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Novel antioxidants are not toxic to normal tissues but effectively kill cancer cells

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Table S1. Genes differentially expressed in EpiOral tissues treated with 1b antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	***Fold change (Log2)***	***Gene Name***
ARRDC4	-1.12	arrestin domain containing 4
JUN	-0.82	Jun oncogene
SOX2	-0.80	SRY (sex determining region Y)-box 2
HBEGF	-0.74	heparin-binding EGF-like growth factor
ADRB2	-0.71	adrenergic, beta-2-, receptor, surface
SERTAD1	-0.69	SERTA domain containing 1
SOX9	-0.59	SRY (sex determining region Y)-box 9
SRXN1	-0.58	sulfiredoxin 1 homolog
ECHDC2	0.58	enoyl Coenzyme A hydratase domain containing 2
LOC158160	0.72	hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2
LOC123688	0.82	aminoglycoside phosphotransferase domain containing 1
DTWD2	0.85	similar to DTW domain containing 2

Table S2. Genes differentially expressed in EpiOral tissues treated with 2a antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	***Fold change (log 2)***	***Gene name***
ADM	1.09	adrenomedullin
ADRB2	-0.86	adrenergic, beta-2-, receptor, surface
ANKRD37	0.91	ankyrin repeat domain 37
DDIT4	1.02	DNA-damage-inducible transcript 4
EGR1	0.71	early growth response 1
LOC440926	-0.59	H3 histone, family 3B (H3.3B); H3 histone, family 3A pseudogene; H3 histone, family 3A; similar to H3 histone, family 3B; similar to histone H3.3B
MIR1974	1.44	microRNA 1974
OVOL2	-0.64	ovo-like 2 (Drosophila)
PFKFB3	0.83	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
PPIB	-0.65	peptidylprolyl isomerase B (cyclophilin B)
RNU4-2	0.63	RNA, U4 small nuclear 2; RNA, U4 small nuclear 1; RNA, U4 small nuclear 1B
SGK1	-0.58	serum/glucocorticoid regulated kinase 1
SNORD56	0.66	small nucleolar RNA, C/D box 56; small nucleolar RNA, C/D box 56B
SOX2	-0.69	SRY (sex determining region Y)-box 2
SPRR2C	-0.62	small proline-rich protein 2C (pseudogene); small proline-rich protein 2G

Table S3. Genes differentially expressed in EpiOral tissues treated with 2b antioxidant compound (1.5 fold cut-off). No genes were differentially regulated at more than 2 fold cut-off.

SYMBOL	***Fold (log 2)***	***Gene name***
ADRB2	-0.75	adrenergic, beta-2-, receptor, surface
AGAP8	0.57	ArfGAP with GTPase domain, ankyrin repeat and PH domain 8
HBEGF	-0.75	heparin-binding EGF-like growth factor
PHF23	-0.58	PHD finger protein 23
PTPLAD2	0.57	protein tyrosine phosphatase-like A domain containing 2

Table S4. Genes differentially expressed in EpiOral tissues treated with 1a antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	***Fold (log 2)***	***Gene name***
ADM	2.82	adrenomedullin
ADRB2	-1.24	adrenergic, beta-2-, receptor, surface
ANKRD37	2.11	ankyrin repeat domain 37
ANKRD38	-0.64	ankyrin repeat domain 38
BHLHB2	0.63	Class E basic helix-loop-helix protein 40
C1orf74	-0.67	chromosome 1 open reading frame 74
CDK5R1	-0.64	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
CYP1B1	-0.65	cytochrome P450, family 1, subfamily B, polypeptide 1
DDIT4	1.80	DNA-damage-inducible transcript 4
DUSP1	1.50	dual specificity phosphatase 1
DUSP6	-0.94	dual specificity phosphatase 6
DYRK2	-0.61	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
EGR1	1.27	early growth response 1
FAM84B	-0.74	family with sequence similarity 84, member B
FAT2	-0.68	FAT tumor suppressor homolog 2 (Drosophila)
FERMT1	-0.71	fermitin family homolog 1 (Drosophila)
FLRT3	-0.65	fibronectin leucine rich transmembrane protein 3
FTSJD1	-0.61	FtsJ methyltransferase domain containing 1
GFOD1	-0.62	glucose-fructose oxidoreductase domain containing 1
HBEGF	-0.77	heparin-binding EGF-like growth factor
HES1	0.91	hairy and enhancer of split 1, (Drosophila)
HES5	-1.12	hairy and enhancer of split 5 (Drosophila)
HSZFP36	-0.60	small RNA
IER3	0.95	immediate early response 3
IER5	-0.93	immediate early response 5
IRX3	-0.81	iroquois homeobox 3
IRX5	-0.91	iroquois homeobox 5
KIAA0182	-0.61	KIAA0182
MEX3C	-0.61	mex-3 homolog C (C. elegans)
MMP10	-0.63	matrix metallopeptidase 10 (stromelysin 2)
MYC	-0.85	v-myc myelocytomatosis viral oncogene homolog (avian)
PLAGL2	-0.58	pleiomorphic adenoma gene-like 2; similar to pleiomorphic adenoma gene-like 2
PPP1R3C	1.45	protein phosphatase 1, regulatory (inhibitor) subunit 3C
RND3	-0.87	Rho family GTPase 3
SERPINE1	-0.80	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
SFRS6	-0.60	splicing factor, arginine/serine-rich 6; similar to arginine/serine-rich splicing factor 6
SFRS7	-0.60	splicing factor, arginine/serine-rich 7, 35kDa
SLC16A9	-0.61	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)
SNORA12	-1.67	small nucleolar RNA, H/ACA box 12
SOX2	-0.78	SRY (sex determining region Y)-box 2
SOX21	-0.97	SRY (sex determining region Y)-box 21
SOX9	-0.68	SRY (sex determining region Y)-box 9

SPRY2	-0.89	sprouty homolog 2 (Drosophila)
STK40	-0.71	serine/threonine kinase 40
TP53INP1	-0.66	tumor protein p53 inducible nuclear protein 1
TRIB1	-0.95	tribbles homolog 1 (Drosophila)
TSC22D2	-0.63	TSC22 domain family, member 2
ZBED5	-0.97	zinc finger, BED-type containing 5
ZC3H12C	-0.78	zinc finger CCCH-type containing 12C
ZFP36	1.11	zinc finger protein 36, C3H type, homolog (mouse)
ZNF217	-0.68	zinc finger protein 217
ZNF281	-0.63	zinc finger protein 281

Table S5. Genes differentially expressed in EpiGingival tissues treated with 1b antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	***Fold (log 2)***	***Gene name***
ABCA12	-0.66	ATP-binding cassette, sub-family A (ABC1), member 12
ANXA9	-0.77	annexin A9
ARG1	-0.78	arginase, liver
ARID5B	-0.65	AT rich interactive domain 5B (MRF1-like)
ASPRV1	-0.65	aspartic peptidase, retroviral-like 1
ATP10B	-0.90	ATPase, class V, type 10B
C10orf116	0.62	chromosome 10 open reading frame 116
C5orf46	-0.62	chromosome 5 open reading frame 46
CFLAR	-0.75	CASP8 and FADD-like apoptosis regulator
CLDN17	-0.64	claudin 17
CYP2C18	-0.63	cytochrome P450, family 2, subfamily C, polypeptide 18
CYP4B1	-0.61	cytochrome P450, family 4, subfamily B, polypeptide 1
CYP4F22	-0.63	cytochrome P450, family 4, subfamily F, polypeptide 22
DSC1	-0.79	desmocollin 1
DSG1	-0.66	desmoglein 1
EDN1	0.92	endothelin 1
EHF	-0.67	ets homologous factor
ELOVL4	-0.58	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
FETUB	-0.72	fetuin B
FLG	-0.71	filaggrin
FLG2	-0.89	filaggrin family member 2
FLJ22536	-0.61	hypothetical locus LOC401237
FLJ22662	-0.81	feline leukemia virus subgroup C cellular receptor family, member 2
FLVCR2	-0.60	
GLRX	-0.58	glutaredoxin (thioltransferase)
HAL	-0.70	histidine ammonia-lyase
HRNR	-0.80	hornerin
HSD17B4	-0.58	hydroxysteroid (17-beta) dehydrogenase 4
HSDL2	-0.69	hydroxysteroid dehydrogenase like 2
IQCG	-0.63	IQ motif containing G
KLK13	-0.75	kallikrein-related peptidase 13
KRT2	-0.75	keratin 2
LASS3	-0.60	LAG1 homolog, ceramide synthase 3
LCE1C	-0.83	late cornified envelope 1C
LOC100129144	-0.61	similar to hCG2042189
LOC100130246	-1.35	
LOC730833	-1.14	
LOC731486	-0.66	
LPHN2	-0.77	latrophilin 2
LY6G6C	-0.59	lymphocyte antigen 6 complex, locus G6C
MED27	-1.12	similar to cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa; mediator complex subunit 27; CRSP8 pseudogene
MYO1G	-0.66	myosin IG

PLA2G4D	-0.78	phospholipase A2, group IVD (cytosolic)
RNASE7	-0.58	ribonuclease, RNase A family, 7
RPTN	-0.92	repetin
SASH1	-0.69	SAM and SH3 domain containing 1
SH3BGRL2	-0.81	SH3 domain binding glutamic acid-rich protein like 2
SH3GL3	-0.68	SH3-domain GRB2-like 3
SPINK5	-0.66	serine peptidase inhibitor, Kazal type 5
SRPK1	-0.61	SFRS protein kinase 1
TAOK1	-0.68	TAO kinase 1
TCN1	-0.64	transcobalamin I (vitamin B12 binding protein, R binder family)
TGM5	-0.68	transglutaminase 5
TMPRSS11B	-0.63	transmembrane protease, serine 11B
TP53INP2	-0.77	tumor protein p53 inducible nuclear protein 2
ZNF91	-0.78	zinc finger protein 91

Table S6. Genes differentially expressed in EpiGingival tissues treated with 2a antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	*Fold (log 2)*	*Gene name*
ALDH1A3	0.66	aldehyde dehydrogenase 1 family, member A3
ALPP	-0.87	alkaline phosphatase, placental (Regan isozyme)
ALS2CR14	-0.63	
ANKRD30B	-0.62	ankyrin repeat domain 30B
ARG1	-0.59	arginase, liver
ARL16	-0.63	ADP-ribosylation factor-like 16
BLZF1	-0.69	basic leucine zipper nuclear factor 1
BMS1P5	-0.66	BMS1 pseudogene 5
C13orf15	0.64	chromosome 13 open reading frame 15
C14orf153	-0.72	chromosome 14 open reading frame 153
C14orf85	-0.65	
C15orf52	-0.59	chromosome 15 open reading frame 52
C15orf63	-0.84	chromosome 15 open reading frame 63; small EDRK-rich factor 2
C2orf69	-0.84	chromosome 2 open reading frame 69
C9orf130	-0.59	chromosome 9 open reading frame 130
C9orf80	-0.76	chromosome 9 open reading frame 80
CATSPER2	-0.66	cation channel, sperm associated 2
CCBE1	-0.76	collagen and calcium binding EGF domains 1
CCL20	0.63	chemokine (C-C motif) ligand 20
CD83	0.68	CD83 molecule
CEP27	-0.64	
CFLAR	-0.67	CASP8 and FADD-like apoptosis regulator
CGN	-0.66	cingulin
CRCP	-0.66	CGRP receptor component
CXCL1	0.58	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
DDX51	-0.75	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51
DKFZp434K191	-0.77	
DTWD2	-0.81	similar to DTW domain containing 2; DTW domain containing 2
DUSP19	-0.71	dual specificity phosphatase 19
EDN1	0.70	endothelin 1
EIF2AK4	-0.77	eukaryotic translation initiation factor 2 alpha kinase 4
EVI5	-0.67	ecotropic viral integration site 5
FAM175A	-0.85	family with sequence similarity 175, member A
FAM3D	-0.74	family with sequence similarity 3, member D
FKBP14	-0.73	FK506 binding protein 14, 22 kDa
FLG	-0.66	filaggrin
FLJ25363	-0.89	similar to hypothetical protein FLJ25976
FLJ35390	-0.88	hypothetical LOC255031
FLJ44124	-0.72	hypothetical LOC641737
FLJ46309	-0.65	

GFOD1	-0.59	glucose-fructose oxidoreductase domain containing 1
HIATL2	-1.05	hippocampus abundant transcript-like 2
HNRNPU	-0.62	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
HSD17B7	-0.84	hydroxysteroid (17-beta) dehydrogenase 7
LOC100128062	-0.61	
LOC100128084	-0.82	hypothetical LOC100128084
LOC100128288	-0.62	hypothetical protein LOC100128288
LOC100128505	-0.66	similar to hCG2021201
LOC100128510	-0.61	hypothetical protein LOC100128510
LOC100129211	-0.73	
LOC100129502	-0.83	hypothetical protein LOC100129502
LOC100129905	-0.66	
LOC100130053	-1.12	
LOC100130168	-0.70	hypothetical protein LOC100130168
LOC100130276	-0.66	hypothetical protein LOC100130276
LOC100130598	-0.63	
LOC100131718	-1.14	
LOC100131989	-0.97	
LOC100132391	-0.67	
LOC100132585	-0.92	hypothetical LOC100132581; similar to speedy homolog A; WBSCR19-like protein 5-like; speedy homolog E8 (Xenopus laevis), pseudogene
LOC100132727	-0.82	
LOC100133019	-0.62	similar to hCG1983765
LOC100133298	-0.77	
LOC100133516	-0.96	
LOC100133772	-0.61	similar to MCT; solute carrier family 16, member 5 (monocarboxylic acid transporter 6)
LOC100190938	-0.64	hypothetical LOC100190938
LOC255167	-0.61	hypothetical LOC255167
LOC389765	-1.02	similar to KIF27C
LOC399900	-0.78	hypothetical LOC399900
LOC401098	-0.90	hypothetical LOC401098
LOC401640	0.60	
LOC440157	-0.65	hypothetical gene supported by BC066547
LOC441087	-0.78	hypothetical gene supported by AK125735
LOC644250	-0.74	
LOC644642	-0.67	
LOC645452	-0.86	
LOC646786	-0.60	
LOC648852	-0.69	
LOC648921	-0.90	
LOC653158	-0.68	
LOC653829	-0.62	
LOC728105	-0.72	
LOC728205	-0.59	

LOC728620	-0.67	
LOC728809	-0.73	hypothetical LOC728809
LOC729120	-0.75	
LOC729603	-0.63	calcium binding protein P22 pseudogene
LOC730060	-0.66	hypothetical LOC730060
LOC730313	-0.79	
LPHN2	-0.61	latrophilin 2
LRAP	-0.70	
LRRC37B2	-1.05	leucine rich repeat containing 37, member B2
MAGT1	-0.87	magnesium transporter 1
MBD4	-0.83	methyl-CpG binding domain protein 4
MCART1	-0.92	mitochondrial carrier triple repeat 1
MFSD11	-0.61	major facilitator superfamily domain containing 11
MMP3	0.81	matrix metallopeptidase 3 (stromelysin 1, progelatinase)
MT1E	0.59	metallothionein 1L (gene/pseudogene); metallothionein 1E; metallothionein 1 pseudogene 3; metallothionein 1J (pseudogene)
NUBPL	-0.97	nucleotide binding protein-like
PIP5K2B	-0.75	
PLA2G2D	-0.79	phospholipase A2, group IID
PLDN	-0.68	pallidin homolog (mouse)
PNPT1	-0.71	polyribonucleotide nucleotidyltransferase 1
POF1B	-0.67	premature ovarian failure, 1B
PPP1R3C	0.62	protein phosphatase 1, regulatory (inhibitor) subunit 3C
PRO1853	-0.72	
QRFPR	-0.78	pyroglutamylated RFamide peptide receptor
RAXL1	-0.81	
RGS17	-0.60	regulator of G-protein signaling 17
RHBDL2	-0.72	rhomboid, veinlet-like 2 (Drosophila)
RPL7L1	-0.58	ribosomal protein L7-like 1; ribosomal protein L7 pseudogene 14; ribosomal protein L7 pseudogene 21; ribosomal protein L7 pseudogene 22; ribosomal protein L7 pseudogene 46
RPTN	-0.60	repetin
SHROOM4	-0.68	shroom family member 4
SMCR5	-0.67	Smith-Magenis syndrome chromosome region, candidate 5 (non-protein coding)
SNAPC1	-0.73	small nuclear RNA activating complex, polypeptide 1, 43kDa
SPINK5	-0.59	serine peptidase inhibitor, Kazal type 5
TAOK1	-0.75	TAO kinase 1
TMEM106A	-0.92	hypothetical LOC728772; transmembrane protein 106A
TMEM17	-0.82	transmembrane protein 17
TMEM45B	-0.69	transmembrane protein 45B
TP53INP2	-0.69	tumor protein p53 inducible nuclear protein 2
USP49	-0.78	ubiquitin specific peptidase 49
XPNPEP3	-0.62	X-prolyl aminopeptidase (aminopeptidase P) 3, putative
XRCC2	-0.60	X-ray repair complementing defective repair in Chinese hamster cells 2
ZNF223	-0.89	zinc finger protein 223
ZNF394	-0.64	zinc finger protein 394

ZNF486	-0.59	zinc finger protein 486
ZNF549	-0.75	zinc finger protein 549
ZNF69	-0.59	zinc finger protein 69
ZNF738	-0.96	zinc finger protein 738
ZNF786	-0.80	zinc finger protein 786
ZNF91	-0.86	zinc finger protein 91

Table S7. Genes differentially expressed in EpiGingival tissues treated with 2b antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	*Fold (log 2)*	*Gene name*
CCL20	0.70	chemokine (C-C motif) ligand 20
LOC100130246	-1.09	
LOC646786	-0.60	
LOC648390	0.65	
MED27	-0.88	similar to cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa; mediator complex subunit 27; CRSP8 pseudogene
TAOK1	-0.66	TAO kinase 1
TMEM45B	-0.60	transmembrane protein 45B
ZNF91	-0.69	zinc finger protein 91

Table S8. Genes differentially expressed in EpiGingival tissues treated with 1a antioxidant compound (1.5 fold cut-off). Genes differentially regulated at more than 2 fold cut-off are in red.

SYMBOL	***Fold (log 2)***	***Gene name***
ADM	0.70	adrenomedullin
BTG2	0.60	BTG family, member 2
CD83	0.74	FLJ22662
CDC42EP4	0.69	CDC42 effector protein (Rho GTPase binding) 4
DEFB4	0.63	
EDN1	1.09	endothelin 1
FLJ22662	-0.72	
IGFBP3	1.01	insulin-like growth factor binding protein 3
IL1F9	0.66	interleukin 1 family, member 9
IRF1	0.73	interferon regulatory factor 1
PPP1R3C	1.38	protein phosphatase 1, regulatory (inhibitor) subunit 3C
RNASE7	-0.96	ribonuclease, RNase A family, 7
S100A7	-0.79	S100 calcium binding protein A7
TNFAIP3	0.75	tumor necrosis factor, alpha-induced protein 3
ZNF395	0.65	zinc finger protein 395

Table S9. Genes differentially expressed in MCF-7/DOX cells treated with 1a and 1b antioxidant compounds (1.5 fold cut-off).

Dox_106 ONLY

SYMBOL	***Fold***
ADC	0.75771
ADRA1B	0.853348
BAT2D1	0.446098
C11orf10	0.666188
C16orf68	-0.73791
CALM3	0.903387
CAMK2N1	0.612474
CELSR3	0.955295
CHIC2	0.796941
CIC	0.552443
DACT3	1.123064
DNPEP	0.507162
ESPL1	0.892412
ETFDH	0.63956
EVI5L	0.702996
FAM53C	0.767975
FLOT2	0.910955
FOXO4	0.849295
HNRPR	0.480605
HOXA9	0.589548
IFT20	0.435192
LGALS1	1.258598
MBD6	0.877138
MDH2	0.709728
MGST3	0.978228
MLL5	0.847924
MYH10	0.590052
NDUFS4	0.465082
NR2F2	0.470414
OSR1	1.128449
PHC1	-0.49413
PPP4C	0.554091
PSENEN	0.619038
PYGL	0.892884
RAB12	0.541072
RN7SL1	0.453105
RNU4-1	-0.56835
RPRC1	0.424729
RSBN1	0.861488
RSPRY1	0.48187

Dox_1E_ONLY

SYMBOL	***Fold***
CYCSP52	-0.62166
LOC653994	-0.88086
MRPS30	-0.54535
NDUFA3	0.559712
PPP3R1	-0.63045
PSMD14	-0.83059
YWHAB	-0.64605

Common in 106 and 1e

	106	***1E***
EIF4G2	-0.81524	-0.55272
HEXB	0.771492	0.549012
NT5DC2	1.255453	0.794597

SEC11C	-0.45032
SFRS5	0.469174
SLC25A40	1.069229
SSBP2	0.624226
TAF15	0.573244
THRA	0.833
TOB1	0.55799
TP53BP1	0.603477
TUBB2B	0.742257
VPS37D	1.249846
XRCC1	0.951829

Table S10. Genes differentially expressed in MCF-7/CIS cells treated with 1a and 1b antioxidant compounds (1.5 fold cut-off).

Cis_1e_ONLY

SYMBOL	***Fold***
ANXA2P2	1.596063
ATP1A1	-1.03032
BAT2D1	-1.12143
BZW2	-1.0406
CHD4	-1.38716
CHIC2	1.049065
CHPF2	-1.03047
COPB1	-1.13418
CRYAB	1.274261
DNAJA1	-1.08602
DNPEP	-1.28634
E2F3	-0.98534
ENO3	-1.21868
EXT1	-1.18031
FAM120A	-1.03076
GGNBP2	-0.9523
H3F3A	-1.34728
KARS	-1.11506
KIAA0196	-1.00456
KIAA0261	-1.49738
LASP1	-0.98613
LOC100008588	1.382722
MDH1	-1.02147
MT1A	2.302722
MTHFD1	-1.12307
NAG18	1.281688
NFIX	-1.14973
PDGFA	-1.07687
PSMD1	-1.00757
PURB	-1.53049
RN7SK	6.093691
RN7SL1	1.69044
RNU11	1.972105
RNU1-3	2.933885
RNU1-5	2.883961
RNU1A3	2.702857
RNU1F1	2.675404
RNU1G2	2.951732
RNU5A	1.542016
RNU6-1	1.379539

Cis_106_ONLY

SYMBOL	***Fold***
ACTR1A	0.974304
AMD1	-0.99254
CALM3	1.075784
CELSR3	1.230935
CXorf56	-1.08643
CYCSP52	-1.2547
FLOT2	1.604271
FST	-1.3886
GTF2A2	-1.11167
HINT1	-1.2263
HNRPR	-1.10885
LOC728937	-0.98004
MED25	1.016188
MIR21	1.088675
PSENEN	1.248256
PSMC4	-1.16609
RPS4X	-2.05271
RSBN1	1.047825
SDHB	1.212738
SMS	-1.04767
SNORD62B	1.307799
TRAPPC3	1.172093
TRIP6	1.016845
UBQLN2	-1.19023
VPS37D	1.288699

Common in 106 and 1E

	106	**1e**
GMPS	-1.3152	-1.13499
NUP153	-1.3696	-1.52659
PPA1	-1.59763	-1.20682

RNU6-15	1.343619
RSPRY1	-0.95813
SERTAD2	-1.40228
SFRS2	-1.20178
SLMAP	-1.43483
SNX27	-0.98026
SRF	-1.36313
TNPO3	-1.26176
TRIP4	-0.97146
TUBA1A	-1.76773
TUBA3E	-1.38303
TUBB4Q	-1.31534
UBAP2L	-1.0714
UBR4	-0.9959
WDR57	-1.03687
ZNF207	-1.0055
ZNF674	1.216681