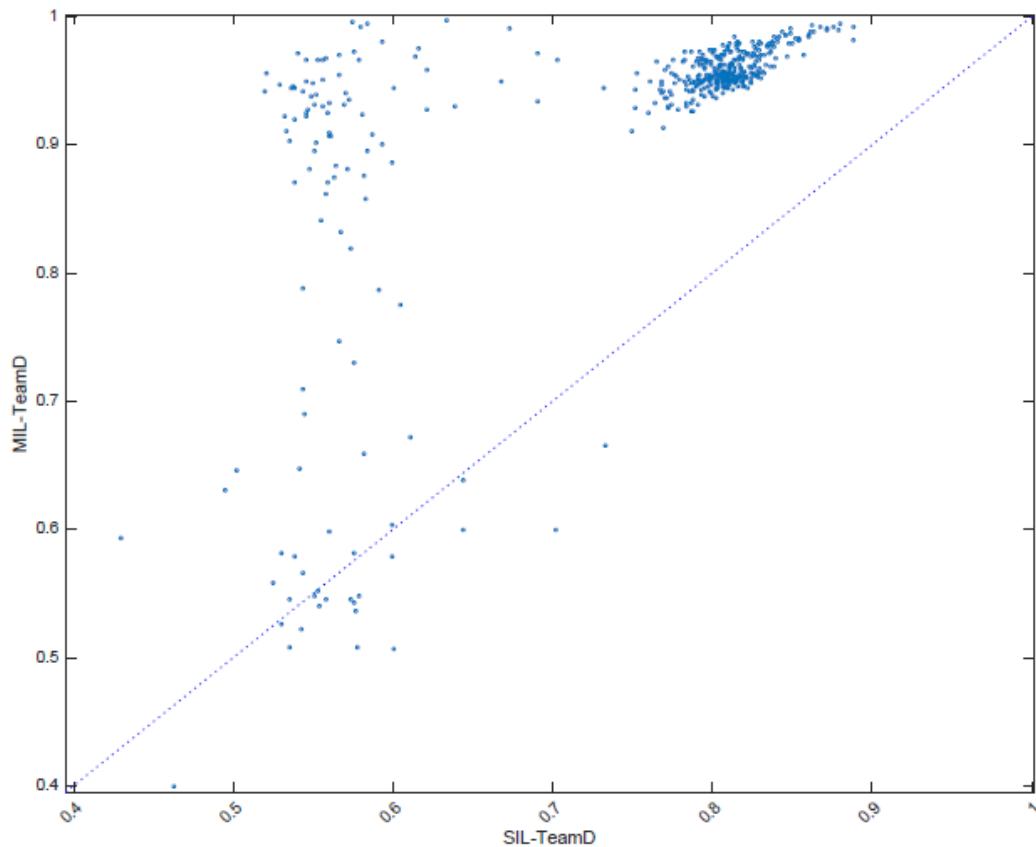
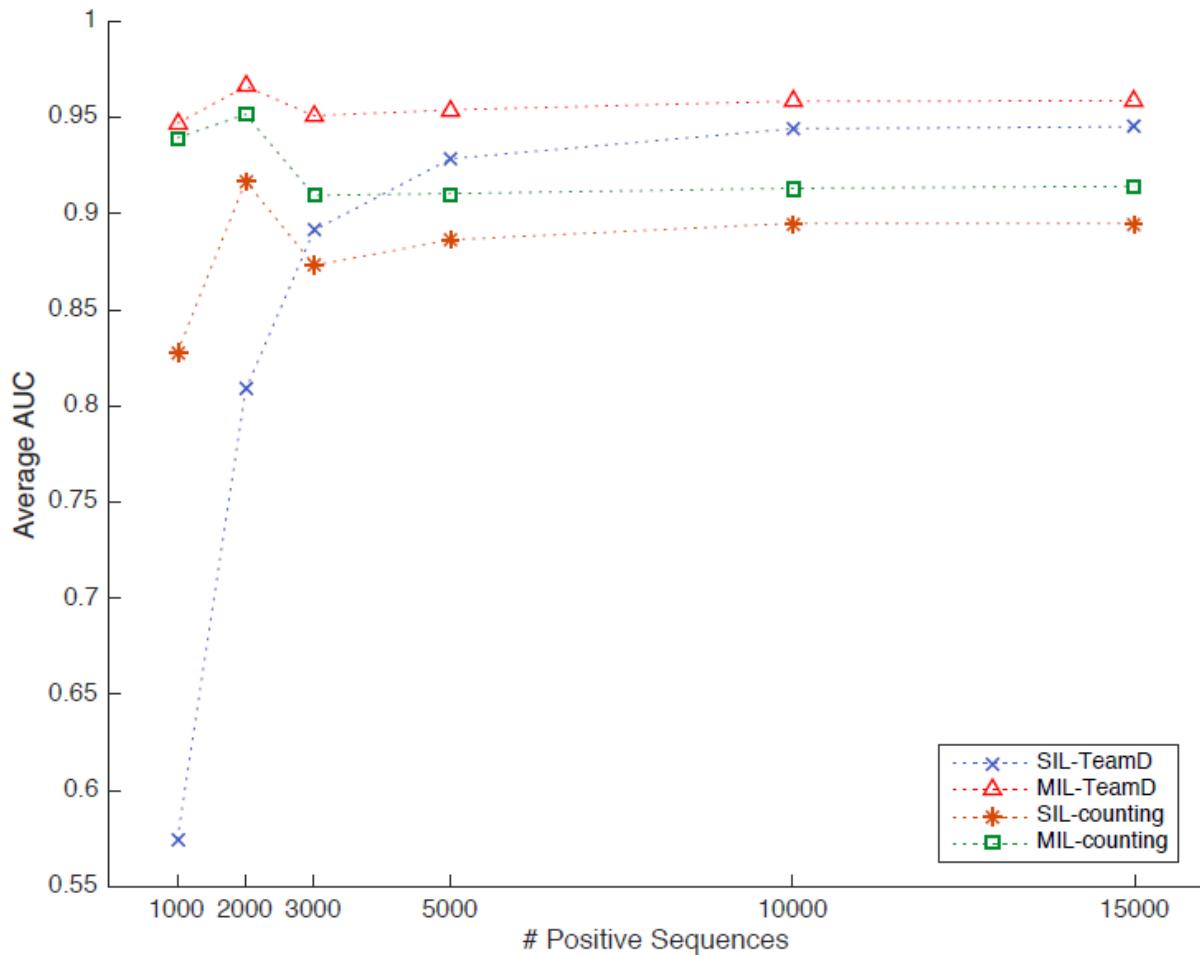


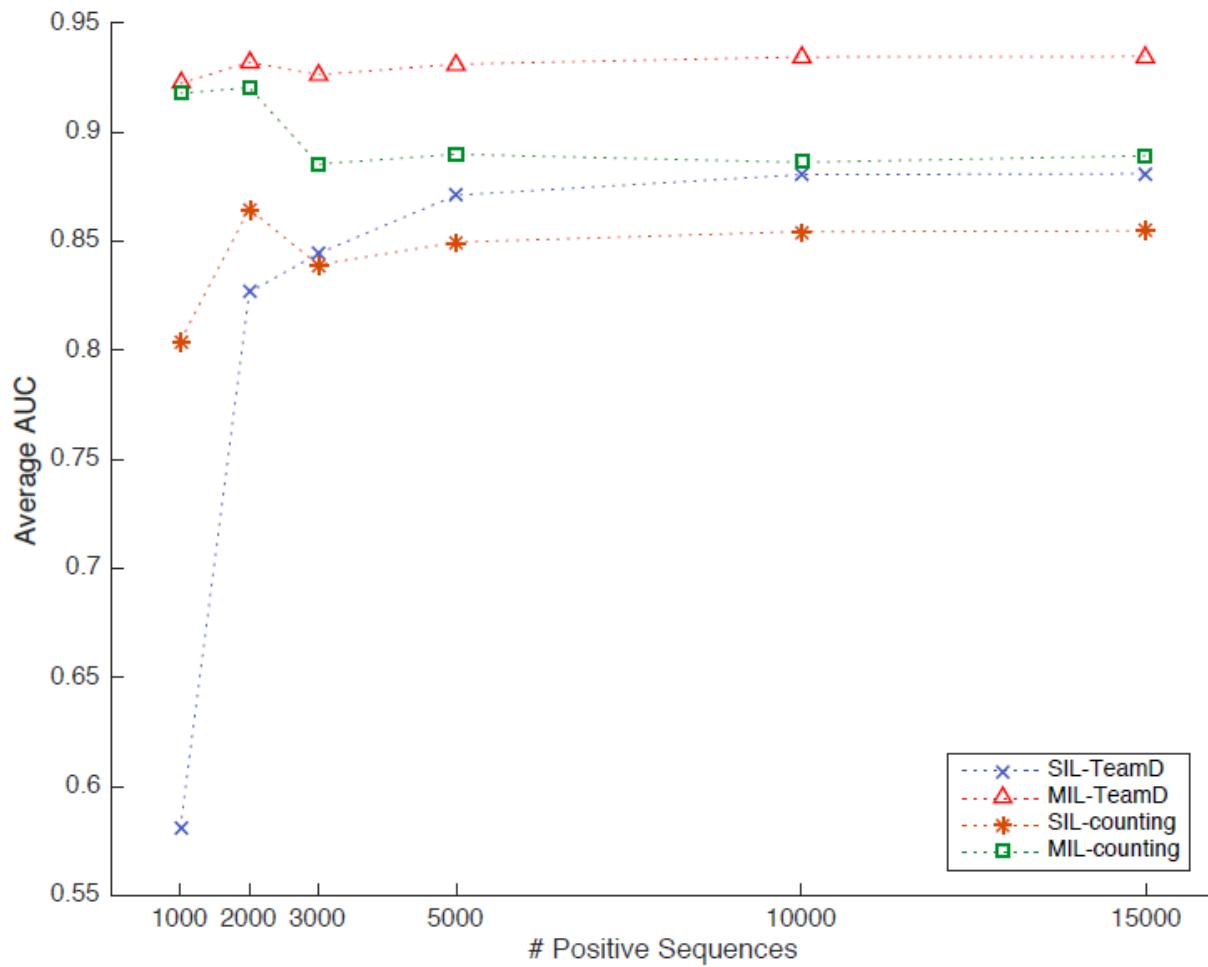
**Supplemental Fig. 1.** AUC comparison between MIL-TeamD and SIL-TeamD on 495 ENCODE ChIP-Seq data.



**Supplemental Fig. 2.** Effect of number of positive sequences on MIL performance for the four selected TFs (Gata2, Gata3, Mef2c, and Nanog)



**Supplemental Fig. 3.** Effect of number of positive sequences on MIL performance for 100 randomly sampled TFs from ENCODE



**Supplemental Fig. 4** Top-5 motifs found by HOMER from CI, TI and TF1 sequences for each TF

(a)  
GATA2

	CIMs		TIMs		TFIMs	
	Logo	Best match	Logo	Best match	Logo	Best match
1		GATA3		GATA3		GATA5
2		Tcf12		GCN4		BAS1
3		GATA3(Zf)		FOXP1		SOK2
4		RUNX		PB0012		SPIB
5		FZF1		Tcf12		RTG3

(b)  
GATA3

	CIMs		TIMs		TFIMs	
	Logo	Best match	Logo	Best match	Logo	Best match
1		GATA(Zf)		PHA-4(Forkhead)		FOXD2
2		FOXD2		GATA3(Zf)		MAFG
3		GATA(Zf)		TEAD3		GATA3
4		GATA3(Zf)		GATA(Zf)		TEC1
5		AP-2gamma		RTG3		MBP1

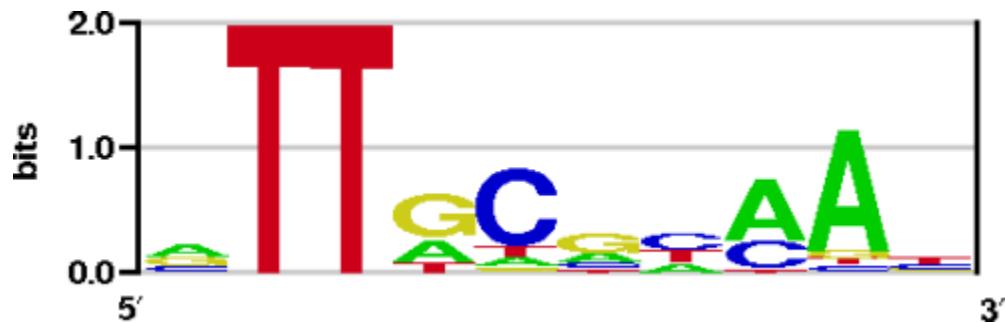
(c)  
MEF2C

	CIMs		TIMs		TFIMs	
	Logo	Best match	Logo	Best match	Logo	Best match
1		Mef2c		Mef2c		br(var.2)
2		GCN4		RUNX1		RUNX1
3		RUNX2		GCR2		AP-1(bZIP)
4		PU.1:IRF8		GCN4		Tgif2
5		SpiB		PU.1-IRF		MF0009.1

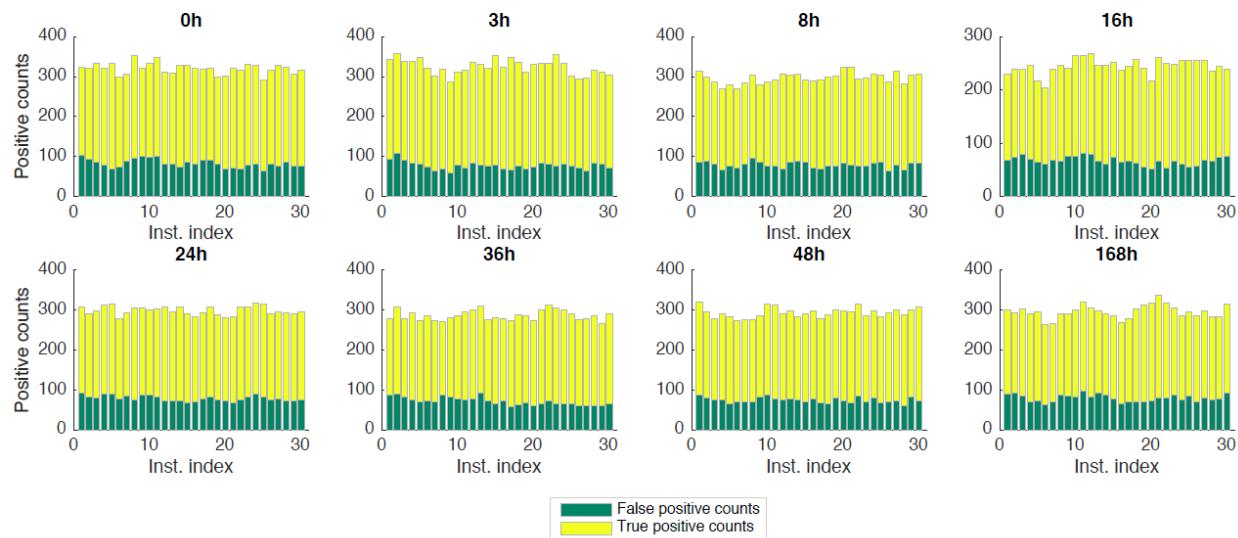
(d)  
NANOG

	CIMs		TIMs		TFIMs	
	Logo	Best match	Logo	Best match	Logo	Best match
1		Sox3(HMG)		Sox2		Sox4(HMG)
2		Zic(Zf)		Brm1		BARHL2
3		Pou5fl		Nanog		PHD1
4		Nanog		PHD1		MIG2
5		Bm1		vvl		TEC1

**Supplement Fig. 5** PBM-derived Cebpb motif ([Weirauch et al. 2014](#))

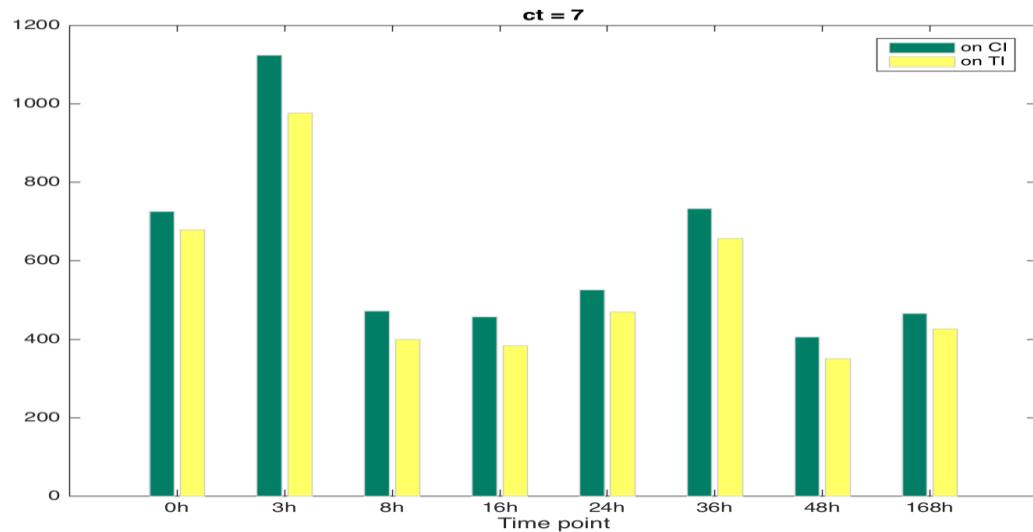


**Supplemental Fig. 6** Number of predicted positive instances at each instance location for Cebpb ChIP-Seq data

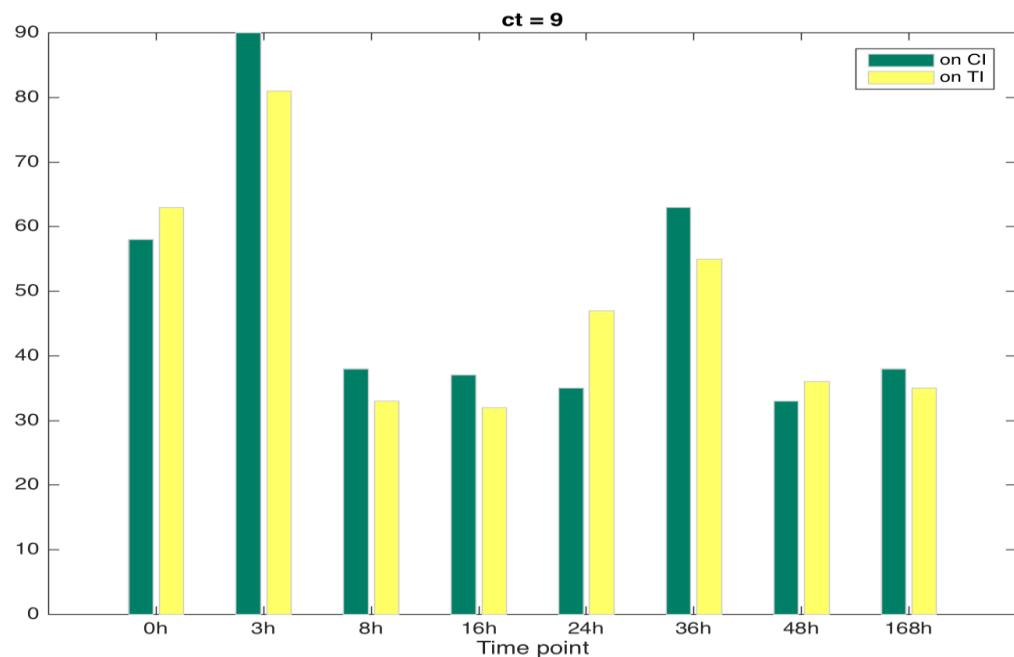


**Supplemental Fig. 7** Occurrence of Cebpb binding sites in TI and CI, returned by HOMER using different score cutoffs

(a) cutoff = 7.0



(b) cutoff = 9.0



**Supplemental table 1.** Possible co-factors for Gata2, Gata3, Mef2c, and Nanog found by our method on each type of sequences.

<b>Gata2</b>	
CI	SPI1, JUND, NHLH1, NFE2, MAFF, MAFG, TCF7L2
TI	SPI1, TBX2, JUND, RUNX1;, NHLH1, NFE2, RBPJ, MAFF, MAFG, RUNX2, ETS1, FLI1, TCF7L2
TFI	SPI1, RELA
TI unique to CI	TBX2, RUNX1;, RBPJ, RUNX2, ETS1, FLI1
TFI unique to CI	RELA
<b>Gata3</b>	
CI	FOXJ2, FOXA1, FOXA2, IKZF1, TEAD3, FOXD1
TI	FOXJ2, SPI1, FOXA1, FOXA2, FOXG1, TEAD3, ELF3, ETS1, ETV1, FOXD1
TFI	FOXJ2, FOXA1, LEF1, HOXA10, FOXA2, ZEB1, FOXD1
TI unique to CI	SPI1, FOXG1, ELF3, ETS1, ETV1
TFI unique to CI	LEF1, HOXA10, ZEB1
<b>Mef2c</b>	
CI	SPI1, TBX2, JUND, RUNX1;, GABPA, RUNX2, ETS1, CEBPA
TI	SPI1, JUND, RUNX1;, FOXL1, RUNX2
TFI	ESRRA, SPI1, EGR2, JUND, ZIC3, ZBTB7B, RUNX1;, TGIF1, RUNX2, KLF6, CEBPA
TI unique to CI	FOXL1
TFI unique to CI	ESRRA, EGR2, ZIC3, ZBTB7B, TGIF1, KLF6
<b>Nanog</b>	
CI	SOX4, MNX1, ZIC3, SOX17, GBX2, SOX2, NFATC1
TI	SOX4, MNX1, LEF1, ZIC3, SOX17, SP3, SOX2, FOXG1, PAX4, KLF6
TFI	SPI1, CTCF, NFATC1, ELF3, ETS1, KLF6
TI unique to CI	LEF1, SP3, FOXG1, PAX4, KLF6
TFI unique to CI	SPI1, CTCF, ELF3, ETS1, KLF6

**Supplemental table 2.** Possible co-factors for Cebpb at different time points during liver regeneration (Jakobsen et al., 2013) found by our method on each type of sequences.

<b>0h</b>	
CI	LEF1
TI	EGR2, FOXA2, MEF2A
TFI	FOXA2
TI unique to CI	EGR2, FOXA2, MEF2A
TFI unique to CI	FOXA2
<b>3h</b>	
CI	SP3, FOXA2, ESR2, NFIX
TI	SPI1, ITGA2, SP3, FOXA2, IKZF1, ESR2, ETS1
TFI	RELA
TI unique to CI	SPI1, ITGA2, IKZF1, ETS1
TFI unique to CI	RELA
<b>8h</b>	
CI	ESR2, NFIX
TI	USF2, BHLHE41, ATF3, USF1, PAX3, RELA
TFI	RELA
TI unique to CI	USF2, BHLHE41, ATF3, USF1, PAX3, RELA
TFI unique to CI	RELA
<b>16h</b>	
CI	
TI	RELA
TFI	CTCF, RELA, CREB1
TI unique to CI	RELA
TFI unique to CI	CTCF, RELA, CREB1
<b>24h</b>	
CI	
TI	MAFF, RELA
TFI	RELA
TI unique to CI	MAFF, RELA
TFI unique to CI	RELA
<b>36h</b>	
CI	HOXA10
TI	ESR2, NFIX, RELA
TFI	CTCF
TI unique to CI	ESR2, NFIX, RELA

TFI unique to CI	CTCF
<b>48h</b>	
CI	EGR2, SP3, MAFF, MAFG, FOXO4, RELA
TI	RELA
TFI	RELA
TI unique to CI	
TFI unique to CI	
<b>168h</b>	
CI	RELA
TI	
TFI	
TI unique to CI	
TFI unique to CI	