International Journal of
Molecular Sciences

MDPI

Article

Peak Scores Significantly Depend on the Relationships between Contextual Signals in ChIP-Seq Peaks

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Table S1. Independent variables obtained when constructing a multiple regression model to assess the dependence of the *ln(PS)* value in the ChIP-Seq experiment with the FoxA2 transcription factor on the presence of IUPAC motifs in these peaks. Multiple regression coefficients were calculated using the Statistica system (Statsoft™, Tulsa, USA).

Independent variable	The value of the regression coefficient	p - value
TRTWKACH	0.064945	0.000003
RTTKACHY	0.027893	0.039629
TMAAYANS	0.057817	0
TWKACHYW	0.027454	0.006242
TTKRTYTW	-0.0183	0.106331
TKAHYTWK	0.004714	0.556024
TRTTKRTY	0.022418	0.110034
GRMCTHNG	0.003873	0.669797
RAAYHAAY	-0.00456	0.71945
TTRNGHAA	0.024021	0.031108
KACDTWGN	0.028459	0.011256
GGGGHGGG	0.020249	0.464922
GKDCRNAG	-0.00612	0.507082
RAGKYCAN	0.013327	0.267003
GGGHGGGG	-0.00193	0.941753
TAAHYABW	-0.02715	0.006997
ARMYAAGV	0.014113	0.179725
TGYGTACH	-0.00186	0.951609
RTWKACHR	-0.0171	0.166124
AGKTCRND	-0.01803	0.149243
TRTWTGCW	0.033065	0.070134
CCRCCCCB	-0.08112	0.000936
TGNMCTYW	-0.00413	0.67892
ACBTWGNH	-0.00567	0.522861
TAYRCARN	0.004306	0.741284
AAAMAAAR	-0.004	0.379818
CGSCBBCG	0.003226	0.874502

VTTNGCTN	-0.00846	0.398943
ATMMAYAN	-0.01157	0.34691
WTRTTTGY	-0.02029	0.214387
TCRAYADW	0.021752	0.090305
GGYGGSGS	-0.02072	0.314472
GTACRCAH	0.004619	0.897252
TTYGCTYW	0.025579	0.163475
GCGGNGCG	0.04153	0.288321
TDCHTAAB	-0.01677	0.238398
TNGCTHWG	-0.00426	0.709402
RRGRCRGR	-0.0052	0.587477
GCGYKCGN	0.010204	0.901432
CGMRCGCV	-0.07895	0.325373
RSDYRGTG	0.013789	0.15695
GYMCTNBG	0.013578	0.137178
AAMYAYBR	-0.00129	0.885633
GGVVRWGG	0.001835	0.831654
ARYBAATB	0.002026	0.871641
ACWVAGMW	0.006341	0.498484
TTKTTTTS	-0.01969	0.297221
TNACYMWG	-0.01787	0.05649
AMCTYWGN	0.005755	0.537538
ANCRAHGV	0.018936	0.058036
CGBTCGVN	0.118823	0.006146
CGGHGCGB	-0.03953	0.265681
GTGTACWY	0.054044	0.060788
YTGYCYTN	0.014752	0.116004
TTSGYWRN	0.018182	0.040455
GGGCNGGG	-0.00008	0.997041
MYTMACYN	-0.00111	0.915654
CKTYGGHN	0.004876	0.729611
TCSCKHCS	-0.01649	0.333777
AKAYVAAY	-0.00738	0.617441
AACAWGVV	0.032637	0.004226
WRCCBTDG	-0.00361	0.733808
GCGDCSGS	0.001905	0.952881
CTYRGMMB	0.007255	0.436816
AAAAAAAT	-0.04381	0.229676
ATTKCDHA	0.020283	0.151477
TRATTRRY	0.03743	0.032885
DGGRKGMG	-0.01986	0.105866
TTNRTTCW	-0.03517	0.016293

CCGNMKCS	0.034576	0.050553
GCAHRCRS	-0.01072	0.389983
TNCKWATB	0.020401	0.142042
GGWGRVHG	0.024464	0.008203
ATYGATYR	-0.01486	0.552127
AWGCVABS	-0.00066	0.952915
WSCSTRKS	0.018255	0.033926
YCWCYGWV	0.004817	0.601776
CWMYGTNR	0.001395	0.880217
ASSSAGGV	0.001651	0.881211
CGYCGCSB	-0.00872	0.756327
CAWACAAR	0.009464	0.60626
GGHYRGGG	-0.00534	0.729401
AARWRCAA	-0.00721	0.635604
ATBATTAA	-0.0153	0.680502
GHGGKMGG	0.011976	0.514792
AGWCBWYG	0.012495	0.440684
AATYATTA	-0.00379	0.931667
WMHTAACY	-0.01141	0.500393
GNCWCYGH	0.010461	0.243576
HTAACCHB	0.008789	0.565996
ARKSSAAA	0.021976	0.060556
CBWATCDV	0.014192	0.266432
CTRSGHWB	0.000268	0.975205
GBCKTDGB	0.015655	0.131419
CGVRCGGS	0.006716	0.808555
KGKCMYYG	0.003218	0.760706
TGSMTDCB	-0.00391	0.701575
TTGCDWCA	0.019258	0.355813
HCGBTCGV	-0.11369	0.043413
CSWVGCTV	-0.01206	0.289738
GGCRGGAV	0.046776	0.009803
TGWMCCYW	-0.00206	0.885991
ATTKCRWC	-0.01219	0.646997
TNSVDTTC	-0.00034	0.968723
ACDWGGHH	0.001697	0.856515
GCGMCGMG	0.007786	0.864423
TTKACWRA	0.033587	0.035103
DAHGAAAR	-0.00644	0.657093
GCBWAKGR	-0.00908	0.560534
GGHNGAGH	0.021662	0.040533
KRAGCBAN	0.026475	0.009812

DRGRMAAG	-0.00716	0.502581
YRTCKHYS	-0.00863	0.391891
TTTGWATY	0.011182	0.676263
HCCWWCCS	0.007283	0.643497
ACVCWRMS	0.023771	0.010771
TGGGGNKG	-0.0204	0.244909
DRATKTCR	-0.00083	0.95523
GGCSMCGC	0.00678	0.837769
CRTGCGCR	0.047644	0.191893
WCCCCVVC	0.04015	0.01686
TCKWYCYN	-0.00397	0.711223
YRGKTCRB	0.017374	0.224318
SRCWCAGN	-0.01564	0.099753
AMVCAYAG	0.03683	0.00944
CTMACTVN	-0.01458	0.330524
CGNMYCGG	0.08602	0.008174
TACRCAYD	-0.00512	0.811333
RTTYGMAY	0.029037	0.123496
CKTCCGKN	0.0739	0.044389
YKCKTBCB	0.010328	0.27771
TMAYYTYB	-0.00848	0.370015
AGCGYKCG	0.039415	0.620771
RCCHMGTG	0.021349	0.190224
WTWCAAAR	0.005842	0.734245
AWCVSWGM	0.008588	0.361091
KNGMAAYG	-0.00087	0.947455
CTTBGWTS	0.00698	0.701813
CTBCSTSK	-0.01883	0.096703
KGKGCGTG	-0.00189	0.95178
GTBCMHGG	0.020722	0.098363
MCGGAMGK	-0.04252	0.372464
WNGRATKR	-0.01159	0.250609
RWCGBTCG	-0.07535	0.206749
TCCWSSYC	0.02072	0.092817
TDCKGWTK	-0.00501	0.682396
RCTCYGDV	0.013253	0.171227
GGKTCRKD	-0.00751	0.660859
ACRMRCAC	-0.00527	0.19023
DNCKCACB	0.01557	0.191313
RATMTTTG	0.020472	0.335884
KTTCWBTK	-0.00235	0.802398
ACATAGHH	-0.00382	0.871105

MGGCKKGS	0.020086	0.171724
CCTSGRMK	0.036704	0.015545
TATCTWRK	0.028604	0.304342
MKCYACCV	-0.00645	0.688424
TRCYMAGV	-0.00137	0.908218
TTAWYTDA	0.022748	0.241918
GGCSGSCG	0.026619	0.428897
SRTGGTGS	-0.02642	0.24453
AWGRAAAA	0.004712	0.831298
GMGBWGGG	-0.01411	0.397874
RCSRATCG	-0.032	0.481291
WCSGBBCG	0.033847	0.149445
GHRGNTGG	-0.00703	0.554474
RCWCAGKM	0.019598	0.114461
TWTRTASW	-0.00697	0.69251
TDCTYTTY	0.006017	0.669828
GAHBTCAY	0.006527	0.660263
TGTGGACW	0.103851	0.000909
YWRGAAYB	-0.00396	0.702522
TGCAATSB	0.026351	0.265777
RGAAYTSR	-0.02954	0.069598
GCTCRCYS	0.032263	0.172095
TBRCTMAY	-0.00666	0.63315
KMCRAMGV	0.004017	0.790012
TGMMCYGW	-0.01006	0.522609
TRGTTHTB	0.000909	0.951084
AMVYATVC	-0.00731	0.583863
AAWTAAMR	0.007168	0.68754
TKMGTYAY	0.023544	0.236221
TTAAAAAW	-0.05005	0.119039
AWTCGWTV	0.033755	0.422023
AGKYCABC	0.010805	0.50076
GTCCMCAD	-0.00069	0.97725
TRGRAAAW	-0.00471	0.78652
GSARHGGR	-0.0236	0.040487
TKASACAK	0.007172	0.670823
KRATKAAR	-0.02418	0.163617
WGCGGYSG	0.084659	0.021616
ATCGATHY	0.026319	0.530421
CKTGCKTV	-0.00029	0.989536
TWWKTAAY	-0.05389	0.001453
CGDSASCG	0.04324	0.203914

RGAAAARH	-0.01602	0.309993
GGWAGSNG	0.023198	0.144094
GCRGGMMG	-0.01102	0.575352
GCTMAGCD	-0.00019	0.993453
GCCCHSGM	-0.00688	0.685831
AYAAGCDA	-0.00893	0.732848
CGKKACGB	0.028595	0.484864

Table S2. Independent variables obtained when constructing a multiple regression model to assess the dependence of the ln(PS) value in the ChIP-Seq experiment with the FoxA2 transcription factor on the presence of the most significant ($P_{Bonf}(n,N) < 10^{-30}$) IUPAC motifs. Multiple regression coefficients were calculated using Statistica (Statsoft™, Tulsa, USA).

Independent variable	The value of the regression coefficient	p - value
TRTWKACH	0.066537	0.000001
RTTKACHY	0.020576	0.127869
TMAAYANS	0.051297	0
TWKACHYW	0.021614	0.028887
TTKRTYTW	-0.01798	0.087215
TKAHYTWK	-0.00452	0.558784
TRTTKRTY	0.025957	0.056908
GRMCTHNG	0.007598	0.389525
RAAYHAAY	-0.02022	0.079725
TTRNGHAA	0.014906	0.161514
KACDTWGN	0.025535	0.015482
GGGGHGGG	0.008683	0.743245
GKDCRNAG	-0.00599	0.494705
RAGKYCAN	0.019199	0.075093
GGGHGGGG	0.00606	0.803012
TAAHYABW	-0.03378	0.000422
ARMYAAGV	0.02232	0.020651
TGYGTACH	0.01832	0.50862
RTWKACHR	-0.01418	0.219779
AGKTCRND	-0.01949	0.05581
TRTWTGCW	0.021962	0.185892
CCRCCCCB	-0.05688	0.017154
TGNMCTYW	-0.00593	0.535821
ACBTWGNH	-0.00828	0.3323
TAYRCARN	0.00643	0.603919
AAAMAAAR	-0.00702	0.110747
CGSCBBCG	0.040932	0.014188
VTTNGCTN	-0.00617	0.51208
ATMMAYAN	-0.0153	0.197303

WTRTTTGY	-0.01027	0.452303
TCRAYADW	0.006622	0.598369
GGYGGSGS	-0.01007	0.572261
GTACRCAH	-0.00787	0.816082
TTYGCTYW	0.016563	0.35154
GCGGNGCG	0.032148	0.281616
TDCHTAAB	-0.021	0.132216
TNGCTHWG	0.005806	0.58342
RRGRCRGR	0.009095	0.265196
GCGYKCGN	0.115472	0.009763
CGMRCGCV	-0.13168	0.009819
RSDYRGTG	0.013772	0.127386
GYMCTNBG	0.01683	0.055736
AAMYAYBR	-0.00362	0.679905
GGVVRWGG	0.000316	0.967446
ARYBAATB	0.007057	0.523718
ACWVAGMW	0.003306	0.705764
TTKTTTTS	-0.03302	0.062233
TNACYMWG	-0.01257	0.158219
AMCTYWGN	-0.00054	0.952723
ANCRAHGV	0.018453	0.040805

Table S3. Independent variables obtained when constructing a multiple regression model to assess the dependence of the *ln(PS)* value in the ChIP-Seq experiment with the Sp1 transcription factor on the presence of IUPAC motifs in these peaks. Multiple regression coefficients were calculated using the Statistica system (Statsoft™, Tulsa, USA).

Independent variable	**The value of the regression coefficient**	**p - value**
RCSAATSR	-0.03968	0.149248
ATTSGHYR	0.06863	0.009941
RRCSAATS	-0.07458	0.021391
GRGGYGGG	-0.00775	0.635139
GGGYGGGG	-0.03714	0.052744
WTGTAGTY	0.0723	0.072885
TGTAGTYY	0.25583	0
CSAATSRV	0.141722	0
GGCGGGRC	-0.02481	0.298582
TACAWNTC	-0.10395	0.031145
RKGGGYGG	0.004386	0.762046
ANWTGTAG	0.155459	0.000388
ACAWNTCC	-0.00684	0.845511
TBYBATTG	0.05046	0.00207
GGGANWTG	0.147136	0

TTGGYTRN	0.025576	0.139164
RCWTMCKG	0.018955	0.303513
GCGGGRCB	-0.02321	0.306679
CGSAHGYG	-0.01685	0.31289
AWYTCCCA	0.007676	0.782633
GCGCABGC	0.029531	0.178375
AATBARMD	-0.01655	0.225488
WGGGYGGG	0.042234	0.038834
WRGGGGYG	0.002944	0.852301
GGARGBGG	0.014922	0.23332
TKCYGGGW	0.051412	0.00338
CTTCCKGB	-0.04694	0.011891
RGGCGGGH	0.050394	0.001738
ATTSGYYY	0.076936	0.00512
AABATGGC	0.043041	0.320513
TATTGGHY	0.172836	0.000022
GGGHSGWG	-0.02572	0.047439
TRCGCAYG	-0.05127	0.104776
RTGACGTM	-0.02342	0.553568
TTCCKRTY	0.008231	0.68229
GGGAGGGG	-0.04261	0.127127
TGWCGTMA	-0.00789	0.86545
CGGKRCBD	0.029378	0.019498
RCSAATAG	-0.02511	0.61291
ACGWCAYB	-0.00523	0.871806
GGCSGWRC	-0.01065	0.5993
GGGGAGGG	-0.02574	0.33396
GKAAGTRH	-0.00409	0.833201
WHTCCCAG	0.008707	0.67101
ATKCTGGG	-0.01669	0.657205
CSAATAGV	0.020195	0.642444
RGTGGGBG	-0.02822	0.097165
GCAVGCGC	0.025662	0.302115
GADSGMGG	0.025278	0.051817
TCSRCCCC	-0.01803	0.424184
KGGGCGTG	0.001341	0.964425
RABBGACR	0.075836	0
TCYRGGWH	0.005942	0.660425
CAMTCAVS	-0.03009	0.102829
GGGCGTGG	-0.05943	0.169547
TRATTSGA	0.01216	0.785801
GATTSGAY	-0.03686	0.437022

AGGNNGGG	-0.01015	0.365549
AHDCRMAB	0.004712	0.53238
DACTTCCG	0.003082	0.903334
TTGGTCNR	0.079731	0.000773
TAGTYYWH	0.050178	0.015284
TSGMTRHB	-0.0117	0.299792
TTTRHWTW	-0.03734	0.037889
WKCAAAKN	-0.04326	0.004714
GGWGGGGH	-0.02704	0.124095
ATGGCRRC	-0.01606	0.556384
CCATSTTK	-0.02915	0.444397
GTCAYGTG	-0.09834	0.001426
TGANTGAC	0.134395	0.000061
AVHGAYAR	-0.04384	0.001981
GGCGTGGY	-0.00237	0.94732
ABATGGCG	-0.0142	0.753224
GCSGWGCB	0.029308	0.078454
AYGATTSG	0.242444	0
GGATTSGH	0.121602	0.000005
ACGSAHGY	0.053019	0.026689
GVATKCTG	0.058493	0.038876
AGATAAGV	-0.12972	0.000021
CGCAGGCG	-0.0377	0.310418

Table S4. Independent variables obtained when constructing a multiple regression model to assess the dependence of the ln(PS) value in the ChIP-Seq experiment with the FoxA2 transcription factor on the presence of the most significant ($P_{Bonf}(n,N) < 10^{-30}$) target IUPAC motifs. Multiple regression coefficients were calculated using Statistica (Statsoft™, Tulsa, USA).

Independent variable	The value of the regression coefficient	p - value
TRTWKACH	0.055717	0.000001
RTTKACHY	0.027913	0.02056
TMAAYANS	0.047318	0.000001
TWKACHYW	0.019684	0.04549
TTKRTYTW	-0.02034	0.046044
TKAHYTWK	-0.00736	0.313546
TRTTKRTY	0.025064	0.063592
RAAYHAAY	-0.02213	0.050214
TTRNGHAA	0.004312	0.643176
KACDTWGN	0.020031	0.035274
TAAHYABW	-0.03625	0.000121
ARMYAAGV	0.019283	0.037902
TGYGTACH	0.015768	0.493004

TRTWTGCW	0.018187	0.258766
AAAMAAAR	-0.00935	0.024866
ATMMAYAN	-0.01295	0.267248
WTRTTTGY	-0.01487	0.272732
TCRAYADW	0.003956	0.751831
GTACRCAH	-0.00138	0.965276
TTYGCTYW	0.015228	0.362641
TNGCTHWG	0.006644	0.521259
TNACYMWG	-0.01242	0.160252

Estimation of the binomial probability to observe a motif in at least n of N sequences of the analyzed set for random reasons

The value of $P_{Bonf}(n,N)$ was calculated as follows. Consider a motif **M** = m_1, m_2, .., m_k of length *k* written in the 15-letter IUPAC code. The probability of observing the motif **M** at a certain position of a DNA sequence can be estimated based on a Markov chain of order *r*:

$$P(M)=\frac{P(m_1,m_{r+1})P(m_2,m_{r+2})..P(m_{k-r},m_k)}{P(m_2,m_{r+1})P(m_3,m_{r+2})..P(m_{k-r},m_{k-1})}$$

$P(m_i,m_{i+r})$ is the frequency of occurrence of the motif m_i, m_{i+1}, .., m_{i+r} in the set **Pos**. Alternatively, *P(M)* can be calculated assuming equal frequencies of the mononucleotide "background" context ($P_A = P_T = P_G = P_C = 0.25$).

Then, the probability *p* that a motif of length *k* occurs in a DNA sequence of length *L* at least once is

$$p=1-e^{-(L-k+1)*P(M)}$$

It may be noted that *Q* - expected representation of the motif in the **Pos** set is equal to *p*.

The statistical significance of observing the motif in at least *n* out of *N* sequences in the set Pos can be estimated by using the binomial criterion as

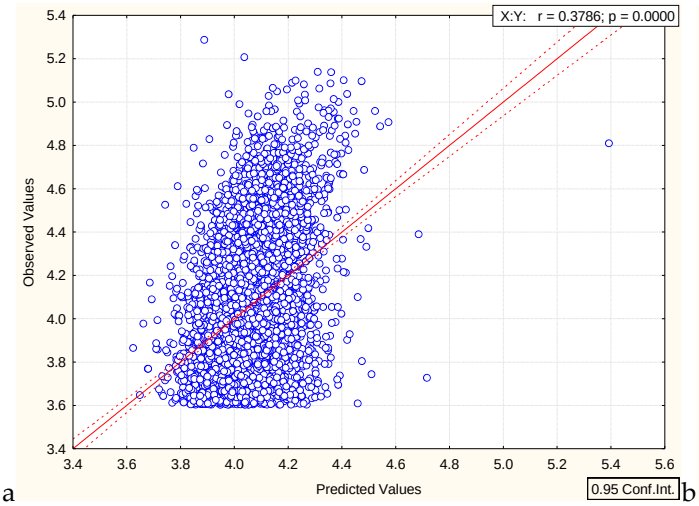
$$P_{one}(n,N)=\sum_{i=n}^{N}C_N^i p^i(1-p)^{N-i}$$

Because the number of motifs being tested for significance is large, we use the Bonferroni correction for multiple comparisons.

$$P_{Bonf}(n,N)=P_{one}(n,N)*15^k$$

Assessment of the dependence of ChIP-seq peak scores in experiments with nine transcription factors on the presence of significant IUPAC motifs in their ChIP-seq peaks

CEBPA



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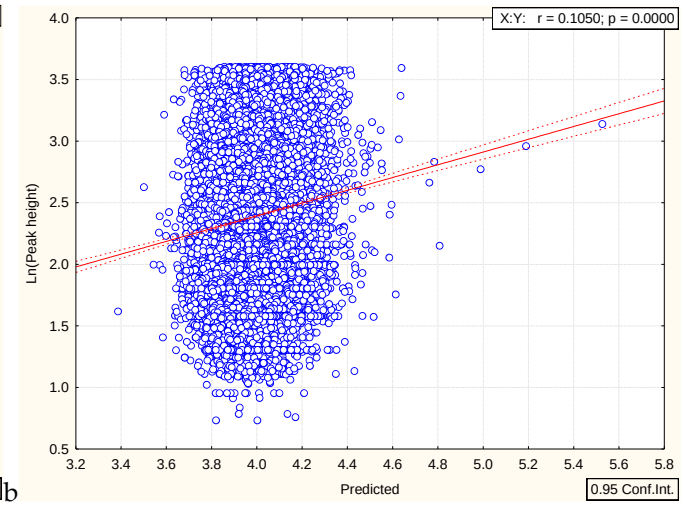

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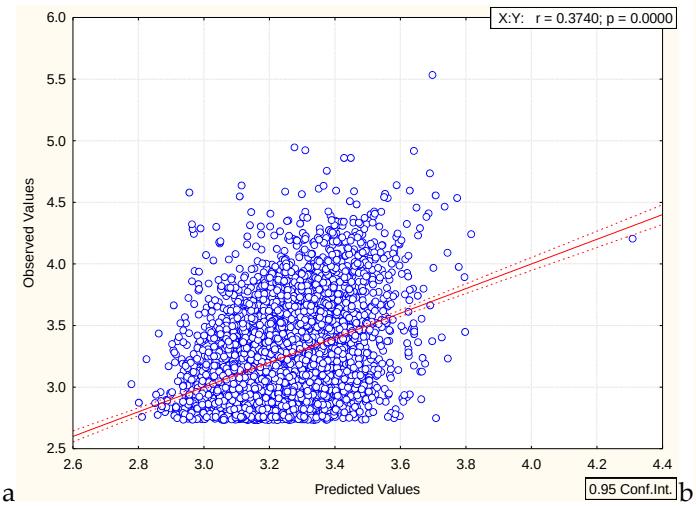

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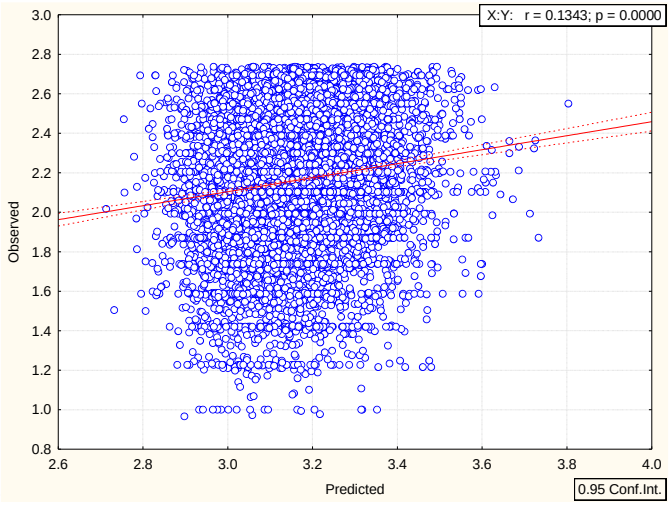

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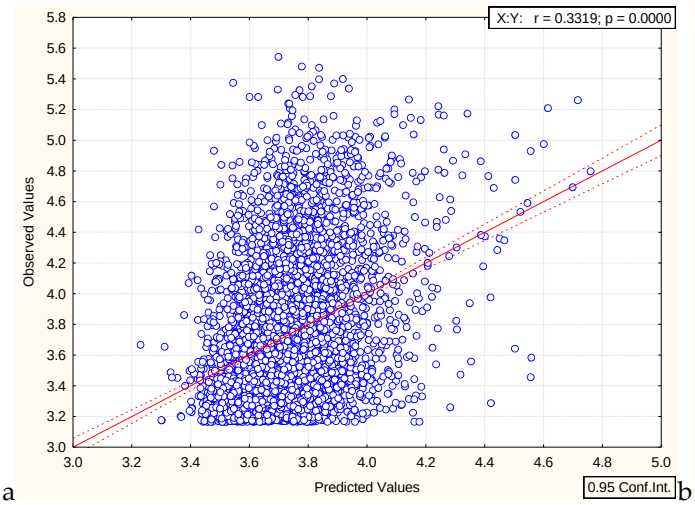
NFE2L2



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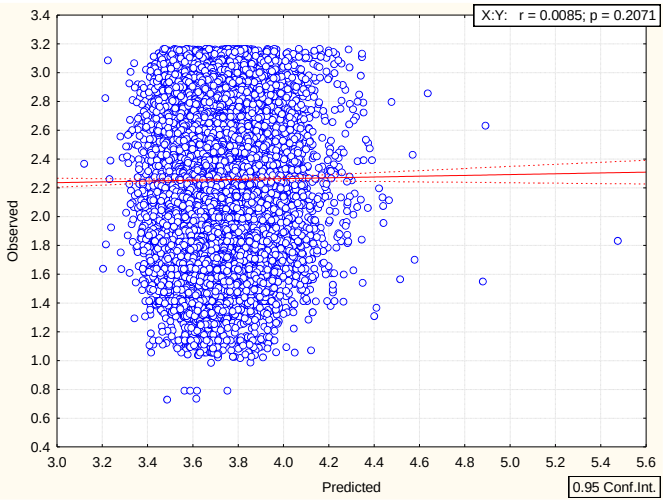
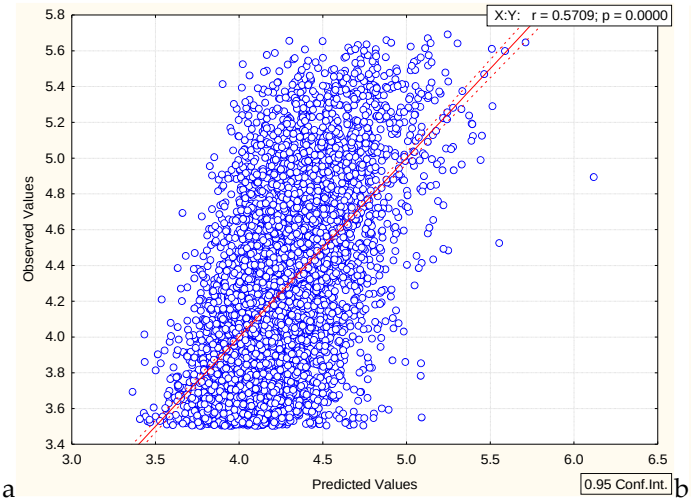


b

SP1



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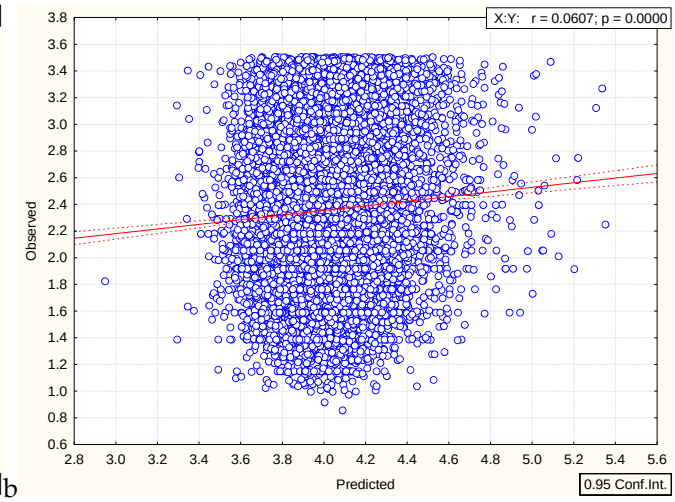

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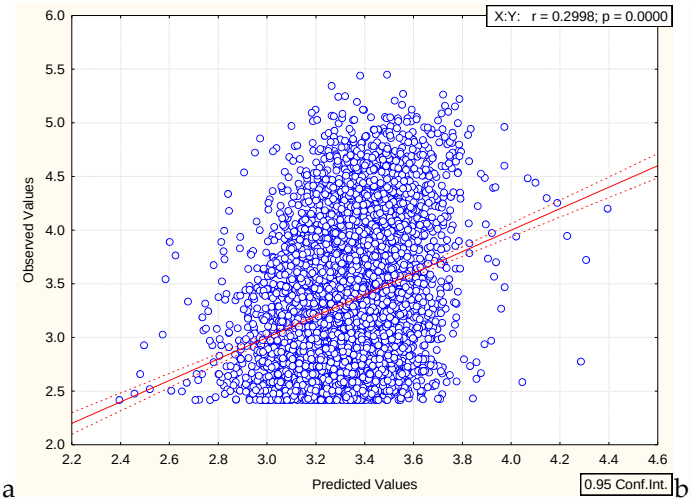
GATA1



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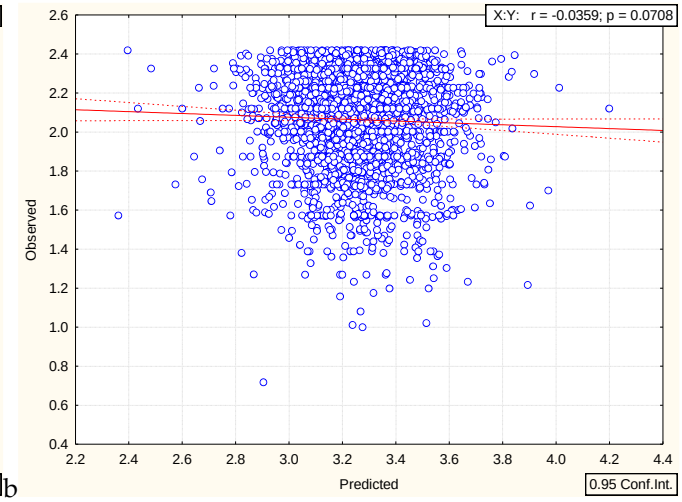
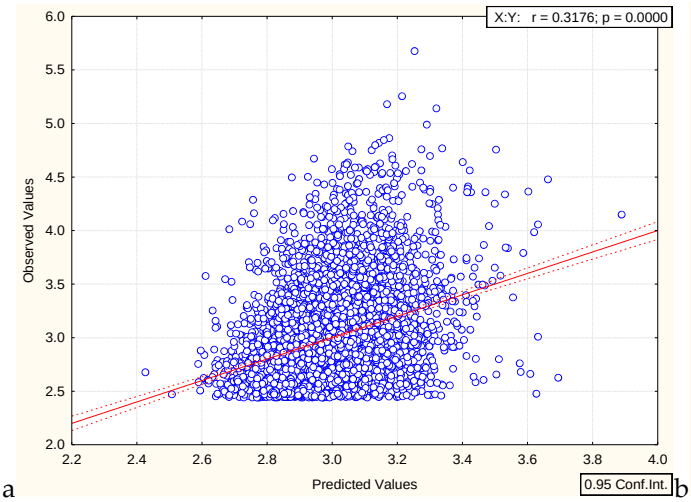


b

FOXO1



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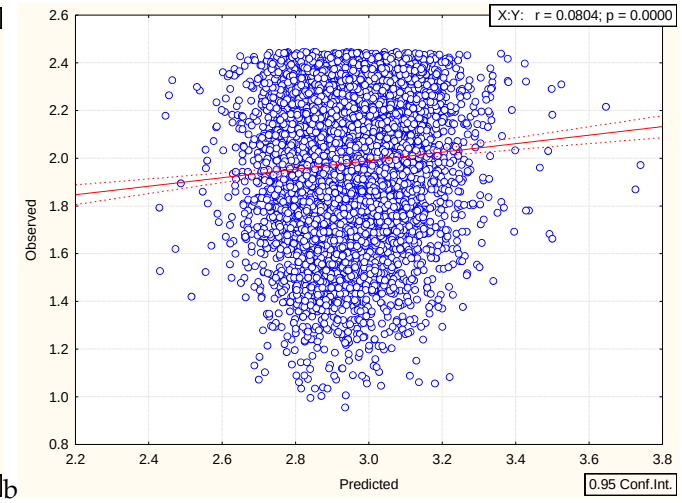

b

NFYA

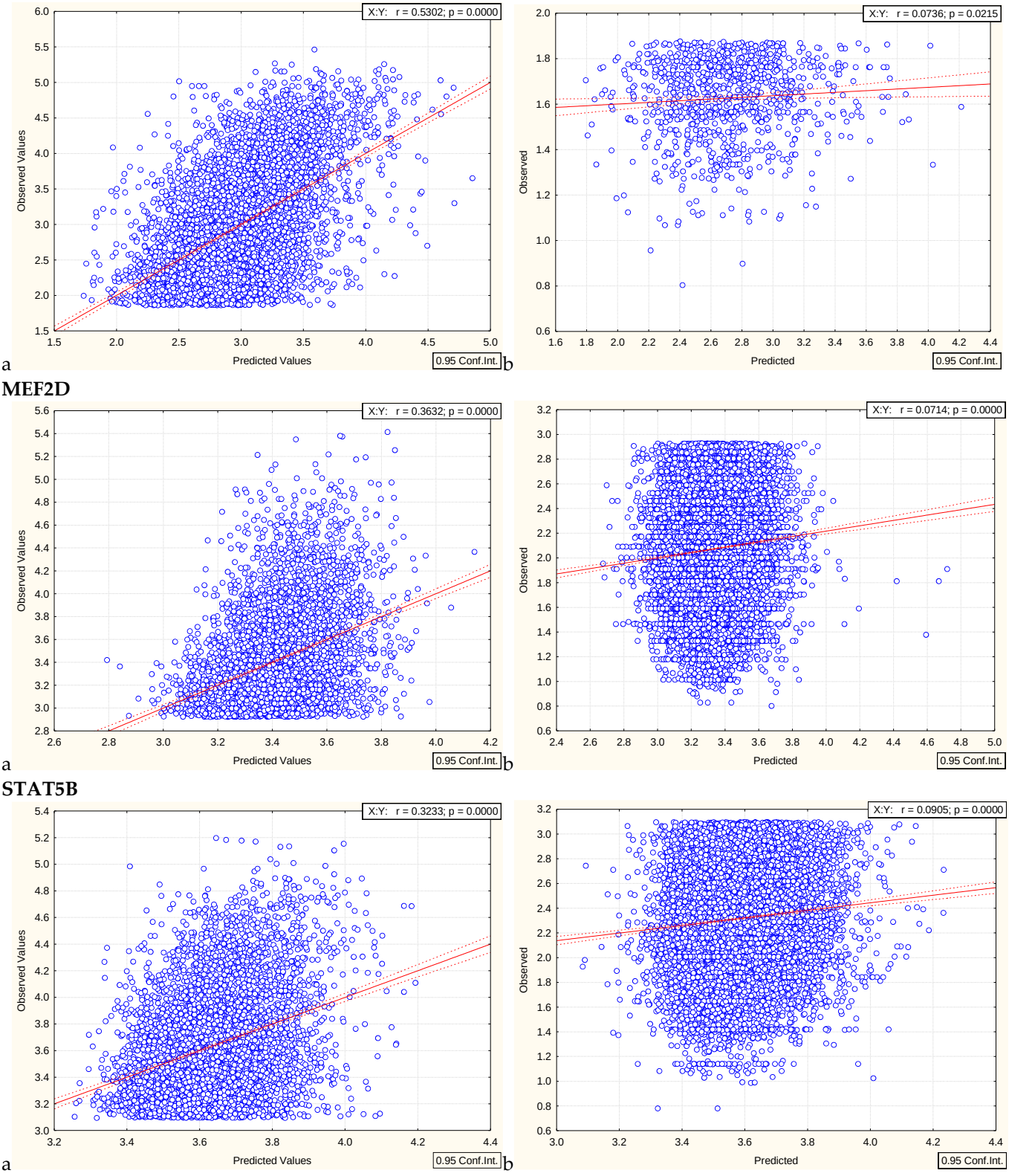

Figure S1. Dependence of the observed values of $ln(PS)_{Obs}$ for ChIP-seq peak sequences in the training (a) and control (b) sets on their expected value in experiments with nine transcription factors. Solid and dashed lines represent the regression line and the bounds of its 95% confidence interval as calculated using STATISTICA (StatSoft™, Tulsa, USA). *r* is the linear correlation coefficient and *p* is its statistical significance.

Estimation of the influence of the boundary value q_0 on the number of IUPAC motifs considered

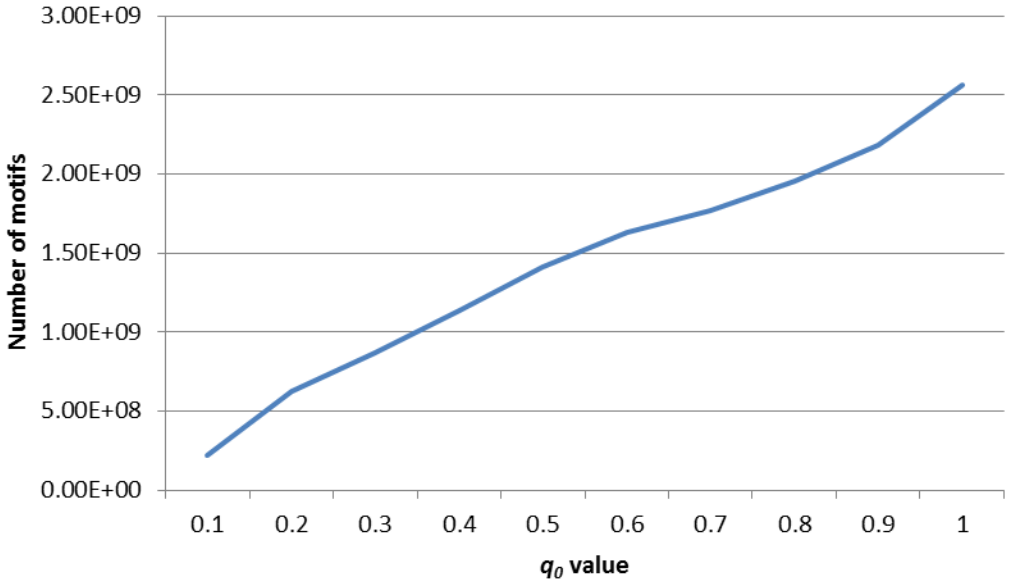

Figure S2. The dependence of the number of the motifs being considered (*y*-axis) on the boundary value q_0, the occurrence of the motifs by chance (*x*-axis). The search was carried out in a set of 1000 randomly generated 200-bp DNA sequences.