

combp results

Guannan Shen

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Contents

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## [1] "/home/guanshim/Documents/gitlab/ECCHO_github/DataProcessed/combp"

## X.chrom      start      end      min_p n_probes      z_p z_sidak_p
## 1 chr7 157644160 157644606 0.010140      4 3.773e-05 0.81280
## 2 chr7 95026248 95026299 0.089060      1 2.900e-04 1.00000
## 3 chr6 170535854 170535905 0.041730      1 2.582e-04 1.00000
## 4 chr6 147124930 147125453 0.038620      6 1.479e-05 0.42890
## 5 chr6 164506981 164507215 0.055410      2 3.534e-04 1.00000
## 6 chr6 30297174 30297678 0.001693     11 1.277e-06 0.04895
##      refGene_name refGene_distance      refGene_feature
## 1      PTPRN2      0      intron
## 2      PON3      -561      intergenic
## 3      LOC154449      27516      intergenic
## 4      ADGB;KATNBL1P6      0;0      intron;nc_exon
## 5      LOC102724152      -414465      intergenic
## 6 TRIM39;TRIM39-RPP21      0;0 intron+cds;intron+cds
##      cpGISlandExt_name cpGISlandExt_distance cpGISlandExt_feature
## 1      CpG: 19      -3194      <NA>
## 2      CpG: 58      126      shore
## 3      CpG: 68      5182      <NA>
## 4      CpG: 24      204685      <NA>
## 5      CpG: 52      113157      <NA>
## 6      CpG: 103      2103      shore

##      pid infant_sex maternal_age      Race birth_weight
## 1 10010      Female      24      All others      3562
## 2 10012      Female      28 Non-Hispanic white      3270
## 3 10015      Female      28      All others      3588
## 4 10019      Female      21 Non-Hispanic white      3308
## 5 10023      Female      31 Non-Hispanic white      3115
## 6 10032      Female      31      All others      3208
##      ipv3_pp_fm_pct Chol_IPV3 FFA_IPV3 Gluc_IPV3 HDL_IPV3 Insu_IPV3 Trig_IPV3
## 1      14.60      39      105      110      19      10      21
## 2      10.65      58      719      144      21      11      78
## 3      13.20      81      382      80      30      13      32
## 4      11.50      37      133      84      18      8      24
## 5      6.60      50      570      125      24      31      50
## 6      10.30      73      251      87      34      10      77
##      Leptin_actual_ng_ml_      Bcell      CD4T      CD8T      Gran
## 1      16.843 0.11754765 0.16278378 0.1834083 0.40891895
## 2      24.391 0.10578653 0.11867605 0.2077634 0.31831334
## 3      12.291 0.16126622 0.25813746 0.3092699 0.09279149
## 4      20.658 0.14345471 0.19545818 0.1212067 0.36735010
## 5      21.292 0.04381055 0.02577342 0.1384002 0.52990516
## 6      17.368 0.15614951 0.14449892 0.1568786 0.27863095
##      Mono      NK      nRBC PFHXS_ng_ml PFOA_ng_ml PFOS_ng_ml
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## 1 0.09978678 0.000000000 0.07360455      0.4      2.1      3.5
## 2 0.10946521 0.131339579 0.04937575      0.9      1.9      6.5
## 3 0.15924291 0.007852405 0.08165615      3.8      1.7      6.3
## 4 0.14560996 0.000000000 0.06125634      0.4      3.0      7.6
## 5 0.09781404 0.056007693 0.12422596      1.2      2.4      7.6
## 6 0.04487677 0.052744528 0.20331001      0.9      0.9      3.1
##      lnpfhxs      lnpfoa      lnpfos
## 1 -0.9162907  0.7419373 1.252763
## 2 -0.1053605  0.6418539 1.871802
## 3  1.3350011  0.5306283 1.840550
## 4 -0.9162907  1.0986123 2.028148
## 5  0.1823216  0.8754687 2.028148
## 6 -0.1053605 -0.1053605 1.131402

## [1] 4.943e-13 6.985e-04

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X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_distance	refGene_fea
chr11	6291339	6292947	12	0.0000000	CCKBR	0	intron+utr3
chr13	52419265	52419765	8	0.0000028	TMEM272	0	TSS+exon+
chr11	32449163	32450743	11	0.0000144	WT1	0;0	nc_intron+
chr16	857454	858550	6	0.0002707	PRR25	0	intron+cds
chr5	83016630	83017972	10	0.0042280	HAPLN1	0	TSS+exon+
chr14	106321551	106322480	7	0.0056520	MIR4507	1812	intergenic
chr16	57391655	57392249	4	0.0081880	CCL22	-445	intergenic
chr5	141488016	141488662	9	0.0265300	NDFIP1	0	TSS+intron
chr13	107354273	107355044	9	0.0291100	LINC00443	29745	intergenic
chr3	49236376	49237551	9	0.0299500	CCDC36	0;0	TSS+intron
chr22	19949585	19950217	8	0.0341900	COMT	0;0	TSS+utr5+
chr11	58830191	58830908	4	0.0374200	LOC283194	-4266	intergenic
chr8	1899943	1900451	5	0.0441700	ARHGEF10	0	intron
chr6	30297174	30297678	11	0.0489500	TRIM39;TRIM39-RPP21	0;0	intron+cds;
chr17	2907678	2908420	6	0.0658200	RAP1GAP2	0	intron
chr22	50585197	50585478	8	0.1052000	MOV10L1	0	intron
chr2	3704363	3705322	8	0.1192000	ALLC	-467	intergenic
chrX	8751190	8751738	7	0.1393000	FAM9A	7097	intergenic

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_c
chr16	8806359	8807077	12	0.0000002	ABAT	0;0
chr7	95025194	95026723	25	0.0000011	PON3	0
chr5	126408756	126409604	13	0.0000022	C5orf63	0
chr8	143859143	143860041	12	0.0000099	LYNX1-SLURP2;LYNX1	0;0
chr20	62178498	62179803	7	0.0000133	SRMS	0
chr1	248099757	248101060	13	0.0000153	OR2L13	0
chr6	291687	293336	10	0.0000822	DUSP22	0;0
chr6	30094300	30095853	30	0.0000956	TRIM40	-8063
chr15	34501719	34503044	11	0.0004745	KATNBL1	0
chr2	114035983	114037111	5	0.0006693	PAX8	0
chr16	88843923	88845255	8	0.0027820	PIEZO1	0
chr6	42927281	42928971	30	0.0042370	CNPY3-GNMT;CNPY3-GNMT;GNMT;GNMT	0;0;0;0
chr6	33872251	33873783	8	0.0065580	MIR7159	5274
chr17	71898027	71898955	7	0.0066980	LINC00469	-73351
chr20	36148133	36149506	39	0.0081610	BLCAP	0;0

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_c
chr17	767301	767431	3	0.0118100	NXN	0;0
chr15	93616424	93617219	14	0.0159700	RGMA	0;0;0;0
chr16	857454	858550	6	0.0162900	PRR25	0
chr20	62209427	62209916	4	0.0184700	HELZ2	-3835
chr4	53010	53413	9	0.0226800	ZNF718;ZNF718;ZNF595;ZNF595	0;0;0;0
chr5	132113386	132114674	11	0.0236800	SEPT8	0
chr10	21456020	21456090	2	0.0279800	NEBL	0
chr17	79919578	79919778	2	0.0395700	NOTUM	-515
chr1	203044677	203045280	5	0.0402000	PPFIA4	0
chr13	51639953	51640493	5	0.0469500	GUCY1B2	0
chr12	133003394	133003979	3	0.0477500	FBRSL1	-62757
chr12	131196378	131196516	3	0.0573400	RIMBP2	0
chr12	131118426	131118705	4	0.0643400	RIMBP2	0
chr10	135160697	135161098	8	0.0700000	PRAP1	0
chr19	51774377	51775162	6	0.0728100	LINC01872	0
chr17	80189381	80190205	9	0.1437000	SLC16A3	0;0
chr2	74347215	74347827	5	0.1531000	TET3	11913
chr11	57003857	57004345	3	0.1685000	APLNR	0;0
chrX	53448902	53449951	12	0.1696000	SMC1A;RIBC1;SMC1A	0;0;0
chr2	75937660	75938810	12	0.1893000	GCFC2	0;0
chr11	1989186	1990486	8	0.1931000	MRPL23	11357

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_distance	r
chr13	52419265	52419765	8	0.0000002	TMEM272	0	T
chr11	128554586	128556662	10	0.0000338	LOC101929538;FLI1	0;0	n
chr7	95025194	95026723	25	0.0001908	PON3	0	T
chr11	14280333	14281104	5	0.0014920	SPON1	0	i
chr12	739280	740389	4	0.0024660	NINJ2;LOC100049716;NINJ2;NINJ2	0;0;0;0	n
chr3	49170496	49171394	10	0.0033400	LAMB2	-13	i
chr18	72916012	72916827	4	0.0053410	ZADH2	0;0	i
chr11	58830191	58830908	4	0.0120900	LOC283194	-4266	i
chr1	156211409	156212056	10	0.0165600	BGLAP;PMF1-BGLAP	0;0	T
chr15	42565872	42566713	12	0.0181300	GANC	0;0	i
chr8	28174192	28175514	10	0.0193900	PNOC	0	T
chr2	239139911	239140961	10	0.0198200	LOC643387;LINC02610	0;0	n
chr16	857454	858550	6	0.0205900	PRR25	0	i
chr11	2464822	2465542	15	0.0255900	KCNQ1	-678	i
chr11	1990900	1991239	3	0.0435600	MRPL23	13071	i
chr7	56515510	56516555	12	0.0454400	LOC650226	0	n
chr4	53010	53413	9	0.0545000	ZNF718;ZNF718;ZNF595;ZNF595	0;0;0;0	n
chr12	127630314	127630863	3	0.0695700	LINC02405	-85372	i
chr11	66102055	66102737	6	0.1298000	RIN1	0	i
chr5	138713750	138714390	7	0.1304000	SLC23A1	0	i
chr10	1505595	1506226	4	0.1408000	ADARB2	0	i
chr3	138763424	138764244	9	0.1480000	PRR23C	0	T
chr19	54484823	54485781	8	0.1500000	CACNG8;MIR935	0;0	i
chr1	2120985	2121775	6	0.1583000	FAAP20	0;0;0;0	n
chr11	57003857	57004345	3	0.1619000	APLNR	0;0	c
chr16	88952491	88953495	3	0.1713000	CBFA2T3;LOC101927793	0;0	i
chr19	51815281	51815709	4	0.1824000	IGLON5	0	i

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_distance
chr6	32119616	32121617	45	0.0000196	PPT2;LOC100507547;PRRT1;PRRT1	0;0;0;0
chr6	30078632	30079713	20	0.0000251	TRIM31-AS1;TRIM31;TRIM31	0;0;0
chr6	30038754	30039852	38	0.0000489	RNF39	0
chr6	53530503	53530679	6	0.0001051	KLHL31	0
chr1	39249315	39249715	5	0.0002384	RRAGC	54153
chr8	105379368	105380036	6	0.0007721	DCSTAMP	10451
chr8	689326	690110	5	0.0016010	LOC401442;DLGAP2;DLGAP2	0;0;0
chr7	18534872	18535837	9	0.0036910	HDAC9	0;0;0;0
chr7	94953653	94954506	11	0.0047640	PON1	0
chr20	48185517	48186225	3	0.0051400	PTGIS	-843
chr1	161008127	161009028	11	0.0052520	TSTD1	0
chr3	30936070	30936582	9	0.0113200	GADL1	0
chr7	134464123	134464462	6	0.0127600	CALD1	0
chr5	27038605	27038887	5	0.0133600	CDH9	0
chr7	42896343	42897368	5	0.0135100	C7orf25	51503
chr3	183959000	183959904	10	0.0149300	VWA5B2;MIR1224	0;0
chr14	24422368	24423250	9	0.0176200	DHRS4-AS1;DHRS4-AS1;DHRS4	0;0;0
chr20	31366437	31366537	3	0.0636300	DNMT3B	0
chr5	162864768	162865287	4	0.1323000	CCNG1	0;0;0;0
chr19	310296	310563	3	0.1334000	MIER2	0

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_distance	refGene_type
chr6	31733619	31734631	19	0.0000000	VWA7	0	intro
chr7	94953653	94954506	11	0.0000003	PON1	0	TSS
chr6	30038754	30039852	38	0.0000032	RNF39	0	intro
chr3	45077070	45078126	9	0.0000080	CLEC3B	0	utr3
chr8	16859045	16860172	11	0.0000259	FGF20	0	TSS
chr10	82295394	82296242	6	0.0000413	LOC101929574	0	nc_
chr4	187219230	187220029	5	0.0000811	F11-AS1	0	nc_
chr6	32846924	32847896	20	0.0001919	LOC100294145	-14056	inter
chr10	32216031	32216441	6	0.0007851	ARHGAP12	0	intro
chr1	228890820	228891357	5	0.0009195	RHOU	8404	inter
chr19	45448413	45449352	7	0.0011770	APOC4;APOC4-APOC2;APOC2	0;0;0	utr3
chr12	95840313	95841465	7	0.0012260	METAP2	-26356	inter
chr10	35894012	35894481	7	0.0045960	GJD4	0	TSS
chr13	100217962	100219064	6	0.0088890	TM9SF2	1660	inter
chr6	31275148	31276488	18	0.0098580	LINC02571	-5734	inter
chr6	32551749	32552721	8	0.0118000	HLA-DRB1	0	intro
chr11	126455596	126456702	7	0.0160100	KIRREL3	0	intro
chr1	206786000	206786231	5	0.0258500	EIF2D	-96	inter
chr16	31711160	31711262	2	0.0285100	CLUHP3	-671	inter
chr10	77871618	77872509	8	0.0292000	LRMDA	0;0	intro
chr6	79339195	79339569	3	0.0400000	IRAK1BP1	-237698	inter
chr1	26880207	26881060	6	0.0465200	MIR1976;RPS6KA1	0;0	nc_
chr8	38831508	38832779	8	0.0494900	HTRA4	0	TSS
chr5	66461884	66462713	4	0.0542200	MAST4	0	cds
chr11	93398567	93398618	1	0.0886700	CEP295	0	intro
chr15	26873818	26875065	7	0.0944900	GABRB3	0;0;0;0	TSS
chr10	134775542	134776101	5	0.1178000	LINC01166;LINC01167	0;0	nc_
chr22	27834439	27834680	3	0.1267000	LINC02554	120638	inter
chr13	110521956	110522348	5	0.1442000	IRS2	-83026	inter

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_distance	refGene_feature
chr1	39249315	39249715	5	0.1776000	RRAGC	54153	intron
chr1	224032648	224033261	4	0.1831000	TP53BP2	0;0	intron

X.chrom	start	end	n_probes	z_sidak_p	refGene_name	refGene_distance	refGene_feature
chr1	75198211	75199547	12	0.0000000	TYW3;TYW3;CRYZ	0;0;0	TSS+intron
chr11	2919689	2920840	18	0.0000054	SLC22A18AS	0;0	intron+cds;
chr6	31690725	31692426	37	0.0000149	MPIG6B	0	TSS+intron
chr19	1851750	1852216	5	0.0000604	KLF16	181	intergenic
chr1	39249315	39249715	5	0.0000988	RRAGC	54153	intergenic
chr6	30420981	30421706	14	0.0001013	HLA-E	-35579	intergenic
chr1	26880207	26881060	6	0.0002795	MIR1976;RPS6KA1	0;0	nc_exon;int
chr6	30419201	30419663	7	0.0002947	HLA-E	-37622	intergenic
chr22	45704675	45705563	9	0.0006802	FAM118A	0;0	TSS+intron
chr10	35893437	35894481	9	0.0035980	GJD4	0	TSS+exon+
chr12	54446019	54446627	10	0.0045140	HOXC4	0	intron+utr5
chr20	57426538	57428083	47	0.0052370	GNAS	0;0;0	intron+utr5
chr7	155150681	155151478	5	0.0063150	BLACE	0	nc_intron+
chr7	94953653	94954506	11	0.0106900	PON1	0	TSS+intron
chr18	7011217	7011514	4	0.0116100	LAMA1	0	intron+cds
chr11	2154386	2155572	6	0.0169100	IGF2;INS-IGF2;MIR483	0;0;0	intron+cds;
chr11	118986793	118987204	3	0.0229600	C2CD2L	0	utr3+cds
chr7	1094737	1095771	7	0.0309800	GPR146;GPR146;C7orf50	0;0;0	intron+utr5
chr12	54454163	54454496	5	0.0600800	FLJ12825	0	nc_intron
chr10	88427813	88428480	11	0.0928600	LDB3	0;0;0	TSS+utr5+
chr15	40571997	40572845	5	0.1337000	ANKRD63	0	exon
chr4	72897281	72898263	8	0.1394000	NPFFR2	0	TSS+intron
chr2	382090	382407	3	0.1808000	LINC01865	45036	intergenic