

Supplemental Table S1. Chromosomal positions and GFP levels of all 90 clones. GFP levels are ²log-transformed FACS values. Chromosome (chr) and position are according to UCSC build HG15. Orientation (Or.) gives the orientation of the GFP gene. For each integration site, the distance to the closest transcriptional start site (TSS) and closest 3' end of nearby transcriptional units (TU) are given. Genes of integration sites within the boundaries of either a TU or RefSeq Gene (UCSC build HG15) are denoted with their respective TU and RefSeq names. For RefSeqs, the location (intronic or exonic) is given.

Clone	GFP	Chr	Position (bp)	Or.	Closest TSS (bp)	Closest 3' (bp)	TU	RefSeq	Location
1	15.03	chr01	147,439,327	+	5,401	6,302	29379_1_0_0_m	GPP34R	intron
2	14.77	chr01	147,154,880	+	42,660	66,330	29956_1_0_0		
3	14.76	chr01	222,091,466	-	71,088	3,491	14838_1_0_0	ENAH	exon
4	11.48	chr01	233,857,961	+	127,578	435,916	90821_1_0_1_m	RYP2	intron
5	11.44	chr01	74,177,374	+	42,072	42,972	150926_1_0_0_m	LOC51086	intron
6	14.89	chr01	27,989,763	+	60,499	22,745		FLJ13171	intron
7	13.75	chr01	142,969,173	+	33,112	48,939	8121_1_0_1_m	LOC64182	intron
8	14.92	chr01	147,782,760	+	26,770	96,495	78524_1_0_0_m	HTCD37	exon
9	12.03	chr01	186,072,100	-	138,999	178,405			
10	14.33	chr01	222,148,669	-	36,335	99,430	32399_1_0_0_m	LOC113521	intron
11	15.00	chr02	27,553,790	-	3,899	2,595	78436_2_0_0	SNX17	intron
12	9.18	chr02	47,640,318	+	52,502	27,760	78934_2_0_0	MSH2	intron
13	14.48	chr02	175,991,105	+	6,001	13,904	80285_2_0_0_m	ATF2	intron
14	13.18	chr02	219,056,736	-	10,898	26,359	83583_2_1_0	ARPC2	intron
15	13.93	chr03	57,617,332	+	20,521	127,008	4007_3_0_0_m		
16	11.43	chr03	95,653,525	+	335,876	337,877			
17	14.39	chr04	106,530,000	-	27,930	18,956	301149_4_0_0		
18	13.00	chr04	107,623,087	-	7,504	40,503	8115_4_0_0_m	MGC16169	intron
19	14.50	chr04	140,768,756	+	72,391	9,963	125034_4_0_0	TBDN100	intron
20	14.80	chr04	181,567,748	-	696,893	669,018			
21	13.68	chr05	37,540,117	+	160,664	177,388	16079_5_0_0_m	FLJ10233	intron
22	14.37	chr05	102,533,147	+	46,325	36,620	26179_5_0_0	KIAA0433	intron
23	13.20	chr05	179,074,133	-	26,680	13,767	289064_5_0_0	RUFY1	intron
24	11.76	chr06	20,858,584	+	146,522	436,590	279893_6_0_1_m	FLJ20342	intron
25	14.16	chr06	30,579,894	+	5,033	10,194	117406_6_0_0_m	GNL1	intron
26	14.20	chr06	36,021,683	-	24,699	58,745	79107_6_0_0_m	MAPK14	intron
27	11.41	chr06	64,891,793	+	545,569	515,020			
28	12.03	chr06	65,629,349	-	191,987	193,585			
29	15.54	chr06	85,661,065	-	311,687	291,657			
30	11.57	chr06	132,876,683	-	3,667	11,792			
31	14.23	chr06	144,776,604	+	158,067	328,398		UTRN	intron
32	14.55	chr06	157,110,972	-	55,309	101,353	73287_6_0_0	ELD/OSA1	intron
33	15.16	chr07	25,402,585	+	103,631	133,961			
34	13.55	chr07	34,737,746	-	23,681	41,324	11217_7_0_2		
35	12.21	chr07	129,595,397	-	24,701	20,243	27027_7_0_0_m	TSGA14	intron
36	10.79	chr08	52,248,150	-	286,568	205,173			
37	12.57	chr08	88,588,553	+	131,415	124,408			
38	11.29	chr08	135,269,962	-	683	2,592	15611_8_0_0		
39	13.61	chr09	64,303,116	-	35,193	182,130	7535_9_1_0		
40	14.26	chr09	93,857,411	-	35,034	16,722	89563_9_0_0	NCBP1	intron
41	15.17	chr09	126,314,425	+	29,056	34,317	6639_9_0_0	GPR107	intron
42	15.69	chr09	133,462,798	+	12,544	16,741			
43	11.20	chr10	3,661,685	+	17,597	15,851			
44	9.76	chr10	38,468,753	+	12,689	10,997	307098_10_0_0	ZNF33A	intron
45	15.31	chr10	119,900,480	+	37,080	4,828	173656_10_0_0	Rab11-FIP2	intron

Clone	GFP	Chr	Position (bp)	Or.	Closest TSS (bp)	Closest 3' (bp)	TU	RefSeq	Location
46	15.06	chr10	135,117,757	+	14,450	25,664		PAO	intron
47	14.98	chr10	135,392,859	+	93,871	109,343			
48	15.08	chr11	608,505	+	15,207	20,767	130541_11_0_0		
49	15.95	chr11	9,348,732	-	26,737	7,378	174905_11_0_0		
50	10.38	chr11	24,181,344	+	315,966	359,315			
51	15.54	chr11	65,131,852	-	2,372	1,999	31130_11_0_0	TM7SF2	intron
52	13.40	chr11	125,926,081	-	62,070	1,230			
53	15.14	chr12	54,371,293	-	12,319	11,087	89232_12_0_0_m	CBX5	intron
54	11.99	chr12	77,021,339	-	29,631	58,493			
55	15.13	chr12	125,094,712	-	22,250	60,600			
56	12.04	chr13	82,121,723	-	2,000,679	1,981,677			
57	11.77	chr13	84,801,702	-	679,300	698,302			
58	15.47	chr15	61,413,481	-	37,780	1,862	251636_15_0_0_m	USP3	intron
59	15.02	chr15	71,106,112	+	185,313	67,407	90408_15_0_0_m	NEO1	intron
60	15.03	chr15	71,491,763	+	9,930	31,537	6354_15_0_0_m	SDFR1	intron
61	14.57	chr15	76,440,160	-	31,487	21,160		CHRNA5	intron
62	14.95	chr15	97,561,872	-	137,059	42,638			
63	14.31	chr16	126,954	-	1,905	40,572	19699_16_0_0	CGTHBA	intron
64	15.20	chr16	2,115,845	-	9,978	28,246	75813_16_0_0	PKD1	intron
65	14.25	chr16	24,944,610	-	9,478	79,742	14169_16_0_0_m	RICH1	intron
66	15.41	chr16	28,869,476	-	3,180	14,588			
67	13.77	chr16	29,939,527	-	1,805	253	274580_16_0_0		
68	14.89	chr16	46,599,239	+	6,242	22,995	322901_16_0_0		
69	14.63	chr16	66,446,522	-	19,554	59,861	255606_16_0_0		
70	14.45	chr16	75,157,724	-	29,612	48,268	296460_16_0_0_m	CFDP1	intron
71	13.49	chr17	5,248,695	-	19,049	32,564	172108_17_0_0	NUP88	intron
72	15.30	chr17	7,724,958	-	6,364	22,238	333414_17_0_0_m		
73	14.12	chr17	29,545,889	-	47,273	51,425	93207_17_0_0_m	NF1	intron
74	15.13	chr17	57,648,459	-	19,213	13,932			
75	11.48	chr17	73,499,283	+	7,964	171	64593_17_0_0	ATP5H	intron
76	16.07	chr17	80,190,246	-	3,510	10,687			
77	14.30	chr18	2,733,319	+	3,845	61,697	8118_18_0_0_m		
78	14.10	chr19	2,445,675	-	48,717	5,010			
79	14.86	chr19	2,942,532	+	26,643	4,897	332173_19_0_0	TLE2	intron
80	14.30	chr19	4,208,172	-	915	21,096	21811_19_0_0	FLJ10374	intron
81	7.91	chr19	21,129,018	+	52,332	13,936	135553_19_0_0_m		
82	14.43	chr19	50,274,303	-	18,487	3,418			
83	14.94	chr19	53,743,550	+	12,101	35,156	94581_19_0_0		
84	12.66	chr19	55,143,583	-	35,757	12,161			
85	14.43	chr20	42,974,443	+	40,296	9,122	179718_20_0_0	MYBL2	intron
86	14.93	chr20	52,914,674	-	51,360	25,123			
87	14.34	chr22	16,228,932	-	102,249	116,630			
88	14.86	chr22	38,146,670	-	7,527	10,506	83869_22_0_0_m	FLJ20232	intron
89	13.29	chrX	65,756,836	-	4,673	233,890		OPHN1	intron
90	15.22	chrX	94,073,570	-	19,722	98,131		DIAPH2	intron