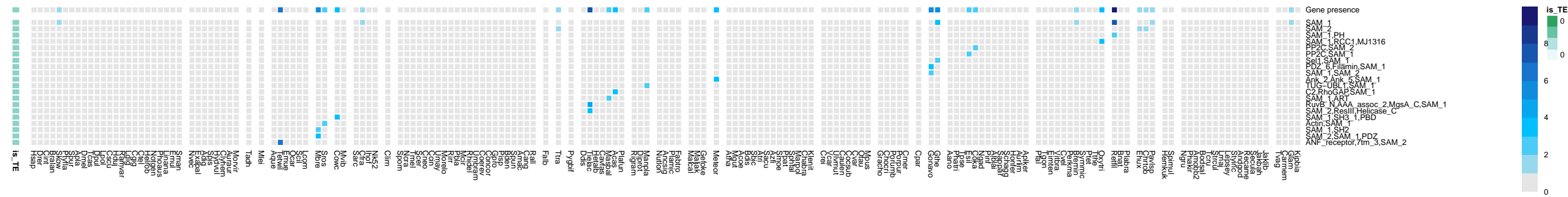
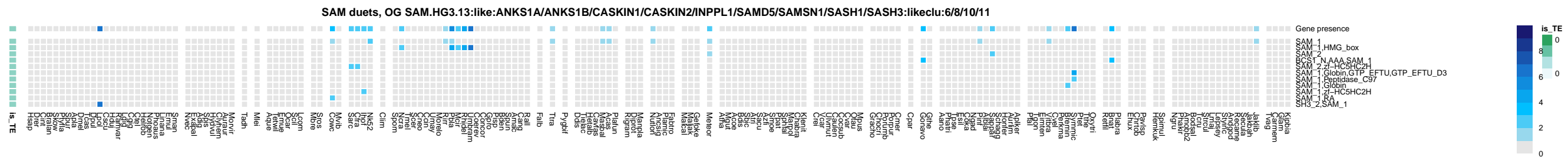
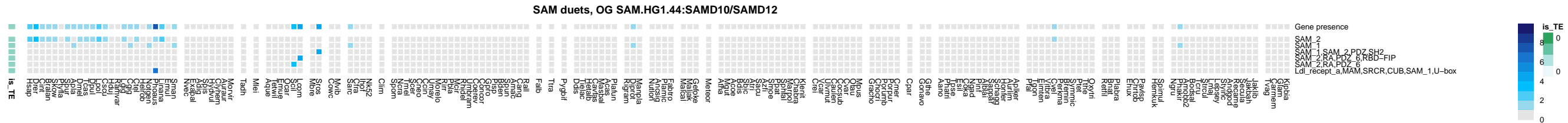
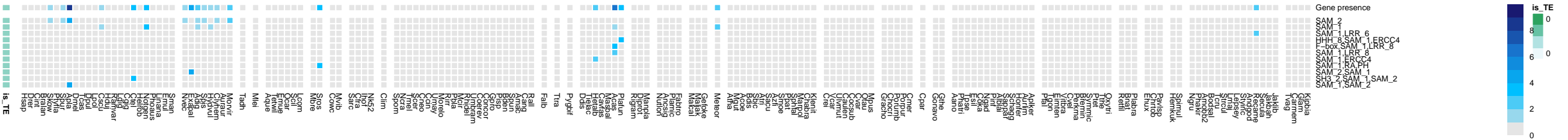


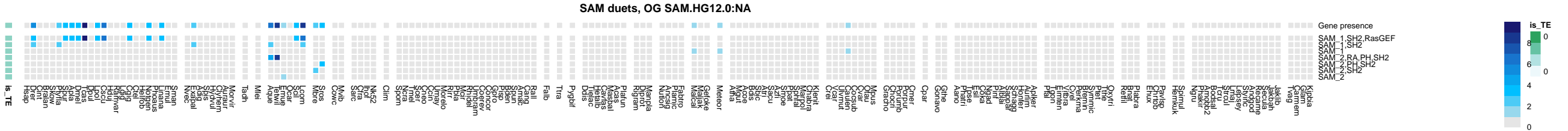
uets, OG SAM.HG1.1:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKSR1/CNKSR2/CNKSR3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SARM1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:2/3/6/12/13/14/18/38/39/40/42/44/46



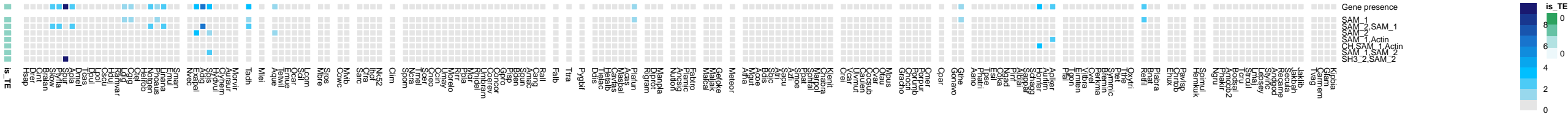


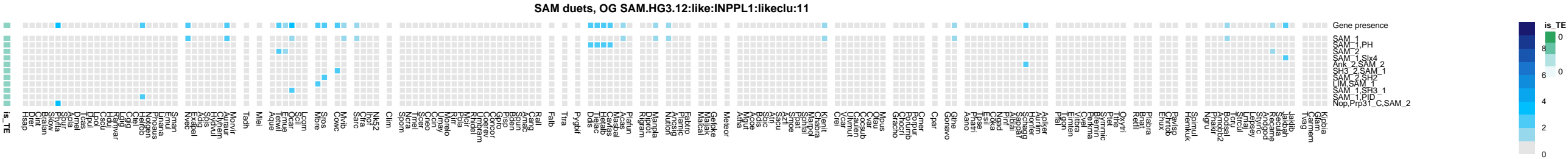


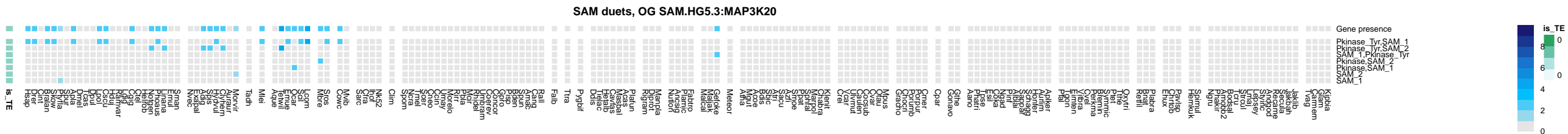




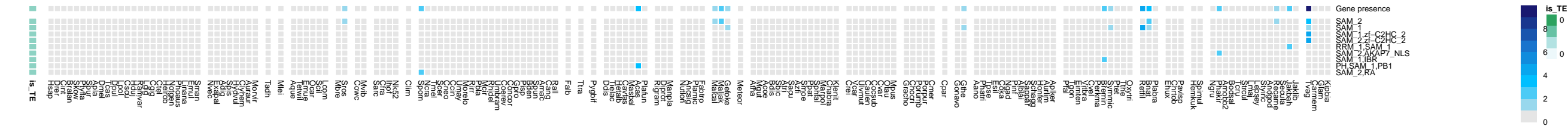
SAM duets, OG SAM.HG3.0:like:ANKS1A/ANKS1B/CASKIN1/CASKIN2/INPL1/SAMD5/SAMSN1/SASH1/SASH3:likeclu:6/8/10/11



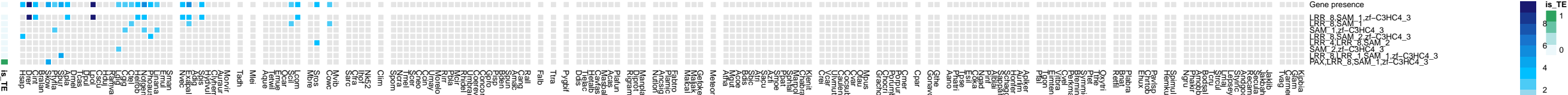


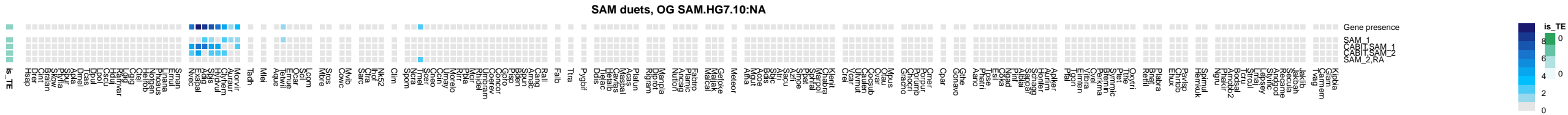


SAM duets, OG SAM.HG1.26:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKSRI1/CNKSRI2/CNKSRI3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46

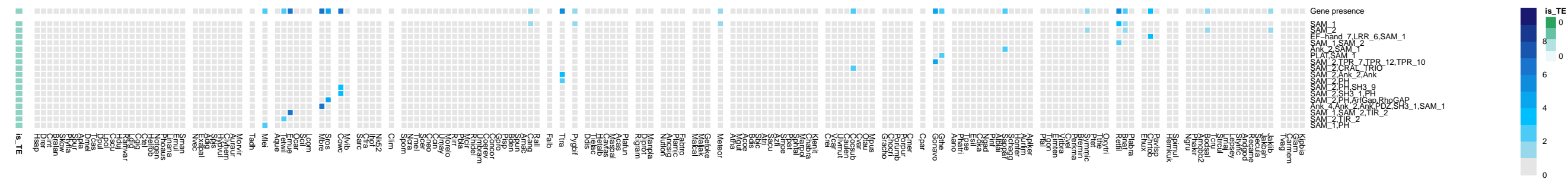


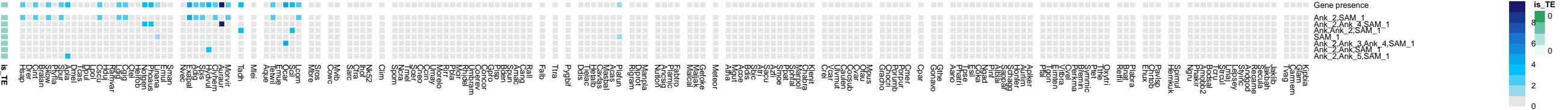
SAM duets, OG SAM.HG11.1:LRSAM1

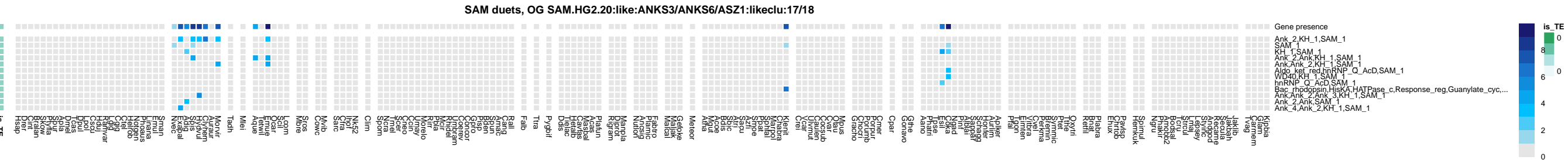


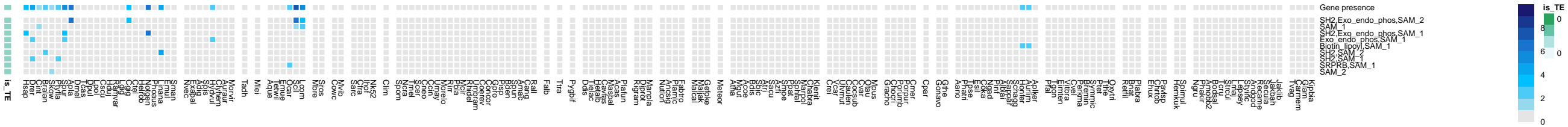


AM duets, OG SAM.HG1.32:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKSR1/CNKSR2/CNKSR3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46

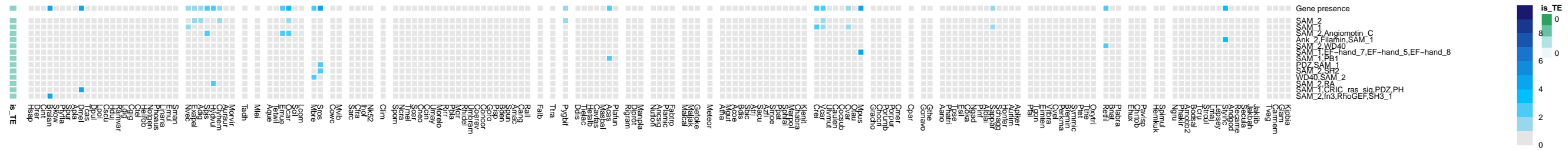


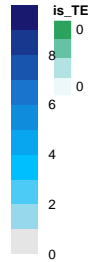
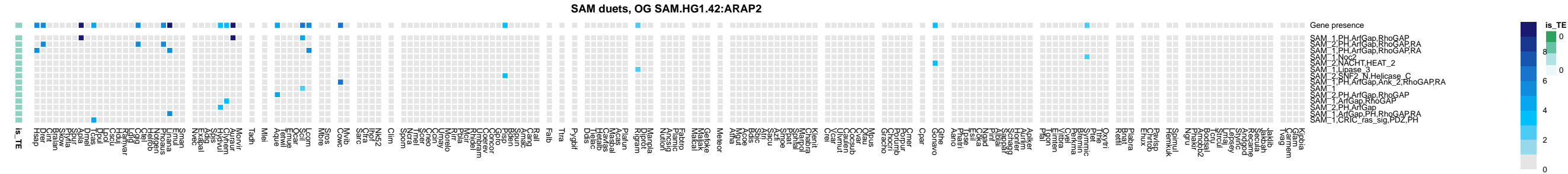


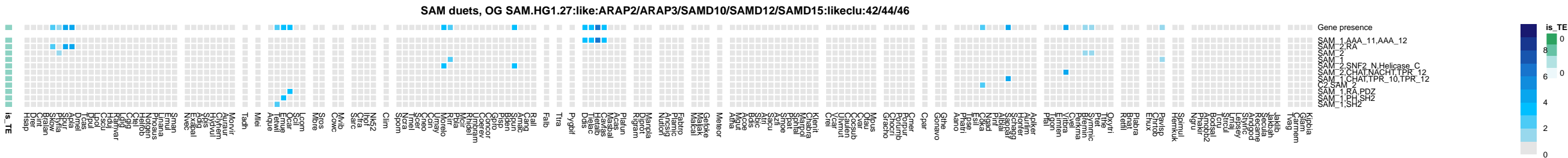


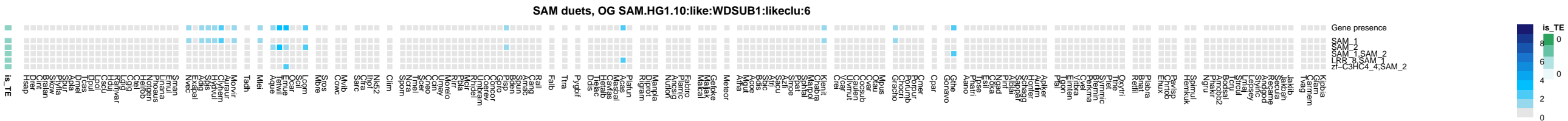


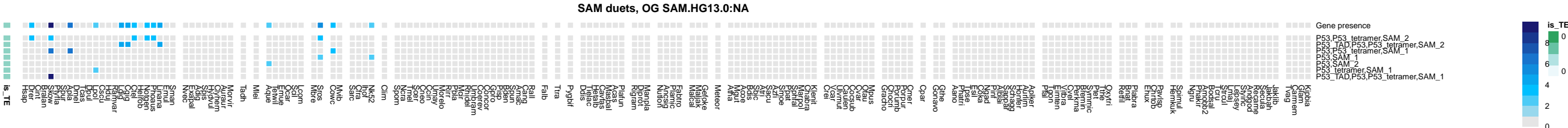
M duets, OG SAM.HG1.23:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46

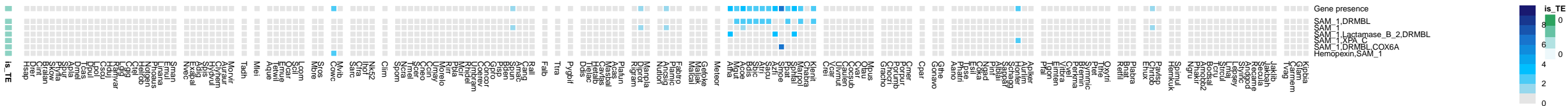




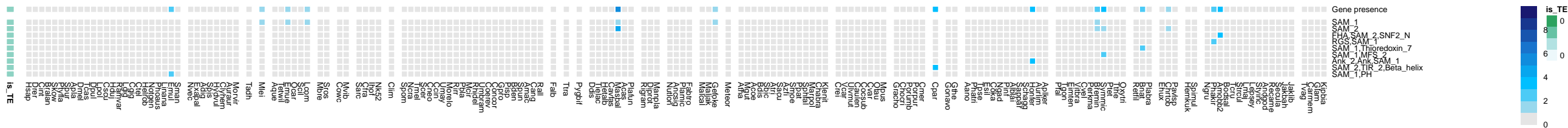


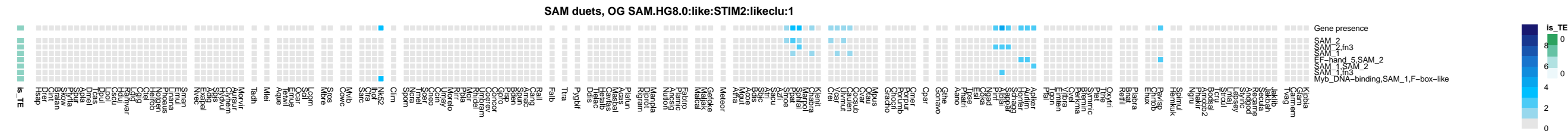


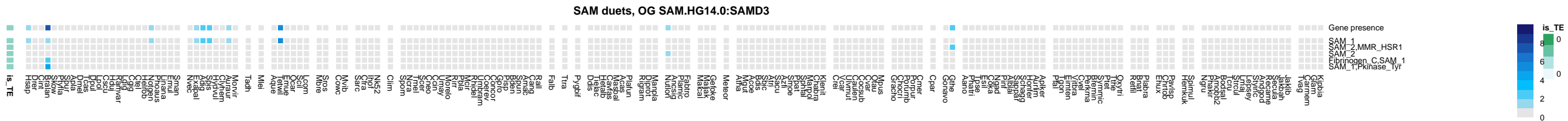


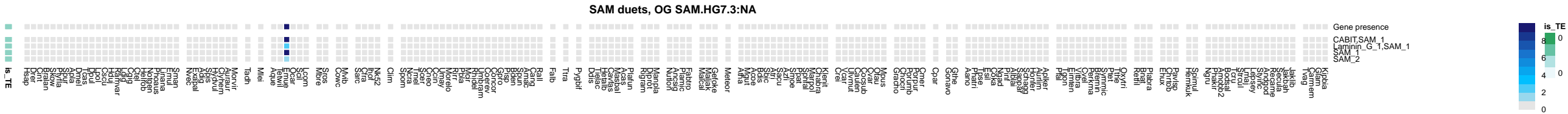


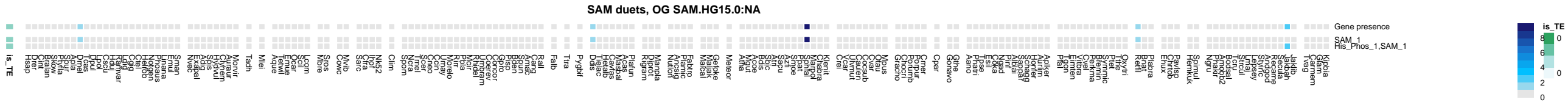
SAM duets, OG SAM.HG2.0:like:ANKS3/ANKS4B/ANKS6/ASZ1/BICC1/DDHD2/SEC23IP/TNKS/TNKS2/USH1G:likeclu:5/10/11/15/17/18











is_TE



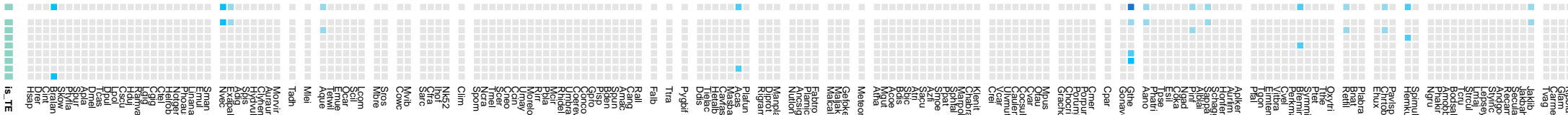
0 2 4 6 8

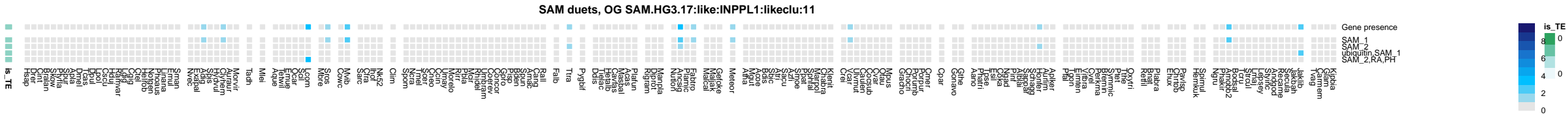
Gene presence

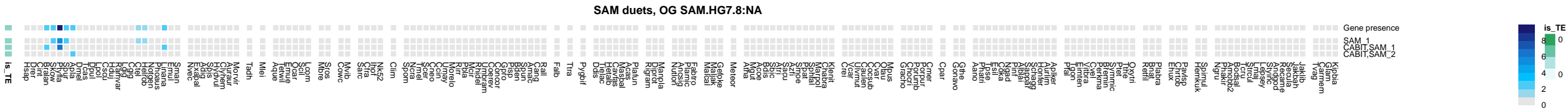


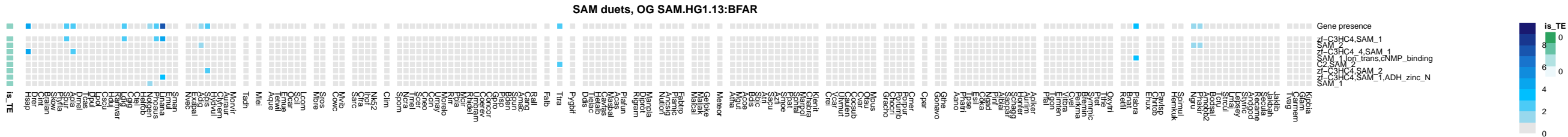
SAM_2
SAM_1
PEST, SAM_2
SAM_1, Dynamin, N
SAM_1, Bromodomain, SAM_1
P, X, PDZ, 6, SAM_2
RasGEF, SAM_2
Roc, COR, SAM_2

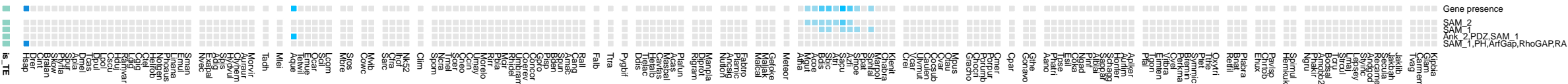
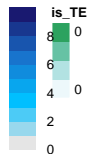
SAM duets, OG SAM.HG7.1:NA

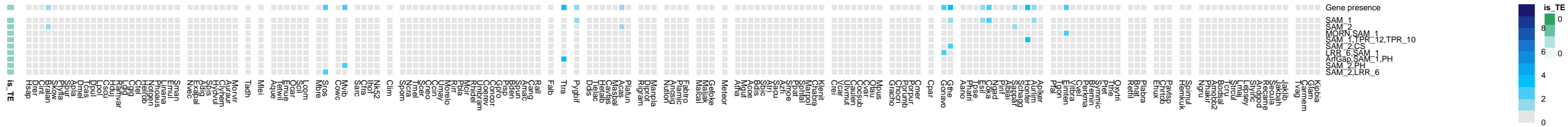


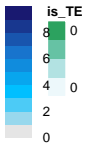






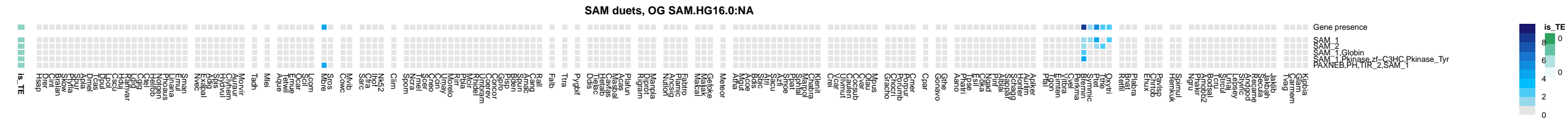


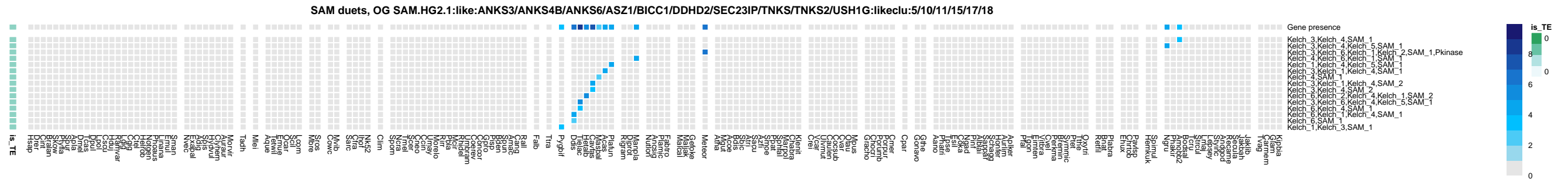


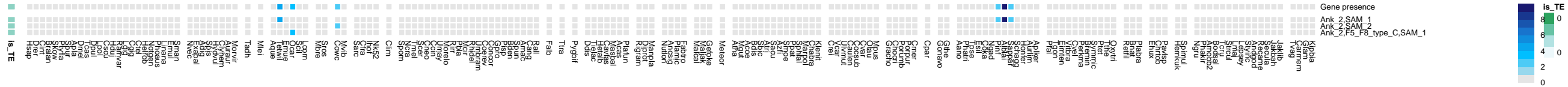


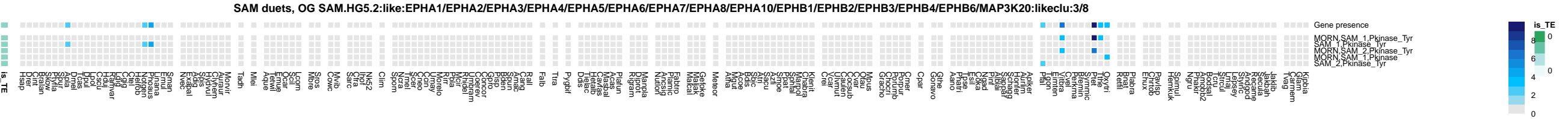
SAM duets, OG SAM.HG7.6:NA

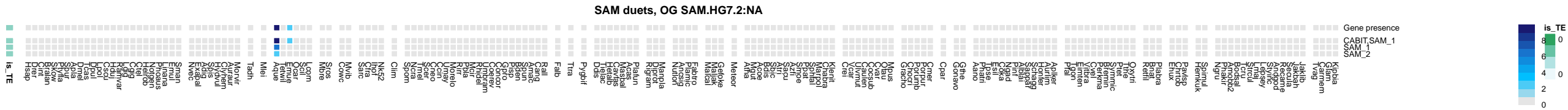


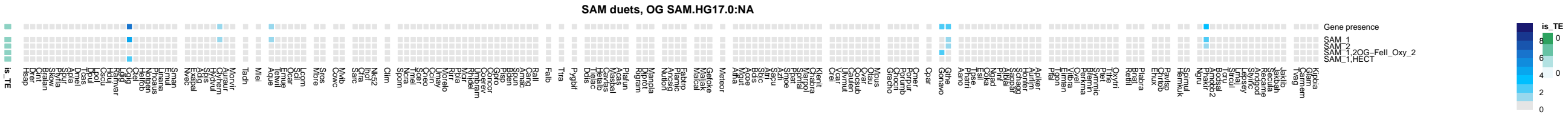


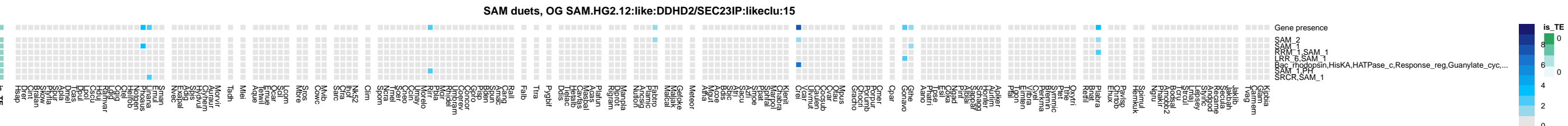


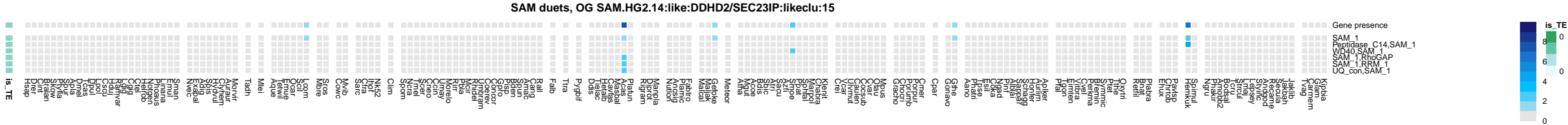




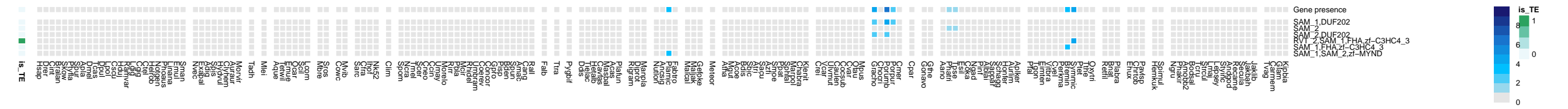




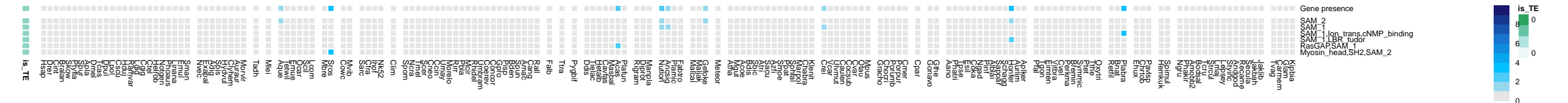




AM duets, OG SAM.HG1.24:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKSR1/CNKSR2/CNKSR3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46



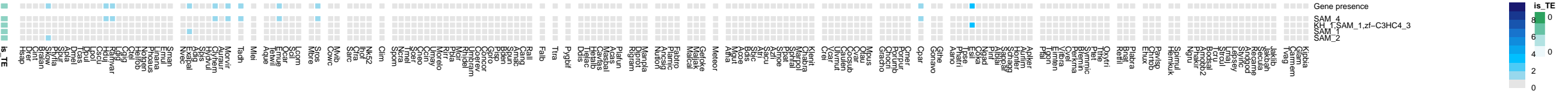
SAM duets, OG SAM.HG1.30:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46

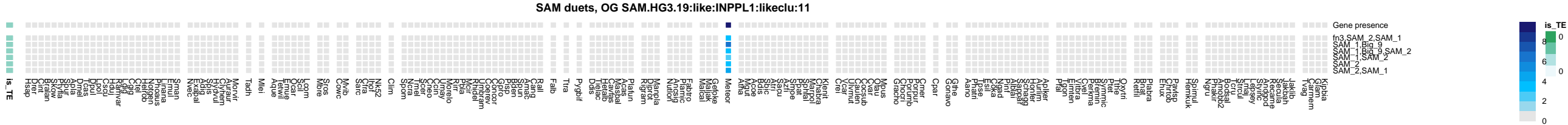


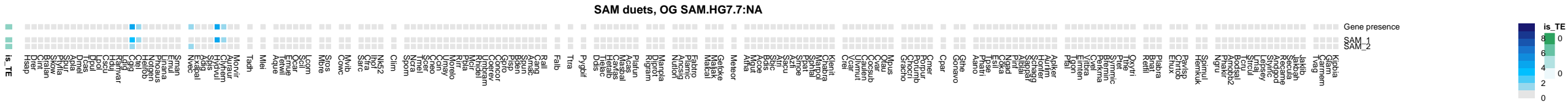
is_TE

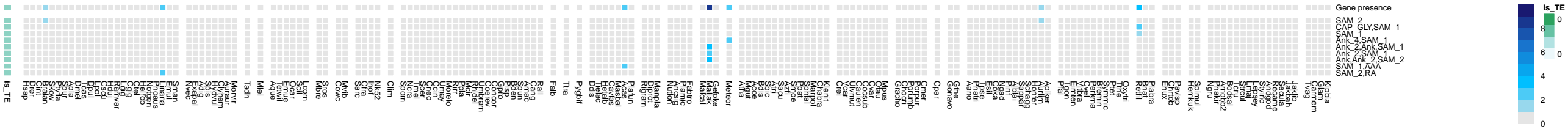


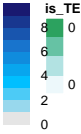
SAM duets, OG SAM.HG11.0:like:LRSAM1:likeclu:1





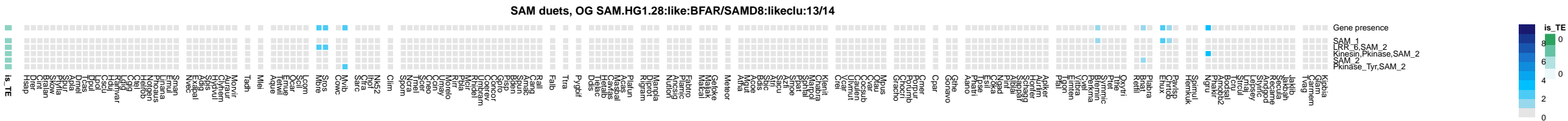




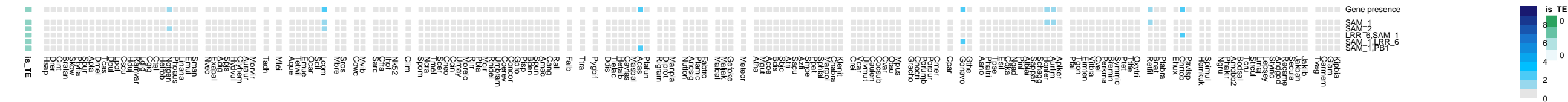


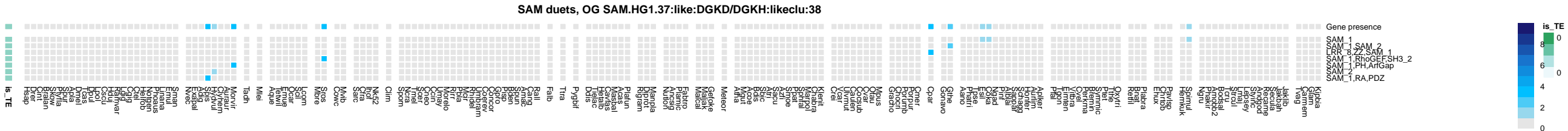
SAM duets, OG SAM.HG7.21:NA

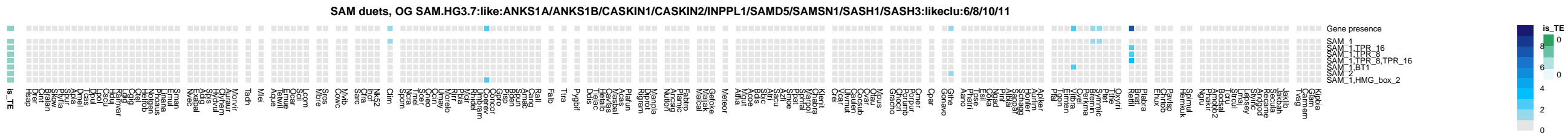


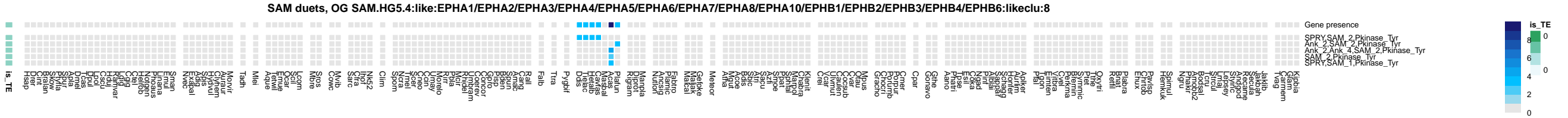


SAM duets, OG SAM.HG1.36:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:liieclu:3/6/12/13/14/18/38/39/40/42/44/46

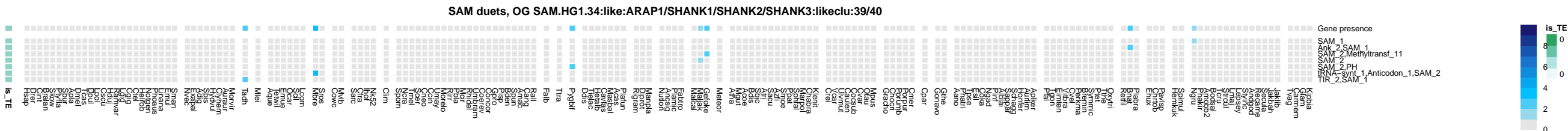




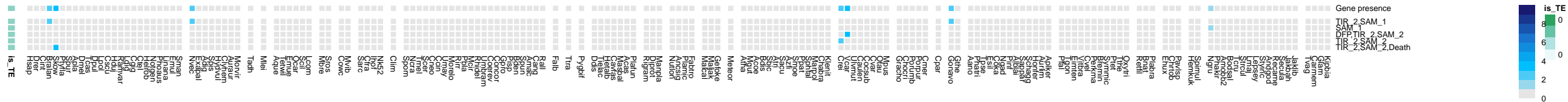


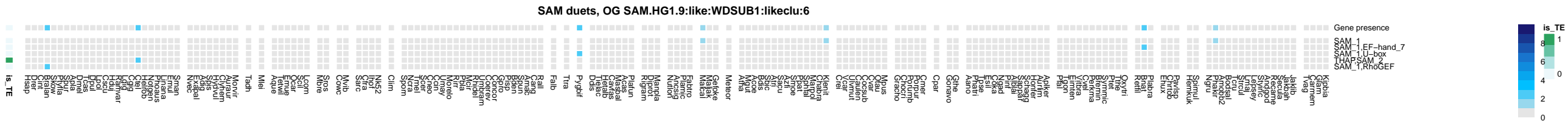


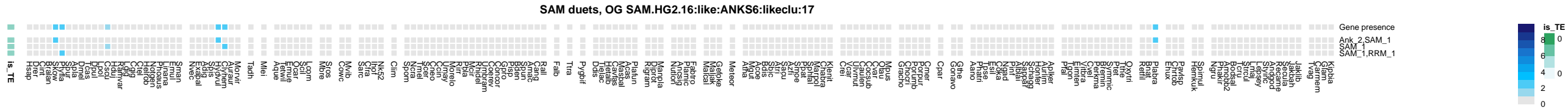


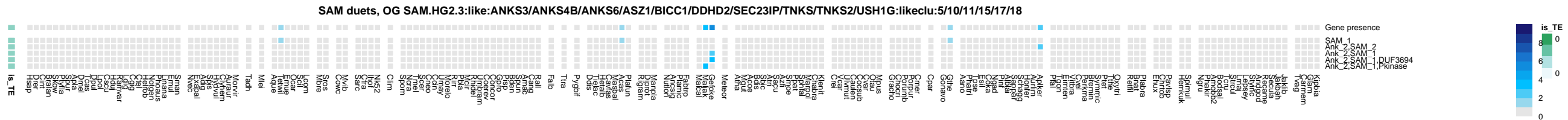


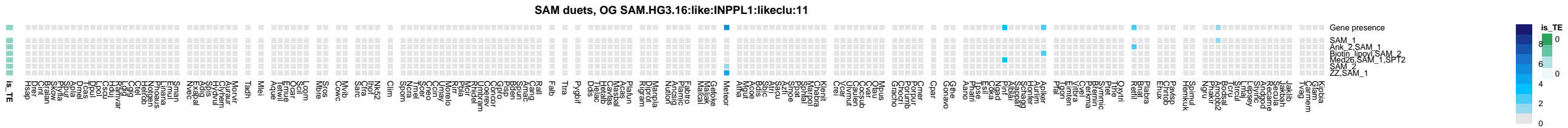
SAM duets, OG SAM.HG1.35:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:like:clu:3/6/12/13/14/18/38/39/40/42/44/46

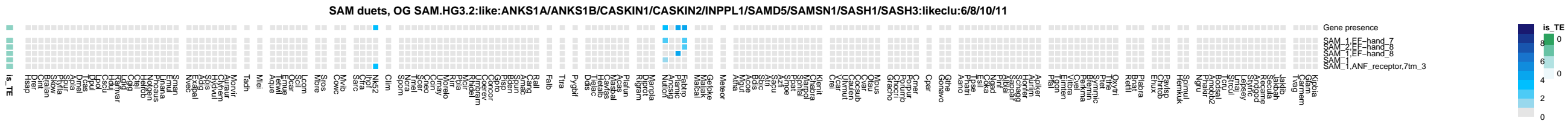








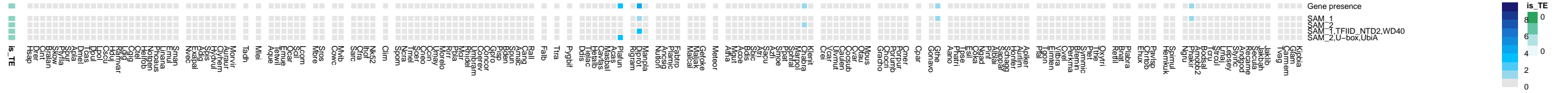


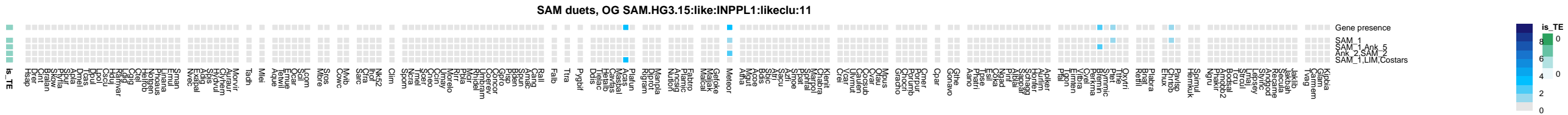


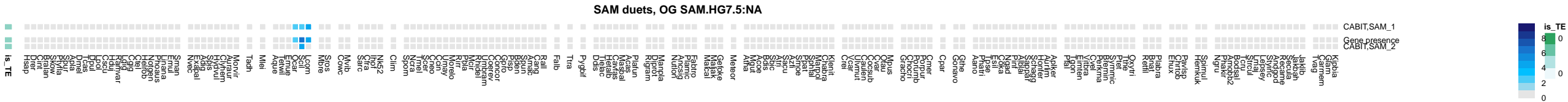
is_TE

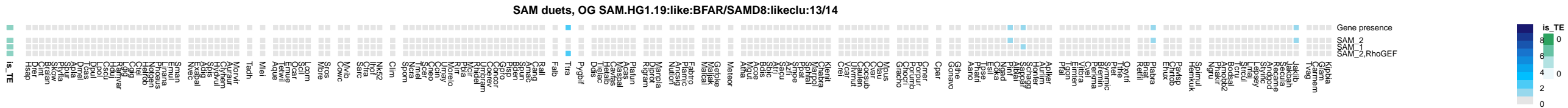


SAM duets, OG SAM.HG1.43:like:SAMD10/SAMD12:likeclu:44

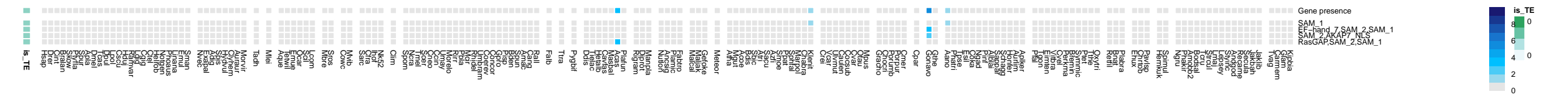


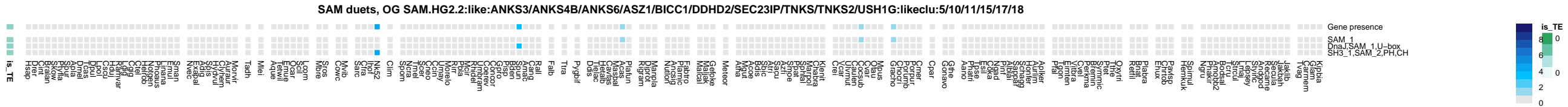


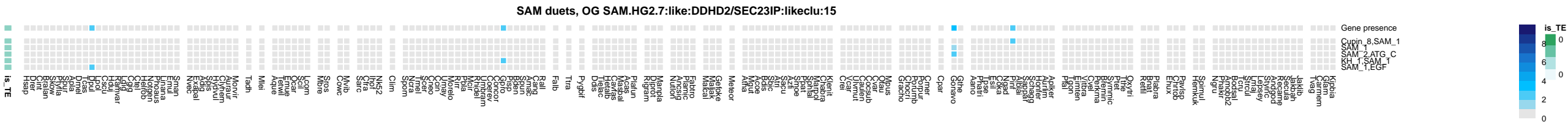


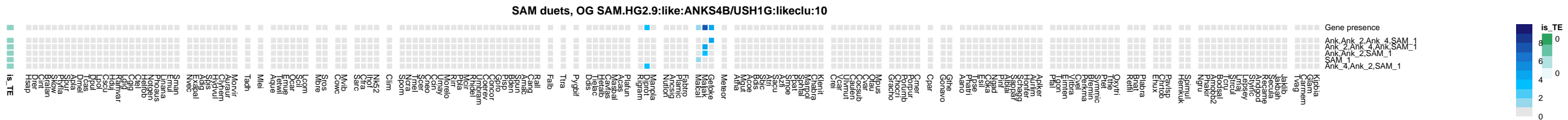


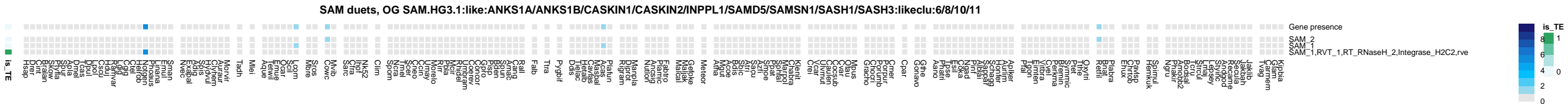
SAM duets, OG SAM.HG1.31:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46

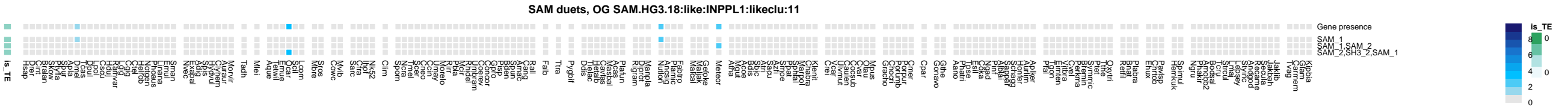


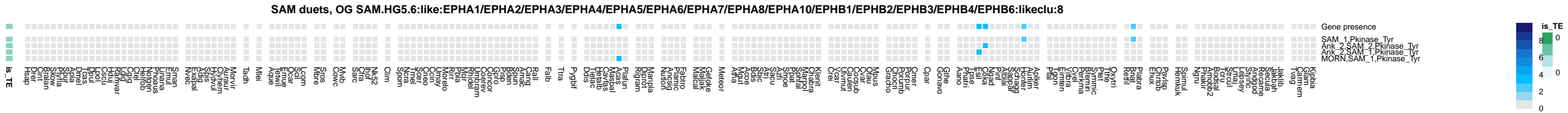


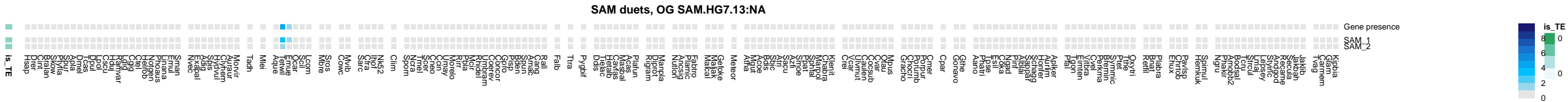




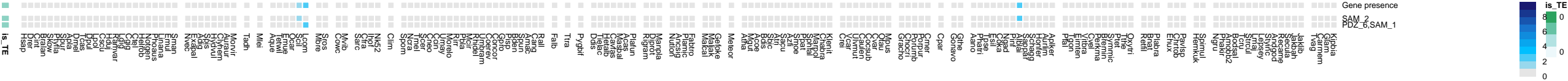




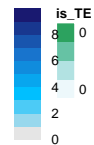




SAM duets, OG SAM.HG1.15:like:AL357075.4/CNKS2/CNKS3:likeclu:12



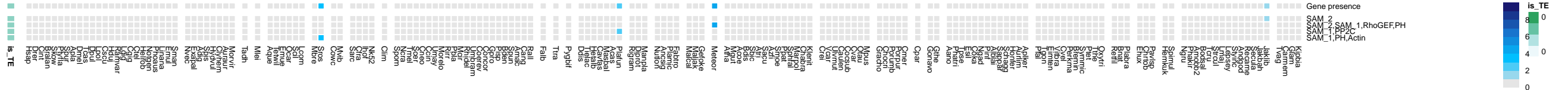
M duets, OG SAM.HG1.5:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SARM1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:2/3/6/12/13/14/18/38/39/40/42/44/46

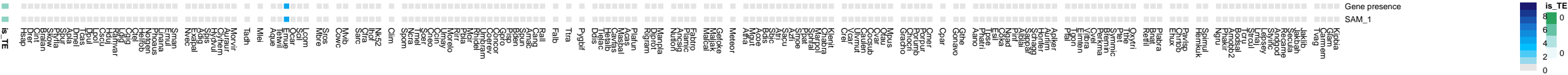


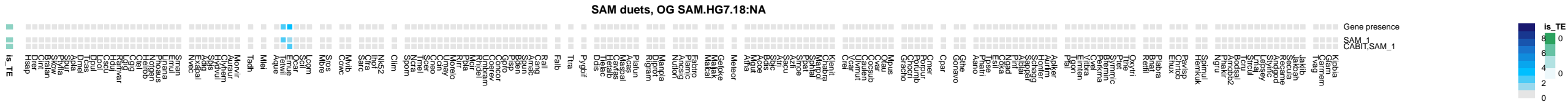
is_TE



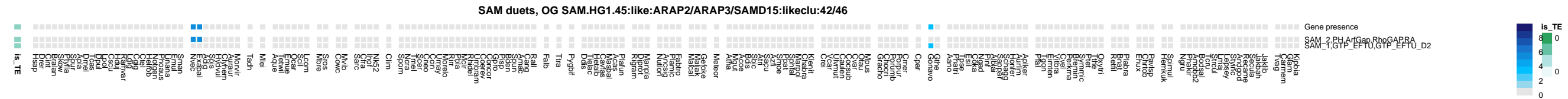
SAM duets, OG SAM.HG3.5:like:SAMD5/SAMSN1/SASH1/SASH3:likeclu:6

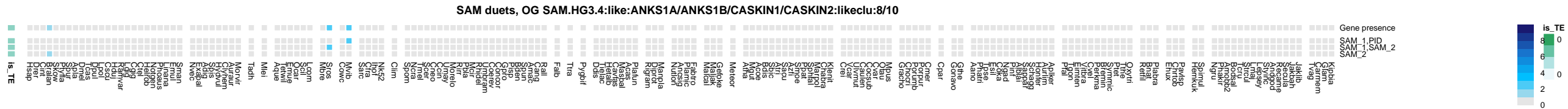


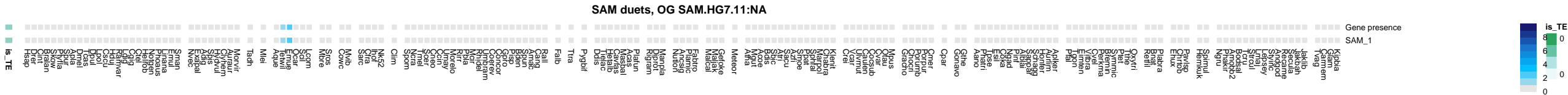


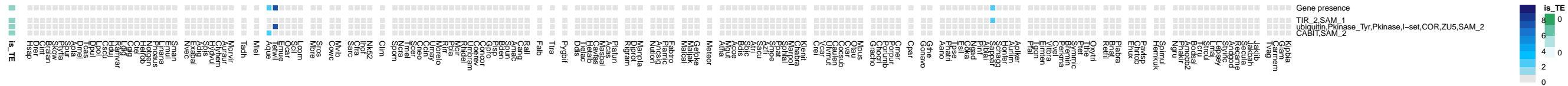




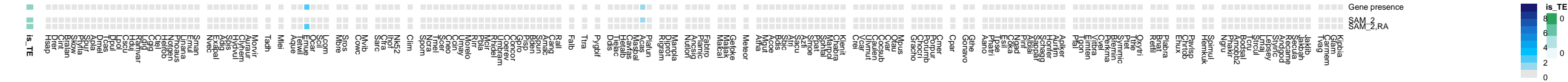




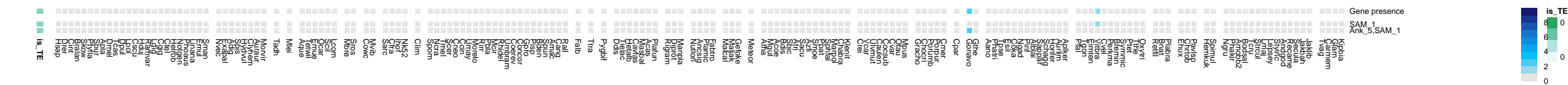




SAM duets, OG SAM.HG1.33:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKS1/CNKS2/CNKS3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46

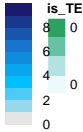


AM duets, OG SAM.HG1.4:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKSRI1/CNKSRI2/CNKSRI3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SARM1/SHANK1/SHANK2/SHANK3/WDSUB1:likeclu:2/3/6/12/13/14/18/38/39/40/42/44/46



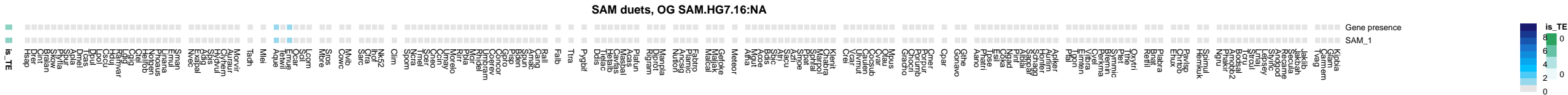


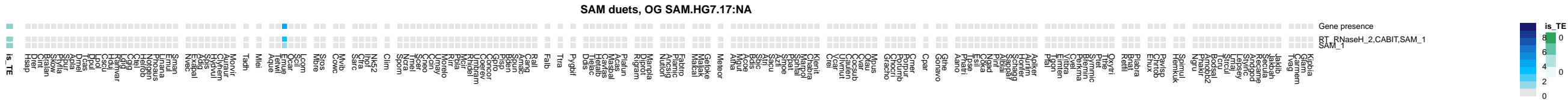


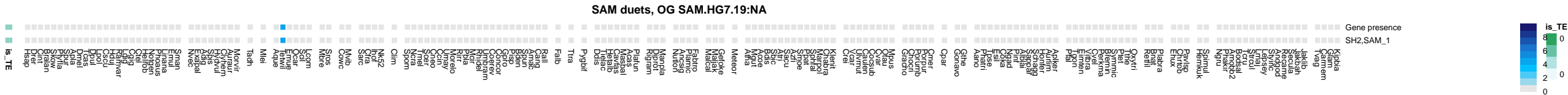


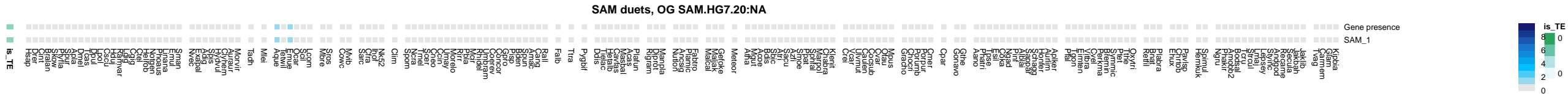
SAM duets, OG SAM.HG7.12:NA

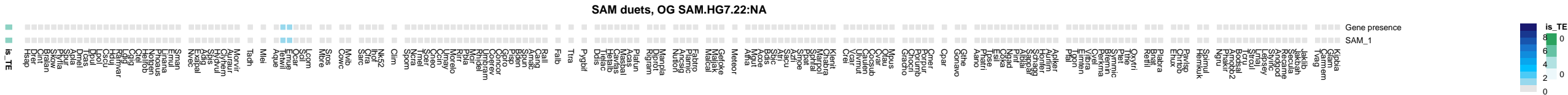


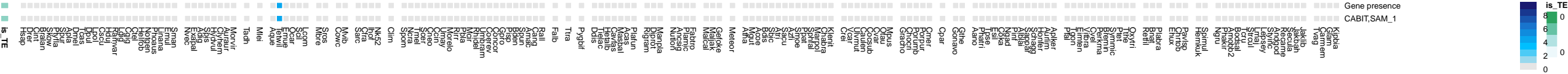


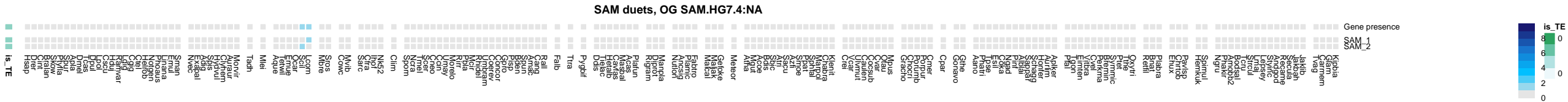


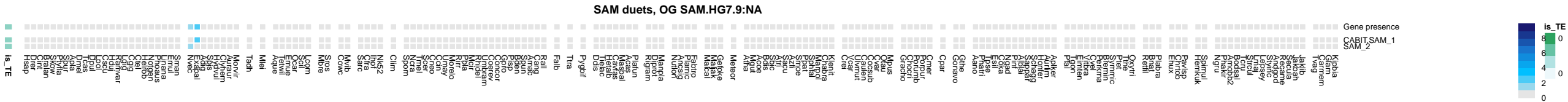


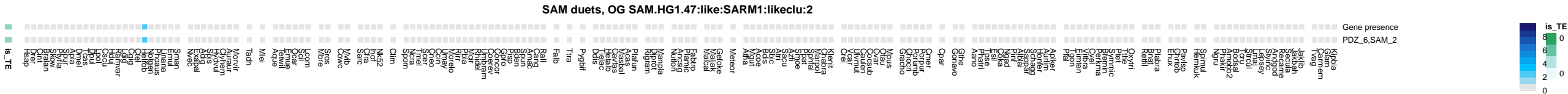


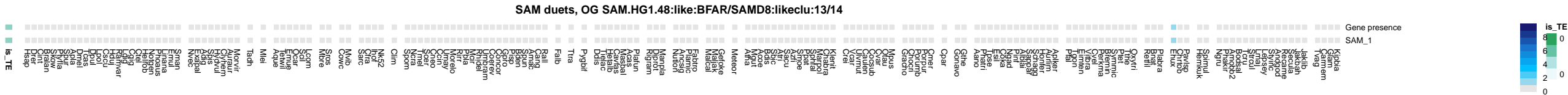




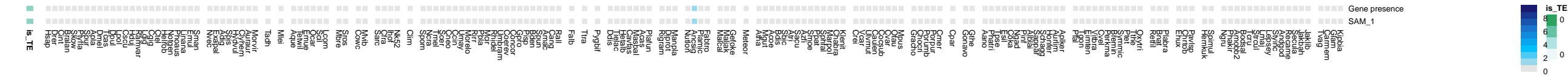


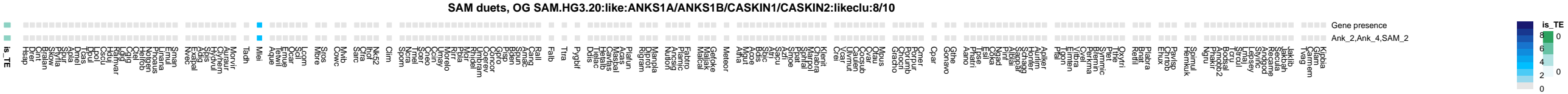






SAM duets, OG SAM.HG1.49:like:AL357075.4/ARAP1/ARAP2/ARAP3/BFAR/CNKSR1/CNKSR2/CNKSR3/DGKD/DGKH/PPP1R9A/SAMD8/SAMD10/SAMD12/SAMD14/SAMD15/SAMHD1/SHANK1/SHANK2/SHANK3/WDSUB1.1:likeclu:3/6/12/13/14/18/38/39/40/42/44/46





SAM duets, OG SAM.HG5.10::like:EPHA1/EPHA2/EPHA3/EPHA4/EPHA5/EPHA6/EPHA7/EPHA8/EPHA10/EPHB1/EPHB2/EPHB3/EPHB4/EPHB6/MAP3K20::likeclu:3/8

