Supplementary Table 3. Genome-wide expression analysis of sh-p105 cells treated with vehicle vs. sh-p105 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	1.620650	20.75548645	7.73E-11	0.0000042	GDF15 /// LOC100292463	growth differentiation factor 15 /// similar to growth differentiation factor 15	100292463 /// 9518	19p13.11	YES
202284_s_at	0.922874	14.35487549	5.71E-09	0.0001362	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1026	6p21.2	YES
207813_s_at	0.963293	14.02171158	7.47E-09	0.0001362	FDXR	ferredoxin reductase	2232	17q24-q25	YES
237737_at	0.853938	12.71013739	2.29E-08	0.0003129	LOC100289026	similar to hCG1744891	100289026	---	YES
1559462_at	0.930399	12.22237523	3.56E-08	0.0003895	---	---	---	---	YES
236640_at	-0.717386	-10.22338716	2.59E-07	0.0021283	LOC399959	Hypothetical LOC399959	399959	11q24.1	YES
203409_at	0.650551	10.17721875	2.72E-07	0.0021283	DDB2	damage-specific DNA binding protein 2, 48kDa	1643	11p12-p11	YES
218346_s_at	0.671656	9.77278549	4.24E-07	0.0028963	SESN1	sestrin 1	27244	6q21	YES
1555786_s_at	0.579254	9.49911721	5.76E-07	0.0029713	C14orf34	chromosome 14 open reading frame 34	645687	14q22.3	
204780_s_at	0.617602	9.451057183	6.09E-07	0.0029713	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
201236_s_at	0.826902	9.415419015	6.34E-07	0.0029713	BTG2	BTG family, member 2	7832	1q32	YES
238733_at	0.884952	9.390489092	6.52E-07	0.0029713	---	---	---	---	YES
229868_s_at	1.311703	9.286411985	7.35E-07	0.0030915	LOC100287132	hypothetical protein LOC100287132	100287132	19p13.11	YES
239814_at	0.631694	9.122543569	8.89E-07	0.0034734	---	---	---	---	
201061_s_at	0.596538	8.932516235	1.11E-06	0.0040572	STOM	stomatin	2040	9q34.1	YES
205543_at	0.571807	8.855661359	1.22E-06	0.0041691	HSPA4L	heat shock 70kDa protein 4-like	22824	4q28	YES
204781_s_at	0.495217	8.135050207	2.97E-06	0.0084026	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
238364_x_at	0.565576	8.13055041	2.99E-06	0.0084026	GLI4	GLI family zinc finger 4	2738	8q24.3	
225842_at	-0.500197	-8.117276308	3.04E-06	0.0084026	PHLDA1	pleckstrin homology-like domain, family A, member 1	22822	12q15	
1558846_at	0.498705	8.099020986	3.11E-06	0.0084026	PNLIPRP3	pancreatic lipase-related protein 3	119548	10q25.3	
1566147_a_at	0.732125	8.070685087	3.23E-06	0.0084026	LOC375010	ankyrin repeat domain 20 family, member A pseudogene	375010	1q21.1	YES
227863_at	-0.562050	-7.960279441	3.72E-06	0.0087544	LOC402778	CD225 family protein FLJ76511	402778	11p15.5	
238232_at	0.943308	7.877297547	4.14E-06	0.0087544	---	---	---	---	
1554015_a_at	0.490561	7.876145475	4.15E-06	0.0087544	CHD2	chromodomain helicase DNA binding protein 2	1106	15q26	
226093_at	0.490768	7.876501384	4.15E-06	0.0087544	DCP1B	DCP1 decapping enzyme homolog B (S. cerevisiae)	196513	12p13.33	YES
209773_s_at	0.423316	7.817146237	4.48E-06	0.0087544	RRM2	ribonucleotide reductase M2	6241	2p25-p24	
200974_at	0.523183	7.81366715	4.50E-06	0.0087544	ACTA2	actin, alpha 2, smooth muscle, aorta	59	10q23.3	YES
209806_at	-0.491508	-7.769822194	4.77E-06	0.0087544	HIST1H2BK	histone cluster 1, H2bk	85236	6p21.33	YES
239870_at	0.863530	7.766091457	4.79E-06	0.0087544	SPATS1	spermatogenesis associated, serine-rich 1	221409	6p21.1	
208890_s_at	0.608812	7.764681082	4.80E-06	0.0087544	PLXNB2	plexin B2	23654	22q13.33	YES
220818_s_at	0.558542	7.721839341	5.08E-06	0.0089649	TRPC4	transient receptor potential cation channel, subfamily C, member 4	7223	13q13.1-q13.2	
215407_s_at	0.730492	7.658344364	5.53E-06	0.0094477	ASTN2	astrotactin 2	23245	9q33.1	
218634_at	0.482353	7.420039607	7.62E-06	0.0126208	PHLDA3	pleckstrin homology-like domain, family A, member 3	23612	1q31	
209375_at	0.451249	7.368716001	8.17E-06	0.0127813	XPC	xeroderma pigmentosum, complementation group C	7508	3p25	YES
201060_x_at	0.485216	7.367557063	8.18E-06	0.0127813	STOM	stomatin	2040	9q34.1	YES
228176_at	0.672300	7.288493061	9.12E-06	0.0138478	S1PR3	sphingosine-1-phosphate receptor 3	1903	9q22.1-q22.2	YES
219508_at	0.456304	7.262071985	9.46E-06	0.0139726	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	9245	15q21.3	
218248_at	0.424573	7.220481838	1.00E-05	0.0144091	FAM111A	family with sequence similarity 111, member A	63901	11q12.1	
235063_at	0.393013	7.157565193	1.09E-05	0.0151761	C20orf196	chromosome 20 open reading frame 196	149840	20p12.3	
215719_x_at	0.592430	7.146167394	1.11E-05	0.0151761	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
240228_at	0.687953	7.126187537	1.14E-05	0.0152241	CSMD3	CUB and Sushi multiple domains 3	114788	8q23.3	
220623_s_at	0.586785	6.98815598	1.39E-05	0.0180400	TSGA10	testis specific, 10	80705	2q11.2	YES
222879_s_at	0.523327	6.874603097	1.63E-05	0.0204055	POLH	polymerase (DNA directed), eta	5429	6p21.1	
215977_x_at	0.394300	6.868676324	1.64E-05	0.0204055	GK	glycerol kinase	2710	Xp21.3	
214696_at	-0.381561	-6.752585813	1.94E-05	0.0234991	C17orf91	chromosome 17 open reading frame 91	84981	17p13.3	
225381_at	-0.443490	-6.726633602	2.01E-05	0.0234991	LOC399959	hypothetical LOC399959	399959	11q24.1	
215364_s_at	0.449246	6.724618572	2.02E-05	0.0234991	KIAA0467	KIAA0467	23334	1p34.2	
209301_at	0.563566	6.676877558	2.16E-05	0.0240133	CA2	carbonic anhydrase II	760	8q22	
236105_at	0.628684	6.649402409	2.25E-05	0.0240133	ZBTB10	zinc finger and BTB domain containing 10	65986	8q13-q21.1	
235251_at	-0.468699	-6.647428348	2.26E-05	0.0240133	---	---	---	---	
60084_at	-0.477132	-6.64136502	2.28E-05	0.0240133	CYLD	cylindromatosis (turban tumor syndrome)	1540	16q12.1	
208257_x_at	0.453865	6.627386471	2.33E-05	0.0240133	PSG1	pregnancy specific beta-1-glycoprotein 1	5669	19q13.2	
240259_at	0.679901	6.627075001	2.33E-05	0.0240133	FLRT2	Fibronectin leucine rich transmembrane protein 2	23768	14q24-q32	
210046_s_at	0.403229	6.530480613	2.68E-05	0.0271554	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	3418	15q26.1	
204566_at	0.561175	6.511788646	2.76E-05	0.0274066	PPM1D	protein phosphatase, Mg2+/Mn2+ dependent, 1D	8493	17q23.2	
200798_x_at	-0.502992	-6.492073004	2.84E-05	0.0277125	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	4170	1q21	
204803_s_at	0.518074	6.42354654	3.14E-05	0.0301382	RRAD	Ras-related associated with diabetes	6236	16q22	
1555623_at	-0.866557	-6.410693768	3.20E-05	0.0301906	---	---	---	---	
206039_at	0.422015	6.395719458	3.27E-05	0.0303486	RAB33A	RAB33A, member RAS oncogene family	9363	Xq26.1	
225803_at	0.433874	6.365370539	3.43E-05	0.0309646	FBXO32	F-box protein 32	114907	8q24.13	
225912_at	0.625730	6.359946737	3.45E-05	0.0309646	TP53INP1	tumor protein p53 inducible nuclear protein 1	94241	8q22	YES
213293_s_at	0.426763	6.320348547	3.67E-05	0.0319229	TRIM22	tripartite motif-containing 22	10346	11p15	
209709_s_at	0.356596	6.318089769	3.68E-05	0.0319229	HMMR	hyaluronan-mediated motility receptor (RHAMM)	3161	5q33.2-qter	YES
226552_at	-0.377600	-6.291841559	3.83E-05	0.0326868	IER5L	immediate early response 5-like	389792	9q34.11	
216252_x_at	0.520116	6.278501574	3.90E-05	0.0326868	FAS	Fas (TNF receptor superfamily, member 6)	355	10q24.1	YES
204774_at	0.425515	6.271463065	3.95E-05	0.0326868	EVI2A	ecotropic viral integration site 2A	2123	17q11.2	
1556496_a_at	-0.526914	-6.258008214	4.03E-05	0.0328594	---	---	---	---	
217920_at	0.424788	6.24092634	4.13E-05	0.0332228	MAN1A2	mannosidase, alpha, class 1A, member 2	10905	1p13	
205733_at	0.365998	6.202096908	4.38E-05	0.0343442	BLM	Bloom syndrome, RecQ helicase-like	641	15q26.1	
206239_s_at	0.519974	6.199882879	4.40E-05	0.0343442	SPINK1	serine peptidase inhibitor, Kazal type 1	6690	5q32	
210559_s_at	0.380993	6.188007239	4.48E-05	0.0344768	CDK1	cyclin-dependent kinase 1	983	10q21.1	
212298_at	-0.402586	-6.169143862	4.61E-05	0.0349874	NRP1	neuropilin 1	8829	10p12	
209648_x_at	-0.458447	-6.158004798	4.69E-05	0.0350985	SOCS5	suppressor of cytokine signaling 5	9655	2p21	
221611_s_at	0.481379	6.143388324	4.79E-05	0.0352140	PHF7	PHD finger protein 7	51533	3p21.1	
240969_at	0.493112	6.13812732	4.83E-05	0.0352140	---	---	---	---	
1553348_a_at	0.440738	6.124779213	4.93E-05	0.0353159	NFX1	nuclear transcription factor, X-box binding 1	4799	9p13.3	
204011_at	-0.367115	-6.119009721	4.97E-05	0.0353159	SPRY2	sprouty homolog 2 (Drosophila)	10253	13q31.1	
231180_at	0.512656	6.093443495	5.17E-05	0.0362547	---	---	---	---	
213139_at	-0.385191	-6.066395054	5.39E-05	0.0364912	SNAI2	snail homolog 2 (Drosophila)	6591	8q11	
1554783_s_at	0.728941	6.061593632	5.43E-05	0.0364912	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	9181	1q21-q22	
219655_at	0.574472	6.057416788	5.47E-05	0.0364912	C7orf10	chromosome 7 open reading frame 10	79783	7p14.1	YES
237352_at	-0.447874	-6.05663111	5.47E-05	0.0364912	---	---	---	---	
229711_s_at	0.472421	6.019758455	5.79E-05	0.0379516	MDM2	Mdm2 p53 binding protein homolog (mouse)	4193	12q14.3-q15	YES
215785_s_at	0.402287	6.015517713	5.83E-05	0.0379516	CYFIP2	cytoplasmic FMR1 interacting protein 2	26999	5q33.3	
226800_at	0.527267	5.971554837	6.24E-05	0.0397661	EFCAB7	EF-hand calcium binding domain 7	84455	1p31.3	
209230_s_at	0.482496	5.970104834	6.25E-05	0.0397661	NUPR1	nuclear protein, transcriptional regulator, 1	26471	16p11.2	
210416_s_at	0.356868	5.961032015	6.34E-05	0.0398658	CHEK2	CHK2 checkpoint homolog (S. pombe)	11200	22q11|22q12.1	
222162_s_at	-0.376227	-5.941223246	6.54E-05	0.0406436	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	9510	21q21.2	
223196_s_at	0.379700	5.921114661	6.75E-05	0.0414635	SESN2	sestrin 2	83667	1p35.3	
208107_s_at	0.386089	5.90475031	6.92E-05	0.0418264	LOC81691	exonuclease NEF-sp	81691	16p12.3	
206157_at	-0.495451	-5.898246042	6.99E-05	0.0418264	PTX3	pentraxin 3, long	5806	3q25	
215205_x_at	0.394994	5.894250438	7.04E-05	0.0418264	NCOR2	nuclear receptor co-repressor 2	9612	12q24	
227230_s_at	0.326073	5.875902914	7.24E-05	0.0425793	KIAA1211	KIAA1211	57482	4q12	
241553_at	0.660557	5.8477461	7.57E-05	0.0440240	GSG1	germ cell associated 1	83445	12p13.1	
1552519_at	0.371931	5.835832027	7.71E-05	0.0443818	ACVR1C	activin A receptor, type IC	130399	2q24.1	
208025_s_at	-0.348982	-5.828649008	7.80E-05	0.0444173	HMGA2	high mobility group AT-hook 2	8091	12q15	
204958_at	0.449661	5.797177238	8.19E-05	0.0461884	PLK3	polo-like kinase 3 (Drosophila)	1263	1p34.1	
206587_at	-0.462800	-5.755524933	8.75E-05	0.0487674	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2)	10693	17q12	
203214_x_at	0.343780	5.747090354	8.87E-05	0.0487674	CDK1	cyclin-dependent kinase 1	983	10q21.1	
219643_at	-0.581421	-5.739665141	8.97E-05	0.0487674	LRP1B	low density lipoprotein receptor-related protein 1B	53353	2q21.2	
224753_at	0.361744	5.737141063	9.01E-05	0.0487674	CDCA5	cell division cycle associated 5	113130	11q12.1	