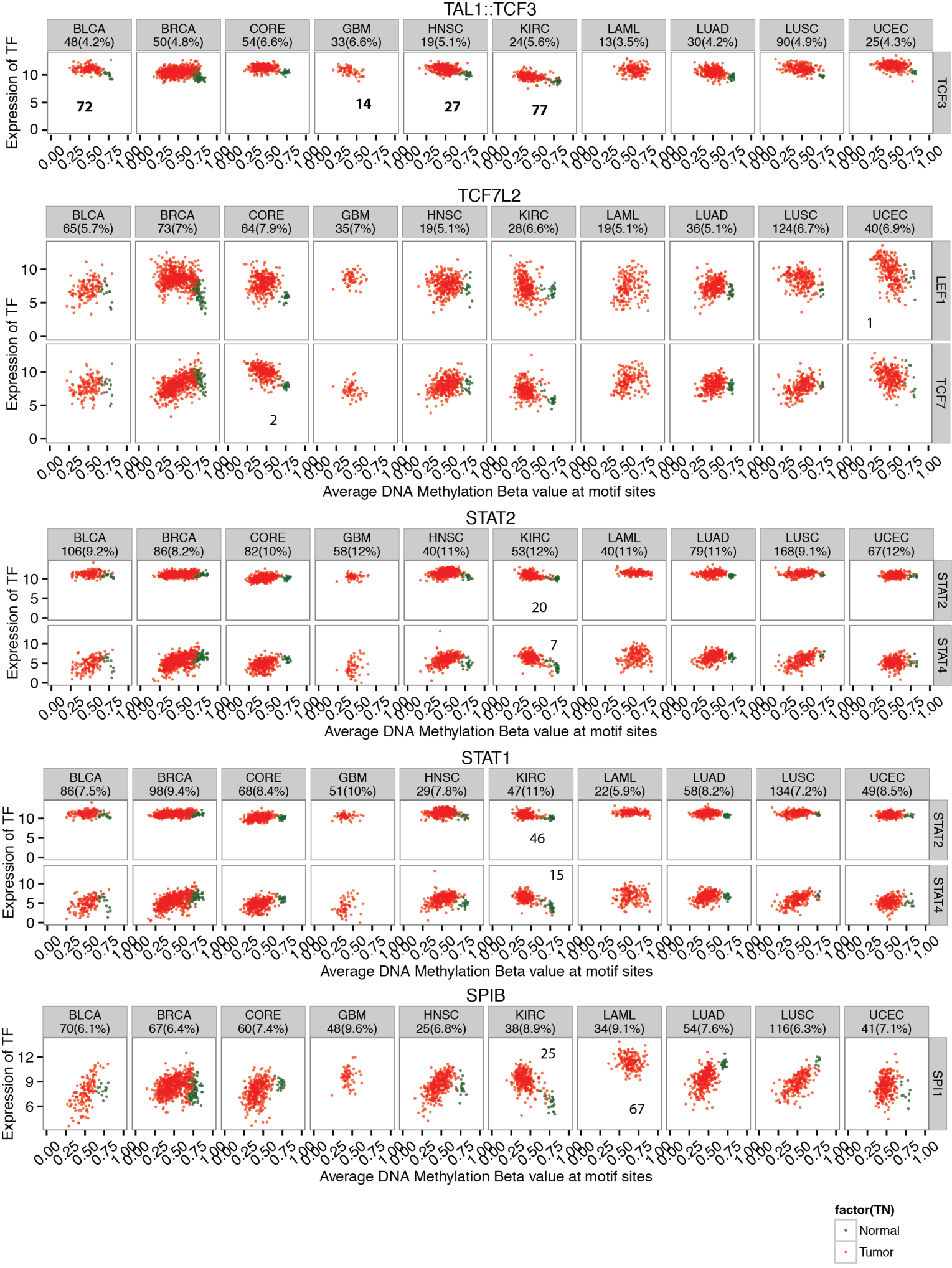
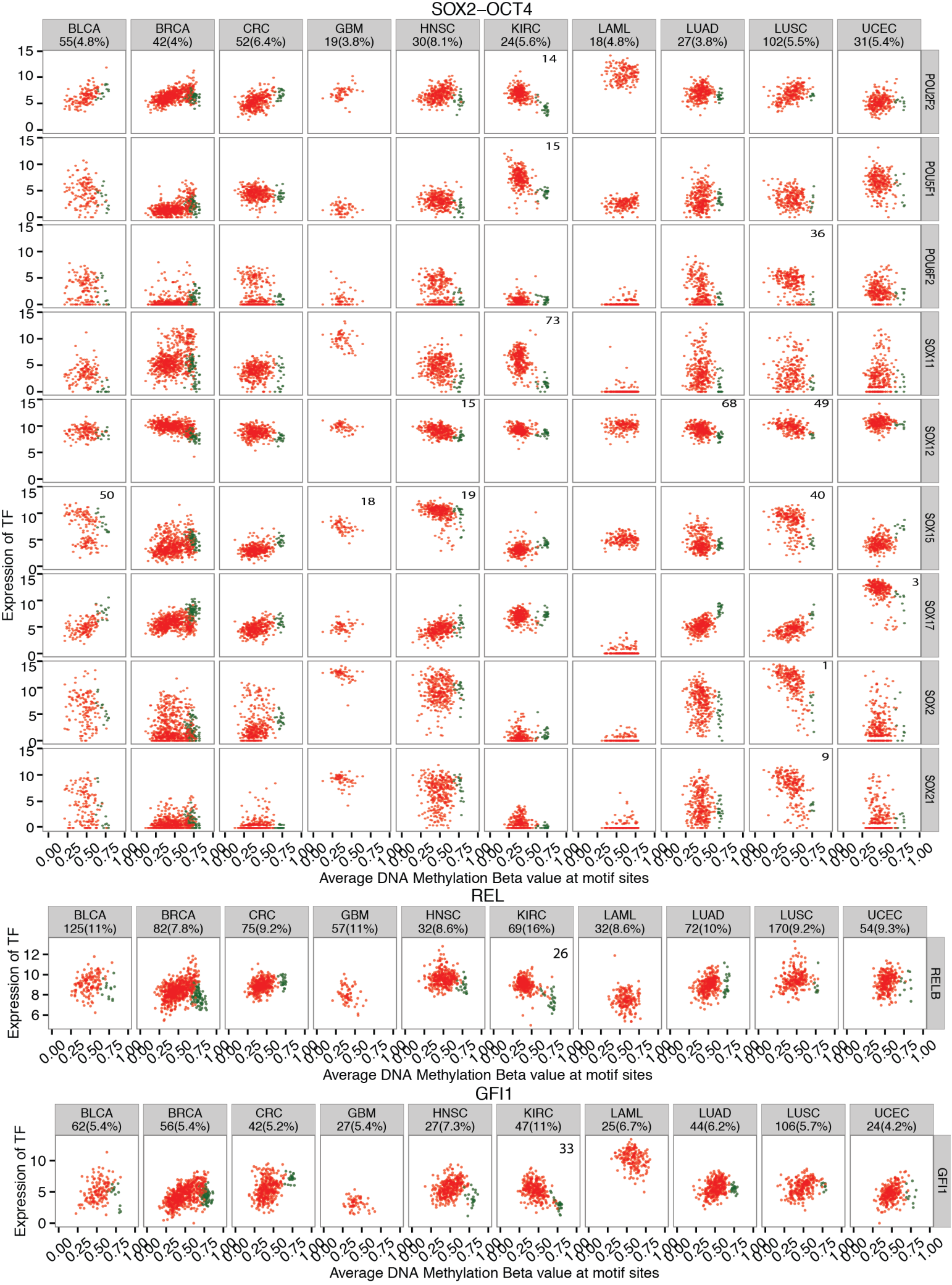
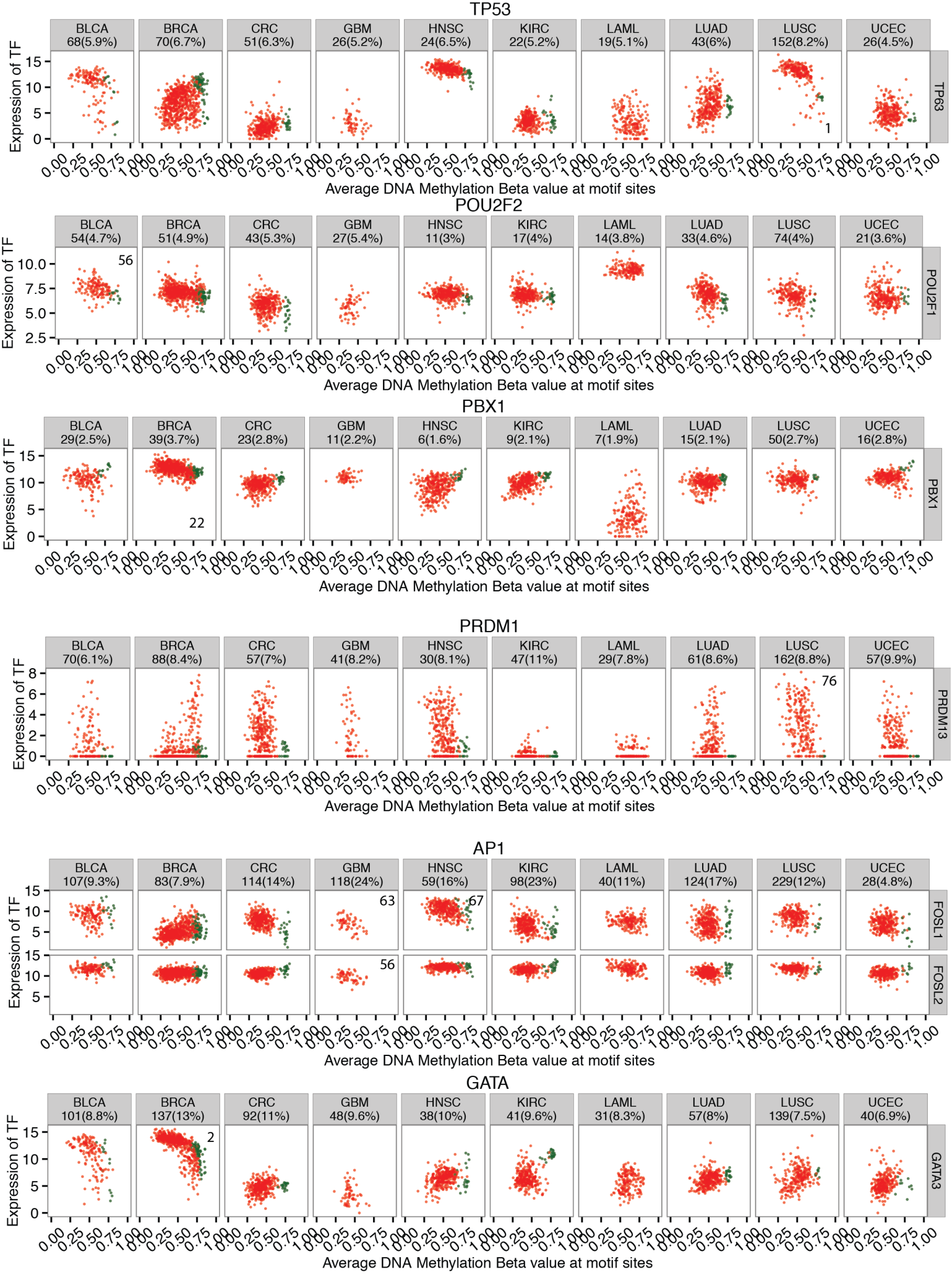
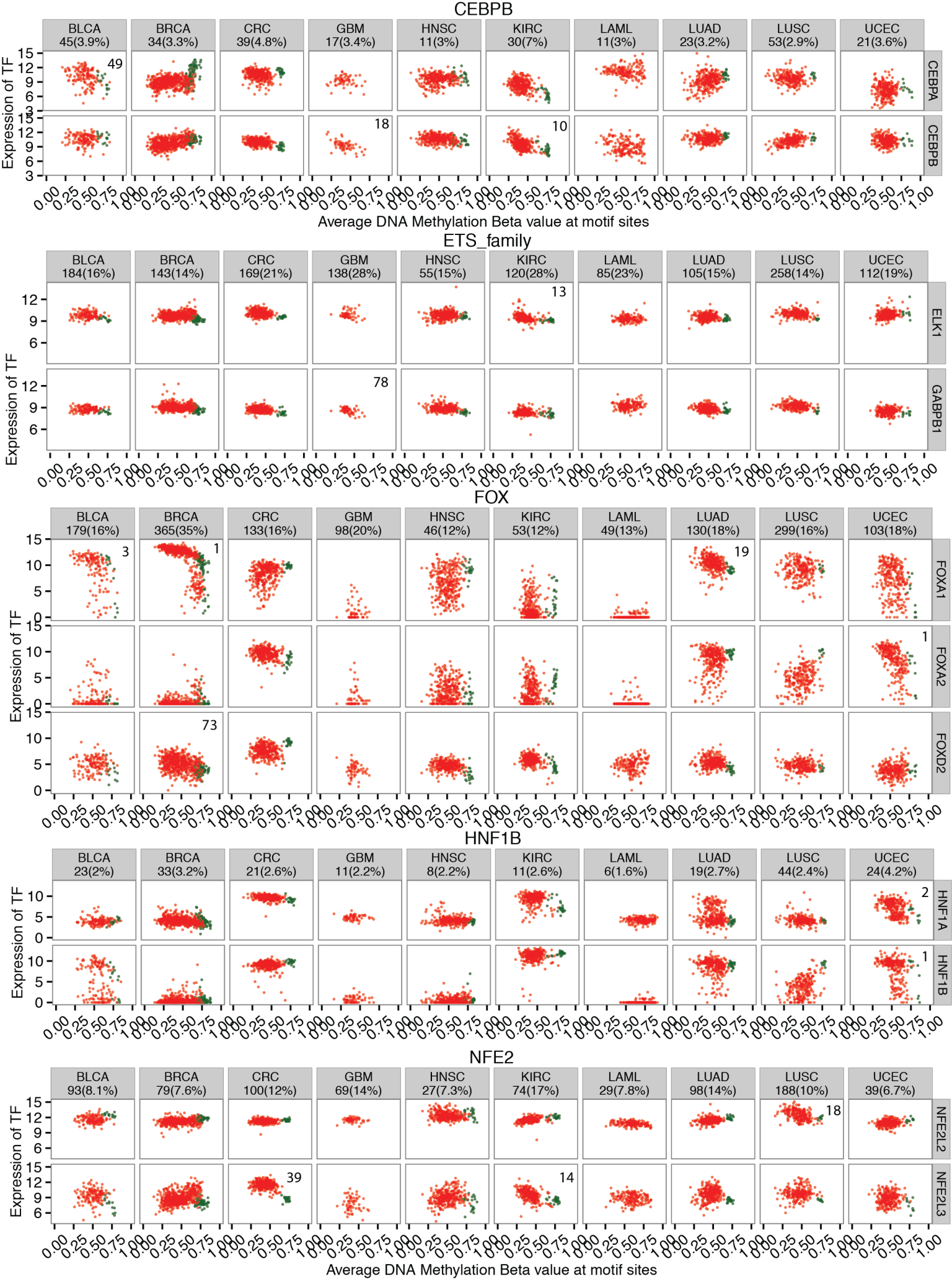
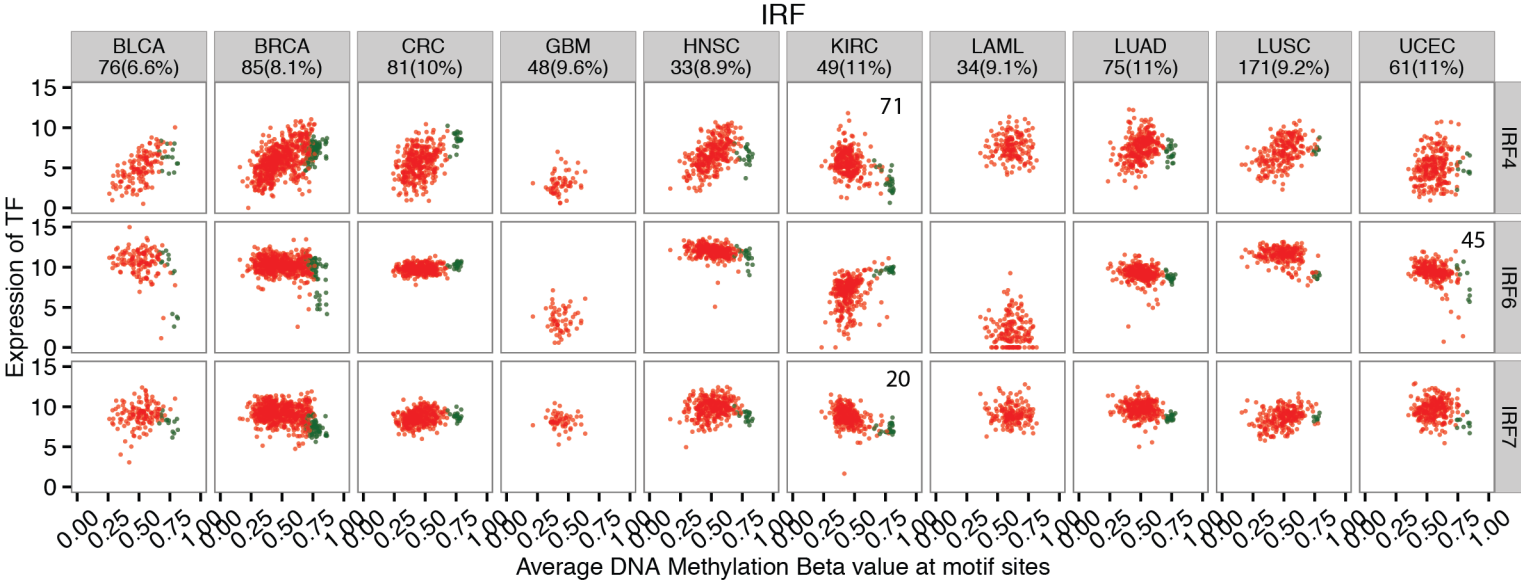
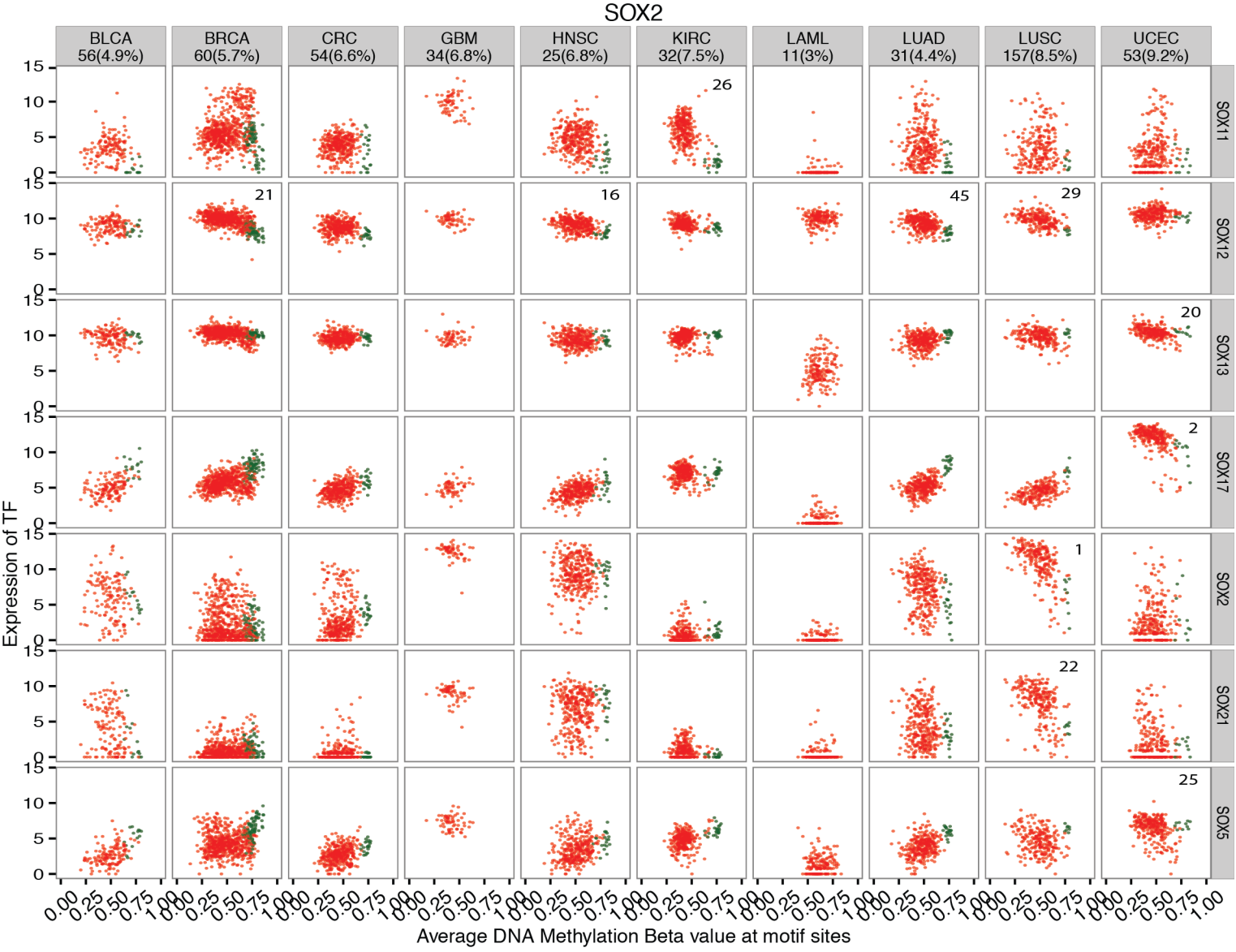

TAL1::TCF3
BLCA 48(4.2%)
BRCA 50(4.8%)
CORE 54(6.6%)
GBM 33(6.6%)
HNSC 19(5.1%)
KIRC 24(5.6%)
LAML 13(3.5%)
LUAD 30(4.2%)
LUSC 90(4.9%)
UCEC 25(4.3%)
TCF3
72
14
27
77
TCF7L2
BLCA 65(5.7%)
BRCA 73(7%)
CORE 64(7.9%)
GBM 35(7%)
HNSC 19(5.1%)
KIRC 28(6.6%)
LAML 19(5.1%)
LUAD 36(5.1%)
LUSC 124(6.7%)
UCEC 40(6.9%)
LEF1
TCF7
1
2
STAT2
BLCA 106(9.2%)
BRCA 86(8.2%)
CORE 82(10%)
GBM 58(12%)
HNSC 40(11%)
KIRC 53(12%)
LAML 40(11%)
LUAD 79(11%)
LUSC 168(9.1%)
UCEC 67(12%)
STAT2
STAT4
20
7
STAT1
BLCA 86(7.5%)
BRCA 98(9.4%)
CORE 68(8.4%)
GBM 51(10%)
HNSC 29(7.8%)
KIRC 47(11%)
LAML 22(5.9%)
LUAD 58(8.2%)
LUSC 134(7.2%)
UCEC 49(8.5%)
STAT2
STAT4
46
15
SPIB
BLCA 70(6.1%)
BRCA 67(6.4%)
CORE 60(7.4%)
GBM 48(9.6%)
HNSC 25(6.8%)
KIRC 38(8.9%)
LAML 34(9.1%)
LUAD 54(7.6%)
LUSC 116(6.3%)
UCEC 41(7.1%)
SPI1
25
67
Expression of TF
Average DNA Methylation Beta value at motif sites
factor(TN)
Normal
Tumor


SOX2−OCT4
BLCA 55(4.8%)
BRCA 42(4%)
CRC 52(6.4%)
GBM 19(3.8%)
HNSC 30(8.1%)
KIRC 24(5.6%)
LAML 18(4.8%)
LUAD 27(3.8%)
LUSC 102(5.5%)
UCEC 31(5.4%)
POU2F2
POU5F1
POU6F2
SOX11
SOX12
SOX15
SOX17
SOX2
SOX21
Expression of TF
Average DNA Methylation Beta value at motif sites
REL
BLCA 125(11%)
BRCA 82(7.8%)
CRC 75(9.2%)
GBM 57(11%)
HNSC 32(8.6%)
KIRC 69(16%)
LAML 32(8.6%)
LUAD 72(10%)
LUSC 170(9.2%)
UCEC 54(9.3%)
RELB
Expression of TF
Average DNA Methylation Beta value at motif sites
GFI1
BLCA 62(5.4%)
BRCA 56(5.4%)
CRC 42(5.2%)
GBM 27(5.4%)
HNSC 27(7.3%)
KIRC 47(11%)
LAML 25(6.7%)
LUAD 44(6.2%)
LUSC 106(5.7%)
UCEC 24(4.2%)
GFI1
Expression of TF
Average DNA Methylation Beta value at motif sites


TP53
BLCA 68(5.9%)
BRCA 70(6.7%)
CRC 51(6.3%)
GBM 26(5.2%)
HNSC 24(6.5%)
KIRC 22(5.2%)
LAML 19(5.1%)
LUAD 43(6%)
LUSC 152(8.2%)
UCEC 26(4.5%)
TP63
Expression of TF
Average DNA Methylation Beta value at motif sites
POU2F2
BLCA 54(4.7%)
BRCA 51(4.9%)
CRC 43(5.3%)
GBM 27(5.4%)
HNSC 11(3%)
KIRC 17(4%)
LAML 14(3.8%)
LUAD 33(4.6%)
LUSC 74(4%)
UCEC 21(3.6%)
POU2F1
PBX1
BLCA 29(2.5%)
BRCA 39(3.7%)
CRC 23(2.8%)
GBM 11(2.2%)
HNSC 6(1.6%)
KIRC 9(2.1%)
LAML 7(1.9%)
LUAD 15(2.1%)
LUSC 50(2.7%)
UCEC 16(2.8%)
PRDM1
BLCA 70(6.1%)
BRCA 88(8.4%)
CRC 57(7%)
GBM 41(8.2%)
HNSC 30(8.1%)
KIRC 47(11%)
LAML 29(7.8%)
LUAD 61(8.6%)
LUSC 162(8.8%)
UCEC 57(9.9%)
PRDM13
AP1
BLCA 107(9.3%)
BRCA 83(7.9%)
CRC 114(14%)
GBM 118(24%)
HNSC 59(16%)
KIRC 98(23%)
LAML 40(11%)
LUAD 124(17%)
LUSC 229(12%)
UCEC 28(4.8%)
FOSL1
FOSL2
GATA
BLCA 101(8.8%)
BRCA 137(13%)
CRC 92(11%)
GBM 48(9.6%)
HNSC 38(10%)
KIRC 41(9.6%)
LAML 31(8.3%)
LUAD 57(8%)
LUSC 139(7.5%)
UCEC 40(6.9%)
GATA3


CEBPB
BLCA 45(3.9%)
BRCA 34(3.3%)
CRC 39(4.8%)
GBM 17(3.4%)
HNSC 11(3%)
KIRC 30(7%)
LAML 11(3%)
LUAD 23(3.2%)
LUSC 53(2.9%)
UCEC 21(3.6%)
CEBPA
CEBPB
Expression of TF
Average DNA Methylation Beta value at motif sites
ETS_family
BLCA 184(16%)
BRCA 143(14%)
CRC 169(21%)
GBM 138(28%)
HNSC 55(15%)
KIRC 120(28%)
LAML 85(23%)
LUAD 105(15%)
LUSC 258(14%)
UCEC 112(19%)
ELK1
GABPB1
FOX
BLCA 179(16%)
BRCA 365(35%)
CRC 133(16%)
GBM 98(20%)
HNSC 46(12%)
KIRC 53(12%)
LAML 49(13%)
LUAD 130(18%)
LUSC 299(16%)
UCEC 103(18%)
FOXA1
FOXA2
FOXD2
HNF1B
BLCA 23(2%)
BRCA 33(3.2%)
CRC 21(2.6%)
GBM 11(2.2%)
HNSC 8(2.2%)
KIRC 11(2.6%)
LAML 6(1.6%)
LUAD 19(2.7%)
LUSC 44(2.4%)
UCEC 24(4.2%)
HNF1A
HNF1B
NFE2
BLCA 93(8.1%)
BRCA 79(7.6%)
CRC 100(12%)
GBM 69(14%)
HNSC 27(7.3%)
KIRC 74(17%)
LAML 29(7.8%)
LUAD 98(14%)
LUSC 188(10%)
UCEC 39(6.7%)
NFE2L2
NFE2L3


IRF
BLCA 76(6.6%)
BRCA 85(8.1%)
CRC 81(10%)
GBM 48(9.6%)
HNSC 33(8.9%)
KIRC 49(11%)
LAML 34(9.1%)
LUAD 75(11%)
LUSC 171(9.2%)
UCEC 61(11%)
IRF4
IRF6
IRF7
71
45
20
Expression of TF
Average DNA Methylation Beta value at motif sites


SOX2
BLCA 56(4.9%)
BRCA 60(5.7%)
CRC 54(6.6%)
GBM 34(6.8%)
HNSC 25(6.8%)
KIRC 32(7.5%)
LAML 11(3%)
LUAD 31(4.4%)
LUSC 157(8.5%)
UCEC 53(9.2%)
SOX11
SOX12
SOX13
SOX17
SOX2
SOX21
SOX5
26
21
16
45
29
20
2
1
22
25
Expression of TF
Average DNA Methylation Beta value at motif sites