

Table S9. Gene Ontology enrichment analysis on *Nkx2-5*⁺ EB CPs (*P*<0.05)

GO biological process complete	Background frequency	Sample frequency	expected	Fold Enrichment	+/-	P value	
mesenchyme morphogenesis	31	6	0.4	15	+	2.90E-02	Smad4, Lef1, Snai1, Notch1, Ctnnb1, Rbpj
mRNA processing	338	20	4.42	4.53	+	2.31E-04	C1qbp, Zrsr2, Lsm6, Clns1a, Srrm1, Pabpc2, Prpf4, Kin, Celf6, Cpsf2, Eftud2, Zpr1, Tsen15, Pde12, Ppil3, Pabpc1, Strap, Prpf39, Fam103a1, Scaf4
mRNA metabolic process	395	22	5.16	4.26	+	1.35E-04	C1qbp, Zrsr2, Lsm6, Clns1a, Srrm1, , Auh, Pabpc2, Prpf4, Kin, Celf6, Cpsf2, Eftud2, Mex3d, Zpr1, Tsen15, Pde12, Ppil3, Pabpc1, Strap, Prpf39, Fam103a1, Scaf4
RNA processing	590	23	7.71	2.98	+	2.97E-02	C1qbp, Zrsr2, Lsm6, Wdhd1, Clns1a, Srrm1, Pabpc2, Prpf4, Noc4l, Kin, Celf6, Cpsf2, Eftud2, Zpr1, Tsen15, Pde12, Ppil3, Pabpc1, Strap, Prpf39, Fam103a1, Scaf4, Cih1a
regulation of transcription from RNA polymerase II promoter	1560	46	20.38	2.26	+	1.52E-03	Klf13, Cbx2, Hmg20a, Insig2, Smad4, C1qbp, E2f8, Ctbp2, Evx1, Lhx2, Rfx1, Taf4a, Scap, Lef1, Lef1, Mtf1, Rnf2, Cbfa2t2, Zpr1, Etv2, Sall4, Per1, Itgb1bp1, Snai1, Wdr61, Skil, Rbck1, Triap1, Foxk2, Setdb1, Strap, Ecm1, Gal, Notch1, Irf1, Ctnnb1, Rbpj, Med14, Hexim1, Strn3, Tcf3, Wwc2, Sap130, Dab2ip, Cry1, Crtc3
RNA metabolic process	2532	74	33.08	2.24	+	1.50E-07	Hmg20a, Zrsr2, Smad4, C1qbp, Lsm6, Klf13, Cbx2, Chaf1b, Wdhd1, E2f8, Clns1a, Ctbp2, Prpf4, Setd1b, Kdm4b, Rfx1, Auh, Taf4a, Lhx2, Srrm1, Pabpc2, Med23, Pcgf3, Kin, Celf6, Lef1, Atoh8, Noc4l, Elp4, Mtf1, Rnf2, Cpsf2, Dna2, Sall4, Eftud2, Zpr1, Mex3d, Atg5, Etv2, Tsen15, Per1, Cdca7, Vps36, Wdr61, Setdb1, Itgb1bp1, Snai1, Cdca7l, Skil, Pde12, Adnp2, Foxk2, Ppil3, Strap, Notch1, Irf1, Zkscan1, Chaf1a, Thap1, Pabpc1, Hexim1, Tcf3, Ctnnb1, Rbpj, Med14, Atmin, Prpf39, Scaf4, Cih1a, Cry1

							,Crtc3,Fam103a1,Sap130,Mier3
positive regulation of nucleobase-containing compound metabolic process	1408	40	18.39	2.17	+	2.56E-02	Klf13,Insig2,Smad4,E2f8,Ctbp2,Evx1,Nif3l1,Tinf2,Lhx2,Taf4a,Scap,Lef1,Mtf1,Cbfa2t2,Ube2v2,Zpr1,Dna2,Etv2,Sall4,Per1,Irgb1bp1,Snai1,Wdr61,Rbck1,Trip1,Foxk2,Gal,Notch1,Irf1,Pabpc1,Ctnnb1,Rbpj,Rnf219,Med14,Strn3,Cdc42,Tcf3,Atmin,Dab2ip,Crtc3
nucleic acid metabolic process	3007	85	39.28	2.16	+	1.57E-08	Hmg20a,Zrsr2,Smad4,C1qbp,Lsm6,Klf13,Cbx2,Chaf1b,Wdhd1,E2f8,Clns1a,Ctbp2,Prpf4,Setd1b,Kdm4b,Rfx1,Auh,Taf4a,Tinf2,Lhx2,Srrm1,Pabpc2,Med23,Pcgf3,Kin,Un g,Celf6,Lef1,Atoh8,Noc4l,Msh6,Ncapg2,Rfc5,Elp4,Mtf1,Rnf2,Ncapd2,Cpsf2,Dna2,Bahcc1,Sall4,Ube2v2,Eftud2,Zpr1,Mex3d,Atg5,Etv2,Tsen15,Per1,Cdca7,Vps36,Wdr61,Setdb1,Irgb1bp1,Snai1,Cdca7l,Skil,Pde12,Adnp2,Foxk2,Exo1,Ppil3,Strap,Notch1,Irf1,Zkscan1,Chaf1a,Thap1,Pabpc1,Hexim1,Tcf3,Ctnnb1,Rbpj,Med14,Atmin,Prpf39,Scaf4,Cirh1a,Cry1,Crtc3,Fam103a1,Smardc1,Sap130,Mier3,Dtl
gene expression	2679	74	35	2.11	+	2.01E-06	Hmg20a,Zrsr2,Smad4,C1qbp,Lsm6,Mrlp15,Klf13,Cbx2,Chaf1b,Wdhd1,E2f8,Clns1a,Ctbp2,Prpf4,Setd1b,Kdm4b,Rfx1,Taf4a,Lhx2,Srrm1,Pabpc2,Med23,Pcgf3,Kin,Celf6,Lef1,Atoh8,Noc4l,Elp4,Mtf1,Rnf2,Eif3m,Cpsf2,Sall4,Eftud2,Zpr1,Eif1a,Etv2,Tsen15,Per1,Cdca7,Vps36,Wdr61,Setdb1,Eif2d,Irgb1bp1,Snai1,Cdca7l,Skil,Pde12,Adnp2,Foxk2,Ppil3,Strap,Notch1,Irf1,Zkscan1,Chaf1a,Thap1,Eif1a,Pabpc1,Hexim1,Tcf3,Ctnnb1,Rbpj,Med14,Atmin,Prpf39,Scaf4,Cirh1a,Cry1,Crtc3,Fam103a1,Sap130,Mier3,Eif1a
nucleobase-containing compound metabolic process	3714	99	48.52	2.04	+	3.53E-09	Psmc2,C1qbp,Lsm6,Klf13,Cbx2,Chaf1b,Wdhd1,Clns1a,Hmg20a,Zrsr2,Smad4,Dpyl5,Rab34,E2f8,Ctbp2,Atp6v1g1,Prpf4,Setd1b,Kdm4b,Tinf2,Lhx2,Pabpc2,Rfx1,Auh,T

							af4a,Srrm1,Med23,P cgf3,Celf6,Noc4l,Rab 18,Rfc5,Mtf1,Kin,Ung ,Lef1,Atoh8,Msh6,Nc apg2,Elp4,Cpsf2,Dna 2,Sall4,Ube2v2,Eftud 2,Etv2,Rnf2,Ncapd2, Bahcc1,Zpr1,Mex3d, Atg5,Tsen15,Per1,W dr61,Papss1,Itgb1bp 1,Snai1,Adnp2,Foxk2 ,Cdca7,Vps36,Setdb 1,Cdca7l,Skil,Pde12, Exo1,Notch1,Irf1,Nt5 c2,Chaf1a,Thap1,Pa bpc1,Ppil3,Strap,Zks can1,Dlg3,Fut8,Hexi m1,Cdc42,Ctnnb1,Ad al,Tcf3,Rbpj,Med14, Atmin,Prpf39,Cirh1a, Cry1,Fam103a1,Sma rcad1,Sap130,Mier3, Dtl,Cenpe,Scaf4,Crtc 3,Spast,Rragc
negative regulation of macromolecule metabolic process	1783	47	23.29	2.02	+	2.46E-02	
RNA biosynthetic process	1901	50	24.83	2.01	+	1.21E-02	
cellular nitrogen compound metabolic process	3977	103	51.96	1.98	+	5.60E-09	
transcription, DNA-templated	1894	49	24.74	1.98	+	2.47E-02	
nucleic acid-templated transcription	1894	49	24.74	1.98	+	2.47E-02	
cellular aromatic compound metabolic process	3880	100	50.69	1.97	+	1.98E-08	
heterocycle metabolic process	3848	99	50.27	1.97	+	3.01E-08	
organic cyclic compound metabolic process	4065	103	53.11	1.94	+	2.19E-08	
nitrogen compound metabolic process	4295	108	56.11	1.92	+	7.50E-09	
regulation of transcription, DNA-templated	2798	70	36.55	1.92	+	4.06E-04	
nucleobase-containing compound biosynthetic process	2121	53	27.71	1.91	+	2.52E-02	
regulation of nucleic acid-templated transcription	2811	70	36.72	1.91	+	4.87E-04	
regulation of RNA biosynthetic process	2817	70	36.8	1.9	+	5.29E-04	
regulation of RNA metabolic process	2899	72	37.87	1.9	+	3.29E-04	
regulation of nucleobase-containing compound metabolic process	3156	78	41.23	1.89	+	8.97E-05	
cellular nitrogen compound biosynthetic process	2229	55	29.12	1.89	+	2.31E-02	
organelle organization	2322	57	30.33	1.88	+	1.72E-02	
cellular macromolecule biosynthetic process	2589	63	33.82	1.86	+	5.92E-03	
regulation of cellular macromolecule biosynthetic process	3061	74	39.99	1.85	+	6.02E-04	
macromolecule	2613	63	34.14	1.85	+	8.09E-	

biosynthetic process						03	
cellular macromolecule metabolic process	5071	122	66.25	1.84	+	2.06E-09	
regulation of gene expression	3350	80	43.76	1.83	+	2.47E-04	
regulation of nitrogen compound metabolic process	3377	80	44.12	1.81	+	3.50E-04	
regulation of macromolecule biosynthetic process	3173	74	41.45	1.79	+	2.50E-03	
cellular component organization	3866	90	50.51	1.78	+	7.81E-05	
cellular component organization or biogenesis	3998	93	52.23	1.78	+	4.04E-05	
regulation of cellular biosynthetic process	3287	74	42.94	1.72	+	9.66E-03	
macromolecule metabolic process	5678	126	74.18	1.7	+	2.24E-07	
cellular biosynthetic process	3254	72	42.51	1.69	+	2.64E-02	
regulation of biosynthetic process	3358	74	43.87	1.69	+	2.14E-02	
regulation of macromolecule metabolic process	4530	99	59.18	1.67	+	2.61E-04	
organic substance biosynthetic process	3349	73	43.75	1.67	+	3.78E-02	
biosynthetic process	3415	74	44.61	1.66	+	3.93E-02	
cellular metabolic process	6983	149	91.23	1.63	+	1.15E-08	
primary metabolic process	7178	151	93.77	1.61	+	2.28E-08	
regulation of primary metabolic process	4476	94	58.47	1.61	+	4.59E-03	
regulation of cellular metabolic process	4677	98	61.1	1.6	+	2.54E-03	
regulation of metabolic process	5339	111	69.75	1.59	+	3.63E-04	
organic substance metabolic process	7455	153	97.39	1.57	+	1.12E-07	
metabolic process	8031	160	104.92	1.53	+	2.66E-07	
cellular process	12681	209	165.66	1.26	+	7.68E-04	
biological process	20617	287	269.34	1.07	+	1.72E-02	
Unclassified	1658	4	21.66	< 0.2	-	0.00E+00	
neurological system process	1822	4	23.8	< 0.2	-	2.49E-03	
sensory perception	1525	2	19.92	< 0.2	-	1.91E-03	
sensory perception of smell	1099	1	14.36	< 0.2	-	4.54E-02	
detection of stimulus involved in sensory perception	1173	1	15.32	< 0.2	-	1.75E-02	
detection of stimulus	1266	1	16.54	< 0.2	-	5.22E-03	
G-protein coupled receptor signaling pathway	1840	1	24.04	< 0.2	-	2.42E-06	