



COMPLETE SCREENING OF EXONS 2, 3, AND 4 OF *KRAS* AND *NRAS* GENES REVEALS A HIGHER NUMBER OF CLINICALLY RELEVANT MUTATIONS THAN FOOD AND DRUG ADMINISTRATION QUANTITATIVE POLYMERASE CHAIN REACTION-BASED COMMERCIAL KITS

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Table S1. Primer sequences and PCR product lengths

Primer name	Primer sequences	Genetic region	Fragment length
K2F	TGTGTGACATGTTCTAATATAGTCAC	<i>KRAS</i> Exon 2 (NC_000012.12)	216 bp
K2R	AGAATGGTCCTGCACCAGTAA		
K3F	ACTGTGTTTCTCCCTTCTCAG	<i>KRAS</i> Exon 3 (NC_000012.12)	282 bp
K3R	TGCATGGCATTAGCAAAGAC		
K4F	TCCAGAGAACAATTAAGAGAG	<i>KRAS</i> Exon 4 (NC_000012.12)	355 bp
K4R	AACCAAAGCCAAAAGCAGTACC		
N2F	CTCGCCAATTAACCCTGATT	<i>NRAS</i> Exon 2 (NC_000001.11)	213 bp
N2R	CCGACAAGTGAGAGACAGGA		
N3F	ACACCCCAGGATTCTTACAGA	<i>NRAS</i> Exon 3 (NC_000001.11)	126 bp
N3R	GACTTGCTATTATTGATGGC		
N4F	CCACTGTACCCAGCCTAATCTTG	<i>NRAS</i> Exon 4 (NC_000001.11)	257 bp
N4R	GCAAACCTCTGCACAAATGCTGA		

PCR: polymerase chain reaction.

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ANALYSIS OF THE ENDOMETRIAL TRANSCRIPTOME AT THE TIME OF IMPLANTATION IN WOMEN RECEIVING A SINGLE POST-OVULATORY DOSE OF LEVONORGESTREL OR MIFEPRISTONE

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Table S1. Comparison of gene directionality of 60 common differentially expressed genes in endometrial biopsies between T-LNG and ERA

Gene symbol	Gene name	ERA (FC)	T-LNG (FC)
GPX3	Glutathione peroxidase 3 (plasma)	35.49	3.66
LIF	Leukemia inhibitory factor (cholinergic differentiation factor)	15.03	2.14
CXCL14	Chemokine (C-X-C motif) ligand	14.02	2.23
C4BPA	Complement component 4 binding protein, alpha	13.14	2.64
TSPAN8	Tetraspanin 8	12.90	1.55
GADD45A	Growth arrest and DNA damage-inducible, alpha	8.25	1.69
NNMT	Nicotinamide N-methyltransferase	7.74	1.62
DPP4	Dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2)	7.72	2.57
S100P	S100 calcium-binding protein P	6.95	1.30
SNX10	Sorting nexin 10	6.56	1.93
CP	Ceruloplasmin (ferroxidase)	6.34	1.64
ADRA2A	Adrenergic, alpha-2A, receptor	5.78	2.50
TAGLN	Transgelin	5.71	1.61
THBS2	Thrombospondin 2	5.17	1.60
SERPING1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary), transcript variant 1	5.16	1.72
AOX1	Aldehyde oxidase 1	4.82	2.69
CYP3A5	Cytochrome P450, family 3, subfamily A, polypeptide 5	4.82	2.58
DHRS3	Dehydrogenase/reductase (SDR family) member 3	4.72	2.08
MYL9	Myosin, light polypeptide 9, regulatory, transcript variant 2	4.72	1.42
HABP2	Hyaluronan-binding protein 2	4.09	5.20
TBC1D2	TBC1 domain family, member 2	4.07	1.26
CDA	Homo sapiens cytidine deaminase (CDA), mRNA [NM_001785]	4.00	1.94
IMPA2	Inositol(myo)-1(or 4)-monophosphatase 2 3.91 2	3.91	1.78
XCL2	Chemokine (C motif) ligand 2	3.73	1.43
CLDN10	Claudin 10, transcript variant 1	3.68	2.06
COTL1	Coactosin-like 1 (Dictyostelium)	3.58	1.52
SYNE2	Spectrin repeat containing, nuclear envelope 2, transcript variant 5	3.52	1.88
PROS1	Homo sapiens protein S (alpha)	3.28	1.45
HLA-DOB	Major histocompatibility complex, class II, DO	-11.06	-2.35
CTNNA2	Catenin (cadherin-associated protein), alpha 2	-8.02	-2.00
NR4A2	Nuclear receptor subfamily 4, group A, member 2, transcript variant 1	-7.05	-2.00
DUOX1	Dual oxidase 1, transcript variant 1	-6.61	-3.05
LRP4	Low-density lipoprotein receptor-related protein 4	-5.87	-1.37
SLC16A6	Solute carrier family 16 (monocarboxylic acid transporters), member 6	-5.61	-2.14
EDN3	Endothelin 3, transcript variant 3	-5.30	-1.45
ANK3	Ankyrin 3, node of Ranvier (ankyrin G), transcript variant 1	-4.79	-2.73
CAPN6	Calpain 6 (CAPN6)	-4.76	-5.17
HPGD	Hydroxyprostaglandin dehydrogenase 15-(NAD)	-4.72	-2.00
SLC7A1	Solute carrier family 7 (cationic amino acid transporter, yb system), member 1	-4.72	-1.65
MMP26	Matrix metalloproteinase 26	-4.66	-5.90
LRRC17	Leucine-rich repeat-containing 17, transcript variant 2	-4.64	-1.67
ALPL	Alkaline phosphatase, liver/bone/kidney	-4.44	-2.14
HEY2	Hairy/enhancer-of-split related with YRPW motif 2	-4.07	-1.97
COBL	Cordon-bleu homolog (mouse)	-3.99	-1.79
SERPINA5	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	-3.84	-2.73
CREB3L1	cAMP responsive element-binding protein 3-like 1	-3.77	-1.55
IDH1	Isocitrate dehydrogenase 1 (NADPp), soluble	-3.68	-1.61
CBR3	Carbonyl reductase 3	-3.66	-1.72
ADAMTS8	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8	-3.59	-2.48
BIRC3	Baculoviral IAP repeat-containing 3 (BIRC3), transcript variant 1	-3.58	-1.75
DFNB31	Deafness, autosomal recessive 31	-3.54	-2.19
KCNJ2	Potassium inwardly-rectifying channel, subfamily J, member 2	-3.47	-1.60
BARD1	BRCA1-associated RING domain 1	-3.47	-1.78
MAP2K6	Mitogen-activated protein kinase 6, transcript variant 1	-3.45	-2.58
NDRG2	NDRG family member 2, transcript variant 1	-3.40	-1.35
LRRC1	Leucine-rich repeat-containing 1	-3.23	-3.16
RASSF2	Ras association (RalGDS/AF-6) domain family 2, transcript variant 1	-3.19	-1.43
OPRK1	Opioid receptor, kappa 1	-3.17	-1.66
STEAP4	STEAP family member 4	-3.04	-1.79
HEY1	Hairy/enhancer-of-split related with YRPW motif 1	-3.03	-1.95

FC: fold change; ERA: endometrial receptivity array (22).
Negative values mean down-regulation.*Corresponding author:
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Table S2. Gene directionality of differentially expressed common genes in endometrial biopsies between T-MFP and ERA

Gene symbol	Gene name	ERA (FC)	T-MFP (FC)
PAEP	Progesterone-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein) (PAEP), transcript variant 2	31.43	-13.00
C4BPA	Complement component 4 binding protein, alpha	13.14	-5.43
MAOA	Monoamine oxidase A, nuclear gene encoding mitochondrial protein	9.39	-4.99
GADD45A	Growth arrest and DNA damage-inducible, alpha	8.25	-1.66
NNMT	Nicotinamide N-methyltransferase	7.74	-1.85
SCGB2A2	Secretoglobulin, family 2A, member 2	7.43	-3.43
SNX10	Sorting nexin 10	6.56	-1.53
CP	Ceruloplasmin (ferroxidase)	6.34	-3.60
EFNA1	Ephrin-A1, transcript variant 1	5.77	-2.19
KLRC1	Killer cell lectin-like receptor subfamily C, member 1, transcript variant 2	5.75	-2.07
TAGLN	Transgelin	5.71	-1.64
SLC15A1	Solute carrier family 15 (oligopeptide transporter), member 1	5.59	-6.41
THBS2	Thrombospondin 2	5.17	-2.55
HPSE	Heparanase	5.17	-5.62
SERPING1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary), transcript variant 1	5.16	-2.38
CRISP3	Cysteine-rich secretory protein 3	5.09	-21.71
RPRM	Reprimo, TP53 dependent G2 arrest mediator candidate	5.03	-1.50
EDNRB	Endothelin receptor type B, transcript variant 2	4.89	-3.03
ABLIM3	Actin-binding LIM protein family, member 3	4.87	-1.61
GLIPR1	GLI pathogenesis-related 1 (glioma)	4.83	-2.00
CTSW	Cathepsin W	4.78	-2.03
AQP3	Aquaporin 3 (Gill blood group)	4.63	-1.68
S100A4	S100 calcium-binding protein A4, transcript variant 1	4.59	-1.30
NKG7	Natural killer cell group 7 sequence	4.42	-1.66
ARG2	Arginase, type II, nuclear gene encoding mitochondrial protein	4.35	-7.95
ANXA4	Annexin A4	4.27	-2.62
ARID5B	AT-rich interactive domain 5B (MRF1-like)	4.19	-1.56
SPP1	Secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	4.15	-11.00
DKK1	Dickkopf homolog 1 (<i>Xenopus laevis</i>)	4.10	-8.22
HABP2	Hyaluronan-binding protein 2	4.09	-1.72
GZMA	Granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	4.07	-2.75
C10orf10	Chromosome 10 open reading frame 10	3.98	-6.68
STAR	Steroidogenic acute regulator, nuclear gene encoding mitochondrial protein, transcript variant 1	3.93	-1.83
LMOD1	Leiomodin 1 (smooth muscle)	3.92	-2.01
HAND2	Heart and neural crest derivatives expressed 2	3.91	-2.06
CXCL13	Chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	3.90	-9.19
RARRES3	Retinoic acid receptor responder (tazarotene induced) 3	3.79	-1.49
MT2A	Metallothionein 2A	3.72	-3.16
RRAS	Related RAS viral (r-ras) oncogene homolog	3.70	-1.80
COTL1	Coactosin-like 1 (Dictyostelium)	3.58	-1.42
ID4	Inhibitor of DNA-binding 4, dominant negative helix-loop-helix protein	3.56	-2.33
LMCD1	LIM and cysteine-rich domains 1	3.53	-1.61
MFAP5	Microfibrillar-associated protein 5	3.42	-3.86
MT1G	Metallothionein 1G	3.41	-71.01
CLDN4	Claudin 4	3.41	-2.11
PTPRR	Protein tyrosine phosphatase, receptor type, R, transcript variant 1	3.40	-2.04
DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52, transcript variant 2	3.38	-2.43
HAL	Histidine ammonia-lyase	3.37	-2.01
ADAMTS1	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	3.32	-4.86
PROS1	Homo sapiens protein S (alpha)	3.28	-1.40
FOSL2	FOS-like antigen 2	3.26	-2.27
AMIGO2	Adhesion molecule with Ig-like domain 2	3.20	-1.85
POLD4	Polymerase (DNA-directed), delta 4	3.16	-1.38
GBP2	Guanylate-binding protein 2, interferon-inducible	3.14	-4.08
GABARAPL1	GABA(A) receptor-associated protein-like 1	3.13	-1.89
MT1H	Metallothionein 1H	3.12	-48.84
ATP6V1A	ATPase, H _b transporting, lysosomal 70 kDa, V1 subunit A	3.04	-1.49
IL15	Interleukin 15, transcript variant 1	3.03	-4.26
BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51), transcript variant 2	3.02	-2.27
TRH	Thyrotropin-releasing hormone	-21.69	7.31
HLA-DOB	Major histocompatibility complex, class II, DO	-11.06	-2.55
CSRP2	Cysteine and glycine-rich protein 2	-9.62	1.80
SLC15A2	Solute carrier family 15 (H _b /peptide transporter), member 2	-8.44	2.62
SFRP4	Secreted frizzled-related protein 4	-8.33	3.76
NR4A2	Nuclear receptor subfamily 4, group A, member 2, transcript variant 1	-7.05	-2.17
DUOX1	Dual oxidase 1, transcript variant 1	-6.61	-3.51
KIF20A	Kinesin family member 20A	-6.33	2.11
PENK	Proenkephalin	-6.16	1.68
EDN3	Endothelin 3, transcript variant 3	-5.30	1.78
GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	-4.85	3.23
CAPN6	Calpain 6 (CAPN6)	-4.76	-2.53
MMP26	Matrix metalloproteinase 26	-4.66	-8.40
LRRC17	Leucine-rich repeat-containing 17, transcript variant 2	-4.64	1.66
KCNQ1	Potassium voltage-gated channel, subfamily G, member 1, transcript variant 1	-4.63	1.48
SOX17	SRY (sex determining region Y)-box 17	-4.24	1.81
TOP2A	Topoisomerase (DNA) II alpha 170 kDa	-3.98	2.51
SPDEF	SAM pointed domain-containing ets transcription factor	-3.78	5.54
KMO	Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-3.78	3.14
ATP1B1	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	-3.73	1.84
ADAMTS8	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 8	-3.59	-3.78
BIRC3	Baculoviral IAP repeat-containing 3 (BIRC3), transcript variant 1	-3.58	-2.50
PLA1A	Phospholipase A1 member A	-3.42	1.61
PBK	PDZ-binding kinase	-3.42	2.08
PRC1	Protein regulator of cytokinesis 1 (PRC1), transcript variant 1	-3.29	1.65
MSX1	Msh homeobox homolog 1 (<i>Drosophila</i>)	-3.26	1.93
LRRC1	Leucine-rich repeat-containing 1	-3.23	-3.60
EPHB3	EPH receptor B3	-3.20	1.52

FC: fold Change; ERA: endometrial receptivity array (22).
Negative values mean down-regulation.



PROGNOSTIC SIGNIFICANCE OF THE *MAD1L1* 1673 G:A POLYMORPHISM IN OVARIAN ADENOCARCINOMAS

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Table S1. Clinical and histopathological variables of patients with ovarian adenocarcinoma treated at the National Cancer Institute – Mexico from 2005 to 2018 (n = 118)

Variable	Mean	SD
Age, years	52.12	11.78
BMI, kg/m ²	27.18	5.27
Variable	Median	Q1-Q3
Initial CA 125, U/mL	935.50	159.50-2770.20
Initial HE4, U/mL	50.40	36.23-82.58
Tumor Size, cm	11.50	5.87-18.00
Variable	n	%
BMI, kg/m²		
Underweight (<18.5)	3	2.54
Normal weight (18.5-24.9)	41	34.75
Overweight (25-29.9)	45	38.14
Obesity (≥30)	29	24.58
Initial ECOG performance status		
0	89	75.42
1	21	17.80
2	7	5.93
3	1	0.85
Histological type		
High-grade papillary serous	58	49.15
Low-grade papillary serous	7	5.93
Endometrioid	21	17.80
Clear cell	11	9.32
Mixed histology/other	21	17.80
FIGO clinical stage		
I	25	21.19
II	5	4.24
III	57	48.31
IV	31	26.27
Cytoreduction		
Taken to cytoreduction	113	95.76
Optimal cytoreduction	85	75.22*
Chemotherapy		
Received neoadjuvancy	74	62.71
Received adjuvancy	90	76.27
Recurrence/progression of disease		
Neither	40	33.90
Recurrence or progression	78	66.10
Sensitivity to chemotherapy		
Non-platin sensitive	58	49.15
Platin sensitive/no recurrence	60	50.85
Site of recurrence		
Peritoneal	16	20.51**
Nodal	23	29.48**
Distance	27	34.61**
Undetermined/other	12	15.38**
<i>MAD1L1</i> genotype		
Wild type	26	22.03
Heterozygous	49	41.53
Homozygous polymorphic	43	36.44

*Including only patients taken to cytoreduction.

**Including only patients with recurrence/progression of disease.

SD: standard deviation; Q1-Q3: first quartile-third quartile; BMI: body mass index; ECOG: Eastern Cooperative Oncology Group; FIGO: International Federation of Gynecology and Obstetrics.

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Table S2. Sociodemographic, clinical, anatomical, and histopathological variables in relation to platin sensitivity of patients with ovarian adenocarcinoma, treated at the National Cancer Institute – Mexico from 2005 to 2018 (n = 118)

Variable	Non-platin sensitive ^a (n = 58)		Platin sensitive ^b (n = 60)		p-value*
	Mean	SD	Mean	SD	
Age, years	51.50	11.90	52.71	11.73	0.577
BMI, kg/m ²	26.94	5.50	27.39	5.08	0.642
Variable	Median	Q1-Q3	Median	Q1-Q3	p-value*
Initial CA125, IU/mL	1506.50	415.80-3823.50	324.50	93.50-2094.00	0.150
Initial HE4, IU/mL	116.15	84.83-172.80	49.05	36.23-73.03	0.285
Tumor size, cm	6.00	4.15-7.00	16.00	12.00-21.50	<0.001
Variable	n	%	n	%	p-value**
Initial ECOG performance status					
0	40	68.97	49	81.67	0.141
1	15	25.86	6	10.00	
2	3	5.17	4	6.67	
3	0	0.00	1	1.67	
Histological type					
High-grade papillary serous	44	75.86	19	31.67	<0.001
Low-grade papillary serous	0	0.00	2	3.33	
Endometrioid	5	8.62	16	26.67	
Clear cell tumor	2	3.45	9	15.00	
Other/mixed histology	7	12.07	14	23.33	
FIGO clinical stage					
I	0	0.00	26	43.33	<0.001
II	1	1.72	3	5.00	
III	35	60.34	22	36.67	
IV	22	37.93	9	15.00	
Cytoreduction					
Yes	53	91.38	60	100.00	0.061
Optimal cytoreduction^c					
Yes	29	54.72	56	93.33	<0.001
Chemotherapy					
Received neoadjuvancy	53	89.83	21	35.00	<0.001
Received adjuvancy	43	72.88	47	78.33	1.000
Recurrence/progression of disease					
Recurrence or progression	58	100.00	20	33.33	<0.001
Site of recurrence^d					
Peritoneal	5	8.62	4	20.00	0.035
Nodal	11	18.97	5	25.00	
Distant	25	43.10	9	45.00	
Multiple locations/other	17	29.31	2	10.00	
MAD1L1 genotype					
Wild type	7	12.07	19	31.67	0.024
Heterozygous	25	43.10	24	40.00	
Polymorphic	26	44.83	17	28.33	

*p-value calculated using Student's t-test.

**p-value calculated using Chi-squared test.

^aDefined as patients who had a recurrence of disease before 1 year after the end of treatment or with progression of disease.^bDefined as patients who did not recur after treatment or who recurred over a year after the end of treatment.^cConsidering only patients who were cytoreduced.^dConsidering only patients with recurrence/progression of disease.

SD: standard deviation; Q1-Q3: first quartile-third quartile; FIGO: International Federation of Gynecology and Obstetrics; MAD1: mitotic arrest deficiency 1. ECOG: Eastern Cooperative Oncology Group; BMI: body mass index.



SCREENING TOOL FOR RESTRICTIVE AND OBSTRUCTIVE VENTILATORY ABNORMALITIES IN A POPULATION-BASED SURVEY

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Table S1: Prediction of pre-bronchodilator ventilatory spirometric abnormalities from pre-bronchodilator 6 s pocket spirometry

Spirometry parameters	AUC ^a	Sensitivity (95% CI)	Specificity (95% CI)	PPV ^b (95% CI)	NPV ^c (95% CI)	Best cutoff point ^d
FEV₁ %P						
Restrictive	91.8 (88.4-95.3)	87.5 (77.6-94.1)	84.3 (81.2-87.0)	38.7 (31.1-46.6)	98.4 (96.9-99.2)	87
Obstructive	89.0 (82.3-95.7)	81.3 (63.6-92.8)	84.6 (81.6-87.3)	21.0 (14.2-29.2)	98.9 (97.6-99.6)	87
Any ventilatory abnormality	91.0 (87.7-94.2)	84.8 (76.4-91.0)	84.3 (81.2-87.0)	47.1 (39.8-54.5)	97.1 (95.3-98.3)	87
FEV₆ %P						
Restrictive	87.1 (82.1-92.2)	88.9 (79.3-95.1)	75.8 (72.3-79.1)	29.4 (23.4-35.9)	98.4 (96.8-99.3)	85
Obstructive	73.3 (64.3-82.4)	62.5 (43.7-78.9)	77.4 (73.9-80.6)	11.7 (7.2-17.6)	97.2 (95.4-98.5)	84
Any ventilatory abnormality	82.9 (78.2-87.6)	80.0 (71.1-87.2)	75.8 (72.3-79.1)	35.3 (29.2-41.7)	95.8 (93.7-96.4)	85
FEV₁/FEV₆ %P						
Restrictive	61.2 (54.8-67.5)	62.5 (50.3-73.6)	60.1 (56.2-64.0)	15.1 (11.2-19.6)	93.4 (90.6-95.6)	105
Obstructive	83.0 (74.4-91.7)	66.7 (48.2-82.0)	89.0 (86.3-91.3)	23.9 (15.6-33.9)	98.1 (96.6-99.0)	97
Any ventilatory abnormality	67.9 (62.3-73.5)	69.5 (59.8-78.1)	60.1 (56.2-64.0)	22.3 (17.9-27.2)	92.3 (89.3-94.7)	105
Crude FEV₁/FEV₆						
Restrictive	60.2 (53.7-66.7)	73.6 (61.9-83.3)	46.0 (42.1-50.0)	13.4 (10.2-17.1)	93.9 (90.7-96.3)	88
Obstructive	80.7 (71.8-89.7)	63.6 (45.1-79.6)	88.5 (85.8-90.9)	22.3 (14.4-32.1)	97.9 (96.4-98.9)	79
Any ventilatory abnormality	66.6 (61.0-72.3)	67.6 (57.8-76.4)	60.0 (56.0-63.8)	21.8 (17.4-26.7)	91.8 (88.8-94.3)	86

^aArea under the curve; ^bpositive predictive value; ^cnegative predictive value; ^dby the highest Youden index, affording the same value to sensitivity and specificity; FEV₁: forced expiratory volume in 1 s; %P: percentage of predicted.

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Table S2. Prediction of post-bronchodilator ventilatory abnormalities from pre-bronchodilator 6 s pocket spirometer

Spirometry parameters	AUC ^a	Sensitivity (95% CI)	Specificity (95% CI)	PPV ^b (95% CI)	NPV ^c (95% CI)	Best cutoff point ^d
FEV₁ %P						
Restrictive	91.7 (88.1-95.2)	88.7 (78.1-95.3)	82.1 (78.7-85.1)	34 (26.9-41.0)	98.6 (97.1-99.4)	87
Obstructive	89.0 (77.6-1.00)	81.3 (54.4-96.0)	93.9 (91.7-95.7)	26.5 (14.9-41.1)	99.5 (98.4-99.9)	82
Any ventilatory abnormality	91.2 (87.5-94.9)	88.5 (79.2-94.6)	82.1 (78.7-85.1)	39.4 (32.1-47.1)	98.2 (96.6-99.2)	87
FEV₆ %P						
Restrictive	90.4 (86.8-94.0)	91.9 (82.2-97.3)	75.3 (71.6-78.7)	28.1 (22.0-34.8)	98.9 (97.4-99.6)	85
Obstructive	73.3 (57.8-87.3)	50.0 (24.7-75.3)	90.9 (88.2-93.1)	12.9 (5.7-23.9)	98.5 (97.1-99.4)	77
Any ventilatory abnormality	86.8 (82.3-91.2)	85.9 (76.2-92.7)	75.3 (71.6-78.7)	31.5 (25.3-38.2)	97.6 (95.7-98.8)	84
FEV₁/FEV₆ %P						
Restrictive	54.0 (46.7-61.3)	58.1 (44.8-70.5)	52.6 (48.5-56.7)	11.4 (8.1-15.4)	92.3 (88.9-94.9)	106
Obstructive	83.1 (71.1-95.0)	68.8 (41.3-89.0)	88.8 (86.0-91.3)	14.3 (7.4-24.1)	99.1 (97.8-99.7)	97
Any ventilatory abnormality	60.0 (53.1-66.9)	61.5 (49.8-72.3)	54.1 (50.0-58.2)	15.0 (11.3-19.5)	91.4 (88.0-94.1)	106
CRUDE FEV₁/FEV₆						
Restrictive	52.6 (45.1-60.2)	80.6 (68.6-89.6)	26.1 (22.6-29.8)	10.3 (7.7-13.3)	92.8 (87.7-96.2)	90
Obstructive	82.0 (70.7-93.3)	64.7 (38.3-85.8)	92.2 (89.8-94.2)	19.3 (10.0-31.9)	98.9 (97.6-99.6)	76
Any ventilatory abnormality	59.0 (52.0-65.9)	55.7 (44.1-66.9)	59.6 (55.5-63.5)	15.5 (11.5-20.3)	91.0 (87.6-93.6)	86

^aArea under the curve; ^bpositive predictive value; ^cnegative predictive value; ^dby the highest Youden index, affording same value to sensitivity and specificity; FEV₁: forced expiratory volume in 1 s; %P: percentage of predicted.



ECHINOCOCCUS GRANULOSUS HAPLOTYPES IN THE SCIENTIFIC LITERATURE

Supplementary Table 1. *Echinococcus granulosus* haplotypes informed in the literature

Reference	Haplotypes informed in literature*	Gene	Country
Alvarez-Rojas (2017)	EG01 (JQ250806); EGp1 (AB522646); EgAus03 (KT968704); EgAus02 (KT968703); EgRUS7 (AB777904); EgCL1-EgCI21 (KX227116-KX227136)	cox1	Chile
Andresiuk (2013)	C1-C7; N1-N3 (KC579441-KC579451)	cox1 and nad1	Argentina
Barazesh (2019)	H1 (MF544127); H2 (MG672258); H3 (MH542404); H4 and H5 (MH542399, MH542406, and MH542395)	cox1 and nad1	Iran
Bold (2019)	H1 (EcMGL2); H2 (No registered); H3 (EcMGL15); H4 (No registered)	cox1	Mongolia
Boufana (2015)	EGUK01-EGUK03 (AF346403; AB786665; AF346403)	cox1	UK
Boufana (2014)	EgTu01-EgTu39 (KM014606-KM014644)	cox1	Tunisia
Correa (2018)	H1-H11 (MF421702-MF421712)	cox1	Chile
De la Rue (2011)	H1 (M84661); H2 (AF458872); H3 (EF367289); H4 (No registered)	cox1	Brazil
Farhadi (2015)	EGH1-EGH13 (KP859559-KP859571)	cox1	Iran
Gorgani-Firouzjaee (2018)	H1 ([EgS2] MF346705; [EgB2] MF625021); H2 ([EgS1] MF625022); H3 ([EgS12] MF625020); H4 ([EgB6] MF449137); H5 ([EgB1] MF346706); H6 ([EgHum5] MG099696); H7 ([EgHum4] MG099695); H8 ([EgS11] MF625018); H9 ([EgS6] MF449131); H10 ([EgB3] MF625019)	cox1	Iran
Guo (2018)	H1-H15 (MH211191-MH211205)	cox1	China
Hajjalilo (2012)	H1 ([IRCO1] HM563001, HM563009-11; [IRND1] HM563023-26); H2 ([IRCO1] HM563011, [IRND2] HM563027); H3 ([IRCO1] HM563011, [IRND3] HM563028); H4 ([IRCO1] HM563010, [IRND4] HM563029); H5 ([IRCO1] HM563010, [IRND6] HM563031); H6 ([IRCO2] HM563012, HM563013, [IRND1] HM563023, HM563026); H7 ([IRCO2] HM563012, [IRND3] HM563028); H8 ([IRCO3] HM563014, [IRND5] HM563030); H9 ([IRCO4] HM563016, [IRND7] HM563032); H10 ([IRCO4] HM563017, [IRND8] HM563033); H11 ([IRCO4] HM563015, [IRND9] HM563034); H12 ([IRCO5] HM563018, HM563019, [IRND10] HM563035, HM563036); H13 ([IRCO6] HM563020, [IRND11] HM563037)	cox1 and nad1	Iran
Hammad (2018)	Hap_5; Hap_6; Hap_7; Hap_8; Hap_9 (no registered)	cox1	Iraq
Han (2019)	EgQH1 (MG674403); EgQH2 (MG674404); EgQH3 (MG674405); EgQH4 (MG674406); EgQH5 (MG674407); EgQH6 (MG674408); EgQH7 (MG674409); EgQH8 (MG674410); EgQH9 (MG674411); EgQH10 (MG674412); EgQH11 (MG674413); EgQH12 (MG674414); EgQH13 (MG674415); EgQH14 (MG674416); EgQH15 (MG674417); EgQH16 (MG674418); EmQH1 (MG674419); EsQH1 (MG674420)	cox1	Tibet (China)
Jafari (2018)	IfnN1 (KX186691.1); IfnC1 (KU360325.1); IfnN2 (KU925412.1); IfnC2 (KT254124.1); IfnN3 (KY495928.1); IfnC3 (EF367259.1); IfnN4 (HM853647.1); IfnC4 (KU360316.1); IfnN5 (KX298249.1); IfnC5 (KX269858.1); IfnN6 (KF437795.1); IfnC6 (KU360299.1); IfnN7 (GQ168810.1); IfnC7 (DQ269944.1); IfnN8 (KX010894.1); IfnC8 (KX010872.1); IfnN9 (KP751440.1)	cox1 and nad1	Iran
Kinkar (2017)	SPA5 (KY766886); SPA1 (KY766900); SPA2 (KY766896); SPA4 (KY766897); SPA3 (KY766903)	Whole mitochondrial genome	Spain
Kinkar (2017)	FIN1 (KY766884)	Whole mitochondrial genome	Algeria (patient detected in Finland)
Kinkar (2017)	TUN1 (KY766885)	Whole mitochondrial genome	Túnez
Kinkar (2017)	ARG1 (KY766882)	Whole mitochondrial genome	Argentina
Kinkar (2017)	IND2 (KY766891); IND1 (KY766902)	Whole mitochondrial genome	India
Kinkar (2017)	CHI1 (KY766890)	Whole mitochondrial genome	Chile
Kinkar (2017)	TUR4 (KY766888); TUR1 (KY766901); TUR2 (KY766904); TUR3 (KY766898)	Whole mitochondrial genome	Turkey
Kinkar (2017)	FRA3 (KY766889); FRA1 (KY766893); FRA2 (KY766892)	Whole mitochondrial genome	France
Kinkar (2017)	ALB1 (KY766883)	Whole mitochondrial genome	Albania
Kinkar (2017)	IRA4 (KY766887); IRA3 (KY766899); IRA1 (KY766894); IRA2 (KY766895);	Whole mitochondrial genome	Iran
Karamian (2017)	Cox1-Elran-1 (KP751430); Cox1-Elran-2 (KP751426)	cox1	Iran
Konyaev (2013)	EgRUS7 (AB777904); EgRUS10 (AB777907); EgRUS11 (AB777908); EgRUS8 (AB777905); EgRUS9 (AB777906); EcRUS7 (AB777914)	cox1	Russia
Laatamna (2019)	EG01 (JQ250806); EG40 (AB688617); EgA01 (KX020323); EgA16 (KX020337); EgAus03 (KT968704); EgAlg01 (MG808282); EgAlg02 (MG808283); EgAlg03 (MG808284); EgAlg04 (MG808285); EgAlg05 (MG808286); EgAlg06 (MG808287); EgAlg07 (MG808288); EgAlg08 (MG808289); EgAlg09 (MG808290); EgAlg10 (MG808291); EgAlg11 (MG808292); EgAlg12 (MG808293); EgAlg13 (MG808294); EgAlg14 (MG808295); EgAlg15 (MG808296); EgAlg16 (MG808297); EgAlg17 (MG808298); EgAlg18 (MG808299); EgAlg19 (MG808300); EgAlg20 (MG808301); EgAlg21 (MG808302); EgAlg22 (MG808303); EgAlg23 (MG808304); EgAlg24 (MG808305); EgAlg25 (MG808306); EgAlg26 (MG808307); EgAlg27 (MG808308); EgAlg28 (MG808309); EgAlg29 (MG808310); EgAlg30 (MG808311); EgAlg31 (MG808312); EgAlg32 (MG808313); EgAlg33 (MG808314); EgAlg34 (MG808315); EgAlg35 (MG808316); EgAlg36 (MG808317); EgAlg37 (MG808318); EgAlg38 (MG808319); EgAlg39 (MG808320); EgAlg40 (MG808321); EgAlg41 (MG808322); EgAlg42 (MG808323); EgAlg43 (MG808324); EgAlg44 (MG808325); EgAlg45 (MG808326); EgAlg46 (MG808327); EgAlg47 (MG808328); EgAlg48 (MG808329); EgAlg49 (MG808330); EgAlg50 (MG808331); EgAlg51 (MG808332); EgAlg52 (MG808333); EgAlg53 (MG808334); EgAlg54 (MG808335); EgAlg55 (MG808336); EgAlg56 (MG808337); EgAlg57 (MG808338); EgAlg58 (MG808339); EgAlg59 (MG808340); EgAlg60 (MG808341); EgAlg61 (MG808342); EgAlg62 (MG808343); EgAlg63 (MG808344); EgAlg64 (MG808345); EgAlg65 (MG808346); EgAlg66 (MG808347); EgAlg67 (MG808348); EgAlg01X (MG808349)	cox1	Algeria
Laurimäe (2018)	IRA3 (MH300931); IRA4 (MH300932)	Whole mitochondrial genome	Iran
Laurimäe (2018)	ARG4 (MH300955); ARG5 (MH300956); ARG6 (MH300957); ARG7 (MH300958); ARG8 (MH300959); ARG9 (MH300960); ARG10 (MH300961); ARG11 (MH300962); ARG12 (MH300963); ARG13 (MH300964); ARG14 (MH300965); ARG15 (MH300966); ARG16 (MH300967); ARG17 (MH300968); ARG18 (MH300969); ARG19 (MH300970)	Whole mitochondrial genome	Argentina
Laurimäe (2018)	KEN2 (MH300937); KEN3 (MH300938)	Whole mitochondrial genome	Kenya
Laurimäe (2018)	SUD1 (MH300939); SUD2 (MH300940); SUD3 (MH300941); SUD4 (MH300942); SUD5 (MH300943); SUD6 (MH300944); SUD7 (MH300945); SUD8 (MH300946); SUD9 (MH300947); SUD10 (MH300948); SUD11 (MH300949); SUD12 (MH300950); SUD13 (MH300951); SUD14 (MH300952);	Whole mitochondrial genome	Sudan
Laurimäe (2018)	MAU1 (MH300953); MAU2 (MH300954)	Whole mitochondrial genome	Mauritania
Laurimäe (2018)	Gmon (MH300971)	Whole mitochondrial genome	Mongolia
Laurimäe (2018)	MEX1 (MH300972); MEX2 (MH300973); MEX3 (MH300974); MEX4 (MH300975); MEX5 (MH300976); MEX6 (MH300977); MEX7 (MH300978); MEX8 (MH300979); MEX9 (MH300980); MEX10 (MH300981)	Whole mitochondrial genome	Mexico
Laurimäe (2018)	FRA2 (MH300987); FRA3 (MH300988); FRA4 (MH300989); FRA5 (MH300990); FRA6 (MH300991); FRA7 (MH300992); FRA8 (MH300993); FRA9 (MH300994); FRA10 (MH300995); FRA11 (MH300996); FRA12 (MH300997); FRA13 (MH300998); FRA14 (MH300999); FRA15 (MH301000); FRA16 (MH301001); FRA17 (MH301002); FRA18 (MH301003); FRA19 (MH301004); FRA20 (MH301005); FRA21 (MH301006); FRA22 (MH301007); FRA23 (MH301008); FRA24 (MH301009); FRA25 (MH301010); FRA26 (MH301011); FRA27 (MH301012); FRA28 (MH301013); FRA29 (MH301014); FRA30 (MH301015); FRA31 (MH301016); FRA32 (MH301017)	Whole mitochondrial genome	France
Laurimäe (2018)	POL1 (MH301003); POL2 (MH301004); POL3 (MH301005); POL4 (MH301006); POL5 (MH301007)	Whole mitochondrial genome	Poland
Laurimäe (2018)	LIT1 (MH301020)	Whole mitochondrial genome	Lithuania
Laurimäe (2018)	UKR1 (MH301021); UKR2 (MH301022)	Whole mitochondrial genome	Ukraine
Laurimäe (2018)	SER1 (MH300984)	Whole mitochondrial genome	Serbia
Laurimäe (2018)	ROM2 (MH300983)	Whole mitochondrial genome	Romania
Oskoueji (2016)	S1 (no registered); S2 (no registered); S3 (no registered); S4 (no registered); S5 (no registered); S6 (no registered); S7 (no registered); S8 (no registered); S9 (KJ540227); S10 (no registered); S11 (no registered); S12 (no registered); S13-S18 (no registered); S19 (KJ540229); S20 (KJ540231); S21-S23 (no registered)	cox1	Iran
Marinova (2017)	H1 ([C1] KR070964, [N1] KR070984, [S1] KR070969, [L1] KR070973, [ATP1] KR070978); H2 ([C1] KR070964, [N3] KR070986, [S1] KR070969, [L1] KR070973, [ATP1] KR070978); H3 ([C1] KR070964, [N5] KR070988, [S1] KR070969, [L2] KR070974, [ATP1] KR070978); H4 ([C1] KR070964, [N2] KR070985, [S1] KR070969, [L1] KR070973, [ATP1] KR070978); H5 ([C1] KR070964, [N6] KR070989, [S1] KR070969, [L1] KR070973, [ATP1] KR070978); H6 ([C1] KR070964, [N4] KR070987, [S1] KR070969, [L1] KR070973, [ATP2] KR070979); H7 ([C2] KR070965, [N1] KR070984, [S1] KR070969, [L1] KR070973, [ATP1] KR070978); H8 ([C1] KR070964, [N8] KR070991, [S1] KR070969, [L1] KR070973, [ATP1] KR070978); H9 ([C3] KR070966, [N7] KR070990, [S2] KR070970, [L4] KR070976, [ATP4] KR070981); H10 ([C3] KR070966, [N7] KR070990, [S2] KR070970, [L3] KR070975, [ATP3] KR070980); H11 ([C3] KR070966, [N7] KR070990, [S3] KR070971, [L3] KR070975, [ATP3] KR070980); H12 ([C3] KR070966, [N7] KR070990, [S2] KR070970, [L3] KR070975, [ATP5] KR070982); H13 ([C4] KR070967, [N7] KR070990, [S2] KR070970, [L3] KR070975, [ATP3] KR070980); H14 ([C5] KR070968, [N9] KR070992, [S4] KR070972, [L5] KR070977, [ATP6] KR070983)	cox1, nad1, rns5, rrr1, atp6	Bulgaria
Matini (2019)	Hamc1 (MG792551); Hamc2 (MG792552); Hamc3 (MG792553); Hamc4 (MG792554); Hamc5 (MG792555); Hamc6 (MG792556); Hamc7 (MG792557); Hamc8 (MG792558); Hamc9 (MG792559); Hamc10 (MG792560); Hamc11 (MG792561); Hamc12 (MG792562); Hamc13 (MG792563)	cox1	Iran
Metwally (2018)	Echs1-Echs12 (no registered); Echc1 (no registered); Echc2 (no registered)	cox1	Saudi Arabia
Moro (2009)	Egra-A (AB458672); Egra-B (AB458673); Egra-C (AB458674); Egra-D (AB458675); Egra-E (AB470527); Ecan-A (AB458676); Ecan-B (AB458677); Ecan-C (AB458678)	cox1	Peru
Nikmanesh (2014)	H1 (KF612381, KF612357); H2 (KF612356); H3 (KF612390, KF612360); H4 (KF612380, KF612358); H5 (KF612376, KF612349); H6 (KF612395, KF612350); H7 (KF612396, KF612355); H8 (KF612394, KF612343); H9 (KF612386, KF612351); H10 (KF612397, KF612369); H11 (KF612400, KF612372)	cox1 and nad1	Iran
Orsten (2018)	TUK01-TUK28 (no registered)	cox1	Turkey
Parsa (2012)	H1 ([Lor1] JN604097, [Lor2] JN604107); H2 ([Lor1] JN604097, [Lor3] JN604108); H3 ([Lor1] JN604097, [Lor4] JN604109); H4 ([Lor1] JN604097, [Lor5] JN604110); H5 ([Lor1] JN604097, [Lor6] JN604111); H6 ([Lor2] JN604098), [Lor7] JN604107); H7 ([Lor3] JN604099), [Lor8] JN604106); H8 ([Lor4] JN604100), [Lor9] JN604101); H9 ([Lor5] JN604101), [Lor10] JN604107); H10 ([Lor6] JN604102), [Lor11] JN604107); H11 ([Lor7] JN604103), [Lor12] JN604112); H12 ([Lor8] JN604104), [Lor13] JN604112); H13 ([Lor9] JN604105), [Lor14] JN604112)	cox1 and nad1	Iran
Pezeshki (2012)	H1 (AB677806+AB677815); H2 (AB677806+AB677816); H3 (AB677806+AB677817); H4 (AB677806+AB677819); H5 (AB677807+AB677815); H6 (AB677808+AB677815); H7 (AB677809+AB677818); H8 (AB677810+AB677815); H9 (AB677811+AB677815); H10 (AB677811+AB677821); H11 (AB677812+AB677815); H12 (AB677813+AB677815)	cox1 and nad1	Iran
Pour (2011)	G1a (HM130574, HM130575, HM130576, HM130577, HM130578); G1b (HM130579, HM130580, HM130581, HM130582, HM130583, HM130584, HM130585); G1γ (HM130586, HM130587, HM130588, HM130589, HM130590, HM130591); G1δ (HM130593, HM130594, HM130595, HM130596)	cox1	Iran
Rodríguez-Prado (2014)	KF734649-KF734660	cox1	Mexico
Roinioti (2016)	KT285513; KT285514; KT285515; KT285516; KT285517; KT285518; KT285519; KM245580; KMS21206; KT184863; KT184864; KT184865; KT184866; KT285520	cox1	Greece
Rostami (2015)	IREG1 (KF443137); IREG2 (KF443138); IREG3 (KF443139); IREG4 (KF443140); IREG5 (KF443141); IREG6 (KF443142); IREG7 (KF443143); IREG8 (KF443144); IREG9 (KF443145); IREG10 (KF443146); IREG11 (KF443147); IREG12 (KF443148); IREG13 (KF443149); IREG14 (KF443150); IREG15 (KF443151); IREG16 (KF443152); IREG17 (KF443153); IREG18 (KF443154); IREG19 (KF443155); IREG20 (KF443156); IREG21 (KF443157); IREG22 (KF443158); IREG23 (KF443159); IREG24 (KF443160); IREG25 (KF443161); IREG26 (KF443162); IREG27 (KF443163); IREG28 (KF443164); IREG29 (KF443165); IREG30 (KF443166); IREG31 (KF443167); IREG32 (KF443168); IREG33 (KF443169); IREG34 (KF443170); IREG35 (KF443171); IREG36 (KF443172); IREG37 (KF443173); IREG38 (KF443174); IREG39 (KF443175); IREG40 (KF443176); IREG41 (KF443177); IREG42 (KF443178); IREG43 (KF443179); IREG44 (KF443180); IREG45 (KF443181); IREG46 (KF443182); IREG47 (KF443183); IREG48 (KF443184); IREG49 (KF443185); IREG50 (KF443186); IREG51 (KF443187); IREG52 (KF443188); IREG53 (KF443189); IREG54 (KF443190); IREG55 (KF443191); IREG56 (KF443192); IREG57 (KF443193); IREG58 (KF443194); IREG59 (KF443195); IREG60 (KF443196); IREG61 (KF443197); IREG62 (KF443198)	cox1	Iran
Shang (2019)	G1-G34 (KX685889 - KX685927)	cox1	China
Sharbatkhori (2016)	H1 ([Golc1] KMS13626, [Golc1-1] KT074941, [Golc1-2] KT074942, [Golc1] KMS13634, [Golc1-1] KT074936, [Golc1-3] KT074938); H2 ([Golc1] KMS13626, [Golc3] KMS13636); H3 ([Golc1-1] KT074941, [Golc1-2] KT074942, [Golc1-3] KT074943, [Golc4] KMS13637, [Golc4-1] KT074939, [Golc4-2] KT074940); H4 ([Golc2] KMS13627, [Golc2-1] KT074944, [Golc2-2] KT074945, [Golc2-3] KT074946, [Golc2-4] KT074947); H5 ([Golc2-1] KT074938); H6 ([Golc2-1] KT074945, [Golc2-2] KT074946, [Golc2-3] KT074947); H7 ([Golc3] KMS13635); H8 ([Golc4-1] KT074948, [Golc4-2] KT074939); H9 ([Golc5] KMS13630, [Golc5-1] KT074937); H10 ([Golc6] KMS13631, [Golc6-1] KT074938); H11 ([Golc6] KMS13631, [Golc6-1] KT074938); H12 ([Golc6] KMS13631, [Golc6-1] KT074938); H13 ([Golc7] KMS13632, [Golc7-1] KT074938); H14 ([Golc7] KMS13632, [Golc7-1] KT074939); H15 ([Golc8] KMS13633, [Golc8-1] KMS13638)	cox1 and nad1	Iran
Shariatzadeh (2015)	AZE03 (KP723338); AZE11 (KT154000); AZE01 (KT153999); AZE02 (KT153998); AZE04 (KT153997); AZE05 (KT153996); AZE10 (KT153995)	cox1	Iran
Sharifyazdi (2011)	Camel A CO1 (HM626405), Camel B CO1 (HM626406), Camel A ND1 (HQ585933), Camel B ND1 (HQ585934), Microvariant (HM626405)	cox1, nad1, its1	Iran
Soriano (2010)	G1nqnA; G1nqnB; G1nqnC; G6nqn; (GU980906-14)	cox1	Argentina
Spotin (2016)	IR2; IR3; IR5; IR6; IR7; IR8; IR10; IR12; IR13; IR14; IR17; IR18; IR19; IR22; IR34; IR35; IR36; IR38; IR39; IR43; IR44; IR47; IR48; IR49	cox1	Iran
Yan (2018)	HLN1; YLY1; YLY2; YLY3; YLY4; YLY5; YLY6; YLY7; YLY8; YLY9; YLY10; YLY11; YLY12; YLY13; YLY14; YLY15; YLY16; YLY17; YLY18; YLY19; YLY20; YLY21; YLY22; YLY23; YLY24; YLY25; YLY26; YLY27; YLY28; YLY29; YLY30; YLY31; YLY32; YLY33; YLY34; YLY35; YLY36; YLY37; YLY38; YLY39; YLY40; YLY41; YLY42; YLY43; YLY44; YLY45; YLY46; YLY47; YLY48; YLY49; YLY50; YLY51; YLY52; YLY53; YLY54; YLY55; YLY56; YLY57; YLY58; YLY59; YLY60; YLY61; YLY62; YLY63; YLY64; YLY65; YLY66; YLY67; YLY68; YLY69; YLY70; YLY71; YLY72; YLY73; YLY74; YLY75; YLY76; YLY77; YLY78; YLY79; YLY80; YLY81; YLY82; YLY83; YLY84; YLY85; YLY86; YLY87; YLY88; YLY89; YLY90; YLY91; YLY92; YLY93; YLY94; YLY95; YLY96; YLY97; YLY98; YLY99; YLY100; YLY101; YLY102; YLY103; YLY104; YLY105; YLY106; YLY107; YLY108; YLY109; YLY110; YLY111; YLY112; YLY113; YLY114; YLY115; YLY116; YLY117; YLY118; YLY119; YLY120; YLY121; YLY122; YLY123; YLY124; YLY125; YLY126; YLY127; YLY128; YLY129; YLY130; YLY131; YLY132; YLY133; YLY134; YLY135; YLY136; YLY137; YLY138; YLY139; YLY140; YLY141; YLY142; YLY143; YLY144; YLY145; YLY146; YLY147; YLY148; YLY149; YLY150; YLY151; YLY152; YLY153; YLY154; YLY155; YLY156; YLY157; YLY158; YLY159; YLY160; YLY161; YLY162; YLY163; YLY164; YLY165; YLY166; YLY167; YLY168; YLY169; YLY170; YLY171; YLY172; YLY173; YLY174; YLY175; YLY176; YLY177; YLY178; YLY179; YLY180; YLY181; YLY182; YLY183; YLY184; YLY185; YLY186; YLY187; YLY188; YLY189; YLY190; YLY191; YLY192; YLY193; YLY194; YLY195; YLY196; YLY197; YLY198; YLY199; YLY200; YLY201; YLY202; YLY203; YLY204; YLY205; YLY206; YLY207; YLY208; YLY209; YLY210; YLY211; YLY212; YLY213; YLY214; YLY215; YLY216; YLY217; YLY218; YLY219; YLY220; YLY221; YLY222; YLY223; YLY224; YLY225; YLY226; YLY227; YLY228; YLY229; YLY230; YLY231; YLY232; YLY233; YLY234; YLY235; YLY236; YLY237; YLY238; YLY239; YLY240; YLY241; YLY242; YLY243; YLY244; YLY245; YLY246; YLY247; YLY248; YLY249; YLY250;		