

Appendix 3. Genetic and physical distances and PCR amplification primers for markers used in linkage analysis of chromosome 17 and association analysis of the RUNX1 and RAPTOR loci.

Marker Name	Alias	Genetic distance from p-terminus (Kosambi cM) †	Genetic distance from p-terminal marker (Haldane cM) ‡	Physical distance from p-terminus (bp) §	Amplification primers¶
AFM234wg3	D17S849	0.63	0.25	417,451	CAATTCTGTTCTAAGATTATTTTGG CTCTGGCTGAGGAGGC
GTAT1A05	D17S1308	1.13	0.25	608,007	TGTGAAACTTTTGTTCATCACTATAACC TTGGTGACAAAGAAAGTCTCC
AFM177xh6	D17S796	16.59	18.32	6,452,214	CAATGGAACCAAATGTGGTC AGTCCGATAATGCCAGGATG
GATA158H04		16.81	18.54	6,533,729	ACATACAGCACAGGCCAAAT CCAGTCTTCCGTCCTACTATGC
GATA8C04	D17S974	28.70	31.83	10,719,385	AGACCCTGTCTCAGATAGATGG TAAAATAGAAAGTGCCCCTCC
ATA78D02N*		36.83	40.61	13,317,440	GGCAAGAGTTTTCCCATTTT GGCAAGAGAACTCACGTAA
AFM192yh2	D17S799	37.00	40.78	13,371,696	ATTGCCAGCCGTCAGTT GACCAGCATATCATTATAGACAAGC
GATA185H04	D17S2196	47.32	52.16	17,465,099	CCAACATCTAGAATTAATCAGAATC ATATTTCAATATTGTAACCAGTCC
AFM026vh7	D17S783	50.91	55.88	25,457,788	AGGACTCGAAATGCTTTCAT TAACAGAAAACCTTGGAGCCG
GGAA9D03	D17S1294	52.78	57.79	28,527,909	TGGCATGCAATTGTAGTCTC TTCTTTCCTTACTAAGTTGAGAACG
GATA25A04	D17S1299	69.60	77.38	39,367,629	TAGCACTTGAGCACACATGG GTGCATTATGGGGACCATTA

Appendix 3. Continued (page 2 of 5).

Marker Name	Alias	Genetic distance from p-terminus (Kosambi cM) †	Genetic distance from p-terminal marker (Haldane cM) ‡	Physical distance from p-terminus (bp) §	Amplification primers¶
AFM200zf4	D17S800	69.67	77.45	39,429,607	GGTCTCATCCATCAGGTTTT ATAGACTGTGTACTGGGCATTGA
AFM095tc5	D17S787	85.01	95.11	53,756,701	TGGGCTCAACTATATGAACC TTGATACCTTTTTGAAGGGG
AAT245*		87.17	97.32	55,77,4591	GCCAAGGCAGGAGGATTACT CCTTTACCACTTGTGGCACTT
GATA49C09	D17S1290	88.27	98.43	56,806,181	GCAACAGAGCAAGACTGTC GGAAACAGTTAAATGGCCAA
ATA43A10	D17S2193	99.34	110.72	67,144,939	AAGCACAGAACTGTTTGGG AAGTAAGGGCCTGAAAAAGAC
AFMa112yb5	D17S1786	101.10	112.51	68,091,874	GAGACTCTGTATGGCACCC AAACTGGATAACGCCCTG
GATA31B11	D17S2059	102.96	114.40	69,098,201	TGTAATGCTTGTGCAGATGG TGCAGTGATTTTACATTGC
GATA28D11	D17S1301	113.59	126.15	73,278,071	AAAGAAGATGAAATTGCCATG TAAAAGAATGAAGGTAAAAATGTG
rs745318		113.67	126.24	73,360,921	AACCTTCTTTCACCTCATCTTT CAATGTGGCTTTTAGGTAAG
rs734232		113.67	126.24	73,362,854	AGGTAGAAATTGAGAAATGGTAAG GTAAATATCCCCGTTAGACAAG
rs895691		113.68	126.24	73,363,423	AGACCCAGGTCCCTGATACC CCTCTGACAAGGAGCAGGAG

Appendix 3. Continued (page 3 of 5).

Marker Name	Alias	Genetic distance from p-terminus (Kosambi cM) †	Genetic distance from p-terminal marker (Haldane cM) ‡	Physical distance from p-terminus (bp) §	Amplification primers¶
AFM049xc1	D17S785	115.34	127.93	75,028,564	ATCCCTGGAGAGTGAAAATG AAGGCCAACCTGAAAATAA
AFM107ye3	D17S937	118.10	130.77	75,944,548	CATGGAGGGACTTGCG TTCCCAGAACCCGGTTT
AFM267xh1	D17S939	118.45	131.12	76,059,359	AGCTATAAGTAACCATGTTTNTGG TACAGTGCAAACCTCCTACCG
TTCA006M*		118.89	131.56	76,200,179	TCCCCACGTAAGCATTCTC AGAGGCGCTTGCTAAACAAAG
AFM210xa5	D17S802	120.83	133.54	76,831,785	GCCACCTGCCCTCAA CTGCCAGCAGAGGCCA
UT952	D17S674	120.84	133.55	76,905,489	GTGACTTGGTGCTGCACCCTCC GACACAGGGCGAGGCTCTG
AFMb310yf5	D17S1847	123.75	136.54	77,621,984	GATCACCAGGAACACCC TCTTCAGAGCTTGCCAG
AFM163yg1	D17S836	125.04	137.85	77,897,068	GTGCATCTGGCTTCATGTTC AGCTTCCACACACTAGGTGC
AFMa238yb5	D17S1806	126.14	138.96	78,042,795	GATGTGCTTATTTGAAACCTGC TGTAACGTCCACCAGCAGAG
AFMb019zg5	D17S1830	129.57	142.53	78,496,285	GGGAGACTCCATCTCAAAA ATTTGCCCATCTGCTTT
AFM044xg3	D17S784	129.62	142.53	78,502,392	GAGTCTCCTAAATGCTGGGG AGCTCCTGCACAGTTCTTAAATA
AAT09*		131.61	144.67	79,300,708	TTGGGATGGTGAAAAGGTTT TGCTCACGGTTGTCTGTAG

Appendix 3. Continued (page 4 of 5).

Marker Name	Alias	Genetic distance from p-terminus (Kosambi cM) †	Genetic distance from p-terminal marker (Haldane cM) ‡	Physical distance from p-terminus (bp) §	PCR amplification primers¶
rs1564864		131.71	144.67	79,342,164	GGCTAGTAATGAGTAAAATGGATG GGGCCTCCACTAGACAAAGT
rs2019154		131.74	144.67	79,354,463	GGTTCTGAGTTTTTGTCTGTTTG GGTGCTGTGCCTCTGAAG
rs869190		131.78	144.67	79,368,712	GCACTTAAGTAAGGAGGAGTGAT AGTCTCTGGCACACACTAACA
AFM217yd10	D17S928	135.67	148.80	80,931,803	TAAACGGCTACAACACATACA ATTTCCCCTGGCTG

*Marker name comes from human STRP screening set 13 of the Marshfield Center for Medical Genetics (<http://research.marshfieldclinic.org/genetics>).

† Sex-averaged genetic map distances from the p-terminus of chromosome 17 were derived from the deCODE map¹. Distances for markers not in the deCODE map were interpolated based on the physical locations of the markers in the July 2003 human genome assembly (NCBI Build 34, <http://genome.usc.edu/>).

‡ Genetic map distances from the p-terminal marker of the analysis set used for nonparametric multipoint linkage analysis by Merlin version 0.10.6². They were derived by first converting the deCODE genetic distances from Kosambi cM to Haldane cM and then adjusting distances for four sets of tightly linked markers (D17S849 + D17S1308, rs745318 + rs734232 + rs895691, D17S1830 + D17S784, and AAT095 + rs1564864 + rs2019154 + rs869190) that were clustered and treated as single markers by Merlin to avoid positive bias of the LOD scores³.

§ Physical locations of markers are from the July 2003 human genome assembly (NCBI Build 34, <http://genome.usc.edu/>). Locations of the 32 microsatellite markers are denoted by the midpoint of the amplicon; the 6 SNPs are denoted by their actual location.

¶ The sequence of the forward PCR primer for the marker amplicon is listed first, followed by the reverse primer, both in the 5' to 3' direction.

Appendix 3. Continued (page 5 of 5).

References

1. Kong A, Gudbjartsson DF, Sainz J, *et al.* A high-resolution recombination map of the human genome. *Nat Genet* 2002;31(3):241-7.
2. Abecasis GR, Cherny SS, Cookson WO, *et al.* Merlin--rapid analysis of dense genetic maps using sparse gene flow trees. *Nat Genet* 2002;30(1):97-101.
3. Abecasis GR, Wigginton JE. Linkage analysis with markers that are in linkage disequilibrium [abstract]. *Am J Hum Genet* 2004.