

Probe_Set_ID	Symbol	Protein_Pr	Array_Add	Probe_Typ	Probe_Sta	SEQUENCE	Chromoso	Probe_Chr
ILMN_1653412	RAXL1	NP_11614	3830382	S	2182	TTGAGACC	19	-
ILMN_1654320	LOC64425	XP_93429	940386	S	259	AAGTGGA	13	-
ILMN_1656233	LOC64386	XP_93860	3610465	I	3261	GGAGCCC	7	+
ILMN_1656393	PPP2R3A	NP_87162	540041	A	4082	CACTCCAG	3	+
ILMN_1658921	LOC64485	XP_93931	2360053	I	879	CCCAGCGC	1	+
ILMN_1659878	PAK2	XP_94160	6110608	I	1688	AGAGGTGCGGTTCGATCGGCCGAAG		
ILMN_1660942	LOC65335	XP_93940	4540653	I	2039	AAGTAGAC	16	-
ILMN_1672661	SP110	NP_00450	70338	A	1274	GGTGGAT	2	-
ILMN_1675258	LOC44126	NP_00101	3840102	S	2048	CAGGCCCC	7	-
ILMN_1676665	CUEDC1	NP_06041	2680725	S	2114	GCAGCAG	17	-
ILMN_1677262	LOC731706		4180564	S	466	AGCCTGAGCTGCTGGAAACTATTC		
ILMN_1677843	RAB24	NP_57013	4730156	A	1124	TGGAACGGAGACAGCATTGGGCT		
ILMN_1678757	BCYRN1		2450154	S	57	GGAGGAT	2	+
ILMN_1680279	USP49	NP_06103	7320088	S	2818	TCCTAGCT	6	-
ILMN_1685628	C15orf51		5910131	I	3782	AGCTCACACCACTGCAGTCCAGCC		
ILMN_1688490	PTP4A2	XP_95000	5360603	I	2364	ACTCTGGCCTGGGTGATAGAGCG		
ILMN_1688666	HIST1H2B	NP_00351	5720433	S	352	GCCGTAC	6	+
ILMN_1690114	PTPLAD2	NP_00101	1470091	S	3665	GAGACAG	9	-
ILMN_1691428	PSMD12	XP_00113	1440131	I	2849	TGCAGTGGATCCCAGCACTTTGGG		
ILMN_1691881	IL4R	NP_00100	1770678	I	962	GGGGAAT	16	+
ILMN_1692145	ZNF14	NP_06635	2340674	S	2358	AGGCCAA	19	-
ILMN_1693789	ALPP	NP_00162	4230088	S	2672	TCTATGCG	2	+
ILMN_1694399	ICA1	NP_07168	6560411	I	543	GGATCAC	7	-
ILMN_1695468	SRPK2	NP_87263	2350072	I	107	CTGGCCAT	7	-
ILMN_1696027	LOC642333		1010296	A	611	GGCCGGGAAGCTAAAAGACAAGT		
ILMN_1697304	FARSLB	NP_00567	460128	S	2992	CAGTCCCA	2	-
ILMN_1697377	LOC64984	XP_94399	4830300	S	644	GGACAGTGTCTTTTGACCAACCAC		
ILMN_1699383	LOC44260	XP_94092	5360300	A	2603	TTTTGGAGGTCATGGCGGGAGGA		
ILMN_1700182	LOC400721		5890162	S	5744	AAGGTCATGCCACTGCACTCCAGC		
ILMN_1709164	RUNDC2B	NP_00101	4780064	I	1140	GAGCTGG	16	+
ILMN_1710362	LOC64459	XP_93279	1510196	S	3719	TGGTGAT	1	-
ILMN_1711073	LOC65348	XP_93920	3890053	I	5975	TCTGTAC	2	-
ILMN_1713319	PBLD	NP_07141	1340474	I	2137	GGAGTTCC	10	-
ILMN_1713706	ZNF786	NP_68962	4200541	S	3091	TGGGAGG	7	-
ILMN_1721204	CSF2RA	XP_94759	5340037	I	1791	CCGTTGCACTCCAGCCTGGGTAAC		
ILMN_1721349	DKFZp564I	NP_11549	5700139	S	2093	GATATGA	X	-
ILMN_1722223	LOC72857	XP_00112	5270575	A	224	AGAATCAC	5	+
ILMN_1726636	HECTD2	NP_77576	2230408	I	1864	ATTGAGTA	10	+
ILMN_1730678	ANKRD30E	NP_00102	1690184	I	2942	CATGCACC	18	+
ILMN_1731203	KIAA1618	NP_06600	4570561	I	4774	CAAGGCA	17	+
ILMN_1732311	CEP152	NP_05580	3930370	S	4067	AGGCAGA	15	-
ILMN_1733983	LOC65331	XP_93821	7320170	I	1162	CAGTGGCT	5	+
ILMN_1734991	PPM1B	NP_00102	3450026	I	1448	GTAATCCT	2	+
ILMN_1736008	YRDC	NP_07891	1340491	S	1263	AAGTCTCA	1	-
ILMN_1737878	FLJ34047	NP_77594	4850735	S	2829	TACTCTTG	5	-
ILMN_1738482	CEP27	NP_06056	3850524	S	1256	AGTCATGA	15	+
ILMN_1739283	UPF2	NP_05635	2230307	I	5	GCTGGAG	10	-

ILMN_1740165	C14orf102 NP_06044	3140358 I	161 GAAGCAG	14 -
ILMN_1743476	LOC65382 XP_94089	7100044 A	3711 GTTTTGGAGGTCATGGTGGGAGG	
ILMN_1745931	FLJ43663 XP_93563	3930180 A	1437 AGGACAA	7 -
ILMN_1746919	LOC64388 XP_93697	3180482 S	1616 CTA <del>CTCGG</del>	12 +
ILMN_1748090	SLC2A11 NP_00102	2750091 A	1397 TGTCCAC	22 +
ILMN_1750093	SDHALP1	6420674 I	10150 GATTGTGCCACCGTACTCCAGCCT	
ILMN_1755114	EIF2AK4 NP_00101	3370471 S	5290 ATGGATCA	15 +
ILMN_1756998	LOC64769 XP_94184	2970600 S	3 GCCACAAATAGAAAAGTTTTCTGC	
ILMN_1759872	LOC64350 XP_93324	70286 A	2564 GTGGAAT	18 -
ILMN_1766176	RAP1A NP_00101	3060692 I	188 GGTGATTA	1 +
ILMN_1771320	FLJ38717 NP_00100	990100 S	2559 TTGCAGGC	6 +
ILMN_1772492	MCART1 NP_21948	1980521 S	1556 CCTAGCTG	9 -
ILMN_1776290	LOC65359 XP_93974	430209 I	6963 GTGATGTC	2 -
ILMN_1778202	FLJ40722 XP_94718	2600632 I	2233 CTGGCGTTCACACCAGCCTGGCC	
ILMN_1778457	IL18 NP_00155	5890196 S	1038 TGTGGTG	11 -
ILMN_1780496	MGC1276 XP_93557	4490338 I	1659 GCCGTGCG	1 -
ILMN_1783060	SLC25A20 XP_00113	770255 I	561 GTAAGGTTGTCTACTCAGGAGGCT	
ILMN_1784554	LOC64738 XP_94155	6040181 S	837 AAATCAAAACTACTATGAGGCCGG	
ILMN_1785703	LMOD3 NP_93801	4250609 S	3155 CCCTAGAA	3 -
ILMN_1787314	ALS2CR14 NP_83994	4900215 S	830 TTTTCTTC	2 -
ILMN_1795461	LOC72985 XP_00113	5720204 S	1261 AGGGCTTA	1 -
ILMN_1798581	MCM8 NP_87795	6270082 A	3364 CAGTGAGC	20 +
ILMN_1805668	ZNF486 XP_37115	2070471 A	3074 CATTGCAC	19 +
ILMN_1806999	MGC4093 NP_08505	270519 S	895 GGGGACA	19 -
ILMN_1809750	TDRD1 NP_94209	270301 S	3989 TTTATTAC	10 +
ILMN_1811221	SLC5A8 NP_66601	4010021 S	3702 GTAATCTG	12 -
ILMN_1812105	PIP5K2B NP_61963	6370093 I	1324 TTGAACCC	17 -
ILMN_1812640	AHR NP_00161	840189 S	4990 GGCCAAG	7 +
ILMN_1814039	LOC65308 XP_93608	6860064 I	6448 TGATGTGT	2 -
ILMN_1814204	C21orf55 NP_06030	4390136 S	1982 TTTTTTGA	21 -
ILMN_1815578	ZNF223 NP_03749	4760767 S	2321 TGACCTAT	19 +
ILMN_1751351	FLJ90086 XP_37182	5050181 A	4017 AAAAGAG	6 -
ILMN_1759250	TAP2 NP_06131	1780528 A	1448 GGTTTTCT	6 -
ILMN_1760509	EOMES NP_00543	6760075 S	2643 GTCCAGGA	3 -
ILMN_1773650	LRRN3 NP_06080	7380181 S	2676 GCTGCCTC	7 +
ILMN_1783795	BTNL3 NP_00669	3180082 A	1714 CTCCATCC	5 +
ILMN_1793461	LOC65360 XP_49771	730468 S	12 GGACCATC	1 -
ILMN_1796335	AYTL1 NP_06030	5670100 S	1697 GACAACCC	16 +
ILMN_1343293	TXN	4260048 S	72 GCAGATCGAGAGCAAGACTGCTTT	
ILMN_1651228	RPS28 NP_00102	7510672 S	329 CGCCACAC	19 +
ILMN_1651498	GADD45G NP_00669	70376 S	923 GCCCTGGA	9 +
ILMN_1651850	RPS16 NP_00101	130768 S	496 GCGCTCGC	19 -
ILMN_1651964	ABCC5 NP_00101	7610097 I	1804 CCGTCGGA	3 -
ILMN_1652003	GNG10 NP_00101	4590608 S	292 GCCTTCAA	9 +
ILMN_1652128	LMBRD1 NP_06083	4590301 S	1576 CTGGTTCT	6 -
ILMN_1652230	LOC64736 XP_94152	3870088 S	27 CCACGCGCGAAAATTCGGCCAGGC	
ILMN_1652631	C9orf19 NP_07173	4280253 S	1778 GCAGCTCC	9 +
ILMN_1652736	RPS6KA3 NP_00457	5890647 I	7247 G <del>TACTTAT</del> X	-

ILMN_1653567	LOC39003	XP_37234	2140537	S	108	TGGAACTC	11	-
ILMN_1653871	PBEF1	NP_00573	3800243	I	1544	CGTCTTCAAGGACCCAGTTGCTGA		
ILMN_1654516	TMPIT	NP_11413	5560577	S	1055	CCACAAGT	7	-
ILMN_1656057	PLAU	NP_00264	1740349	S	2049	GTGGTCTT	10	+
ILMN_1656676	ZYG11B	NP_07892	4610019	S	6333	GGAAGTT	1	+
ILMN_1656961	CD82	NP_00222	6770594	A	1323	GGCAGC	11	+
ILMN_1657317	POLR2J	NP_00622	4810594	S	627	TGTGGACT	7	-
ILMN_1657398	LOC28475	NP_00100	870349	S	4094	CTGGTAGC	20	+
ILMN_1657497	KIAA0319	NP_05562	5910102	S	6659	CAGCCTGT	6	-
ILMN_1657515	RPS6KA5	NP_00474	2030482	I	3521	GGGGCAT	14	-
ILMN_1657996	LOC64203	XP_94119	360128	S	3	GTCTTCACATCTACCTTTCTATGTC		
ILMN_1658798	MEGF9	NP_00107	7560615	A	857	GGCTCTGTCAGCCATGTGACTGTA		
ILMN_1658957	LOC653635		3990128	S	2595	GGGGGCT	1	-
ILMN_1659047	HIST2H2A	NP_00350	1030039	S	1	CGACTTTC	1	-
ILMN_1659437	TXNL5	NP_11612	830047	S	378	CACCTCAA	17	+
ILMN_1659490	LOC65315	XP_93190	5820682	I	2213	GCTACTCA	5	+
ILMN_1660357	LOC64182	XP_94066	3180246	S	121	GGGAGGAAGGAACGAGGCAAGG		
ILMN_1660498	RPS27	NP_00102	5290523	S	36	CACGAGA	1	+
ILMN_1660549	GPR177	NP_00100	540288	I	1848	TGTTTCAGC	1	-
ILMN_1661196	CSF2RA	NP_75844	4570168	A	1147	ATTCACCC		X
ILMN_1661461	LOC28354	XP_37845	870575	A	4193	GCCTCATG	14	-
ILMN_1661466	LOC64642	XP_94636	520209	S	189	CAGTGACCAGGTTACCTACAGTAG		
ILMN_1661636	ZMYM2	NP_00344	6040079	A	4512	CAAGTTTA	13	+
ILMN_1662617	PPP2R3C	NP_06038	2760110	S	1264	GCTACCAT	14	-
ILMN_1662846	GPR160	NP_05518	6180427	S	1437	TGCCCCCT	3	+
ILMN_1662865	FLJ11151	NP_06081	7550519	S	2496	CAGGTGT	16	-
ILMN_1663422	Rgr	NP_70584	3440253	S	2648	GCTCTGCA	22	+
ILMN_1663437	EFCBP2	NP_06193	6770669	S	1468	CCACGCAT	16	+
ILMN_1664047	CACNA1E	NP_00071	2760452	S	9561	CACTGCAC	1	+
ILMN_1664577	DLD	NP_00009	1690671	S	1675	CCTGGGAC	7	+
ILMN_1664698	UNC119	NP_00513	1570164	A	1267	CATGAGG	17	-
ILMN_1664706	LOC65360	XP_49771	6650593	S	133	ATGGCCCC	1	-
ILMN_1664750	TMBIM4	NP_05714	5270356	S	610	GGAGTTGGTCTTAGCCGCTGCAGC		
ILMN_1664802	WSB1	NP_05644	6650575	A	2671	CTGTTTCT	17	+
ILMN_1665384	SH3BP5L	NP_08514	7320112	S	2889	AGATCTGC	1	-
ILMN_1665557	USP15	NP_00630	70767	S	4159	GCTGGGG	12	+
ILMN_1665781	LOC39046	XP_37252	6130672	S	61	AACCACCC	14	+
ILMN_1665982	AKTIP	NP_07192	2360414	A	1431	ATGTTAGC	16	-
ILMN_1666376	TRIM56	NP_11222	1780647	S	3115	GGGCCAA	7	+
ILMN_1666480	CDC123	NP_00601	6110379	S	1191	ACCGGCT	10	+
ILMN_1667162	NKX3-1	NP_00615	4670735	S	2969	CCATCTTG	8	-
ILMN_1667319	LPPR2	NP_07357	3140274	S	2354	GCTTGCCC	19	+
ILMN_1667460	SULF2	NP_94099	5270762	A	3335	CAGGACA	20	-
ILMN_1667561	IFRD1	NP_00154	3780243	A	1957	GACAAGA	7	+
ILMN_1667970	LOC72882	XP_00112	3060348	S	35	TGCGCGC		X
ILMN_1667985	NTNG2	NP_11592	6270382	S	2101	GGACCCC	9	+
ILMN_1668379	LOC39147	XP_94237	2630253	A	601	CCTGCTCGGTGCACTCTCTGCAGG		
ILMN_1669177	DHRS12	NP_00102	4890114	A	562	ACCCGGCC	13	-

ILMN_1669608	PDE7A	NP_00259	6960221 I	2530 GCTGAATC	8 -
ILMN_1669790	MNDA	NP_00242	6380228 S	1318 AACTGAG/	1 +
ILMN_1670130	ARID3A	NP_00521	4260446 S	2546 CCACACACTCACCCTCCCAGCTTC	
ILMN_1670821	CYorf15A	NP_00100	2190192 S	1688 TTGATGCAY	+
ILMN_1671516	CIR	NP_00487	2640088 A	1294 AGGGAGA	2 -
ILMN_1671933	CLCC1	NP_00104	20674 S	4235 CTTCTCTGGACATGCGCGTTTGAG/	
ILMN_1672004	TOB1	NP_00574	2470477 S	892 CCAATGG/	17 -
ILMN_1672988	LMNB1	NP_00556	4900048 S	2443 GGGAGGG	5 +
ILMN_1673113	F2RL1	NP_00523	5690201 S	2245 CAGACTGC	5 +
ILMN_1674590	LOC65257	XP_94719	3180192 S	537 GAGATGATGTGTGGTCCCCTGAA	
ILMN_1674650	C9orf95	NP_06035	7320079 S	1013 CTCCTCT/	9 -
ILMN_1675117	HSD17B11	NP_05732	2190475 I	465 ATGCTGGT	4 -
ILMN_1675424	SIRPB1	NP_00605	1570402 S	3692 CTCCTCT/	20 -
ILMN_1675939	IFNGR1	NP_00040	1500446 S	1771 CGGAACA/	6 -
ILMN_1676016	NBPF9	XP_93911	6270324 I	582 TATTTCTG/	1 -
ILMN_1676480	LOC65405	XP_94877	7400592 S	941 TGGGATTCGGCCTCTGGAAAGTGC	
ILMN_1676737	Septin 2	NP_00100	780431 I	352 TTTTTTGT/	2 +
ILMN_1676767	CLEC4D	NP_52512	3990328 S	1551 GCCAAAG/	12 +
ILMN_1677511	PTGS2	NP_00095	1470682 S	3943 GCCTATGT	1 -
ILMN_1678170	MME	NP_00921	240608 A	5051 GAGTCTGCCTCCATGCTGCAGTGT	
ILMN_1678690	UPB1	NP_05741	7160367 S	1915 GAAATTCT	22 +
ILMN_1678707	TAF15	NP_63196	5960128 A	1913 TTGCCAGA/	17 +
ILMN_1678799	RAPGEF1	NP_94137	6100576 I	65 AAGAGAT/	9 -
ILMN_1678939	VNN2	NP_51104	5570673 A	1770 CTCCAGCT	6 -
ILMN_1679666	SCGB3A1	NP_44309	2060543 S	221 ATCCCCGT	5 -
ILMN_1679920	LOC65189	XP_94624	1570750 S	7 TTGGGCTTCACCCATAACCCACTGC	
ILMN_1680314	TXN	NP_00332	830762 S	43 CGTCAGAC	9 -
ILMN_1681130	ACP6	NP_05744	3180376 S	1595 TGCCGAG/	1 -
ILMN_1681683	LOC65091	XP_94951	4250543 S	1385 GTAGTCTGCAGATGTGGATCCTAA	
ILMN_1681888	PRKAR2A	NP_00414	4900593 S	2304 GGGTCTGC	3 -
ILMN_1682165	NT5C2	NP_03636	520647 S	3272 CTTCCATT/	10 -
ILMN_1682443	UBE2D3	NP_87161	4640110 A	2052 TGGTGTGC	4 -
ILMN_1682699	PBX2	NP_00257	5550500 S	3106 GGGAGGCATGGGCCGGGGGCAG/	
ILMN_1682757	PFKFB2	NP_00620	3190326 I	6815 GGGCTGA/	1 +
ILMN_1683250	LOC44073	XP_93878	270768 A	111 TGGCTAG/	1 -
ILMN_1683494	TMEM154	NP_68989	7650379 S	2498 TCCAACCC	4 -
ILMN_1683959	THRAP2	NP_05615	1990332 S	9174 GGGGAAA	12 -
ILMN_1684054	ASAH1	NP_80859	840161 I	261 GCTCTTCTTTGCCTCTGCTGGAGTC	
ILMN_1684585	ACSL1	NP_00198	4880717 S	3553 GGGGTCT/	4 -
ILMN_1685312	PSG11	NP_00277	3400292 I	413 TTCCAATG	19 -
ILMN_1685493	TMCC3	NP_06574	2650152 S	4505 GGGCAAA/	12 -
ILMN_1686116	THBS1	NP_00323	5910376 S	4947 CAGTCTAA	15 +
ILMN_1686464	SLCO4C1	NP_85132	770717 S	4454 CTCCCACC	5 -
ILMN_1686750	MGEA5	NP_03634	1010402 S	4955 CACAGGT/	10 -
ILMN_1686862	HLX1	NP_06877	1400706 S	1612 CACGGAG/	1 +
ILMN_1686981	SULF2	NP_06132	1850056 I	2862 GTTTCAGC	20 -
ILMN_1687057	RBM7	NP_05717	5390326 S	1656 AGTGCCCA/	11 +
ILMN_1687384	IFI6	NP_00202	4390176 A	743 TGCGCCG/	1 -

ILMN_1687805	LOC65189	XP_946248	5130273	S	131	TGGAATTTGCAAAGCTGCCAAAGC	
ILMN_1688580	CAMP	NP_004331	6400736	S	644	AGAGTCCT	3 +
ILMN_1689004	TNFRSF12	NP_057721	2190008	S	634	CAGAAAGC	16 +
ILMN_1689955	C19orf40	NP_689471	7150189	S	676	GGAGCAGC	19 +
ILMN_1691364	STAT1	NP_644671	3190133	I	2595	CGCCATCA	2 -
ILMN_1691508	PLAUR	NP_001001	6130594	I	1107	TCAGCCAT	19 -
ILMN_1691574	LOC64606	XP_938468	2450014	S	1382	TGTATAGT	16 -
ILMN_1693394	BCKDK	NP_005871	5390056	S	1742	AGCACCAAC	16 +
ILMN_1693494	CMTM1	NP_851811	4830017	A	704	CACCCCCG	16 +
ILMN_1693740	LOC64783	XP_948141	2600669	S	2498	TAAGATCATGTCACTGCACTCCAGC	
ILMN_1694075	GADD45A	NP_001911	3140239	S	659	CTGCACTG	1 +
ILMN_1694584	CLTCL1	NP_009021	5090026	I	4593	G TTCAGGTGCATTGCGGCCTATCTC	
ILMN_1694742	RPS29	NP_001021	1990753	A	63	GCGAAAA	14 -
ILMN_1695435	LOC65361	XP_933480	5670544	S	713	ATGCTGGC	1 +
ILMN_1695853	CLK4	NP_065711	6510110	S	2086	GGGTGATC	5 -
ILMN_1696162	MME	NP_000891	2360400	I	28	AGATGTGCAAGTGGCGAAGCTTG	
ILMN_1696187	PYGL	NP_002851	4610113	S	2494	ATCCAAAC	14 -
ILMN_1696466	ROPN1L	NP_114121	1050240	S	740	GGGCCCGC	5 +
ILMN_1696704	TLE4	NP_008931	6290170	S	4048	GGCATGCT	9 +
ILMN_1698213	RBM3	NP_001011	7380612	A	346	GAGGTGG X	+
ILMN_1699015	LOC440926		4590593	A	143	CGTACAAAGCAGACTGCCCGCAA	
ILMN_1699331	IFIT1	NP_001531	6220673	I	108	GATGCAGC	10 +
ILMN_1699687	USP9Y	NP_004641	6290398	S	9257	GTGTAGCC Y	+
ILMN_1700610	CLEC7A	NP_922941	1090170	A	43	CCTAGCCC	12 -
ILMN_1700896	SAP30	NP_003851	2510133	S	873	CAGATCTC	4 +
ILMN_1701242	UTY	NP_872601	5310196	I	4730	TGCCTTCT Y	-
ILMN_1701747	PFN2	NP_444251	4210246	I	620	GGTGATGC	3 -
ILMN_1701957	MXD1	NP_002341	2260239	S	5318	TTTTGGGC	2 +
ILMN_1702168	HSD17B12	NP_057221	3290411	S	1747	GTACCACT	11 +
ILMN_1703720	SF3B14	NP_057131	1410315	S	199	TTCATCAG	2 -
ILMN_1704385	LOC34737	XP_943021	5900072	A	1	ATACCATGGCTCGTACAAGGTGGA	
ILMN_1704476	LOC28315	NP_001021	4810324	A	314	GCATGCCA	11 -
ILMN_1705477	CAMK1D	NP_065131	3930653	I	1347	GCATCTGC	10 +
ILMN_1705605	LOC653635		2480278	S	2417	ACACCAGC	1 -
ILMN_1706502	EIF2AK2	NP_002751	1190349	S	2728	CGTTCTCT	2 -
ILMN_1708485	BIN3	NP_061151	7550392	S	1578	TTGTGCTGTAACCTTAGGCGAGCAG	
ILMN_1708841	GOLPH3	NP_071411	4780114	S	2120	GGGAAGA	5 -
ILMN_1708936	EXOSC3	NP_001001	1980743	A	721	CAGGTCAAC	9 -
ILMN_1709707	LOC64749	XP_948031	6560128	I	589	AGGCCCTTTGCCTTACAGAGAAG	
ILMN_1710974	RGS2	NP_002911	5690500	S	865	CCTCACTG	1 +
ILMN_1711156	LOC64589	XP_933951	7570673	S	83	TGTGGCGC	8 -
ILMN_1711617	GMFG	NP_004861	4250452	S	469	TCCTCAGG	19 -
ILMN_1711729	LOC64496	XP_933140	2600187	S	1	CAAAATGC X	-
ILMN_1712389	CKLF	NP_057411	2000551	A	174	ACATCGCC	16 +
ILMN_1712596	NUDT16P		6420402	S	1354	AGAGCCTC	3 +
ILMN_1712688	LOC65350	XP_932860	160494	S	3717	TGGTGATC	1 -
ILMN_1712918	NQO2	NP_000891	870400	S	621	CGGGAGG	6 +
ILMN_1713636	S100A6	NP_055431	1500553	S	527	GGAGTATC	1 -

ILMN_1714065	FAM101B	XP_001126	2350093	S	5	CTCCCACCAGCCTCTTAACTACTTG	
ILMN_1714418	FAM101B	NP_87436	940246	S	292	CCTGGCTCCCGGCTGTGCGCTGAG	
ILMN_1714848	ZNF354A	NP_00564	2850670	S	2312	TGTCACGT	5 -
ILMN_1714991	S100A9	NP_00295	830400	S	506	GCCTGTTATGTCAAACGTCTTGGC	
ILMN_1715693	LOC44016	XP_49857	1190731	S	115	TCCTGCAGCTGTGTTTGAACAGGT	
ILMN_1715809	OGFRL1	NP_07885	2750315	S	1038	AAAGGAG	6 +
ILMN_1716465	RBP7	NP_44319	4810131	S	421	GTGCAAAC	1 +
ILMN_1717371	C22orf34	NP_00103	5910682	S	1303	TGCTTTCT	22 -
ILMN_1718303	PVRL2	NP_00284	2570544	S	1789	CTGGACGGCTCCCTCATCTCACGG	
ILMN_1719951	FLJ31951	NP_65332	2490437	S	2719	GGGTGGG	5 -
ILMN_1719988	HAL	NP_00209	6660327	S	2301	GGGCAGT	12 -
ILMN_1720604	ARSG	NP_05577	5420379	S	1739	GTTAGCCT	17 +
ILMN_1721116	USP10	NP_00514	1980021	S	2458	GATCAACCAGTACCAGGTGGTGA	
ILMN_1721648	EXOC8	NP_78707	5130491	S	4522	GGAACCTC	1 -
ILMN_1721729	PPARBP	NP_00476	6760373	S	5590	GGGTTCA	17 -
ILMN_1722076	DHRS8	XP_00113	1570553	A	1604	CCTACCCATTGCCACTCTGTTTCCT	
ILMN_1723079	LTB4R	NP_85804	3120735	S	2942	TGAGAGCC	14 +
ILMN_1723320	FLJ37307		5490440	A	3986	GTCTTCCT	13 -
ILMN_1723486	HK2	NP_00018	4760768	S	6532	GAGCACAC	2 +
ILMN_1723909	LOC40217	NP_00101	4050056	S	1350	ACTGCATC	4 -
ILMN_1724315	LMTK2	NP_05573	4050040	S	5327	GGATCTTC	7 +
ILMN_1724407	TACC3	NP_00633	2630544	S	2550	GGAGCAG	4 +
ILMN_1724533	LY96	NP_05617	6980474	S	505	TGGGAGCC	8 +
ILMN_1725427	B2M	NP_00403	6290114	S	402	GTGGGATC	15 +
ILMN_1726289	C12orf35	NP_06063	3310446	S	5367	ACGGAAG	12 +
ILMN_1726786	TNRC6B	NP_00102	2600386	A	15415	CTAGGCAC	22 +
ILMN_1727603	ZKSCAN1	NP_00343	1580187	S	5035	ATCCTCAG	7 +
ILMN_1728639	FCGR3B	NP_00056	3990360	S	1450	GAGCCCTC	1 -
ILMN_1728677	CREB5	NP_00101	4220026	I	40	GAGCTCTC	7 +
ILMN_1728724	IL17RA	NP_05515	3870110	S	2932	CAGGGGA	22 +
ILMN_1728844	PTPRN2	NP_57085	6580717	A	4200	CCGATTCCG	7 -
ILMN_1729294	RNF130	NP_06090	5670603	S	1503	CCTCAGGA	5 -
ILMN_1729421	LOC64975	XP_94705	70041	A	190	GGGGTAGAAGTTATGCTTGTGTTT	
ILMN_1729659	TNNI2	NP_00327	6350142	S	274	GTGAGGG	11 +
ILMN_1729801	S100A8	NP_00295	6280576	S	253	TAACTTCC	1 -
ILMN_1730454	FOLR3	NP_00079	2230601	S	759	GCCCCGTC	11 +
ILMN_1730928	CDK5R1	NP_00387	770484	S	3133	CCCTCAGT	17 +
ILMN_1731048	TLR1	NP_00325	5080398	S	2736	GTGAGTG	4 -
ILMN_1731546	RPL26	NP_00097	2000025	S	57	CTTCCCTT	17 -
ILMN_1731785	ORM2	NP_00059	6370202	S	473	GCTGTTCC	9 +
ILMN_1735014	KLF6	NP_00129	5260397	I	1330	CCCTTCCG	10 -
ILMN_1735506	CYSLTR1	NP_00663	4810204	S	1218	TGCAGAA(X	-
ILMN_1735955	LOC64403	XP_93237	4290669	S	283	CAAACCTG	8 -
ILMN_1736190	CYP4F3	NP_00088	650164	S	4625	CTATCTAT	19 +
ILMN_1736982	PHACTR1	NP_11221	3800095	S	1803	AGATAAGC	6 +
ILMN_1737426	PCMTD1	NP_44316	240037	S	3666	TCTAGCAT	8 -
ILMN_1738243	RPS29	NP_00102	5960026	I	194	TGGACTAA	14 -
ILMN_1738643	LOC64496	XP_93313	70221	S	430	CTATGCCA	19 -

ILMN_1738821	GOLGA2	NP_00447	5390445	S	3921	CCATCTTC	9 -
ILMN_1739263	LOC64328	XP_93327	4230615	S	68	GGCCAGG	9 +
ILMN_1739423	RN7SK		5080673	S	257	CGTAGGG	6 +
ILMN_1739587	UTY	NP_00905	5420224	I	6354	GCTATACTY	-
ILMN_1739622	PPP1R12A	NP_00247	4180280	S	4479	ACATCTTT	12 -
ILMN_1739876	RAB3GAP1	NP_03636	6330561	S	3989	CATGGAG	2 +
ILMN_1741073	FCAR	NP_57981	6860239	I	1361	CTGCACAC	19 +
ILMN_1741917	OSCAR	NP_57012	2190609	A	983	AACGGTCC	19 -
ILMN_1743034	KIF1B	NP_90432	3170719	I	5646	GCCCAGG	1 +
ILMN_1743281	PHF3	NP_05596	2510687	S	6079	GGAGAAA	6 +
ILMN_1746020	MDM4	NP_00238	4490671	S	2032	CTTCTGCC	1 +
ILMN_1746276	EPC1	NP_07948	2680010	S	2756	ACACAGTA	10 -
ILMN_1746577	RAE1	NP_00360	4850138	A	1662	CTAAGGG	20 +
ILMN_1746864	PSCDBP	NP_00427	5390195	S	1719	GGGGTTA	2 -
ILMN_1747047	ZNF346	NP_03641	3420373	S	2662	GTGTCCAC	5 +
ILMN_1747205	JDP2	NP_56973	3180379	S	1608	GCCAGGG	14 +
ILMN_1748366	SLC5A9	NP_00101	70270	S	2889	CTGTATTT	1 +
ILMN_1748767	LOC73074	XP_00112	4920408	S	228	TGTGGCGCTCCGTGAAATTAGACG	
ILMN_1748915	S100A12	NP_00561	10279	S	241	TCCAAGGC	1 -
ILMN_1749006	RCSD1	NP_44309	3140280	S	2692	TGCAAGG	1 +
ILMN_1749673	CSF2RA	NP_75844	4150246	A	1244	CCGCCTCCX	+
ILMN_1750880	AMN1	NP_99722	3990719	S	1629	CCACGCTT	12 -
ILMN_1750961	TM6SF1	NP_07537	10541	S	964	GGAGGTC	15 +
ILMN_1751051	C7orf25	NP_07695	4570397	S	1351	CAGCCCA	7 -
ILMN_1751749	SYNJ2	NP_00388	5900592	S	6404	CAAAGAA	6 +
ILMN_1753712	STX10	NP_00375	3190681	S	685	TGGTGTGC	19 -
ILMN_1753819	RFFL	NP_00101	5870551	A	3411	GGGCAGA	17 -
ILMN_1754395	ADCK4	NP_07915	1690221	S	1907	GGAACTCC	19 -
ILMN_1754859	TRIM25	NP_00507	2850576	S	5462	CAGCCTGA	17 -
ILMN_1755049	ANKRD44	NP_71018	4730377	S	2988	CCTACAAG	2 -
ILMN_1755077	HEBP2	NP_05513	5090184	S	804	CGATGAG	6 +
ILMN_1755115	RPL23	NP_00096	4120707	S	321	TCCAGCAC	17 -
ILMN_1756506	CYorf15B	NP_11596	4730458	S	4976	AGCAGTG(Y	+
ILMN_1758418	TNFSF13B	NP_00656	460608	S	634	GGCAACTC	13 +
ILMN_1758658	FADD	NP_00381	1940035	S	1558	CTCTGAGA	11 +
ILMN_1759208	RGS18	NP_57013	1240438	S	1787	GGGGAAG	1 +
ILMN_1759613	PNMA6A	NP_11627	6760270	S	1892	GATGGCG(X	+
ILMN_1760347	SRGN	NP_00271	650541	S	482	CCTTAGGT	10 +
ILMN_1760542	PSMA1	NP_68387	20451	I	233	CCTTGGCC	11 -
ILMN_1760779	ENSA	NP_99705	1110685	A	236	GCCTGAG	1 -
ILMN_1761411	C10orf119	NP_07911	4830192	S	4030	CAGCGTTA	10 -
ILMN_1763260	HIF1A	NP_00152	2850288	I	2496	TTACAGCA	14 +
ILMN_1763408	RBMXL1	NP_06255	5080093	S	3210	CTCCCCGT	1 -
ILMN_1763452	EVI2B	NP_00648	2030593	S	1401	CCTCCCAA	17 -
ILMN_1763809	IRS2	NP_00374	6980095	S	6369	GTA ACTCC	13 -
ILMN_1763837	ANPEP	NP_00114	1770605	S	3149	CTCCAGCC	15 -
ILMN_1764082	MBOAT1	XP_00113	5810731	A	2451	GAGCTGAAGAGGGGCTGCTGTTT	
ILMN_1764396	HDAC4	NP_00602	5960341	S	8280	GGTGATG	2 -

ILMN_1764415	ZNF585A	NP_68986	460504	I	5	CGGAAGT	19	-
ILMN_1765061	OXER1	NP_68376	510491	S	1501	GTGGGTGGCAGGGAGAGAAACCC		
ILMN_1765122	MAP3K2	NP_00660	2320296	A	3192	GCAGCCTC	2	-
ILMN_1767809	LOC55289	NP_00411	5820176	S	337	AACCGCCT	9	+
ILMN_1768117	RBM25	NP_06706	840075	S	4100	ACACACCT	14	+
ILMN_1768394	ARPC5	NP_00570	3930243	S	1767	CGAGTAGC	1	-
ILMN_1769705	LOC44009	NP_00101	4730100	S	307	TTCAACAC	12	-
ILMN_1769734	NT5C3	NP_00100	3780689	A	962	ACTCCCAA	7	-
ILMN_1769741	RPL32	NP_00100	2340373	I	1	GACCTCCT	3	-
ILMN_1769764	ANKRD55	NP_07894	4670056	S	1969	CTGCCAAC	5	-
ILMN_1769937	LOC64982	XP_94730	5550364	A	192	GGCCTTCTCACCTAACGCCACCAAI		
ILMN_1770161	BST1	NP_00432	4920243	S	1081	GTAAGTGC	4	+
ILMN_1770244	CBX1	NP_00679	2450446	S	1745	AGAGGAAI	17	-
ILMN_1770831	LOC64197	XP_94084	6040114	S	7	CTAATAACAGTGACCTCCCGCCAI		
ILMN_1771048	LOC65315	XP_93190	3460735	A	194	TATAAGAT	5	+
ILMN_1771664	CLEC4E	NP_05517	940754	S	1426	GGCTGTAA	12	-
ILMN_1771815	C20orf43	NP_05749	4050537	S	1458	TCCCTCTG	20	+
ILMN_1772163	PRKY	NP_00275	2900048	S	6641	ATCTGGCCY		+
ILMN_1772387	TLR2	NP_00325	1260008	S	3246	GCCACAA	4	+
ILMN_1773154	NFKBIA	NP_06539	4570154	S	992	GAGGACG	14	-
ILMN_1773757	SLC26A8	NP_44319	6650717	A	2874	GCAGCGTI	6	-
ILMN_1775268	HECW2	NP_06581	3140541	S	6706	CTGGGACC	2	-
ILMN_1775444	FLJ12078		7150039	A	2413	GGGGTGAAGTGGAAAATCCAGGG		
ILMN_1776195	TMSB4Y	NP_00419	4150095	S	1360	AGTGGCG`Y		+
ILMN_1776515	MPPE1	NP_07556	780168	A	2114	TCGTCACTCACATGCACGACAGTCI		
ILMN_1776649	LRRK2	NP_94098	1450523	A	7502	CACAGCTA	12	+
ILMN_1777565	TAP2	NP_00053	2970240	I	5257	ACTTGCCCT	6	-
ILMN_1778709	PICALM	NP_00909	1580364	I	1560	CTGTAGAT	11	-
ILMN_1778930	CHD7	NP_06025	4640750	S	10019	TGTCCCGA	8	+
ILMN_1779228	CDH2	NP_00178	4780376	S	4032	GCCTCTGT	18	-
ILMN_1779572	LOC44045	XP_94027	7510424	I	895	GTCCATCA	17	-
ILMN_1781198	PPP1R3D	NP_00623	6400064	S	3031	GGCCTTCA	20	-
ILMN_1782459	OSBPL8	NP_00100	3830138	A	6974	CCTGCAGT	12	-
ILMN_1783085	IL8RB	NP_00154	2710437	S	2541	GGAGGGG	2	+
ILMN_1783675	ASB8	NP_07700	4280114	S	2124	GGCAGTTC	12	-
ILMN_1783805	PNMA3	NP_03749	2490113	S	3474	CGGGACCTGTGTGGGACCTGTGTC		
ILMN_1784300	TUBA4A	NP_00599	380731	S	1391	GAGGGAG	2	-
ILMN_1784380	DTX3L	NP_61214	2850100	S	4588	GGGATTAC	3	+
ILMN_1785167	OSBPL9	NP_07886	6020685	A	2397	GCTTCCCT	1	+
ILMN_1785345	GPR84	NP_06510	2370576	S	1181	GCATCAAC	12	-
ILMN_1785615	SUMO1P1		5340050	S	447	GACTTTCCAGTTGGCCCTGATTTTC		
ILMN_1786847	TGM3	NP_00323	3440754	S	2485	TGATCCCC	20	+
ILMN_1787186	NOV	NP_00250	6420367	S	1974	TGAGGCC	8	+
ILMN_1787378	ADD3	NP_05843	1690273	I	2132	GATGACG	10	+
ILMN_1787808	CEP63	NP_07945	1090300	S	2450	GGAAGAGGAGGAACTGAGGTCTC		
ILMN_1787897	CXCL1	NP_00150	6130576	S	792	GGCTGGC	4	+
ILMN_1788143	LINS1	NP_00103	730491	A	1016	GAAACCATCTTGCATGCTAGAAGT		
ILMN_1788439	LOC44119	NP_00101	2060113	S	1600	GAAAACCC	7	-



ILMN_1788701	PSIP1	NP_15009	1240541	I	3023	TGAATATT	9	-
ILMN_1790412	FLJ39639	XP_37093	5420452	A	2341	GCTTTACG	16	+
ILMN_1790625	CBX3	NP_05767	4880020	I	37	TCCCCCTT	7	+
ILMN_1790689	CRISPLD2	NP_11366	6060224	S	4224	ACGGCGTI	16	+
ILMN_1790715	LOC65310	XP_93630	3800139	I	1	TGCCGACT	1	+
ILMN_1790891	CKAP4	NP_00681	6770348	S	2458	CTGCCTCC	12	-
ILMN_1790985	dJ341D10	NP_00100	4180402	S	1152	TCAGGGGT		+
ILMN_1791253	FBXL13	NP_65946	5050653	S	2503	CCCTCCAC	7	-
ILMN_1791536	BTAF1	NP_00396	1820546	S	6646	CTGGGCAK	10	+
ILMN_1792207	MLX	NP_73375	5820021	A	2409	GAGATGTC	17	+
ILMN_1792997	NPTN	NP_03656	5360338	A	1992	GGGCTTA	15	-
ILMN_1794223	COX7B	NP_00185	70722	S	141	TCAGCAA		+
ILMN_1794333	POU2F1	NP_00268	3850554	S	2380	TCCAAGGC	1	+
ILMN_1796138	BMX	NP_00171	5560451	A	1987	ACAGGCTT		+
ILMN_1796316	MMP9	NP_00498	4150224	S	2049	GCTTCTAC	20	+
ILMN_1796642	NCF2	NP_00042	7050360	S	2056	GGGGAGA	1	-
ILMN_1797207	TTY15		2570082	S	4933	GGCTGCA		+
ILMN_1797745	MAP4K4	NP_66371	2450170	A	6802	GCAGGGA	2	+
ILMN_1797875	ALOX5AP	NP_00162	4180411	S	664	TCTATTGG	13	+
ILMN_1798233	PSMB9	NP_68375	6130669	A	767	TGGGAAA	6	+
ILMN_1798804	SRPK1	NP_00312	3460674	S	4153	GGCAGCT	6	-
ILMN_1799030	CMTM2	NP_65327	5080300	S	763	CCACTTCA	16	+
ILMN_1799106	MOSC1	NP_07358	1980082	S	1680	GGACCCCT	1	+
ILMN_1799644	IBRDC2	NP_87743	5910037	S	4431	GTTGTGAC	6	+
ILMN_1799848	ANKRD22	NP_65319	4200543	S	609	CCTCTGCT	10	-
ILMN_1800638	CUGBP2	NP_00102	6110672	I	2065	CCCGGTGC	10	+
ILMN_1800695	LOC64822	XP_94401	3780189	S	2404	TAAGTTAGCCCTTTGGGTAAGAGT		
ILMN_1801216	S100P	NP_00597	2640609	S	378	AATGATGC	4	+
ILMN_1801776	PSG9	NP_00277	1050465	S	404	TCCAACGC	19	-
ILMN_1801866	BRWD1	NP_38750	430400	I	12653	AAAGGCTI	21	-
ILMN_1802096	ABTB1	NP_74202	5670424	A	1913	CCATTCAG	3	+
ILMN_1802348	SLC36A4	NP_68952	2350195	S	2320	GGAAAAG	11	-
ILMN_1802758	ZNF281	NP_03661	6940113	S	2768	GACACCCA	1	-
ILMN_1802799	C1orf108	NP_07887	1690673	A	1613	CAGGCCCC	1	+
ILMN_1803500	ANP32A	NP_00629	3360546	S	987	TCTGATTG	15	-
ILMN_1803953	LOC38878	XP_94504	1440259	A	219	GGCGAAGTCGTCAGACCAAAAGG		
ILMN_1805064	SCARNA9		840639	S	46	GCCAAATC	11	+
ILMN_1805104	ABAT	NP_06573	1030685	A	4303	AACTCAGCAGAAGCTGGTAAAAAC		
ILMN_1806122	CHD8	NP_06597	5310433	S	7016	GGCCCCATTGCTTGGGCGGCTGCT		
ILMN_1806224	KIAA0492	XP_94938	1090609	A	5727	GGCCCTATACCTGATCACCTCTAA		
ILMN_1807003	ANXA11	NP_66587	7380450	I	338	TCACAGTT	10	-
ILMN_1807529	PADI4	NP_03651	5310653	S	2163	GTCCCAGT	1	+
ILMN_1809585	KIAA0319L	NP_87262	150392	I	5065	GGACAGG	1	-
ILMN_1810229	ARID4A	NP_07537	3830228	A	4318	GCCAAAGTATATGTTTCAGCAGTGT		
ILMN_1811330	FLJ20152	NP_06187	1230022	S	2592	AGGTACAC	5	-
ILMN_1811608	FLJ14107		2900008	S	1503	CACTCAGCACCCCTCCCAAAGAG		
ILMN_1811616	KIAA1706	NP_08513	6250685	S	4375	CCCAGGA	7	+
ILMN_1812571	RAB35	NP_00685	5340243	S	2738	GTGGGGA	12	-

ILMN_1812856	ZSWIM1	NP_54217	1260082	S	2094	CTGACTCA	20	+
ILMN_1813139	ANKDD1A	NP_87436	3290296	S	2807	TCGGGGAAACTGTGTGTGCTGAAC		
ILMN_1813455	SP110	NP_53634	10546	I	1934	CTTGAAGC	2	-
ILMN_1813746	CORO2A	NP_00338	4590554	A	1976	CGCTGAA	9	-
ILMN_1814153	IL9R	NP_00217	290424	A	1990	CTCTGAG		+
ILMN_1815121	PLAGL1	NP_00107	2230475	A	2085	CCATCCCTCATGTGTTCTCAGCTGC		
ILMN_1815668	GTF2IP1		6200438	S	2314	CAGCTGG	7	-
ILMN_2038776	TXN		7610747	S	23	CATCGGTCCTTACAGCCGCTCGTC		



89852902- Homo sapiens chromosome 14 o binding [gc FLJ14051; NM_01797 mRNA	blue
ATCACCTG/ PREDICTED: Homo sapiens similar to Williams Beuren s XM_93580 mRNA	blue
13044316: PREDICTED: Homo sapiens hypothetical protein FLJ436 XM_93054 lncRNA	blue
8382616-8 PREDICTED: Homo sapiens hypothetical protein LOC64: XM_93187 mRNA	blue
22556843- Homo sapi membrane transport [ glucose tra MGC1188: NM_0010: mRNA	blue
5GGCGACA Homo sapiens succinate dehydrogenase cor SDHAL1 NR_00326 mRNA	blue
38114867- Homo sapi cytosolic ri regulation transferas GCN2; KIA, NM_0010: mRNA	blue
AAATGTAC PREDICTED: Homo sapiens similar to dicer1 (LOC64769 XM_93674 mRNA	blue
22002600- PREDICTED: Homo sapiens similar to Dihydrofolate red XM_92815 mRNA	blue
11197165( Homo sapi membrane small GTP: nucleotide RAP1; KRE' NM_0010: mRNA	blue
42861220- Homo sapiens FLJ38717 protein (FLJ38717), FLJ40915 NM_0010( mRNA	blue
37875474- Homo sapi integral to transport [ binding [gc CG7943; N NM_0334: mRNA	blue
11071486: PREDICTED: Homo sapiens similar to RAN-binding prot: XM_93465 mRNA	blue
AACATGAC PREDICTED: Homo sapiens hypothetical protein FLJ407 XM_94209 mRNA	blue
11151924: Homo sapi extracellul: immune re interleukin MGC1232( NM_0015( mRNA	blue
16829066- PREDICTED: Homo sapiens hypothetical protein MGC1: XM_93048 mRNA	blue
'AAGGTGG( PREDICTED: Homo sapiens solute carrier family 25 (car: XM_00113 mRNA	blue
iGCACAGT( PREDICTED: Homo sapiens hypothetical protein LOC64: XM_93646 mRNA	blue
69239594- Homo sapi actin cytoskeleton [gc tropomyos: DKFZp313: NM_1982: mRNA	blue
20339862: Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) NM_1782: mRNA	blue
15574998: PREDICTED: Homo sapiens similar to Fc receptor-like 5 XM_00113 mRNA	blue
5923495-5 Homo sapi nucleus [gc DNA replic DNA-depe: MGC4816; NM_1828( mRNA	blue
20171476- PREDICTED: Homo sapiens zinc finger protein 486 (ZNF: XM_37115 mRNA	blue
46552207- Homo sapiens hypothetical protein MGC4093 (MGC40: NM_0305: mRNA	blue
11598153: Homo sapiens tudor domain con zinc ion bir FLJ21082 NM_1987: mRNA	blue
10007363: Homo sapi membrane ion transp: transporte SMCT; MG NM_1459: mRNA	blue
34185801- Homo sapi endoplasr cell surfac: 1-phospha Pip4k2B; P NM_1386: mRNA	blue
17351414- Homo sapi nucleus [gc response t transcription factor ac NM_0016: mRNA	blue
11285135: PREDICTED: Homo sapiens similar to RAN-binding prot: XM_93099 mRNA	blue
33779905- Homo sapiens chrom: protein fol unfolded p C21orf78 NM_0178: mRNA	blue
49263889- Homo sapi nucleus [gc regulation DNA binding [goid 36: NM_0133( mRNA	blue
42178233- PREDICTED: Homo sapiens similar to AI661453 protein XM_37182 mRNA	grey
32906458- Homo sapi TAP compl immune re tapasin bir RING11; P: NM_0188: mRNA	grey
27732933- Homo sapi nucleus [gc morphoge transcripti: TBR2 NM_0054: mRNA	grey
11055200: Homo sapi membrane [goid 160: transferas NLRR-3; NI NM_0183: mRNA	grey
18036576: Homo sapi membrane lipid metabolism [goid: BTNLR NM_0067( mRNA	grey
14806725: PREDICTED: Homo sapiens similar to H3 histone, family XM_49771 mRNA	grey
54174433- Homo sapi membrane metabolisr acyltransfe FLJ20481; NM_0178: mRNA	grey
TCAGGAA( Homo sapiens thioredoxin (TXN), mRNA. NM_0033: mRNA	turquoise
8293227-8 Homo sapi intracellul: protein bic structural constituent NM_0010: mRNA	turquoise
91411148- Homo sapiens growth cell differe protein bir DDIT2; CR: NM_0067( mRNA	turquoise
44615731- Homo sapi ribosome [ protein bic structural constituent NM_0010: mRNA	turquoise
18518435: Homo sapi integral to transport [ ATPase act MOAT-C; p NM_0010: mRNA	turquoise
11347139: Homo sapi heterotrim G-protein ( GTPase activity [goid : NM_0010: mRNA	turquoise
70442883- Homo sapiens LMBR1 domain containing 1 (ba810: NM_0183( mRNA	turquoise
5TTCTCGCT PREDICTED: Homo sapiens similar to 40S ribosomal prc XM_93643 mRNA	turquoise
36153798- Homo sapi membrane [goid 16020] [eviden: GLIPR2; G: NM_0223: mRNA	turquoise
20078363- Homo sapiens ribosor skeletal de transferas: pp90RSK2; NM_0045: mRNA	turquoise

4316893-4 PREDICTED: Homo sapiens similar to Ssu72 RNA polymerase II subunit 72	XM_37234 mRNA	turquoise
TCCCAACA, Homo sapiens pre-B-cell pyridine nucleotidyl transferase	DKFZP666I NM_00574 mRNA	turquoise
75454418- Homo sapiens integral to membrane [goid 16021] [evidence 1]	NM_03192 mRNA	turquoise
75346964- Homo sapiens extracellular blood coagulation factor serine-type 1	UPA; URK; NM_00265 mRNA	turquoise
53063842- Homo sapiens zyg-11 homolog B binding [gc FLJ13456; ]	NM_02464 mRNA	turquoise
44597523- Homo sapiens plasma membrane [gc protein bir SAR2; TSP1]	NM_00225 mRNA	turquoise
10190085- Homo sapiens DNA-directed transcription factor	RPB11; MCMC NM_00625 mRNA	turquoise
58332875- Homo sapiens hypothetical protein LOC284	FLJ46426 NM_00100 mRNA	turquoise
24652407- Homo sapiens membrane homophilic calcium ion channel	DLX2; DYLL1 NM_01480 mRNA	turquoise
90407224- Homo sapiens nucleus [gc response to stress transferase	RLPK; MSP NM_00475 mRNA	turquoise
ACATGTGC, PREDICTED: Homo sapiens hypothetical protein LOC64	XM_93610 lncRNA	turquoise
GTCCACAT, Homo sapiens membrane [goid 1602] receptor	EGFL5 NM_00108 mRNA	turquoise
3756-3805 PREDICTED: Homo sapiens similar to CXYorf1-related protein	XR_01761.1 mRNA	turquoise
14808089- Homo sapiens chromosomal nucleosomal DNA binding	H2a-615; H2A.1 NM_00351 mRNA	turquoise
6486367-6 Homo sapiens thioredoxin-like 5 electron carrier	TRP14; MCMC NM_03275 mRNA	turquoise
60710651- PREDICTED: Homo sapiens similar to hypothetical protein	XM_92681 mRNA	turquoise
AGCTAAAG PREDICTED: Homo sapiens hypothetical protein LOC64	XM_93557 lncRNA	turquoise
15222988- Homo sapiens ribosome [protein biogenesis RNA binding	MPS-1; MFM1 NM_00105 mRNA	turquoise
68336908- Homo sapiens G protein-coupled receptor positive regulator	C1orf139; NM_00100 mRNA	turquoise
1388309-1 Homo sapiens integral to plasma membrane receptor	CSF2R; CSF2R NM_17224 mRNA	turquoise
38299200- PREDICTED: Homo sapiens hypothetical protein LOC28	XM_37845 lncRNA	turquoise
TGACTGCC PREDICTED: Homo sapiens hypothetical protein LOC64	646424 (LC) XM_94126 mRNA	turquoise
19558234- Homo sapiens nucleus [gc regulation zinc ion binding	RAMP; SCL NM_00345 mRNA	turquoise
34634020- Homo sapiens protein phosphatase calcium ion dependent	G5pr; FLJ212 NM_01791 mRNA	turquoise
17128557- Homo sapiens membrane G-protein-coupled receptor	GPCR1; GP1R NM_01437 mRNA	turquoise
12664737- Homo sapiens hypothetical protein hydrolase	CSTP1 NM_01834 mRNA	turquoise
22371126- Homo sapiens intracellular small GTP-binding guanyl-nucleotide	MGC11967; NM_15361 mRNA	turquoise
82593742- Homo sapiens cytoplasmic antibiotic resistance oxidoreductase	NECAB2 NM_01906 mRNA	turquoise
18003717- Homo sapiens voltage-gated calcium ion channel voltage-gated	CACH6; BII1 NM_00072 mRNA	turquoise
10734697- Homo sapiens mitochondrial electron transport disulfide oxidoreductase	E3; PHE3; INM_00010 mRNA	turquoise
23897916- Homo sapiens cytosolic [gc phototransduction [gc HRG4	NM_00514 mRNA	turquoise
14805181- PREDICTED: Homo sapiens similar to H3 histone, family	XM_49771 mRNA	turquoise
AGCCCTTC, Homo sapiens membrane [goid 16020] [evidence 1]	CGI-119; ZNF119 NM_01605 mRNA	turquoise
22664611- Homo sapiens intracellular intracellular signaling	SWIP1; WIP1 NM_01562 mRNA	turquoise
24707151- Homo sapiens SH3-binding domain protein	FLJ33845; NM_03064 mRNA	turquoise
61085713- Homo sapiens ubiquitin ubiquitin-cysteine peptidase	MGC13198; NM_00631 mRNA	turquoise
34459695- PREDICTED: Homo sapiens similar to SMT3 suppressor	XM_37252 mRNA	turquoise
52083405- Homo sapiens AKT interacting ubiquitin-cysteine ubiquitin-protein	FTS; FT1 NM_02247 mRNA	turquoise
10052019- Homo sapiens intracellular [goid 562 zinc ion binding	DKFZP667C NM_03096 mRNA	turquoise
12331650- Homo sapiens cell division cell cycle [goid 7049]	C10orf7; DNM1 NM_00602 mRNA	turquoise
23592413- Homo sapiens nucleus [gc regulation sequence-specific	NKX3A; BAK1 NM_00616 mRNA	turquoise
11337048- Homo sapiens lipid phosphate phosphatase zinc ion binding	FLJ13055; NM_02275 mRNA	turquoise
45720017- Homo sapiens endoplasmic reticulum metabolic hydrolase	MGC12641; NM_19855 mRNA	turquoise
11190318- Homo sapiens interferon-gamma cell differentiation binding	gc PC4; TIS7 NM_00155 mRNA	turquoise
11485989- PREDICTED: Homo sapiens similar to SMT3 suppressor	XM_00112 mRNA	turquoise
13410774- Homo sapiens membrane cell differentiation GPI anchor	baA479K20. NM_03255 mRNA	turquoise
ACTTTCCCA, PREDICTED: Homo sapiens similar to F15D3.1a (LOC39	XM_93727 mRNA	turquoise
51243958- Homo sapiens dehydratase metabolic oxidoreductase	FLJ13639 NM_00105 mRNA	turquoise

66796993- Homo sapi cell fractio signal tran: hydrolase : HCP1; PDE NM_00260 mRNA	turquoise
15708427- Homo sapi nucleus [g: cellular de: DNA bindir PYHIN3 NM_00243 mRNA	turquoise
:TCGTGTCC Homo sapi nucleus [g: regulation transcripti E2FBP1; BF NM_00522 mRNA	turquoise
20210812- Homo sapiens chromosome Y open reading MGC13173 NM_00100 mRNA	turquoise
17492157- Homo sapi nucleus [g: transcripti: protein binding [goid : NM_00488 mRNA	turquoise
GGTGGAGC Homo sapi nucleus [g: chloride tr: chloride ch RP11-475E NM_00104 mRNA	turquoise
46295471- Homo sapiens transdu: negative r: SH3/SH2 a MGC10479 NM_00574 mRNA	turquoise
12620016- Homo sapi nucleus [goid 5634] [e: structural i: MGC11141 NM_00557 mRNA	turquoise
76166279- Homo sapi plasma me blood coag thrombin r PAR2; GPR NM_00524 mRNA	turquoise
VTGGTATCA PREDICTED: Homo sapiens similar to Fc fragment of IgC XM_94209 mRNA	turquoise
76866031- Homo sapiens chrom: pyridine n: kinase acti NRK1; bA2 NM_01788 mRNA	turquoise
88514916- Homo sapiens hydrox metabolisr oxidoredu: DHRS8; PA NM_01624 mRNA	turquoise
1491641-1 Homo sapi integral to cell surface receptor I SIRP-BETA: NM_00606 mRNA	turquoise
13756055- Homo sapi integral to response t cytokine bi CD119; IFN NM_00041 mRNA	turquoise
14606854- PREDICTED: Homo sapiens neuroblastoma breakpoint f XM_93402 mRNA	turquoise
VTGGTAGT PREDICTED: Homo sapiens similar to hypothetical LOC: XM_94367 lncRNA	turquoise
24190563- Homo sapi contractile cell cycle [i: GTPase acti KIAA0158; NM_00100 mRNA	turquoise
8565844-8 Homo sapi membrane immune re sugar bindi CLEC6; MC NM_08038 mRNA	turquoise
18490806- Homo sapi nucleus [g: physiologi: oxidoredu: PHS-2; CO: NM_00096 mRNA	turquoise
TCGAGTGG Homo sapi plasma me cell-cell sig zinc ion bir MGC12668 NM_00728 mRNA	turquoise
23252401- Homo sapiens ureido: nitrogen c: zinc ion bir BUP1 NM_01632 mRNA	turquoise
31198110- Homo sapi nucleus [goid 5634] [e: RNA polym: TAFII68; T: NM_13921 mRNA	turquoise
13357493- Homo sapi intracellul: small GTP: guanyl-nuc DKFZp781I NM_19867 mRNA	turquoise
13310682- Homo sapi membrane nitrogen c: hydrolase : FOAP-4; GI NM_07848 mRNA	turquoise
17995025- Homo sapi extracellul: regulation cytokine a: MGC8786; NM_05286 mRNA	turquoise
:CATGGCC PREDICTED: Homo sapiens similar to ribosomal protein XM_94115 mRNA	turquoise
11205355- Homo sapiens thio red cell motilit thiol-disulf DKFZp686I NM_00332 mRNA	turquoise
14558593- Homo sapiens acid phosphatase hydrolase : PACPL1; A: NM_01636 mRNA	turquoise
CTCCTGCG PREDICTED: Homo sapiens hypothetical protein LOC65: XM_94441 mRNA	turquoise
48763124- Homo sapi plasma me intracellul: kinase acti MGC3606; NM_00415 mRNA	turquoise
10483792- Homo sapi cytosol [goid 5829] [e: hydrolase : cN-II; NT5E NM_01222 mRNA	turquoise
10393633- Homo sapiens ubiquit ubiquitin c ligase activ E2(17)KB3: NM_18188 mRNA	turquoise
TTCTCTCTCT Homo sapi nucleus [g: regulation sequence-: G17; PBX2 NM_00258 mRNA	turquoise
20531752- Homo sapiens 6-phos metabolisr kinase acti DKFZp781I NM_00621 mRNA	turquoise
22972970- PREDICTED: Homo sapiens hypothetical LOC440731, tr: XM_93369 lncRNA	turquoise
15376725- Homo sapi integral to membrane [goid 1602 FLJ32028 NM_15268 mRNA	turquoise
11488107- Homo sapi nucleus [g: regulation receptor a: PROSIT24C NM_01533 mRNA	turquoise
:CGGGGAG Homo sapi lysosome [ceramide r transferas: AC; FLJ220 NM_17792 mRNA	turquoise
18591394- Homo sapi membrane metabolisr ligase activ FACL2; LA: NM_00199 mRNA	turquoise
48220757- Homo sapi extracellul: pregnancy [goid 7565 MGC22484 NM_00278 mRNA	turquoise
93486339- Homo sapi membrane [goid 16020] [eviden: KIAA1145 NM_02069 mRNA	turquoise
37676117- Homo sapi extracellul: cell motilit signal tran: TSP; THBS; NM_00324 mRNA	turquoise
10159841- Homo sapi membrane transport [ transporte OATP-M1; NM_18099 mRNA	turquoise
10353434- Homo sapiens mening glycoprote hyaluronoi MEA5; FLJ: NM_01221 mRNA	turquoise
21912437- Homo sapi nucleus [g: regulation sequence-: HB24 NM_02199 mRNA	turquoise
45721550- Homo sapi endoplasr metabolisr hydrolase : MGC12641 NM_01883 mRNA	turquoise
11378458- Homo sapiens RNA bi: meiosis [g: RNA bindir FLJ11153 NM_01609 mRNA	turquoise
27865202- Homo sapi membrane anti-apopt protein bir IFI-6-16; 6- NM_00203 mRNA	turquoise

CTTAGACA PREDICTED: Homo sapiens similar to ribosomal protein XM_94115 mRNA	turquoise
48241909- Homo sapi extracellular region [goid 5576] [ LL37; FALL NM_00434 mRNA	turquoise
3012033-3 Homo sapi membrane cell differe receptor a CD266; TM NM_01663 mRNA	turquoise
38159368- Homo sapi nucleus [gc DNA repair DNA bindir FLJ46828; NM_15226 mRNA	turquoise
19154862: Homo sapi nucleus [gc transcripti transcripti ISGF-3; ST/ NM_13926 mRNA	turquoise
48842368- Homo sapi plasma me cell motilit GPI anchor CD87; UPA NM_00100 mRNA	turquoise
3067402-3 PREDICTED: Homo sapiens hypothetical protein LOC641 XM_93337 mRNA	turquoise
31031334- Homo sapi alpha-keto branched c kinase activity [goid 1 NM_00588 mRNA	turquoise
65170462- Homo sapi integral to chemotaxi cytokine a CKLFH; CKI NM_18130 mRNA	turquoise
ACTGAGCA. PREDICTED: Homo sapiens hypothetical protein LOC641 XM_94304 lncRNA	turquoise
67924838- Homo sapi nucleus [gc apoptosis [goid 6915] GADD45; I NM_00192 mRNA	turquoise
GTACAAGG Homo sapi clathrin co morphoge binding [gc CLH22; CL1 NM_00705 mRNA	turquoise
49122497- Homo sapi ribosome [ protein bic structural constituent NM_00103 mRNA	turquoise
14808981( PREDICTED: Homo sapiens similar to Histone H2A.o (H2 XM_92838 mRNA	turquoise
17796264: Homo sapi nucleus [gc protein arr ATP bindin DKFZp686; NM_02066 mRNA	turquoise
ACCGAGAG Homo sapi plasma me cell-cell sig zinc ion bir NEP; MGC: NM_00090 mRNA	turquoise
50441973- Homo sapiens phosphr glycogen n pyridoxal phosphate k NM_00286 mRNA	turquoise
10514353- Homo sapiens ropporin 1-like (ROPN1L), mRASP; FLJ25 NM_03191 mRNA	turquoise
81530777- Homo sapi nucleus [gc regulation of transcrip BCE-1; ESG NM_00700 mRNA	turquoise
48319749- Homo sapiens RNA bi RNA proce RNA bindir RNPL; IS1-I NM_00101 mRNA	turquoise
TCGACCG( PREDICTED: Homo sapiens H3 histone, family 3A pseud XR_01783: mRNA	turquoise
91149642- Homo sapi cytoplasm immune re binding [gc RNM561; I NM_00154 mRNA	turquoise
13481379- Homo sapiens ubiquit ubiquitin-c calcium-de DFFRY; SP: NM_00465 mRNA	turquoise
10174011- Homo sapi integral to phagocyto pattern rex BGR; DECT NM_19795 mRNA	turquoise
17453502: Homo sapi nucleus [gc regulation transcription corepre: NM_00386 mRNA	turquoise
13918925- Homo sapi nucleus [goid 5634] [e binding [gc UTY1; DKF: NM_18265 mRNA	turquoise
15116681: Homo sapi actin cytos regulation actin bindi D3S1319E; NM_05302 mRNA	turquoise
70023312- Homo sapi nucleus [gc cell prolife transcripti MGC10465 NM_00235 mRNA	turquoise
43834109- Homo sapi membrane metabolisr oxidoredu KAR NM_01614 mRNA	turquoise
24150565- Homo sapi nucleus [gc nuclear mf RNA bindir Ht006; SF3 NM_01604 mRNA	turquoise
CTGCCCGC PREDICTED: Homo sapiens similar to H3 histone, family XM_93792 mRNA	turquoise
11856670: Homo sapiens hypothetical protein LOC283: MGC12544 NM_00103 mRNA	turquoise
12907768- Homo sapi nucleus [gc protein arr calmodulir CKLiK; CaV NM_02035 mRNA	turquoise
3934-3983 PREDICTED: Homo sapiens similar to CXYorf1-related p XR_01761: mRNA	turquoise
37187233- Homo sapi intracellul: immune re transferas PRKR; PKR NM_00275 mRNA	turquoise
iAGGAAAC( Homo sapi cytoskelet: barrier sep cytoskelet: MGC14978 NM_01868 mRNA	turquoise
32161087- Homo sapi membrane [goid 16020] [evidenc FLJ90675; NM_02213 mRNA	turquoise
37770607- Homo sapi cytoplasm rRNA proci exonuclea: RP11-3J10 NM_00100 mRNA	turquoise
AGCAGACA PREDICTED: Homo sapiens similar to CG7889-PA, transi XM_94293 mRNA	turquoise
19104754: Homo sapiens regulat regulation calmodulir GOS8 NM_00292 mRNA	turquoise
67689479- PREDICTED: Homo sapiens hypothetical protein LOC641 XM_92886 mRNA	turquoise
44510871- Homo sapi intracellul: protein arr enzyme ac MGC12686 NM_00487 mRNA	turquoise
56780689- PREDICTED: Homo sapiens similar to Ubiquinol-cytochr XM_92804 mRNA	turquoise
65144146- Homo sapi integral to macropha: chemokine UCK-1; CKI NM_01632 mRNA	turquoise
132565798 Homo sapiens nudix (nucleoside diphosphat FLJ20525 NR_00294 mRNA	turquoise
14307218: PREDICTED: Homo sapiens similar to peptidyprolyl isor XM_92776 mRNA	turquoise
2962146-2 Homo sapiens NAD(P) electron tr zinc ion bir DHQV; DIA NM_00090 mRNA	turquoise
15177380( Homo sapi ruffle [goic cell-cell sig protein ho PRA; CABP NM_01462 mRNA	turquoise

CCTGAGGA PREDICTED: Homo sapiens family with sequence similar to XM_00112 mRNA	turquoise
GGCTTTGTC Homo sapiens family with sequence similar to MGC45871 NM_18270 mRNA	turquoise
17807132: Homo sapiens nucleus [glucuronidase RNA polymerase II; TCF1 NM_00564 mRNA	turquoise
CTGTGGGG Homo sapiens extracellular cell-cell signaling signal transduction CFAG; MAF NM_00296 mRNA	turquoise
CATTACC PREDICTED: Homo sapiens hypothetical LOC440160 (LOC XM_49857 mRNA	turquoise
72067992- Homo sapiens membrane [glycophorin receptor and CD331H24. NM_02457 mRNA	turquoise
9998450-9 Homo sapiens retinol transport [retinal binding CRBP4; MAF NM_05296 mRNA	turquoise
48399408- Homo sapiens chromosome 22 open reading frame 34 NM_00103 mRNA	turquoise
CGGGCAGT Homo sapiens plasma membrane homophilic protein homolog PVRR2; HV NM_00285 mRNA	turquoise
15851759( Homo sapiens hypothetical protein protein bir DKFZp686I NM_14472 mRNA	turquoise
94892061- Homo sapiens cytosol [glucosyltransferase lyase activity HSTD; histone NM_00210 mRNA	turquoise
63928321- Homo sapiens endoplasmic reticulum metabolic hydrolase KIAA1001 NM_01496 mRNA	turquoise
ACCAACTC Homo sapiens ubiquitin ubiquitin-c ubiquitin thiolase MGC2621; NM_00515 mRNA	turquoise
22953563( Homo sapiens exocyst protein transmembrane protein bir Exo84p; SE NM_17587 mRNA	turquoise
34816549- Homo sapiens nucleus [glucuronidase DNA binding TRIP2; PPA NM_00477 mRNA	turquoise
GAGAGATA PREDICTED: Homo sapiens dehydrogenase/reductase (NADPH) XM_00113 mRNA	turquoise
23855914- Homo sapiens integral to cell motility nucleotide LTBR1; P21 NM_18165 mRNA	turquoise
51285425- PREDICTED: Homo sapiens hypothetical protein FLJ373 XR_00060: lncRNA	turquoise
74973428- Homo sapiens mitochondrion glycolysis [kinase activity HKII; HXK2 NM_00018 mRNA	turquoise
54546773- Homo sapiens ribosome [protein biogenesis structural constituent NM_00101 mRNA	turquoise
97673262- Homo sapiens integral to membrane transferase KIAA1079; NM_01491 mRNA	turquoise
1716348-1 Homo sapiens transforming, acidic coiled-coil MGC13324 NM_00634 mRNA	turquoise
75103777- Homo sapiens plasma membrane cellular density coreceptor MD-2 NM_01536 mRNA	turquoise
42795187- Homo sapiens extracellular immune response MHC class I receptor alpha NM_00404 mRNA	turquoise
32030109- Homo sapiens chromosome 12 open reading frame FLJ20696; NM_01816 mRNA	turquoise
39061214- Homo sapiens trinucleotide repeat nucleotide KIAA1093 NM_00102 mRNA	turquoise
99472880- Homo sapiens nucleus [glucocorticoid regulation zinc ion binding MGC13842 NM_00343 mRNA	turquoise
15986014( Homo sapiens membrane immune response receptor alpha CD16b; FC gamma 2R1 NM_00057 mRNA	turquoise
28692285- Homo sapiens nucleus [glucocorticoid positive response sequence-1 CRE-BPA NM_00101 mRNA	turquoise
15970908- Homo sapiens integral to cell surface receptor alpha hIL-17R; IL-17R1 NM_01433 mRNA	turquoise
15702493( Homo sapiens integral to protein arrangement transmembrane PTPRP; ICA NM_13084 mRNA	turquoise
17932641( Homo sapiens integral to apoptosis   zinc ion binding G1RZFP; N NM_01843 mRNA	turquoise
CTCCAGGC PREDICTED: Homo sapiens hypothetical protein LOC641 XM_94196 lncRNA	turquoise
1818688-1 Homo sapiens troponin regulation actin binding DA2B; AMI NM_00328 mRNA	turquoise
15162923( Homo sapiens extracellular inflammatory calcium ion channel CFAG; 60B NM_00296 mRNA	turquoise
71528496- Homo sapiens membrane folic acid transporter folic acid binding FR-gamma NM_00080 mRNA	turquoise
27841663- Homo sapiens cyclin-dependent brain development cadherin beta p35nck5a; NM_00388 mRNA	turquoise
38474336- Homo sapiens plasma membrane positive response transferase KIAA0012; NM_00326 mRNA	turquoise
8226343-8 Homo sapiens large ribosomal protein biogenesis structural constituent NM_00098 mRNA	turquoise
11613369( Homo sapiens extracellular acute-phase binding [glucanase AGP2; AGF NM_00060 mRNA	turquoise
3811452-3 Homo sapiens nucleus [glucocorticoid B cell differentiation transcript BGF; ZF9; 5 NM_00130 mRNA	turquoise
77415032- Homo sapiens membrane respiratory leukotriene receptor CYSLTR; M NM_00663 mRNA	turquoise
3918-3967 PREDICTED: Homo sapiens similar to similar to RPL23A1 XM_92728 mRNA	turquoise
15634207- Homo sapiens endoplasmic reticulum leukotriene iron ion binding CPF3; CYP4 NM_00089 mRNA	turquoise
13391737- Homo sapiens phosphatase and protein phosphatase RPEL; MGC NM_03094 mRNA	turquoise
52892908- Homo sapiens protein protein membrane protein-L-1 FLJ10883 NM_05293 mRNA	turquoise
49120092- Homo sapiens ribosome [protein biogenesis structural constituent NM_00103 mRNA	turquoise
193631-19 PREDICTED: Homo sapiens hypothetical protein LOC641 XM_92804 mRNA	turquoise



13005821	Homo sapi Golgi apparatus [goid protein bir MGC2067	NM_0044	mRNA	turquoise
89330079-	PREDICTED: Homo sapiens similar to 40S ribosomal prc	XM_92818	mRNA	turquoise
52968633-	Homo sapiens RNA, 7SK, nuclear (RN7SK) or 7SK	NR_00144.	mRNA	turquoise
13869775-	Homo sapi nucleus [goid 5634] [ε binding [gc UTY1; DKF.	NM_0071	mRNA	turquoise
78692404-	Homo sapi actin cytos regulation signal tran: MGC1330	NM_0024	mRNA	turquoise
13564383	Homo sapi soluble fra regulation Rab GTPas RAB3GAP; NM_0122	mRNA	turquoise	
60091988-	Homo sapi plasma me immune re receptor a CD89	NM_1332	mRNA	turquoise
59290134-	Homo sapiens osteoclast-associa receptor a MGC3361	NM_1307	mRNA	turquoise
10289291-	Homo sapi microtubul neuomus ATPase act KIAA0591; NM_1834	mRNA	turquoise	
64481496-	Homo sapiens PHD fir regulation zinc ion bir MGC1422	NM_0151	mRNA	turquoise
20278583	Homo sapi nucleus [gc protein sta zinc ion bir MDMX; Dk	NM_0023	mRNA	turquoise
32597972-	Homo sapi nucleus [gc chromatin transcripti Epl1; DKFZ	NM_0252	mRNA	turquoise
55386776-	Homo sapi cytoskelet mitotic spi RNA bindir MIG14; M	NM_0036	mRNA	turquoise
15797981	Homo sapi membrane regulation protein bir CASP; CYTI	NM_0042	mRNA	turquoise
17642594	Homo sapi nucleus [gc apoptosis   zinc ion bir Zfp346; JA	NM_0122	mRNA	turquoise
75006821-	Homo sapi nucleus [gc regulation protein dir JUNDM2	NM_1304	mRNA	turquoise
48486565-	Homo sapi membrane ion transp transporte MGC1325	NM_0010	mRNA	turquoise
TTATCAGA	PREDICTED: Homo sapiens similar to H3 histone, family	XM_00112	mRNA	turquoise
15161298	Homo sapi insoluble fixenobiotic zinc ion bir CAAF1; CA	NM_0056	mRNA	turquoise
16594166	Homo sapiens RCSD domain cont kinase acti RP3-503M	NM_0528	mRNA	turquoise
1388406-1	Homo sapi integral to plasma me receptor a CSF2R; CSF	NM_1722	mRNA	turquoise
31715625-	Homo sapiens antagonist of mitotic exit network 1 hon	NM_2073	mRNA	turquoise
81587223-	Homo sapi membrane [goid 16020] [evidence NAS]; int	NM_0230	mRNA	turquoise
42915789-	Homo sapiens chromosome 7 open reading MGC2821; NM_0240	mRNA	turquoise	
15843922	Homo sapiens synaptojanin 2 (SY RNA bindir KIAA0348; NM_0038	mRNA	turquoise	
13116239-	Homo sapi membrane protein transport [goi SYN10; hsy	NM_0037	mRNA	turquoise
30360904-	Homo sapi membrane ubiquitin c zinc ion bir RNF189; R	NM_0010	mRNA	turquoise
45889570-	Homo sapiens aarF domain cont kinase acti COQ8; FLJ	NM_0248	mRNA	turquoise
52320501-	Homo sapiens tripartite motif-co zinc ion bir Z147; ZNF	NM_0050	mRNA	turquoise
19756814	Homo sapiens ankyrin repeat domain 44 (A MGC7044	NM_1536	mRNA	turquoise
13877579	Homo sapiens heme binding protein 2 (HEBI RP3-422G	NM_0143	mRNA	turquoise
34260200-	Homo sapi ribosome [ protein bic structural ( MGC1173	NM_0009	mRNA	turquoise
20225225-	Homo sapiens chromosome Y open reading frame 15B	NM_0325	mRNA	turquoise
10772071	Homo sapi integral to immune re tumor nec ZTNF4; TAI	NM_0065	mRNA	turquoise
69730861-	Homo sapi cytoplasm antimicrob protein kin GIG3; MOF	NM_0038	mRNA	turquoise
19042121	Homo sapiens regulat negative re signal tran: RGS13	NM_1307	mRNA	turquoise
15199374	Homo sapiens paraneoplastic antigen like 6 MGC1582	NM_0328	mRNA	turquoise
70533801-	Homo sapiens serglycin (SRGN), mRNA. PRG1; PPG	NM_0027	mRNA	turquoise
14589154-	Homo sapi nucleus [gc ubiquitin-c threonine MGC2285	NM_1489	mRNA	turquoise
14886661	Homo sapiens endosu transport [ ion channe MGC4319; NM_2071	mRNA	turquoise	
12157899	Homo sapiens chromosome 10 open readin FLJ36756; NM_0248	mRNA	turquoise	
61282171-	Homo sapi nucleus [gc positive re transcripti HIF-1alpha	NM_0015	mRNA	turquoise
89219327-	Homo sapiens RNA binding motif protein, X-KAT3	NM_0196	mRNA	turquoise
26655419-	Homo sapi integral to plasma membrane [gc EVDB; D17	NM_0064	mRNA	turquoise
10920476	Homo sapiens insulin glucose m receptor activity [goic	NM_0037	mRNA	turquoise
88129409-	Homo sapi ER-Golgi in angiogene: metallope APN; gp15	NM_0011	mRNA	turquoise
CCGAATG	PREDICTED: Homo sapiens membrane bound O-acyltra	XM_00113	mRNA	turquoise
23963544	Homo sapi nucleus [gc B cell diffe transcripti HD4; HDA	NM_0060	mRNA	turquoise

42355401- Homo sapi nucleus [g]regulation zinc ion bir FLJ23765; NM_15265 mRNA	turquoise
:ACCTAGGC Homo sapi integral to G-protein (5-oxo-6E,8 GPR170; G NM_14896 mRNA	turquoise
12778030 Homo sapi nucleus [g]protein arr transferas MEKK2; M NM_00666 mRNA	turquoise
11343382 Homo sapiens hypothetical protein LOC552891 (LOC55 NM_00412 mRNA	turquoise
72657673- Homo sapiens RNA bi nuclear m f mRNA binc S164; MG NM_02123 mRNA	turquoise
18186212( Homo sapi Arp2/3 prc cell motilit structural ( ARC16; dJ1 NM_00571 mRNA	turquoise
31836086- Homo sapi chromosor nucleosom DNA binding [goid 36; NM_00101 mRNA	turquoise
33021836- Homo sapi endoplasr nucleotide hydrolase : MGC2733; NM_00106 mRNA	turquoise
12856899- Homo sapi ribosome [ protein bic structural ( PP9932 NM_00106 mRNA	turquoise
55431745- Homo sapiens ankyrin repeat domain 55 (A FLJ11795; NM_02466 mRNA	turquoise
:ATGGTGT PREDICTED: Homo sapiens similar to 60S ribosomal prc XM_94221 mRNA	turquoise
15342563- Homo sapi membrane developm e hydrolase : CD157 NM_00433 mRNA	turquoise
43502841- Homo sapi chromatin chromatin chromatin M31; HP1 NM_00686 mRNA	turquoise
:GTCCTGT( PREDICTED: Homo sapiens similar to general transcript XM_93575 mRNA	turquoise
60706623- PREDICTED: Homo sapiens similar to hypothetical prot e XM_92681 mRNA	turquoise
8577850-8 Homo sapi membrane immune re sugar bindi CLECSF9; N NM_01435 mRNA	turquoise
54527196- Homo sapiens chromosome 20 open readin; HSPC164; ! NM_01646 mRNA	turquoise
7309013-7 Homo sapiens proteir protein arr ATP binding [goid 552 NM_00276 mRNA	turquoise
15484653( Homo sapi plasma me induction c transferas CD282; TIL NM_00326 mRNA	turquoise
34940976- Homo sapi nucleus [g]cytoplasm ubi quitin p IKBA; NFKE NM_02052 mRNA	turquoise
36019743- Homo sapi integral to transport [ transporte TAT1; FLJ3 NM_05296 mRNA	turquoise
19677239; Homo sapi intracellul e ubi quitin c ligase activ DKFZp686I NM_02076 mRNA	turquoise
:CAAGTTTC PREDICTED: Homo sapiens hypothetical protein FLJ120 XR_00126; lncRNA	turquoise
14326989- Homo sapi cytoskelet r regulation actin bindi TB4Y; MG NM_00426 mRNA	turquoise
:CTTGTTCC Homo sapiens metallophosphoe: hydrolase activity [goi NM_02307 mRNA	turquoise
39045111- Homo sapiens leucine small GTP e binding [g RIPK7; RO NM_19857 mRNA	turquoise
32901537- Homo sapi TAP compl protein cor tapasin bir APT2; RIN NM_00054 mRNA	turquoise
85379025- Homo sapi coated pit protein cor clathrin bir LAP; CALM NM_00716 mRNA	turquoise
61941594- Homo sapi nucleus [g]chromatin ATP bindin FLJ20361; NM_01778 mRNA	turquoise
23784959- Homo sapi membrane homophilic calcium ior CDw325; C NM_00179 mRNA	turquoise
60232730- PREDICTED: Homo sapiens similar to pleckstrin homolo XM_93518 mRNA	turquoise
57945667- Homo sapiens proteir glycogen n protein ph PPP1R6; D NM_00624 mRNA	turquoise
75269880- Homo sapiens oxyster lipid transport [goid 6 ORP8; MG NM_00106 mRNA	turquoise
21870990; Homo sapi integral to neutrophil receptor a CD182; CN NM_00155 mRNA	turquoise
46828278- Homo sapiens ankyrir intracellular signaling FLJ21255; NM_02409 mRNA	turquoise
:CTGTGGTC Homo sapiens paraneoplastic an zinc ion bir MGC13275 NM_01336 mRNA	turquoise
21982328; Homo sapi microtubul microtubu GTP bindin TUBA1; H2 NM_00606 mRNA	turquoise
12377564; Homo sapiens deltex 3-like (Dros zinc ion bir BBAP NM_13828 mRNA	turquoise
52026216- Homo sapiens oxyster lipid transport [goid 6 FLJ14629; NM_02458 mRNA	turquoise
53042762- Homo sapi membrane G-protein ( receptor a GPCR4; EX NM_02037 mRNA	turquoise
:AACCATGT Homo sapiens SUMO1 pseudogene 1 (SUMO1P1) on cl NR_00218; mRNA	turquoise
2269595-2 Homo sapi cornified e skin develc GTPase act MGC12624 NM_00324 mRNA	turquoise
12050538; Homo sapi extracellul: regulation growth fac IGFBP9; N NM_00251 mRNA	turquoise
11188207( Homo sapi membrane [goid 160; calmodulir ADDL NM_01682 mRNA	turquoise
ATCACATT( Homo sapi centrosome [goid 581 protein bir MGC78416 NM_02518 mRNA	turquoise
74955506- Homo sapi extracellul: negative r e enzyme ac GROa; GR NM_00151 mRNA	turquoise
TATTACCT( Homo sapiens lines homolog 1 (Drosophila) FLJ10583; NM_00104 mRNA	turquoise
5426395-5 Homo sapiens similar to zinc finger protein 469 (LOC44 NM_00101 mRNA	turquoise

15454347- Homo sapi nucleus [gcrregulation DNA bindir MGC74712; NM_03322; mRNA	turquoise
3257423-3 PREDICTED: Homo sapiens hypothetical protein FLJ396 XM_37093; lncRNA	turquoise
26207885- Homo sapi nucleus [gcrchromatin chromatin HP1-GAM1; NM_01658; mRNA	turquoise
83500277- Homo sapi extracellular region [goid 5576] [ DKFZP434I; NM_03147; mRNA	turquoise
29648-296 PREDICTED: Homo sapiens similar to Proline-rich nucle; XM_93121; mRNA	turquoise
10515631; Homo sapi membrane fraction [goid 5624] [ p63; CLIM1; NM_00682; mRNA	turquoise
100100006; Homo sapiens dJ341D10.1 (novel protein) (dJ341D10.1; NM_00100	turquoise
10224110; Homo sapi cytoplasm ubiquitin c transferas; Fbl13; FLJ3; NM_14503; mRNA	turquoise
93779668- Homo sapi nucleus [gcrnegative r; ATP bindin TAF172; KI; NM_00397; mRNA	turquoise
37978594- Homo sapi nucleus [gcrregulation transcripti; TCFL4; MX; NM_17060; mRNA	turquoise
71639809- Homo sapi integral to positive re cell adhesi; SDFR1; GP; NM_01242; mRNA	turquoise
77044806- Homo sapi membran; electron tr oxidoreductase activi; NM_00186; mRNA	turquoise
16565165; Homo sapi nucleus [gcrregulation sequence-; OCT1; OTF; NM_00265; mRNA	turquoise
15477974- Homo sapiens BMX n; mesoderm transferas; PSCTK2; P; NM_00172; mRNA	turquoise
44078320- Homo sapi extracellul; peptidogly zinc ion bir MMP-9; GI; NM_00495; mRNA	turquoise
18179160; Homo sapi cytosol [gocellular de; electron c; p67phox; I; NM_00043; mRNA	turquoise
13313238- Homo sapiens testis-specific transcript, Y-lin; DKFZP434I; NR_00154; mRNA	turquoise
10187692; Homo sapiens mitoge protein kin transferas; KIAA0687; NM_14568; mRNA	turquoise
30236347- Homo sapi membran; leukotrien; enzyme ac FLAP NM_00162; mRNA	turquoise
32935355- Homo sapi cytosol [goimmune re threonine ; MGC70470; NM_14895; mRNA	turquoise
35908947- Homo sapi nucleus [gcrprotein kin transferas; SFRSK1 NM_00313; mRNA	turquoise
65179379- Homo sapi membran; chemotaxi; cytokine a; MGC39436; NM_14467; mRNA	turquoise
21905403; Homo sapiens MOCO sulphurase C-terminal; FLJ22390; NM_02274; mRNA	turquoise
18576492- Homo sapi integral to ubiquitin c ligase activ; KIAA0161; NM_18275; mRNA	turquoise
90572750- Homo sapiens ankyrin repeat domain 22 (A); MGC22805; NM_14455; mRNA	turquoise
11411493- Homo sapiens CUG tri neuromus; RNA bindir BRUNOL3; NM_00102; mRNA	turquoise
TCCAAGTG PREDICTED: Homo sapiens hypothetical protein LOC64; XM_93891; mRNA	turquoise
6749666-6 Homo sapi nucleus [goid 5634] [ r; magnesiun; MIG9 NM_00598; mRNA	turquoise
48463849- Homo sapi membran; defense response [go; PSG11 NM_00278; mRNA	turquoise
39484301- Homo sapi nucleus [gcrregulation of transcri; C21orf107; NM_03365; mRNA	turquoise
128882396; Homo sapiens ankyrir protein bic protein bir; BPOZ; PP2; NM_17202; mRNA	turquoise
92520593- Homo sapiens solute carrier family 36 (prot; FLJ38932; NM_15231; mRNA	turquoise
198642746; Homo sapi DNA-direct transcripti; DNA bindir; FLJ12859; NM_01248; mRNA	turquoise
39243212- Homo sapiens chromosome 1 open reading STRF2; FLJ; NM_02455; mRNA	turquoise
66859320- Homo sapi nucleus [gcrintracellul; transferas; C15orf1; P; NM_00630; mRNA	turquoise
ATGGCTCA PREDICTED: Homo sapiens hypothetical gene supporte; XM_93995; mRNA	turquoise
93094373- Homo sapiens small Cajal body-specific RNA Z32; mgU2; NR_00256; lncRNA	turquoise
ATGGGGGA Homo sapi mitochond neurotrans; pyridoxal r; NPD009; G; NM_02068; mRNA	turquoise
GTATTTTC; Homo sapi chromatin chromatin hydrolase ; KIAA1564; NM_02092; mRNA	turquoise
AAACATGA; PREDICTED: Homo sapiens KIAA0492 protein (KIAA049; XM_94429; mRNA	turquoise
81930715- Homo sapi nucleus [gcrimmune re calcium-de; ANX11; CA; NM_14586; mRNA	turquoise
17562982- Homo sapi nucleus [gcrchromatin protein-ar; PADI5; PDI; NM_01238; mRNA	turquoise
35677307- Homo sapi membran; homophilic; calcium ior; PP791; RP; NM_18268; mRNA	turquoise
GCCCAGGA; Homo sapi chromatin transcripti; transcripti; RBP1; RBP; NM_02300; mRNA	turquoise
16526589- Homo sapiens hypothetical protein FLJ2015; FLJ22179; NM_01900; mRNA	turquoise
CGCCCCCT; PREDICTED: Homo sapiens hypothetical protein FLJ141; XR_01796; mRNA	turquoise
36307365- Homo sapi intracellular [goid 562 sequence-specific DN; NM_03063; mRNA	turquoise
119017396; Homo sapi membran; small GTP; GTP bindin; RAB1C; H-; NM_00686; mRNA	turquoise

43947237- Homo sapiens zinc finger, SWIM- zinc ion bir C20orf162	NM_080606 mRNA	turquoise
5AGTACGT( Homo sapiens ankyrin signal transduction protein bir	MGC12030( NM_182706 mRNA	turquoise
23074466( Homo sapiens nucleus [growth regulation] zinc ion bir	FLJ22835; NM_080422 mRNA	turquoise
99926695- Homo sapiens coronin nitrogen catabolite-inducible	WDR2; CLI NM_003388 mRNA	turquoise
15489351( Homo sapiens integral to cell proliferation receptor a	CD129 NM_002188 mRNA	turquoise
5CACTGGCT( Homo sapiens nucleus [growth] positive regulatory DNA binding	MGC12627; NM_001088 mRNA	turquoise
74241769- Homo sapiens general transcription factor II WSCR7	NR_002200 mRNA	turquoise
5GACTCCA( Homo sapiens thioredoxin (TXN), mRNA.	NM_003322 mRNA	turquoise