

ProbiD	Insulin_avg_Zscore	Insulin_1_z	Insulin_2_z	Insulin_3_z	cg_list	probe_table::seq
2503	-3,795213953	-4,41	-4,27	-2,71	CG16833	TCACAAATCGCGAGGCAAAGTGGCATACTATGCATT
2167	-2,67428805	-2,27	-2,64	-3,11	CG3779	GATCCCGATATATATATATGATCGCGCCCATCAATTTA
9803	-3,182700166	-3,50	-2,53	-3,52	CG7450	TTTCTATGAAAATCGAGTAAAAGCGCATGCAACAAG
13105	3,047838566	2,33	2,76	4,05	CG3937	TGGACGGACTTGAGCCAACTGACTTGCGCGTAACCA
19591	-3,071113543	-3,81	-2,73	-2,68	CG3725	GATTGGATTGGATAGGTGGCCACTGAACGAAGAGGA
19589	-2,791024802	-3,41	-2,19	-2,78	CG3725	AACAACCTTGATTTATAAAGGCCACTGAACGAAGAGGA
690	2,571097436	2,84	2,38	2,49	CG3365	ATTCGAGATTCAAAACGCAGCGCGGTCTGACGCCGCC
17582	2,834298354	2,52	3,19	2,80	CG18076	GCCGAGAAGCGGATCAAGCAAGCAGTATTCGAGAAG
7742	3,360529791	2,67	3,92	3,50	CG11486	TATCTTTTGGATTTTTCAGATACGGCTGCTATGGATC
6166	-2,375902553	-3,18	-1,85	-2,10	CG9177	CATCAAATATAACAATAAGAAAACACCAGCAAAAAAAA
6943	-2,533491916	-2,12	-2,14	-3,34	CG1417	ATAAATAATAAGAACGAACAACAACCGAGATTGGAG
12702	-2,540219015	-2,20	-2,20	-3,22	CG3731	GCGCAGCGCAGTACATTGGCTATTGAACGAATTAAT
7640	-3,040893764	-3,14	-2,90	-3,08	CG16758	GGTTCTCAACGAAGACAGTATCCCTATGAGGTCAT
3512	3,962668583	4,69	3,39	3,81	CG10334	AGCTAAATCCCAAAGTAATTTTCTAACACACACACAC
9940	-2,396322188	-1,83	-2,45	-2,92	CG4899	CTGGCCGCTGGAGCAGCGAAGGTGGCCATCATTGAT
11759	-2,984943773	-3,03	-2,84	-3,09	CG18466	AAAAGAAGTCACAATAAGCAACATGGCTCAAATTAT
4877	-3,989334153	-4,13	-4,15	-3,68	CG3168	AGAGAATAGCAACAAGAAACCGCTAAGCGAGGCAGA
17509	-2,8185317	-3,32	-2,64	-2,49	CG4832	CTCGGATTTACAATAAATAGTCGCTGCAAAATCTA
7487	-2,968924539	-2,33	-3,43	-3,14	CG7995	AACAATCGAATACAAAAAGCAGCATGCCGAGGGCA
19194	3,111642673	2,74	3,50	3,10	CG13499	CACAGAAACGAGGTAGGTGCGAGGTGGAGGCGGCGG
7708	-2,423686269	-2,00	-2,92	-2,35	CG2103	ACATATGTCTGCGATAAGACCACGTTGCGAGTGCCGC
14212	-2,566472275	-2,24	-2,99	-2,47	CG5854	CTGTTCTGATTTTGGGTGGCTGCGGCTTCATTGGAC
7483	-2,712896373	-3,16	-2,94	-2,04	CG7995	GGGGCAGTGCTAATGTGGGCAGCATGCCGAGGGCA
7644	-4,771924473	-4,16	-5,00	-5,16	CG16758	GCCCCAGGAGAATCCCACCGGCAATGAAAAATCCA
3509	3,527618602	3,77	3,33	3,48	CG10334	AGCTAAATCCCAAAGTAAATACACACATCACCCCTA
15811	-2,34893186	-2,43	-2,50	-2,12	CG8276	TAGGTGTTTTCTAACGTTGGTACATCTCAACGGAGT
15318	-3,337784673	-3,28	-4,04	-2,69	CG7950	ATATCTGGACGTGAAGATATAATTACGTTTTTAAT
6948	2,563643434	2,73	2,09	2,88	CG1417	CGAGAAACGTGAAGTTGAATCTCCGCTCCAGTGC
3638	3,236900476	3,48	3,03	3,20	CG9326	ACGATACCTCCGATAACGCCCGCTTCGCAACTCGA
7037	2,776081304	2,37	3,33	2,62	CG1210	AATGTGTGCTGCTAGCTGTTAAAGTATGCGAGAAGC
1137	-2,780215648	-3,22	-3,09	-2,03	CG10021	TCAAAATTGTCCCTTAGTAATCGTATTAACAGAAGT
14087	-2,606481584	-2,93	-2,66	-2,23	CG17894	GAGCTTCAACAAGATAAAGGACAAGAACATGAGAAT
16498	3,767050837	3,45	3,94	3,91	CG11804	AAGTAGCGGACCGTGAAGCTCCCTTAAACGCTTAAA
8446	-2,454349543	-2,19	-2,45	-2,72	CG8588	GGACGCGAGGTGGGAGCGATCACCCAAGTACTGTG
18801	-2,450058138	-2,69	-2,21		CG8201	AAGAAAAAAACACAGAAAAATTTAACAAAGTACTCT
13310	-2,670706202	-3,55	-2,16	-2,30	CG18617	TAATTCTCGTCGGCGGAGGGAACGTAAGCAGTCGCC
17075	-3,339648543	-2,85	-4,08	-3,09	CG30035	ATTTGTACCTTCTCCCAGGTCTTGGCTGCTCTGAGT
8987	-2,389301993	-2,83	-2,62	-1,72	CG6767	TACGATTGGAATTTAGGAGTCGTGCGCCATCTCG
6016	3,25542479	2,59	2,14	5,04	CG8948	AGTCCGTTCTTGATGAAAGAAGGATTACCAATATGC
10045	-2,493151751	-2,24	-2,61	-2,62	CG9674	AAATAATCTACGATCACGTGTGATTGTTCAAGCTGA
10094	-2,785409147	-3,51	-2,52	-2,33	CG11661	ACTCTGGGTTTTTGTGGCGAGCAGGACATGGATC
13446	3,123692428	2,66	3,60	3,12	CG31175	CAAGCGTGGCATTACAGGTGACCCGATTGCGAGAGC
11407	2,988915513	3,07	4,03	1,86	CG10279	CGGCAGCATGCGAGCAAAGGCCACACACGATCGCGA
9145	-5,191961027	-5,70	-5,18	-4,69	CG7958	GAAGCGCAATTCAAAAAGAAAAATGATGAAATGAA
16895	-2,4421665	-2,48	-2,30	-2,54	CG2368	AATATAAATAGCGAAAAGTACTGCGAGTATACACA
10602	-3,135024026	-3,23	-2,72	-3,45	CG5683	CAGCCACAAAATGGAAGGCACAGCAGCAACAACA
17593	3,272021661	2,43	3,63	3,76	CG18076	TCCACGCAGCGCAGAGAGATCTCCGATATTGTTGTG
16589	-3,222170303	-3,33	-3,14	-3,20	CG1516	TATGGTACGAAAAGTCAAATACATTTAAGTCCTAGG
8445	-5,298595167	-4,16	-6,79	-4,94	CG8588	GGACGCGAGGTGGGAGCGAAAGCAAAAGACGGTGAC
14882	2,591733474	3,50	2,88	1,40	CG14253	AAGTGGTACGCTACGAACATATAGTAATATGTCTCA
7740	4,490538245	4,16	4,66	4,65	CG11486	ATTATCAAATGCCAGTGTATACGGCTGCTATGGATC
1188	-2,330284038	-2,19	-2,87	-1,93	CG3714	GGAACGGATCAAAAAACCGACAATTGCAAAACAAT
16060	4,079590883	3,61	4,77	3,87	CG1600	CAATTCACAAGTAAAAGTTGGAACAACAGATACCTC
5723	3,043356608	3,09	3,08	2,96	CG1771	ATGTTTCGGATATCACATTTGTTTTAGTGGGAGCTCC
2091	3,160478506	2,64	3,86	2,98	CG12437	GGTTAAATTTCTCTCAGAGAAGTTCTGAATGCATG
16171	-2,43895671	-2,97	-1,36	-2,98	CG1882	CATAGCCAGCGGCTAGAGGATCCCGCAACAATAGA
18456	3,701203422	3,73	3,99	3,39	CG33130	CGAAGCGGACGAGAGAGGCGATTTTGTGCTGCGG
14959	2,985080559	3,19	3,34	2,43	CG5643	AAGTCCGGATGCTCGAAGTGAACACCAGCAAGCAGC
3052	2,998508471	2,34	2,90	3,75	CG31732	GAAATACCGAATTTCTTGCTGCACGAGATCACCCGG
1136	-3,004476806	-3,47	-3,17	-2,37	CG10021	GCTAGTGTGTGTGTGTGTAATCGTATTACAGAAGT
12382	-3,650474057	-5,27	-2,88	-2,81	CG10120	AAATTTTCGATGAAAATGGCAGCGGTTTTATCCAC
13470	-6,316767204	-6,66	-6,03	-6,26	CG6231	CATATATAAATAACTACAGACCAAGCCAAAGGAACAA
19102	-2,356950707	-2,15	-2,83	-2,10	CG9696	CAGCCACAACGCAACAGCCATGAGCGATCTAACTG
9171	-2,38273921	-1,89	-2,40	-2,86	CG7888	ACAGCAACAACAACACCATCATGACCAAGAATGGAC
5447	-2,627428631	-3,03	-1,86	-2,99	CG1743	GTGCATTGAAAAATCAGTATGTCCGCTAGGATCCT

12780	-5,279569592	-4,25	-6,31		CG4898	AATTACCCAAAAATTAACAAAAACACAAGTGCAGC
15158	2,733985346	3,05	3,70	1,46	CG2005	GTGGCCATGCAAAAAGAGTGCCAAAATGGAAATCAT
16280	-3,209571573	-3,36	-3,34	-2,93	CG11546	CGACATCAAAGCACGAGAATCAGTAACAGGATCAAG
6937	-5,139591129	-4,36	-6,33	-4,72	CG32527	GGCAATAATATCATTCAACGTAATATGTTTGGAT
5804	2,67894396	2,57	2,44	3,03	CG11111	AAATCCGCGGCGCAGAAGGTACCTGGAAGAAAGAC
14530	-2,63399259	-3,54	-1,72		CG13636	AGGAACTTATTTTTACATTTAAAGGACGAGAGTGCA
3507	-3,03906259	-3,52	-2,79	-2,81	CG10334	GGGTGTTTTTGTGTGCATATACACATCACCCCTA
14900	4,030980834	3,56	4,26	4,27	CG6134	ACTATCCGGACCTTTCAGACGAGCGATTCTTTGCA
5829	3,073891493	2,89	2,20	4,13	CG32626	GCGACATGTAAGTCGCCAGTGATCTCGCCGATTAC
13095	3,378130006	3,71	2,79	3,63	CG3937	CTCTCTAGCAGAGGAAAACCTGAAGTCAGAATGCCTA
13473	-5,807987829	-6,07	-4,97	-6,39	CG6231	CTTGCGGCGCATCTCTGGACCAAGCCAAAGGAACAA
14221	-3,431097273	-2,87	-4,23	-3,19	CG5320	GCATGTATCACCTGAAGAATCAACCCTAAGGAGTAC
10603	-4,115304625	-4,11	-3,98	-4,26	CG5683	AAAGCCCGCCAAAAAAGGCACTAGCAGCAACAACA
14905	2,673017648	3,07	2,78	2,17	CG6134	CCAGATCAGTACTTCAAAGGACGGACACGGAGGTG
7738	4,002530412	3,12	4,33	4,56	CG11486	ACAATTTCTTCCCGCAGATAATGTGCTCGACTTAT
12712	2,922603068	2,78	2,45	3,54	CG6904	GTCGACAATTGTTCAACTATGAATCGTCGCTTTTCG
13220	-2,900162065	-2,24	-3,24	-3,21	CG31243	CCGAATAATAACAAACTAAGCATCAAAGTGAGGAT
10488	-2,622396458	-2,68	-2,53	-2,66	CG32425	GTGGAACAAGGCAGCAGTTAATTGCAACTCGAAGG
3791	-2,902628114	-2,53	-3,65	-2,53	CG2201	CAGCATTTCATAGCAATGCCACCCCTGAGGAAATT
14411	3,474927353	2,82	3,66	3,95	CG6643	TAAGTAAACCGTCTTAAGCGATAACAGTCCATGGT
17622	3,528885034	4,40	4,37	1,82	CG6692	TCGCAGAGGGCACAATTGATTCCAGAACAATCACA
16775	2,616832148	2,03	2,64	3,18	CG18408	TACCGCCTTCCGTCCAGGCCCGTCCGTGCTACAAGA
7616	2,698857208	3,10	2,84	2,15	CG32306	ATTTTCCCGATATCGAAAAACCATTGCGGCCTCAA
5349	-4,976662377	-4,62	-5,75	-4,56	CG16944	GAAACACAAATACAAATTTGAATCGTACATCCACTA
18568	-2,675007718	-3,37	-2,56	-2,10	CG5119	ATCGAGCGTGTGTTGAGAATGGTCTAGGAATGTTG
2490	-2,532351346	-2,99	-1,32	-3,29	CG6647	TTGTGGTCATGTGAGGAGATGGCTCCTCCATCATAC
10487	3,187999461	2,84	3,81	2,91	CG32425	TCTCCTGCTTAAAGCCTGCACCGCCAGCAACGTCG
13090	-3,023117988	-3,36	-3,39	-2,32	CG3962	CCAGGGAGAGCAATGTAAGGCTGAGATGAGCAACA
14216	-2,455476117	-2,33	-2,28	-2,75	CG5320	AAAGAATCATTAATGACGAATCCGTTCAAGAGTCCC
13604	3,653438036	4,29	3,08	3,59	CG4257	AAAAAGGCAATCTGAAAGTTTCTCCTTCAACCAT
14901	3,553918469	3,57	4,05	3,04	CG6134	CATGCCCATACCCACCCAAAACCTTCTGCACGAATGT
16789	-2,73167048	-2,30	-3,08	-2,82	CG18408	TGAAGGTAACCTGTCCAGAGCTTTGGCCAAGGAATC
7641	-2,433503597	-3,41	-1,38	-2,51	CG16758	AACTCCAGAAAGTCTGCTGTATCCCTATGAGGTCAT
13610	-2,693055443	-2,70	-3,03	-2,35	CG4241	GTGCTAACAAAAACAAAGTCCCCAGTCCGAGTCT
13748	-2,449587037	-2,33	-2,57		CG17299	GATATAAAGATTTATTAGTTTTCGGCGAGCCGCACA
9424	-2,407906253	-2,94	-2,16	-2,13	CG32103	CGCGGGGAAATTTCGATACAGCTACTGTTTTCCATTT
8035	-4,679520129	-4,62	-4,33	-5,09	CG15009	CCCTGATTAATGGAGGCGAAAATGAATTTACATGTG
9292	-3,792635473	-3,06	-5,01	-3,31	CG11658	AGCCACAGCAATTTCTCGTTAAATCAAACGCGTTTC
5143	-4,032638321	-3,92	-3,29	-4,88	CG12737	AAATATATCGAGCATAAGTCCAGCTTGACGGGCAA
17569	2,57695391	2,69	2,46	2,58	CG18076	AGAACGATCCTTGTGCGCGGACGAACACTTGGCCG
5325	3,864612934	3,30	4,79	3,51	CG33175	GTGATGGATGCCATAGCCTGCTCAGCTCGCTGGCC
2869	-2,346999154	-1,93	-2,48	-2,63	CG16885	GAGCGAACCAACCAACAACAACCGCCAACGTACGAC
18566	-2,42615383	-2,55	-2,09	-2,64	CG5119	CATCGAGAACGAAAAGAAGTAGACCTGATCACCAAA
10494	3,010928025	3,04	2,96	3,03	CG5059	CCGGCTAACGAATCGAACAATCTTGATCGAACTCA
15545	5,986221963	6,27	6,37	5,32	CG11525	AAACGCGAGGGCATCCGGCTCGTAAGTTTTATTTG
11080	2,853559026	2,79	2,87	2,91	CG9765	CAAGCCATGAGTGGCGAGTGATCCGTTGGCGGTG
17917	2,682192596	2,52	3,34	2,20	CG30084	ACGGCTGTCTGTGAGAAAGTGCACAGGAGGCTCAAA
8577	-2,462798336	-2,68	-2,25	-2,46	CG17888	TTAGCCAGCCAGCTCAGGCAGGAAATCTCCGTTTT
647	2,552030255	1,94	2,34	3,38	CG4280	CGCATATAAACGCTTCTGGCACCAAAAGGTAAGGGA
16793	-2,557762717	-2,50	-2,12	-3,05	CG18408	ACACCGTTCGACGGATCAGACGTGAACATCCACTCA
532	-2,969276067	-2,95	-3,27	-2,69	CG2674	CCTTTGTTCAAACCCACACTCCACCAACAATTTAGC
18850	-2,403334858	-2,47	-2,11	-2,63	CG9854	CTACACAGGAAGAAAAGGCATTTTTATTAAGCGCAGT
12485	-2,378522543	-2,84	-1,68	-2,62	CG8863	TTCTACAAAAAAAATGGTAAACAGCAAAACAAATG
7737	3,91967329	2,95	2,99	5,82	CG11486	CTCATTAAAGTAATTACGTGACGCGCCTCAATTGT
11687	-2,379896395	-1,56	-2,26	-3,32	CG8036	TAGAGGTGACCAGCTCAACCATCCACATCATGTGC
537	-3,10278466	-3,17	-3,08	-3,06	CG2674	AAGAATACACCCCAATGACAAAATGTGCGACCCAAA
6430	-3,177480716	-2,66	-3,44	-3,43	CG5172	ATGGAGGTGGCAATCAAGGTGGCCACGAGGACAAG
15542	-3,603564985	-3,55	-3,47	-3,79	CG11525	CAAATGGCTGTAAAAACGTAAGTGGCCAGCCCTCA
17344	-6,052627427	-6,49	-5,55	-6,13	CG8772	AGAGGATAATGCCAAGCTCAGTCAGAGACGCCACTA
2634	-3,759659553	-3,57	-5,08	-2,62	CG6756	GTAAGTTTTTAAAAAAGTTTCATCACACATAACACA
16907	3,264944413	3,88	3,39	2,52	CG2368	CTGGCTTGGCGAGAAAGATGCATTAAAGAACCCAAA
16989	3,778521638	4,03	3,62	3,68	CG12313	ATTGTGCGCCTTTAAAAATAAGAGCTAAGTAGATGAT
10091	-2,655696096	-1,89	-2,71	-3,37	CG11661	TTCCGCGACACAGCTACCCCTTGAACCAGATCTTC
14427	2,958310599	2,92	2,93	3,02	CG13624	TCGTTTTTATACATTCAGTTGGCATTAAATAGTG
19932	-2,326499812		-2,70	-1,95	CG9380	CATTGTTGACTATATAGCTTATGTTATACAGCAGCT
11294	3,13772617	3,34	3,54	2,53	CG2922	ATATCCTTGGGTGAAAGCCAATTTATTGTATGAGTC

17431	2,616825842	2,52	2,91	2,42	CG17054	AAGCTGATGATCGGCAATGCTTTCCGGCGCAACATG
1953	3,147290607	2,95	3,13	3,36	CG8222	CGATCAATGAACAACAATTGCCTTTGCAGCAGTTCT
7633	-2,420644152	-3,47	-2,05	-1,74	CG1146	GACACCACTTGAAGAAAGAGTGTATGTATGTCATAA
17807	-2,866357282	-2,29	-2,65	-3,66	CG8095	GAGCCTGCGACCCAATGGCATCATTGTGGGAGCCCC
4375	2,547567704	3,51	2,26	1,87	CG7981	TGAGGAAGCGCAGCTTCGGCGCTACCCCGCCACCCA
3840	3,374365514	4,14		2,60	CG2238	CGACTGTGAAGACTTAGTGTCAACTTCACCGTCGAC
1949	2,853186433	2,92	3,40	2,24	CG8222	GAGATGACCAGCATAGAAAAGACGGCAAACCGCTGC
5326	4,344231981	4,11	4,86	4,06	CG33175	GGCATTGGCGTTCCCTGGCGGCAAAGGAGCACGTA
10339	-2,561657213	-3,06	-2,65	-1,97	CG8533	CCGGTTATATATTCCAAGATCAACCTAACATCCTGG
12381	-3,352454149	-3,29	-3,28	-3,49	CG10120	CAGAAAACTTTTGGACCCACGCCGGTTTATCCAC
13471	-4,577166928	-4,47	-4,81	-4,46	CG6231	TATCTGGCCTTTAAAAGTACCAAGCCAAAGGAACAA
13509	-4,42167155	-4,37	-4,81	-4,09	CG4608	TTCGCTCTACTACGATTTCTGTGTCTGCAGCTAAT
5033	-5,198272891	-6,16	-5,18	-4,26	CG2252	CATATGAAAAAGCTAAAATTGCAACTTTTAAACAAT
13410	-2,575963902	-2,44	-2,50	-2,78	CG5558	GGAGCCAAAGAAAGAACAACCTTGGCGGAGGCCTTGA
1364	2,705674283	2,72	2,39	3,01	CG14029	AGTCATAAATACGGCTAATTCGCCGCATCCAAGCTC
8574	-2,962225374	-2,88	-3,06	-2,94	CG17888	TTCAGCCAGCCAGCTCAGGCAAATCCACATCGAATA
2502	-2,422502768	-2,42	-2,60	-2,25	CG16833	TTTGCTATTAGTTATATTTTTTGCCTCCATTTTAC
15701	-3,979083643	-2,37	-3,74	-5,83	CG30438	ATATCAATAAAAAAAAAAACAACATGCTTAAAAAAAT
5346	-3,33794831	-3,52	-3,54	-2,95	CG16944	ATCCATAACATCACAAAGCAAAATGGGCAAGGATTT
15258	-2,584601538	-2,39	-2,87	-2,49	CG7816	TGTTACAGCTGAATAACGCCGAGTCAATCATCGATCA
17341	-4,420463106	-4,42	-4,86	-3,97	CG8772	CCACTATTTCGATGCGGCCCATCGCGAGCAGGAGCA
10722	-2,545502643	-3,42	-2,03	-2,19	CG7145	GCCTGAAACTCACAAAAATAGCAAATTTCTAGGTG
12970	2,619935724	2,80	2,73	2,33	CG6963	TTCACCGGAGTCCACCGGTGGCGGTGGCCACAAC
16880	2,537551015	2,29	2,65	2,67	CG12052	AGCAACGGGATCCCCAAGATTTCCGTACTAACCTGGT
10183	-3,424295293	-3,17	-3,85	-3,25	CG3979	TGACTAATCATCACCGATCTACAGCCACCGCCA
3107	3,212470787	3,49	2,70	3,44	CG12448	TGCATTAAGGGAATCTGATCTGCTAAGTAAGATCGA
7484	-2,614821752	-2,89	-2,96	-2,00	CG7995	GGGGCAGTGCTAATGTGGCATGACCGAGGGCAAGAA
13472	-5,124714494	-5,49	-5,01	-4,87	CG6231	AGAGTTTCTCACAGGCCAAGCAAGCCAAAGGAACAA
5803	2,791471964	2,69	3,18	2,50	CG11111	AAATCCGCGGCGCAGAAGGCTGCATGAACAAGCAAC
7481	-3,414504373	-4,35	-2,15	-3,74	CG2086	CTGCAAAAAGAAGAGAATATATAACGTAGACGGTTGT
204	-2,80733677	-2,52	-2,46	-3,44	CG1507	ATGGCATCTCAGGATCAAAATATAATGTTGCAAAATA
2106	3,341987814	2,98	3,90	3,14	CG9520	AAGGAAGAGCAAACGAAGAAAATGTAAGGAGAAGCT
2814	-3,389205207	-4,69	-2,20	-3,28	CG9239	TGCAGTCTTTGCTCAGACGAAGTGTAAATCGACA
1510	-2,361338628	-2,42	-2,38	-2,28	CG31641	GAAAAAGTTCAAAACTCGAACGTCGCGCTGAGCTC
17806	2,559031267	2,88	2,44	2,36	CG8095	TGTCATCCGCCAGACCAGCATATTGTGGGAGCCCC
6981	-3,984908466	-3,99	-3,05	-4,91	CG14619	CTAAACGACAGCAGCAAGACGTTGGCGAGAAGTGGC
11685	-3,568917728	-3,28	-2,32	-5,10	CG8036	AAAGCTAATAAGGATAAGCGCCGACGATAGACGATA
5293	-2,352437052	-2,48	-2,28	-2,30	CG32684	AAAGGAGAGCGAAGAGAAAGAACTGAGAAAACATA
12851	-2,742265933	-2,93	-2,69	-2,61	CG14869	ATGAAGCGTATCAGTGAGTTTGATACGACCACGCAG
13967	-3,629333517	-4,57		-2,69	CG7059	AATGCGCGAAATTCAGGCCTCCCAATTTATGACGAA
13091	-3,433743732	-3,43	-4,48	-2,39	CG3962	AAATAAATAAATACAGATAGGCTGAGATGAGCAACA
10935	2,730819249	3,04	2,52	2,64	CG1106	ACAGCCGTTTCAAATAGACCTGCTTGTGTTTTTGGC
9000	-3,234480971	-2,91	-3,24	-3,56	CG18177	CGAAATGTGAACAAGGAGGACAAGGGCATCTGCCG
3008	-2,849398639	-2,21	-2,95	-3,40	CG4170	GAAACACTGAAAATTAAGAGCAAAAAGGCAATTTAAA
7642	-2,546223694	-2,35	-2,01	-3,28	CG16758	CACTCCACAGAGCCTGCTGTATCCCTATGAGGTCTAT
12216	-4,481058199	-4,09	-4,84	-4,52	CG17342	AGGCAGCAACATGTTAGACGGCAGAAATGAGCTGA
1955	2,966861103	2,35		3,58	CG8222	CAGAAACACCCAAATAAATGCAACGCTAAGTGAGCA
8072	4,05059997	4,12	3,16	4,87	CG11347	ACATTGTGGAGAAGGAAGACGAGGAGGACGACTCCC
4879	-4,374000131	-5,24	-3,72	-4,16	CG3168	GCGGAAAACAGCCACAAAACCGCTAAGCGAGGCAGA
5368	-2,609194405	-1,61	-3,16	-3,06	CG1637	ACCCAGTATATACATCGTGTGACGCTGTCCACCTG
8189	-3,142470765	-2,83	-3,05	-3,55	CG10645	AAAATCACCGAGAGCAAGTTCTTCAAATGGGTTGAC
10961	-3,11168404	-3,61	-2,61		CG32490	AGCTCGACGATTTTACAAAACCTGAAAAATCAAATAG
20057	-2,650337348	-3,17	-2,37	-2,41	CG11961	GAGGAGAAAAGATCGAAGGCTCAGCCCAATGGCTGT
10496	-4,536445185	-4,49	-4,32	-4,80	CG5059	GCGAAGATTTGCTGGGCGAATCTTGGATCGAACTCA
10505	-2,934094931	-3,43	-3,47	-1,90	CG4365	TTGGAGAAAAAACAACCTTGCAAAAACCTACGAAAAAG
3396	2,610177086	3,38	2,50	1,94	CG10473	TTTTCTTATCAAGAAAAGATCTTTCCAGCGCTCGCAG
2926	2,923788355	2,86	3,14	2,77	CG4551	AATTGGTCTGTCATAAAGAAATCTTTATGTTTTGCG
3510	2,940877937	3,67	2,66	2,50	CG10334	CGCACACACACACGCATGTTTTCTAAACACACACAC
2082	-2,54615235	-1,93	-2,93	-2,78	CG9310	CTGGCCATTGAGCTTTAATTGCCGTCATTACTTCA
16159	-2,608931093	-2,66	-2,40	-2,77	CG1553	GTAATAAAAAAACTCGTGAACCTTCCAGAAATAGAA
4771	-2,330733036	-1,43	-3,34	-2,22	CG3187	GCATCTCGACGGAATCGGATTGACTTCCAAAAGCTT
6334	-2,579082471	-2,74	-2,34	-2,66	CG4429	TGAATAGAGGATACAATGATCGGCGCAAAATCGTG
11295	3,031413127	2,59	3,57	2,94	CG2922	GCTCATAAGAAAAGAGAGCAATTTATTGTATGAGTC
10184	-2,653012678	-2,38	-2,91	-2,67	CG3979	ACCGAACTACAAAATGATCTACACGCCACCGCCA
14162	-2,842067027	-2,65	-3,21	-2,67	CG10365	GTACAAAACCACTACAAAATCTCAATTCACCTTGG
13096	2,639058007	3,11	2,32	2,48	CG3937	CAATTGTAACACATCAAGCTGAAGTCAGAAATGCCTA

7890	2,795182781	2,46	3,01	2,92	CG12008	TGCGAACGAGTTTGCAAAGTTGGGGAAATACACGCT
926	-2,44361289	-2,59	-3,23	-1,51	CG16987	AATGGATTATTAATTTGGACGAAACTTAACGAAAAG
18960	-2,718917707	-2,19	-3,25		CG3216	CATCTGTCTTCTGCAAAAGCAGATGAAGCTCAGCAA
3010	-4,129208439	-4,24	-4,37	-3,77	CG4170	AAAAAGTATCCATAGATGAGCAAAAAGGCAATTAAA
16448	-2,687229368	-2,68	-2,71	-2,67	CG8026	GGGCTCATGGCAGCTTGAGTTTGAGGGCTACAGAGG
1739	4,36512876	3,86	5,12	4,11	CG5973	TTTGTGTGATTTTTGCGCTTGAACCGGTGAACAAC
9351	4,268197793		4,56	3,98	CG6928	AAACATTTGTTTAAATACAAATAGAAGCCATGAGCC
18221	-2,368499851	-1,85	-2,49	-2,77	CG8098	TGGAGCAACAGCCGCAGAGATGCTTTGCCACCCGGT
16449	-3,081924243	-2,89	-3,73	-2,62	CG8026	ACGCCAACATCTGCATGCCTGCGTCTTTTCATTTG
12486	-2,486880293	-2,13	-2,99	-2,35	CG8863	AAACTTCAAAAATTTTCGTA AACAGCAAAACAAATG
7734	2,57196327	2,22	3,29	2,20	CG11486	CAAAGTGAACATGACTGTCGACGCGCCTCAATTGT
8579	-4,551029173	-4,99	-4,11		CG17888	TTCTGAGAATAAGAAAAGCACAAATTTTTTTTCAGA
9622	-2,404621855	-3,05	-1,05	-3,11	CG17364	GTGGATGAAAACCAGGAGTATCCTCCCCGGCTGGAA
19723	-3,916302818	-5,18	-3,51	-3,06	CG3318	ATCGTCGTCAAGGATCGTCCAGAGAACAAGAGATCC
11134	-2,708200655	-3,19	-2,15	-2,79	CG31543	GGAACTTTTGGACAAGCGTGAGCGCCGCTATGAGGA
19222	-2,537899103	-2,45	-2,86	-2,30	CG13503	ACAAATCAGCGGAAACGATGGCTATTCCGCCACCC
17941	-2,639872207	-2,55	-2,60	-2,76	CG8256	TAGCATCCAGAGCACTAGCCCAATAAATACTCGAT
10632	2,896323096	2,46	3,05	3,17	CG7611	TTAAGAAATGCTTTTACGGAATATAATGTGCTATAC
8071	-6,97595766	-6,07	-6,15	-8,71	CG11347	GTTTTGCGCATCCATAAGCTTCTACGCTACGAAGAA
20044	2,54706282	2,29	2,67	2,68	CG11949	AAGTCCTCAGGCAGACGTGCTGATGCTACACCACC
5322	4,713256613	5,43	4,42	4,29	CG33175	CCAGCGAATGCATCATGGAACAAGTGAACCCATTCC
5350	-2,80375488	-3,13	-1,69	-3,59	CG16944	AGAAGTTATCAACTGAAGTGAATCGTACATCCACTA
12170	-2,519199561	-1,69	-2,96	-2,90	CG31305	GACACGAGCTGATCACCTAATTTCCACCTAACA
11583	-3,024189132	-2,15	-2,98	-3,94	CG32466	ACGCGTTACCGGACAAGGTGGCCTGGGCTGTTGGCGC
8989	-3,126236548	-3,61	-2,95	-2,82	CG6767	CAAGATAAAAAAGACAAGTTGGCAGGAGTGAAGAT
7482	-4,468792572	-4,54	-4,45	-4,41	CG2086	ACCGTCTTCTTGCCAAGTTGAATCCGGTTTAACTCT

ProbID	Wingless_avg_Zscore	Wingless_1	Wingless_2	Wingless_3	cg_list	probe_table::seq
13603	3,001204712	2,88	2,49	3,64	CG4257	GGTGGTTGTGTACCAAAGTTTCTCCTTCTAACCAT
13105	2,257054194	2,70	2,33	1,74	CG3937	TGGACGGAAGTTGAGCCAACTGACTTGGCGGTAACCA
17665	-3,542617306	-2,74	-3,93	-3,97	CG8468	GAACAAGAACAGATAAAAACCACATCAAATTTCTTTG
4868	-2,221214652	-3,17	-1,70	-1,80	CG4523	AAATTGGCTGCCAGGCAACCCACACAGATATCGAAA
14671	-6,269928408	-5,25	-6,90	-6,66	CG17383	TAACAATTCATGGGTCAATATCTCGAATTCGCAATAT
12702	-2,268328007	-3,16	-1,81	-1,84	CG3731	CGCGAGCGCAGTACATTTGGCTATTGAACGAATTAAT
13098	2,391799477	2,94	2,89	1,35	CG3937	CTAGTCGATTGCCAAGTTTGGCTGTCCAGAGAAAAGC
11643	-4,80426179	-5,15	-5,45	-3,82	CG2747	TGTGCACGAAGTGAACCGATCGTTTATAAACAGCGA
18369	2,452900807	2,55	2,56	2,25	CG15611	TCTGCTGGACAGCGATAGCCACGAGGATGAGGACAC
5315	5,705388651	5,40	5,40	6,32	CG33175	GGCAGCGGATCCCTGGACTGGCGCTCCAGCTGCCTT
12172	2,794898354	2,19	3,20	2,99	CG31305	CCCATCATTCACTTTTCGGCGCTGGTCTGGTGACGC
16498	-2,283236873	-2,15	-1,57	-3,12	CG11804	AAGTAGCGGACCGTGAAGCTCCCTTAAACGCTTAAA
8446	-3,320188427	-3,66	-2,49	-3,81	CG8588	GGACGCGAGGTGGGAGCGATCACCCAACCTGACTGTG
15148	-3,298119373	-4,06	-3,06	-2,77	CG11956	ACTGAGGCTCTGGCAACGATTATACTTTCTCTATGC
7614	-3,044670612	-3,85	-2,12	-3,16	CG32306	AATTCCTGGTCTGTGCAGGTGAGTACGACCAGTTT
8445	-5,765525642	-5,86	-5,13	-6,31	CG8588	GGACGCGAGGTGGGAGCAATAAGCAAAAAGACGGTGAC
14882	4,578310197	6,02	2,96	4,76	CG14253	AAGTGGTACGCTACGAACATAGTAATATGTCTCA
7902	-3,172873749	-3,92	-3,12	-2,48	CG10579	TTTTCAAAGTGCAGATATTCGGAGCGCGAAGTGCGG
1536	-3,09135574	-2,87	-3,34	-3,07	CG11050	GGAACCTCTTGCACCCAGACGCCACTTGCACATCAC
12629	-3,963441275	-4,21	-4,60	-3,08	CG8651	GCAACAACAACAACAATAAGCGCGCTTGACCCGAA
608	-3,926109294	-3,09	-4,14	-4,55	CG3625	CTAACGTTCTGGATGCGATAATTCAGGCACTGTAC
7901	-3,517977317	-3,83	-3,14	-3,59	CG10579	CAACAAATGCTAAAGATGGCGTCAACATGCGCGAGA
14669	-4,770487098	-3,82	-4,93	-5,56	CG17383	GCTTGTGTTTGTGTTGTCGATCTCGAATTCGCAATAT
19110	-3,08026105	-2,83	-2,48	-3,93	CG10497	AAATACGAGAGGAAAAGCCGCGCGCAGATACGATA
5829	-4,224020762	-3,79	-4,20	-4,68	CG32626	GCGACATGTAAGTCGCCAGTGATCTCGCCGATTAC
9880	3,357943863	3,24	4,28	2,55	CG32156	CGCCACTGCCTCCTGCGGATTTGTGAGCATAGCTCG
14221	-3,344400782	-4,04	-3,30	-2,70	CG5320	GCATGTATCACCTGAAGAATCAACCCTAAGGAGTAC
12823	-2,59576777	-1,88	-2,39	-3,52	CG31302	GAACCATATCAAAGAGTGAACCTCGAAGAAGAAGTGA
14453	2,237544108	2,73	1,75	2,24	CG5794	AGAATCTCCTGGAGCTCTATGAGGTGCGCGTGGCCA
7900	-2,954863186	-2,65	-3,08	-3,13	CG10579	GCCAGTAAAACGTGCAGCTGACATACGCATACAAA
13604	4,333784614	4,69	3,64	4,67	CG4257	AAAAAGGCAATCTGAAAAGTTTCTCCTTCTAACCAT
10880	2,25169292	2,43	2,19	2,14	CG6143	AAATCGCCGTTGCAACACCTTTTAAATAAATTTCC
13610	2,289498998	3,02	1,17	2,68	CG4241	GTGCTAACAAAAACAAGGTCCCCACGTCGAGTCT
7245	-2,088919833	-2,61	-1,84	-1,82	CG12038	GCGGTGAAGGTAGGTGCGCTGGCCCGGCACAACGAT
7615	-2,850123709	-2,80	-2,38	-3,38	CG32306	ATTATTTTCTGTTTTCGGAAACCATTGCGGCCTCAA
89	2,037958018	2,24	2,55	1,32	CG1674	TCAAGGCGCAATACAAATGCCGTTGCTTCTCGCCA
16158	-3,329879859	-1,52	-4,30	-4,17	CG1553	AAACTATAAAATAGCCAGAACCTTCCAGAAATAGAA

5742	-3,302626977	-3,51	-2,48	-3,92	CG1630	TCGCCGCCGCGTCTATATAAATACATAGATAGTTGC
14884	3,19192769	3,83	2,41	3,34	CG14253	CCACTGGAAAACACATATCAAGACCCATAAAAATCG
7909	-2,950153858	-2,90	-3,08	-2,87	CG10579	CAAATTGCAGATATGGAGACTGGCGCAGCACGGACA
6222	3,418715777	3,46	2,36	4,44	CG3525	TAGCACCTAATAGCCGTTCTTTTCGTGATATAGTCG
18441	-2,617579328	-2,89	-2,64	-2,32	CG33130	CGCTAATGAATCTGTGCGGTCCTAAACTCTATAAAC
16939	-2,450967934	-2,32	-3,32	-1,70	CG30015	CACAAGTAATCCGAAAGACCACCAACAAAAGAGAT
18445	-2,055826313	-2,50	-1,61	-2,06	CG33130	ACTCCCTCACTGTAAAAGAGTACCCCGATGATTATC
9879	3,272322824	3,65	3,43	2,74	CG32156	CTCACCGCCCTGCACCAGGCGTGCATAGACGACAAT
10203	9,575485759	9,78	8,44	10,51	CG9739	AACGGAATGGAAAAATGTTAGACCACGCCGTTTGT
5826	-4,52218419	-3,76	-4,25	-5,56	CG32626	GCCCGATGATTGCAAATGGCAGGCTACAGGACCTAG
7633	-3,467488248	-2,63	-4,88	-2,89	CG1146	GACACCACTTGAAGAAAGAGTGATGTGATGCATAA
3659	4,261114611	4,83	4,78	3,17	CG9339	GCTTCCAGTTCAGTCCAGGCAAGGAACCGGCACTGC
14674	-5,921695427	-4,88	-6,29	-6,60	CG17383	TAAATTGTATTTCTCGAGGAATGGAGAACCTGTGCG
11642	9,912087559	9,88	9,56	10,30	CG2747	TATCTCCGAGGCGCGCAGATCGTTTATAAACAGCGA
6390	-2,260509237	-2,85	-2,02	-1,91	CG4829	CAGTTATATATAGCTGCGCTCCATCACAATCCCAGC
2183	2,039306272	1,53	2,85	1,73	CG33298	AGCCTCATCAATCTATAGAATCACCGATTATGGGTC
9876	2,567774584	2,45	2,75	2,50	CG32156	GGGAATTTTCGCGGGAAAGCAAGCAGGAAAAGAAGAA
14034	-2,480123233	-2,86	-2,02	-2,56	CG7023	ATCAAGGCGGAAGCACAGAAACGGAACGGGAACCA
13967	3,939545993	2,62	3,34	5,85	CG7059	AATGCGCGAAATTCAGGCCTCCCAATTTATGACGAA
13601	2,692863007	2,83	1,62	3,63	CG4257	GATCGAAGACAGGATAATGTCCGAACAAATAACGCC
17863	2,119487357	1,96	3,06	1,34	CG16801	GACTCCTGCCGCCGCCCTCACTGGGCAGTTTGCCGA
2926	-2,584894262	-2,40	-2,42	-2,93	CG4551	AATTGGTCTGTCATAAAGAAATCTTTATGTTTTGCG
5741	-3,51219625	-3,94	-2,31	-4,29	CG1630	TGGCTCGGGGTCTCGTCTAAATACATAGATAGTTGC
14486	-3,079061231	-3,48	-3,37	-2,38	CG10693	GCAAATTCGATGACTTAGGTGATATCACTCGTGACA
926	-4,634453095	-5,66	-4,31	-3,93	CG16987	AATGGATTATTAATTTGGACGAAACTTAACGAAAAG
6618	-3,081038054	-3,04	-4,19	-2,01	CG6103	GAAGTGGCTACCAAGGATGTGCAGTCCGTGATACAG
9016	-2,485283064	-2,03	-3,17	-2,26	CG8177	GACGAAACACAGAAAGTGCGCCGCGTAAACTAAAAC
11090	-2,696353598	-2,94	-2,88	-2,26	CG31536	GGAAGAGGAGTACACCAGTGGTCAATCCCCGGCGGA
7905	-2,976313212	-3,70	-2,64	-2,59	CG10579	TTTCCGAAAAAAGAGTATAATATTTGACCTCGTT
16496	2,434679007	2,17	2,91	2,22	CG11804	CTCCTTCAGCTTGTAACGCTCCCTTAAACGTTAAA
19154	-3,301749962	-3,64	-3,77	-2,49	CG10433	TGGAGTGCTGCTACGAACTCCGATCAAACCCAACAC
11133	-2,052280448	-2,42	-2,16	-1,58	CG31543	TATAATATAACCGCCGGTTGAGCGCCGCTATGAGGA
10204	-6,322840872	-6,93	-7,12	-4,91	CG9739	AAGCAGTGACAATCAATCCTGGGCGGAATCGAATGA
15145	-2,812630138	-3,05	-2,86	-2,52	CG11956	TAGGCAGCAAAAAGCGCGTTTTGGTAATGAAGTGGT
11134	-2,363468783	-2,93	-2,66	-1,50	CG31543	GGAACTTTTGGACAAGCGTGAGCGCCGCTATGAGGA
19222	-2,94225084	-3,42	-3,04	-2,37	CG13503	ACAAATCAGCGGGAAACGATGGCTATTCCGCCACCC
9877	2,570953852	2,17	2,70	2,84	CG32156	GGGAATTTTCGCGGGAAAGGAAAAGAAGAAGCAGCAG
14670	8,6994043	7,78	11,41	6,92	CG17383	GGCGCAGCCTCCAAAAGATCTCGAATTCGCAATAT
11583	-3,048115377	-4,01	-3,49	-1,65	CG32466	ACGCGGTTACCGGACAAGGTGGCTGGGTCTGGGCG
16388	2,167164634	1,85	2,05	2,60	CG8224	CATCATCTTCAGCTACAGTTGCATGGTTGTCAAGTA