Enhancer Predictions for the Encyclopedia - part 3

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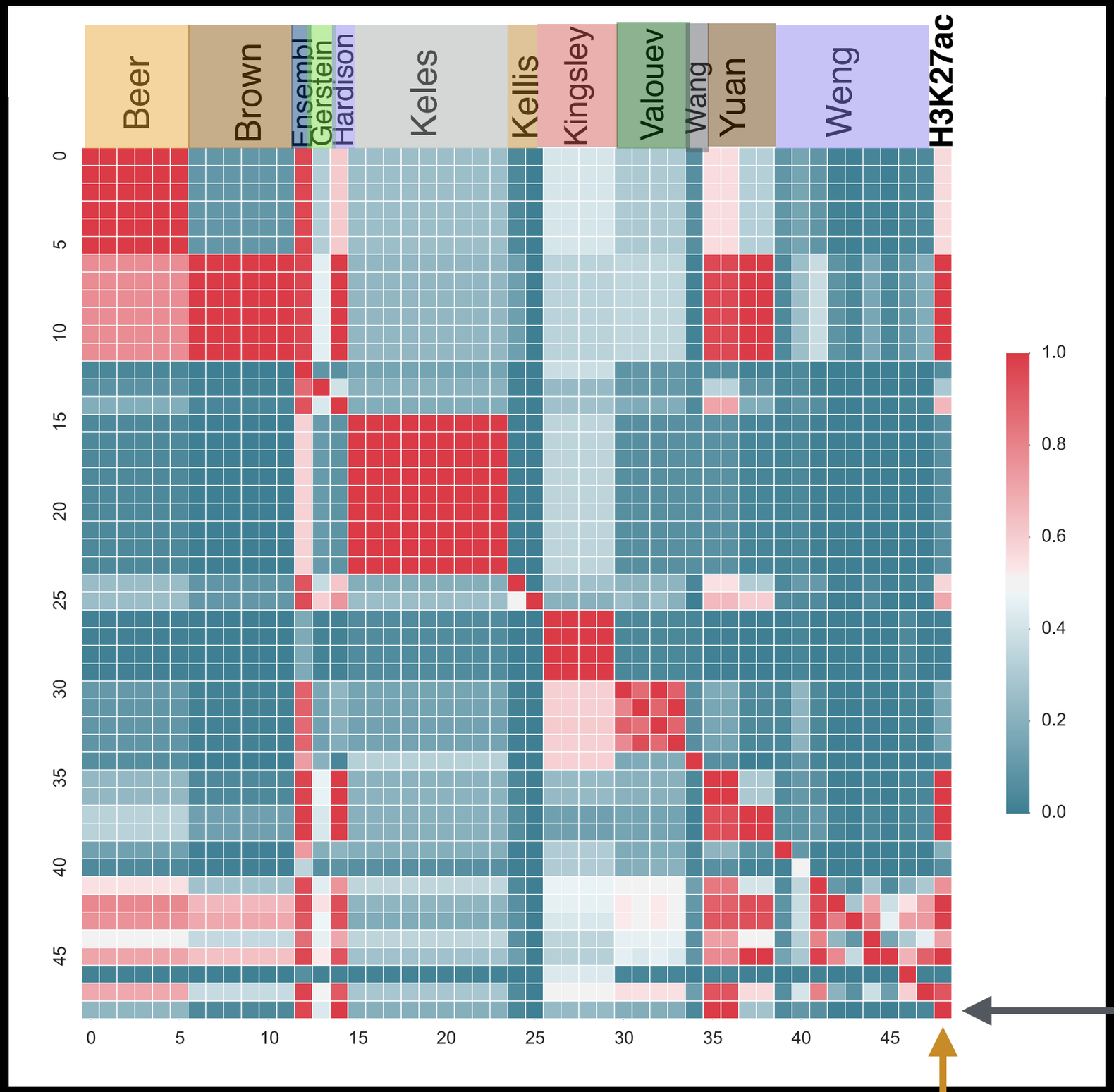
Similarity between Ensemble ranking and all prediction methods + H3K27ac peak ranking

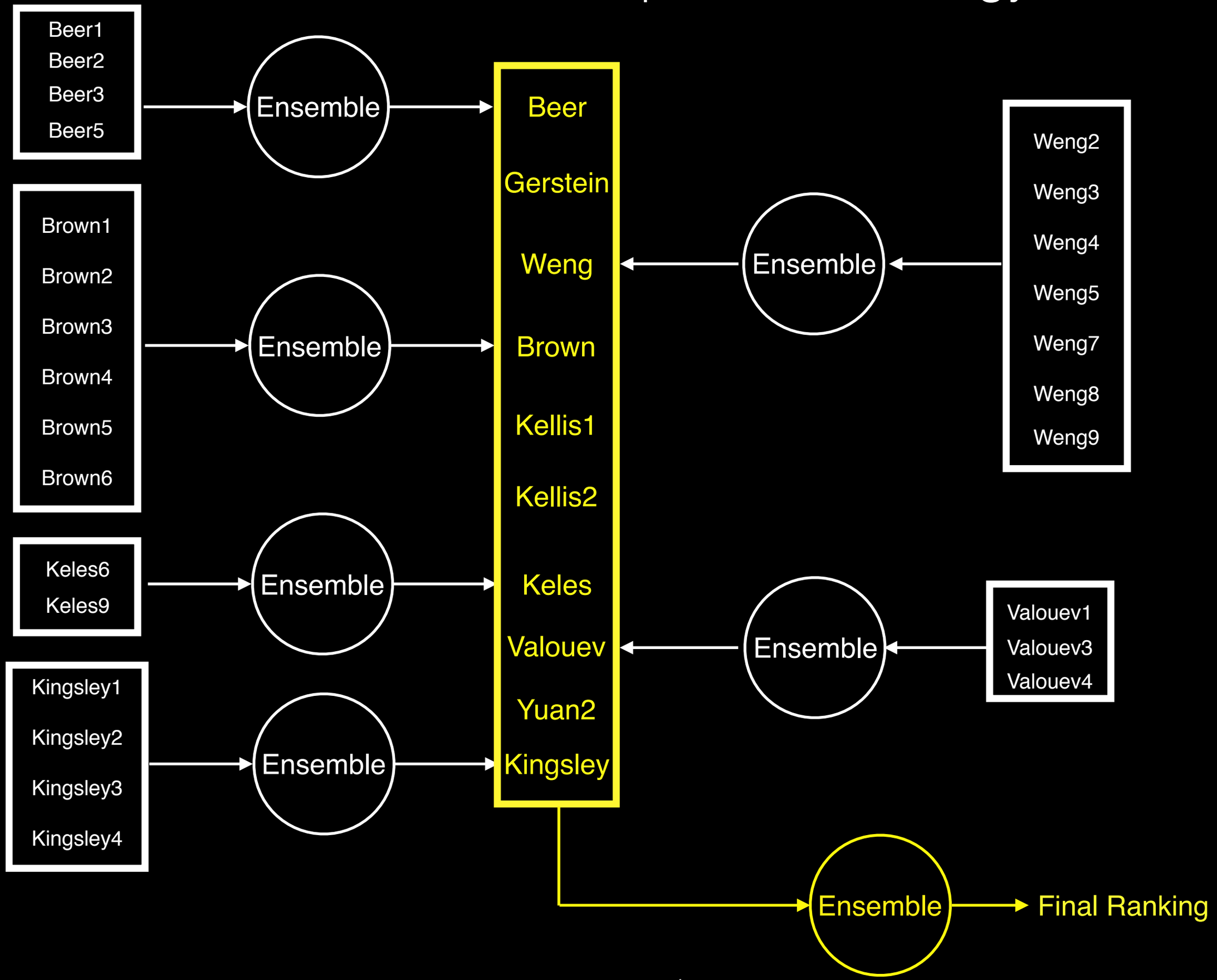
Overlap between different methods and H3K27ac peaks - forebrain



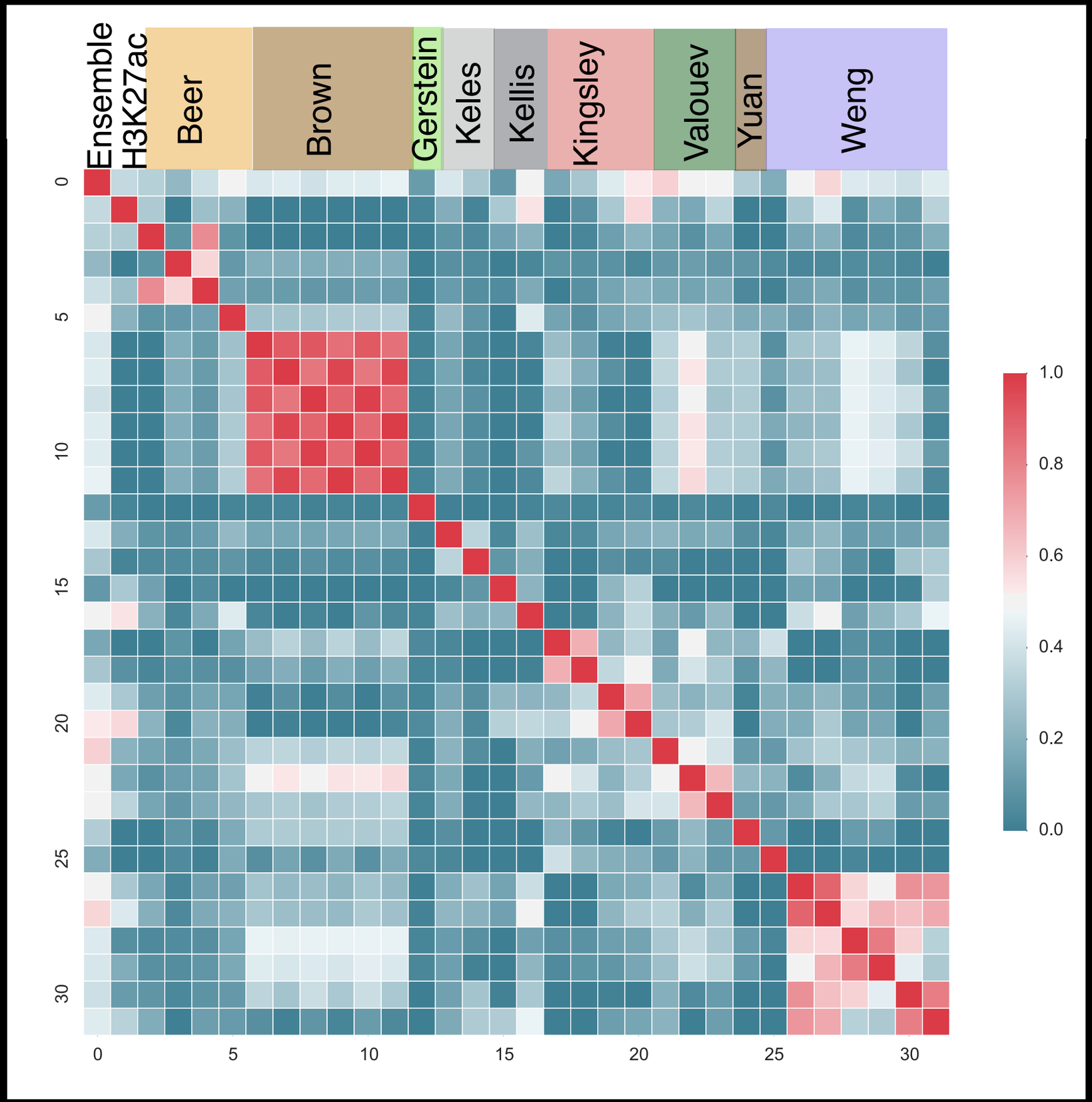
Fraction of H3K27ac peaks predicted to be an enhancer

Fraction of predictions overlapping H3K27ac peaks

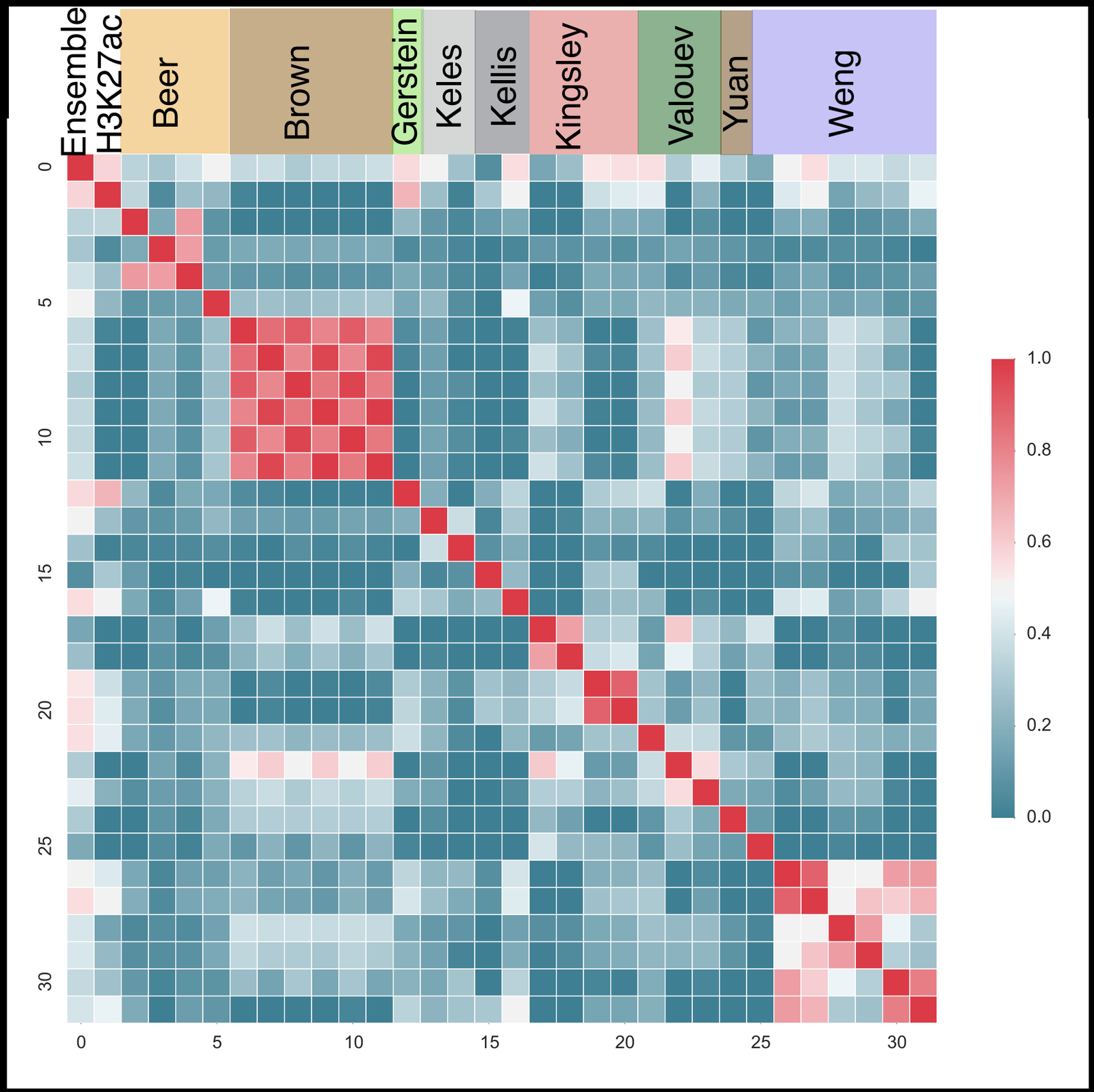
The final unsupervised strategy



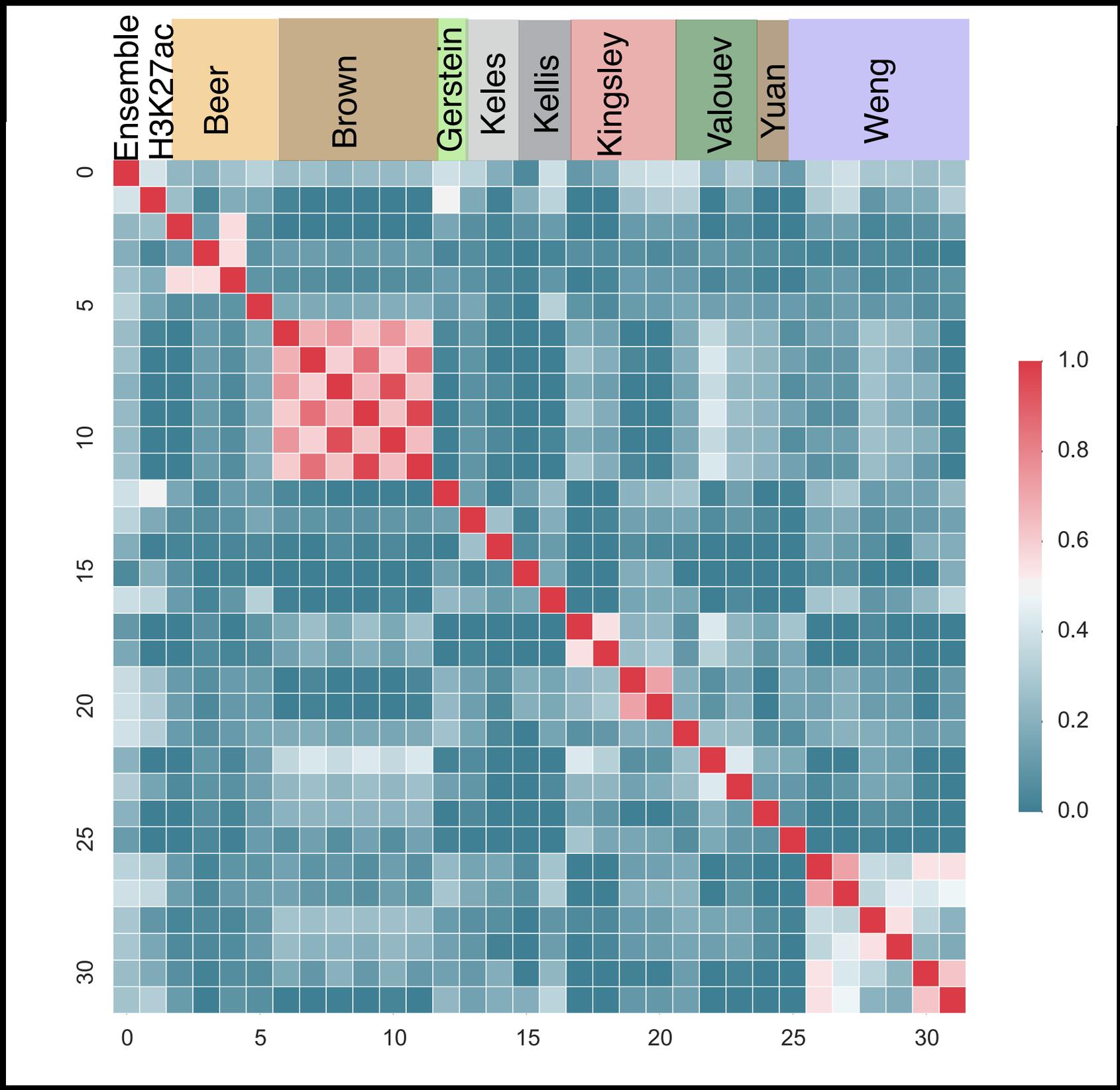
Pearson Correlation between different groups for H3K27ac peaks



Spearman rank correlation between all methods for H3K27ac peaks

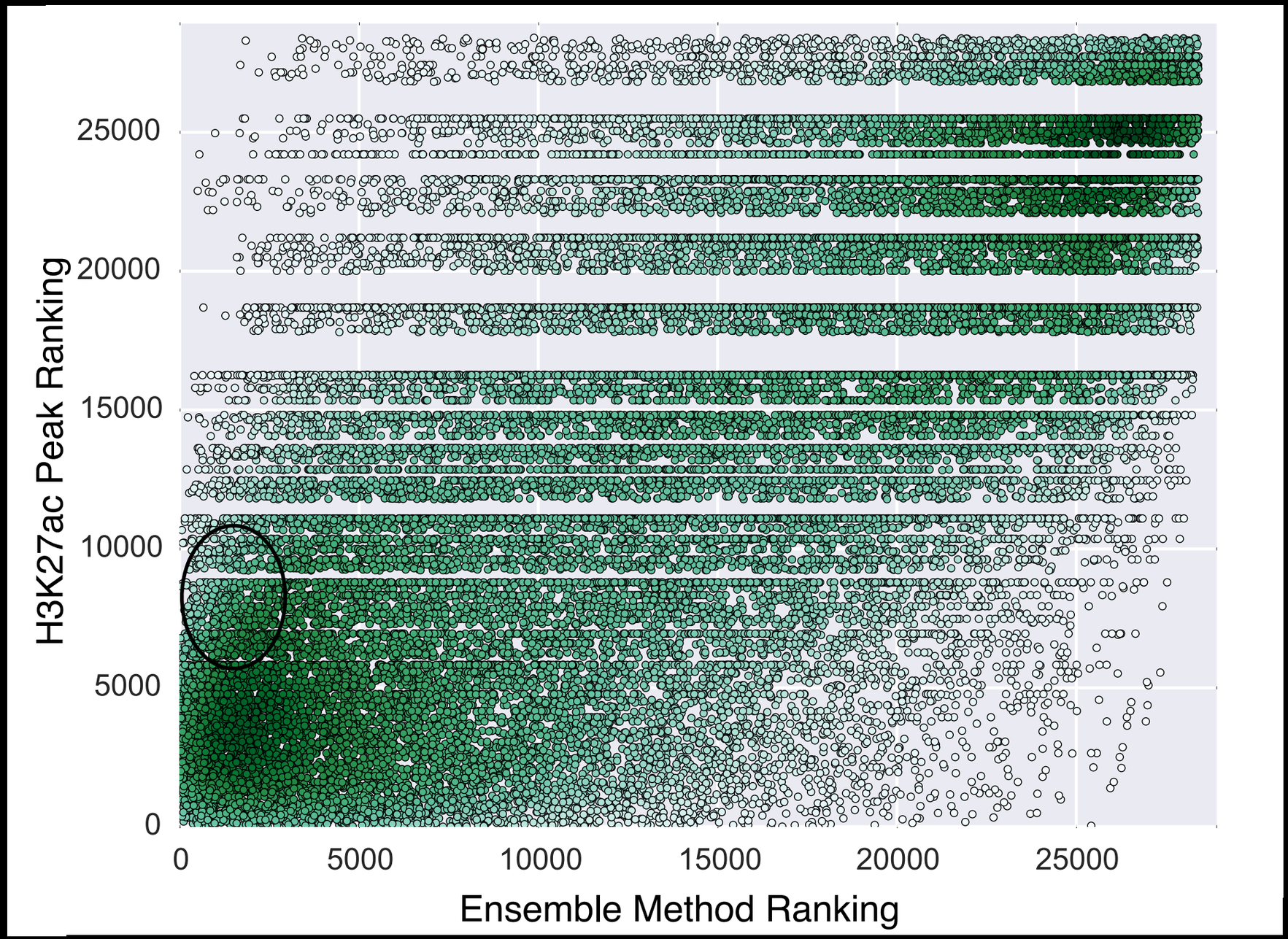


Kendall's tau correlation



Fraction of pairs with concordant ordering

Comparison of ranking between H3K27ac peaks and Ensemble method



Spearman Ranking Correlation = 0.58

Simple Models Continued

- Signal based model (average model)
- Peak based model (q-value of peak)
- Linear Regression models for combining two marks
- Logistic Regression models for combining two marks
- DNase-Seq signal is made by averaging two biological replicates (each biological replicate is actually made by combining 4-6 technical replicates).
- DNA-me is only CpG signal in one of the replicates for that tissue.

Accuracy of different experimental datasets to predict **forebrain** enhancers

	Signal		Peak - 10%(50%)	
Method	**AUROC**	**AUPR**	**AUROC**	**AUPR**
H3K27ac	**0.81**	**0.45**	**0.73 (0.62)**	**0.41 (0.39)**
P300 signal	0.48	0.18		
H3K27ac + P300 logistic	0.59	0.44		
H3K27ac + P300 linear	0.81	0.45		
H3K4me1	0.72	0.28	0.66 (0.51)	0.30 (0.20)
H3K27ac + H3K4me1 log	0.57	0.43	0.37 (0.35)	0.54 (0.52)
H3K27ac + H3K4me1 lin	0.80	0.44	0.74 (0.62)	0.37 (0.38)
H3K4me2	0.74	0.31	0.65 (0.55)	0.28 (0.26)
H3K27ac + H3K4me2 log	0.81	0.45	0.41 (0.34)	0.53 (0.52)
H3K27ac + H3K4me2 lin	0.81	0.45	0.71 (0.63)	0.41 (0.37)
H3K4me3	0.70	0.27	0.55 (0.51)	0.23 (0.20)
H3K27ac + H3K4me3 log	0.59	0.47	0.42 (0.44)	0.55 (0.53)
H3K27ac + H3K4me3 lin	0.81	0.47	0.73 (0.62)	0.42 (0.39)
H3K9ac	0.65	0.24	0.58 (0.5)	0.25 (0.18)
H3K27ac + H3K9ac log	0.60	0.52	0.44 (0.45)	0.55 (0.54)
H3K27ac + H3K9ac lin	0.83	0.50	0.74 (0.62)	0.43 (0.41)
DNA-me	0.72	0.29		
H3K27ac + DNA-me log	0.60	0.52		
H3K27ac + DNA-me lin	0.82	0.46		
GC	0.45	0.15		
H3K27ac + GC log	0.57	0.45		
H3K27ac + GC lin	0.81	0.45		
Null model	0.50	0.16	0.50	0.16
Matched Filter			0.80	0.42

Accuracy of different experimental datasets to predict **heart** enhancers

	Signal		Peak - 10%(50%)	
Method	**AUROC**	**AUPR**	**AUROC**	**AUPR**
H3K27ac	0.89	0.50	0.86 (0.80)	0.44 (0.43)
P300 signal	0.61	0.12		
H3K27ac + P300 lin	0.89	0.50		
H3K27ac + P300 log	0.68	0.51		
H3K4me1	0.81	0.20	0.80 (0.63)	0.33 (0.29)
H3K27ac + H3K4me1 lin	0.89	0.52	0.86 (0.80)	0.43 (0.42)
H3K27ac + H3K4me1 log	0.63	0.48	0.40 (0.37)	0.59 (0.58)
H3K4me2	0.76	0.17	0.72 (0.59)	0.17 (0.15)
H3K27ac + H3K4me2 lin	0.90	0.51	0.86 (0.80)	0.45 (0.44)
H3K27ac + H3K4me2 log	0.63	0.47	0.44 (0.43)	0.61 (0.60)
H3K4me3	0.76	0.13	0.57 (0.52)	0.12 (0.11)
H3K27ac + H3K4me3 lin	0.90	0.51	0.85 (0.80)	0.47 (0.45)
H3K27ac + H3K4me3 log	0.63	0.46	0.45 (0.42)	0.61 (0.59)
H3K9ac	0.83	0.27	0.74 (0.56)	0.24 (0.19)
H3K27ac + H3K9ac lin	0.89	0.52	0.85 (0.80)	0.47 (0.45)
H3K27ac + H3K9ac log	0.63	0.46	0.45 (0.43)	0.60 (0.59)
DNA-me	0.37	0.06		
H3K27ac + DNA-me lin	0.89	0.50		
H3K27ac + DNA-me log	0.89	0.50		
GC	0.53	0.11		
H3K27ac + GC lin	0.89	0.50		
H3K27ac + GC log	0.64	0.46		
Null model	0.50	0.07	0.50	0.07
Matched Filter			0.88	0.48

Accuracy of different experimental datasets to predict **midbrain** enhancers

	Signal		Peak - 10%(50%)	
Method	**AUROC**	**AUPR**	**AUROC**	**AUPR**
H3K27ac	0.78	0.43	0.72 (0.61)	0.41 (0.37)
P300	0.52	0.18		
H3K27ac + P300 lin	0.78	0.43		
H3K27ac + P300 log	0.58	0.46		
H3K4me1	0.76	0.30	0.73 (0.56)	0.33 (0.24)
H3K27ac + H3K4me1 lin	0.79	0.41	0.75 (0.64)	0.37 (0.32)
H3K27ac + H3K4me1 log	0.56	0.40	0.35 (0.35)	0.54 (0.52)
H3K4me2	0.75	0.30	0.67 (0.57)	0.29 (0.27)
H3K27ac + H3K4me2 lin	0.78	0.43	0.70 (0.63)	0.40 (0.35)
H3K27ac + H3K4me2 log	0.56	0.45	0.39 (0.35)	0.53 (0.52)
H3K4me3	0.70	0.26	0.56 (0.52)	0.24 (0.23)
H3K27ac + H3K4me3 lin	0.78	0.434	0.71 (0.60)	0.41 (0.37)
H3K27ac + H3K4me3 log	0.57	0.45	0.40 (0.37)	0.54 (0.52)
H3K9ac	0.69	0.26	0.61 (0.53)	0.26 (0.25)
H3K27ac + H3K9ac lin	0.79	0.46	0.72 (0.60)	0.42 (0.37)
H3K27ac + H3K9ac log	0.58	0.47	0.44 (0.40)	0.55 (0.52)
DNase	0.78	0.37	0.68 (0.52)	0.32 (0.36)
H3K27ac + DNase lin	0.79	0.43	0.74 (0.61)	0.38 (0.38)
H3K27ac + DNase log	0.57	0.45	0.44 (0.40)	0.55 (0.52)
GC	0.46	0.14		
H3K27ac + GC lin	0.77	0.41		
H3K27ac + GC log	0.57	0.47		
Null model	0.50	0.15	0.50	0.15
Matched Filter			0.78	0.42

Accuracy of different experimental datasets to predict **limb** enhancers

	Signal		Peak - 10%(50%)	
Method	**AUROC**	**AUPR**	**AUROC**	**AUPR**
H3K27ac	0.78	0.31	0.73 (0.60)	0.31 (0.27)
P300 signal	0.55	0.15		
H3K27ac + P300 lin	0.77	0.31		
H3K27ac + P300 log	0.54	0.33		
H3K4me1	0.74	0.23	0.72 (0.53)	0.25 (0.16)
H3K27ac + H3K4me1 lin	0.78	0.30	0.75 (0.61)	0.27 (0.24)
H3K27ac + H3K4me1 log	0.52	0.26	0.27 (0.17)	0.52 (0.50)
H3K4me2	0.79	0.19	0.61 (0.53)	0.18 (0.15)
H3K27ac + H3K4me2 lin	0.78	0.32	0.72 (0.59)	0.32 (0.27)
H3K27ac + H3K4me2 log	0.53	0.28	0.22 (0.23)	0.51 (0.51)
H3K4me3	0.62	0.15	0.51 (0.5)	0.12 (0.11)
H3K27ac + H3K4me3 lin	0.79	0.33	0.73 (0.60)	0.33 (0.27)
H3K27ac + H3K4me3 log	0.53	0.30	0.25 (0.23)	0.52 (0.51)
H3K9ac	0.63	0.16	0.53 (0.50)	0.14 (0.12)
H3K27ac + H3K9ac lin	0.80	0.35	0.74 (0.60)	0.35 (0.29)
H3K27ac + H3K9ac log	0.53	0.30	0.30 (0.30)	0.53 (0.51)
DNase	0.75	0.34	0.76 (0.52)	0.33 (0.26)
H3K27ac + DNase lin	0.82	0.37	0.79 (0.61)	0.34 (0.28)
H3K27ac + DNase log	0.53	0.28	0.29 (0.20)	0.53 (0.51)
DNA-me	0.64	0.16		
H3K27ac + DNA-me lin	0.78	0.31		
H3K27ac + DNA-me log	0.52	0.28		
GC	0.44	0.10		
H3K27ac + GC lin	0.78	0.32		
H3K27ac + GC log	0.53	0.30		
Null model	0.50	0.10		
Matched Filter			0.79	0.32

Accuracy of different experimental datasets to predict **hindbrain** enhancers

	Signal		Peak - 10%(50%)	
Method	**AUROC**	**AUPR**	**AUROC**	**AUPR**
H3K27ac	0.73	0.30	0.69 (0.60)	0.29 (0.28)
H3K4me1	0.66	0.20	0.58 (0.50)	0.20 (0.18)
H3K27ac + H3K4me1 lin	0.73	0.29	0.69 (0.60)	0.26 (0.28)
H3K27ac + H3K4me1 log	0.52	0.30	0.19 (0.16)	0.50 (0.50)
H3K4me2	0.68	0.23	0.60 (0.53)	0.23 (0.20)
H3K27ac + H3K4me2 lin	0.73	0.30	0.70 (0.60)	0.29 (0.27)
H3K27ac + H3K4me2 log	0.52	0.34	0.17 (0.16)	0.50 (0.50)
H3K4me3	0.64	0.19	0.54 (0.51)	0.19 (0.17)
H3K27ac + H3K4me3 signal	0.73	0.31	0.68 (0.59)	0.30 (0.28)
H3K27ac + H3K4me3 log	0.52	0.33	0.28 (0.21)	0.51 (0.50)
H3K9ac	0.64	0.19	0.56 (0.51)	0.20 (0.17)
H3K27ac + H3K9ac	0.73	0.33	0.69 (0.60)	0.32 (0.29)
H3K27ac + H3K9ac log	0.53	0.33	0.31 (0.28)	0.52 (0.51)
DNase	0.69	0.29	0.65 (0.50)	0.29 (0.26)
H3K27ac + DNase	0.76	0.34	0.72 (0.60)	0.31 (0.29)
H3K27ac + DNase log	0.52	0.33	0.31 (0.28)	0.52 (0.51)
GC	0.47	0.13		
H3K27ac + GC	0.72	0.30		
H3K27ac + GC log	0.78	0.32		
Null model	0.50	0.13	0.50	0.13
Matched Filter			0.73	0.31

Accuracy of different experimental datasets to predict **neuralTube** enhancers

	Signal		Peak - 10%(50%)	
Method	**AUROC**	**AUPR**	**AUROC**	**AUPR**
H3K27ac	**0.74**	**0.25**	**0.69 (0.58)**	**0.24 (0.22)**
H3K4me1	**0.69**	**0.15**	**0.64 (0.51)**	**0.16 (0.11)**
H3K27ac + H3K4me1 lin	**0.71**	**0.24**	**0.71 (0.58)**	**0.21 (0.23)**
H3K27ac + H3K4me1 log	**0.52**	**0.29**	**0.18 (0.19)**	**0.51 (0.50)**
H3K4me2	**0.69**	**0.17**	**0.62 (0.52)**	**0.18 (0.13)**
H3K27ac + H3K4me2 lin	**0.74**	**0.25**	**0.71 (0.57)**	**0.24 (0.22)**
H3K27ac + H3K4me2 log	**0.52**	**0.29**	**0.20 (0.19)**	**0.51 (0.50)**
H3K4me3	**0.65**	**0.14**	**0.54 (0.52)**	**0.15 (0.13)**
H3K27ac + H3K4me3 lin	**0.74**	**0.26**	**0.68 (0.58)**	**0.25 (0.23)**
H3K27ac + H3K4me3 log	**0.52**	**0.29**	**0.20 (0.31)**	**0.51 (0.51)**
H3K9ac signal	**0.64**	**0.15**	**0.59 (0.51)**	**0.17 (0.14)**
H3K27ac + H3K9ac lin	**0.75**	**0.27**	**0.69 (0.58)**	**0.27 (0.24)**
H3K27ac + H3K9ac log	**0.52**	**0.29**	**0.27 (0.29)**	**0.52 (0.51)**
DNase signal	**0.78**	**0.27**	**0.78 (0.57)**	**0.27 (0.22)**
H3K27ac + DNase lin	**0.77**	**0.26**	**0.79 (0.62)**	**0.28 (0.23)**
H3K27ac + DNase log	**0.52**	**0.27**	**0.29 (0.29)**	**0.52 (0.51)**
GC	**0.48**	**0.09**		
H3K27ac + GC	**0.73**	**0.25**		
H3K27ac + GC log	**0.52**	**0.30**		
Null model	**0.50**	**0.09**	**0.50**	**0.09**
Matched Filter			**0.74**	**0.26**

Table per tissue - rows are candidate - columns and features/ genomic coordinates/positive-negative/peak q-value/ signal/ empty if not a peak

Correlation between DNase and H3K27ac in each cell type (both signal and q-value)

UCSC genome tracks - for the rest of the tissues

Also try peak models with signal values

Plot linear regression and logistic regression models

Signal for single feature ranking