---	
217168_s_at	-0.47557235	-6.12601403	4.92E-05	0.04505211	HERPUD1	ocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain mem	9709	16q12.2-q13	
228620_at	0.600746772	6.1162946	4.99E-05	0.04505211	---	---	---	---	
201061_s_at	0.408183651	6.11210921	5.03E-05	0.04505211	STOM	stomatin	2040	9q34.1	YES
235534_at	0.519974802	6.10049006	5.12E-05	0.045120932	---	---	---	---	