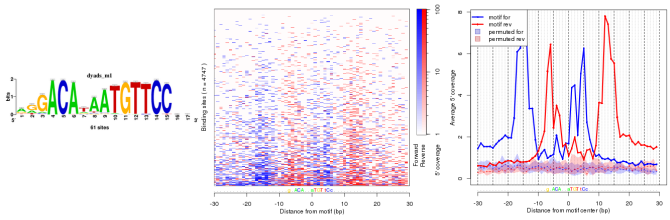
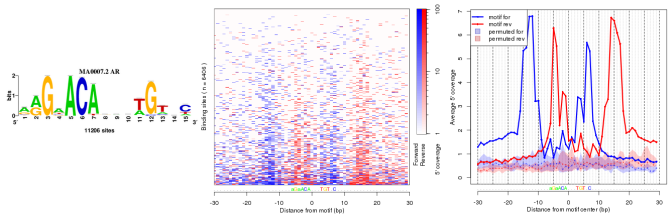
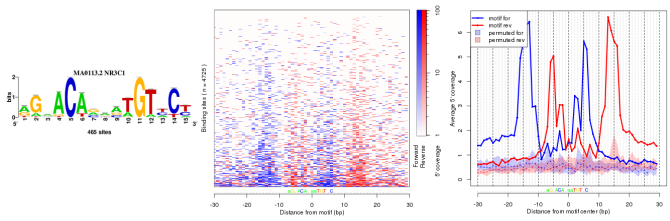
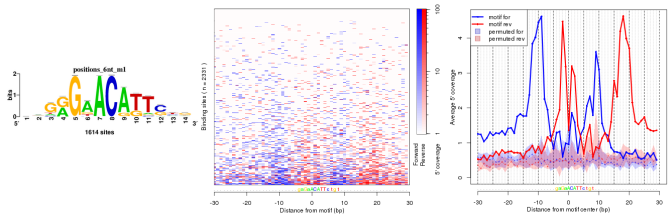
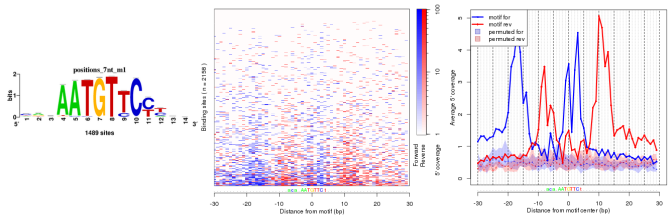
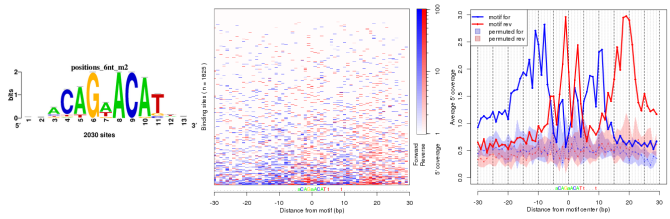
Supplementary data 2

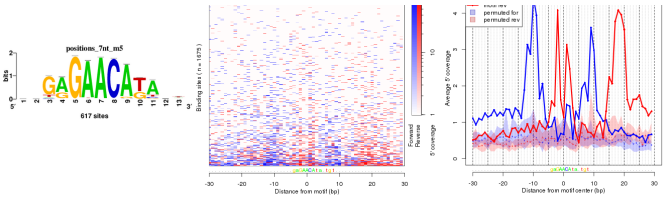
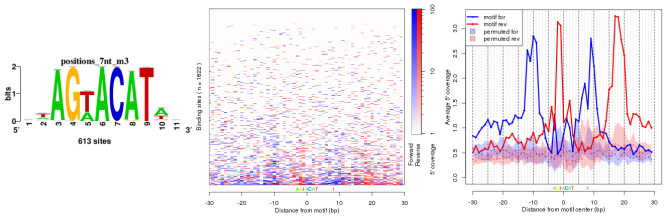
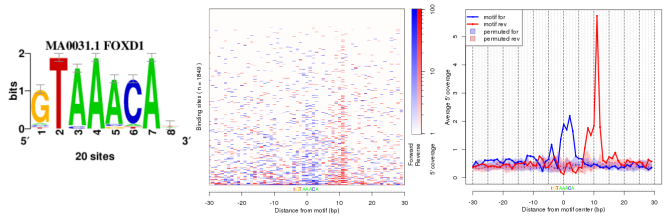
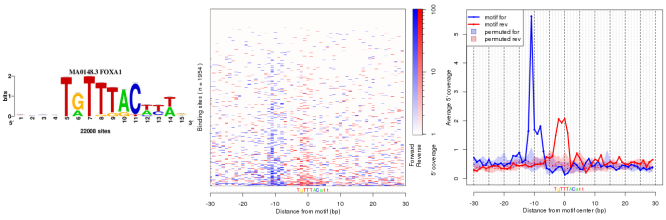
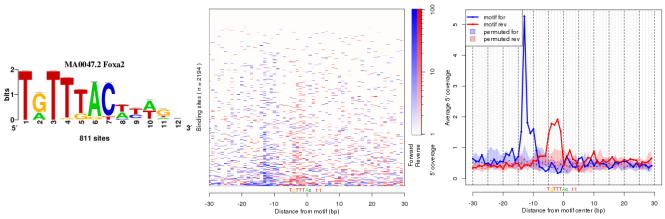
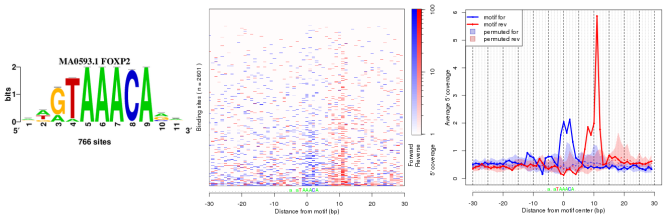
Starick, Ibn-Salem, Jurk et al *ChIP-exo signal associated with DNA-binding motifs provide insights into the genomic binding of the glucocorticoid receptor and cooperating transcription factors.*

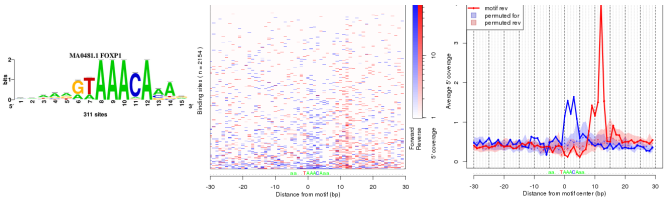
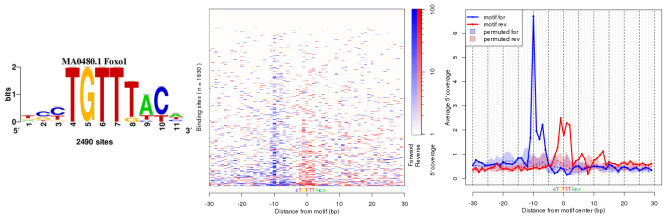
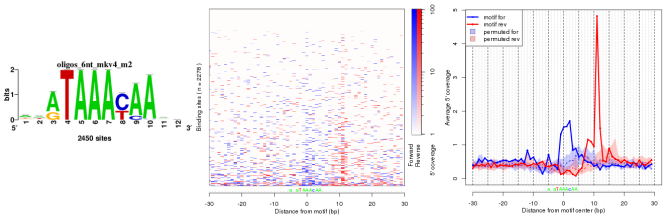
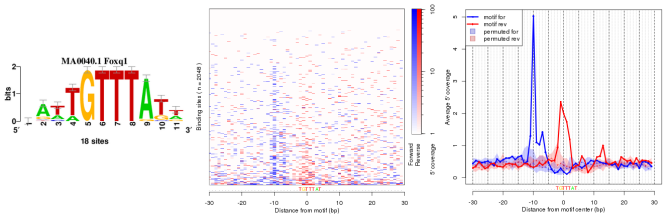
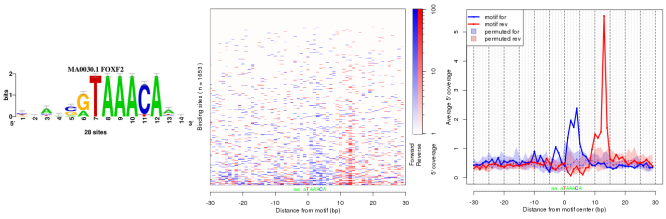
Table presenting the profiles obtained with ExoProfiler in IMR90 cell line.

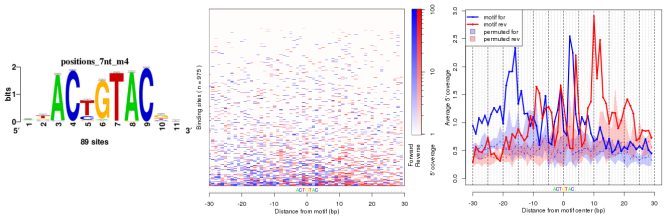
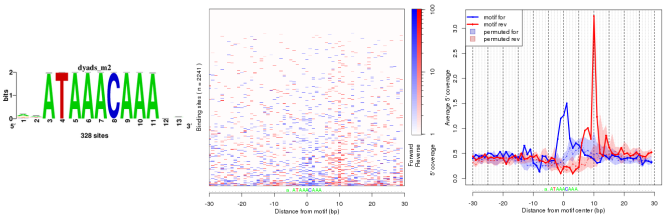
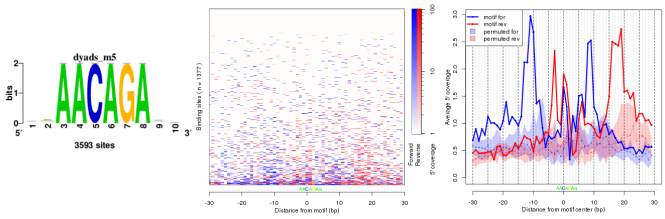
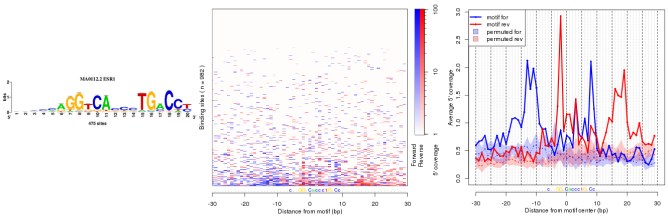
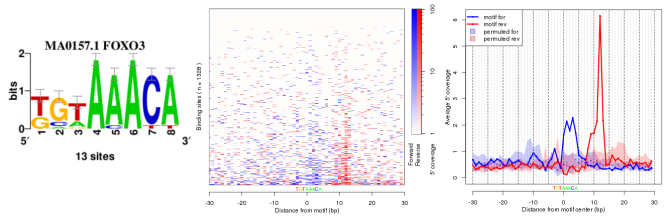
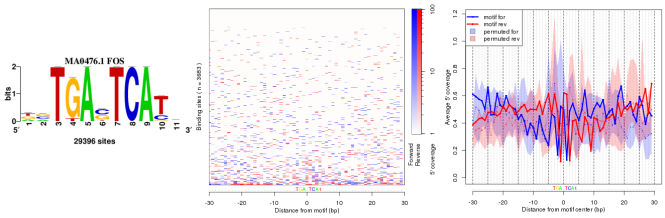
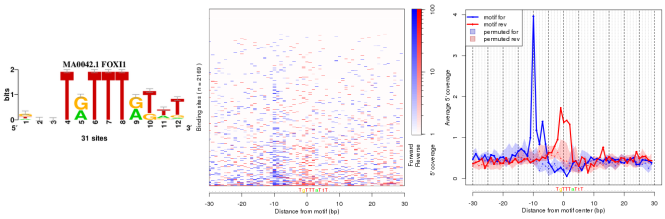
Here, ChIP-seq peaks were limited to ±30 bp around the peak summit. The motifs were obtained from JASPAR vertebrates only or discovered for this peak dataset with the program RSAT *peak-motifs*.
The table displays the profiles for all motifs; the following information are indicated: the provenance (JASPAR ID or de novo) and its name (from JASPAR, or for de novo motifs: name of the most similar motif within JASPAR, similarity values taken from *peak-motifs* result), the class and family of TF (information from JASPAR), motif logo, heatmap and profile, number of sites contributing to the profile, coverage p-value.

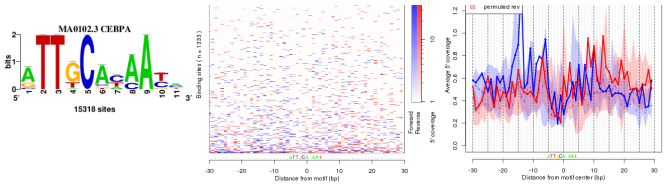
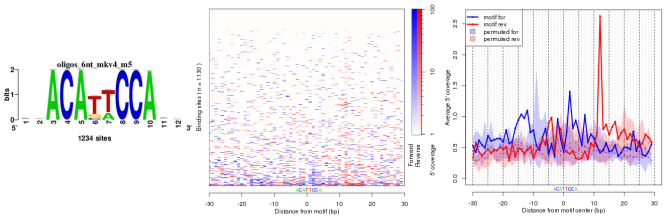
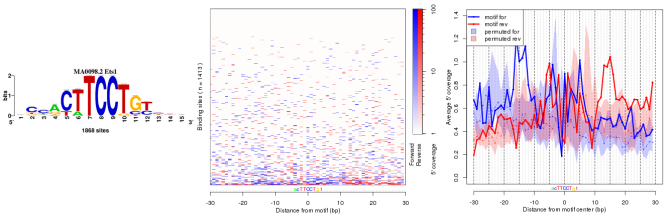
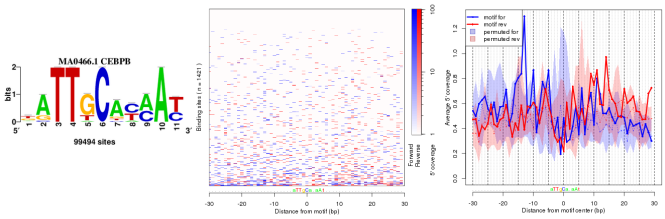
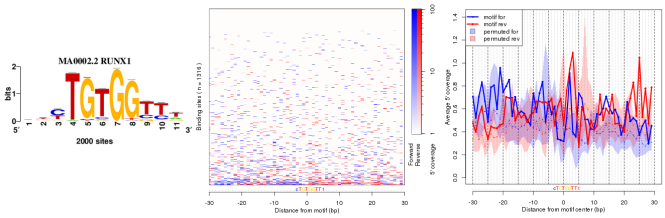
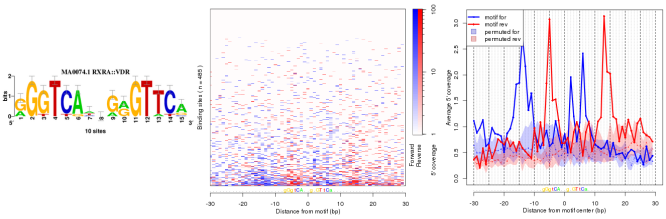
Table can be sorted by clicking on the column headers. For our analyses, this table was sorted on the coverage p-value (last column), lowest values first.

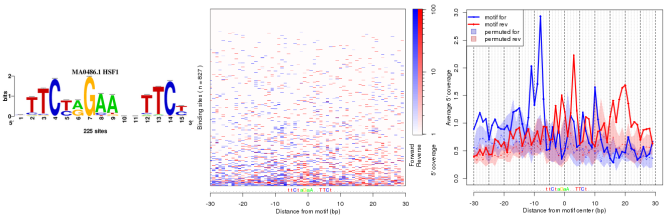
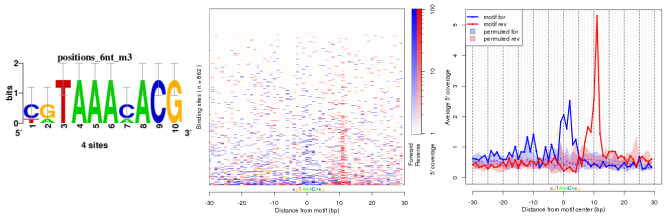
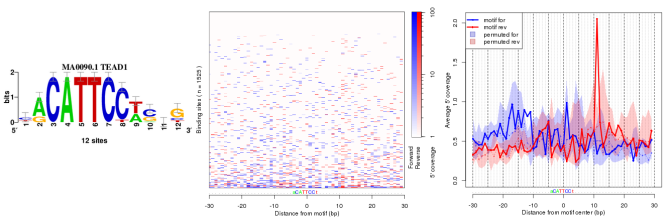
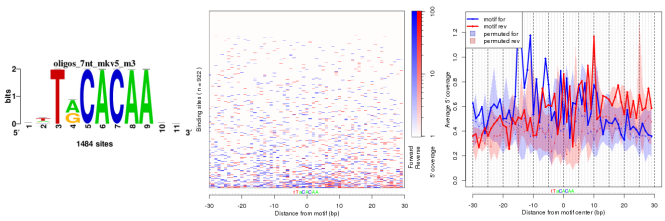
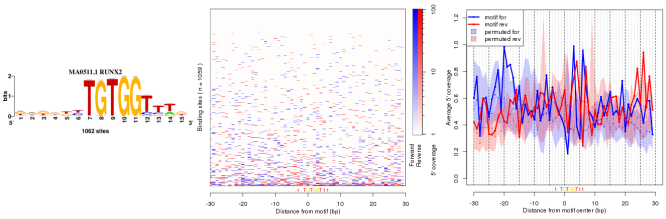
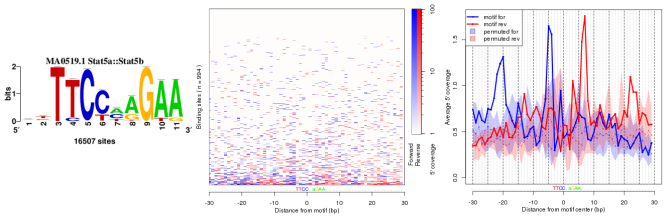
Factor/motif	Class	Family	Logo and exo-profile	Sites	Coverage p-value ▾
peaks-motifs de novo discovery **dyads_m1** Most similar motif in JASPAR: **NR3C1**	-	-		4747	0
MA0007.2 **AR**	Zinc-coordinating	Hormone-nuclear Receptor		6406	0
MA0113.2 **NR3C1**	Zinc-coordinating	Hormone-nuclear Receptor		5446	0
peaks-motifs de novo discovery **positions_6nt_m1** Most similar motif in JASPAR: **NR3C1**	-	-		2331	7.6484320503644e-153
peaks-motifs de novo discovery **positions_7nt_m1** Most similar motif in JASPAR: **NR3C1**	-	-		2158	3.51766965091321e-140
peaks-motifs de novo discovery **positions_6nt_m2** Most similar motif in JASPAR: **NR3C1**	-	-		1825	1.08207690980014e-84
					

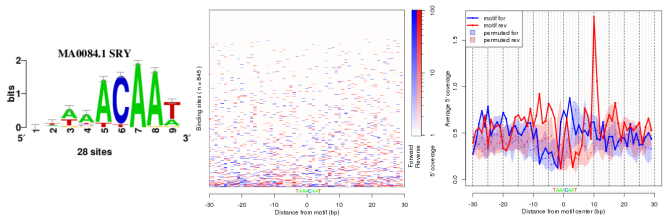
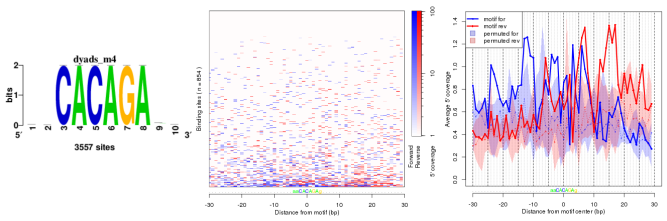
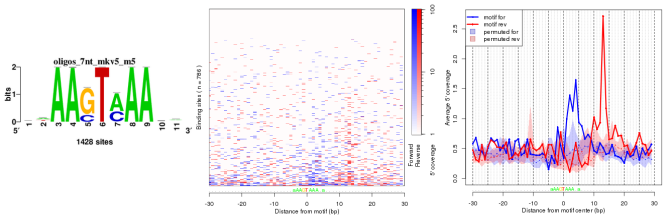
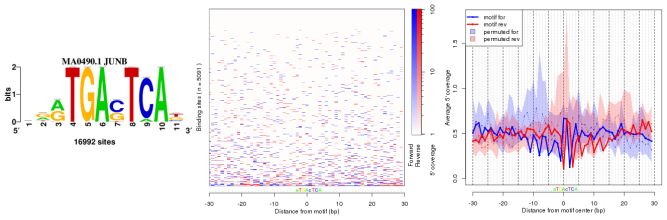
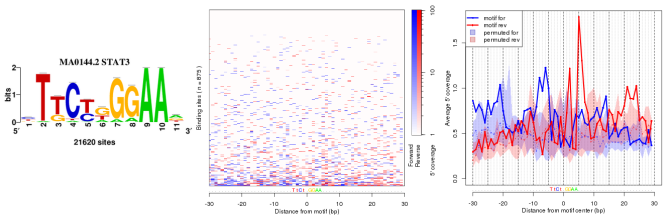
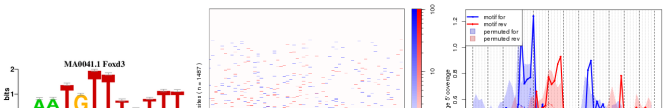
peaks-motifs de novo discovery **positions_7nt_m5** Most similar motif in JASPAR: **AR**	-	-		1675	2.03885290161182e-79
peaks-motifs de novo discovery **positions_7nt_m3** Most similar motif in JASPAR: **NR3C1**	-	-		1822	3.12451482639409e-77
MA0031.1 **FOXD1**	Winged Helix-Turn-Helix	Forkhead		1849	4.49121080362848e-46
MA0148.3 **FOXA1**	Winged Helix-Turn-Helix	Forkhead		1954	4.23150393132508e-44
MA0047.2 **Foxa2**	Winged Helix-Turn-Helix	Forkhead		2194	4.59197499137264e-41
MA0593.1 **FOXP2**	Winged Helix-Turn-Helix	Forkhead		2601	1.0560916695928e-40

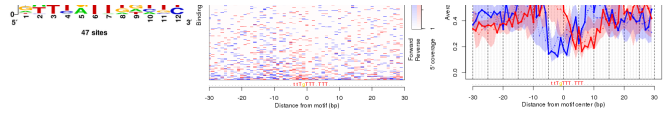
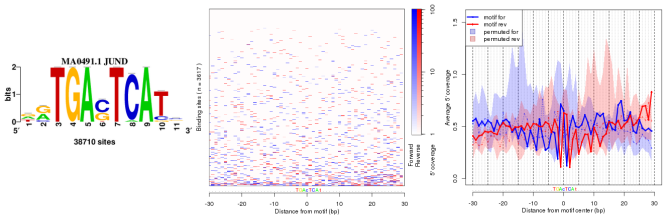
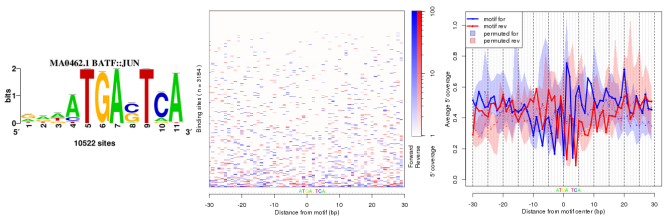
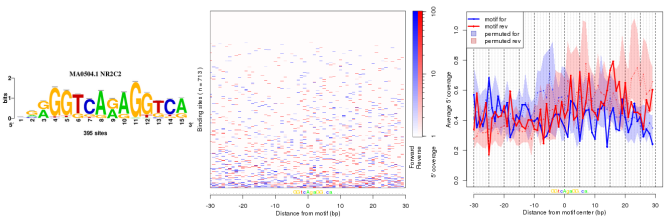
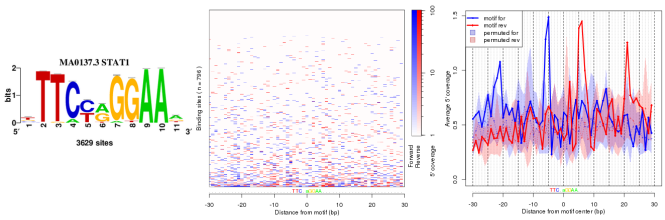
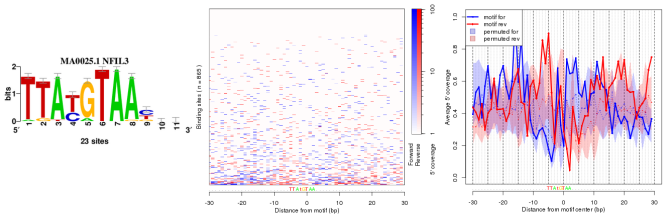
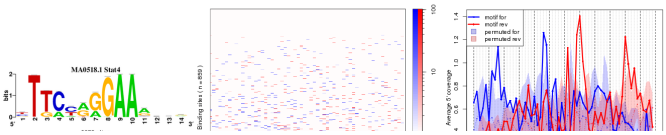
MA0481.1 **FOXP1**	Winged Helix-Turn-Helix	Forkhead		2154	3.99171738733038e-38
MA0480.1 **Foxo1**	Winged Helix-Turn-Helix	Forkhead		1630	2.57865464984525e-37
peaks-motifs de novo discovery **oligos_6nt_mkv4_m2** Most similar motif in JASPAR: **FOXP1**	-	-		2278	1.22386621222197e-33
MA0040.1 **Foxq1**	Winged Helix-Turn-Helix	Forkhead		2048	2.43935496405333e-32
MA0030.1 **FOXF2**	Winged Helix-Turn-Helix	Forkhead		1653	4.63705298388167e-29
peaks-motifs de novo discovery					

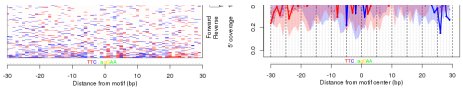
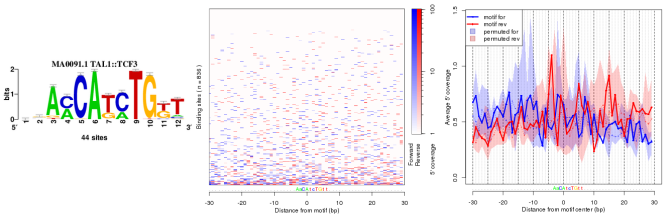
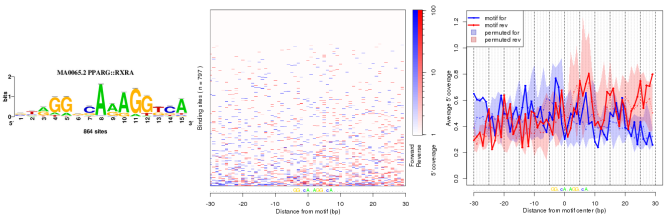
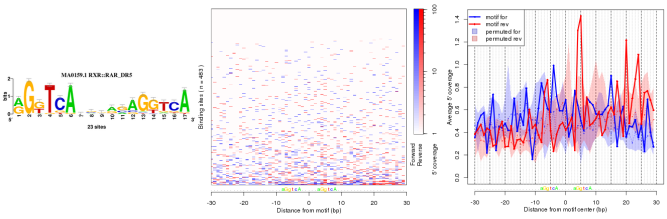
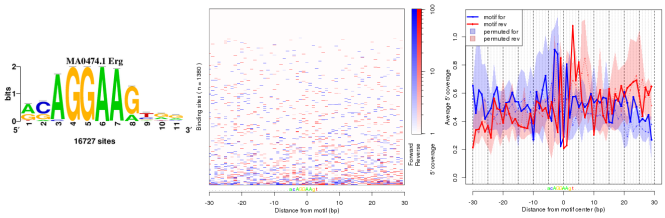
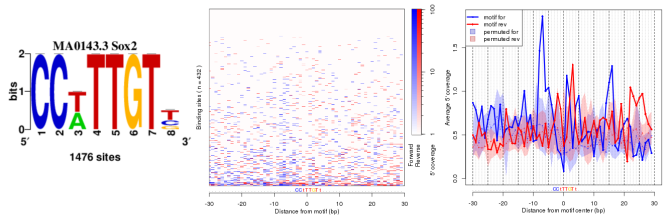
positions_7nt_m4 Most similar motif in JASPAR: **no match**	-	-		975	7.78453602586915e-28
peaks-motifs de novo discovery **dyads_m2** Most similar motif in JASPAR: **FOXP1**	-	-		2241	3.49587115619 83e-27
peaks-motifs de novo discovery **dyads_m5** Most similar motif in JASPAR: **FOXO3**	-	-		1377	1.07937586662635e-23
MA0112.2 **ESR1**	Zinc-coordinating	Hormone-nuclear Receptor		995	1.58989155855649e-21
MA0157.1 **FOXO3**	Winged Helix-Turn-Helix	Forkhead		1328	1.18056872694808e-19
MA0476.1 **FOS**	Zipper-Type	Leucine-Zipper		4781	7.48361482735651e-17
MA0042.1 **FOXI1**	Winged Helix-Turn-Helix	Forkhead		2169	1.32378885419659e-16
					

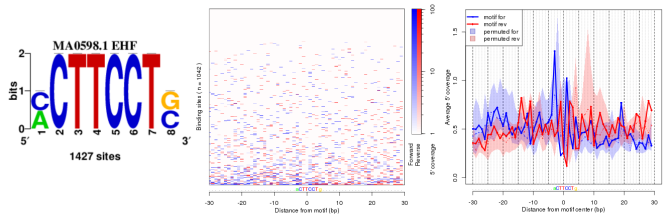
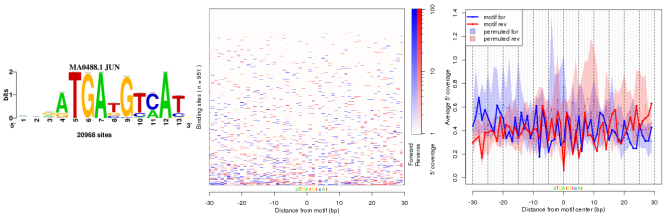
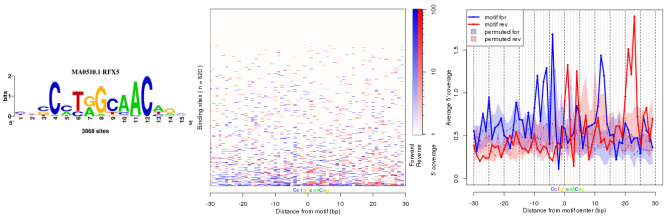
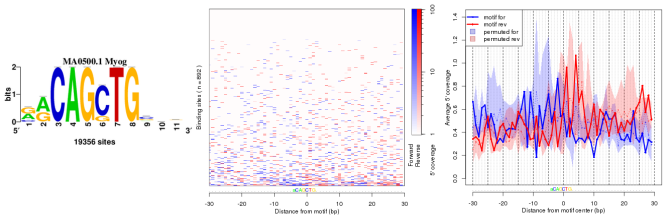
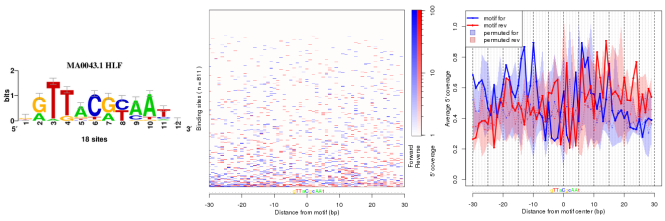
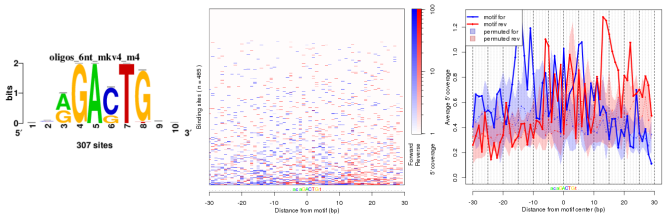
MA0102.3 **CEBPA**	Zipper-Type	Leucine Zipper		1333	1.82047788387476e-16
peaks-motifs de novo discovery **oligos_6nt_mkv4_m5** Most similar motif in JASPAR: **TEAD1**	-	-		1130	1.09549433426823e-15
MA0098.2 **Ets1**	Winged Helix-Turn-Helix	Ets		1413	2.41392734793751e-14
MA0466.1 **CEBPB**	Zipper-Type	Leucine-Zipper		1421	1.69831565425716e-13
MA0002.2 **RUNX1**	Ig-fold	Runt		1316	8.93179154000296e-13
MA0074.1 **RXRA::VDR**	Zinc-coordinating	Hormone-nuclear Receptor		485	2.8222672462489e-11

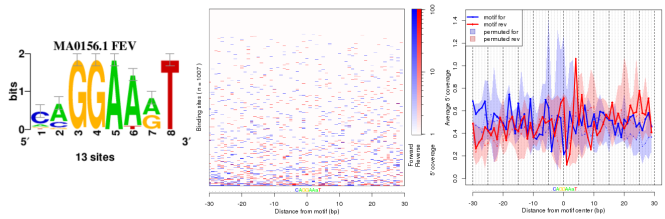
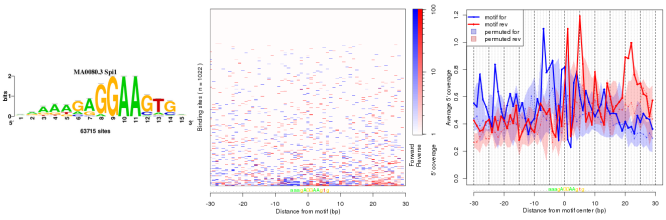
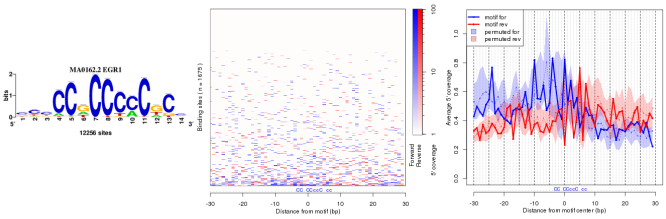
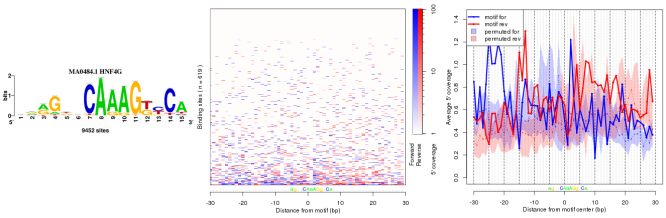
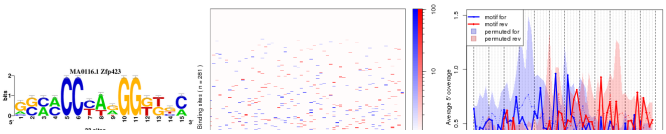
MA0486.1 **HSF1**	Winged Helix-Turn-Helix	HSF		827	4.19949736616783e-11
peaks-motifs de novo discovery **positions_6nt_m3** Most similar motif in JASPAR: **FOXO3**	-	-		864	6.00817485313302e-11
MA0090.1 **TEAD1**	Helix-Turn-Helix	Homeo		1525	4.42370836416079e-10
peaks-motifs de novo discovery **oligos_7nt_mkv5_m3** Most similar motif in JASPAR: **CEBPA**	-	-		922	9.13676637209637e-10
MA0511.1 **RUNX2**	Other	Runt		1059	1.34664982128199e-09
MA0519.1 **Stat5a::Stat5b**	Other	STAT		994	1.18243949876918e-08

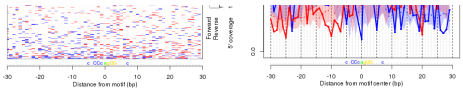
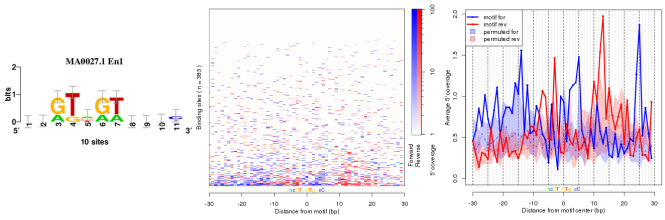
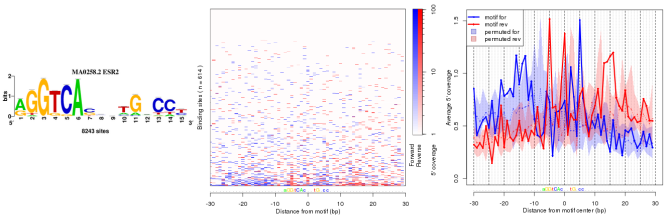
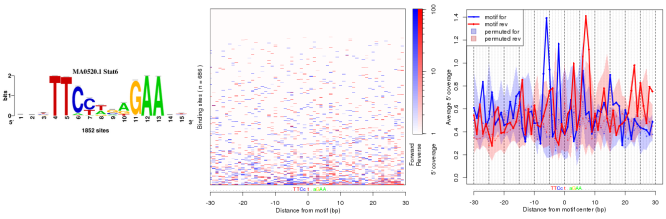
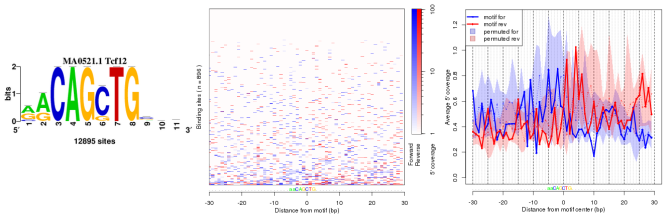
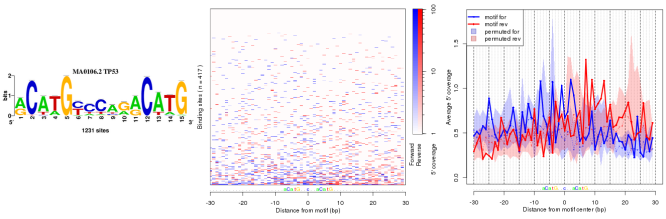
MA0084.1 **SRY**	Other Alpha-Helix	High Mobility Group box (HMG)		845	1.38914048905346e-08
peaks-motifs de novo discovery **dyads_m4** Most similar motif in JASPAR: **RUNX1**	-	-		854	2.32932876433485e-07
peaks-motifs de novo discovery **oligos_7nt_mkv5_m5** Most similar motif in JASPAR: **FOXD1**	-	-		786	2.50831244075935e-07
MA0490.1 **JUNB**	Zipper-Type	Leucine-Zipper		5091	3.6665521542343e-07
MA0144.2 **STAT3**	Ig-fold	Stat		971	4.23241334622616e-07
MA0041.1	Winged Helix-Turn-	Forkhead		1487	8.09679418205736e-07

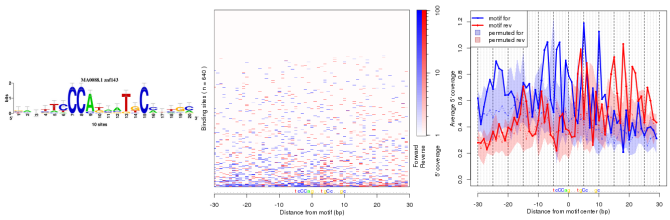
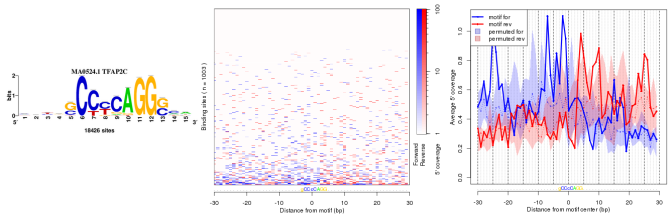
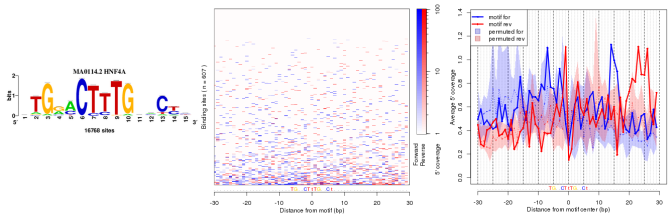
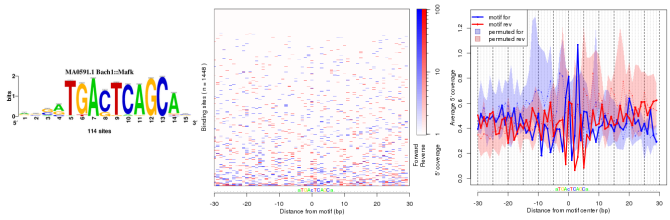
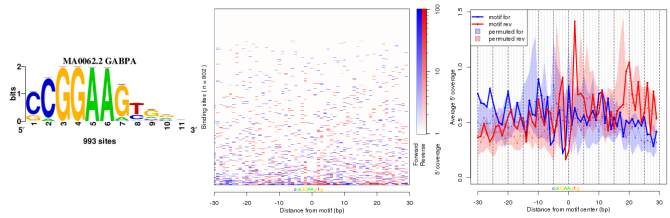
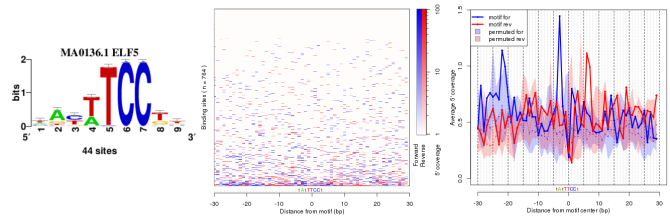
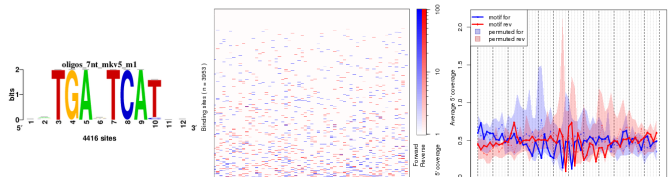
Foxd3	Helix				
MA0491.1 **JUND**	Zipper-Type	Leucine-Zipper		5257	9.45617251321679e-07
MA0462.1 **BATF::JUN**	Zipper-Type	Leucine-Zipper		3184	4.56203850255607e-06
MA0504.1 **NR2C2**	Zinc-coordinating	Hormone-nuclear Receptor		713	5.78695776146218e-06
MA0137.3 **STAT1**	Ig-fold	Stat		990	6.39253273924696e-06
MA0025.1 **NFIL3**	Zipper-Type	Leucine Zipper		865	1.19282211535992e-05
MA0518.1 **Stat4**	Other	STAT		859	3.9121430981811e-05

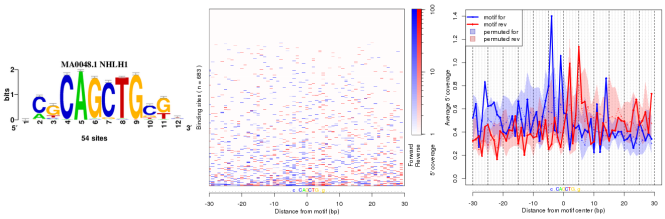
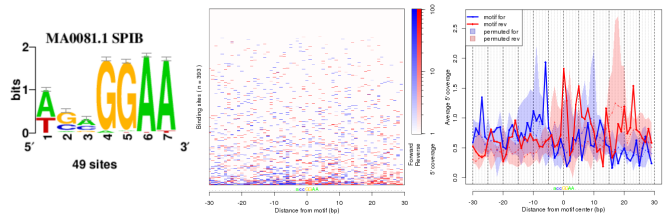
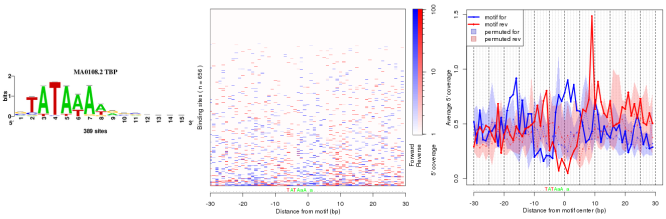
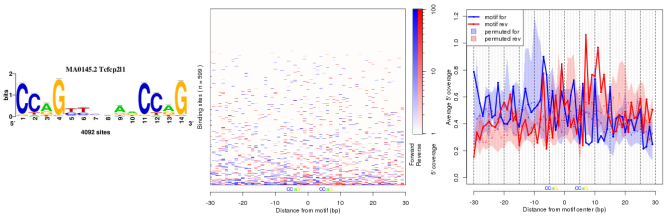
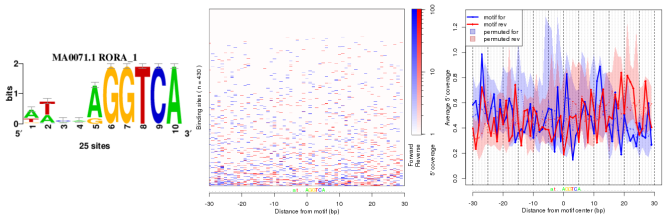
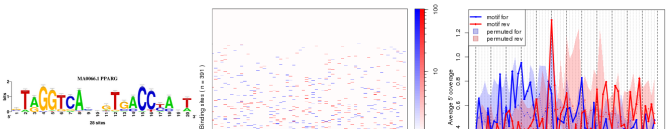
					
MA0091.1 **TAL1::TCF3**	Zipper-Type	Helix-Loop-Helix		836	8.61319069330976e-05
MA0065.2 **PPARG::RXRA**	Zinc-coordinating	Hormone-nuclear Receptor		797	0.00018832778358369
MA0159.1 **RXR::RAR_DR5**	Zinc-coordinating	Hormone-nuclear Receptor		483	0.000208374262875992
MA0474.1 **Erg**	Winged Helix-Turn-Helix	ETS		1380	0.000230007148981826
MA0143.3 **Sox2**	Other Alpha-Helix	High Mobility Group box (HMG)		432	0.000416155067541784

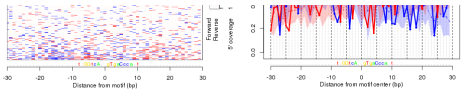
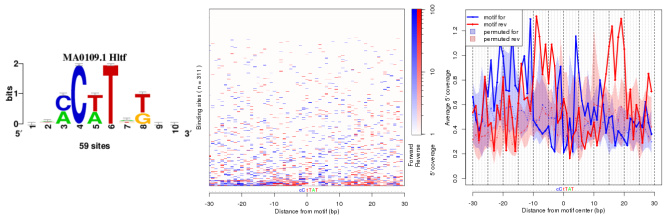
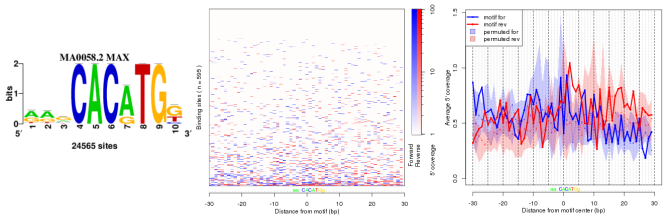
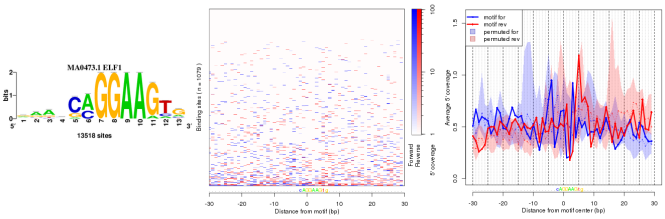
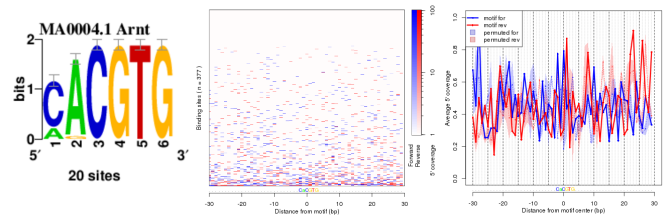
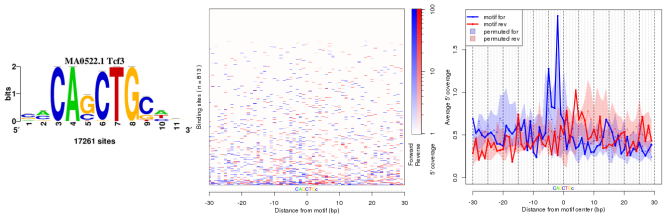
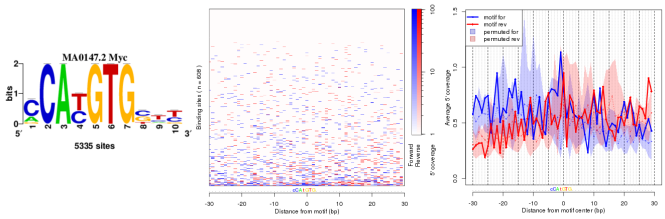
MA0598.1 **EHF**	Winged Helix-Turn-Helix	ETS		1042	0.000480306553380232
MA0488.1 **JUN**	Zipper-Type	Leucine-Zipper		951	0.000624662576451088
MA0510.1 **RFX5**	Winged Helix-Turn-Helix	RFX		620	0.00067970247027751
MA0500.1 **Myog**	Zipper-Type	Helix-Loop-Helix		892	0.000767168494416453
MA0043.1 **HLF**	Zipper-Type	Leucine Zipper		952	0.000823400659650455
peaks-motifs de novo discovery **oligos_6nt_mkv4_m4** Most similar motif in JASPAR: **no match**	-	-		485	0.00101766137890243

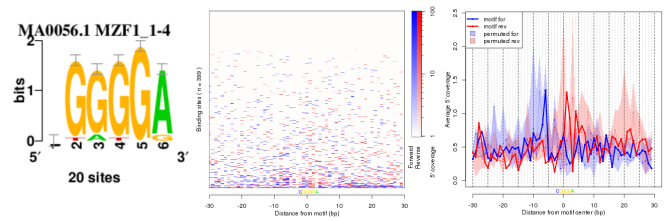
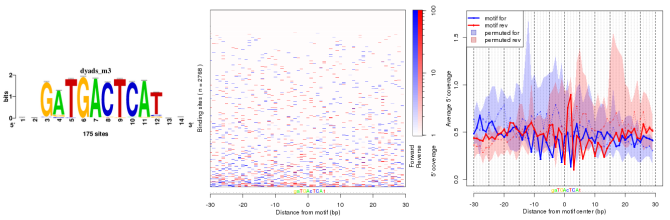
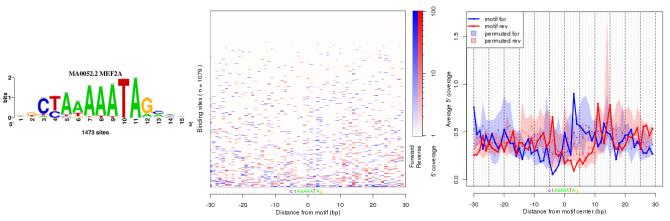
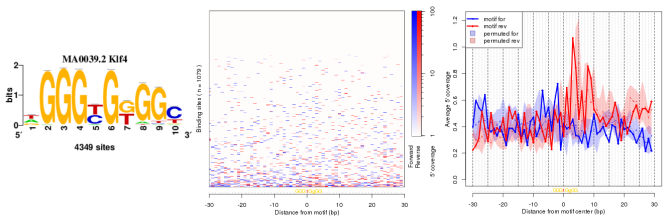
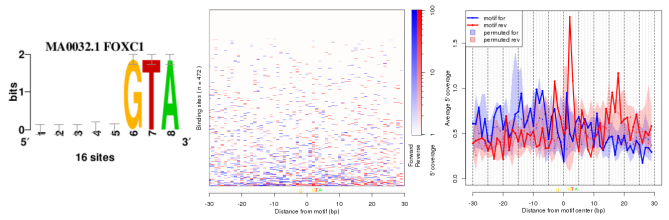
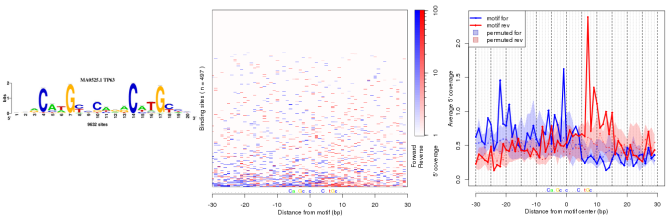
MA0156.1 **FEV**	Winged Helix-Turn-Helix	Ets		1007	0.00104345410857944
MA0080.3 **Spi1**	Winged Helix-Turn-Helix	Ets		1022	0.00127709428898886
MA0162.2 **EGR1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		1675	0.00155680570056084
MA0484.1 **HNF4G**	Zinc-coordinating	Hormone-nuclear Receptor		619	0.00214489153997349
					

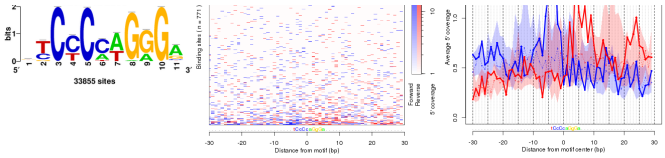
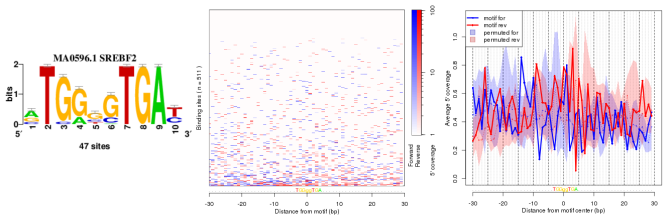
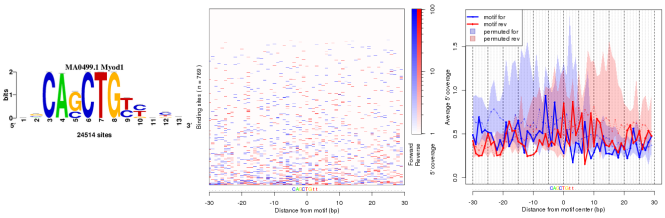
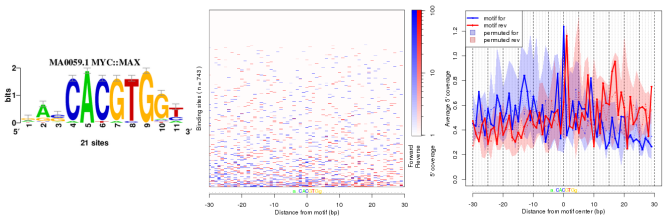
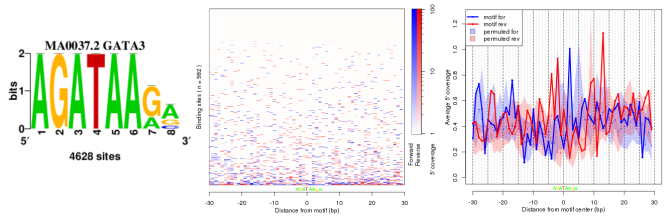
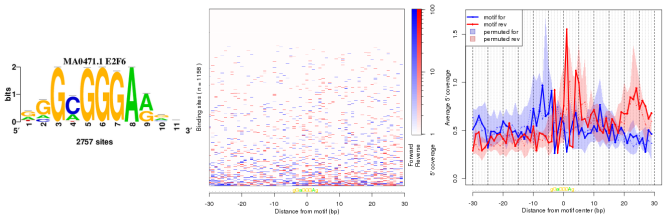
MA0116.1 **Zfp423**	Zinc-coordinating	BetaBetaAlpha-zinc finger		327	0.00231344393798243
MA0027.1 **En1**	Helix-Turn-Helix	Homeo		383	0.00248195909745266
MA0258.2 **ESR2**	Zinc-coordinating	Hormone-nuclear Receptor		682	0.00250579272770723
MA0520.1 **Stat6**	Other	STAT		686	0.00252942991239785
MA0521.1 **Tcf12**	Zipper-Type	Helix-Loop-Helix		896	0.00319389811577332
MA0106.2 **TP53**	Zinc-coordinating	Loop-Sheet-Helix		417	0.00352369089012948

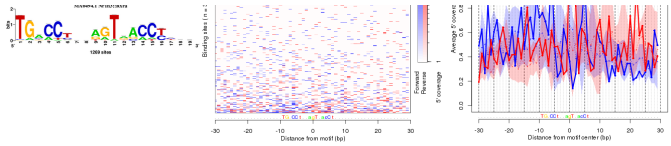
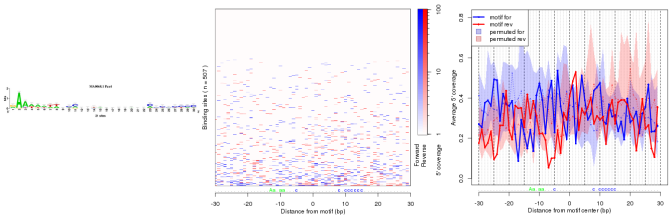
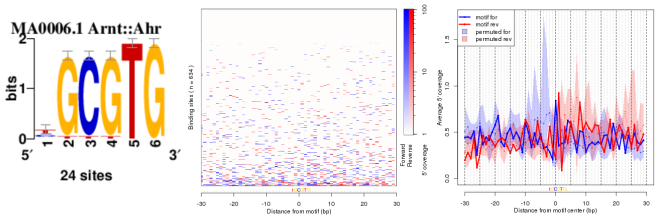
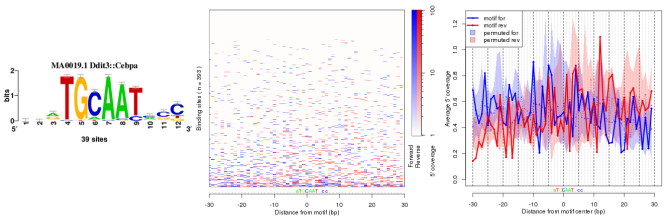
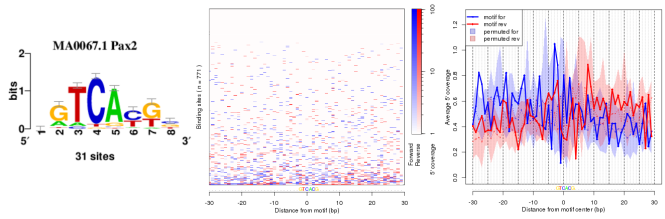
MA0088.1 **znf143**	Zinc-coordinating	BetaBetaAlpha-zinc finger		640	0.003984932888394
MA0524.1 **TFAP2C**	Zipper-Type	Helix-Loop-Helix		1003	0.00438767891428064
MA0114.2 **HNF4A**	Zinc-coordinating	Hormone-nuclear Receptor		607	0.00565504518682653
MA0591.1 **Bach1::Mafk**	Zipper-Type	Leucine-Zipper		1525	0.00570333950599349
MA0062.2 **GABPA**	Winged Helix-Turn-Helix	Ets		902	0.00685419043629559
MA0136.1 **ELF5**	Winged Helix-Turn-Helix	Ets		764	0.00803287309888239
peaks-motifs de novo discovery **oligos_7nt_mkv5_m1** Most similar motif in JASPAR: **FOS**	-	-		3953	0.0161926102625433

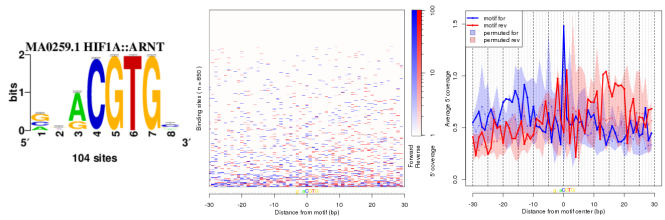
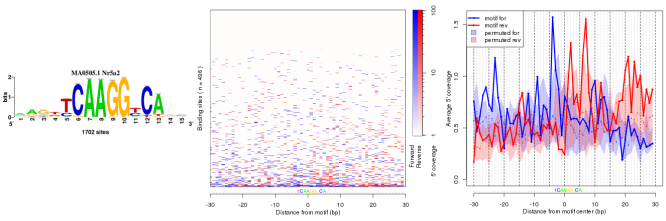
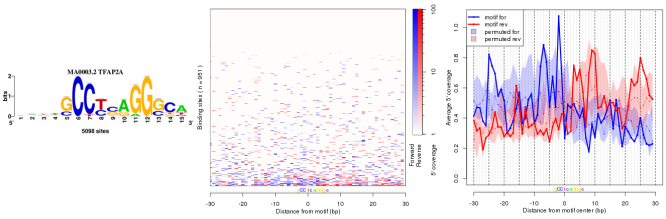
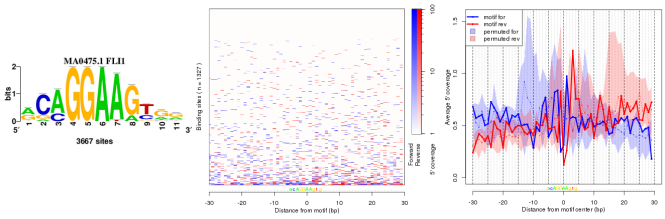
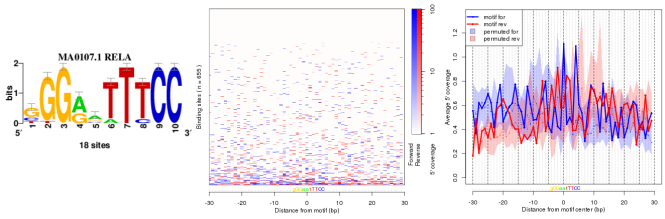
					
MA0048.1 **NHLH1**	Zipper-Type	Helix-Loop-Helix		1010	0.0204372839692601
MA0081.1 **SPIB**	Winged Helix-Turn-Helix	Ets		393	0.0234816883117741
MA0108.2 **TBP**	Beta-sheet	TATA-binding		656	0.025177112849857
MA0145.2 **Tcfcp2l1**	Other	CP2		710	0.0256010752634432
MA0071.1 **RORA_1**	Zinc-coordinating	Hormone-nuclear Receptor		430	0.0326530735291033
MA0066.1 **PPARG**	Zinc-coordinating	Hormone-nuclear Receptor		391	0.0366902896092156

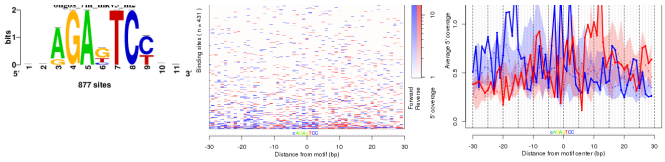
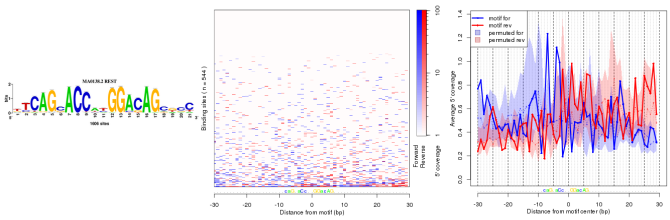
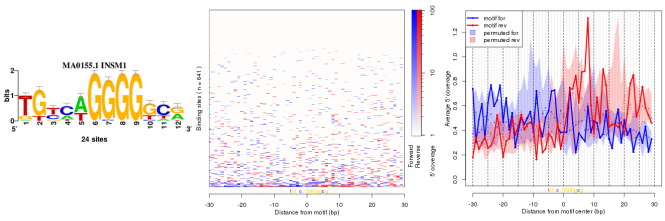
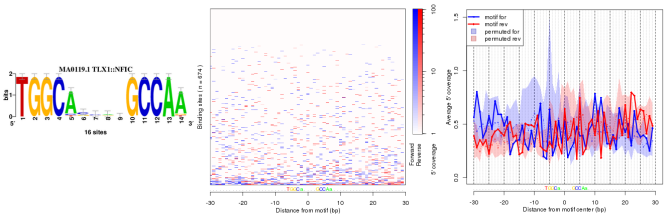
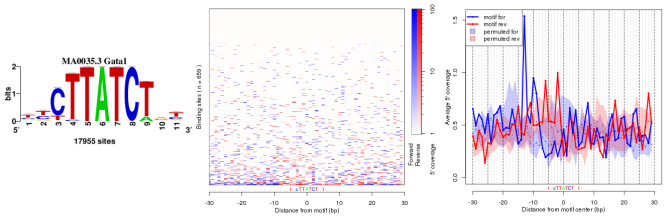
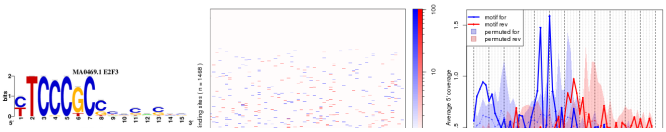
					
MA0109.1 **Hltf**	Zinc-coordinating	GATA		312	0.0416190328012254
MA0058.2 **MAX**	Zipper-Type	Helix-Loop-Helix		595	0.0462753676723501
MA0473.1 **ELF1**	Winged Helix-Turn-Helix	ETS		1079	0.0506398977427855
MA0004.1 **Arnt**	Zipper-Type	Helix-Loop-Helix		647	0.0507508061519212
MA0522.1 **Tcf3**	Other Alpha-Helix	High Mobility Group (Box)		813	0.057721714706671
MA0147.2 **Myc**	Zipper-Type	Helix-Loop-Helix		608	0.0580931669032525

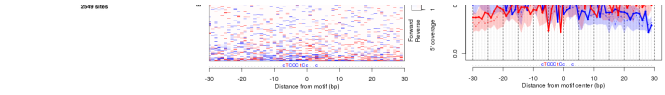
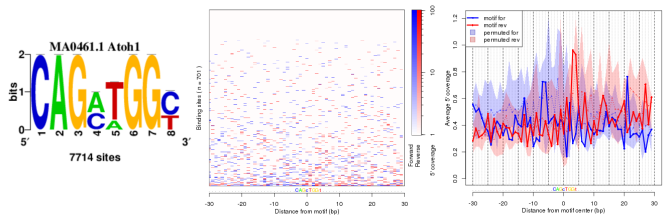
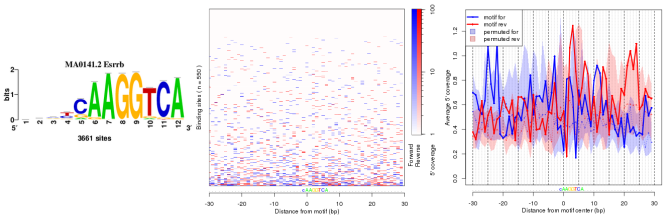
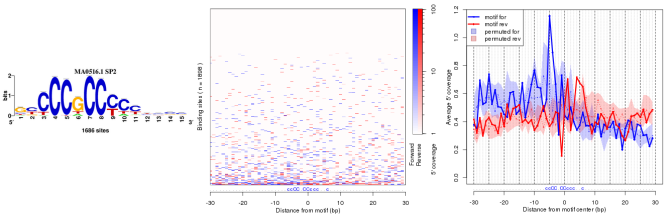
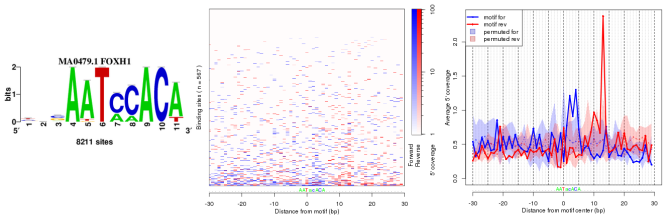
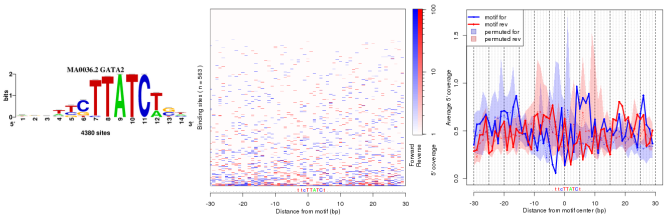
MA0056.1 **MZF1_1-4**	Zinc-coordinating	BetaBetaAlpha-zinc finger		399	0.0615687876335193
peaks-motifs de novo discovery **dyads_m3** Most similar motif in JASPAR: **FOSL2**	-	-		2768	0.062156700192963
MA0052.2 **MEF2A**	Other Alpha-Helix	MADS		1079	0.065122604733139
MA0039.2 **Klf4**	Zinc-coordinating	BetaBetaAlpha-zinc finger		1079	0.0651612670726308
MA0032.1 **FOXC1**	Winged Helix-Turn-Helix	Forkhead		473	0.068536444559146
MA0525.1 **TP63**	Zinc-coordinating	Loop-Sheet-Helix		557	0.0729148841020679
					

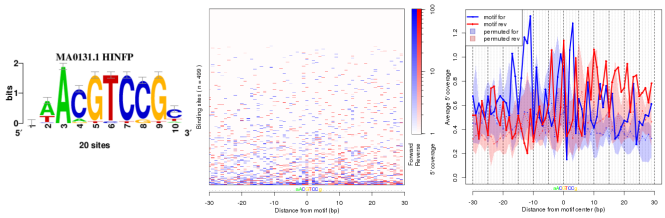
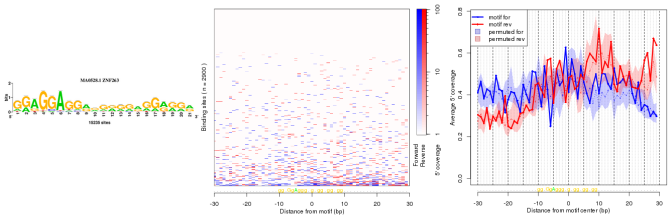
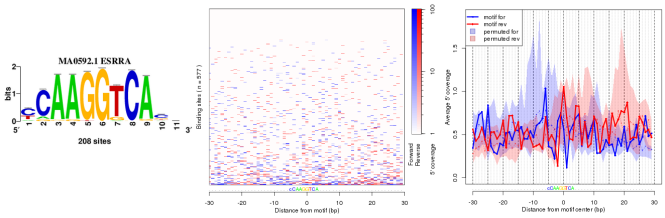
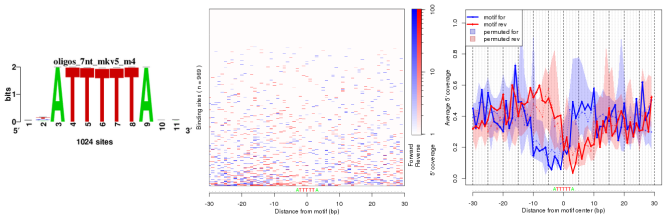
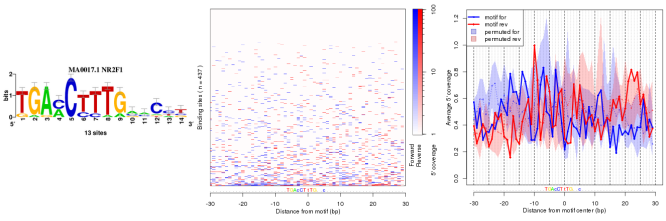
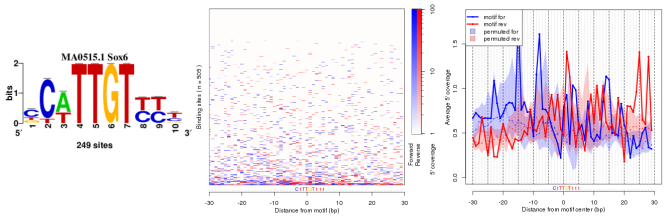
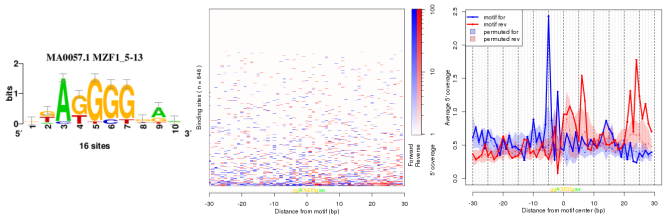
MA0154.2 **EBF1**	Zipper-Type	Helix-Loop-Helix		771	0.0831758701283423
MA0596.1 **SREBF2**	Zipper-Type	Helix-Loop-Helix		513	0.0990809960496176
MA0499.1 **Myod1**	Zipper-Type	Helix-Loop-Helix		769	0.10218294215897
MA0059.1 **MYC::MAX**	Zipper-Type	Helix-Loop-Helix		743	0.102585063812316
MA0037.2 **GATA3**	Zinc-coordinating	GATA		582	0.103546557390364
MA0471.1 **E2F6**	Winged Helix-Turn-Helix	E2F		1158	0.105741025542785
					

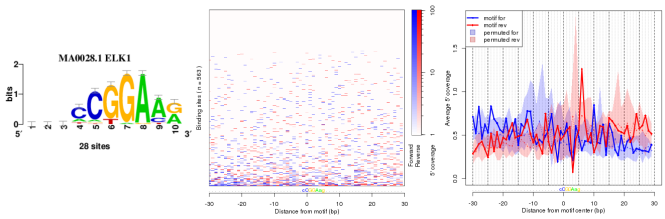
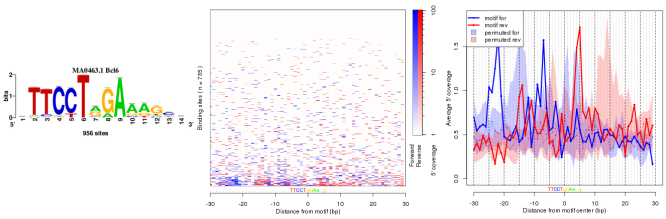
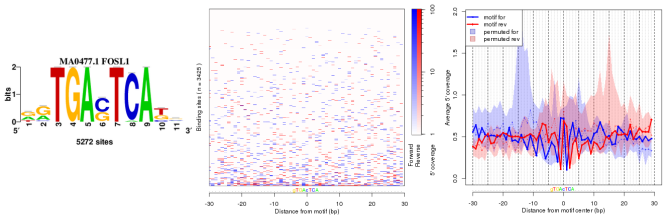
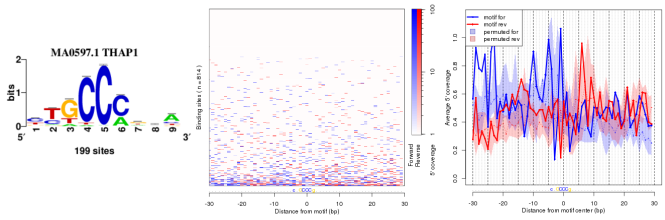
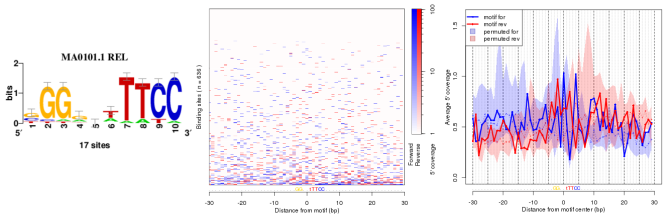
MA0494.1 **Nr1h3::Rxra**	Zinc-coordinating	Hormone-nuclear Receptor		379	0.105876899193544
MA0068.1 **Pax4**	Helix-Turn-Helix	Homeo		509	0.110004954169175
MA0006.1 **Arnt::Ahr**	Zipper-Type	Helix-Loop-Helix		704	0.114762150810417
MA0019.1 **Ddit3::Cebpa**	Zipper-Type	Leucine Zipper		393	0.121760463472309
MA0067.1 **Pax2**	Helix-Turn-Helix	Homeo		771	0.124076205527151
MA0259.1 **HIF1A::ARNT**	Zipper-Type	Helix-Loop-Helix		941	0.127166263922089

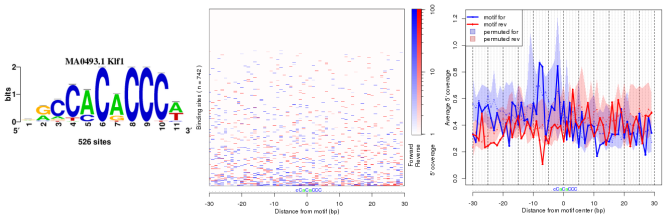
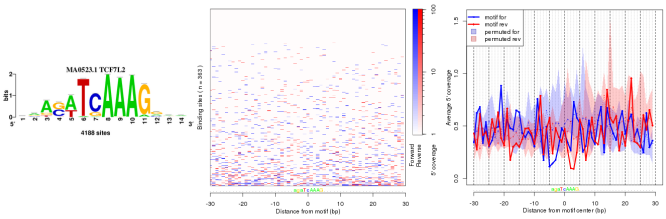
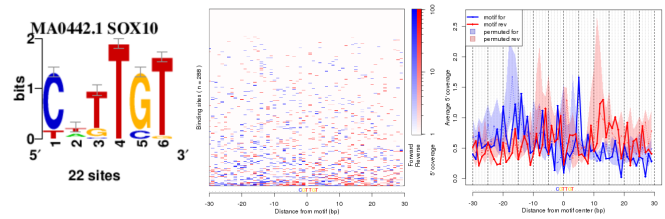
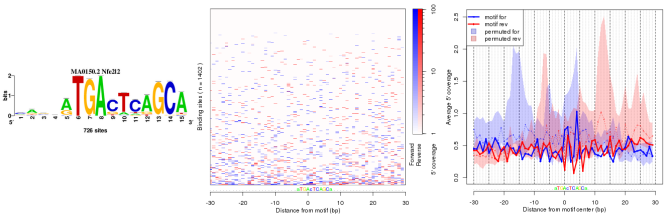
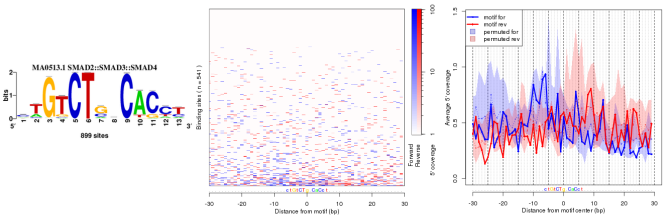
					
MA0505.1 **Nr5a2**	Zinc-coordinating	Hormone-nuclear Receptor		496	0.129250925262028
MA0003.2 **TFAP2A**	Zipper-Type	Helix-Loop-Helix		951	0.139076289226506
MA0475.1 **FLI1**	Winged Helix-Turn-Helix	ETS		1327	0.140805488622663
MA0107.1 **RELA**	Ig-fold	Rel		671	0.141943934209372
					

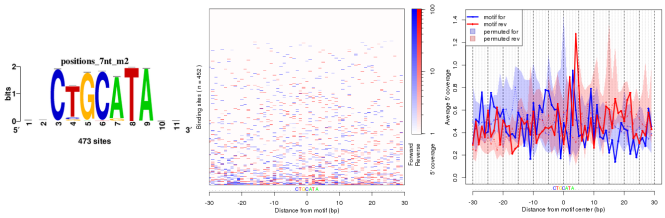
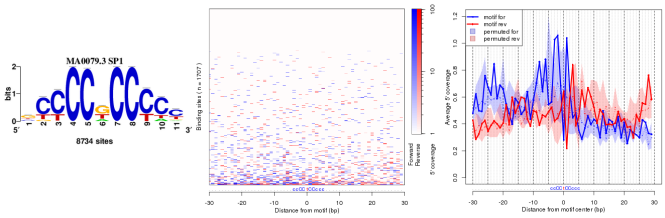
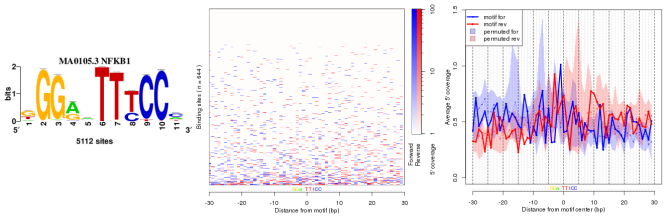
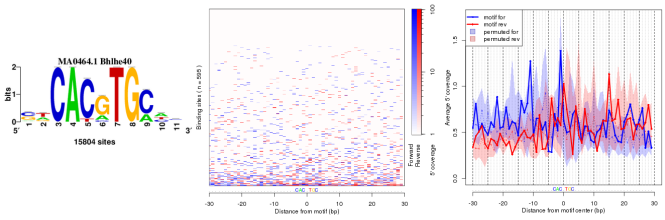
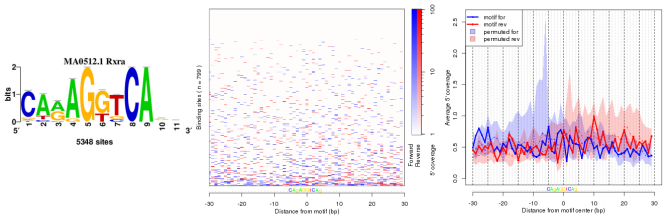
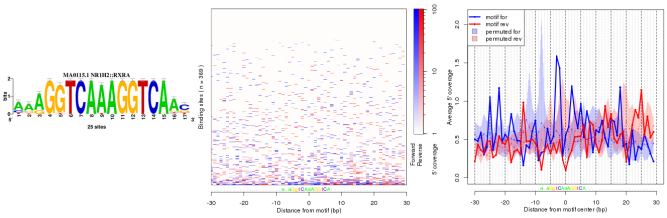
peaks-motifs de novo discovery **oligos_7nt_mkv5_m2** Most similar motif in JASPAR: **no match**	-	-		438	0.156453743912521
MA0138.2 **REST**	Zinc-coordinating	BetaBetaAlpha-zinc finger		544	0.156723736354918
MA0155.1 **INSM1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		641	0.168203056821478
MA0119.1 **TLX1::NFIC**	Helix-Turn-Helix::Other	Homeo::Nuclear Factor I-CCAAT-binding		674	0.168915130035081
MA0035.3 **Gata1**	Zinc-coordinating	GATA		659	0.170799762695913
MA0469.1 **E2F3**	Winged Helix-Turn-Helix	E2F		1468	0.173666628461744

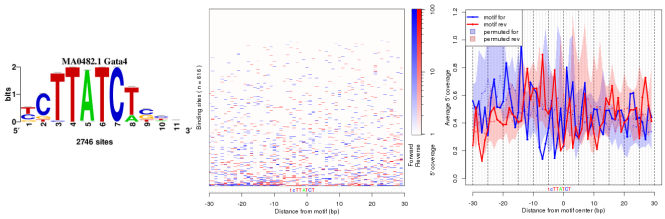
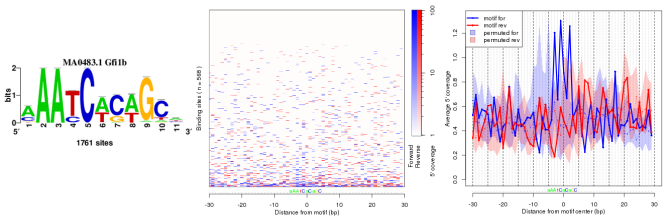
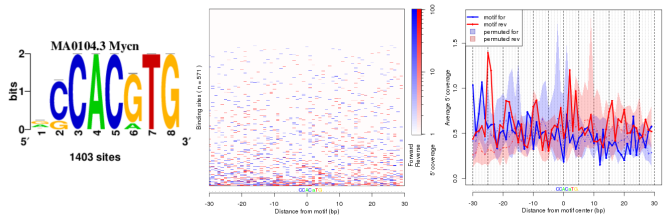
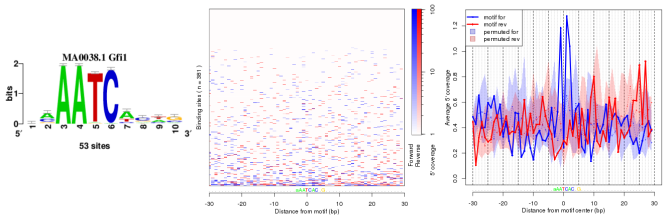
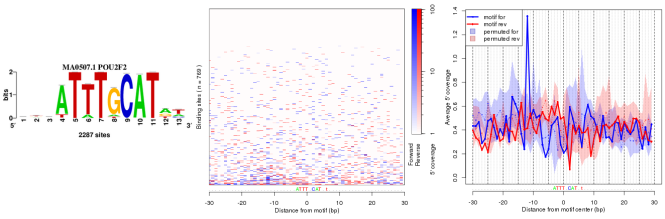
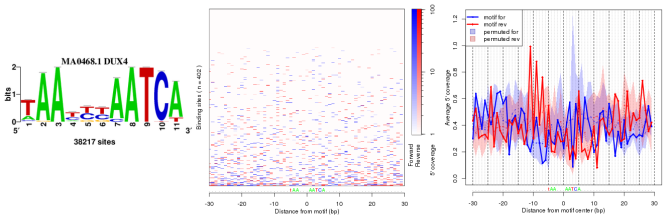
					
MA0461.1 **Atoh1**	Zipper-Type	Helix-Loop-Helix		701	0.176198390608434
MA0141.2 **Esrrb**	Zinc-coordinating	Hormone-nuclear Receptor		550	0.177250282145084
MA0516.1 **SP2**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		1898	0.181517447418176
MA0479.1 **FOXH1**	Winged Helix-Turn-Helix	Forkhead		567	0.183120706866782
MA0036.2 **GATA2**	Zinc-coordinating	GATA		563	0.188137663212389
MA0131.1	Zinc-	BetaBetaAlpha-		400	0.196192976202682

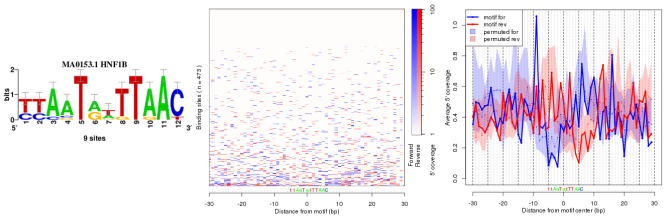
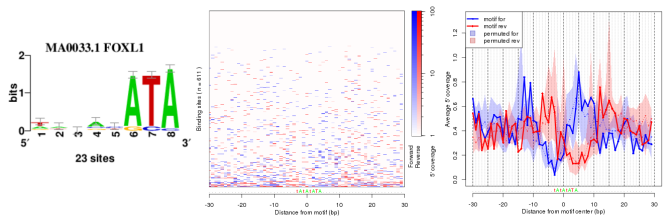
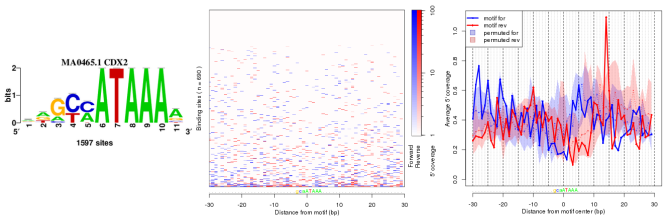
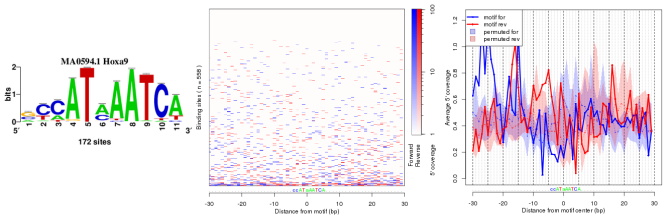
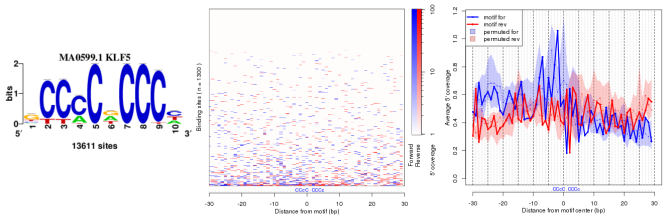
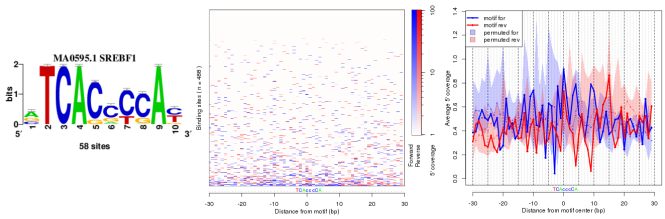
HINFP	coordinating	zinc finger			
MA0528.1 **ZNF263**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		2900	0.211052292796158
MA0592.1 **ESRRA**	Zinc-coordinating	Hormone-nuclear Receptor		577	0.238691775089503
peaks-motifs de novo discovery **oligos_7nt_mkv5_m4** Most similar motif in JASPAR: **MEF2C**	-	-		969	0.243590722448478
MA0017.1 **NR2F1**	Zinc-coordinating	Hormone-nuclear Receptor		437	0.281681725787941
MA0515.1 **Sox6**	Other Alpha-Helix	High Mobility Group (Box)		505	0.305547002673673
MA0057.1 **MZF1_5-13**	Zinc-coordinating	BetaBetaAlpha-zinc finger		646	0.306799342388098

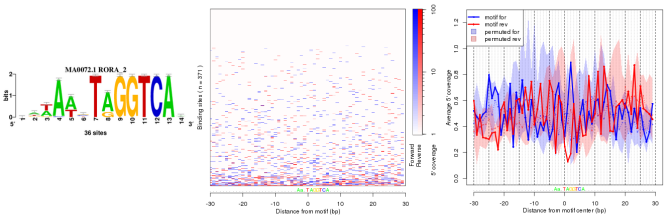
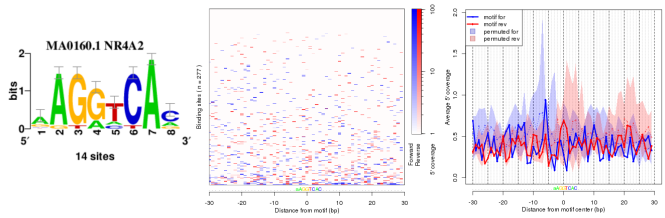
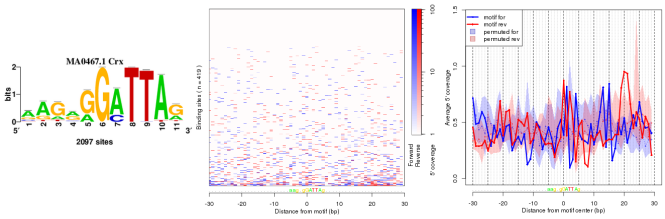
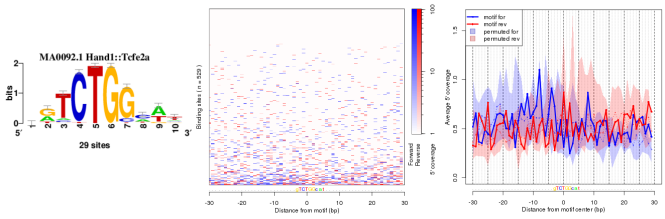
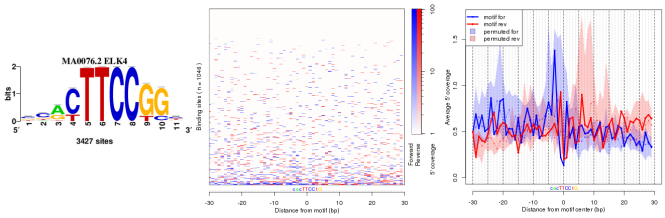
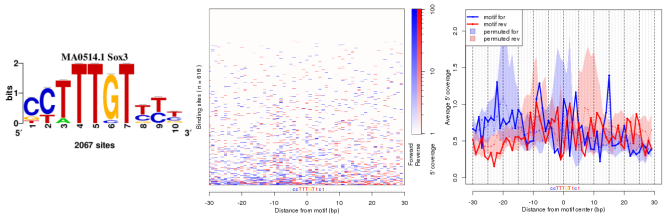
MA0028.1 **ELK1**	Winged Helix-Turn-Helix	Ets		571	0.310441986171705
MA0463.1 **Bcl6**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		735	0.31666364287263
MA0477.1 **FOSL1**	Zipper-Type	Leucine-Zipper		5015	0.324636258019575
MA0597.1 **THAP1**	Zinc-coordinating	THAP		814	0.325377890601038
MA0101.1 **REL**	Ig-fold	Rel		636	0.385105637457213

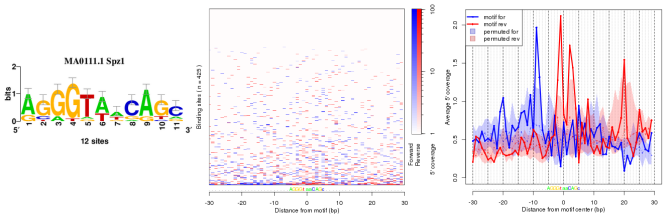
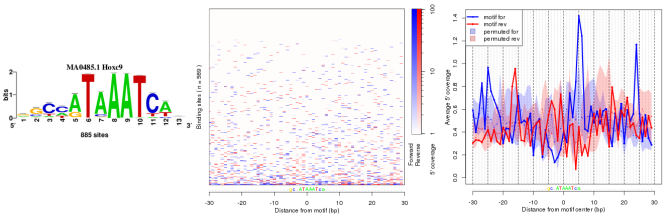
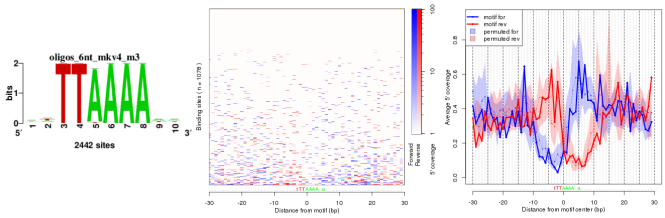
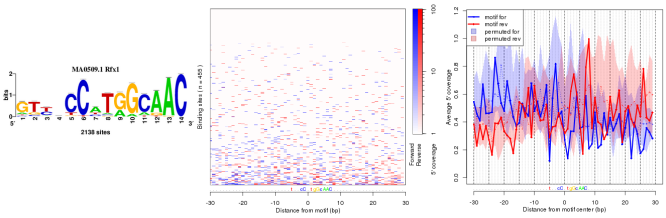
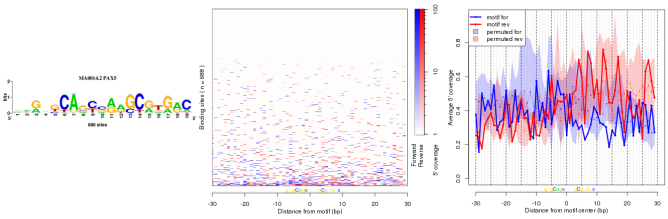
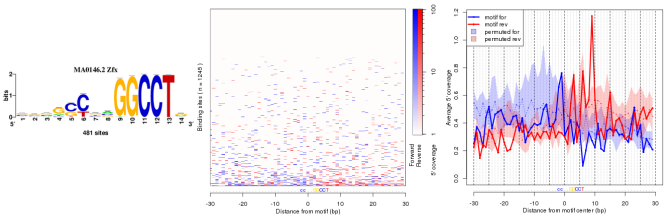
MA0493.1 **Klf1**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		742	0.399090451754216
MA0523.1 **TCF7L2**	Other Alpha-Helix	High Mobility Group (Box)		363	0.412150640780457
MA0442.1 **SOX10**	Other Alpha-Helix	High Mobility Group box (HMG)		288	0.417102347174032
MA0150.2 **Nfe2l2**	Zipper-Type	Leucine Zipper		1402	0.443480347729068
MA0513.1 **SMAD2::SMAD3::SMAD4**	Zinc-coordinating	MH1		541	0.485095916035726

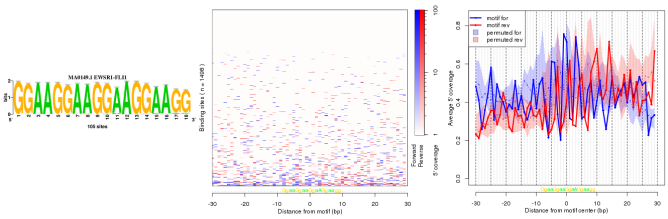
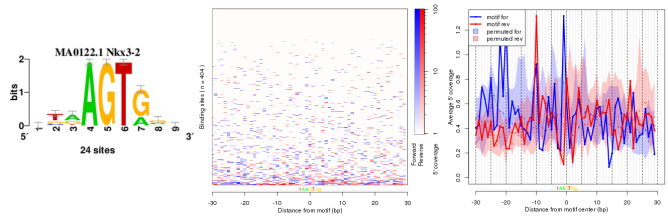
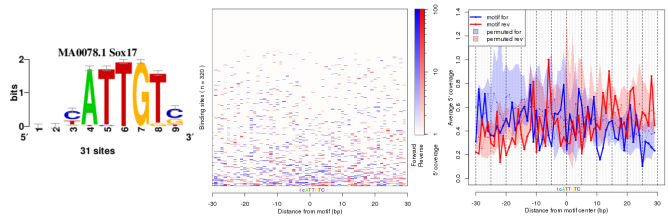
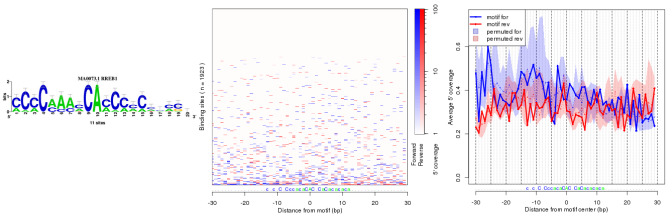
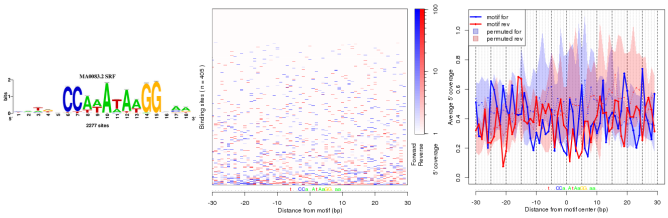
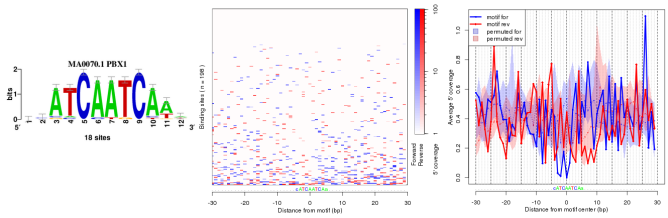
peaks-motifs de novo discovery **positions_7nt_m2** Most similar motif in JASPAR: **no match**	-	-		452	0.515927179563035
MA0079.3 **SP1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		1707	0.517149504189253
MA0105.3 **NFKB1**	Ig-fold	Rel		644	0.527108287271448
MA0464.1 **Bhlhe40**	Zipper-Type	Helix-Loop-Helix		595	0.532700199868295
MA0512.1 **Rxra**	Zinc-coordinating	Hormone-nuclear Receptor		799	0.541750035712442
MA0115.1 **NR1H2::RXRA**	Zinc-coordinating	Hormone-nuclear Receptor		369	0.552248512190603

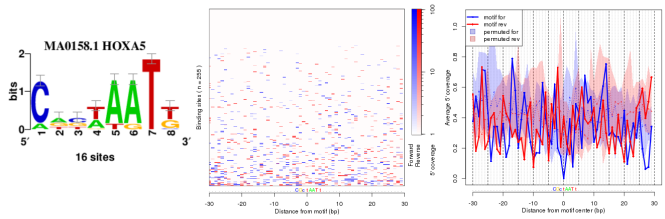
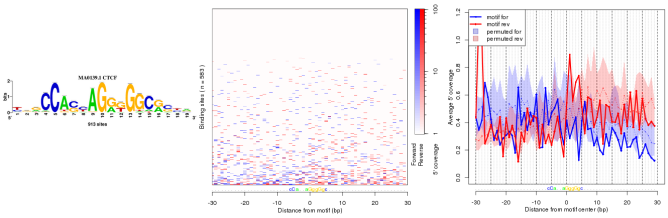
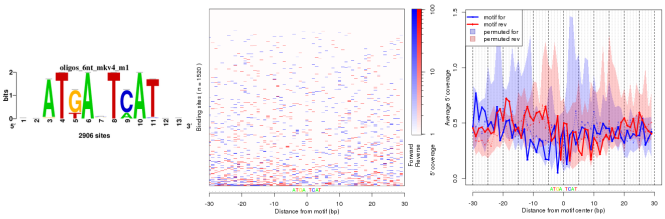
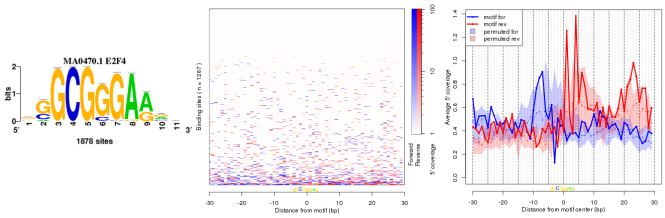
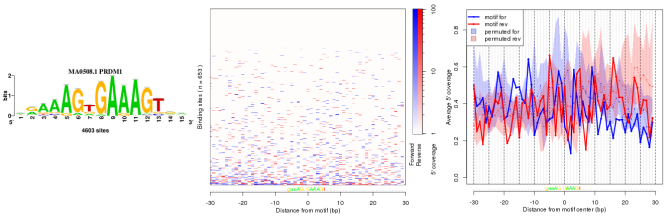
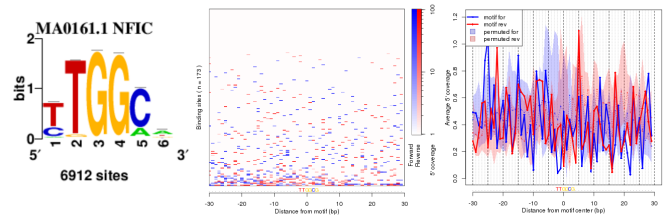
MA0482.1 **Gata4**	Zinc-coordinating	GATA		616	0.56010750038511
MA0483.1 **Gfi1b**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		568	0.564330780472825
MA0104.3 **Mycn**	Zipper-Type	Helix-Loop-Helix		572	0.576523457820495
MA0038.1 **Gfi1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		381	0.583659757961658
MA0507.1 **POU2F2**	Helix-Turn-Helix	Homeodomain		769	0.583777081645438
MA0468.1 **DUX4**	Helix-Turn-Helix	Homeodomain		402	0.600835931416878

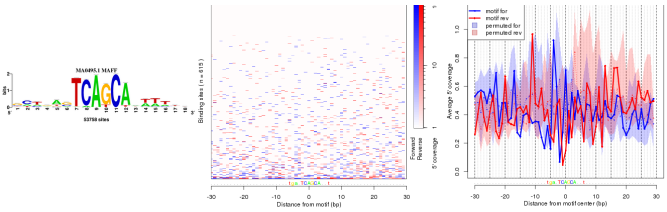
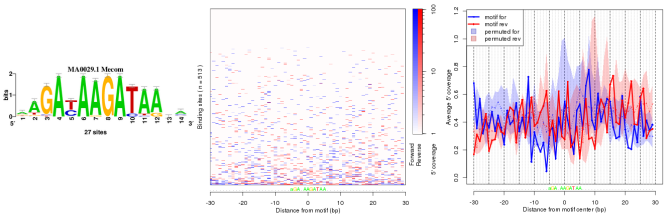
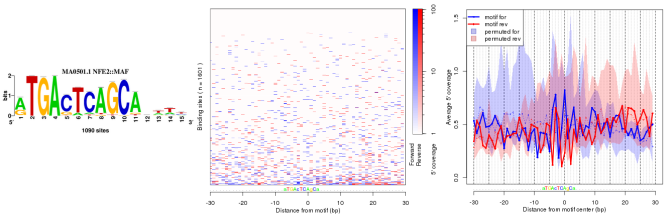
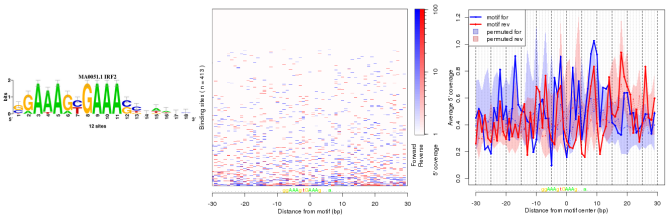
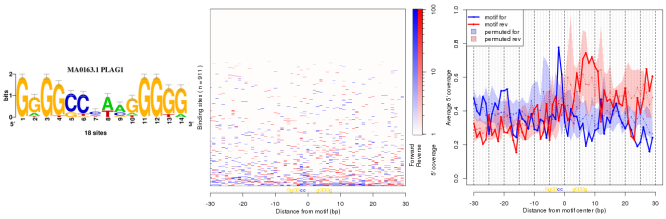
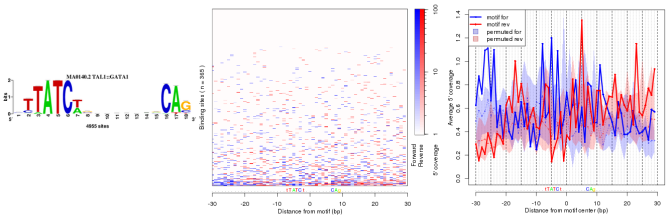
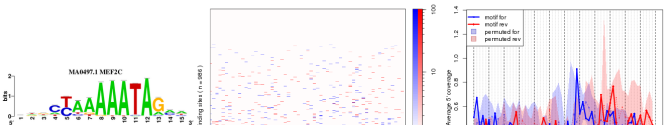
MA0153.1 **HNF1B**	Helix-Turn-Helix	Homeo		473	0.643142201245918
MA0033.1 **FOXL1**	Winged Helix-Turn-Helix	Forkhead		730	0.647988477296055
MA0465.1 **CDX2**	Helix-Turn-Helix	Homeodomain		690	0.657356753274894
MA0594.1 **Hoxa9**	Helix-Turn-Helix	Homeodomain		558	0.666764427087013
MA0599.1 **KLF5**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		1300	0.666912198289041
MA0595.1 **SREBF1**	Zipper-Type	Helix-Loop-Helix		495	0.674104203643864

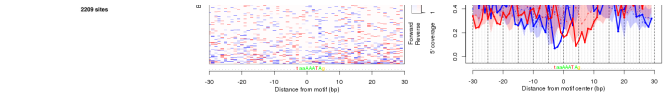
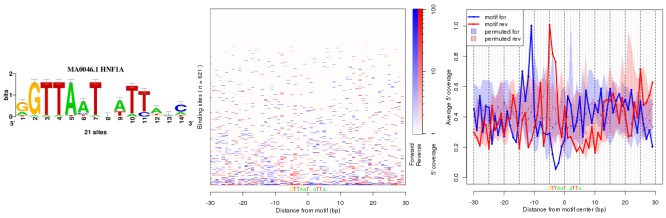
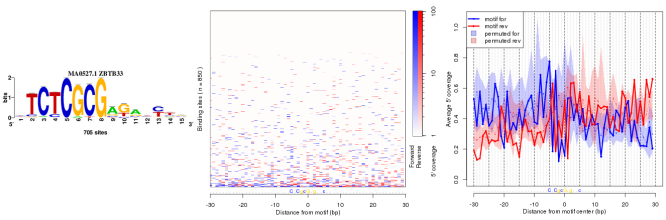
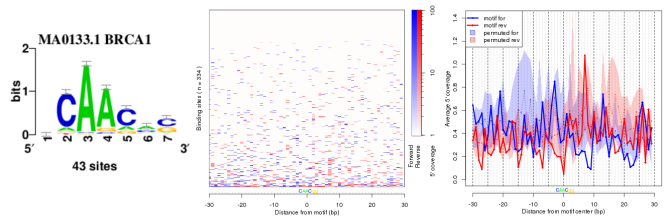
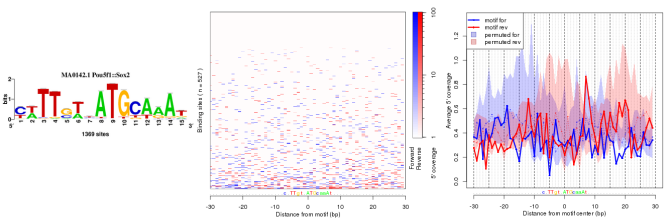
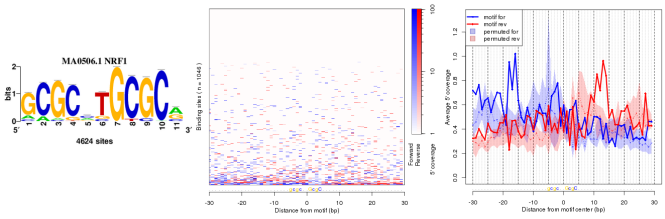
MA0072.1 **RORA_2**	Zinc-coordinating	Hormone-nuclear Receptor		371	0.703708175046292
MA0160.1 **NR4A2**	Zinc-coordinating	Hormone-nuclear Receptor		277	0.709508491544734
MA0467.1 **Crx**	Helix-Turn-Helix	Homeodomain		419	0.711395097620089
MA0092.1 **Hand1::Tcfe2a**	Zipper-Type	Helix-Loop-Helix		529	0.713697888023799
MA0076.2 **ELK4**	Winged Helix-Turn-Helix	Ets		1046	0.716261043709482
MA0514.1 **Sox3**	Other Alpha-Helix	High Mobility Group (Box)		618	0.730206699366209

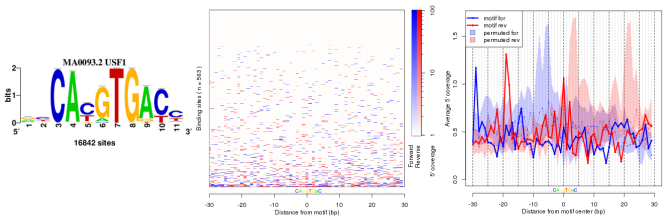
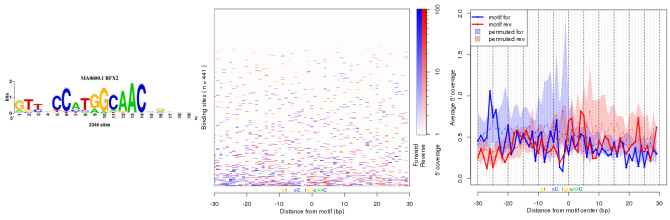
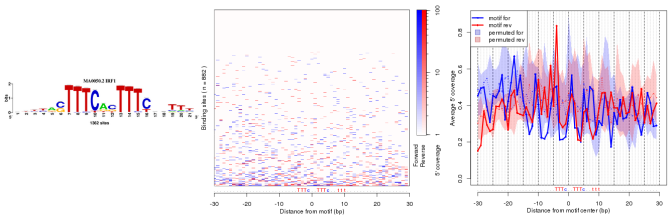
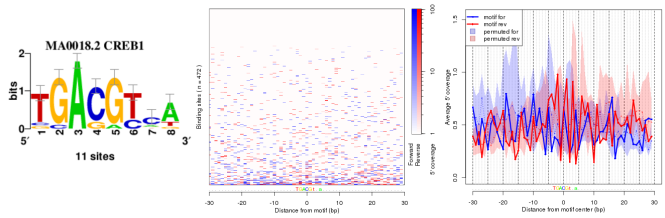
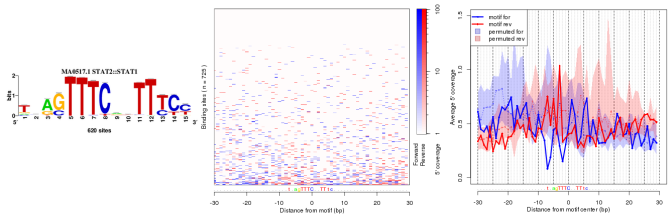
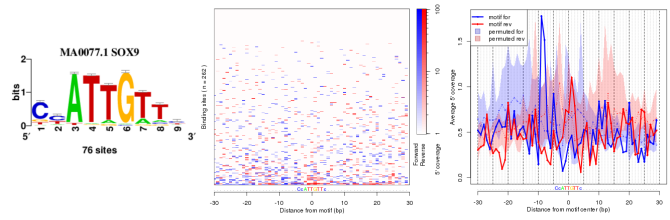
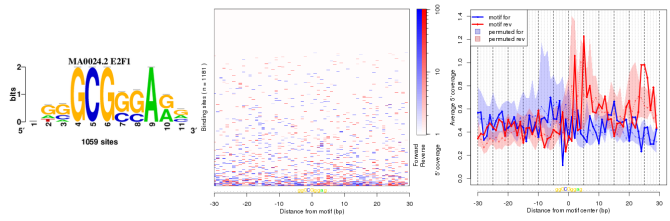
MA0111.1 **Spz1**	Other	Other		425	0.741502397349324
MA0485.1 **Hoxc9**	Helix-Turn-Helix	Homeodomain		589	0.748664759205412
peaks-motifs de novo discovery **oligos_6nt_mkv4_m3** Most similar motif in JASPAR: **ARID3A**	-	-		1078	0.761944111509578
MA0509.1 **Rfx1**	Winged Helix-Turn-Helix	RFX		489	0.789250961419959
MA0014.2 **PAX5**	Helix-Turn-Helix	Homeo		688	0.791743042733607
MA0146.2 **Zfx**	Zinc-coordinating	BetaBetaAlpha-zinc finger		1262	0.794886627817549

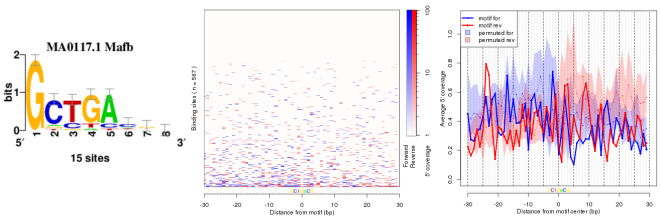
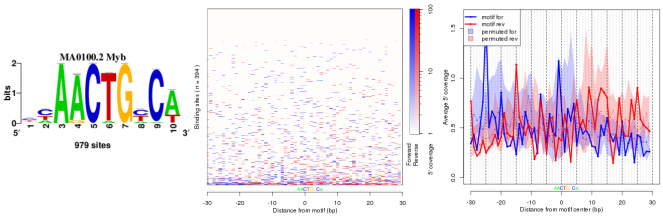
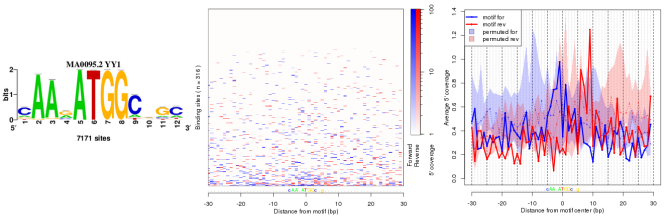
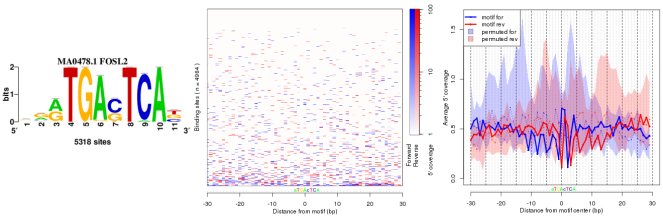
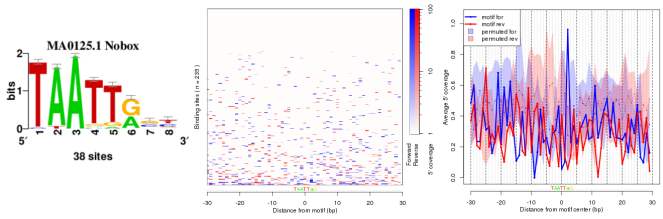
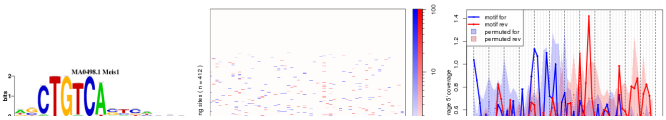
MA0149.1 **EWSR1-FLI1**	Winged Helix-Turn-Helix	Ets		1498	0.808125456811774
MA0122.1 **Nkx3-2**	Helix-Turn-Helix	Homeo		405	0.80930947246343
MA0078.1 **Sox17**	Other Alpha-Helix	High Mobility Group box (HMG)		320	0.823459148473264
MA0073.1 **RREB1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		1923	0.845438635994866
MA0083.2 **SRF**	Other Alpha-Helix	MADS		405	0.848626077821076
MA0070.1 **PBX1**	Helix-Turn-Helix	Homeo		198	0.855691153261962

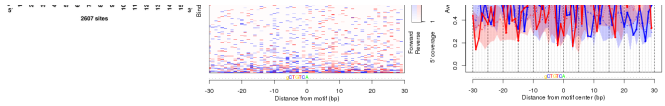
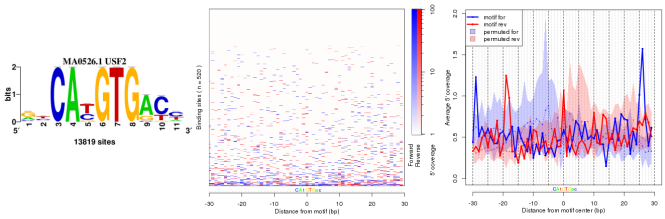
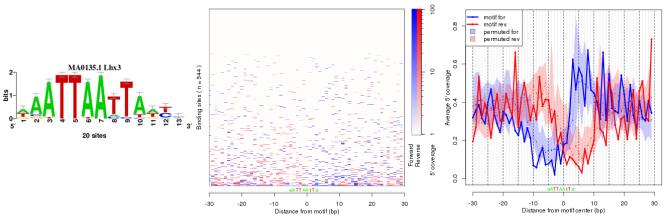
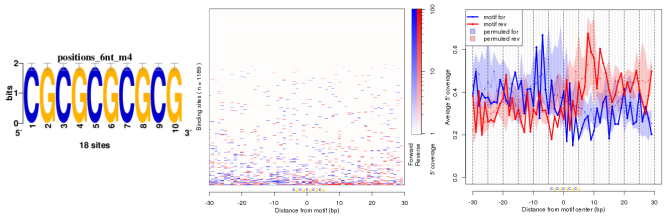
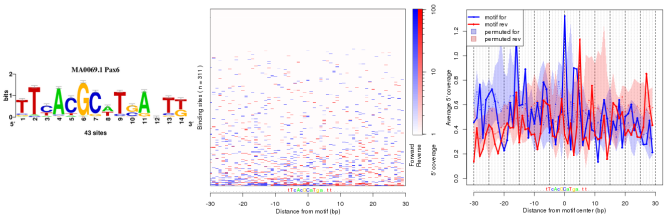
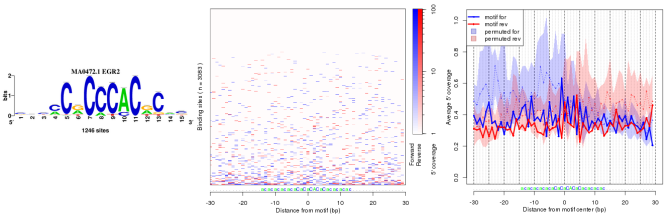
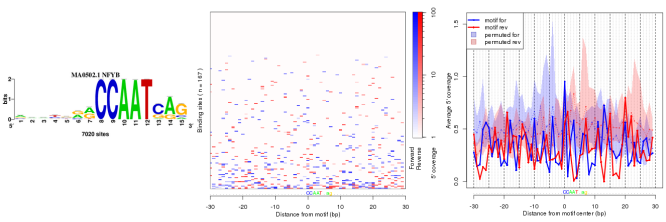
MA0158.1 **HOXA5**	Helix-Turn-Helix	Homeo		255	0.8581210250052
MA0139.1 **CTCF**	Zinc-coordinating	BetaBetaAlpha-zinc finger		583	0.859133091691821
peaks-motifs de novo discovery **oligos_6nt_mkv4_m1** Most similar motif in JASPAR: **JUND**	-	-		3040	0.863117394968998
MA0470.1 **E2F4**	Winged Helix-Turn-Helix	E2F		1267	0.863299438959019
MA0508.1 **PRDM1**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		653	0.863480964826342
MA0161.1 **NFIC**	Other	NFI CCAAT-binding		173	0.877789793949493

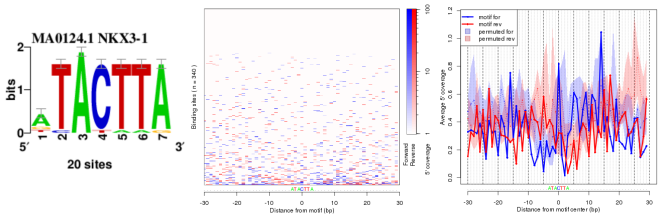
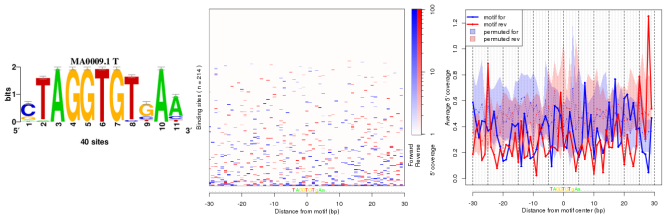
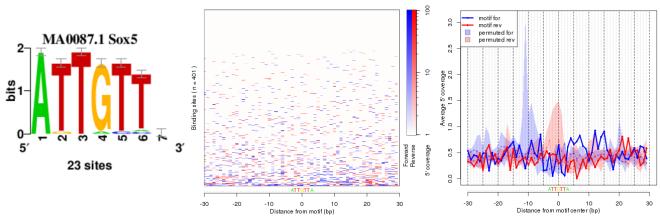
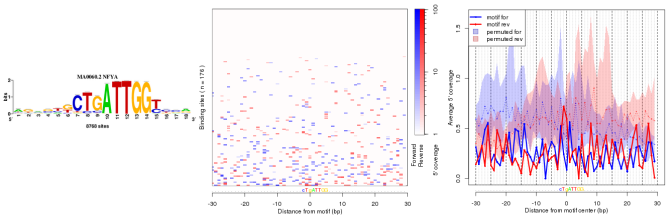
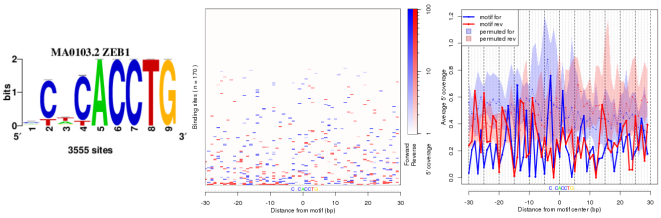
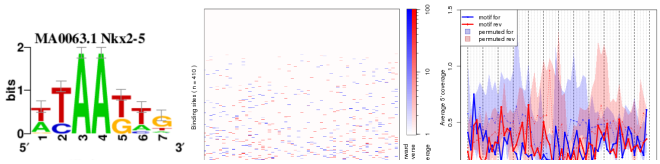
MA0495.1 **MAFF**	Zipper-Type	Leucine-Zipper		615	0.882580996641004
MA0029.1 **Mecom**	Zinc-coordinating	BetaBetaAlpha-zinc finger		513	0.883338852617938
MA0501.1 **NFE2::MAF**	Zipper-Type	Leucine-Zipper		1601	0.883953638914765
MA0051.1 **IRF2**	Winged Helix-Turn-Helix	IRF		413	0.889533529472367
MA0163.1 **PLAG1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		911	0.896877658723152
MA0140.2 **TAL1::GATA1**	Zipper-Type	Helix-Loop-Helix		365	0.904121967561927
MA0497.1 **MEF2C**	Other Alpha-Helix	MADS		986	0.904286910638692

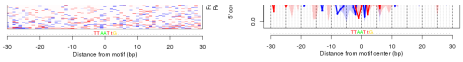
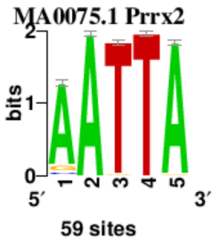
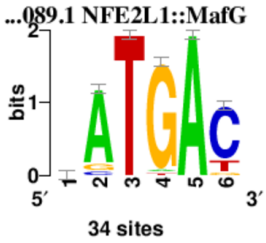
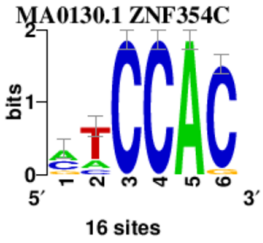
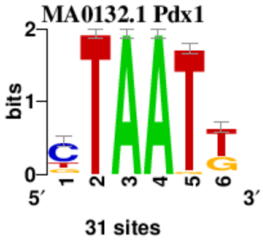
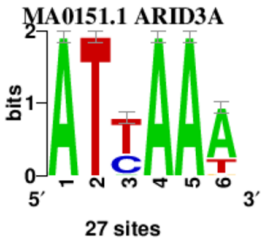
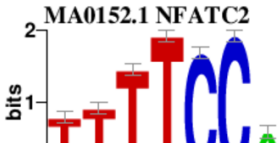
					
MA0046.1 **HNF1A**	Helix-Turn-Helix	Homeo		632	0.921889193228842
MA0527.1 **ZBTB33**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		850	0.92427942278078
MA0133.1 **BRCA1**	Other	Other		334	0.924398422853223
MA0142.1 **Pou5f1::Sox2**	Helix-Turn-Helix	Homeo		527	0.93661035863463
MA0506.1 **NRF1**	Other	NRF		1046	0.941292516855448
MA0093.2 **USF1**	Zipper-Type	Helix-Loop-Helix		563	0.9419500865533

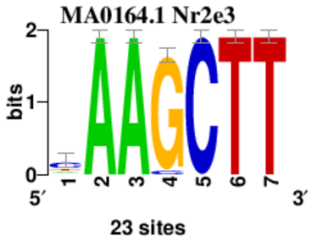
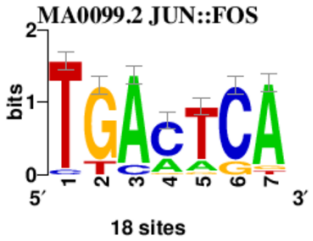
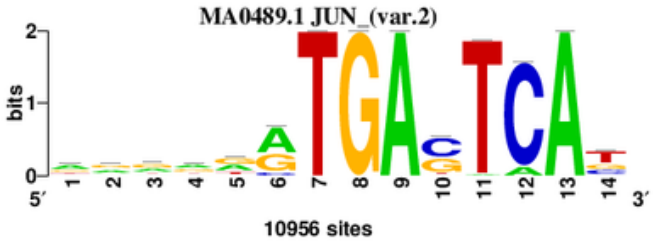
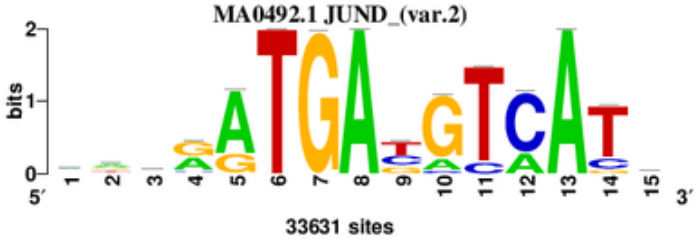
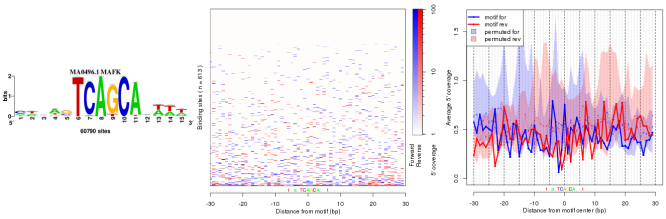
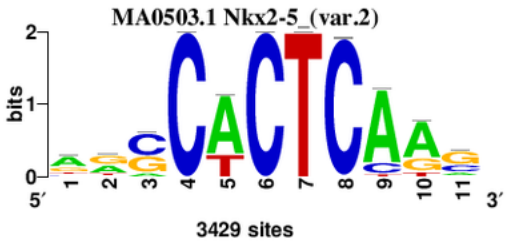
					
MA0600.1 **RFX2**	Winged Helix-Turn-Helix	RFX		441	0.945975258870561
MA0050.2 **IRF1**	Winged Helix-Turn-Helix	IRF		882	0.949553842666775
MA0018.2 **CREB1**	Zipper-Type	Leucine Zipper		532	0.95830203977225
MA0517.1 **STAT2::STAT1**	Other	STAT		725	0.964477590507233
MA0077.1 **SOX9**	Other Alpha-Helix	High Mobility Group box (HMG)		262	0.964662644063331
MA0024.2	Winged Helix-Turn-	E2F		1181	0.974001383288818

E2F1					
MA0117.1 **Mafb**	Zipper-Type	Leucine Zipper		583	0.982444028708434
MA0100.2 **Myb**	Helix-Turn-Helix	Myb		394	0.985738012519309
MA0095.2 **YY1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		316	0.987289917782374
MA0478.1 **FOSL2**	Zipper-Type	Leucine-Zipper		4964	0.98742546672963
MA0125.1 **Nobox**	Helix-Turn-Helix	Homeo		235	0.994028227250405
MA0498.1 **Meis1**	Helix-Turn-Helix	Homeodomain		412	0.996640526982052

					
MA0526.1 **USF2**	Zipper-Type	Helix-Loop-Helix		520	0.996998228915274
MA0135.1 **Lhx3**	Helix-Turn-Helix	Homeo		544	0.997476971052255
peaks-motifs de novo discovery **positions_6nt_m4** Most similar motif in JASPAR: **NRF1**	-	-		2378	0.9975543969116
MA0069.1 **Pax6**	Helix-Turn-Helix	Homeo		311	0.998430762197329
MA0472.1 **EGR2**	Zinc-coordinating	BetaBetaAlpha-zinc Finger		3083	0.998605015219158
MA0502.1 **NFYB**	Other Alpha-Helix	NF-Y CCAAT-Binding		167	0.999493101828354

MA0124.1 **NKX3-1**	Helix-Turn-Helix	Homeo		340	0.999726770693167
MA0009.1 **T**	Beta-Hairpin-Ribbon	T		214	0.999940710134937
MA0087.1 **Sox5**	Other Alpha-Helix	High Mobility Group box (HMG)		401	0.999993250772955
MA0060.2 **NFYA**	Other Alpha-Helix	NFY CCAAT-binding		176	0.999996203486472
MA0103.2 **ZEB1**	Zinc-coordinating	BetaBetaAlpha-zinc finger		170	0.999999977614683
MA0063.1 **Nkx2-5**	Helix-Turn-Helix	Homeo		410	0.999999979579607

			17 sites 		
MA0075.1 **Prrx2**	Helix-Turn-Helix	Homeo		0	1
MA0089.1 **NFE2L1::MafG**	Zipper-Type	Leucine Zipper		0	1
MA0130.1 **ZNF354C**	Zinc-coordinating	BetaBetaAlpha-zinc finger		0	1
MA0132.1 **Pdx1**	Helix-Turn-Helix	Homeo		0	1
MA0151.1 **ARID3A**	Helix-Turn-Helix	Arid		0	1
MA0152.1 **NFATC2**	Ig-fold	Rel		0	1

					
MA0164.1 **Nr2e3**	Zinc-coordinating	Hormone-nuclear Receptor		0	1
MA0099.2 **JUN::FOS**	Zipper-Type	Leucine Zipper		0	1
MA0489.1 **JUN (var.2)**	Zipper-Type	Leucine-Zipper		0	1
MA0492.1 **JUND (var.2)**	Zipper-Type	Leucine-Zipper		0	1
MA0496.1 **MAFK**	Zipper-Type	Leucine-Zipper		613	1
MA0503.1 **Nkx2-5 (var.2)**	Helix-Turn-Helix	Homeodomain		0	1