

Supplementary Table 5: Proteins covered exclusively by population specific peptides.

Accession number	Protein Name	Gene name	Sequence coverage	Protein Score	Postulated Biological process^a
Protein group covered by peptides which were not detected in control samples					
LG3BP_HUMAN	Galectin-3-binding protein precursor	LGALS3BP	8,2%	240	Signal transduction, metastatic process
PABP1_HUMAN	Polyadenylate-binding protein 1	PABPC1	4,9%	155	mRNA stabilization
PSA_HUMAN	Puromycin-sensitive aminopeptidase	NPEPPS	6,0%	271	zinc metallopeptidase, cell migration
UGPA_HUMAN	UTP-glucose-1-phosphate uridylyltransferase	UGP2	7,5%	108	glucose metabolic process
THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	7,3%	104	lipid metabolic process
SEPT9_HUMAN	Septin-9	SEPT9	5,3%	98	cytokinesis, cell motility and polarity
STOM_HUMAN	Stomatin	STOM	28,1%	404	unknown
Protein group covered by peptides which were not detected in tumorous samples					
Q13576_HUMAN	Ras GTPase-activating-like protein	IQGAP2	3,8%	257	regulation of cell motility and cell morphogenesis
ADH1G_HUMAN	Alcohol dehydrogenase 1C	ADH1C	9,6%	160	cellular alcohol metabolic process
ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial precursor	ALDH2	9,5%	232	carbohydrate metabolic process, cellular alcohol metabolic process
DAD1_HUMAN	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit DAD1	DAD1	17,7%	95	anti-apoptosis
ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial precursor	ETFA	17,1%	209	respiratory chain
F16P1_HUMAN	Fructose-1,6-bisphosphatase 1	FBP1	9,2%	97	hexose metabolic process
IGHA1_HUMAN	Ig alpha-1 chain C region	IGHA1	9,9%	186	immune response

a) Postulated biological process was determined by Gene Ontology (GO) and bibliographic features