

Supporting Information

Table S1. The 237 villi-specific genes.

A1BG
ABHD14B
ANKLE2
ARHGDI1A
BRE
C9orf116
CBY1
CD81
CDK16
CGN
CHRD
COL5A1
CYBA
DPCD
FAM193B
FTH1
GGT1
GPX3
H1FX
HLA-E
HNMT
HRAS
IFT80
L3MBTL2
MGAT4B
MRPS2
MT1G
MT1L
NUAK2
PCAT6
PFKM
PIAS3
PKP2
PTPRCAP
RAVER1
RTN4RL2
SERPING1
SEZ6L2
SOX13

STAT3
TBCK
TMEM238
TMEM9
TRABD
TRMU
TTC21B
UBTF
USP11
VAC14
WDR54
ACPP
ADCK2
ANKFY1
AP5S1
ARPC2
ATP6V1A
BCL10
C16orf70
C17orf80
C1orf109
CARKD
CASP7
CDC16
CEP290
CHM
CIRH1A
CUTC
DDX52
DEFB1
DNAJC10
FAM60A
FBXL12
FERMT2
FRA10AC1
G3BP1
GNAQ
GPATCH11
GSE1
GSTM3
GUSBP1
ICE1
ING1
ITPA

LOC220729
MAPKAPK5-AS1
MARCH5
MBTD1
MFSD7
MRPL28
MRRF
NEK6
NUPR1
PAX8
PAXBP1
PNRC2
PPP2R5A
PPTC7
PTPRE
RBKS
RCC1
RGL3
RIT1
RNF41
RPE
RRP1
SIRT1
SLC15A4
SMARCC1
SNAPC5
SRBD1
SRSF11
STAG1
SYNJ2
SYTL3
TCEAL5
TMEM194A
TMEM251
TOP1
TOP1P2
YBEY
ZFP62
ZFX
ZNF426
ACSL1
ACSL4
AREL1
ARHGAP21

ARHGEF17
ARPC5
ATAD1
ATG4B
BCL2L13
C5orf45
CAPN10
CCDC186
CCSER2
CDK10
CLPX
CLU
CNST
COL6A1
COL6A2
CRKL
CST3
CST5
CXCL14
CYP2W1
DAXX
DGKA
DIRC1
EMILIN1
ERVH-4
FAM43B
FOXO1
GADD45A
GAST
GP9
INPP5E
JUP
KCNK3
KGFLP1
KIF3A
LLGL2
LOC101929918
LOC283788
LOC390705
LOC642236
LOC649294
LRFN1
LRRN2
LYPD5

MAPKAPK2
ME2
MED8
MIB2
MRE11A
MRPL2
MTF1
NFKBIE
OBFC1
ODF2
ORAI2
PCCA
PCOLCE
PHF1
PLA2G6
PPME1
PPP1R12C
PPP2R3B
PTEN
PTPN6
R3HDM4
RAB1B
RAC2
RAP2B
RBM15
RBM42
RHBDL1
RIMKLB
RNF141
RNF214
RNPEPL1
RPS6KA2
S100A16
SEC63
SERHL2
SIAE
SIGIRR
SKI
SLC25A29
SLC50A1
SLIT1
SOD2
SPATA13
SPATA20

SRPK2
 SSBP4
 ST6GAL1
 SUSD3
 TGFBRAP1
 TLN1
 TMEM101
 TPCN1
 TSC2
 TSC22D1
 TSKU
 UBE2D1
 UBE2G2
 UCP2
 VEGFA
 VPS18
 VPS36
 WARS
 WDR25
 ZBTB48
 ZNF33A
 ZYX

Legend: We defined villi-specific genes as those with mean expression levels in the villus samples greater than three SDs above the mean of the mature placenta samples (SD: Standard Deviation).

Table S2. Changes in the expression of villi-specific genes in TCGA.

CancerName	NO.cancerSample	NO.normalSample	NO.gene	NO.upGene	NO.downGene
BRCA	1093	112	214	112	72
KIRC	533	72	214	106	74
LUAD	515	59	214	112	59
THCA	501	59	37	17	12
PRAD	497	52	214	87	77
COADREAD					
D	379	51	214	91	82
LUSC	501	51	214	101	81
LIHC	371	50	214	112	54
HNSC	520	44	214	85	56
COAD	285	41	214	92	77
STAD	415	35	214	86	54
KIRP	290	32	214	91	80
KICH	66	25	214	63	90

UCEC	176	24	214	93	57
BLCA	408	19	214	80	55
ESCA	184	11	214	78	33
READ	94	10	214	82	49
CHOL	36	9	213	115	48
GBM	153	5	214	98	44
GBMLGG	669	5	214	95	35

Legend: The 20 cancer types from TCGA, each cancer type had at least five normal samples, and we used t-tests to determine whether the genes were differentially expressed between the cancer and normal samples (p value <0.05).