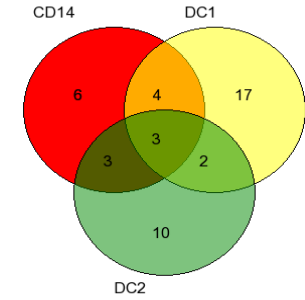


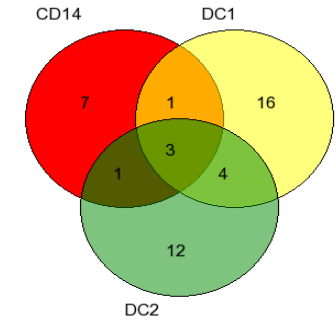
ST1a. All peaks motifs

CD14				DC1			DC2				
motif	Name	p Value	log P-pvalue	motif	Name	p Value	log P-pvalue	motif	Name	p Value	log P-pvalue
	VDR	1e-559	-1.29E+03		SFP11	1e-1362	-3.14E+03		VDR	1e-555	-1.28E+03
	SFP11	1.00E-293	-6.76E+02		CEBP(bZIP)	1e-1148	-2.65E+03		CEBP-AP1	1.00E-124	-2.87E+02
	CEBP(bZIP)	1.00E-206	-4.75E+02		BATF(bZIP)	1e-1061	-2.44E+03		SFP11	1.00E-118	-2.73E+02
	BRCA1	1.00E-35	-8.23E+01		VDR	1e-999	-2.30E+03		BATF(bZIP)	1.00E-117	-2.70E+02
	JUN	1.00E-31	-7.16E+01		RELA	1e-356	-8.22E+02		NR2F2	1.00E-44	-1.03E+02
	SPI1	1.00E-28	-6.53E+01		Ddit3::Cebpa	1.00E-229	-5.28E+02		RELA	1.00E-35	-8.07E+01
	NKX2-5	1.00E-26	-6.12E+01		IRF2	1.00E-207	-4.79E+02		PAX2	1.00E-34	-7.91E+01
	CEBP-AP1	1.00E-22	-5.11E+01		JUN	1.00E-190	-4.38E+02		MYBL2	1.00E-30	-7.12E+01
	CEBP-AP1	1.00E-20	-4.72E+01		RUNX2(Runt)	1.00E-170	-3.92E+02		BRCA1	1.00E-26	-6.11E+01
	RUNX(Runt)	1.00E-19	-4.50E+01		IRF4	1.00E-102	-2.36E+02		NR4A2	1.00E-26	-6.01E+01
	MEIS1	1.00E-15	-3.63E+01		CEBPB	1.00E-95	-2.21E+02		STAT1	1.00E-23	-5.49E+01
	CEBP(bZIP)	1.00E-15	-3.63E+01		USF2	1.00E-92	-2.13E+02		RXRA	1.00E-19	-4.55E+01
	CEBPB	1.00E-15	-3.48E+01		BRCA1	1.00E-87	-2.03E+02		GF1B	1.00E-18	-4.28E+01
	SP2	1.00E-15	-3.63E+01		EGR2	1.00E-67	-1.56E+02		NKX2-5	1.00E-18	-4.20E+01
	IRF3	1.00E-19	-3.07E+01		TFAP4	1.00E-51	-1.18E+02		CEBPA	1.00E-18	-4.28E+01
	RUNX-AML(Runt)	1.00E-13	-3.16E+01		IRF1	1.00E-31	-7.37E+01		DCE_5_II	1.00E-14	-3.30E+01
	ESRRA	1.00E-12	-2.81E+01		HRE(HSF)	1.00E-41	-9.51E+01		SPI1	1.00E-12	-2.89E+01
	NKX2-2	1.00E-12	-2.79E+01		SRF	1.00E-31	-7.37E+01		ELF5	1.00E-12	-2.81E+01
					NKX2-3	1.00E-31	-7.27E+01				
					LXRE(NR/DR4)	1.00E-25	-5.80E+01				
					X-box(HTH)	1.00E-24	-5.72E+01				
					RUNX-AML(Runt)	1.00E-24	-5.56E+01				
					BATF::JUN	1.00E-24	-5.53E+01				
					NKX3-1	1.00E-23	-5.41E+01				
					IRF9	1.00E-19	-4.52E+01				
					E2F4	1.00E-15	-3.51E+01				



ST1b. canonical VDRE motifs

CD14				DC1				DC2			
Motif	Name	p Value	log P-pvalue	Motif	Name	p Value	log P-pvalue	Motif	Name	p Value	log P-pvalue
	VDR	1e-854	-1.97E+03		VDR	1e-2960	-6.82E+03		VDR	1e-800	-1.84E+03
	SP11	1.00E-110	-2.55E+02		SP11	1.00E-220	-5.08E+02		CEBPB	1.00E-82	-1.90E+02
	CEBPA	1.00E-73	-1.70E+02		CEBP	1.00E-160	-3.70E+02		BATF	1.00E-54	-1.26E+02
	JUND	1.00E-39	-9.08E+01		BATF	1.00E-160	-3.69E+02		EHF	1.00E-51	-1.18E+02
	AP-1	1.00E-38	-8.86E+01		PITX1	1.00E-73	-1.69E+02		IRF4	1.00E-39	-9.01E+01
	SOX10	1.00E-21	-5.04E+01		RELA	1.00E-51	-1.19E+02		PITX1	1.00E-27	-6.35E+01
	SP1	1.00E-19	-4.44E+01		IRF1	1.00E-44	-1.03E+02		RELA	1.00E-21	-4.96E+01
	MAFK	1.00E-16	-3.73E+01		THAP1	1.00E-35	-8.18E+01		EHF	1.00E-18	-4.17E+01
	ARID5A	1.00E-16	-3.69E+01		MYB	1.00E-29	-6.88E+01		THAP1	1.00E-17	-3.95E+01
	CTCF	1.00E-15	-3.46E+01		DDIT3	1.00E-29	-6.79E+01		MZF1	1.00E-16	-3.84E+01
	SP1	1.00E-14	-3.43E+01		ELF5	1.00E-23	-5.40E+01		INSM1	1.00E-16	-3.84E+01
	MYB	1.00E-14	-3.31E+01		CEBP-AP1	1.00E-23	-5.30E+01		SP11	1.00E-13	-3.22E+01
	NFI3	1.00E-13	-3.18E+01		NFYB	1.00E-23	-5.30E+01		HNF1A	1.00E-13	-3.22E+01
	NR4A2	1.00E-12	-2.91E+01		HNF4A	1.00E-22	-5.28E+01		STAT5	1.00E-13	-3.22E+01
					RHOX6	1.00E-22	-5.19E+01		ESRRB	1.00E-13	-3.22E+01
					CEBP-AP1	1.00E-20	-4.78E+01		JUND	1.00E-13	-3.09E+01
					GF11	1.00E-20	-4.78E+01		GLI3	1.00E-12	-2.94E+01
					GATA3	1.00E-19	-4.48E+01		PITX3	1.00E-12	-2.88E+01
					JUN::FOS	1.00E-19	-4.42E+01		IRF9	1.00E-12	-2.82E+01
					ZNF143 STAF	1.00E-18	-4.22E+01		ZNF410	1.00E-12	-2.81E+01
					MYC	1.00E-17	-4.14E+01				
					PITX1	1.00E-17	-3.99E+01				
					PLAG1	1.00E-16	-3.76E+01				
					NR1D1	1.00E-15	-3.58E+01				
					EGR2	1.00E-12	-2.90E+01				



ST1c. non canonical VDRE motifs

CD14		CD14	CD14	CD14	DC1		DC1	DC1	DC2		DC2	DC2	DC2	
Motif		Name	p Value	log P-pvalue	Motif		Name	p Value	log P-pvalue	Motif		Name	p Value	log P-pvalue
ATGATGCAATAT		CEBPB	1.00E-197	-4.54E+02	AASAGGAAGT		SP1	1e-1145	-2.64E+03	ATTATGCAATAT		CEBPB	1.00E-122	-2.82E+02
AASAGGAAGT		SP1	1.00E-178	-4.11E+02	ATAATGCAATAT		CEBPA	1e-1038	-2.39E+03	AGCGTTCAAT		RXRA	1.00E-80	-1.85E+02
ATGACTCA		AP-1	1.00E-91	-2.12E+02	ATAATGCAATAT		BATF	1e-894	-2.06E+03	AACAGGAAGT		SP1	1.00E-78	-1.80E+02
GCGCTCTAG		NKX2-5	1.00E-24	-5.68E+01	TGTGCAAT		CEBPA	1e-360	-8.31E+02	ATGACTCAAT		AP-1	1.00E-73	-1.69E+02
AACCACATGACT		RUNX1	1.00E-22	-5.27E+01	GGCAATTCCT		RELA	1.00E-293	-6.75E+02	GGTCAAGGCG		USF1	1.00E-19	-4.52E+01
AACCCG		GEM1	1.00E-20	-4.71E+01	ACCAATGAC		NFE2L1::MatG	1.00E-219	-5.06E+02	TTTCCCACTCATCTC		SOX13	1.00E-18	-4.37E+01
AACCATAGAGAC		RUNX1	1.00E-19	-4.50E+01	ATGAACCTT		RXRA	1.00E-199	-4.60E+02	AAACCICCAAGACTTC		ZNF281	1.00E-18	-4.36E+01
GGGTTAACCCTG		PTX1	1.00E-16	-3.84E+01	TAACCACAAG		RUNX family	1.00E-176	-4.07E+02	GGAATTCCTCA		REL	1.00E-18	-4.30E+01
GTGAACAAACCACA		RUNX1	1.00E-15	-3.63E+01	TTTTCAGGAA		STAT1	1.00E-96	-2.21E+02	TTTCCGGAA		STAT4	1.00E-17	-4.06E+01
CGTAAC		ELK1	1.00E-15	-3.56E+01	GTGTTGGGG		EGR2	1.00E-72	-1.68E+02	AACCGTTGAAC		TCF7L2	1.00E-17	-4.04E+01
AGCCCAAGCACTT		NKX2-1	1.00E-14	-3.45E+01	CCCATTAAGCAATAAC		LHX9	1.00E-45	-1.04E+02	GTTACG		HLF	1.00E-16	-3.83E+01
TGTGACACATTGAC		JUND	1.00E-14	-3.45E+01	TTCCCCAAGTGC		TCFAP2B	1.00E-42	-9.72E+01	AAASCACAATGACCTC		VDR	1.00E-14	-3.27E+01
TAGTGCATTGAGTAC		NRS2	1.00E-14	-3.45E+01	CGFAAGCG		GABPA	1.00E-36	-8.49E+01	CATCGGCT		TAL1::TCF3	1.00E-14	-3.23E+01
CAAAAAGGAGGGTGT		FOXO1	1.00E-12	-2.88E+01	CAGCTG		TFAP4	1.00E-36	-8.32E+01	TAGTCTCACCCTGC		KLF1	1.00E-13	-3.13E+01
					GAAACTCGGT		IRF4	1.00E-33	-7.76E+01	TTCCAAGTACTCCA		RBPJ1	1.00E-13	-3.15E+01
					ATCACATG		MAX	1.00E-33	-7.63E+01	CTTCCTAATGATGAAA		DDIT3	1.00E-13	-3.13E+01
					SAAATAAGCAATTCAT		DUX4	1.00E-33	-7.62E+01					
					TCITAAGAAA		STAT6	1.00E-30	-7.13E+01					
					AATGTACTTAATCCA		NKX2-3	1.00E-30	-7.01E+01					
					CTAGAGGGCC		NKX2-5	1.00E-28	-6.88E+01					
					ATCAIACAGTATTTGT		ARID5A	1.00E-24	-5.57E+01					
					CATCATGTGICACT		JUND	1.00E-23	-5.35E+01					
					ACCATAGAGA		RUNX-AML	1.00E-22	-5.13E+01					
					GIACCTCATATAAGTG		NKX2-5	1.00E-21	-5.02E+01					
					TATACAGTTCAGTAGT		RXRA	1.00E-20	-4.75E+01					
					TTTTCAAGATGAAAA		MAFB	1.00E-17	-4.00E+01					
					TTGCAAGCACTGCACT		ZBTB3	1.00E-16	-3.71E+01					
					GCAAACTCCAGTCTT		HNFA	1.00E-13	-3.08E+01					

