

	AI?	Gene Expression log2 (Tumor/Normal)						Allelic Imbalance (AI)						neighbor concord?	adhesion/ECM/lumina?					
		Patient 33		Patient 8		Patient 51		Patient 33		Patient 8		Patient 51								
		8	33	51	1->2	2->1	2->2	1->2	2->1	2->2	1->2	2->1	2->2							
DST	●●●	-1.3	0.1	1.0		L>F						G>R					chr6 -	56,596,090	dystronin isoform 1e precursor	member of the plakun protein family of adhesion junction plaque proteins. some isoforms are expressed in epithelial tissue, anchoring keratin-containing intermediate
PERP	●●●	0.7	0.0	0.7			3 (2)					Syn, R->P					chr6 -	138,461,949	PERP, TP53 apoptosis effector	downregulation of PERP correlated with metastatic capacity of human melanoma cell lines
FAT2	●●●	0.1	0.3	1.9								Syn		S->L, I	I->M, Syn		chr5 -	150,896,272	FAT tumor suppressor homolog 2	Drosophila and human homolog is a tumor suppressor gene
MALAT1	●●●	0.3	-0.6	0.3		NC						NC				NC	chr11 +	65,026,161	metastasis associated lung adenocarcinoma transcript 1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding) (MALAT1), non-coding RNA.
DS3C	●●●	0.6	0.5	1.1			3					3, K>R, S->T				3 (3)	chr18 +	26,850,414	desmocollin 3 associated Dsc3a preproprotein	a calcium-dependent glycoprotein that is a member of the desmocollin subfamily. cell adhesion and desmosome formation.
CD44	●●●	-0.9	0.5	1.3		Syn, I						K>R				I/NSS	chr11 +	35,163,759	CD44 molecule	adhesion molecule involved in migration, cell fusion and resorption in osteoclasts that also plays a role in cellular metastasis.
GIB2	●●●	0.6	-0.7	1.2								W->C				I, 3	chr13 -	19,662,360	gap junction protein, beta 2	forms gap junctions; may play a role in epididymal development
CTNND1	●●●	1.2	0.0	1.0		I, 3										I, 3	chr11 +	57,314,519	catenin, delta 1 isoform 1A	member of the Armadillo protein family, which function in adhesion between cells and signal transduction. Multiple translation initiation codons
CND1	●●●	3.7	-0.1	1.2			3	3									chr11 +	69,171,738	cyclin D1	regulatory subunit of CDK4 or CDK6; involved in regulation of the G1/S transition of the cell cycle
DSP	●●●	-0.1	-0.3	1.6		I->F, Syn							Syn				chr6 +	7,509,407	desmoplakin isoform I	Desmosomes are intercellular junctions that tightly link adjacent cells. Desmoplakin is an obligate component of functional desmosomes that anchors intermediate filaments to plakophilin 1 and plakoglobin. The C-terminus of desmoplakin binds with intermediate filaments. In the mid-region of desmoplakin, a coiled-coiled rod domain is resp
PKP1	●●●	0.0	0.6	1.5		I, I/NSS										I	chr1 +	199,543,971	plakophilin 1	may be involved in molecular recruitment and stabilization during desmosome formation.
S100A2	●●●	0.1	0.7	1.3		I/NSS										I/NSS	chr1 -	151,802,569	S100 calcium binding protein A2	a member of the S100 family of proteins containing 2 EF-hand calcium-binding motifs. S100 proteins are involved in the regulation of cell cycle progression and differe
SKP1	●●●	0.2	-0.6	-0.4									5			5	chr5 -	133,530,302	S-phase kinase-associated protein 1	component of SCF complexes, which are composed of this protein, cyclin 1, a ring-box protein, and one member of the F-box family of proteins. This protein binds diere
NCRNA00084	●●●	0.4	0.1	-0.3			NC (5)		NC			NC (3)					chr11 +	64,956,406	0	0
POLR2A	●●●	-0.5	1.2	0.4									Syn			3	chr17 -	7,343,614	polymerase (RNA) II (DNA directed) polypeptide	largest subunit of RNA polymerase II, the polymerase responsible for synthesizing messenger RNA in eukaryotes. The product of this gene contains a carboxy terminal
KRT14	●●●	-0.5	0.4	0.9								Syn, I/NSS					chr17 -	36,994,366	keratin 14	member of the keratin family, the most diverse group of intermediate filaments. a type I keratin, is usually found as a heterodimer with two keratin 5 molecules, a
KIF9	●●●	-0.6	-2.1	-2.0		III							NC				chr11 -	1,974,311	0	0
RUNX1	●●●	0.6	1.0	-0.4									III				chr21 +	35,212,715	runt-related transcription factor 1	putative transcription factor that may be involved in skeletal muscle gene regulation; human homolog is associated with a form of acute myeloid leukemia
KRT1	●●●	0.8	-3.0	1.5		3										Syn	chr12 -	51,357,622	keratin complex 2, basic, gene 1	0
MAP4	●●●	-1.5	-0.1	-1.0													chr3 -	47,897,033	microtubule-associated protein 4	a major non-neuronal microtubule-associated protein. This protein contains a domain similar to the microtubule-binding domains of neuronal microtubule-associated
KRT6A	●●●	-1.8	-0.1	0.9			3 (2), I (3)									I, 3	chr12 -	51,170,336	keratin 6A	The protein encoded by this gene is a member of the keratin gene family. The type I cytokeratins consist of basic or neutral proteins which are arranged in pairs of he
HSPG2	●●●	0.1	0.4	-1.1												R->H	chr1 -	22,078,830	heparan sulfate proteoglycan 2	Heparan sulfate proteoglycan is a major component of basement membranes, where the molecule may be involved in the stabilization of other molecules as well as b
HNRNPH1	●●●	-0.1	-0.5	-0.3												I	chr5 -	178,978,556	heterogeneous nuclear ribonucleoprotein H1	interacts with PKC-zeta and GABA(C) receptors to form ternary postsynaptic complex in the retina
SCSTM1	●●●	0.3	0.9	-0.7												Syn (2)	chr5 +	179,189,065	sequestosome 1 isoform 1	...
HLA-A	●●●	-0.3	0.3	0.5												3	chr6 +	30,019,971	major histocompatibility complex, class I, A	HLA-A belongs to the HLA class I heavy chain paralogues. This class I molecule is a heterodimer consisting of a heavy chain and a light chain (beta-2 microglobulin). Cla
NDST1	●●●	-0.3	0.0	-0.7			Syn										chr5 +	149,892,916	N-deacetylase/N-sulfotransferase (heparan	enzyme that catalyzes the transfer of sulfate from 3'-phosphoadenosine 5'-phosphosulfate to the nitrogen of glucosamine in heparan sulfate
EIF4G1	●●●	0.8	1.2	0.6												Syn	chr3 +	185,525,445	eukaryotic translation initiation factor 4	a component of the protein complex EIF4F, which is involved in the recognition of the mRNA cap, ATP-dependent unwinding of 5'-terminal secondary structure, and ri
EPN2	●●●	-0.8	0.3	0.4			I									3	chr17 +	19,130,952	epin 2 isoform b	may mediate membrane dynamics at the cell surface
PITX1	●●●	-0.9	-0.7	-2.8			Syn	I								Syn	chr5 -	134,394,593	paired-like homeobox domain 1	paired-like homeobox transcription factor; transcription regulator of pituitary genes; genetic marker for nascent Rathke's pouch, precursor of anterior and intermedia
ALDH3A1	●●●	-0.9	1.4	-2.4			3	Syn								D->G	chr17 -	19,585,628	aldehyde dehydrogenase 3A1	aldehyde dehydrogenase that is expressed during hepatocarcinogenesis
CTSB	●●●	0.4	1.4	-0.5												3, L->V	chr8 -	11,750,249	cathepsin B preproprotein	lysosomal peptidase
ACTG1	●●●	0.5	0.4	0.7												V->I	chr17 -	77,093,008	actin, gamma, cytoplasmic 1	Actins are highly conserved proteins that are involved in various types of cell motility, and maintenance of the cytoskeleton. The beta and gamma actins co-exist in m
ZFP36L1	●●●	-0.5	-0.4	0.1			3									G->S	chr14 -	68,326,833	zinc finger protein 36, C3H type-like 1	putative nuclear transcription factor; member of the TIS11 family of early response genes; may regulate the response to growth factors [RGD].
ANKA1	●●●	-3.5	-2.2	-1.0												I/NSS	chr9 +	74,965,864	annexin A1	plays a role in regulation of insulin secretion; may inhibit phospholipase A2
SH3PXD2A	●●●	-0.2	0.6	0.4												3	chr10 +	105,474,464	SH3 and PX domains 2A	...
PHK8	●●●	-0.2	0.3	0.4				I (2)								I	chr16 +	46,172,823	phosphorylase kinase, beta	expression in regenerating muscle may be correlated with that of other phosphorylase kinase subunits
SRRM2	●●●	-0.4	0.9	-0.1													chr16 +	2,751,872	serine/arginine repetitive matrix 2	...
TMEM107	●●●	2.5	0.2	0.9												3	chr17 -	8,918,790	transmembrane protein 107 isoform 1	...
HLA-DRB6	●●●	-0.9	0.1	-1.2												NC	chr6 -	32,632,112	major histocompatibility complex, class II, DR beta 6	Homo sapiens major histocompatibility complex, class II, DR beta 6 (pseudogene) (HLA-DRB6), non-coding RNA.
ALKBH5	●●●	-0.9	1.6	0.4												3	chr17 +	18,040,792	alkB, alkylation repair homolog 5	...
BAT2L	●●●	-1.1	1.2	0.4												R->L	chr9 +	133,330,347	HLA-B associated transcript 2-like	...
CDKN2AIPNL	●●●	1.2	-0.3	-0.2													chr5 -	133,610,065	CDKN2A interacting protein N-terminal like	...
AHNK	●●●	-0.2	0.0	0.5			Syn										chr11 -	62,014,250	AHNK nucleoprotein isoform 3	...
COL1A1	●●●	4.5	1.1	-1.1													chr17 -	45,625,227	alpha 1(I) type I collagen preproprotein	pro-alpha1 chains of type I collagen whose triple helix comprises two alpha1 chains and one alpha2 chain. Type I is a fibril-forming collagen found in most connective t
COL4A1	●●●	2.3	0.4	-1.5												A->T, Syn	chr13 -	109,678,404	alpha 1(IV) type IV collagen preproprotein	syndrome type VIIA, Ehlers-Danlos syndrome Classical type, Caffey Disease and idiopathic osteoporosis. Reciprocal translocations between chromosomes 17 and 22, w
FAM129B	●●●	-1.2	-0.2	-0.7												3, I	chr9 -	129,344,264	hypothetical protein LOC362115	the major type IV alpha collagen chain of basement membranes. Like the other members of the type IV collagen gene family, this gene is organized in a head-to-head
ITGB4	●●●	1.1	4.2	2.5												Syn (2)	chr17 +	71,248,932	integrin beta 4	beta subunit of integrin alpha6/beta4 which is a cell surface receptor for laminin; involved in hemidesmosome formation.
KRT13	●●●	-7.2	-1.7	-6.4												Syn	chr17 +	36,913,075	keratin 13	human homolog plays a role in epidermal development
KRT5	●●●	-0.5	-0.3	1.6			3, I (2), Syn (2)									S->G	chr12 -	51,197,568	keratin 5	cytoskeletal intermediate filament protein; provides a cortical scaffold to primary spermatocytes
PID1	●●●	-1.4	-3.5	-3.6												I	chr2 -	229,720,617	phosphotyrosine interaction domain containing 1	0
PLEC1	●●●	1.7	1.7	1.0													chr8 -	145,076,101	plectin 1	cytoskeletal cross-linking protein; interacts with all three major groups of cytoskeletal proteins, actin filaments, microtubules, and intermediate filaments
TGM3	●●●	-3.9	-2.3	-7.1			3										chr20 +	2,247,169	transglutaminase 3 precursor	Transglutaminases are enzymes that catalyze the crosslinking of proteins by epsilon-gamma glutamyl lysine isopeptide bonds. Involved the later stages of cell envelop