

Supplementary table 1. Genes methylated in normal PBL identified by MCAM

Accessions	ProbeName	GeneName	Probe location	CGI status	Length of fragment (bp)	Signal intensity		Ratio
						PBL	Fully Methylated	
NM_003689	A_17_P00075036	AKR7A2	chr1:019383581-019383626	dense-CGI	984	10452.36	6731.86	1.6
NM_033504	A_17_P00124074	TMEM54	chr1:033036997-033037057	dense-CGI	680	141113.40	86066.53	1.6
NM_004983	A_76_P0126357	KCNJ9	chr1:156866801-156866741	dense-CGI	451	19734.75	13601.73	1.5
NM_181644	A_17_P00747943	DKFZp761N1114	chr1:202269905-202269950	dense-CGI	946	7772.31	4430.39	1.8
NM_152666	A_76_P0131246	FLJ40773	chr1:239013571-239013631	dense-CGI	636	7671.34	4372.15	1.8
NM_017629	A_76_P0107188	EIF2C4	chr1:35942233-35942293	dense-CGI	734	11668.28	7907.43	1.5
NM_017629	A_76_P0113819	EIF2C4	chr1:35942573-35942513	dense-CGI	734	10845.13	7022.15	1.5
NM_033067	A_76_P0130086	DMRTB1	chr1:53637013-53637073	dense-CGI	439	16330.39	8934.06	1.8
NM_033067	A_76_P0120255	DMRTB1	chr1:53637327-53637267	dense-CGI	439	45641.77	14552.37	3.1
NM_152607	A_76_P0110290	FLJ40201	chr1:54983818-54983878	dense-CGI	834	26899.86	13808.98	1.9
NM_148974	A_76_P0118935	TNFRSF25	chr1:6460664-6460724	dense-CGI	727	46329.66	18875.07	2.5
NM_005185	A_17_P07043884	CALML3	chr10:005557309-005557354	dense-CGI	711	171667.40	106915.90	1.6
NM_020397	A_17_P07078152	CAMK1D	chr10:012431606-012431651	dense-CGI	719	8392.39	5517.84	1.5
NM_213569	A_17_P07118013	NEBL	chr10:021503345-021503390	dense-CGI	741	15513.33	6391.28	2.4
NM_012071	A_17_P07122048	COMMD3	chr10:022645335-022645380	dense-CGI	573	8749.29	4479.65	2.0
NM_024747	A_76_P0102707	HPS6	chr10:103806097-103806157	dense-CGI	777	8379.04	5282.70	1.6
NM_005308	A_76_P0132627	GRK5	chr10:120956830-120956890	dense-CGI	297	6944.75	4290.36	1.6
NM_198148	A_17_P07543440	CPXM2	chr10:125641023-125641068	dense-CGI	184	128245.60	71545.90	1.8
NM_145235	A_76_P0131620	FANK1	chr10:127574692-127574632	dense-CGI	280	283895.10	83181.28	3.4
NM_145235	A_76_P0118561	FANK1	chr10:127574794-127574854	dense-CGI	427	91900.54	36496.09	2.5
NM_145235	A_76_P0123142	FANK1	chr10:127575020-127574960	dense-CGI	427	267142.90	58532.60	4.6
NM_145235	A_76_P0115092	FANK1	chr10:127575067-127575127	dense-CGI	427	135871.80	64661.97	2.1
NM_145235	A_76_P0116512	FANK1	chr10:127575221-127575161	dense-CGI	427	176919.90	86601.27	2.0
NM_173572	A_17_P07591273	C10orf93	chr10:134606970-134607015	dense-CGI	120	31377.05	18351.36	1.7
NM_052997	A_76_P0116122	ANKRD30A	chr10:37454821-37454881	dense-CGI	1051	20234	8378	2.4
NM_005729	A_76_P0116373	PPIF	chr10:80777447-80777507	dense-CGI	983	7543.16	4870.04	1.5
NM_145869	A_76_P0130924	ANXA11	chr10:81956298-81956238	dense-CGI	707	12048.60	7237.29	1.7
NM_000218	A_17_P07602914	KCNQ1	chr11:002422200-002422245	dense-CGI	711	17951.10	11666.59	1.5
NM_014633	A_76_P0162563	SH2BP1	chr11:10729245-10729185	dense-CGI	694	5561.67	3011.94	1.8
NM_198516	A_76_P0154731	GALNTL4	chr11:11600635-11600575	dense-CGI	982	15871.08	10588.60	1.5
NM_005238	A_17_P08111505	ETS1	chr11:127897129-127897189	dense-CGI	667	12000.29	7149.53	1.7
NM_174902	A_76_P0144849	LOC143458	chr11:35922518-35922578	dense-CGI	658	9185.20	4496.64	2.0
NM_013402	A_76_P0164043	FADS1	chr11:61341379-61341319	dense-CGI	717	10432.34	4573.26	2.3
NM_002032	A_76_P0138536	FTH1	chr11:61491866-61491926	dense-CGI	671	7320.06	4274.11	1.7

NM_022172	A_76_P0149358	PC	chr11:66381380-66381440	dense-CGI	434	35915.96	5004.84	7.2
NM_022172	A_76_P0168886	PC	chr11:66381599-66381539	dense-CGI	434	25164.77	4815.47	5.2
NM_002180	A_76_P0146770	IGHMBP2	chr11:68428192-68428132	dense-CGI	802	12387.38	6573.04	1.9
NM_002180	A_76_P0160801	IGHMBP2	chr11:68428409-68428469	dense-CGI	802	15136.66	7168.29	2.1
NM_024829	A_17_P08205809	FLJ22662	chr12:014612434-014612494	dense-CGI	682	29996.85	15533.65	1.9
NM_138566	A_17_P08373619	GLS2	chr12:055168998-055169058	dense-CGI	637	8759.92	4699.11	1.9
NM_152638	A_17_P08528851	C12orf12	chr12:089850806-089850851	dense-CGI	90	164703.30	46705.02	3.5
NM_152638	A_17_P08528854	C12orf12	chr12:089851148-089851193	dense-CGI	438	284317.70	98058.32	2.9
NM_007076	A_76_P0169197	HYPE	chr12:107411112-107411052	dense-CGI	982	12536.01	7456.58	1.7
NM_152759	A_76_P0143099	MGC35140	chr12:121192977-121192917	dense-CGI	833	21048.40	11975.14	1.8
NM_003428	A_17_P08703726	ZNF84	chr12:132224222-132224267	dense-CGI	384	14209.13	9220.24	1.5
NM_024829	A_76_P0164214	FLJ22662	chr12:14612441-14612501	dense-CGI	682	15417.93	8341.30	1.8
NM_173602	A_76_P0160084	KIAA1463	chr12:49184652-49184712	dense-CGI	999	5293.43	3254.92	1.6
NM_199187	A_76_P0159746	KRT18	chr12:51628458-51628518	dense-CGI	627	8750.81	4159.78	2.1
NM_199187	A_76_P0144369	KRT18	chr12:51628908-51628848	dense-CGI	627	17339.74	8607.13	2.0
NM_018416	A_76_P0152381	FOXJ2	chr12:8075850-8075910	dense-CGI	591	10482.55	4158.62	2.5
NM_020698	A_76_P0170130	TMCC3	chr12:93547055-93546995	dense-CGI	485	5886.93	3333.98	1.8
NM_017826	A_17_P08780520	FLJ20449	chr13:035686476-035686521	dense-CGI	336	283227.80	90167.87	3.1
NM_017826	A_17_P08780521	FLJ20449	chr13:035686608-035686653	dense-CGI	336	277659.30	82892.27	3.3
NM_178861	A_17_P09068707	RNF113B	chr13:097627412-097627457	dense-CGI	359	145160.30	65910.60	2.2
NM_006322	A_76_P0154297	TUBGCP3	chr13:112290572-112290632	dense-CGI	753	4523.53	3009.62	1.5
NM_006322	A_76_P0153182	TUBGCP3	chr13:112290857-112290797	dense-CGI	753	8530.61	4714.42	1.8
NM_024719	A_76_P0163577	GRTP1	chr13:113057389-113057449	dense-CGI	665	40063.51	12487.33	3.2
NM_024719	A_17_P09148213	GRTP1	chr13:113057472-113057532	dense-CGI	665	54645.92	23622.91	2.3
NM_014572	A_76_P0154377	LATS2	chr13:20533769-20533709	dense-CGI	722	11096.36	4955.01	2.2
NM_014572	A_76_P0145455	LATS2	chr13:20534132-20534072	dense-CGI	722	11936.88	6808.95	1.8
NM_016529	A_76_P0157430	ATP8A2	chr13:24940271-24940331	dense-CGI	913	6899.85	3738.15	1.8
NM_017826	A_76_P0138137	FLJ20449	chr13:35686679-35686619	dense-CGI	336	58345.09	32229.54	1.8
NM_025138	A_76_P0144796	C13orf23	chr13:38510129-38510069	dense-CGI	986	19796.09	12180.02	1.6
NM_005845	A_76_P0170084	ABCC4	chr13:94751668-94751728	dense-CGI	371	15180.28	9330.34	1.6
NM_001001715	A_76_P0168210	FARP1	chr13:97627283-97627343	dense-CGI	359	16577.63	10906.35	1.5
NM_001001715	A_76_P0149889	FARP1	chr13:97628419-97628359	dense-CGI	892	39856.88	25827.75	1.5
NM_173159	A_17_P09210464	NPAS3	chr14:032478224-032478275	dense-CGI	245	8792.33	5243.47	1.7
NM_020784	A_17_P09293985	KIAA1344	chr14:052089850-052089895	dense-CGI	675	34725.22	21322.95	1.6
NM_000428	A_17_P09392084	LTBP2	chr14:074148680-074148730	dense-CGI	839	22635.34	12826.74	1.8
NM_006427	A_17_P09532639	SIVA	chr14:104289525-104289570	dense-CGI	362	156208.60	89925.30	1.7
NM_031314	A_76_P0167758	HNRPC	chr14:20807977-20808037	dense-CGI	609	5490.82	3412.85	1.6

NM_002863	A_76_P0144675	PYGL	chr14:50481653-50481593	dense-CGI	932	5277.45	3457.33	1.5
NM_015072	A_76_P0163122	KIAA0998	chr14:75197686-75197626	dense-CGI	870	6098.01	4074.38	1.5
NM_002802	A_76_P0170301	PSMC1	chr14:89792941-89793001	dense-CGI	882	6991.67	4302.91	1.6
NM_006668	A_76_P0137930	CYP46A1	chr14:99220556-99220616	dense-CGI	93	9056.10	5520.57	1.6
NM_007223	A_17_P09604630	GPR	chr15:038000011-038000056	dense-CGI	934	39395.21	25853.55	1.5
NM_182616	A_17_P09822650	MGC61550	chr15:088257492-088257537	dense-CGI	526	134740.70	88569.70	1.5
NM_182616	A_17_P09822652	MGC61550	chr15:088257864-088257920	dense-CGI	526	124906.00	71356.31	1.8
NM_078474	A_76_P0150957	BLP2	chr15:100010193-100010133	dense-CGI	596	4573.47	3049.99	1.5
NM_002487	A_76_P0142717	NDN	chr15:21484094-21484034	dense-CGI	934	6627.05	3565.39	1.9
NM_006293	A_76_P0161092	TYRO3	chr15:39638141-39638201	dense-CGI	487	19852.36	12090.38	1.6
NM_002833	A_76_P0143303	PTPN9	chr15:73659002-73659062	dense-CGI	767	9110.90	5565.12	1.6
NM_002833	A_76_P0160927	PTPN9	chr15:73659335-73659275	dense-CGI	767	6736.34	4550.54	1.5
NM_001004309	A_76_P0165399	MGC75360	chr15:88696820-88696760	dense-CGI	526	18024.57	12345.19	1.5
NM_139057	A_76_P0155590	ADAMTS17	chr15:98699636-98699576	dense-CGI	78	79891.58	47063.05	1.7
NM_003345	A_17_P09885627	UBE2I	chr16:001303985-001304030	dense-CGI	869	148652.70	94503.36	1.6
NM_003345	A_17_P09885628	UBE2I	chr16:001304204-001304249	dense-CGI	869	138268.10	83407.23	1.7
NM_003345	A_17_P09885629	UBE2I	chr16:001304310-001304355	dense-CGI	869	87067.06	50797.81	1.7
NM_032520	A_17_P09885838	GNPTG	chr16:001342115-001342160	dense-CGI	559	31982.06	21491.17	1.5
hsa-mir-193b	A_17_P09939196	hsa-mir-193b	chr16:014304583-014304643	dense-CGI	693	4846.17	3078.26	1.6
NM_001004299	A_17_P09990793	FLJ43980	chr16:045160079-045160124	dense-CGI	855	117657.00	61386.09	1.9
NM_001004299	A_17_P09990795	FLJ43980	chr16:045160429-045160476	dense-CGI	855	78269.37	35733.92	2.2
NM_001004299	A_17_P09990796	FLJ43980	chr16:045160586-045160631	dense-CGI	855	65408.23	29706.27	2.2
NM_001004299	A_17_P09990798	FLJ43980	chr16:045160768-045160813	dense-CGI	855	56969.09	36171.80	1.6
NM_001004299	A_17_P09990799	FLJ43980	chr16:045160893-045160938	dense-CGI	292	91285.31	55555.88	1.6
NM_001039	A_76_P0154863	SCNN1G	chr16:23101213-23101153	dense-CGI	861	12625.44	6530.98	1.9
NM_001039	A_76_P0163901	SCNN1G	chr16:23101331-23101391	dense-CGI	861	10547.67	7178.88	1.5
NM_032815	A_76_P0169233	NFATC2IP	chr16:28864924-28864984	dense-CGI	885	19356.78	5012.99	3.9
NM_020677	A_76_P0140049	HSCARG	chr16:4464619-4464679	dense-CGI	582	22832.07	7172.51	3.2
NM_001004299	A_76_P0162090	FLJ43980	chr16:45160296-45160356	dense-CGI	855	31725.04	12050.92	2.6
NM_001004299	A_76_P0160654	FLJ43980	chr16:45160632-45160572	dense-CGI	855	44045.32	17157.56	2.6
NM_025187	A_76_P0156872	Lin10	chr16:65700790-65700850	dense-CGI	853	18458.00	8123.44	2.3
NM_025187	A_76_P0161518	Lin10	chr16:65701177-65701117	dense-CGI	853	20158.65	5584.08	3.6
NM_025187	A_76_P0143627	Lin10	chr16:65701497-65701557	dense-CGI	853	13065.60	5051.56	2.6
NM_018296mgs	A_76_P0155496	FLJ11004	chr16:65918326-65918266	dense-CGI	654	19857.70	6749.91	2.9
NM_001740	A_76_P0155551	CALB2	chr16:69949901-69949841	dense-CGI	931	21864.00	10476.20	2.1
NM_145254	A_76_P0168189	LOC124491	chr16:74056023-74056083	dense-CGI	930	9795.08	5230.68	1.9
NM_203411	A_17_P10215307	LOC92162	chr17:007698829-007698878	dense-CGI	503	4564.87	3031.63	1.5

NM_203411	A_17_P10215309	LOC92162	chr17:007699255-007699300	dense-CGI	170	69376.05	44760.83	1.5
NM_152599	A_17_P10219538	FLJ35773	chr17:008642920-008642965	dense-CGI	440	118053.80	68690.36	1.7
NM_152599	A_17_P10219539	FLJ35773	chr17:008643040-008643085	dense-CGI	440	174559.20	107492.40	1.6
NM_031934	A_17_P10273427	RAB34	chr17:024068209-024068254	dense-CGI	111	24423.39	14961.56	1.6
NM_031272	A_17_P10395050	TEX14	chr17:054124078-054124138	dense-CGI	427	69670.05	40302.67	1.7
NM_031272	A_17_P10395052	TEX14	chr17:054124266-054124322	dense-CGI	427	88234.02	41275.73	2.1
NM_001017918	A_17_P10411795	CYB561	chr17:058868637-058868682	dense-CGI	473	55758.38	29936.28	1.9
NM_014595	A_17_P10465226	NT5C	chr17:070640212-070640272	dense-CGI	668	85037.62	49991.68	1.7
NM_006937	A_17_P10465390	SUMO2	chr17:070691484-070691544	dense-CGI	462	160301.30	77418.22	2.1
NM_032134	A_17_P10470266	DKFZP434P0316	chr17:071815801-071815846	dense-CGI	721	58431.81	34914.18	1.7
NM_032134	A_17_P10470267	DKFZP434P0316	chr17:071816087-071816133	dense-CGI	721	113629.80	59418.27	1.9
NM_032134	A_17_P10470269	DKFZP434P0316	chr17:071816298-071816358	dense-CGI	721	80574.10	48196.26	1.7
NM_004127	A_17_P10494939	GPS1	chr17:077603092-077603137	dense-CGI	472	35816.61	20234.92	1.8
NM_006224	A_76_P0144375	PITPNA	chr17:1420467-1420527	dense-CGI	599	45144.23	22922.97	2.0
NM_004140	A_76_P0160626	LLGL1	chr17:18069999-18070059	dense-CGI	670	21629.49	11914.57	1.8
NM_003563	A_76_P0154219	SPOP	chr17:45110678-45110738	dense-CGI	723	6184.16	3039.09	2.0
NM_005450	A_76_P0147203	NOG	chr17:52026365-52026305	dense-CGI	94	11100.78	6654.10	1.7
NM_022036	A_76_P0167498	GPRC5C	chr17:69940620-69940680	dense-CGI	793	10779.34	5231.81	2.1
NM_032134	A_76_P0148110	DKFZP434P0316	chr17:71815816-71815876	dense-CGI	721	51022.84	29580.52	1.7
NM_032134	A_76_P0139591	DKFZP434P0316	chr17:71816122-71816062	dense-CGI	721	55902.70	27887.05	2.0
NM_022158	A_76_P0171811	FN3K	chr17:78285648-78285708	dense-CGI	852	29391.33	18994.02	1.5
NM_152599	A_76_P0170038	FLJ35773	chr17:8643173-8643113	dense-CGI	440	62874.66	33475.15	1.9
NM_152599	A_76_P0166389	FLJ35773	chr17:8643660-8643600	dense-CGI	711	26344.05	17079.33	1.5
NM_004853	A_76_P0139484	STX8	chr17:9419648-9419708	dense-CGI	178	12980.93	6728.30	1.9
NM_017876	A_17_P10851094	RNF126	chr19:000599167-000599212	dense-CGI	639	78944.21	30613.27	2.6
NM_001252	A_17_P10870657	TNFSF7	chr19:006542339-006542386	dense-CGI	726	8069.82	4717.47	1.7
NM_015318	A_17_P10872745	ARHGEF18	chr19:007411085-007411130	dense-CGI	272	219582.90	141765.80	1.5
NM_015318	A_17_P10872749	ARHGEF18	chr19:007411500-007411550	dense-CGI	144	219061.70	84061.47	2.6
NM_198537	A_17_P10909602	FLJ44968	chr19:019500851-019500896	dense-CGI	282	289507.60	174848.20	1.7
NM_016573	A_17_P10910019	GMIP	chr19:019601582-019601642	dense-CGI	970	17653.51	12047.80	1.5
NM_016573	A_17_P10910020	GMIP	chr19:019601708-019601759	dense-CGI	970	15811.43	10510.27	1.5
NM_001864	A_17_P10950298	COX7A1	chr19:041334883-041334928	dense-CGI	46	7069.72	4746.05	1.5
NM_170720	A_17_P10983726	KCNJ14	chr19:053656945-053656990	dense-CGI	635	60768.03	36804.84	1.7
NM_170720	A_17_P10983727	KCNJ14	chr19:053657056-053657101	dense-CGI	635	317601.80	216778.70	1.5
NM_014037	A_17_P10986125	SLC6A16	chr19:054519934-054519979	dense-CGI	247	170378.30	115564.40	1.5
hsa-mir-373	A_17_P10998282	hsa-mir-373	chr19:058983592-058983652	dense-CGI	452	113013.90	74697.61	1.5
hsa-mir-373	A_17_P10998283	hsa-mir-373	chr19:058983759-058983806	dense-CGI	452	102716.20	65290.08	1.6

NM_020428	A_76_P0170540	CTL2	chr19:10597571-10597511	dense-CGI	808	101965.40	49272.56	2.1
NM_001004314	A_76_P0139504	FLJ46419	chr19:12063881-12063941	dense-CGI	236	7171.94	3086.83	2.3
NM_052876	A_76_P0165001	BTBD14B	chr19:13090327-13090387	dense-CGI	197	17911.47	9932.79	1.8
NM_001319	A_76_P0157660	CSNK1G2	chr19:1920345-1920405	dense-CGI	866	66025.28	35496.80	1.9
NM_001319	A_76_P0155656	CSNK1G2	chr19:1920682-1920622	dense-CGI	866	81507.98	53435.89	1.5
NM_001319	A_76_P0166824	CSNK1G2	chr19:1920902-1920962	dense-CGI	866	44639.90	25054.68	1.8
NM_033103	A_76_P0147311	RHPN2	chr19:38248272-38248332	dense-CGI	623	18189.22	4784.20	3.8
NM_153233	A_76_P0144613	FLJ36445	chr19:41191713-41191653	dense-CGI	577	13644.44	6560.95	2.1
NM_032878	A_76_P0144186	MGC15677	chr19:41191916-41191976	dense-CGI	577	8037.21	4300.80	1.9
NM_133466	A_76_P0143168	ZNF545	chr19:41601480-41601540	dense-CGI	897	5014.50	3140.47	1.6
NM_002446	A_76_P0145378	MAP3K10	chr19:45389541-45389481	dense-CGI	940	8053.79	5515.70	1.5
NM_004359	A_76_P0149112	CDC34	chr19:481952-482012	dense-CGI	594	5157.16	3378.79	1.5
NM_006509	A_76_P0168981	RELB	chr19:50196731-50196791	dense-CGI	974	23630.10	16244.86	1.5
NM_012155	A_76_P0151874	EML2	chr19:50834612-50834672	dense-CGI	504	10365.56	4410.51	2.4
NM_012155	A_76_P0157099	EML2	chr19:50835314-50835254	dense-CGI	486	44445.14	19320.79	2.3
NM_002516	A_76_P0152224	NOVA2	chr19:51168979-51168919	dense-CGI	863	18516.01	11219.83	1.7
NM_005184	A_76_P0139577	CALM3	chr19:51796420-51796480	dense-CGI	365	8670.05	5187.56	1.7
NM_012423	A_76_P0162252	RPL13A	chr19:54681531-54681471	dense-CGI	626	36738.30	22319.74	1.6
NM_153375	A_76_P0170572	PLAC2	chr19:5518674-5518734	dense-CGI	388	8046.01	5207.14	1.5
NM_020637	A_76_P0166636	FGF22	chr19:590890-590950	dense-CGI	941	8398.25	5443.99	1.5
NM_020637	A_76_P0138985	FGF22	chr19:591123-591063	dense-CGI	941	8557.38	5339.61	1.6
NM_033113	A_76_P0170136	ZEC	chr19:60685097-60685157	dense-CGI	221	14028.89	7643.43	1.8
NM_002579	A_76_P0148961	PALM	chr19:659213-659273	dense-CGI	539	13787.26	7442.32	1.9
NM_207329	A_17_P01092989	MYADML	chr2:033864726-033864772	dense-CGI	738	125364.60	55217.42	2.3
NM_016441	A_17_P01103651	CRIM1	chr2:036495187-036495232	dense-CGI	58	79174.84	48514.01	1.6
NM_004305	A_17_P01467693	BIN1	chr2:127580687-127580732	dense-CGI	568	21605.75	14399.37	1.5
NM_004807	A_76_P0124402	HS6ST1	chr2:128793064-128793124	dense-CGI	911	11827.34	5584.41	2.1
NM_001024655	A_17_P01480852	LOC554226	chr2:132753535-132753580	dense-CGI	577	246469.00	73784.21	3.3
NM_194317	A_17_P01566389	MGC52057	chr2:150012383-150012428	dense-CGI	288	17920.62	10343.38	1.7
NM_019091	A_76_P0105951	PLEKHA3	chr2:179171172-179171112	dense-CGI	982	10766.51	5932.63	1.8
NM_080671	A_17_P01920363	KCNE4	chr2:223742900-223742960	dense-CGI	732	110220.70	44697.46	2.5
NM_080671	A_17_P01920365	KCNE4	chr2:223743151-223743206	dense-CGI	732	134539.80	41098.08	3.3
NM_004504	A_17_P01941996	HRB	chr2:228162755-228162800	dense-CGI	377	25307.44	14098.72	1.8
NM_014808	A_17_P02006784	FARP2	chr2:242014726-242014771	dense-CGI	369	116882.70	66021.25	1.8
NM_032515	A_17_P02007749	BOK	chr2:242218047-242218092	dense-CGI	486	253472.60	144025.70	1.8
NM_003353	A_76_P0101172	UCN	chr2:27442433-27442373	dense-CGI	487	27445.32	10777.89	2.5
NM_003353	A_76_P0134871	UCN	chr2:27442629-27442689	dense-CGI	487	61029.41	29666.90	2.1

NM_207329	A_76_P0117676	MYADML	chr2:33864812-33864872	dense-CGI	738	124430.60	52355.91	2.4
NM_032107	A_17_P11180349	L3MBTL	chr20:041576626-041576671	dense-CGI	968	35078.53	23621.73	1.5
NM_014835	A_17_P11259590	OSBPL2	chr20:060246794-060246839	dense-CGI	445	24199.12	15729.03	1.5
NM_024299	A_17_P11266131	C20orf149	chr20:061623072-061623117	dense-CGI	879	13937.65	8657.18	1.6
NM_003116	A_76_P0144268	SPAG4	chr20:33667310-33667370	dense-CGI	687	19361.02	10044.21	1.9
NM_032107	A_76_P0160826	L3MBTL	chr20:41576078-41576018	dense-CGI	968	17063.93	9941.64	1.7
NM_032107	A_76_P0168505	L3MBTL	chr20:41576277-41576337	dense-CGI	968	67293.29	46203.88	1.5
NM_032107	A_76_P0162004	L3MBTL	chr20:41576836-41576896	dense-CGI	968	28928.74	19343.53	1.5
NM_002466	A_76_P0164621	MYBL2	chr20:41728886-41728946	dense-CGI	799	12350.58	8315.03	1.5
NM_080606	A_76_P0149679	BHLHB4	chr20:61108843-61108783	dense-CGI	621	8884.56	4815.42	1.8
NM_003224	A_76_P0153222	ARFRP1	chr20:61809555-61809615	dense-CGI	901	24709.55	17010.33	1.5
NM_003224	A_76_P0158612	ARFRP1	chr20:61809620-61809560	dense-CGI	901	19692.90	10832.36	1.8
NM_003681	A_17_P11409035	PDXK	chr21:043962474-043962521	dense-CGI	504	16995.76	10793.71	1.6
NM_001112	A_17_P11414955	ADARB1	chr21:045317417-045317465	dense-CGI	510	156663.20	83717.86	1.9
NM_000100	A_76_P0145062	CSTB	chr21:44021096-44021156	dense-CGI	531	10505.55	4169.24	2.5
NM_000100	A_76_P0149818	CSTB	chr21:44021265-44021205	dense-CGI	531	13696.31	4020.68	3.4
NM_032608	A_17_P11450454	MYO18B	chr22:024462570-024462625	dense-CGI	216	182621.30	66418.46	2.7
NM_182527	A_17_P11467043	CABP7	chr22:028440994-028441039	dense-CGI	349	14159.58	8839.28	1.6
NM_002969	A_17_P11549914	MAPK12	chr22:049003080-049003125	dense-CGI	179	75902.12	45816.61	1.7
NM_014339	A_76_P0162426	IL17R	chr22:15940323-15940263	dense-CGI	560	43478.87	24247.25	1.8
NM_001008496	A_76_P0161352	PIWIL3	chr22:23484197-23484257	dense-CGI	673	38955.32	19973.76	2.0
NM_032608	A_76_P0168908	MYO18B	chr22:24462550-24462610	dense-CGI	216	21314.91	11711.27	1.8
NM_021126	A_76_P0151466	MPST	chr22:35744888-35744828	dense-CGI	339	34787.30	12598.30	2.8
NM_033386	A_76_P0146348	MICAL	chr22:36627211-36627151	dense-CGI	531	7552.16	4397.64	1.7
NM_194326	A_76_P0151744	MGC52010	chr22:38253527-38253587	dense-CGI	953	10386.22	7121.54	1.5
NM_001008572	A_76_P0139032	TTL1	chr22:41809720-41809660	dense-CGI	815	15237.20	6669.58	2.3
NM_014838	A_76_P0153973	ZBED4	chr22:48567632-48567572	dense-CGI	730	18577.66	5749.82	3.2
NM_018995	A_76_P0151791	MOV10L1	chr22:48831274-48831214	dense-CGI	412	48244.02	27075.39	1.8
NM_138993	A_76_P0154319	MAPK11	chr22:49011425-49011365	dense-CGI	100	11004.14	7389.25	1.5
NM_138433	A_76_P0140056	MGC16635	chr22:49275930-49275870	dense-CGI	282	9461.76	6102.04	1.6
NM_173472	A_17_P02054408	MGC40179	chr3:010124647-010124692	dense-CGI	653	118971.30	29317.79	4.1
NM_182702	A_17_P02215976	TESSP2	chr3:046850368-046850413	dense-CGI	226	78197.55	38925.04	2.0
NM_000316	A_17_P02216261	PTHR1	chr3:046899111-046899162	dense-CGI	825	41447.04	19369.11	2.1
NM_001009996	A_17_P02224984	DALRD3	chr3:049031854-049031912	dense-CGI	201	64482.08	41751.06	1.5
NM_018446	A_17_P02241308	GLT8D1	chr3:052715643-052715694	dense-CGI	772	7271.37	3356.29	2.2
NM_173472	A_76_P0100081	MGC40179	chr3:10124767-10124707	dense-CGI	653	14249.09	7208.04	2.0
NM_000373	A_76_P0101178	UMPS	chr3:125932275-125932335	dense-CGI	937	9079.30	4617.38	2.0

NM_004766	A_76_P0134539	COPB2	chr3:140590982-140591042	dense-CGI	852	7984.72	5450.64	1.5
NM_002628	A_17_P02668733	PFN2	chr3:151171504-151171549	dense-CGI	668	53204.64	14594.30	3.6
NM_012287	A_76_P0132004	CENTB2	chr3:196644737-196644677	dense-CGI	861	13300.60	6910.03	1.9
NM_012157	A_76_P0105655	FBXL2	chr3:33293827-33293767	dense-CGI	939	4826.91	3327.33	1.5
NM_032432	A_17_P02916222	ABLIM2	chr4:008124914-008124959	dense-CGI	340	219284.90	123658.90	1.8
hsa-mir-95	A_17_P02916223	hsa-mir-95	chr4:008125245-008125297	dense-CGI	464	51721.95	31080.77	1.7
hsa-mir-95	A_17_P02916225	hsa-mir-95	chr4:008125505-008125554	dense-CGI	464	123515.40	64661.40	1.9
NM_031279	A_76_P0117546	AGXT2L1	chr4:110041990-110041930	dense-CGI	867	12026.09	5765.77	2.1
NM_004249	A_76_P0128725	RAB28	chr4:13162523-13162583	dense-CGI	508	8540.91	5763.48	1.5
NM_024605	A_76_P0112585	ARHGAP10	chr4:149010266-149010206	dense-CGI	767	7196.41	4514.38	1.6
NM_144979	A_17_P03544796	MGC27016	chr4:156060209-156060254	dense-CGI	452	225043.00	150692.60	1.5
NM_019039	A_17_P03940109	DDX4	chr5:055068598-055068647	dense-CGI	601	134421.40	88274.76	1.5
NM_153610	A_17_P04042255	CMYA5	chr5:079021681-079021731	dense-CGI	491	163017.10	89916.28	1.8
NM_032028	A_17_P04200892	TSSK1	chr5:112798153-112798198	dense-CGI	138	40687.14	21054.41	1.9
NM_177478	A_17_P04238269	FTMT	chr5:121215812-121215860	dense-CGI	141	174155.30	55990.19	3.1
NM_032151	A_76_P0119507	PCBD2	chr5:134268972-134269032	dense-CGI	928	50803.39	27082.04	1.9
NM_004598	A_76_P0129978	SPOCK	chr5:136861855-136861795	dense-CGI	627	53412.11	18124.98	2.9
NM_018834	A_17_P04318150	MATR3	chr5:138656230-138656276	dense-CGI	328	106370.40	57978.40	1.8
NM_004499	A_76_P0134209	HNRPAB	chr5:177563648-177563708	dense-CGI	373	25273.59	7063.58	3.6
NM_017614	A_76_P0123831	BHMT2	chr5:78401341-78401401	dense-CGI	51	6051.11	4045.47	1.5
NM_001012426	A_17_P04688299	FOXP4	chr6:041621678-041621723	dense-CGI	638	5468.15	3709.09	1.5
NM_002395	A_17_P04859572	ME1	chr6:084198057-084198104	dense-CGI	256	335191.20	191092.30	1.8
NM_001431	A_76_P0104868	EPB41L2	chr6:131426107-131426047	dense-CGI	535	4626.74	3135.91	1.5
NM_130900	A_17_P05165916	RAET1L	chr6:150439001-150439046	dense-CGI	433	57741.53	34954.27	1.7
NM_024630	A_76_P0125040	ZDHHC14	chr6:157773258-157773198	dense-CGI	407	14646.22	9777.20	1.5
NM_005453	A_76_P0123302	ZNF297	chr6:33390476-33390416	dense-CGI	741	17551.46	8253.17	2.1
NM_003958	A_76_P0120490	RNF8	chr6:37429678-37429738	dense-CGI	920	10510.45	6279.18	1.7
NM_018665	A_76_P0124694	DDX43-DPPA5	chr6:74159895-74159835	dense-CGI	909	7936	1745	4.5
NM_016587	A_17_P05373127	CBX3	chr7:026014693-026014738	dense-CGI	785	21393.23	12463.07	1.7
NM_006833	A_17_P05646023	COPS6	chr7:099331429-099331474	dense-CGI	69	47818.11	21153.31	2.3
NM_018412	A_17_P05719978	ST7	chr7:116186936-116186983	dense-CGI	500	19462.97	6245.37	3.1
NM_022742	A_17_P05774712	NAG6	chr7:128025167-128025212	dense-CGI	302	27249.62	18516.11	1.5
NM_005631	A_76_P0102533	SMO	chr7:128422693-128422753	dense-CGI	463	9811.80	5949.10	1.6
NM_177525	A_17_P05781778	MEST	chr7:129724727-129724772	dense-CGI	68	20813.86	5020.17	4.1
NM_005397	A_17_P05785928	PODXL	chr7:130698918-130698963	dense-CGI	571	32811.34	18292.87	1.8
NM_022087	A_76_P0123321	GALNT11	chr7:151160271-151160211	dense-CGI	353	13524.00	6945.67	1.9
NM_014766	A_76_P0118905	SCRN1	chr7:29803068-29803128	dense-CGI	641	10982.69	3795.32	2.9

NM_002314	A_76_P0136886	LIMK1	chr7:72942385-72942445	dense-CGI	624	15955.71	10957.67	1.5
NM_177455	A_76_P0118943	MIST1	chr7:97486413-97486353	dense-CGI	41	6311.07	4220.98	1.5
NM_177455	A_76_P0105863	MIST1	chr7:97486498-97486558	dense-CGI	923	35606.72	20671.77	1.7
NM_015395	A_76_P0112748	DKFZP434B0335	chr7:97526455-97526395	dense-CGI	626	6880.96	3532.51	1.9
NM_018842	A_76_P0125537	BAIAP2L1	chr7:97675452-97675392	dense-CGI	654	8913.91	6043.93	1.5
NM_015359	A_17_P06005545	SLC39A14	chr8:022279743-022279788	dense-CGI	986	72557.73	36419.05	2.0
NM_145003	A_76_P0131682	FLJ31164	chr8:143482539-143482479	dense-CGI	929	11515.42	6242.50	1.8
NM_017527	A_76_P0118015	LY6K	chr8:143778743-143778683	dense-CGI	671	16004.79	8102.56	2.0
NM_024736	A_76_P0110685	GSDMDC1	chr8:144709959-144710019	dense-CGI	881	23620.37	10600.59	2.2
NM_032862	A_17_P06533475	TIGD5	chr8:144751686-144751731	dense-CGI	647	11236.14	7633.10	1.5
NM_017570	A_17_P06535205	OPLAH	chr8:145186857-145186902	dense-CGI	340	279457.90	123717.30	2.3
NM_006765	A_76_P0117875	TUSC3	chr8:15441886-15441826	dense-CGI	849	13579.53	7196.82	1.9
NM_032410	A_76_P0126396	HOOK3	chr8:42871383-42871443	dense-CGI	997	6054.45	4118.11	1.5
NM_144651	A_76_P0132286	FLJ25471	chr8:52484570-52484510	dense-CGI	699	37431.05	6274.63	6.0
NM_144651	A_76_P0100174	FLJ25471	chr8:52484741-52484801	dense-CGI	699	104831.30	69985.01	1.5
NM_018444	A_76_P0124120	PPM2C	chr8:94998448-94998508	dense-CGI	714	29980.73	14822.11	2.0
NM_173549	A_76_P0113505	FLJ39553	chr8:99145683-99145623	dense-CGI	861	34124.72	18492.63	1.8
NM_007179	A_17_P06561914	INSL6	chr9:005175453-005175501	dense-CGI	835	139989.30	29961.59	4.7
NM_007179	A_17_P06561917	INSL6	chr9:005175801-005175846	dense-CGI	835	144513.10	42898.87	3.4
NM_007179	A_17_P06561918	INSL6	chr9:005175919-005175973	dense-CGI	835	128884.80	28854.52	4.5
NM_022160	A_17_P06642800	DMRTA1	chr9:022437022-022437067	dense-CGI	464	8883.00	5783.85	1.5
NM_000907	A_17_P06700226	NPR2	chr9:035782065-035782116	dense-CGI	673	198169.40	117760.80	1.7
NM_000907	A_17_P06700229	NPR2	chr9:035782389-035782434	dense-CGI	673	89462.57	52620.41	1.7
NM_002048	A_17_P06796583	GAS1	chr9:086791323-086791375	dense-CGI	548	28423.79	13645.15	2.1
NM_018376	A_76_P0123843	NIPSNAP3B	chr9:104605245-104605305	dense-CGI	872	13933.29	5587.97	2.5
NM_005156	A_17_P06902904	ROD1	chr9:112175026-112175071	dense-CGI	889	15151.89	9983.28	1.5
NM_006752	A_17_P06993719	SURF5	chr9:133244173-133244218	dense-CGI	732	42040.42	25867.00	1.6
NM_017588	A_17_P06997477	WDR5	chr9:134030323-134030368	dense-CGI	82	35760.66	23100.28	1.5
NM_007179	A_76_P0103962	INSL6	chr9:5175577-5175517	dense-CGI	835	64872.32	13241.98	4.9
NM_007179	A_76_P0136785	INSL6	chr9:5175796-5175856	dense-CGI	835	49591.57	13802.31	3.6
NM_007179	A_76_P0108195	INSL6	chr9:5176120-5176060	dense-CGI	835	39722.64	13437.58	3.0
NM_004148	A_76_P0114598	NINJ1	chr9:92975987-92975927	dense-CGI	281	16797.00	11556.13	1.5
NM_032823	A_76_P0119925	C9orf3	chr9:94568062-94568002	dense-CGI	790	4480.14	3013.19	1.5
NM_005333	A_17_P11586728	HCCS	chrX:010889335-010889382	dense-CGI	250	181950.00	103747.60	1.8
NM_153346	A_17_P11620001	CXorf20	chrX:017998232-017998277	dense-CGI	769	194997.10	56117.67	3.5
NM_153346	A_17_P11620002	CXorf20	chrX:017998415-017998460	dense-CGI	769	114288.40	35135.93	3.3
NM_153346	A_17_P11620004	CXorf20	chrX:017998609-017998656	dense-CGI	769	95611.25	31851.72	3.0



NM_153270	A_17_P11634620	RP11-450P7.3	chrX:021435754-021435799	dense-CGI	182	46969.77	31851.41	1.5
NM_153270	A_17_P11634621	RP11-450P7.3	chrX:021436127-021436172	dense-CGI	260	54291.94	20624.25	2.6
NM_153270	A_17_P11634623	RP11-450P7.3	chrX:021436568-021436614	dense-CGI	334	60315.96	31834.98	1.9
NM_153270	A_17_P11634624	RP11-450P7.3	chrX:021436728-021436773	dense-CGI	369	123195.50	59780.41	2.1
NM_153270	A_17_P11634626	RP11-450P7.3	chrX:021436916-021436973	dense-CGI	369	115856.40	47100.68	2.5
NM_173495	A_17_P11642136	PTCHD1	chrX:023111270-023111316	dense-CGI	445	141025.30	75960.10	1.9
NM_173495	A_17_P11642138	PTCHD1	chrX:023111447-023111492	dense-CGI	445	43825.75	29961.71	1.5
NM_002970	A_17_P11643806	SAT	chrX:023560973-023561018	dense-CGI	189	156528.90	99406.97	1.6
NM_002970	A_17_P11643807	SAT	chrX:023561092-023561143	dense-CGI	174	68867.56	41868.27	1.6
NM_152632	A_17_P11696390	CXorf22	chrX:035697756-035697809	dense-CGI	287	73903.70	37934.15	1.9
NM_004683	A_17_P11737537	RGN	chrX:046694321-046694366	dense-CGI	175	71596.93	46112.87	1.6
NM_017602	A_17_P11742373	DKFZp761A052	chrX:048571696-048571741	dense-CGI	397	88167.30	54069.83	1.6
NM_017602	A_17_P11742374	DKFZp761A052	chrX:048571819-048571865	dense-CGI	397	68324.24	46777.89	1.5
NM_007075	A_17_P11742910	WDR45	chrX:048714316-048714361	dense-CGI	913	36722.05	19756.74	1.9
NM_007075	A_17_P11742912	WDR45	chrX:048714683-048714728	dense-CGI	290	28087.62	15410.06	1.8
NM_006150	A_17_P11743134	LMO6	chrX:048799521-048799576	dense-CGI	747	90187.25	46324.38	1.9
NM_006150	A_17_P11743136	LMO6	chrX:048799699-048799746	dense-CGI	747	120300.20	67459.03	1.8
NM_001025449	A_17_P11744696	LOC158572	chrX:049346621-049346666	dense-CGI	960	40667.22	27957.36	1.5
NM_203407	A_17_P11749495	LOC340602	chrX:050982756-050982801	dense-CGI	576	139297.80	52154.28	2.7
NM_203407	A_17_P11749497	LOC340602	chrX:050983015-050983061	dense-CGI	576	274806.30	82405.10	3.3
NM_203407	A_17_P11749498	LOC340602	chrX:050983158-050983203	dense-CGI	576	99350.83	27833.32	3.6
NM_001002838	A_17_P11755566	WNK3	chrX:054267269-054267314	dense-CGI	845	45930.64	29937.08	1.5
NM_020922	A_17_P11755569	WNK3	chrX:054267992-054268042	dense-CGI	865	14844.20	10191.42	1.5
NM_020922	A_17_P11755570	WNK3	chrX:054268145-054268195	dense-CGI	865	18374.37	12625.81	1.5
NM_004429	A_17_P11774923	EFNB1	chrX:067831313-067831359	dense-CGI	816	155109.30	83588.03	1.9
NM_004429	A_17_P11774925	EFNB1	chrX:067831496-067831549	dense-CGI	816	55928.83	33432.95	1.7
NM_004429	A_17_P11774926	EFNB1	chrX:067831611-067831656	dense-CGI	816	84269.76	46153.66	1.8
NM_053281	A_17_P11813509	DACH2	chrX:085209875-085209934	dense-CGI	361	56375.00	30737.22	1.8
NM_212559	A_17_P11850593	XKRX	chrX:099990331-099990376	dense-CGI	329	56058.63	37837.19	1.5
NM_194324	A_17_P11859126	MGC39900	chrX:103023079-103023126	dense-CGI	711	44056.41	26932.69	1.6
NM_194324	A_17_P11859127	MGC39900	chrX:103023196-103023243	dense-CGI	711	59988.23	33995.80	1.8
NM_153448	A_17_P11859903	ESX1L	chrX:103305662-103305707	dense-CGI	798	45373.50	28508.85	1.6
NM_153448	A_17_P11859905	ESX1L	chrX:103306036-103306091	dense-CGI	890	15404.87	10034.13	1.5
NM_153448	A_17_P11859907	ESX1L	chrX:103306612-103306672	dense-CGI	890	8848.93	6079.62	1.5
NM_198465	A_17_P11866458	NRK	chrX:104872794-104872839	dense-CGI	542	98593.53	58264.72	1.7
NM_198465	A_17_P11866459	NRK	chrX:104872906-104872951	dense-CGI	542	121005.40	64494.82	1.9
NM_032227	A_17_P11881771	RP13-360B22.2	chrX:109052520-109052565	dense-CGI	552	124906.30	81455.91	1.5

NM_006667	A_17_P11914205	PGRMC1	chrX:118151584-118151642	dense-CGI	161	69178.87	44920.33	1.5
NM_024528	A_17_P11916452	NKAP	chrX:118859350-118859395	dense-CGI	342	231236.70	149854.30	1.5
NM_024528	A_76_P0154517	NKAP	chrX:118860151-118860091	dense-CGI	718	9791.32	6323.93	1.5
NM_001167	A_17_P11928544	BIRC4	chrX:122719443-122719488	dense-CGI	443	59361.90	39630.63	1.5
NM_003069	A_17_P11947529	SMARCA1	chrX:128382796-128382841	dense-CGI	363	7664.13	4300.37	1.8
NM_139035	A_17_P11947530	SMARCA1	chrX:128382957-128383002	dense-CGI	363	33322.11	16271.34	2.0
NM_001448	A_17_P11964401	GPC4	chrX:132275637-132275682	dense-CGI	415	72814.28	38967.05	1.9
NM_001448	A_17_P11964402	GPC4	chrX:132275750-132275795	dense-CGI	415	81947.92	56123.79	1.5
NM_004484	A_17_P11967400	GPC3	chrX:132844831-132844876	dense-CGI	424	110516.60	40824.79	2.7
NM_003413	A_17_P11980033	ZIC3	chrX:136374293-136374338	dense-CGI	844	41835.09	28554.42	1.5
NM_003413	A_17_P11980034	ZIC3	chrX:136374560-136374605	dense-CGI	844	37210.39	22073.98	1.7
NM_004114	A_17_P11984298	FGF13	chrX:137518530-137518580	dense-CGI	272	66634.87	37032.13	1.8
NM_004114	A_17_P11984300	FGF13	chrX:137518757-137518802	dense-CGI	272	59912.30	31770.69	1.9
NM_017856	A_76_P0155941	FAM51A1	chrX:13807513-13807573	dense-CGI	471	15484.08	10672.94	1.5
NM_005634	A_17_P11991234	SOX3	chrX:139312476-139312521	dense-CGI	135	16533.91	7988.42	2.1
NM_005634	A_17_P11991236	SOX3	chrX:139312707-139312752	dense-CGI	227	83978.38	43632.68	1.9
NM_005634	A_17_P11991238	SOX3	chrX:139313007-139313059	dense-CGI	618	11700.10	6117.59	1.9
NM_005634	A_17_P11991239	SOX3	chrX:139313120-139313167	dense-CGI	618	40520.99	17843.60	2.3
NM_005634	A_17_P11991241	SOX3	chrX:139313334-139313379	dense-CGI	618	34038.19	15148.43	2.2
NM_005634	A_17_P11991244	SOX3	chrX:139313621-139313667	dense-CGI	464	133299.50	87237.11	1.5
NM_000252	A_17_P12023552	MTM1	chrX:149407378-149407423	dense-CGI	737	39592.52	24593.22	1.6
NM_018558	A_17_P12030849	GABRQ	chrX:151477313-151477358	dense-CGI	472	176160.20	109625.30	1.6
NM_000033	A_17_P12034809	ABCD1	chrX:152511420-152511465	dense-CGI	408	102644.50	65139.23	1.6
NM_001018055	A_17_P12039164	CXorf53	chrX:153863722-153863768	dense-CGI	163	23901.27	15767.17	1.5
NM_018196	A_17_P12040125	TMLHE	chrX:154406066-154406111	dense-CGI	326	53751.85	7761.36	6.9
NM_018196	A_17_P12040127	TMLHE	chrX:154406225-154406270	dense-CGI	326	185565.10	10514.26	17.6
NM_173452	A_17_P00104683	FCN3	chr1:027386026-027386071	sparse-CGI	697	18498.68	11253.62	1.6
NM_144622	A_17_P00522833	DCST2	chr1:151818424-151818469	sparse-CGI	539	302859.30	198406.20	1.5
NM_144622	A_17_P00522835	DCST2	chr1:151818614-151818659	sparse-CGI	539	231890.40	123730.00	1.9
NM_032323	A_17_P00527369	MGC13102	chr1:153068264-153068309	sparse-CGI	362	220963.90	133767.40	1.7
NM_014589	A_76_P0116277	PLA2G2E	chr1:19995868-19995808	sparse-CGI	863	43648.04	24346.57	1.8
NM_080431	A_76_P0118068	ARPM2	chr1:2961405-2961465	sparse-CGI	956	76055.43	29812.32	2.6
NM_152374	A_76_P0131685	FLJ38984	chr1:35854594-35854534	sparse-CGI	693	15998.52	4929.80	3.2
NM_022111	A_76_P0110159	CLSPN	chr1:35905830-35905890	sparse-CGI	670	12080.62	4294.45	2.8
NM_005202	A_76_P0104834	COL8A2	chr1:36235244-36235304	sparse-CGI	669	23076.73	11710.40	2.0
NM_005202	A_76_P0109149	COL8A2	chr1:36235582-36235522	sparse-CGI	669	13515.87	7237.44	1.9

NM_001008211	A_17_P07081450	OPTN	chr10:013180617-013180677	sparse-CGI	262	70502.85	44712.84	1.6
NM_001329	A_76_P0123618	CTBP2	chr10:126844452-126844512	sparse-CGI	638	22576.58	6721.62	3.4
NM_194303	A_17_P07587360	C10orf39	chr10:133804972-133805017	sparse-CGI	496	105358.40	48301.07	2.2
NM_194303	A_17_P07587363	C10orf39	chr10:133805276-133805321	sparse-CGI	496	93812.32	50028.10	1.9
nahsa-mi	A_17_P07592624	hsa-mir-202	chr10:134950565-134950610	sparse-CGI	376	242333.10	106790.40	2.3
nahsa-mi	A_17_P07592625	hsa-mir-202	chr10:134950796-134950841	sparse-CGI	376	144709.80	57937.50	2.5
NM_018109	A_76_P0131571	PAPD1	chr10:30678887-30678827	sparse-CGI	735	62473.07	29446.43	2.1
NM_005343	A_17_P07595093	HRAS	chr11:000524057-000524102	sparse-CGI	602	36070.66	16807.79	2.1
NM_001007139	A_17_P07601611	LOC492304	chr11:002107224-002107269	sparse-CGI	74	58449.41	25604.69	2.3
NM_001007139	A_17_P07601613	LOC492304	chr11:002107406-002107456	sparse-CGI	232	196240.10	114026.50	1.7
NM_021801	A_17_P07612347	MMP26	chr11:004965548-004965608	sparse-CGI	460	29850.95	16390.29	1.8
NM_021801	A_17_P07612349	MMP26	chr11:004965708-004965768	sparse-CGI	460	25654.48	17546.35	1.5
NM_024841	A_17_P07753442	FLJ14213	chr11:036433042-036433093	sparse-CGI	957	40966.58	17247.60	2.4
NM_024841	A_17_P07753443	FLJ14213	chr11:036433255-036433302	sparse-CGI	957	66677.24	23971.64	2.8
NM_024841	A_17_P07753445	FLJ14213	chr11:036433466-036433511	sparse-CGI	957	85598.21	34113.80	2.5
NM_024841	A_17_P07753446	FLJ14213	chr11:036433680-036433725	sparse-CGI	957	61319.08	27184.03	2.3
NM_033456	A_17_P07843990	KCNK7	chr11:065120653-065120698	sparse-CGI	476	110517.70	71994.55	1.5
NM_033456	A_17_P07843992	KCNK7	chr11:065120970-065121015	sparse-CGI	476	154463.60	95291.70	1.6
NM_014312	A_76_P0146215	VSIG2	chr11:124127102-124127042	sparse-CGI	475	26983.17	18508.50	1.5
NM_024841	A_76_P0149802	FLJ14213	chr11:36433042-36432982	sparse-CGI	957	19487.71	8862.16	2.2
NM_024841	A_76_P0137800	FLJ14213	chr11:36433260-36433320	sparse-CGI	957	19455.75	7421.20	2.6
NM_024841	A_76_P0138345	FLJ14213	chr11:36433597-36433537	sparse-CGI	957	30377.98	14292.33	2.1
NM_178443	A_76_P0150518	URP2	chr11:63730129-63730189	sparse-CGI	821	53205.22	35039.66	1.5
NM_002527	A_17_P08171436	NTF3	chr12:005473356-005473409	sparse-CGI	511	97150.26	43062.19	2.3
NM_015899	A_17_P08324274	PLEKHA9	chr12:043854567-043854627	sparse-CGI	320	180587.30	91581.15	2.0
NM_002273	A_17_P08357093	KRT8	chr12:051585330-051585382	sparse-CGI	901	24473.58	16598.65	1.5
NM_002273	A_17_P08357096	KRT8	chr12:051585629-051585684	sparse-CGI	901	29404.87	19607.86	1.5
NM_012240	A_17_P08651863	SIRT4	chr12:119201917-119201977	sparse-CGI	703	7689.29	4913.45	1.6
NM_182613	A_17_P08699957	FLJ33915	chr12:131254585-131254634	sparse-CGI	552	161630.30	74577.48	2.2
NM_182613	A_17_P08699959	FLJ33915	chr12:131254739-131254797	sparse-CGI	675	132438.70	66039.44	2.0
NM_182613	A_17_P08699960	FLJ33915	chr12:131254907-131254952	sparse-CGI	675	198302.50	119917.00	1.7
NM_000131	A_17_P09147062	F7	chr13:112807726-112807786	sparse-CGI	843	67643.49	28463.26	2.4
NM_000131	A_17_P09147066	F7	chr13:112808083-112808128	sparse-CGI	843	55936.17	26345.89	2.1
NM_000131	A_17_P09147068	F7	chr13:112808232-112808277	sparse-CGI	843	54031.59	32006.97	1.7
NM_002929	A_76_P0152494	GRK1	chr13:113369631-113369691	sparse-CGI	278	71975.07	49430.66	1.5
NM_002929	A_17_P09149709	GRK1	chr13:113369705-113369750	sparse-CGI	278	271733.10	115366.60	2.4
NM_001805	A_17_P09166421	CEBPE	chr14:022657964-022658009	sparse-CGI	292	261951.50	139979.00	1.9

NM_002471	A_17_P09167585	MYH6	chr14:022927470-022927516	sparse-CGI	716	33475.38	16718.39	2.0
nahsa-mi	A_17_P09167588	hsa-mir-208	chr14:022927864-022927909	sparse-CGI	812	49941.94	31331.10	1.6
nahsa-mi	A_17_P09167589	hsa-mir-208	chr14:022928149-022928204	sparse-CGI	812	58917.83	40613.47	1.5
NM_002471	A_17_P09167695	MYH6	chr14:022946500-022946545	sparse-CGI	639	172790.50	96286.32	1.8
NM_005794	A_17_P09168801	DHRS2	chr14:023177957-023178002	sparse-CGI	327	129422.60	56584.63	2.3
NM_005794	A_17_P09168802	DHRS2	chr14:023178107-023178157	sparse-CGI	327	172336.30	75197.66	2.3
NM_000359	A_17_P09171116	TGM1	chr14:023801205-023801250	sparse-CGI	737	156757.00	49898.11	3.1
NM_000359	A_17_P09171119	TGM1	chr14:023801524-023801569	sparse-CGI	737	157502.50	54298.37	2.9
NM_000359	A_17_P09171121	TGM1	chr14:023801807-023801860	sparse-CGI	737	93349.16	35551.32	2.6
NM_022137	A_17_P09371850	SMOC1	chr14:069414936-069414981	sparse-CGI	373	80892.39	47307.90	1.7
NM_022137	A_17_P09371852	SMOC1	chr14:069415113-069415159	sparse-CGI	373	78313.00	40200.53	1.9
nahsa-mi	A_17_P09517914	hsa-mir-381	chr14:100582022-100582079	sparse-CGI	395	36740.85	14783.61	2.5
nahsa-mi	A_17_P09517917	hsa-mir-382	chr14:100582283-100582328	sparse-CGI	395	245838.60	133682.20	1.8
NM_001031714	A_17_P09532384	C14orf173	chr14:104246845-104246890	sparse-CGI	370	137344.60	84799.34	1.6
NM_001031714	A_17_P09532398	C14orf173	chr14:104249570-104249615	sparse-CGI	627	102476.20	49385.99	2.1
NM_001031714	A_17_P09532401	C14orf173	chr14:104249845-104249890	sparse-CGI	627	86976.09	32213.07	2.7
NM_001031714	A_17_P09532405	C14orf173	chr14:104250317-104250362	sparse-CGI	684	218123.60	71963.25	3.0
NM_001031714	A_17_P09532406	C14orf173	chr14:104250567-104250612	sparse-CGI	684	118895.50	34772.19	3.4
NM_002471	A_76_P0166242	MYH6	chr14:22946362-22946302	sparse-CGI	639	30476.04	20299.67	1.5
NM_002471	A_76_P0151062	MYH6	chr14:22946583-22946643	sparse-CGI	639	14500.77	9991.76	1.5
NM_015492	A_17_P09763526	DKFZP434H132	chr15:073287131-073287176	sparse-CGI	774	111807.30	69342.25	1.6
NM_015492	A_17_P09763528	DKFZP434H132	chr15:073287268-073287315	sparse-CGI	774	104229.80	65089.93	1.6
NM_015492	A_17_P09763530	DKFZP434H132	chr15:073287511-073287556	sparse-CGI	774	213618.10	130570.20	1.6
NM_015492	A_17_P09763531	DKFZP434H132	chr15:073287731-073287780	sparse-CGI	673	146149.20	76321.94	1.9
NM_015492	A_17_P09763532	DKFZP434H132	chr15:073287880-073287925	sparse-CGI	673	98161.77	48791.78	2.0
NM_015492	A_17_P09763533	DKFZP434H132	chr15:073288018-073288063	sparse-CGI	673	124240.90	55020.27	2.3
NM_022767	A_17_P09817042	ISG20L1	chr15:086970497-086970542	sparse-CGI	287	56007.72	30667.96	1.8
NM_022767	A_17_P09817044	ISG20L1	chr15:086970662-086970707	sparse-CGI	287	153705.00	92934.24	1.7
NM_002569	A_17_P09826190	FURIN	chr15:089220004-089220049	sparse-CGI	559	143814.90	75152.54	1.9
NM_002569	A_17_P09826192	FURIN	chr15:089220243-089220288	sparse-CGI	559	409869.90	226855.50	1.8
NM_145294	A_17_P09882889	LOC197336	chr16:000654982-000655042	sparse-CGI	930	32471.22	17362.42	1.9
NM_145294	A_17_P09882891	LOC197336	chr16:000655462-000655507	sparse-CGI	930	58045.54	39837.40	1.5
NM_005823	A_17_P09883299	MSLN	chr16:000750314-000750359	sparse-CGI	163	89752.76	50464.97	1.8
NM_001025190	A_17_P09883405	MPFL	chr16:000773064-000773109	sparse-CGI	255	122625.90	72634.23	1.7
NM_001025190	A_17_P09883406	MPFL	chr16:000773183-000773228	sparse-CGI	255	242108.40	152384.30	1.6
NM_001025190	A_17_P09883407	MPFL	chr16:000773287-000773332	sparse-CGI	884	117245.50	79523.73	1.5
NM_001025190	A_17_P09883409	MPFL	chr16:000773563-000773608	sparse-CGI	884	89506.80	55581.07	1.6

NM_020825	A_17_P09887226	CRAMP1L	chr16:001645802-001645847	sparse-CGI	419	297404.00	184839.20	1.6
NM_020825	A_17_P09887227	CRAMP1L	chr16:001645932-001645977	sparse-CGI	419	230068.20	132107.30	1.7
NM_020825	A_17_P09887228	CRAMP1L	chr16:001646192-001646237	sparse-CGI	113	66081.00	18216.91	3.6
NM_020825	A_17_P09887229	CRAMP1L	chr16:001646313-001646358	sparse-CGI	121	43707.38	15748.24	2.8
NM_020825	A_17_P09887230	CRAMP1L	chr16:001646421-001646466	sparse-CGI	257	125458.00	79429.24	1.6
NM_020825	A_17_P09887231	CRAMP1L	chr16:001646548-001646593	sparse-CGI	257	26717.10	16282.39	1.6
NM_032271	A_17_P09889373	TRAF7	chr16:002153427-002153472	sparse-CGI	672	158142.40	77559.94	2.0
NM_022452	A_17_P09984069	FBS1	chr16:030583394-030583439	sparse-CGI	330	187114.70	112069.40	1.7
NM_022452	A_17_P09984071	FBS1	chr16:030583535-030583580	sparse-CGI	330	250921.30	138546.60	1.8
NM_022452	A_17_P09984073	FBS1	chr16:030583831-030583885	sparse-CGI	343	176820.30	106964.30	1.7
NM_022452	A_17_P09984074	FBS1	chr16:030583957-030584002	sparse-CGI	343	336368.20	188684.20	1.8
NM_014699	A_17_P09985485	ZNF646	chr16:030995388-030995433	sparse-CGI	739	54340.14	35917.56	1.5
NM_014699	A_17_P09985487	ZNF646	chr16:030995553-030995606	sparse-CGI	739	78030.35	49235.91	1.6
NM_014699	A_17_P09985488	ZNF646	chr16:030995760-030995813	sparse-CGI	739	81582.89	48418.29	1.7
NM_014298	A_76_P0166285	QPRT	chr16:29596462-29596402	sparse-CGI	741	7372.19	5036.71	1.5
NM_005823	A_76_P0138418	MSLN	chr16:750170-750230	sparse-CGI	163	19390.94	12816.68	1.5
NM_001976	A_17_P10203549	ENO3	chr17:004796096-004796141	sparse-CGI	365	143121.00	55391.94	2.6
NM_017986	A_17_P10204000	GPR172B	chr17:004878384-004878429	sparse-CGI	724	128830.00	45389.75	2.8
NM_017986	A_17_P10204002	GPR172B	chr17:004878680-004878732	sparse-CGI	724	55650.78	18188.87	3.1
NM_002055	A_17_P10336411	GFAP	chr17:040348395-040348440	sparse-CGI	215	184335.80	126171.20	1.5
NM_000727	A_17_P10427244	CACNG1	chr17:062470215-062470275	sparse-CGI	464	66406.24	38101.08	1.7
NM_000727	A_17_P10427248	CACNG1	chr17:062470863-062470908	sparse-CGI	652	155033.70	85000.37	1.8
NM_000727	A_17_P10427249	CACNG1	chr17:062471244-062471289	sparse-CGI	652	181952.60	84674.13	2.1
NM_000727	A_17_P10427251	CACNG1	chr17:062471394-062471439	sparse-CGI	652	131920.50	77556.81	1.7
NM_019020	A_17_P10486304	TBC1D16	chr17:075539846-075539891	sparse-CGI	801	71289.43	45418.82	1.6
NM_015229	A_76_P0164446	KIAA0664	chr17:2564825-2564885	sparse-CGI	441	27104.90	14273.80	1.9
NM_080704	A_76_P0156888	TRPV1	chr17:3448578-3448518	sparse-CGI	772	23513.83	13171.17	1.8
NM_021939	A_76_P0166520	FKBP10	chr17:37226714-37226654	sparse-CGI	773	42995.16	14257.92	3.0
NM_021939	A_76_P0162713	FKBP10	chr17:37226935-37226995	sparse-CGI	773	56023.77	17123.33	3.3
NM_002512	A_76_P0165481	NME2	chr17:46595625-46595685	sparse-CGI	703	20296.55	11311.60	1.8
NM_000727	A_76_P0145633	CACNG1	chr17:62470612-62470552	sparse-CGI	464	38070.88	25791.50	1.5
NM_000727	A_76_P0170646	CACNG1	chr17:62470826-62470886	sparse-CGI	652	50670.02	29714.19	1.7
NM_000727	A_76_P0170363	CACNG1	chr17:62471152-62471092	sparse-CGI	652	73839.62	39422.95	1.9
NM_000727	A_76_P0147714	CACNG1	chr17:62471372-62471432	sparse-CGI	652	59067.38	30524.33	1.9
NM_080913	A_76_P0161521	ASGR2	chr17:6960155-6960215	sparse-CGI	887	18612.96	6212.42	3.0
NM_144679	A_76_P0169759	FLJ31528	chr17:76835880-76835820	sparse-CGI	752	23232.84	8064.56	2.9
NM_024619	A_76_P0147485	FN3KRP	chr17:78266817-78266877	sparse-CGI	606	13005.41	4124.69	3.2

NM_002385	A_17_P10833217	MBP	chr18:072858273-072858325	sparse-CGI	465	253573.30	63273.49	4.0
NM_002385	A_17_P10833218	MBP	chr18:072858422-072858467	sparse-CGI	465	192895.80	57385.50	3.4
NM_002385	A_76_P0138649	MBP	chr18:72858199-72858139	sparse-CGI	465	55486.15	34467.91	1.6
NM_002385	A_76_P0168991	MBP	chr18:72858419-72858479	sparse-CGI	465	47065.64	31690.51	1.5
NM_173481	A_17_P10851373	C19orf21	chr19:000701854-000701899	sparse-CGI	626	148338.70	81558.77	1.8
NM_173481	A_17_P10851374	C19orf21	chr19:000701972-000702017	sparse-CGI	626	293962.20	158084.50	1.9
NM_032447	A_17_P10875200	FBN3	chr19:008118152-008118197	sparse-CGI	360	154158.70	105800.80	1.5
NM_020230	A_17_P10880350	PPAN	chr19:010082461-010082512	sparse-CGI	840	66474.46	43175.96	1.5
NM_015329	A_17_P10908721	KIAA0892	chr19:019316769-019316824	sparse-CGI	278	131326.60	82354.85	1.6
NM_015329	A_17_P10908723	KIAA0892	chr19:019316932-019316977	sparse-CGI	278	231922.30	139090.40	1.7
NM_005031	A_17_P10946742	FXYD1	chr19:040321839-040321884	sparse-CGI	773	108167.30	56838.41	1.9
NM_005031	A_17_P10946743	FXYD1	chr19:040321951-040321996	sparse-CGI	773	95149.09	53190.97	1.8
NM_005031	A_17_P10946744	FXYD1	chr19:040322096-040322142	sparse-CGI	773	49300.84	24049.94	2.0
NM_005031	A_17_P10946745	FXYD1	chr19:040322308-040322355	sparse-CGI	773	51047.10	27767.37	1.8
NM_033557	A_17_P10955826	YIF1B	chr19:043487830-043487875	sparse-CGI	777	79172.64	30623.88	2.6
NM_033557	A_17_P10955827	YIF1B	chr19:043488008-043488053	sparse-CGI	777	130026.70	57671.61	2.3
NM_032255	A_17_P10981353	ZNF541	chr19:052739624-052739669	sparse-CGI	319	384305.00	217941.40	1.8
NM_016148	A_17_P10990436	SHANK1	chr19:055911925-055911970	sparse-CGI	192	241668.50	153345.80	1.6
nahsa-mi	A_17_P10993885	hsa-mir-99b	chr19:056887151-056887196	sparse-CGI	957	140232.50	83293.32	1.7
NM_020230	A_76_P0161655	PPAN	chr19:10082596-10082656	sparse-CGI	840	63272.87	35361.97	1.8
NM_020230	A_76_P0149633	PPAN	chr19:10082937-10082877	sparse-CGI	922	9881.81	6610.27	1.5
NM_002566	A_76_P0160011	P2RY11	chr19:10083174-10083234	sparse-CGI	922	11158.09	6662.58	1.7
NM_002566	A_76_P0140436	P2RY11	chr19:10083468-10083408	sparse-CGI	922	26591.03	18018.76	1.5
NM_145045	A_76_P0139614	MGC20983	chr19:11402562-11402502	sparse-CGI	974	29684.40	12293.18	2.4
NM_145045	A_76_P0159745	MGC20983	chr19:11402722-11402782	sparse-CGI	974	21546.15	7856.59	2.7
NM_014173	A_76_P0158141	HSPC142	chr19:17240598-17240538	sparse-CGI	921	12987.69	5811.66	2.2
NM_138442	A_76_P0168653	LOC115098	chr19:17901605-17901545	sparse-CGI	627	23448.62	7185.54	3.3
NM_002248	A_76_P0142429	KCNN1	chr19:17945999-17945939	sparse-CGI	315	21585.64	14328.91	1.5
NM_005755	A_76_P0167462	EBI3	chr19:4175793-4175733	sparse-CGI	624	45448.82	10266.17	4.4
NM_005755	A_76_P0139852	EBI3	chr19:4175850-4175910	sparse-CGI	624	58925.14	13960.73	4.2
NM_005755	A_76_P0171853	EBI3	chr19:4177085-4177025	sparse-CGI	989	23046.21	9207.02	2.5
NM_024907	A_76_P0146922	FBXO17	chr19:44158922-44158862	sparse-CGI	853	16280.70	3420.29	4.8
NM_002774	A_76_P0152931	KLK6	chr19:56165470-56165530	sparse-CGI	836	14304.87	5295.41	2.7
NM_214710	A_76_P0140910	PRSSL1	chr19:646865-646925	sparse-CGI	979	8525.71	4763.05	1.8
NM_173481	A_76_P0151431	C19orf21	chr19:702402-702342	sparse-CGI	547	61776.09	35985.97	1.7
NM_002777	A_76_P0166357	PRTN3	chr19:787874-787814	sparse-CGI	885	13527.73	6097.23	2.2
NM_001004699	A_76_P0144073	OR2Z1	chr19:8701621-8701561	sparse-CGI	627	22845.00	10200.84	2.2

nahsa-mi	A_17_P01897024	hsa-mir-26b	chr2:219092887-219092937	sparse-CGI	500	80170.23	27651.29	2.9
NM_007127	A_76_P0131672	VIL1	chr2:219114241-219114181	sparse-CGI	921	143350.70	56843.03	2.5
NM_022134	A_76_P0119509	GAL3ST2	chr2:242436126-242436186	sparse-CGI	813	24867.87	16808.47	1.5
NM_004118	A_17_P11131771	FKHL18	chr20:029896841-029896886	sparse-CGI	349	206796.80	124046.50	1.7
NM_017454	A_17_P11201303	STAU	chr20:047239193-047239253	sparse-CGI	417	49635.84	32055.69	1.5
NM_178463	A_17_P11261092	C20orf166	chr20:060554500-060554545	sparse-CGI	741	87194.35	50480.90	1.7
NM_178463	A_17_P11261093	C20orf166	chr20:060554829-060554874	sparse-CGI	741	127589.60	86024.93	1.5
NM_152302	A_17_P11262759	C20orf158	chr20:060982210-060982255	sparse-CGI	497	187026.70	109548.10	1.7
NM_152302	A_17_P11262763	C20orf158	chr20:060982594-060982639	sparse-CGI	258	133081.30	70260.35	1.9
NM_198078	A_17_P11401414	C21orf121	chr21:042315307-042315355	sparse-CGI	770	54663.41	36645.57	1.5
NM_000394	A_17_P11406742	CRYAA	chr21:043462122-043462169	sparse-CGI	810	38129.26	19803.71	1.9
NM_000394	A_17_P11406744	CRYAA	chr21:043462341-043462386	sparse-CGI	810	88456.52	43569.80	2.0
NM_206965	A_17_P11419755	FTCD	chr21:046399597-046399642	sparse-CGI	866	156730.80	100103.80	1.6
NM_198078	A_76_P0154234	C21orf121	chr21:42315368-42315308	sparse-CGI	770	55080.23	26625.68	2.1
NM_198078	A_76_P0159293	C21orf121	chr21:42315519-42315579	sparse-CGI	770	35258.58	17881.64	2.0
NM_194309	A_76_P0155335	C21orf125	chr21:43694024-43694084	sparse-CGI	897	54237.84	35347.60	1.5
NM_173510	A_76_P0166146	FLJ33814	chr22:27491893-27491953	sparse-CGI	986	13457.72	3375.04	4.0
NM_153609	A_76_P0143157	TMPRSS6	chr22:35823799-35823859	sparse-CGI	718	46183.60	19696.46	2.3
NM_002673	A_17_P02222378	PLXNB1	chr3:048440760-048440805	sparse-CGI	976	54487.82	31354.17	1.7
NM_001008269	A_17_P02223388	LOC440955	chr3:048634359-048634404	sparse-CGI	638	49767.46	24569.35	2.0
NM_007354	A_17_P02575176	GR6	chr3:129775946-129776006	sparse-CGI	336	169653.00	88917.73	1.9
NM_000174	A_17_P02576773	GP9	chr3:130263520-130263565	sparse-CGI	234	256980.30	98645.30	2.6
NM_139209	A_17_P02631006	GRK7	chr3:142980075-142980120	sparse-CGI	236	238309.80	142238.80	1.7
NM_022147	A_76_P0109614	IFRG28	chr3:188568713-188568653	sparse-CGI	975	8767.08	5147.50	1.7
NM_022147	A_76_P0119753	IFRG28	chr3:188568932-188568992	sparse-CGI	975	7336.84	4119.78	1.8
NM_022304	A_76_P0118603	HRH2	chr5:175042509-175042569	sparse-CGI	957	23461.53	12408.63	1.9
NM_022304	A_17_P04481998	HRH2	chr5:175042608-175042668	sparse-CGI	957	7116.48	4833.93	1.5
NM_022304	A_17_P04482002	HRH2	chr5:175042991-175043037	sparse-CGI	957	55865.70	37693.50	1.5
NM_001031799	A_17_P04496677	RASGEF1C	chr5:179496755-179496801	sparse-CGI	600	201820.90	107221.60	1.9
NM_018950	A_76_P0124503	HLA	chr6:29798665-29798725	sparse-CGI	666	10744.63	3104.45	3.5
NM_002754	A_76_P0120508	MAPK13	chr6:36204659-36204599	sparse-CGI	961	27751.13	8885.33	3.1
NM_001760	A_76_P0114954	CCND3	chr6:42024722-42024782	sparse-CGI	709	23814.86	6658.04	3.6
NM_017781	A_17_P05260811	CYP2W1	chr7:000796070-000796115	sparse-CGI	746	545277.30	335725.40	1.6
NM_017781	A_17_P05260812	CYP2W1	chr7:000796226-000796271	sparse-CGI	92	14180.46	4233.02	3.3
NM_017781	A_17_P05260813	CYP2W1	chr7:000796436-000796481	sparse-CGI	558	71732.40	44602.46	1.6
NM_017781	A_76_P0112037	CYP2W1	chr7:795672-795612	sparse-CGI	746	68839.49	29200.88	2.4
NM_017781	A_76_P0123551	CYP2W1	chr7:795918-795978	sparse-CGI	746	90855.03	38611.56	2.4

NM_017781	A_76_P0107603	CYP2W1	chr7:796462-796522	sparse-CGI	558	78830.77	51823.11	1.5
NM_033512	A_17_P06321832	TSPYL5	chr8:098360078-098360130	sparse-CGI	634	89391.77	49341.48	1.8
NM_033512	A_17_P06321833	TSPYL5	chr8:098360236-098360293	sparse-CGI	634	54092.72	30118.32	1.8
NM_178857	A_76_P0108235	RP1L1	chr8:10566933-10566993	sparse-CGI	899	44357.72	28836.12	1.5
NM_178857	A_76_P0131303	RP1L1	chr8:10567195-10567135	sparse-CGI	611	92283.83	59467.28	1.6
NM_178857	A_76_P0127127	RP1L1	chr8:10567379-10567439	sparse-CGI	611	64864.51	39493.62	1.6
NM_002066	A_17_P06530833	GML	chr8:143912981-143913026	sparse-CGI	967	41528.31	19855.68	2.1
NM_002066	A_76_P0135776	GML	chr8:143913050-143913110	sparse-CGI	967	19461.73	11018.35	1.8
NM_002066	A_76_P0106226	GML	chr8:143913361-143913301	sparse-CGI	967	28659.37	10865.59	2.6
NM_002066	A_76_P0108341	GML	chr8:143913581-143913641	sparse-CGI	967	23038.31	12341.01	1.9
NM_198488	A_17_P06533885	FLJ46072	chr8:144883353-144883398	sparse-CGI	251	142831.70	91567.53	1.6
NM_201379	A_17_P06534808	PLEC1	chr8:145100727-145100772	sparse-CGI	447	328586.00	194666.10	1.7
NM_017767	A_17_P06536092	SLC39A4	chr8:145612601-145612646	sparse-CGI	879	191783.90	111538.00	1.7
NM_017767	A_17_P06536093	SLC39A4	chr8:145612819-145612864	sparse-CGI	879	136890.90	94084.42	1.5
NM_017767	A_17_P06536094	SLC39A4	chr8:145612978-145613023	sparse-CGI	879	161590.50	106179.40	1.5
NM_130849	A_17_P06536095	SLC39A4	chr8:145613159-145613204	sparse-CGI	255	278005.20	176792.30	1.6
NM_013432	A_76_P0104105	NFKBIL2	chr8:145632284-145632224	sparse-CGI	622	171901.60	67956.92	2.5
NM_013432	A_76_P0125551	NFKBIL2	chr8:145632505-145632565	sparse-CGI	622	136458.70	66970.46	2.0
NM_033512	A_76_P0130327	TSPYL5	chr8:98360040-98360100	sparse-CGI	634	32502.56	15475.24	2.1
NM_080655	A_76_P0121584	MGC17337	chr9:100266920-100266860	sparse-CGI	645	15659.90	3871.83	4.0
NM_080655	A_76_P0119922	MGC17337	chr9:100267140-100267200	sparse-CGI	645	14550.66	3781.18	3.8
NM_203305	A_17_P06971430	C9orf132	chr9:127792251-127792299	sparse-CGI	817	44044.75	29124.06	1.5
NM_203305	A_76_P0123284	EEIG1	chr9:127794375-127794315	sparse-CGI	571	17871.01	5090.79	3.5
NM_001013652	A_17_P06972087	LOC389791	chr9:127971170-127971215	sparse-CGI	251	163413.10	66849.98	2.4
NM_002957	A_76_P0109937	RXRA	chr9:134519034-134518974	sparse-CGI	797	40300.63	25020.38	1.6
NM_002957	A_17_P06998812	RXRA	chr9:134519247-134519292	sparse-CGI	797	207960.20	121250.90	1.7
NM_002957	A_76_P0102558	RXRA	chr9:134519255-134519315	sparse-CGI	797	105568.90	53711.25	2.0
NM_002957	A_17_P06998814	RXRA	chr9:134519384-134519429	sparse-CGI	797	266752.10	137082.20	1.9
NM_002957	A_17_P06999040	RXRA	chr9:134555947-134555992	sparse-CGI	957	107583.10	57625.62	1.9
NM_002957	A_17_P06999042	RXRA	chr9:134556104-134556149	sparse-CGI	957	68785.93	39859.59	1.7
NM_001012415	A_76_P0119562	C9orf157	chr9:135817221-135817161	sparse-CGI	557	76108.52	4431.50	17.2
NM_001012415	A_76_P0133879	C9orf157	chr9:135817440-135817500	sparse-CGI	136	22443.88	11935.98	1.9
NM_001012415	A_76_P0116575	C9orf157	chr9:135817779-135817719	sparse-CGI	792	143038.60	68706.64	2.1
NM_001012415	A_76_P0130533	C9orf157	chr9:135817963-135818023	sparse-CGI	792	77610.74	40224.89	1.9
NM_203347	A_17_P07010195	UNQ2541	chr9:136935252-136935297	sparse-CGI	927	65338.01	40506.54	1.6
NM_203347	A_17_P07010196	UNQ2541	chr9:136935451-136935499	sparse-CGI	927	91140.12	52458.37	1.7
NM_001606	A_76_P0135415	ABCA2	chr9:137193230-137193290	sparse-CGI	995	9179.89	4688.06	2.0



NM_001606	A_76_P0126606	ABCA2	chr9:137193569-137193509	sparse-CGI	995	20426.85	7372.86	2.8
NM_001606	A_76_P0116168	ABCA2	chr9:137193715-137193775	sparse-CGI	995	11395.65	5102.68	2.2
NM_000832	A_17_P07011733	GRIN1	chr9:137307716-137307761	sparse-CGI	662	196057.30	111264.80	1.8
NM_205849	A_17_P11576285	FAM9B	chrX:008811102-008811147	sparse-CGI	380	143101.70	40551.93	3.5
NM_174901	A_17_P11596564	FAM9C	chrX:012822539-012822584	sparse-CGI	282	165130.70	66742.09	2.5
NM_130776	A_17_P11751377	XAGE3	chrX:052779864-052779909	sparse-CGI	987	77435.94	20902.85	3.7
NM_145799	A_17_P11915792		6-Sep chrX:118610146-118610191	sparse-CGI	341	162314.90	96657.31	1.7
NM_173493	A_76_P0160780	PASD1	chrX:150402385-150402445	sparse-CGI	713	30335.49	11307.22	2.7
NM_173493	A_76_P0137878	PASD1	chrX:150402669-150402609	sparse-CGI	713	93805.17	39532.15	2.4
NM_173493	A_17_P12027082	PASD1	chrX:150402730-150402777	sparse-CGI	713	108848.40	31618.23	3.4
NM_001011543	A_17_P12029434	MAGEA10	chrX:150977429-150977476	sparse-CGI	536	184215.10	81012.47	2.3
NM_000054	A_17_P12035550	AVPR2	chrX:152691316-152691361	sparse-CGI	707	115530.70	58740.88	2.0
NM_000054	A_17_P12035552	AVPR2	chrX:152691510-152691555	sparse-CGI	707	91864.43	53439.21	1.7
NM_172377	A_17_P12037837	CTAG2	chrX:153445187-153445235	sparse-CGI	810	66070.59	19781.84	3.3
NM_172377	A_76_P0155989	CTAG2	chrX:153445252-153445312	sparse-CGI	810	16232.44	8812.08	1.8
NM_020997	A_17_P00835626	LEFTY1	chr1:222383807-222383860	non-CGI	591	213762.70	129396.00	1.7
NM_198074	A_17_P00929390	OR2C3	chr1:244021534-244021586	non-CGI	829	18343.54	12215.84	1.5
NM_014466	A_76_P0117289	TEKT2	chr1:36216174-36216114	non-CGI	556	10698.42	6321.64	1.7
NM_032807	A_17_P07045601	FBXO18	chr10:005976048-005976095	non-CGI	387	12235.19	4958.40	2.5
NM_002457	A_17_P07597377	MUC2	chr11:001063938-001063983	non-CGI	724	122051.40	83361.12	1.5
NM_002457	A_17_P07597384	MUC2	chr11:001064957-001065002	non-CGI	245	71632.75	38817.61	1.8
NM_006278	A_17_P08100477	ST3GAL4	chr11:125781641-125781686	non-CGI	724	62738.20	42342.93	1.5
NM_006278	A_17_P08100479	ST3GAL4	chr11:125781772-125781817	non-CGI	724	133812.20	78169.30	1.7
NM_004963	A_17_P08206334	GUCY2C	chr12:014740322-014740382	non-CGI	512	111769.30	28162.50	4.0
NM_170754	A_17_P08357622	TENC1	chr12:051730476-051730522	non-CGI	788	260830.50	177945.20	1.5
NM_004963	A_76_P0148090	GUCY2C	chr12:14740507-14740567	non-CGI	512	30442.55	11337.29	2.7
NM_198232	A_17_P09156133	RNASE1	chr14:020340194-020340245	non-CGI	885	38343.78	25051.50	1.5
NM_198232	A_17_P09156135	RNASE1	chr14:020340403-020340463	non-CGI	885	22716.16	15558.98	1.5
NM_198232	A_17_P09156138	RNASE1	chr14:020340677-020340725	non-CGI	885	33999.27	21882.55	1.6
NM_198235	A_17_P09156142	RNASE1	chr14:020341032-020341082	non-CGI	454	60629.86	37894.07	1.6
NM_004050	A_17_P09167177	BCL2L2	chr14:022846548-022846608	non-CGI	415	15344.93	8944.60	1.7
NM_004050	A_17_P09167179	BCL2L2	chr14:022846738-022846795	non-CGI	415	23461.23	13355.41	1.8
NM_015299	A_17_P09172083	KIAA0323	chr14:023967373-023967418	non-CGI	785	71407.78	22362.09	3.2
NM_015299	A_17_P09172086	KIAA0323	chr14:023967665-023967723	non-CGI	785	129785.10	39591.21	3.3
NM_001002236	A_17_P09484734	SERPINA1	chr14:093926976-093927023	non-CGI	449	75640.12	30049.23	2.5
NM_001002236	A_17_P09484736	SERPINA1	chr14:093927140-093927185	non-CGI	449	221345.90	94985.24	2.3

NM_001002236	A_17_P09484738	SERPINA1	chr14:093927348-093927394	non-CGI	449	56231.88	21802.28	2.6
NM_024515	A_17_P09514219	MGC4645	chr14:099917321-099917367	non-CGI	347	142515.10	87295.66	1.6
NM_024515	A_17_P09514221	MGC4645	chr14:099917569-099917614	non-CGI	347	123798.80	63274.41	2.0
NM_002933	A_76_P0149154	RNASE1	chr14:20340559-20340619	non-CGI	885	22549.34	9537.50	2.4
NM_198235	A_76_P0138867	RNASE1	chr14:20341119-20341179	non-CGI	454	31263.73	21089.20	1.5
NM_015299	A_76_P0160969	KIAA0323	chr14:23967814-23967754	non-CGI	785	40568.48	13994.11	2.9
NM_014249	A_17_P09748983	NR2E3	chr15:069889880-069889932	non-CGI	95	7535.99	3188.58	2.4
NM_001013638	A_17_P09883529	LOC388199	chr16:000795533-000795578	non-CGI	891	71599.25	46143.25	1.6
NM_182563	A_17_P09889593	MGC21830	chr16:002201812-002201860	non-CGI	243	139117.20	79804.83	1.7
NM_133450	A_17_P09899494	KIAA1977	chr16:004720167-004720212	non-CGI	821	40131.45	24911.59	1.6
NM_033309	A_17_P10083340	MGC4655	chr16:065743274-065743319	non-CGI	897	65731.69	40691.05	1.6
NM_152456	A_17_P10096539	MGC34647	chr16:069238443-069238488	non-CGI	338	29280.82	16388.84	1.8
NM_152348	A_17_P10191174	FLJ33817	chr17:001576966-001577011	non-CGI	389	165377.30	65755.96	2.5
NM_152348	A_17_P10191176	FLJ33817	chr17:001577145-001577190	non-CGI	389	205586.20	82257.97	2.5
NM_152348	A_17_P10191178	FLJ33817	chr17:001577310-001577355	non-CGI	845	117401.40	67680.97	1.7
NM_152348	A_17_P10191179	FLJ33817	chr17:001577446-001577491	non-CGI	845	98013.57	41415.51	2.4
NM_152348	A_17_P10191181	FLJ33817	chr17:001577628-001577673	non-CGI	845	128098.20	57114.23	2.2
NM_152348	A_17_P10191183	FLJ33817	chr17:001577867-001577913	non-CGI	845	137144.20	67212.12	2.0
NM_152348	A_17_P10191185	FLJ33817	chr17:001577994-001578039	non-CGI	845	124895.70	59971.13	2.1
NM_152348	A_17_P10191187	FLJ33817	chr17:001578127-001578172	non-CGI	807	33401.64	18512.06	1.8
NM_152348	A_17_P10191188	FLJ33817	chr17:001578241-001578286	non-CGI	807	56087.40	25150.44	2.2
NM_145068	A_17_P10197862	TRPV3	chr17:003407727-003407772	non-CGI	541	109192.80	58109.47	1.9
NM_001671	A_17_P10212199	ASGR1	chr17:007023112-007023157	non-CGI	576	219931.20	105558.50	2.1
NM_000691	A_17_P10262154	ALDH3A1	chr17:019592484-019592529	non-CGI	276	158995.50	82659.04	1.9
NM_145110	A_17_P10265718	MAP2K3	chr17:021140991-021141039	non-CGI	789	192612.70	85528.02	2.3
NM_145110	A_17_P10265721	MAP2K3	chr17:021141278-021141323	non-CGI	789	125022.60	47442.46	2.6
NM_145110	A_17_P10265724	MAP2K3	chr17:021141546-021141591	non-CGI	789	175194.00	67604.88	2.6
NM_145110	A_17_P10265725	MAP2K3	chr17:021141708-021141753	non-CGI	130	38372.97	26149.19	1.5
NM_001015002	A_17_P10466810	LLGL2	chr17:071051337-071051389	non-CGI	907	117647.30	75158.59	1.6
NM_207389	A_17_P10491939	FLJ44861	chr17:076753015-076753060	non-CGI	805	77061.43	43380.86	1.8
NM_145068	A_76_P0159219	TRPV3	chr17:3407735-3407795	non-CGI	541	42882.21	16514.81	2.6
NM_004524	A_76_P0160658	LLGL2	chr17:71051540-71051600	non-CGI	907	50151.01	23396.12	2.1
NM_207389	A_76_P0140438	FLJ44861	chr17:76721061-76721001	non-CGI	129	12239.99	6919.87	1.8
NM_207389	A_76_P0162400	FLJ44861	chr17:76753268-76753208	non-CGI	805	19602.75	12318.58	1.6
NM_001611	A_17_P10884783	ACP5	chr19:011549111-011549156	non-CGI	167	67248.20	10920.79	6.2
NM_001611	A_17_P10884784	ACP5	chr19:011549264-011549309	non-CGI	387	177677.30	95560.67	1.9
NM_001611	A_17_P10884787	ACP5	chr19:011549485-011549537	non-CGI	387	185909.30	98980.06	1.9

NM_031941	A_17_P10901543	USHBP1	chr19:017236464-017236510	non-CGI	425	229532.80	155238.90	1.5
NM_007000	A_17_P10948513	UPK1A	chr19:040849595-040849641	non-CGI	787	123292.60	72713.60	1.7
NM_198125	A_17_P10949481	TYROBP	chr19:041091232-041091280	non-CGI	477	10140.81	6922.38	1.5
NM_033068	A_17_P10990581	ACPT	chr19:055985444-055985489	non-CGI	677	133782.60	29325.29	4.6
NM_199250	A_17_P10990628	MGC13170	chr19:055994191-055994236	non-CGI	394	201552.30	107125.50	1.9
NM_199250	A_17_P10990630	MGC13170	chr19:055994396-055994441	non-CGI	394	168035.50	87648.72	1.9
NM_024298	A_17_P10999406	LENG4	chr19:059369527-059369572	non-CGI	373	162373.30	92815.89	1.7
NM_024298	A_17_P10999408	LENG4	chr19:059369732-059369777	non-CGI	373	214380.20	116226.10	1.8
NM_020410	A_76_P0166318	ATP13A1	chr19:19621166-19621106	non-CGI	840	37278.38	24053.18	1.5
NM_020410	A_76_P0146545	ATP13A1	chr19:19621349-19621409	non-CGI	840	83403.66	50537.39	1.7
NM_020410	A_76_P0141526	ATP13A1	chr19:19621688-19621628	non-CGI	840	32173.67	15527.07	2.1
NM_007000	A_76_P0167906	UPK1A	chr19:40849529-40849469	non-CGI	787	61588.52	34002.62	1.8
NM_007000	A_76_P0149255	UPK1A	chr19:40849680-40849740	non-CGI	787	66281.05	34113.76	1.9
NM_172140	A_76_P0152429	IL29	chr19:44478560-44478620	non-CGI	855	25146.31	17306.01	1.5
NM_172140	A_76_P0168944	IL29	chr19:44478892-44478832	non-CGI	855	19913.39	12536.66	1.6
NM_172140	A_76_P0138600	IL29	chr19:44479111-44479171	non-CGI	855	28647.60	16262.84	1.8
NM_006114	A_76_P0160130	TOMM40	chr19:50082773-50082833	non-CGI	793	28454.68	16704.95	1.7
NM_033068	A_76_P0161378	ACPT	chr19:55985071-55985131	non-CGI	677	36599.01	9383.42	3.9
NM_033068	A_76_P0142949	ACPT	chr19:55985410-55985350	non-CGI	677	86579.83	27205.66	3.2
NM_182586	A_17_P00988277	FLJ33534	chr2:011222676-011222723	non-CGI	249	208846.10	103978.40	2.0
NM_080653	A_17_P01152721	ATP6V1E2	chr2:046657832-046657878	non-CGI	341	168126.70	55762.44	3.0
NM_144712	A_17_P01900464	SLC23A3	chr2:219859941-219859996	non-CGI	685	281883.90	89110.92	3.2
NM_144712	A_76_P0135717	SLC23A3	chr2:219860046-219860106	non-CGI	685	69824.07	32069.99	2.2
NM_144712	A_17_P01900466	SLC23A3	chr2:219860082-219860127	non-CGI	685	225585.30	81982.46	2.8
NM_001631	A_76_P0119215	ALPI	chr2:233145814-233145874	non-CGI	845	18802.22	9501.83	2.0
NM_001631	A_17_P01963021	ALPI	chr2:233145862-233145907	non-CGI	259	137456.60	78511.19	1.8
NM_001631	A_17_P01963023	ALPI	chr2:233146128-233146177	non-CGI	621	98862.70	58908.39	1.7
NM_001631	A_76_P0108171	ALPI	chr2:233146153-233146093	non-CGI	621	29233.83	19223.76	1.5
NM_001631	A_17_P01963024	ALPI	chr2:233146301-233146346	non-CGI	621	185335.80	89715.01	2.1
NM_001631	A_76_P0107821	ALPI	chr2:233146330-233146390	non-CGI	621	91549.58	53477.07	1.7
NM_001631	A_76_P0128731	ALPI	chr2:233146670-233146610	non-CGI	621	62294.43	29859.03	2.1
NM_003650	A_17_P11126228	CST7	chr20:024878151-024878196	non-CGI	108	63956.28	42605.03	1.5
NM_174897	A_17_P11136246	BPIL3	chr20:031082616-031082662	non-CGI	741	78682.82	52721.21	1.5
NM_174897	A_17_P11136252	BPIL3	chr20:031083179-031083224	non-CGI	741	101002.40	64034.33	1.6
NM_181467	A_17_P11144308	ITGB4BP	chr20:033336860-033336905	non-CGI	226	105870.30	72586.70	1.5
NM_003349	A_17_P11204511	Kua-UEV	chr20:048179938-048179983	non-CGI	301	77805.24	44163.06	1.8
NM_003650	A_76_P0151084	CST7	chr20:24878164-24878224	non-CGI	108	11049.83	5683.66	1.9

NM_174897	A_76_P0155234	BPIL3	chr20:31082791-31082731	non-CGI	741	58523.04	37241.21	1.6
NM_174897	A_76_P0138396	BPIL3	chr20:31082944-31083004	non-CGI	741	44553.22	26217.39	1.7
NM_174897	A_76_P0162663	BPIL3	chr20:31083231-31083171	non-CGI	741	46376.88	28411.70	1.6
NM_019601	A_17_P11445755	SUSD2	chr22:022901596-022901641	non-CGI	728	77996.01	33630.51	2.3
NM_019601	A_17_P11445756	SUSD2	chr22:022901727-022901772	non-CGI	728	49240.74	16620.20	3.0
NM_019601	A_17_P11445757	SUSD2	chr22:022901846-022901891	non-CGI	728	103668.20	33778.68	3.1
NM_001051	A_17_P11496472	SSTR3	chr22:035933394-035933439	non-CGI	832	43455.07	7287.93	6.0
NM_001051	A_17_P11496473	SSTR3	chr22:035933775-035933820	non-CGI	832	39165.25	5185.08	7.6
NM_025045	A_17_P11499956	BAIAP2L2	chr22:036830994-036831039	non-CGI	550	7155.76	4426.99	1.6
NM_019601	A_76_P0151644	SUSD2	chr22:22901456-22901396	non-CGI	728	33883.27	14650.97	2.3
NM_019601	A_76_P0146131	SUSD2	chr22:22901541-22901601	non-CGI	728	51577.48	17836.94	2.9
NM_019601	A_76_P0158758	SUSD2	chr22:22901871-22901811	non-CGI	728	53019.91	17376.13	3.1
NM_025045	A_76_P0171875	BAIAP2L2	chr22:36830861-36830801	non-CGI	550	16800.87	8562.55	2.0
NM_033199	A_17_P02222985	UCN2	chr3:048576350-048576397	non-CGI	915	40490.75	21443.08	1.9
NM_000094	A_17_P02222986	COL7A1	chr3:048576751-048576796	non-CGI	915	117077.00	58665.12	2.0
NM_003262	A_17_P02758680	TLOC1	chr3:171166382-171166442	non-CGI	460	38448.34	24774.39	1.6
NM_014965	A_76_P0101166	OIP106	chr3:42176114-42176054	non-CGI	771	5883.90	3861.95	1.5
NM_014965	A_76_P0102808	OIP106	chr3:42176334-42176394	non-CGI	771	24195.34	15268.97	1.6
NM_005847	A_17_P04318582	SLC23A1	chr5:138746661-138746720	non-CGI	652	20167.13	11422.59	1.8
NM_152685	A_17_P04318584	SLC23A1	chr5:138746903-138746960	non-CGI	652	19326.65	10583.85	1.8
NM_001264	A_17_P04642515	CDSN	chr6:031196222-031196267	non-CGI	971	34051.28	12040.19	2.8
NM_007109	A_76_P0105664	TCF19	chr6:31237000-31236940	non-CGI	955	39524.10	5682.83	7.0
NM_001013836	A_17_P05266161	MAD1L1	chr7:002042940-002042994	non-CGI	486	122089.00	60425.61	2.0
NM_001013836	A_17_P05266163	MAD1L1	chr7:002043120-002043172	non-CGI	486	97755.44	45411.87	2.2
NM_001013836	A_17_P05266165	MAD1L1	chr7:002043242-002043287	non-CGI	486	104818.60	46290.11	2.3
NM_000385	A_17_P05396989	AQP1	chr7:030723899-030723945	non-CGI	740	85587.13	54886.86	1.6
NM_000385	A_17_P05396991	AQP1	chr7:030724136-030724181	non-CGI	740	111672.80	73294.55	1.5
NM_006213	A_17_P05505786	PHKG1	chr7:055934828-055934885	non-CGI	135	104680.00	70752.33	1.5
NM_002360	A_76_P0116724	MAFK	chr7:1342598-1342538	non-CGI	149	49401.92	21019.69	2.4
NM_005775	A_17_P06006297	SCAM-1	chr8:022468109-022468154	non-CGI	381	382837.80	201370.20	1.9
NM_001013842	A_17_P06006545	LOC541565	chr8:022514554-022514599	non-CGI	710	15508.08	8235.56	1.9
NM_178828	A_17_P06801115	C9orf79	chr9:087727340-087727385	non-CGI	890	23869.79	5594.01	4.3
NM_000476	A_17_P06971105	AK1	chr9:127716130-127716175	non-CGI	642	296627.40	148694.00	2.0
NM_032874	A_17_P07010288	KIAA1984	chr9:136976660-136976705	non-CGI	583	373542.40	210014.90	1.8
NM_000954	A_17_P07011032	PTGDS	chr9:137144596-137144641	non-CGI	427	281192.50	177222.60	1.6
NM_000954	A_17_P07011033	PTGDS	chr9:137144741-137144786	non-CGI	427	181958.30	119273.00	1.5
NM_080877	A_17_P07012140	SLC34A3	chr9:137402226-137402271	non-CGI	543	230358.00	152788.40	1.5

NM_018969	A_17_P11751590	GPR173	chrX:052961420-052961465	non-CGI	526	70814.06	34834.70	2.0
NM_005032	A_17_P11902756	PLS3	chrX:114649878-114649938	non-CGI	408	44336.86	17685.37	2.5
NM_007150	A_17_P12031701	ZNF185	chrX:151757433-151757478	non-CGI	852	46847.97	22496.39	2.1

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