Supplemental Data file

Supplemental data files (Excel):

The first set of 5 files (MACE-data) contains the gene entries with gene identifier, gene symbol, gene name, mean exp, mean mock, fold change log2, pvalue, -log10(pvalue), var-log2, chromosome number (with beginning and end), classification (into pseudogene (PG), non-annotated gene (NA), LINC RNA gene (LINC), MIR gene (MIR), SNO gene (SNO), MT gene (MT) and protein coding gene (PCG)).

Data sets 6 and 7 contain the data used for heatmap analysis.

Data sets 8-12 contain the data used for volcano plot analysis

1. MA4 gene signature.xlsx
2. MA4m gene signature.xlsx
3. A4M gene signature.xlsx
4. MA4_A4M gene signature.xlsx
5. MA4m_A4M gene signature.xlsx
6. Heatmap dataset 1 xlsx
7. Heatmap dataset 2 xlsx
8. MA4 volcano.xlsx
9. MA4m volcano.xlsx
10. A4M volcano.xlsx
11. MA4_A4M volcano.xlsx
12. MA4m_A4M volcano.xlsx

Supplemental Figure legends:

Figure S1: Bioinformatic analysis of MACE-Seq data-I

Heatmaps analysis. MACE experiments were performed and resulting data were analyzed by Bioconductor software to create output Excel files. Various bioinformatic tools were used to analyze these data: heatmaps with http://www.heatmapper.ca/expression/. Only protein coding genes have been analyzed.

Figure S2: Bioinformatic analysis of MACE-Seq data-II

Volcano plot analysis. MACE experiments were performed and resulting data were analyzed by Bioconductor software to create output Excel files. Various bioinformatic tools were used to analyze these data: volcano plots with huygens.science.uva.nl. Only protein coding genes have been analyzed.

Figure S3: Investigation of protein coding genes which are common and unique for MA4 and MA4m cells

From the MACE-Seq data, all protein coding genes were extracted that are expressed only in MA4 or MA4m cells. These gene sets (log2 ± 1) were separated for up- and down-regulated genes and then analyzed for overlapping and idiosyncratic genes. As displayed, MA4 and MA4m share 7 commonly up-regulated genes, while 44 and 61 uniquely up-regulated genes, respectively. Similarly, MA4 and MA4m share 26 commonly down-regulated genes, while 79 and 76 uniquely down-regulated genes, respectively.

Figure S4: Investigation of protein coding genes which are common and unique for CO and COm cells

From the MACE-Seq data, all protein coding genes were extracted that are expressed only in CO or COm cells. These gene sets (log2 ± 2) were separated for up- and down-regulated genes and then analyzed for overlapping and idiosyncratic genes. As displayed, CO and COm share 18 commonly up-regulated genes, while 84 and 18 uniquely up-regulated genes, respectively. Similarly, CO and COm share 7 commonly down-regulated genes, while 112 and 14 uniquely down-regulated genes, respectively.

Figure S1

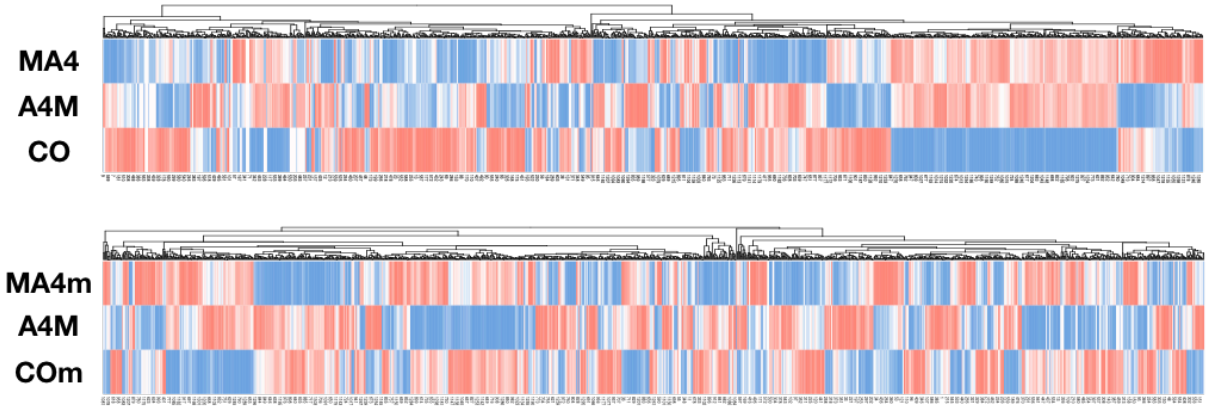


Figure S2

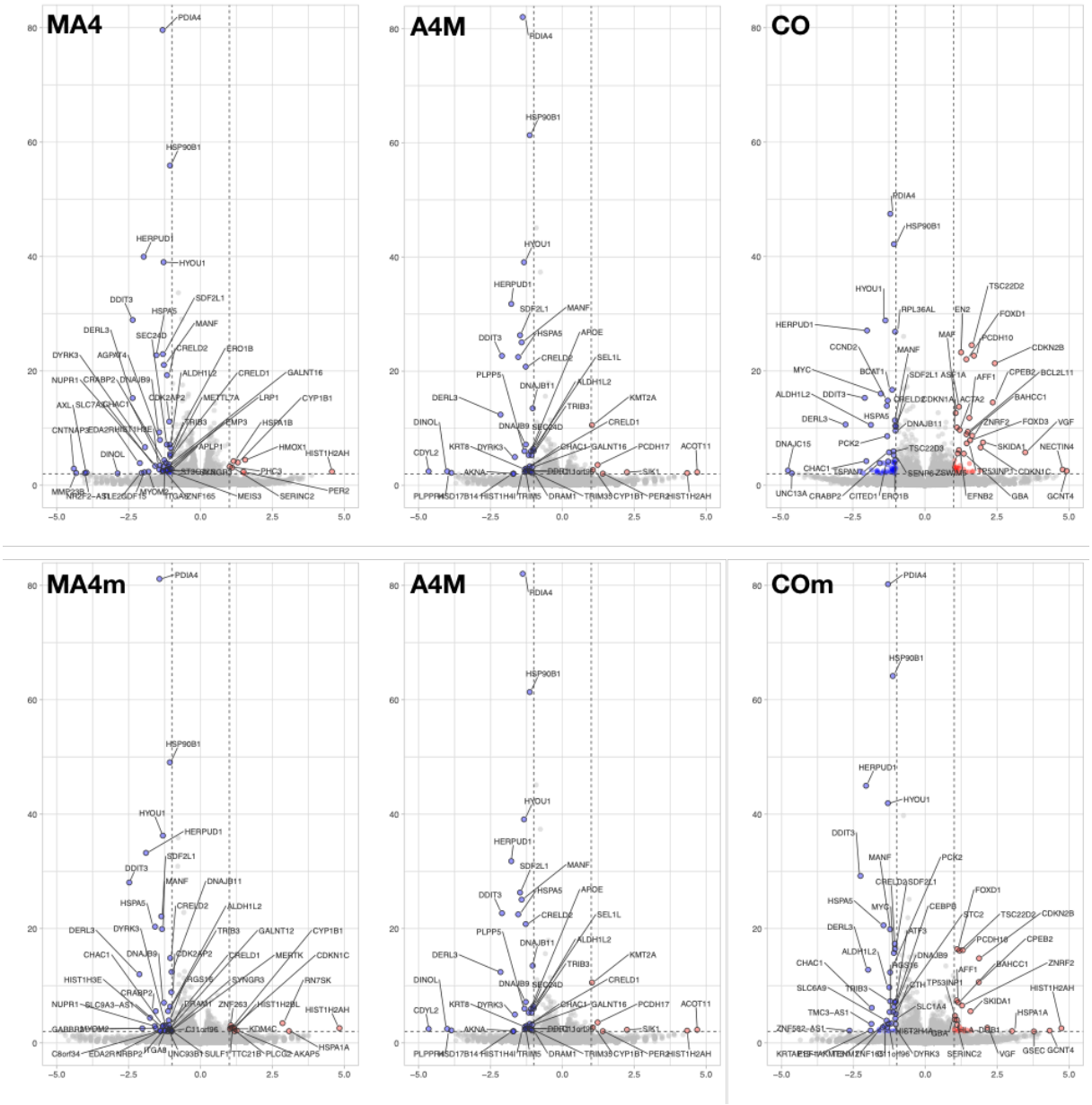
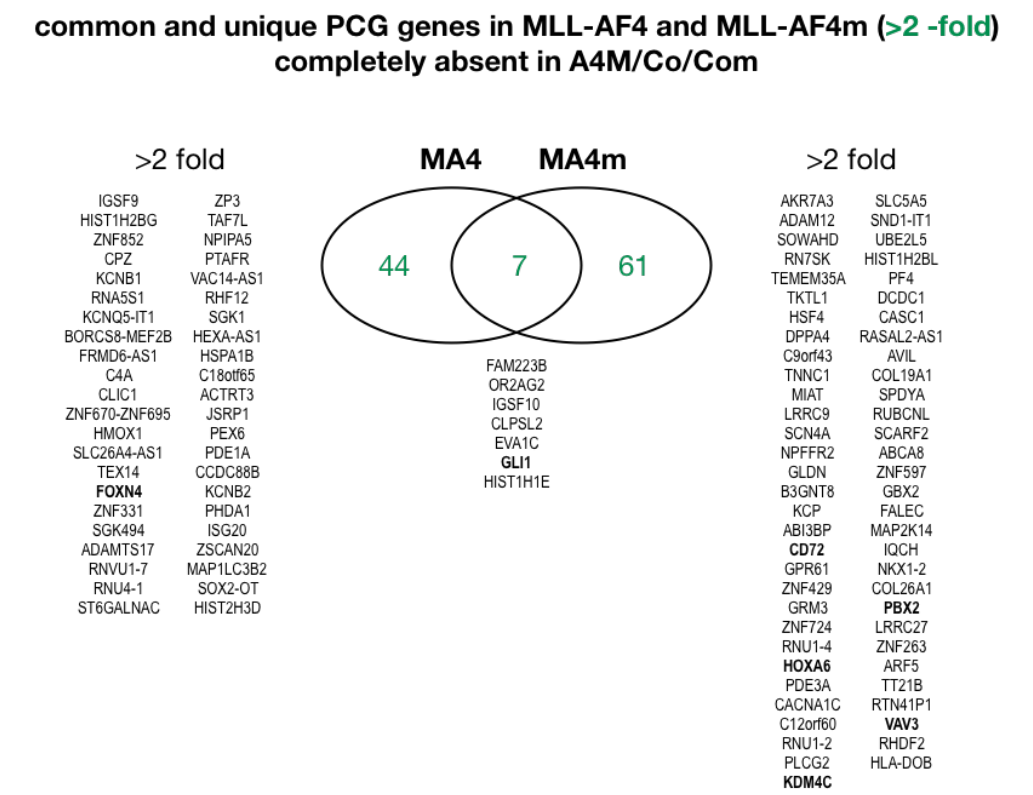


Figure S3


common and unique PCG genes in MLL-AF4 and MLL-AF4m (>2 -fold)
completely absent in A4M/Co/Com
>2 fold
IGSF9
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ZNF852
CPZ
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RNA5S1
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BORCS8-MEF2B
FRMD6-AS1
C4A
CLIC1
ZNF670-ZNF695
HMOX1
SLC26A4-AS1
TEX14
FOXN4
ZNF331
SGK494
ADAMTS17
RNVU1-7
RNU4-1
ST6GALNAC
ZP3
TAF7L
NPIPA5
PTAFR
VAC14-AS1
RHF12
SGK1
HEXA-AS1
HSPA1B
C18otf65
ACTRT3
JSRP1
PEX6
PDE1A
CCDC88B
KCNB2
PHDA1
ISG20
ZSCAN20
MAP1LC3B2
SOX2-OT
HIST2H3D
MA4
MA4m
44
7
61
FAM223B
OR2AG2
IGSF10
CLPSL2
EVA1C
GLI1
HIST1H1E
>2 fold
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LRRC9
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HOXA6
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RNU1-2
PLCG2
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SND1-IT1
UBE2L5
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PF4
DCDC1
CASC1
RASAL2-AS1
AVIL
COL19A1
SPDYA
RUBCNL
SCARF2
ABCA8
ZNF597
GBX2
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MAP2K14
IQCH
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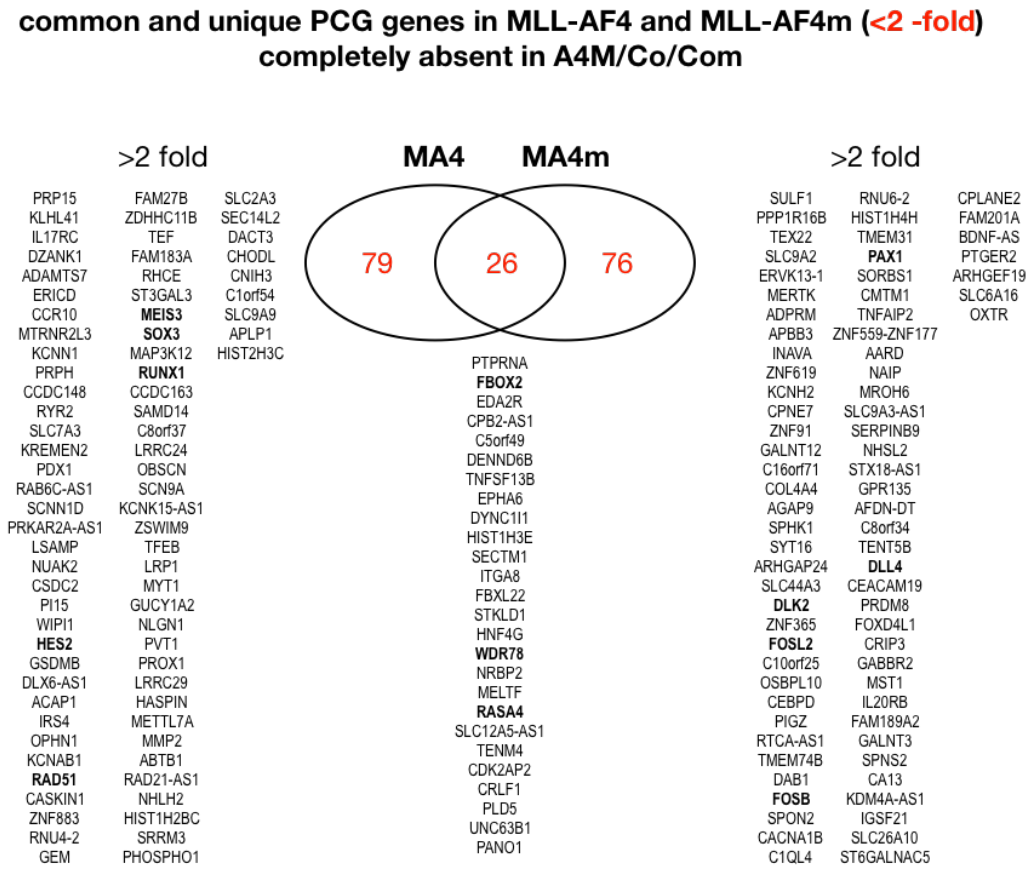
common and unique PCG genes in MLL-AF4 and MLL-AF4m (<2 -fold)
completely absent in A4M/Co/Com
>2 fold
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IL17RC
DZANK1
ADAMTS7
ERICD
CCR10
MTRNR2L3
KCNN1
PRPH
CCDC148
RYR2
SLC7A3
KREMEN2
PDX1
RAB6C-AS1
SCNN1D
PRKAR2A-AS1
LSAMP
NUAK2
CSDC2
PI15
WIPI1
HES2
GSDMB
DLX6-AS1
ACAP1
IRS4
OPHN1
KCNAB1
RAD51
CASKIN1
ZNF883
RNU4-2
GEM
FAM27B
ZDHHC11B
TEF
FAM183A
RHCE
ST3GAL3
MEIS3
SOX3
MAP3K12
RUNX1
CCDC163
SAMD14
C8orf37
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TFEB
LRP1
MYT1
GUCY1A2
NLGN1
PVT1
PROX1
LRRC29
HASPIN
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MMP2
ABTB1
RAD21-AS1
NHLH2
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SRRM3
PHOSPHO1
SLC2A3
SEC14L2
DACT3
CHODL
CNIH3
C1orf54
SLC9A9
APLP1
HIST2H3C
MA4
MA4m
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26
76
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EPHA6
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SECTM1
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FBXL22
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WDR78
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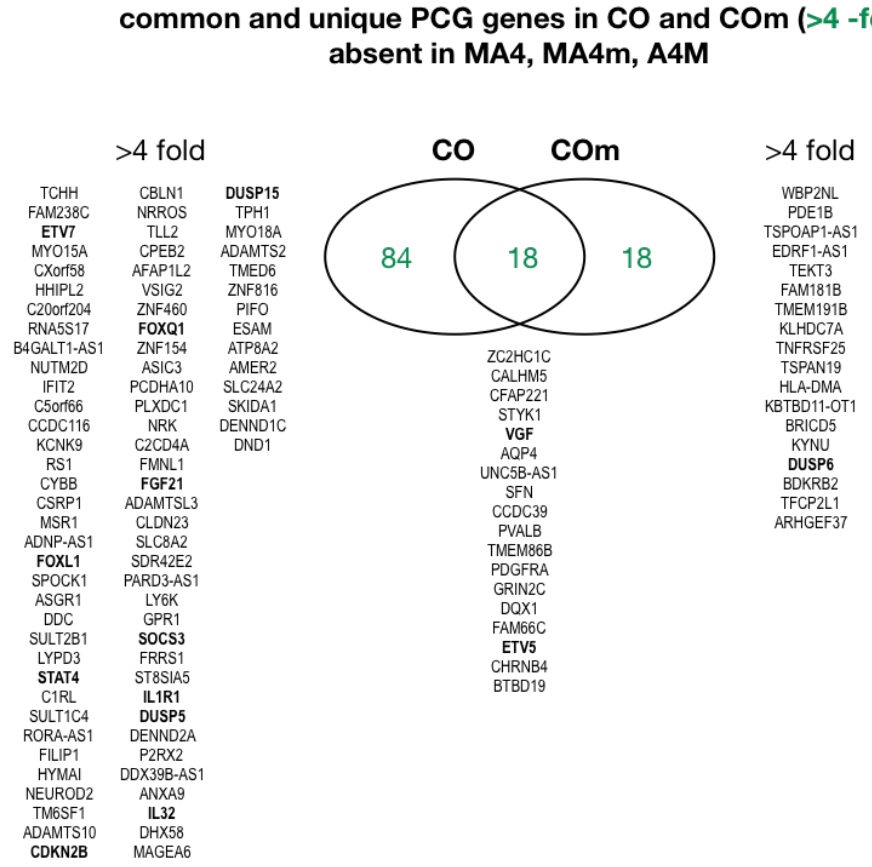
Figure S4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CO
COm
>4 fold
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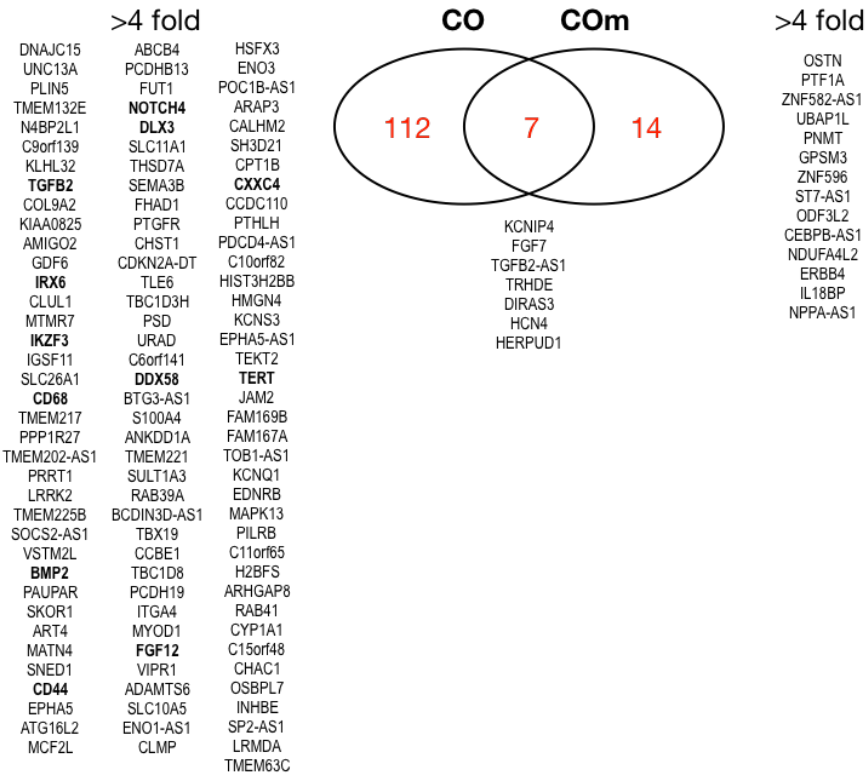
common and unique PCG genes in CO and COm (>4 -fold)
absent in MA4, MA4m, A4M
>4 fold
CO
COm
>4 fold
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CHST1
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