

1 **Supplementary information**

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3 **An altered gene expression profile in tyramine-exposed intestinal cell**  
 4 **cultures supports the genotoxicity of this biogenic amine at dietary**  
 5 **concentrations**

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10 **Table 1S.** Gene expression analysis of tyramine-, histamine- and putrescine-  
 11 exposed HT29 cells compared to untreated HT29 cells using the RT<sup>2</sup> Profiler™ PCR  
 12 Arrays Human Cancer Pathway Finder array (PAHS-033ZC, Qiagen).

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Gene symbol	Description	Tma/Control		Hma/Control		Put/Control	
		Fold change	p-value	Fold change	p-value	Fold change	p-value
<b>Angiogenesis</b>							
ANGPT1	Angiopoietin 1	-1.88	0.1243	-1.49	0.3312	-1.930	0.0922
ANGPT2	Angiopoietin 2	-1.58	0.2391	2.91	0.0536	2.160	0.1380
CCL2	Chemokine (C-C motif) ligand 2	1.37	0.2061	1.14	0.5710	-1.040	0.7618
FGF2	Fibroblast growth factor 2 (basic)	-1.64	0.0249	1.13	0.5383	-1.390	0.4600
FLT1	Fms-related tyrosine kinase 1	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
KDR	Kinase insert domain receptor (a type III receptor tyrosine kinase)	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
PGF	Placental growth factor	4.87	0.0672	1.96	0.1298	-1.210	0.5668
SERPINF1	Serpin peptidase inhibitor, clade F, member 1	-2.22	0.0698	1.25	0.4446	1.420	0.2546
TEK	TEK tyrosine kinase, endothelial	-4.90	0.0574	-2.12	0.2231	-1.560	0.2521
VEGFC	Vascular endothelial growth factor C	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
<b>Apoptosis</b>							
APAF1	Apoptotic peptidase activating factor 1	1.41	0.5716	1.30	0.6237	1.390	0.5301
BCL2L11	BCL2-like 11 (apoptosis facilitator)	2.70	0.1541	1.19	0.5451	1.040	0.9924
BIRC3	Baculoviral IAP repeat containing 3	-2.31	0.1213	-1.22	0.7010	-1.150	0.9962
CASP2	Caspase 2, apoptosis-related cysteine peptidase	-1.27	0.5067	-1.08	0.8029	-1.310	0.5039
CASP7	Caspase 7, apoptosis-related cysteine peptidase	-2.62	0.0356	-1.31	0.2277	-1.060	0.8923

CASP9	Caspase 9, apoptosis-related cysteine peptidase	-1.57	0.2327	-1.04	0.8403	-1.220	0.2304
CFLAR	CASP8 and FADD-like apoptosis regulator	1.04	0.7391	-1.40	0.0469	-1.460	0.0635
FASLG	Fas ligand (TNF superfamily, member 6)	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
NOL3	Nucleolar protein 3 (apoptosis repressor with CARD domain)	-2.27	0.1475	-1.18	0.6041	-1.250	0.3566
XIAP	X-linked inhibitor of apoptosis	-1.79	0.0798	1.00	0.9677	1.070	0.5874
<b>Cell Cycle</b>							
AURKA	Aurora kinase A	-2.57	0.0493	-1.26	0.3667	-1.320	0.4206
CCND2	Cyclin D2	1.39	0.1694	-1.08	0.8743	-1.040	0.7618
CCND3	Cyclin D3	1.12	0.8521	-1.28	0.5541	-1.320	0.4865
CDC20	Cell division cycle 20 homologue ( <i>S. cerevisiae</i> )	-1.50	0.0750	-1.17	0.3774	-1.200	0.6298
E2F4	E2F transcription factor 4, p107/p130-binding	-1.46	0.0274	-1.36	0.0250	-1.320	0.0698
MCM2	Minichromosome maintenance complex component 2	-3.29	0.1065	-2.18	0.2231	-1.730	0.4511
MKI67	Antigen identified by monoclonal antibody Ki-67	-1.51	0.3500	-1.05	0.7903	-1.340	0.5063
SKP2	S-phase kinase-associated protein 2 (p45)	-4.04	0.0599	-1.67	0.2235	-1.560	0.2710
STMN1	Stathmin 1	1.26	0.4939	-1.03	0.9435	-1.180	0.7388
WEE1	WEE1 homologue ( <i>S. pombe</i> )	1.22	0.5274	-1.45	0.4050	-1.320	0.5944
<b>Cellular Senescence</b>							
BMI1	BMI1 polycomb ring finger oncogene	-7.68	0.4092	1.11	0.4282	-1.050	0.5428
ETS2	V-Ets erythroblastosis virus E26 oncogene homologue 2 (avian)	-3.15	0.0291	-1.11	0.6217	-1.080	0.6165
IGFBP3	Insulin-like growth factor binding protein 3	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
IGFBP5	Insulin-like growth factor binding protein 5	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
IGFBP7	Insulin-like growth factor binding protein 7	1.05	0.9042	1.18	0.7192	1.470	0.3433
MAP2K1	Mitogen-activated protein kinase 1	-1.21	0.3543	1.02	0.9950	-1.050	0.7217
MAP2K3	Mitogen-activated protein kinase 3	1.03	0.9574	-1.10	0.8726	-1.410	0.4034
MAPK14	Mitogen-activated protein kinase 14	1.01	0.8941	-1.07	0.6595	1.030	0.8589
SERPINB2	Serpin peptidase inhibitor, clade B (ovalbumin), member 2	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
SOD1	Superoxide dismutase 1, soluble	1.13	0.1821	-1.07	0.7523	-1.120	0.4288
TBX2	T-box 2	1.27	0.3702	-1.16	0.6779	-1.120	0.5295
<b>DNA Damage &amp; Repair</b>							
DDB2	Damage-specific DNA binding protein 2, 48kDa	1.18	0.7198	1.09	0.9518	-1.040	0.8413
DDIT3	DNA-damage-inducible transcript 3	22.37	0.0924	3.52	0.1649	1.000	0.9946
ERCC3	Excision repair cross-complementing rodent repair deficiency, complementation group 3	-2.80	0.0127	-1.09	0.2256	-1.060	0.7288
ERCC5	Excision repair cross-complementing rodent repair deficiency, complementation group 5	-1.64	0.5008	1.01	0.9620	-1.140	0.4275
GADD45G	Growth arrest and DNA-damage-inducible, gamma	6.63	0.0122	1.53	0.0693	1.260	0.2258
LIG4	Ligase IV, DNA, ATP-dependent	1.02	0.8601	1.36	0.1682	1.060	0.8295
POLB	Polymerase (DNA directed), beta	1.58	0.0228	-1.04	0.7872	-1.060	0.6436
PPP1R15A	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	7.98	0.0035	1.32	0.3660	-1.600	0.0221
<b>Epithelial-to-Mesenchymal Transition (EMT)</b>							
CDH2	Cadherin 2, type 1, N-cadherin (neuronal)	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
DSP	Desmoplakin	-1.15	0.6654	-1.21	0.3742	-1.200	0.4693

FOXC2	Forkhead box C2 (MFH-1, mesenchyme forkhead 1)	4.25	0.0971	1.19	0.5013	1.120	0.6930
GSC	Goosecoid homeobox	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
KRT14	Keratin 14	1.20	0.1650	-1.39	0.2777	-1.170	0.3314
OCLN	Occludin	1.90	0.0068	1.15	0.5294	1.070	0.7531
SNAI1	Snail homologue 1 (Drosophila)	7.72	0.1157	1.07	0.7528	1.100	0.6270
SNAI2	Snail homologue 2 (Drosophila)	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
SNAI3	Snail homologue 3 (Drosophila)	1.19	0.6680	1.45	0.3774	1.700	0.1641
SOX10	SRY (sex determining region Y)-box 10	1.93	0.1528	-1.04	0.9625	1.240	0.4950
<b>Hypoxia signalling</b>							
ADM	Adrenomedullin	3.19	0.0989	1.10	0.6212	1.060	0.7108
ARNT	Aryl hydrocarbon receptor nuclear translocator	1.06	0.6516	1.81	0.0167	1.490	0.1144
CA9	Carbonic anhydrase IX	-1.45	0.0806	1.03	0.7780	-1.110	0.6548
EPO	Erythropoietin	1.37	0.2061	-1.07	0.8980	1.740	0.1819
HMOX1	Heme oxygenase (decycling) 1	13.53	0.0519	1.17	0.8034	1.180	0.7442
LDHA	Lactate dehydrogenase A	-2.08	0.0908	1.07	0.9893	1.060	0.9719
SLC2A1	Solute carrier family 2, member 1	-2.24	0.1029	-1.68	0.4578	-1.350	0.6493
<b>Metabolism</b>							
ACLY	ATP citrate lyase	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
ACSL4	Acyl-CoA synthetase long-chain family member 4	-1.50	0.1674	1.10	0.6949	-1.050	0.7660
ATP5A1	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	-1.87	0.0130	-1.15	0.4979	-1.090	0.5969
COX5A	Cytochrome c oxidase subunit Va	-1.18	0.1617	-1.11	0.5265	-1.120	0.4827
<b>CPT2</b>	Carnitine palmitoyltransferase 2	-9.09	0.0002	-2.95	0.0017	-2.180	0.0036
G6PD	Glucose-6-phosphate dehydrogenase	-1.24	0.9599	1.38	0.5701	1.310	0.6428
GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	-2.25	0.0553	-1.62	0.1418	-1.500	0.2296
LPL	Lipoprotein lipase	1.37	0.2061	-1.08	0.8743	-1.040	0.7618
PFKL	Phosphofructokinase, liver	-1.24	0.3087	-1.61	0.1607	-1.480	0.1378
UQCRC1	Ubiquinol-cytochrome c reductase, Rieske iron-sulphur polypeptide 1	-1.35	0.0502	-1.09	0.4166	-1.080	0.6013
<b>Telomeres &amp; Telomerase</b>							
DKC1	Dyskeratosis congenita 1, dyskerin	-1.70	0.2377	-1.17	0.5911	-1.270	0.4944
PINX1	PIN2/TERF1 interacting, telomerase inhibitor 1	-2.31	0.3755	1.04	0.8849	-1.150	0.6328
TEP1	Telomerase-associated protein 1	-1.34	0.3781	-1.35	0.2554	-1.190	0.4046
TERF1	Telomeric repeat binding factor (NIMA-interacting) 1	-1.52	0.4448	-1.21	0.4676	-1.140	0.5530
TERF2IP	Telomeric repeat binding factor 2, interacting protein	2.84	0.1859	-1.06	0.8169	-1.270	0.4599
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	-1.80	0.0690	-1.40	0.0502	-1.150	0.1582
TNKS	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-1.31	0.3000	-1.40	0.2539	-1.520	0.2922
TNKS2	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-2.08	0.1044	-1.14	0.5372	-1.020	0.9441

Genes were sorted by Functional Gene Grouping as outlined by the RT<sup>2</sup> Profiler™ PCR Array Human Cancer PathwayFinder™ Kit. Gene expression levels highlighted in boldface were confirmed by real-time qPCR analysis. Tma: tyramine; Hma: histamine; Put: putrescine.

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20 **Table 2S.** Gene expression of tyramine-exposed HT29 cells compared to untreated  
 21 HT29 cells using the RT<sup>2</sup> PCR Human DNA Damage Signaling Pathway array  
 22 (PAHS-029ZC, Qiagen).

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Gene symbol	Description	Tma/Control	
		Fold change	p-value
<b>ATM / ATR signalling</b>			
ATM	Ataxia telangiectasia mutated	-1.83	0.2063
ATR	Ataxia telangiectasia and Rad3 related	-2.26	0.0531
ATRIP	ATR interacting protein	-2.73	0.0454
BARD1	BRCA1 associated RING domain 1	-3.20	0.1430
BRCA1	Breast cancer 1, early onset	-1.92	0.2411
CDC25A	Cell division cycle 25 homologue A ( <i>S. pombe</i> )	-1.47	0.7119
CHEK1	CHK1 checkpoint homologue ( <i>S. pombe</i> )	-1.38	0.4933
CHEK2	CHK2 checkpoint homologue ( <i>S. pombe</i> )	-1.14	0.6314
CSNK2A2	Casein kinase 2, alpha prime polypeptide	1.47	0.1013
FANCD2	Fanconi anaemia, complementation group D2	-1.33	0.4814
H2AFX	H2A histone family, member X	1.03	0.8531
HUS1	HUS1 checkpoint homologue ( <i>S. pombe</i> )	-1.52	0.1916
MDC1	Mediator of DNA-damage checkpoint 1	-1.56	0.2740
PARP1	Poly (ADP-ribose) polymerase 1	-2.22	0.1493
RAD1	RAD1 homologue ( <i>S. pombe</i> )	1.07	0.8671
RAD17	RAD17 homologue ( <i>S. pombe</i> )	-1.83	0.0860
RAD50	RAD50 homologue ( <i>S. cerevisiae</i> )	-2.12	0.1005
RAD9A	RAD9 homologue A ( <i>S. pombe</i> )	1.10	0.8714
RBBP8	Retinoblastoma binding protein 8	-1.25	0.5131
RNF168	Ring finger protein 168	1.88	0.0783
RNF8	Ring finger protein 8	1.23	0.3715
SMC1A	Structural maintenance of chromosomes 1A	-1.07	0.6662
TOPBP1	Topoisomerase (DNA) II binding protein 1	-1.53	0.2681
TP53	Tumour protein p53	-2.38	0.1091
<b>DNA Damage &amp; Repair</b>			
CDK7	Cyclin-dependent kinase 7	1.65	0.0120
DDB1	Damage-specific DNA binding protein 1, 127kDa	-1.33	0.1018
DDB2	Damage-specific DNA binding protein 2, 48kDa	1.18	0.8008
ERCC1	Excision repair cross-complementing rodent repair deficiency, complementation group 1	-1.34	0.0649
ERCC2	Excision repair cross-complementing rodent repair deficiency, complementation group 2	-2.44	0.0259
LIG1	Ligase I, DNA, ATP-dependent	-1.89	0.2830
NTHL1	Nth endonuclease III-like 1 ( <i>E. coli</i> )	-1.50	0.1470
OGG1	8-oxoguanine DNA glycosylase	-1.03	0.8552

PCNA	Proliferating cell nuclear antigen	-1.69	0.2164
PNKP	Polynucleotide kinase 3'-phosphatase	-1.52	0.0998
RPA1	Replication protein A1, 70kDa	-2.17	0.0614
SIRT1	Sirtuin 1	4.42	0.0645
TP53	Tumour protein p53	-2.38	0.1091
XPA	Xeroderma pigmentosum, complementation group A	-2.19	0.0136
XPC	Xeroderma pigmentosum, complementation group C	-2.17	0.1902
<b>Base Excision Repair (BER)</b>			
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-1.22	0.1716
FEN1	Flap structure-specific endonuclease 1	-1.72	0.1985
LIG1	Ligase I, DNA, ATP-dependent	-1.89	0.2830
MBD4	Methyl-CpG binding domain protein 4	1.11	0.7889
MPG	N-methylpurine-DNA glycosylase	-1.38	0.0541
NTHL1	Nth endonuclease III-like 1 ( <i>E. coli</i> )	-1.50	0.1470
OGG1	8-oxoguanine DNA glycosylase	-1.03	0.8552
PARP1	Poly (ADP-ribose) polymerase 1	-2.22	0.1493
PCNA	Proliferating cell nuclear antigen	-1.69	0.2164
TP53	Tumour protein p53	-2.38	0.1091
UNG	Uracil-DNA glycosylase	-1.69	0.1833
XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	-1.45	0.2931
<b>Mismatch Repair (NMR)</b>			
ABL1	C-abl oncogene 1, non-receptor tyrosine kinase	1.04	0.7511
EXO1	Exonuclease 1	-1.37	0.3610
MLH1	MutL homologue 1, colon cancer, nonpolyposis type 2 ( <i>E. coli</i> )	-1.97	0.0770
MLH3	MutL homologue 3 ( <i>E. coli</i> )	-2.57	0.0115
MSH2	MutS homologue 2, colon cancer, nonpolyposis type 1 ( <i>E. coli</i> )	-2.49	0.1088
MSH3	MutS homologue 3 ( <i>E. coli</i> )	-1.15	0.5562
PCNA	Proliferating cell nuclear antigen	-1.69	0.2164
PMS1	PMS1 postmeiotic segregation increased 1 ( <i>S. cerevisiae</i> )	-3.95	0.0460
PMS2	PMS2 postmeiotic segregation increased 2 ( <i>S. cerevisiae</i> )	-1.44	0.0948
TP73	Tumour protein p73	-1.84	0.2684
<b>Double-Strand Break (DSB) Repair</b>			
ATM	Ataxia telangiectasia mutated	-1.83	0.2063
BLM	Bloom syndrome, RecQ helicase-like	-3.59	0.1165
BRCA1	Breast cancer 1, early onset	-1.92	0.2411
CHEK1	CHK1 checkpoint homologue ( <i>S. pombe</i> )	-1.38	0.4933
H2AFX	H2A histone family, member X	1.03	0.8531
HUS1	HUS1 checkpoint homologue ( <i>S. pombe</i> )	-1.52	0.1916
LIG1	Ligase I, DNA, ATP-dependent	-1.89	0.2830
MDC1	Mediator of DNA-damage checkpoint 1	-1.56	0.2740
MLH1	MutL homologue 1, colon cancer, nonpolyposis type 2 ( <i>E. coli</i> )	-1.97	0.0770
MRE11A	MRE11 meiotic recombination 11 homologue A ( <i>S. cerevisiae</i> )	-1.34	0.4849
NBN	Nibrin	-1.22	0.2421

PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	-1.66	0.1150
RAD50	RAD50 homologue ( <i>S. cerevisiae</i> )	-2.12	0.1005
RAD51	RAD51 homologue ( <i>S. cerevisiae</i> )	-1.44	0.3643
RPA1	Replication protein A1, 70kDa	-2.17	0.0614
TP53BP1	Tumour protein p53 binding protein 1	-1.05	0.7563
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	-3.82	0.1453
XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	-1.30	0.2698
<b>Other DNA Repair Genes</b>			
ATR	Ataxia telangiectasia and Rad3 related	-2.26	0.0531
ATRIP	ATR interacting protein	-2.73	0.0454
ATRX	Alpha thalassaemia/mental retardation syndrome X-linked	-1.52	0.2341
BARD1	BRCA1 associated RING domain 1	-3.20	0.1430
BRIP1	BRCA1 interacting protein C-terminal helicase 1	-2.12	0.2582
CHEK2	CHK2 checkpoint homologue ( <i>S. pombe</i> )	-1.14	0.6314
CIB1	Calcium and integrin binding 1 (calmyrin)	-1.15	0.4901
CRY1	Cryptochrome 1 (photolyase-like)	2.14	0.0496
FANCA	Fanconi anaemia, complementation group A	-1.09	0.7782
FANCD2	Fanconi anaemia, complementation group D2	-1.33	0.4814
FANCG	Fanconi anaemia, complementation group G	1.20	0.9450
<b>GADD45A</b>	Growth arrest and DNA-damage-inducible, alpha	4.94	0.0020
<b>GADD45G</b>	Growth arrest and DNA-damage-inducible, gamma	6.64	0.0131
RAD1	RAD1 homologue ( <i>S. pombe</i> )	1.07	0.8671
RAD17	RAD17 homologue ( <i>S. pombe</i> )	-1.83	0.0860
RAD18	RAD18 homologue ( <i>S. cerevisiae</i> )	-2.03	0.0659
RAD21	RAD21 homologue ( <i>S. pombe</i> )	-1.28	0.4098
RAD51B	RAD51 homologue B ( <i>S. cerevisiae</i> )	1.14	0.7212
RAD9A	RAD9 homologue A ( <i>S. pombe</i> )	1.10	0.8714
RBBP8	Retinoblastoma binding protein 8	-1.25	0.5131
REV1	REV1 homologue ( <i>S. cerevisiae</i> )	-1.10	0.9557
RNF168	Ring finger protein 168	1.88	0.0783
RNF8	Ring finger protein 8	1.23	0.3715
SMC1A	Structural maintenance of chromosomes 1A	-1.07	0.6662
SUMO1	SMT3 suppressor of Mif Two 3 homologue 1 ( <i>S. cerevisiae</i> )	1.00	0.9842
TOPBP1	Topoisomerase (DNA II) binding protein 1	-1.53	0.2681
XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	-1.76	0.3274
<b>Apoptosis</b>			
ATM	Ataxia telangiectasia mutated	-1.83	0.2063
ABL1	C-abl oncogene 1, non-receptor tyrosine kinase	1.04	0.7511
ATM	Ataxia telangiectasia mutated	-1.83	0.2063
BARD1	BRCA1 associated RING domain 1	-3.20	0.1430
BAX	BCL2-associated X protein	-1.28	0.2157
<b>BBC3</b>	BCL2 binding component 3	22.23	0.0055
BRCA1	Breast cancer 1, early onset	-1.92	0.2411
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	7.59	0.1030

CHEK2	CHK2 checkpoint homologue ( <i>S. pombe</i> )	-1.14	0.6314
CIB1	Calcium and integrin binding 1 (calmyrin)	-1.15	0.4901
CSNK2A2	Casein kinase 2, alpha prime polypeptide	1.47	0.1013
<b>PPP1R15A</b>	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	10.19	0.0017
PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	-1.66	0.1150
RAD21	RAD21 homologue ( <i>S. pombe</i> )	-1.28	0.4098
RAD9A	RAD9 homologue A ( <i>S. pombe</i> )	1.10	0.8714
SIRT1	Sirtuin 1	4.42	0.0645
TP53	Tumour protein p53	-2.38	0.1091
TP73	Tumour protein p73	-1.84	0.2684
<b>Cell Cycle</b>			
ATM	Ataxia telangiectasia mutated	-1.83	0.2063
ATR	Ataxia telangiectasia and Rad3 related	-2.26	0.0531
ATRIP	ATR interacting protein	-2.73	0.0454
CDC25A	Cell division cycle 25 homologue A ( <i>S. pombe</i> )	-1.47	0.7119
CDC25C	Cell division cycle 25 homologue C ( <i>S. pombe</i> )	1.01	0.9110
CDK7	Cyclin-dependent kinase 7	1.65	0.0120
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	7.59	0.1030
CHEK1	CHK1 checkpoint homologue ( <i>S. pombe</i> )	-1.38	0.4933
CHEK2	CHK2 checkpoint homologue ( <i>S. pombe</i> )	-1.14	0.6314
<b>DDIT3</b>	DNA-damage-inducible transcript 3	20.20	0.0927
MAPK12	Mitogen-activated protein kinase 12	-1.31	0.3922
MCPH1	Microcephalin 1	1.41	0.0537
MDC1	Mediator of DNA-damage checkpoint 1	-1.56	0.2740
PPM1D	Protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent, 1D	3.94	0.1147
<b>PPP1R15A</b>	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	10.19	0.0017
TP53	Tumour protein p53	-2.38	0.1091
TP73	Tumour protein p73	-1.84	0.2684

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Genes were sorted by Functional Gene Grouping as outlined by the RT<sup>2</sup> Profiler™ PCR Array Human Cancer PathwayFinder™ Kit. Gene expression levels highlighted in boldface were confirmed by real-time qPCR analysis. Tma: tyramine.