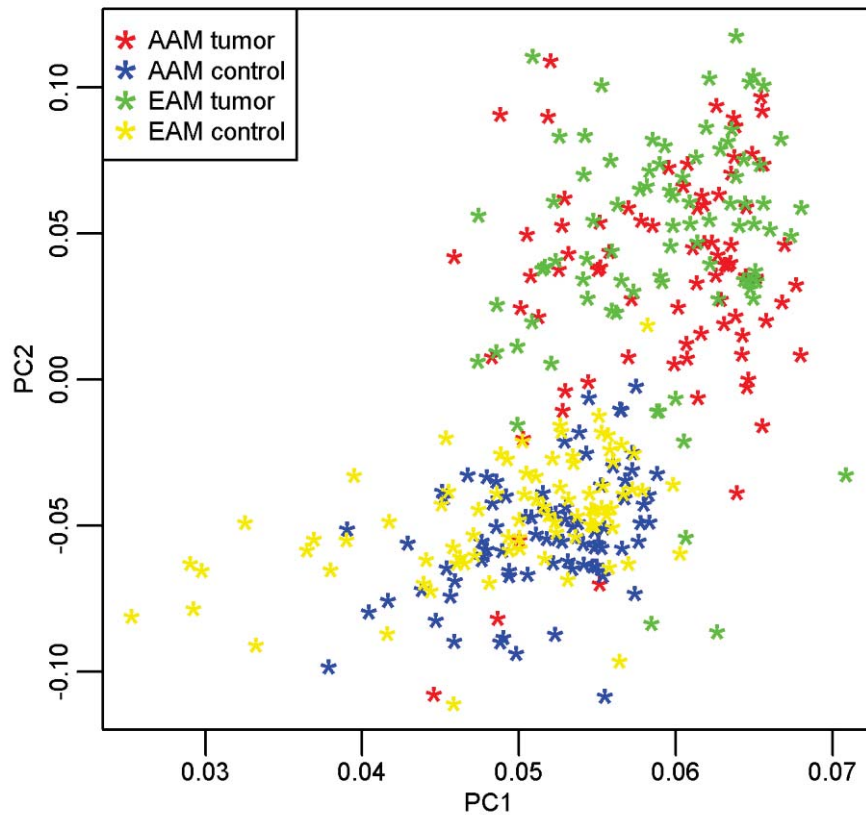


ABCA5	APLP2	CDKN1B	DHCR24	FGFR1	HPGD	LDHB	NFKBIA	PLAUR	SEC14L2	TIMP2
ABCB1	APOD	CDKN2A	DHH	FGFR2	HPN	LEF1	NFKBIB	PLCG1	SEL1L	TIMP3
ABHD2	APOE	CDS2	DHPS	FHIT	HSD17B10	LEPR	NIN	PLD1	SEPT5	TIMP4
ACACA	APRT	CGA	DIABLO	FIGN	HSD17B3	LGALS3BP	NIPAA2	PLD2	SERPINF5	TLR2
ACACB	AR	CHAF1A	DIO2	FLNA	HSD17B4	LIPC	NKX3_1	PLN	SERPINF1	TLR3
ACADSB	ARMET	CHEK2	DLL1	FMR1	HSP90AA1	LIPH	NLRP1	PLS3	SFRP4	TLR4
ACE	ASB2	CHGA	DNAH5	FOLH1	ID4	LOX	NME1	PON1	SGIP1	TMEM176B
ACTA2	ASB5	CLASP2	DNAJB1	FOS	IER3	LTA4H	NOS2	PON2	SGMS1	TMSB15A
ADAMTS9	AZGP1	CLDN5	DPYD	FOXF1	IGF1	LTB4R	NOTCH1	PPARA	SGMS2	TMTC1
ADD2	BCL2	CLU	DPYS	FRZB	IGFBP3	LTB4R2	NOX1	PPARD	SGPP1	TNF
ADIPOQ	BCL2L14	CMA1	DPYSL2	FSTL1	IGFBP6	LTC4S	NOX4	PPARG	SH2D1A	TNFRSF10B
ADIPOR1	BEX4	CNR1	DPYSL3	G6PD	IHH	LUM	NPAT	PPFIA3	SHH	TNFRSF11A
ADIPOR2	BGN	CNR2	DUSP9	GAB1	IKBKG	MAF	NR1H3	PRAME	SLC14A1	TNFRSF13B
ADRB2	BIRC5	CNTNAP2	DVL2	GABRG2	IL10	MAOB	NRIP1	PRKCA	SMAD3	TNFSF11
ADRB3	BLVRA	COL1A1	DVL3	GADD45A	IL10RA	MAPK8	NTN4	PRRT2	SMAD4	TNFSF12
ADSL	BMP2	COL1A2	DYRK1A	GADD45B	IL1B	MDM2	OAT	PRRT2	SMAD7	TP53
AGT	BMP4	COL3A1	E2F3	GARNL3	IL6	MEIS2	OAZ2	PTCH1	SMO	TP73
AGTR1	BMP7	COL4A1	EDNRA	GAS2L3	IL8	MEN1	ODC1	PTCH2	SMOX	TPD52
AHR	BMPR1A	COL5A2	EFNA3	GATM	ILKAP	MGP	OGG1	PTEN	SOCS2	TRAF2
AKAP12	BMPR2	COMT	EGFR	GDF15	IMPA1	MME	OSBPL8	PTGDR	SOD1	TRIM29
AKT1	BRCA1	COX5A	ELAC2	GHR	INHBA	MMP1	OXER1	PTGDS	SOD2	TRPM8
AKT2	BRCA2	CPXM1	EMP1	GHRL	INMT	MMP12	PAICS	PTGER2	SPARC	TRPV6
AKT3	BTG2	CRABP1	EMP2	GLI1	INPP1	MMP13	PAK1	PTGER3	SPHK1	TUSC3
ALCAM	C10ORF11	CRP	EPHB2	GLI2	INPP5D	MMP14	PAOX	PTGER4	SQRDL	TYMS
ALDH1A2	C1QTNF6	CSF2	EPHX2	GLI3	INSIG2	MMP16	PCDH18	PTGES	SRD5A2	UAP1
ALDH1A3	C5ORF26	CSMD1	ERBB2	GPM6B	IRF7	MMP2	PCGEM1	PTGFR	SREBF1	UBE2L6
ALDH2	C7ORF58	CTHRC1	ERBB3	GPR12	ISL1	MMP20	PCM1	PTGIR	SREBF2	UGDH
ALDH9A1	CALM1	CTNNB1	ERBB4	GPX3	ITGA2B	MMP7	PDGFB	PTGIS	SRM	VBP1
ALOX12	CAMKK2	CTSB	ERCC1	GPX4	ITGAV	MMP9	PDGFC	PTGR1	SSBP1	VCAN
ALOX12B	CAPZB	CTSK	ERCC2	GREB1	ITGB3	MOXD1	PDGFD	PTGR2	ST14	VCP
ALOX15	CAV1	CXCL12	ERCC5	GREM1	ITGBL1	MSMB	PDGFRA	PTGS1	ST6GAL1	VDR
ALOX15B	CAV2	CXCR4	ERG	GREM2	ITPR1	MSR1	PDGFRB	PTGS2	STS	VEGFA
ALOX5	CCDC34	CXCR7	ESR2	GRN	ITPR2	MTA1	PDK4	PXN	SUFU	VLDLR
ALOX5AP	CCL2	CYB561	EZH2	GSK3B	ITPR3	MTHFD2	PDPK1	RAD51L1	SULF1	WFDC1
AMACR	CCL5	CYBRD1	F2R	GSTP1	JAG1	MUTYH	PIK3C3	RARB	TBXAS1	WIF1
AMD1	CCND1	CYFIP1	F3	GSTT1	KCNRG	MXI1	PIK3CA	RARRES1	TCF21	WNT1
ANGPTL1	CCND2	CYP11B2	F5	GUCY1A3	KDR	MYB	PIK3CB	RB1	TCF7L1	WNT11
ANKRD17	CD14	CYP17A1	FAAH	GYG1	KHDRBS3	MYC	PIK3R1	REPS2	TCF7L2	WNT2
ANPEP	CD24	CYP19A1	FABP4	HDAC1	KIT	MYLK	PIK3R2	RET	TCL1B	WNT5A
ANTXR1	CD36	CYP1A1	FAM155B	HDAC4	KITLG	MYOCD	PIK3R3	RNASEL	TGFB1	XPA
ANXA1	CD40	CYP1B1	FAM171B	HDAC9	KLF6	MYOF	PLA2G2A	RND3	TGFB111	XPC
ANXA2	CD86	CYP3A4	FASN	HGF	KLF9	NAAA	PLA2G2D	RRN3	TGFB2	XRCC1
ANXA6	CDC14A	CYP7B1	FDFT1	HHIP	KLK2	NAT1	PLA2G4D	S1PR1	TGFB3	XRCC3
AOC3	CDC42EP3	CYSLTR1	FFAR2	HIF1A	KLK4	NCDN	PLA2G6	SALL4	TGFB1	XRCC4
APC	CDH1	CYSLTR2	FGF17	HLA_F	KRT15	NETO2	PLA2G7	SAT1	TGFB2	YIPF1
APC2	CDH11	DAPK1	FGF2	HNF1B	KRT5	NFATC4	PLAT	SATB1	TGFB3	ZADH2
APEX1	CDKN1A	DES	FGF7	HOXB5	LDB2	NFKB1	PLAU	SCD	TIMP1	ZNF10

Supplemental Table 1. List of the 517 genes whose expression was measured by DASL microarray analysis of RNA from FFPE specimens.

Gene	OR	Mean EAM - AAM $\Delta\Delta$Ct	pvalue
AKT1	0.94	0.459	0.041
ALOX15	0.88	-0.584	0.422
CXCR4	0.87	0.834	0.097
ERG	1.62	-1.982	0.003
FASN	0.90	0.504	0.195
IL6	0.78	1.518	0.028
TGFB1	0.91	0.618	0.074
TNF	0.97	0.418	0.467

Supplemental Table 2. Mean difference and t-test p-value between the computed DDCT from EAM minus the computed DDCT from AAM from the validation sample of 16 AAM and 16 EAM. The respective odds ratios from Table 2 are included for comparison purposes. The point estimates for difference in DDCT are all in the same direction (greater than 0 is equivalent to an odds ratio less than 1) as the odds ratios for all genes except ALOX15.



Supplemental Figure 1. Plot of the first 2 principal components, computed from all 517 genes on 163 patient tumor samples (80 AAM, 83 EAM) with the corresponding matched normal samples. Although all of the control samples had a matching tumor sample and thus are expected to be highly correlated with the respective tumor sample, the samples clustered by tumor/control status, regardless of race. This implies that the expression profile of the tumor samples are similar across races and different than the profile of the control samples, which are also similar across races.