

**Supplemental Table 1**

<b>Gene</b>	<b>logFC EA/AA</b>	<b>adj.P.Val</b>
CACNA2 D1	- 1.616486248	2.73234E- 15
RPS28	- 1.583192857	7.98044E- 10
AR	- 1.490650597	2.38261E- 09
CYP4Z1	- 1.447292302	1.2563E-06
IL6ST	-1.39709581	5.56145E- 12
GFRA1	- 1.350601496	0.00012253
KCND3	- 1.319183545	2.55279E- 12
AGTR1	- 1.295185468	1.00719E- 07
PRKG2	- 1.247744271	1.00429E- 18
ADAMTS1 5	- 1.243349701	1.10456E- 09
C7	-1.2367314	9.23632E- 06
IGSF9B	-1.22560262	1.98458E- 11
SLC7A2	- 1.219174304	2.19199E- 08
GPR81	- 1.205194981	9.03106E- 08
EDIL3	- 1.196038236	2.67603E- 11
CYP4B1	- 1.191310314	1.0731E-06
CLIC6	-1.1889956	1.53997E- 07
ERBB4	- 1.185121909	1.38167E- 05
TIMP4	- 1.184578067	3.87282E- 08
THRSP	- 1.180747663	7.73563E- 06

NRK	- 1.172764212	3.89521E- 10
GABRB3	- 1.146063066	1.83977E- 08
FMO2	- 1.131628919	2.03438E- 06
OMD	- 1.122322689	1.03144E- 06
ARHGAP 20	- 1.121317355	4.99001E- 16
CYP2B7P 1	- 1.118740042	0.00032552 6
CDKL5	- 1.114267352	3.01303E- 15
CCNT1	- 1.108688716	4.51526E- 20
CNTN1	- 1.106268555	8.30467E- 10
PTPRT	- 1.104947401	0.00043836
SLC28A3	- 1.097832524	3.16207E- 07
RUNX1T1	- 1.097034394	3.07801E- 12
FAT3	- 1.096850844	1.34563E- 11
ZFPM2	- 1.092742421	2.06064E- 14
CHL1	-1.09142626	1.49816E- 07
RASEF	- 1.086500505	2.37049E- 09
NFATC2	- 1.086065811	1.01759E- 12
OGN	- 1.082412447	1.42436E- 05
KIAA0754	-1.06592747	3.87592E- 14
ADAMTS1 2	- 1.045849428	3.13298E- 09
KLHL4	-1.03585655	1.98589E- 12
PRKG1	- 1.034774571	1.12459E- 10
SLC44A5	- 1.026319148	7.14098E- 08

DDR2	-1.02610626	2.20563E-11
KIRREL	-1.025751468	1.71401E-11
LRRC37A2	-1.02131282	2.3834E-42
TSHZ2	-1.017308713	2.93245E-13
COL10A1	-1.014043685	0.00018806
TNN	-1.014001509	3.27188E-06
AKAP2	-1.004992219	3.01423E-10
GRIK3	-1.002663592	1.41135E-05
FMO1	-1.002428093	1.04516E-09
GGT3P	1.002995458	5.209E-17
KCNG1	1.012630355	3.03523E-08
RNF112	1.015831752	1.4871E-25
P2RY11	1.022090961	5.32665E-13
GPC2	1.025637556	1.47321E-17
MSLN	1.030129161	0.001066345
INE2	1.038603464	4.36059E-12
CCL3L1	1.038777254	4.62231E-18
TSPAN10	1.044760145	2.40626E-24
NACA2	1.053746115	1.67191E-30
COL9A3	1.058009115	3.07866E-11
MAGED4	1.061320144	6.47747E-14
MFSD2B	1.065604315	3.40299E-19
CAPS	1.097430224	8.36083E-17
DLX5	1.10407257	2.02685E-

		10
GJB5	1.1274652	7.11978E-09
COL2A1	1.135461778	5.03194E-06
TUBB8	1.173527118	1.83113E-35
PCSK1N	1.477253295	3.12726E-12
TSIX	1.605997143	2.74797E-22

Gene: gene name

LogFC AA vs EA;  $\text{Log}_2 \left( \frac{\text{mean EA tumor RPKM}}{\text{mean AA tumor RPKM}} \right)$  for each transcript

adj.P.Val: P value adjusted for multiple hypothesis testing with BH method