

Table S1

Top 50 gene up regulated in GH tumors vs Normal

Top 50 gene down regulated in GH tumors vs Normal

Gene	p value	Fold change
GPAM	5.80E-20	13.3261
SLC38A4	4.54E-12	11.0708
CRTAC1	2.49E-10	9.15098
ANLN	5.52E-13	8.56572
MIR7-3	2.80E-13	7.8148
NOX4	7.55E-08	7.42519
UIMC1	1.30E-11	6.58914
MIR27B	3.29E-19	6.21656
ADAMTSL1	3.46E-09	5.34361
RFC1	6.83E-10	5.27605
CBLN1	1.96E-05	4.75386
MIR15A	1.82E-15	4.74236
ST8SIA4	2.22E-13	4.46439
AK5	2.04E-06	4.34198
HEPACAM2	2.58E-06	4.18596
DBC1	2.12E-07	4.14127
CHN2	1.48E-07	4.14068
GALNT5	3.56E-07	4.07638
PLXDC1	1.02E-12	3.94474
LOC121952	6.97E-14	3.90895
HIGD1B	2.29E-16	3.74049
ENPP2	1.01E-05	3.64975
CLSTN2	2.43E-07	3.64525
MIR377	4.32E-11	3.58193
CASP12	5.56E-11	3.57105
CHRN4	9.57E-10	3.48619
RTKN2	2.59E-10	3.47283
CPVL	7.66E-08	3.43645
MIR30E	1.82E-17	3.42594
RGS5	8.94E-09	3.39614
CSGALNACT1	8.85E-07	3.38737
MPEG1	6.11E-09	3.3507
EPB41L4B	3.53E-12	3.2474
MGAM	4.40E-05	3.17652
TRHDE	0.001313	3.04665
CSMD2	2.56E-07	3.04183
TMEM74	5.99E-09	3.02501

Gene	p value	Fold change
GAL	3.29E-18	-80.1988
LHB	1.77E-16	-47.5177
TSHB	1.29E-19	-35.5375
POMC	5.01E-12	-32.6512
CRYAB	1.31E-20	-22.8318
HP	2.22E-13	-20.4309
FSHB	3.15E-11	-20.1862
CHI3L1	1.69E-10	-19.3164
CALB1	1.08E-10	-18.6909
CGA	8.25E-08	-18.4691
GNRHR	7.42E-14	-15.5598
CGB1	2.83E-19	-15.241
SERPINF1	1.52E-12	-15.2225
ASCL1	6.07E-10	-14.9497
GPC4	1.77E-12	-14.7413
SLPI	1.74E-08	-13.8382
SERPINA3	1.04E-09	-13.1348
C7	7.84E-12	-12.4811
PMAIP1	6.34E-12	-12.2092
UGT2B7	4.10E-11	-12.0647
GPR50	4.44E-08	-11.8763
CGB2	1.74E-18	-10.9285
GPC3	1.37E-11	-10.9052
CP	3.27E-11	-10.6246
PCP4L1	5.73E-12	-10.5934
COL6A6	3.35E-14	-10.5374
C13orf36	3.75E-10	-9.99283
LRRTM4	3.24E-09	-9.65104
C4orf31	1.39E-07	-9.47045
UGT2A1	4.54E-12	-9.12288
SPON1	5.71E-07	-9.06451
BBOX1	2.06E-11	-9.01745
IGFBP5	2.17E-13	-8.7876
DGKK	1.53E-09	-8.69226
ADH1B	5.23E-16	-8.50344
TRPM3	2.50E-13	-8.43492
APOD	1.00E-11	-8.36737

GHSR	0.000939	3.00294
ADAMTS14	7.47E-12	2.9632
SHISA3	3.60E-05	2.96027
CD36	6.42E-07	2.8166
CPM	2.28E-05	2.79453
CD79B	3.63E-05	2.7234
MIR29C	8.66E-11	2.70766
IGSF6	2.55E-07	2.66523
TEKT1	1.77E-05	2.65244
KLB	2.83E-06	2.64889
LOC643923	4.21E-06	2.63271
MIR148B	5.56E-12	2.62505
MSL3L2	1.03E-07	2.59965

ESR1	3.73E-12	-8.34413
RGS4	6.03E-09	-8.31069
GJA1	2.12E-14	-8.17594
CGB5	1.74E-17	-8.16953
GPM6B	5.29E-15	-8.09007
SDC4	2.32E-11	-8.08978
CLDN7	1.59E-12	-7.97997
SFRP2	1.41E-15	-7.95603
AVPR1B	4.23E-11	-7.55165
CGB7	1.05E-16	-7.53039
C2orf40	7.20E-09	-7.39104
AREG	1.79E-13	-7.35144
CA8	4.87E-08	-7.34695

Table S2

Top 50 gene up regulated in SG vs DG tumors

Gene	p value	Fold change
CADM2	4.38E-10	21.3069
SLC38A4	1.40E-09	16.4691
SLC24A2	2.27E-08	12.7889
SGCZ	1.90E-07	12.7609
SEMA3A	1.62E-06	10.9913
LGR5	0.000478	10.9466
SYT10	4.61E-06	10.4307
CLVS2	2.88E-06	10.3803
VAT1L	2.81E-06	10.0126
KCNH7	8.77E-07	9.26894
ABI3BP	3.86E-07	9.25909
SLC38A3	1.01E-07	8.91477
KCNQ5	7.40E-05	8.5181
NTNG1	3.24E-09	8.08567
GPR64	5.57E-08	8.0635
MGAM	3.11E-07	7.80602
CASP12	2.68E-13	7.56974
NTS	0.007513	7.56484
KLB	5.88E-11	7.42316
HAL	2.15E-08	7.41204
SV2C	0.000477	7.4118
ADAMTS14	1.32E-16	6.96187
RFTN1	7.11E-13	6.95117
MFAP4	2.03E-07	6.71927
EDIL3	0.007432	6.68923
SHISA3	6.90E-07	6.29855
GNG8	7.25E-13	6.23557
PRDM8	5.05E-07	6.12209
NUAK1	7.19E-13	6.04126
SLCO5A1	1.52E-05	5.90812
RYR2	0.000987	5.86323
PREX2	1.36E-07	5.69319
SPOCK3	0.003537	5.61549
C5orf23	5.65E-05	5.50437
FAM19A2	9.35E-05	5.39674
TIAM1	5.07E-06	5.19031
SLC47A1	0.000132	5.18485

Top 50 gene down regulated in SG vs DG tumors

Gene	p value	Fold change
ESRP1	1.01E-11	-20.145
LMO3	2.63E-05	-18.5692
CGA	0.000211	-14.2351
GPR98	1.94E-13	-12.0741
TRIM36	5.97E-08	-11.2978
CDH1	9.73E-09	-10.432
TMEM30B	1.49E-14	-10.3659
AP1M2	6.13E-14	-10.2069
MAOB	1.61E-08	-9.89205
CCND2	2.03E-09	-9.45764
TRHDE	6.95E-06	-9.15629
ACVR1C	7.64E-10	-9.09927
AKR1B10	1.57E-07	-9.02909
FBXO16	7.30E-10	-8.96672
RHOBTB3	5.08E-11	-8.66724
NKX2-2	6.79E-12	-8.57978
CHML	2.18E-12	-8.06082
VEPH1	4.70E-06	-8.00923
IL13RA2	0.000256	-7.88582
EFEMP1	4.19E-06	-7.8754
GAD1	3.15E-06	-7.45941
NR5A1	1.28E-06	-7.33888
PCK1	6.09E-06	-7.08649
ARHGEF38	1.04E-05	-6.99914
DCX	8.70E-10	-6.64124
HTR4	6.83E-07	-6.60994
MUM1L1	0.000165	-6.46479
TAGLN3	5.19E-06	-6.34963
OPN3	1.06E-09	-6.14448
RAB25	3.03E-07	-6.11629
KCNN2	8.40E-09	-5.96298
OR7C1	1.30E-05	-5.87505
PERP	6.87E-14	-5.87197
TMEM45B	4.08E-05	-5.66893
GJB7	5.40E-05	-5.64009
ST14	7.40E-11	-5.57676
TNR	5.57E-05	-5.52281

ODZ3	3.14E-05	5.1815
CDH20	2.03E-05	5.15039
TTN	3.05E-05	5.0075
NRG3	6.56E-06	4.97905
LRRTM3	0.008887	4.83838
GBP2	7.67E-09	4.80446
SLC17A9	1.22E-15	4.75073
ANTXR2	8.79E-06	4.68765
ACCN1	4.29E-08	4.57425
NPR3	4.36E-05	4.51931
PPAP2B	9.84E-07	4.49604
ANLN	4.48E-05	4.4886
SHISA9	0.000117	4.45559

CA12	6.65E-05	-5.51633
CHMP4C	1.10E-11	-5.45425
LANCL3	7.80E-05	-5.40168
MYO3B	1.18E-06	-5.3692
RNF182	2.60E-05	-5.35039
PLD5	1.62E-05	-5.21593
CDKL5	5.32E-11	-5.19661
MT1F	6.28E-06	-5.06908
FABP6	4.14E-06	-4.94744
NNAT	0.000273	-4.91038
ZFHX4	2.59E-06	-4.89413
KRT23	4.80E-08	-4.83577
SPINT1	6.32E-12	-4.79064

Fig S1

Top IPA canonical pathways Norm vs GH tumor	
Pathway	P-value
Endothelin-1 Signaling	3.58 E -06
cAMP-mediated signaling	8.87 E -06
G-Protein Coupled Receptor Signaling	1.05 E -05
Molecular Mechanisms of Cancer	2.21 E -05
Cell Junction Signaling	2.27 E -05

Top IPA canonical pathways DG vs SG tumor	
Pathway	P-value
Hepatic Fibrosis activation	2.23 E -09
Aryl Hydrocarbon Receptor Signaling	5.77 E -05
Endocytosis signaling	1.15 E -03
Wnt/Ca+ pathway	1.44 E -03
Protein Kinase A Signaling	1.83 E -03

Fig S2

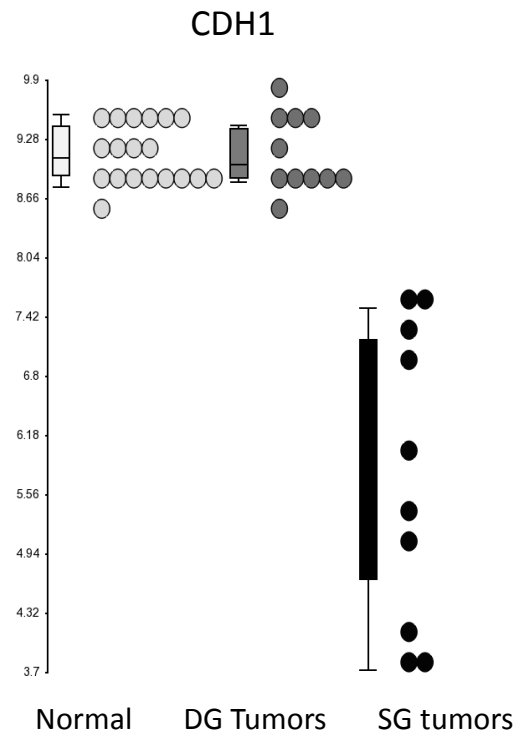


Fig S3

Genes up regulated in EMT	Fold change SG vs DG
MMP2	1.7
NRP1	1.6
PPAP2B	4.5
PRKCA	1.7
VCAN	1.7
EMP3	2.3
IL1R1	3.7
LTBP1	1.7
MME	1.6
SULF1	2.1
ZEB1	1.7
LOX	2
ABCA1	1.9
C5ORF13	1.6
RGS4	1.8

Genes down regulated in EMT	Fold change SG vs DG
CDH1	-10.4
CXADR	-1.9
EPCAM	-2.4
PLXNB1	-1.5
SYK	-1.6
LSR	-2.6
MAP7	-2.2
OCLN	-2.4
PKP2	-2.9
SPINT1	-4.8
GPX3	-2.2
SLC27A2	-2.4
SORL1	1.9
CDS1	-1.6
PLS1	-2
RHOD	-1.9
SLPI	-1.9
TMEM30B	-10.4
TPD52L1	-1.8
TSPAN1	-3
ZNF165	-1.8

Fig S4

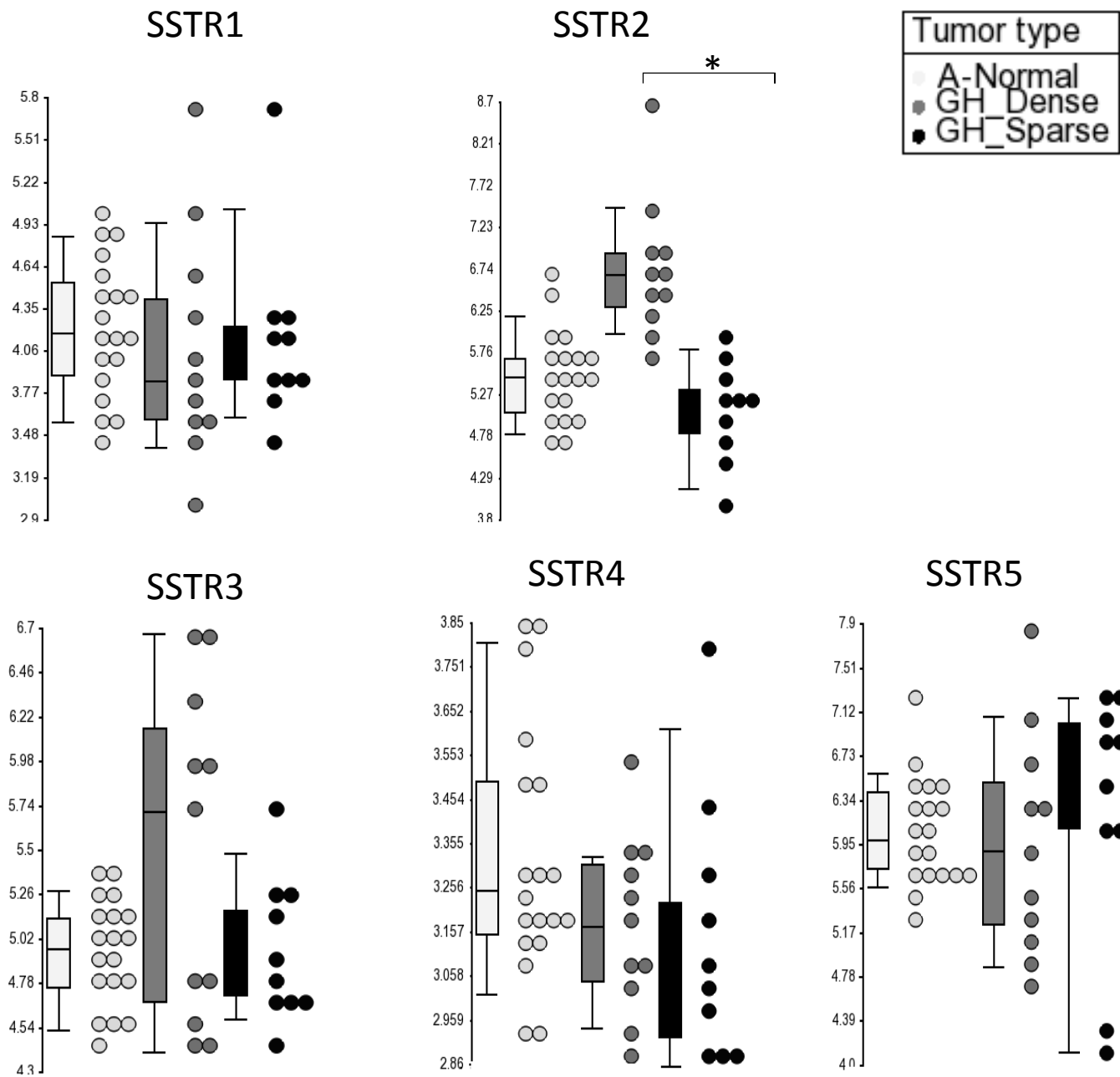


Fig S5

