

Transcripts most-highly co-regulated with AKR1C3 (positive association). All P values<0.001.

GeneSymbol	R value	R2 value
AKR1C3	1	1
AKR1C1	0.94524216	0.893483
AKR1C2	0.935813053	0.875746
AKR1C4	0.886756755	0.786338
AMIGO2	0.675654202	0.456509
KIAA1524	0.652009626	0.425117
LAMB1	0.635375713	0.403702
IGFBP3	0.633829992	0.40174
FGD6	0.596583273	0.355912
CA12	0.576259994	0.332076
FAR2	0.573998341	0.329474
IFI27	0.573286709	0.328658
CKLF	0.565635749	0.319944
UGT2B17	0.563840125	0.317916
IL18	0.562716898	0.31665
LOC728160	0.560990592	0.31471
UGT2B15	0.560990592	0.31471
ST3GAL1	0.559856832	0.31344
OSBPL3	0.558727529	0.312176
GSDMB	0.549991234	0.30249

Transcripts with the most negative association with AKR1C3. All P values<0.001.

GeneSymbol	R value	R2 value
KLK3	-0.714317511	0.51025
ACPP	-0.588004506	0.345749
ABCC4	-0.564390637	0.318537
KLK2	-0.562786881	0.316729
SORD	-0.548272897	0.300603
ALDH1A3	-0.540447988	0.292084
SORD2	-0.539934101	0.291529
KCND3	-0.532286485	0.283329
ALDH6A1	-0.531074288	0.28204
KLK4	-0.530894188	0.281849
TRPM8	-0.52814907	0.278941
SPDEF	-0.516511253	0.266784
SLC45A3	-0.513693514	0.263881
MSMB	-0.512995354	0.263164
FAM13C	-0.512252606	0.262403
C9orf61	-0.500806651	0.250807
LOC100131110	-0.495850304	0.245868
AZGP1	-0.484037215	0.234292
CHRNA2	-0.482433479	0.232742
TBC1D4	-0.479306963	0.229735