#rank	chromosom	start	end	strand	rank	annotation	GeneBank No
ERa_D_1	chr10	95184508	95184988	+	1	FER1L3	NM_013451
ERa_D_2	chr12	15259442	15261654	+	2	RERG	NM_032918
ERa_D_3	chr19	63041816	63042570	+	3	ZNF587	NM_032828
ERa_D_4	chr15	31146630	31149365	+	4	RYR3	NM_001036
ERa_D_5	chr15	69175738	69176648	+	5	THSD4	NM_024817
ERa_D_6	chr19	46118735	46119919	+	6	CYP2A7	NM_000764
ERa_D_7	chr2	2.38E+08	2.38E+08	+	7	MLPH	NM_001042467
ERa_D_8	chr3	13492187	13492938	+	8	HDAC11	NM_024827
ERa_D_9	chr19	63016198	63016884	+	9	ZNF552	NM_024762
ERa_D_10	chr1	1.52E+08	1.52E+08	+	10	TPM3	NM_152263
ERa_D_11	chr10	1.04E+08	1.04E+08	+	11	ARL3	NM_004311
ERa_D_12	chr20	48777653	48778272	+	12	PARD6B	NM_032521
ERa_D_13	chr3	4730400	4731316	+	13	ITPR1	NM_002222
ERa_D_14	chr6	17497321	17497686	+	14	CAP2	NM_006366
ERa_D_15	chr19	63079828	63080540	+	15	ZNF587	NM_032828
ERa_D_16	chr17	72796038	72796720	+	16	SEPT_9	NM_006640
ERa_D_17	chr3	1.97E+08	1.97E+08	+	17	FLJ25996	NM_001001699
ERa_D_18	chr6	12827149	12827933	+	18	PHACTR1	NM_030948
ERa_D_19	chr8	67198844	67199364	+	19	TRIM55	NM_033058
ERa_D_20	chr15	61466609	61468013	+	20	CA12	NM_001218
ERa_D_21	chr17	53333639	53334213	+	21	CUEDC1	NM_017949
ERa_D_22	chr3	1.97E+08	1.97E+08	+	22	TNK2	NM_005781
ERa_D_23	chr1	2.35E+08	2.35E+08	+	23	LGALS8	NM_201545
ERa_D_24	chr8	91065093	91065652	+	24	NBN	NM_001024688
ERa_D_25	chr7	16886759	16887050	+	25	BCMP11	NM_176813
ERa_D_26	chr11	1.2E+08	1.2E+08	+	26	GRIK4	NM_014619
ERa_D_27	chr17	41334105	41334707	+	27	MAPT	NM_005910
ERa_D_28	chr16	46826638	46827941	+	28	ABCC11	NM_032583
ERa_D_29	chr7	1.43E+08	1.43E+08	+	29	PIP	NM_002652
ERa_D_30	chr11	59895048	59895421	+	30	MS4A7	NM_021201
ERa_D_31	chr2	11589741	11590824	+	31	GREB1	NM_014668
ERa_D_32	chr20	19211922	19212624	+	32	SLC24A3	NM_020689
ERa_D_33	chr6	30827231	30827777	+	33	IER3	NM_003897
ERa_D_34	chr1	1.77E+08	1.77E+08	+	34	RALGPS2	NM_018037
ERa_D_35	chr2	1.11E+08	1.11E+08	+	35	RGPD5	NM_032260
ERa_D_36	chr2	1.1E+08	1.1E+08	+	36	RGPD7	NM_001037866
ERa_D_37	chr17	73928737	73929531	+	37	PGS1	NM_024419
ERa_D_38	chr2	1.11E+08	1.11E+08	+	38	RGPD5	NM_032260
ERa_D_39	chr5	43452613	43452959	+	39	CCL28	NM_148672
ERa_D_40	chr12	1.15E+08	1.15E+08	+	40	THRAP2	NM_015335
ERa_D_41	chr17	63803812	63805222	+	41	SLC16A6	NM_004694
ERa_D_42	chr19	46187185	46187510	+	42	CYP2B6	NM_000767
ERa_D_43	chr2	1.05E+08	1.05E+08	+	43	FHL2	NM_201557
ERa_D_44	chr5	1.48E+08	1.48E+08	+	44	SPINK7	NM_032566
ERa_D_45	chr11	66551625	66552475	+	45	SYT12	NM_177963
ERa_D_46	chr1	1.14E+08	1.14E+08	+	46	HIPK1	NM_181358
ERa_D_47	chr16	82537766	82538397	+	47	OSGIN1	NM_013370
ERa_D_48	chr14	73845529	73845977	+	48	ABCD4	NM_005050
ERa_D_49	chr6	20318557	20319869	+	49	E2F3	NM_001949
ERa_D_50	chr17	36944853	36945627	+	50	KRT19	NM_002276

ERa_D_51	chr10	1.04E+08	1.04E+08	+	51	ARL3	NM_004311
ERa_D_52	chr8	87422996	87423753	+	52	WWP1	NM_007013
ERa_D_53	chr10	79301694	79302443	+	53	DLG5	NM_004747
ERa_D_54	chr14	87546280	87547456	+	54	GPR65	NM_003608
ERa_D_55	chr2	1.09E+08	1.09E+08	+	55	LIMS1	NM_004987
ERa_D_56	chr17	63971278	63971915	+	56	WIPI1	NM_017983
ERa_D_57	chr6	1.67E+08	1.67E+08	+	57	CCR6	NM_004367
ERa_D_58	chr2	11596942	11597762	+	58	GREB1	NM_014668
ERa_D_59	chr1	19795350	19796090	+	59	C1orf151	NM_001032363
ERa_D_60	chr21	13978135	13979451	+	60	LOC441956	NM_001013729
ERa_D_61	chr6	42302309	42303560	+	61	TRERF1	NM_033502
ERa_D_62	chr3	4733654	4734576	+	62	ITPR1	NM_002222
ERa_D_63	chr10	1.05E+08	1.05E+08	+	63	C10orf26	NM_017787
ERa_D_64	chr18	14460131	14461422	+	64	ANKRD30B	NM_001029862
ERa_D_65	chr15	19260946	19262127	+	65	POTE15	NM_207355
ERa_D_66	chr12	94016095	94016736	+	66	FGD6	NM_018351
ERa_D_67	chr15	27902389	27903037	+	67	TJP1	NM_003257
ERa_D_68	chr12	2775366	2776518	+	68	FKBP4	NM_002014
ERa_D_69	chr4	37132517	37133029	+	69	C4orf19	NM_018302
ERa_D_70	chr4	6685829	6686198	+	70	MRFAP1	NM_033296
ERa_D_71	chr9	1.27E+08	1.27E+08	+	71	MAPKAP1	NM_001006618
ERa_D_72	chr1	1.45E+08	1.45E+08	+	72	PRKAB2	NM_005399
ERa_D_73	chr12	52663225	52664138	+	73	HOXC10	NM_017409
ERa_D_74	chr17	72793997	72795543	+	74	SEPT_9	NM_006640
ERa_D_75	chr1	2.06E+08	2.06E+08	+	75	CD55	NM_000574
ERa_D_76	chr1	2.01E+08	2.01E+08	+	76	MYOG	NM_002479
ERa_D_77	chr3	1.85E+08	1.85E+08	+	77	MAP6D1	NM_024871
ERa_D_78	chr6	1.52E+08	1.52E+08	+	78	ESR1	NM_000125
ERa_D_79	chr3	1.42E+08	1.42E+08	+	79	SLC25A36	NM_018155
ERa_D_80	chr14	93926562	93927163	+	80	SERPINA1	NM_001002235
ERa_D_81	chr4	39868882	39869125	+	81	RHOH	NM_004310
ERa_D_82	chr9	1.16E+08	1.16E+08	+	82	DFNB31	NM_015404
ERa_D_83	chrX	1.48E+08	1.48E+08	+	83	CXorf40A	NM_178124
ERa_D_84	chr8	1.28E+08	1.28E+08	+	84	FAM84B	NM_174911
ERa_D_85	chr10	61395042	61395713	+	85	CCDC6	NM_005436
ERa_D_86	chr2	96709553	96710293	+	86	LOC90342	NM_001077400
ERa_D_87	chr7	93361657	93362562	+	87	TFPI2	NM_006528
ERa_D_88	chr2	11588563	11588845	+	88	GREB1	NM_014668
ERa_D_89	chr4	1.74E+08	1.74E+08	+	89	GALNT17	NM_001034845
ERa_D_90	chr4	1.41E+08	1.41E+08	+	90	SCOC	NM_032547
ERa_D_91	chr10	1.05E+08	1.05E+08	+	91	NT5C2	NM_012229
ERa_D_92	chr22	19600989	19601418	+	92	CRKL	NM_005207
ERa_D_93	chr19	46095849	46096172	+	93	CYP2A7	NM_000764
ERa_D_94	chr20	17496526	17496909	+	94	DSTN	NM_006870
ERa_D_95	chr1	1.72E+08	1.72E+08	+	95	ZBTB37	NM_032522
ERa_D_96	chr5	1.8E+08	1.8E+08	+	96	SCGB3A1	NM_052863
ERa_D_97	chr15	40350303	40350898	+	97	TMEM87A	NM_015497
ERa_D_98	chr19	46095179	46095397	+	98	CYP2A7	NM_000764
ERa_D_99	chr7	80388226	80388724	+	99	SEMA3C	NM_006379
ERa_D_100	chr13	38156713	38157370	+	100	FREM2	NM_207361
ERa_D_101	chr17	36345213	36345772	+	101	KRT23	NM_015515

ERa_D_102	chr10	1.15E+08	1.15E+08	+	102	CASP7	NM_033340
ERa_D_103	chr22	29262235	29262504	+	103	GAL3ST1	NM_004861
ERa_D_104	chr16	84344286	84344517	+	104	C16orf74	NM_206967
ERa_D_105	chr3	1.9E+08	1.9E+08	+	105	FAM79B	NM_198485
ERa_D_106	chr1	21677686	21678010	+	106	NBPF3	NM_032264
ERa_D_107	chr3	1.69E+08	1.69E+08	+	107	PDCD10	NM_007217
ERa_D_108	chr5	68661571	68661870	+	108	CCDC125	NM_176816
ERa_D_109	chr20	31785368	31785883	+	109	ZNF341	NM_032819
ERa_D_110	chr3	4728431	4729467	+	110	ITPR1	NM_002222
ERa_D_111	chr1	55126444	55126901	+	111	DHCR24	NM_014762
ERa_D_112	chr17	35589834	35590650	+	112	RAPGEFL1	NM_016339
ERa_D_113	chr1	32151929	32152242	+	113	PTP4A2	NM_080391
ERa_D_114	chr16	46841931	46842802	+	114	LONP2	NM_031490
ERa_D_115	chr9	83490582	83491626	+	115	TLE1	NM_005077
ERa_D_116	chr13	92674753	92675717	+	116	GPC6	NM_005708
ERa_D_117	chrX	1.49E+08	1.49E+08	+	117	CXorf40B	NM_001013845
ERa_D_118	chr17	77655078	77655445	+	118	CCDC57	NM_198082
ERa_D_119	chr11	66772232	66773139	+	119	FBXL11	NM_012308
ERa_D_120	chr1	51559514	51560039	+	120	EPS15	NM_001981
ERa_D_121	chr10	99086807	99087455	+	121	FRAT2	NM_012083
ERa_D_122	chr1	1.47E+08	1.47E+08	+	122	NBPF10	NM_001039703
ERa_D_123	chr3	1.58E+08	1.58E+08	+	123	FLJ16641	NM_001004316
ERa_D_124	chr17	43979154	43980185	+	124	HOXB3	NM_002146
ERa_D_125	chr1	2.4E+08	2.4E+08	+	125	RGS7	NM_002924
ERa_D_126	chr1	1.43E+08	1.43E+08	+	126	PPIAL4	NM_178230
ERa_D_127	chr5	96320628	96320934	+	127	LNPEP	NM_175920
ERa_D_128	chr22	34355757	34356192	+	128	LOC284912	NM_203375
ERa_D_129	chr10	76251255	76251998	+	129	MYST4	NM_012330
ERa_D_130	chr1	2.35E+08	2.35E+08	+	130	LGALS8	NM_201545
ERa_D_131	chr13	47568680	47569212	+	131	MED4	NM_014166
ERa_D_132	chr13	32685271	32685615	+	132	STARD13	NM_178006
ERa_D_133	chr16	53518450	53519594	+	133	IRX5	NM_005853
ERa_D_134	chr1	1.44E+08	1.44E+08	+	134	ITGA10	NM_003637
ERa_D_135	chr21	39615377	39615901	+	135	C21orf87	NM_001040140
ERa_D_136	chr3	47459627	47460531	+	136	SCAP	NM_012235
ERa_D_137	chr1	16767140	16767901	+	137	NBPF10	NM_001039703
ERa_D_138	chr11	1.29E+08	1.29E+08	+	138	TMEM45B	NM_138788
ERa_D_139	chr17	23867507	23869378	+	139	FOXN1	NM_003593
ERa_D_140	chr6	35850891	35851148	+	140	UNQ3045	NM_207409
ERa_D_141	chr1	1.45E+08	1.45E+08	+	141	NBPF8	NM_001037501
ERa_D_142	chr1	1.46E+08	1.46E+08	+	142	NBPF8	NM_001037501
ERa_D_143	chr11	60688580	60689336	+	143	VPS37C	NM_017966
ERa_D_144	chr16	31140142	31140671	+	144	TRIM72	NM_001008274
ERa_D_145	chr8	11684528	11685163	+	145	NEIL2	NM_145043
ERa_D_146	chr4	39875978	39876547	+	146	RHOH	NM_004310
ERa_D_147	chr1	1.49E+08	1.49E+08	+	147	PRUNE	NM_021222
ERa_D_148	chr14	63771102	63771385	+	148	ESR2	NM_001437
ERa_D_149	chr11	71184277	71184946	+	149	FAM86C	NM_018172
ERa_D_150	chr1	1.49E+08	1.49E+08	+	150	LASS2	NM_022075
ERa_D_151	chr6	38252707	38253194	+	151	BTBD9	NM_152733
ERa_D_152	chr8	8131660	8132177	+	152	DEFB109	NM_001037380

ERa_D_153	chr12	51625507	51626772	+	153	KRT18	NM_199187
ERa_D_154	chr6	44293984	44294458	+	154	SLC29A1	NM_004955
ERa_D_155	chr5	1.12E+08	1.12E+08	+	155	REEP5	NM_005669
ERa_D_156	chr1	37276854	37277343	+	156	GRIK3	NM_000831
ERa_D_157	chr7	93363161	93364242	+	157	TFPI2	NM_006528
ERa_D_158	chr12	47868178	47868636	+	158	TUBA3	NM_006009
ERa_D_159	chr20	47860642	47861399	+	159	SLC9A8	NM_015266
ERa_D_160	chr8	68417127	68417740	+	160	ARFGEF1	NM_006421
ERa_D_161	chr14	89927354	89927532	+	161	CALM1	NM_006888
ERa_D_162	chr17	36028409	36028985	+	162	SMARCE1	NM_003079
ERa_D_163	chr5	1.5E+08	1.5E+08	+	163	NDST1	NM_001543
ERa_D_164	chr7	1.43E+08	1.43E+08	+	164	PIP	NM_002652
ERa_D_165	chr22	34348876	34349474	+	165	MB	NM_203377
ERa_D_166	chr1	1.47E+08	1.47E+08	+	166	NBPF1	NM_017940
ERa_D_167	chr19	43481353	43481970	+	167	LOC541469	NM_001013617
ERa_D_168	chr6	18494639	18495102	+	168	IBRDC2	NM_182757
ERa_D_169	chr3	1.59E+08	1.59E+08	+	169	VEPH1	NM_024621
ERa_D_170	chr3	1.97E+08	1.97E+08	+	170	PCYT1A	NM_005017
ERa_D_171	chr14	73321297	73322497	+	171	C14orf43	NM_001043318
ERa_D_172	chr1	2.27E+08	2.27E+08	+	172	HIST3H3	NM_003493
ERa_D_173	chr6	1.33E+08	1.33E+08	+	173	LOC285735	NM_001037231
ERa_D_174	chr15	69150352	69150823	+	174	LRRC49	NM_017691
ERa_D_175	chr14	68328207	68328706	+	175	ZFP36L1	NM_004926
ERa_D_176	chr15	37868482	37869083	+	176	FSIP1	NM_152597
ERa_D_177	chr5	96319601	96319946	+	177	LNPEP	NM_005575
ERa_D_178	chr9	1.13E+08	1.13E+08	+	178	EDG2	NM_001401
ERa_D_179	chr2	96776483	96776985	+	179	LMAN2L	NM_030805
ERa_D_180	chr4	69386465	69386929	+	180	TMPRSS11E	NM_014058
ERa_D_181	chr19	18336837	18337122	+	181	PGPEP1	NM_017712
ERa_D_182	chr19	41755415	41756044	+	182	ZNF529	NM_020951
ERa_D_183	chr3	1.35E+08	1.35E+08	+	183	TF	NM_001063
ERa_D_184	chr4	68917167	68917631	+	184	YTHDC1	NM_001031732
ERa_D_185	chr1	1.44E+08	1.44E+08	+	185	NBPF20	NM_001037675
ERa_D_186	chr13	27089716	27090358	+	186	LNX2	NM_153371
ERa_D_187	chr20	52120625	52121008	+	187	BCAS1	NM_003657
ERa_D_188	chr16	87520926	87521372	+	188	CBFA2T3	NM_175931
ERa_D_189	chr15	48844439	48844921	+	189	SPPL2A	NM_032802
ERa_D_190	chr6	47091744	47092360	+	190	GPR110	NM_153840
ERa_D_191	chr3	8517061	8517997	+	191	LMCD1	NM_014583
ERa_D_192	chr13	38157877	38158570	+	192	FREM2	NM_207361
ERa_D_193	chr20	47862154	47862549	+	193	SLC9A8	NM_015266
ERa_D_194	chr10	95188126	95188680	+	194	FER1L3	NM_013451
ERa_D_195	chr1	1.44E+08	1.44E+08	+	195	NOTCH2NL	NM_203458
ERa_D_196	chr10	99197703	99198177	+	196	ZDHHC16	NM_198046
ERa_D_197	chr12	2754887	2755321	+	197	FKBP4	NM_002014
ERa_D_198	chr12	46448453	46448842	+	198	FLJ20489	NM_017842
ERa_D_199	chr8	1963427	1963972	+	199	MYOM2	NM_003970
ERa_D_200	chr3	1.27E+08	1.27E+08	+	200	LOC200810	NM_001015050
ERa_D_201	chr1	1.47E+08	1.47E+08	+	201	NBPF15	NM_173638
ERa_D_202	chr11	72061826	72062193	+	202	PDE2A	NM_002599
ERa_D_203	chr1	1.52E+08	1.52E+08	+	203	C1orf189	NM_001010979

ERa_D_204	chr17	70795080	70795499	+	204	SLC25A19	NM_021734
ERa_D_205	chrX	44288194	44288466	+	205	FUNDC1	NM_173794
ERa_D_206	chr5	1.72E+08	1.72E+08	+	206	LOC153222	NM_153607
ERa_D_207	chr11	1E+08	1E+08	+	207	TMEM133	NM_032021
ERa_D_208	chr7	16810018	16810528	+	208	AGR2	NM_006408
ERa_D_209	chr19	63017220	63017620	+	209	ZNF552	NM_024762
ERa_D_210	chr1	2.23E+08	2.23E+08	+	210	WDR26	NM_025160
ERa_D_211	chr10	125983	126473	+	211	TUBB8	NM_177987
ERa_D_212	chr5	1.8E+08	1.8E+08	+	212	FLT4	NM_182925
ERa_D_213	chr14	64763211	64764004	+	213	MAX	NM_145114
ERa_D_214	chr11	67320739	67321284	+	214	ALDH3B2	NM_001031615
ERa_D_215	chr20	17491255	17491744	+	215	DSTN	NM_006870
ERa_D_216	chr14	77158255	77158944	+	216	SPTLC2	NM_004863
ERa_D_217	chr12	1.23E+08	1.23E+08	+	217	NCOR2	NM_006312
ERa_D_218	chr9	1.35E+08	1.35E+08	+	218	GTF3C4	NM_012204
ERa_D_219	chr14	1.05E+08	1.05E+08	+	219	TMEM121	NM_025268
ERa_D_220	chr15	23657104	23657424	+	220	ATP10A	NM_024490
ERa_D_221	chr8	98719019	98719479	+	221	MTDH	NM_178812
ERa_D_222	chr15	61458644	61459909	+	222	CA12	NM_001218
ERa_D_223	chr8	1.11E+08	1.11E+08	+	223	EBAG9	NM_004215
ERa_D_224	chr4	1.86E+08	1.86E+08	+	224	ACSL1	NM_001995
ERa_D_225	chr1	31432121	31432885	+	225	FAM77C	NM_024522
ERa_D_226	chr20	37022195	37022647	+	226	DHX35	NM_021931
ERa_D_227	chr5	1.51E+08	1.51E+08	+	227	ANXA6	NM_001155
ERa_D_228	chr12	67484360	67485014	+	228	MDM2	NM_006881
ERa_D_229	chr15	69173074	69173579	+	229	LRRC49	NM_017691
ERa_D_230	chr7	94794596	94794769	+	230	PON1	NM_000446
ERa_D_231	chr17	33758417	33758656	+	231	SOCS7	NM_014598
ERa_D_232	chr1	1.17E+08	1.17E+08	+	232	IGSF3	NM_001007237
ERa_D_233	chr3	10127281	10127747	+	233	C3orf24	NM_173472
ERa_D_234	chr1	1.46E+08	1.46E+08	+	234	NBPF14	NM_015383
ERa_D_235	chr6	35857810	35858484	+	235	LOC340204	NM_001010886
ERa_D_236	chr9	12965579	12965789	+	236	MPDZ	NM_003829
ERa_D_237	chr5	1.48E+08	1.48E+08	+	237	SPINK5L2	NM_001001325
ERa_D_238	chr19	50002995	50003199	+	238	BCAM	NM_001013257
ERa_D_239	chr17	23876266	23876758	+	239	FOXN1	NM_003593
ERa_D_240	chr19	46988279	46988498	+	240	CEACAM3	NM_001815
ERa_D_241	chr4	1.07E+08	1.07E+08	+	241	FLJ20184	NM_017700
ERa_D_242	chr12	15264746	15265316	+	242	RERG	NM_032918
ERa_D_243	chr12	53067955	53068241	+	243	ZNF385	NM_015481