Supplementary Table S1. Characteristics of the 24 SNPs included in the MCA assay of 393 cell lines.

SNP ID	Chromosome	Position[1]	ObsHET	PredHET	HWpval	%Geno	MAF	Alleles
rs1040981	chr6	31648763	0.34	0.44	0.6653	99	0.33	A:T
rs1042522	chr17	7520197	0.23	0.43	1.26E-08	98.5	0.32	A:T
rs1143627	chr2	113310858	0.40	0.46	2.60E-05	96.4	0.36	A:T
rs1554606	chr7	22735232	0.34	0.45	1.81E-19	99.7	0.34	A:T
rs1799864	chr3	46374212	0.18	0.23	2.04E-06	99.5	0.13	T:A
rs1800682	chr10	90739943	0.39	0.50	0.0018	99	0.49	T:A
rs1800797	chr7	22732746	0.31	0.41	0.0471	99.5	0.29	A:T
rs1800872	chr1	205013030	0.32	0.43	0.0065	99	0.31	A:T
rs1800896	chr1	205013520	0.34	0.49	3.02E-07	99.7	0.42	T:A
rs1801275	chr16	27281901	0.25	0.34	1.58E-05	98.2	0.22	T:A
rs1805010	chr16	27263704	0.45	0.50	3.00E-04	99	0.48	T:A
rs1805015	chr16	27281681	0.21	0.25	7.94E-07	100	0.15	A:T
rs2234767	chr10	90739236	0.21	0.30	1.11E-05	100	0.19	A:T
rs231775	chr2	204440959	0.40	0.48	8.00E-04	98.7	0.39	T:A
rs3087243	chr2	204447164	0.40	0.49	8.74E-05	99.5	0.41	A:T
rs352140	chr3	52231737	0.40	0.50	2.23E-06	99	0.48	T:A
rs3761623	chrX	12832023	0.11	0.49	1.81E-06	99.2	0.44	T:A
rs3775291	chr4	187241068	0.32	0.41	7.35E-61	99.2	0.29	A:T
rs3788935	chrX	12832580	0.09	0.45	7.02E-59	99.7	0.34	T:A
rs5743305	chr4	187226327	0.34	0.45	2.94E-08	100	0.34	A:T
rs5743836	chr3	52235822	0.16	0.20	6.00E-04	99.2	0.11	A:T
rs603965	chr11	69172091	0.49	0.50	0.0062	98	0.47	A:T
rs7208422	chr17	73642170	0.36	0.50	1.40E-05	96.9	0.49	T:A
rs8177374	chr11	125668053	0.16	0.21	1.30E-07	98.7	0.12	T:A

[1] Chromosome position based on the NCBI Build 36.3; ObsHet, marker's observed heterozygosity; PredHet, marker's predicted heterozygosity; HWpval' Hardy-Weinberg equilibrium p value; %Geno, percentage of non-missing genotypes for this marker; MAF is the minor allele frequency for the marker; Alleles, are the major and minor alleles for this marker.

Table S2. Median fluorescence intensities, calculated ratios and genotype attribution by MCA, exemplarily shown for 12 SNP loci for 13 HEK293T subclones

HEK293T Subclone	SNP 1[a]				SNP 2				SNP 3				SNP 4				SNP 5				SNP 6			
	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype
293T pMC-G-PMS2 10	641	5133	0.12	AA	5658	981	5.77	TT	4739	1413	3.35	TT	265	1713	0.15	AA	4624	471	9.82	TT	3171	4817	0.66	AA
293T pMC-G-MLH1 3	762	4964	0.15	AA	5348	943	5.67	TT	4430	1383	3.20	TT	209	1341	0.16	AA	4778	541	8.83	TT	2847	4403	0.65	AA
293T pMC-G-MLH1 2	594	4779	0.12	AA	5715	960	5.95	TT	4619	1533	3.01	TT	503	2621	0.19	AA	4651	439	10.59	TT	3019	4816	0.63	AA
293T MutLa (mCherry-MLH1 GFP-PMS2)	631	4445	0.14	AA	5504	918	6.00	TT	4448	1326	3.36	TT	578	2770	0.21	AA	4228	481	8.79	TT	3108	4798	0.65	AA
293T MutLb 1 (mCherry-MLH1 GFP-PMS1)	491	4844	0.10	AA	6030	980	6.15	TT	4645	1447	3.21	TT	614	3384	0.18	AA	4553	423	10.76	TT	3140	5113	0.61	AA
293T MutSy 8 (YFP-His-MSH4 CFP-Strep-MSH5)	574	4303	0.13	AA	7039	1218	5.78	TT	4947	1511	3.27	TT	748	3326	0.22	AA	4049	414	9.78	TT	3305	5174	0.64	AA
293T MutLa8 (mCherry-MLH1 GFP-PMS2)	619	4784	0.13	AA	5552	905	6.14	TT	4297	1268	3.39	TT	637	3235	0.20	AA	4281	430	9.97	TT	3066	4750	0.65	AA
293T MutLb 1 (mCherry-MLH1 GFP-PMS1)	577	5276	0.11	AA	6454	796	8.11	TT	4773	1374	3.47	TT	533	3002	0.18	AA	4715	424	11.12	TT	3199	5147	0.62	AA
pMC-G-MLH3delta7 8	760	4534	0.17	AA	4952	754	6.57	TT	4435	1568	2.83	TT	320	1877	0.17	AA	4339	469	9.25	TT	2937	4674	0.63	AA
pMC-G-MLH3delta7 4	658	5223	0.13	AA	5435	711	7.65	TT	4676	1480	3.16	TT	304	1876	0.16	AA	4581	436	10.51	TT	2808	4616	0.61	AA
293T MutLa 1 (mCherry-MLH1 GFP-PMS2)	724	4769	0.15	AA	5745	933	6.16	TT	4524	1434	3.16	TT	387	2158	0.18	AA	4428	468	9.46	TT	2987	4790	0.62	AA
pMC-G-MLH3WT 8	574	4998	0.11	AA	6145	956	6.43	TT	3348	881	3.80	TT	565	2938	0.19	AA	4580	425	10.78	TT	2083	3707	0.56	AA
pMC-G-MLH3WT 12	636	4386	0.15	AA	6401	1220	5.25	TT	4441	1384	3.21	TT	653	3067	0.21	AA	4143	433	9.57	TT	3147	5015	0.63	AA

HEK293T Subclone	SNP 7				SNP 8				SNP 9				SNP 10				SNP 11				SNP 12			
	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype	A_1 (MFI)	A_2 (MFI)	Ratio	Genotype
293T pMC-G-PMS2 10	1438	2189	0.66	AT	33	1677	0.02	AA	165	592	3.59	AT	1453	107	13.58	TT	1215	557	2.18	AA	3594	1400	2.57	TT
293T pMC-G-MLH1 3	1560	2276	0.69	AT	42	1806	0.02	AA	167	573	3.43	AT	1595	118	13.52	TT	1265	608	2.08	AA	3387	1546	2.19	TT
293T pMC-G-MLH1 2	1347	2714	0.50	AT	36	1704	0.02	AA	177	518	2.93	AT	1259	88	14.30	TT	869	421	2.06	AA	3277	1395	2.35	TT
293T MutLa (mCherry-MLH1 GFP-PMS2)	1509	2274	0.66	AT	53	2236	0.02	AA	154	526	3.41	AT	1351	92	14.68	TT	971	500	1.94	AA	3454	1310	2.64	TT
293T MutLb 1 (mCherry-MLH1 GFP-PMS1)	1482	2301	0.64	AT	37	1788	0.02	AA	178	579	3.25	AT	1138	74	15.48	TT	793	387	2.05	AA	3452	1394	2.48	TT
293T MutSy 8 (YFP-His-MSH4 CFP-Strep-MSH5)	1636	2530	0.65	AT	36	1582	0.02	AA	153	530	3.46	AT	1319	78	16.91	TT	840	427	1.97	AA	3136	1201	2.61	TT
293T MutLa8 (mCherry-MLH1 GFP-PMS2)	1394	2056	0.68	AT	42	1902	0.02	AA	174	533	3.07	AT	1356	85	15.95	TT	998	557	1.79	AA	3053	1103	2.77	TT
293T MutLb 1 (mCherry-MLH1 GFP-PMS1)	1595	2526	0.63	AT	38	1851	0.02	AA	193	628	3.26	AT	1531	93	16.46	TT	1035	492	2.10	AA	3406	1243	2.74	TT
pMC-G-MLH3delta7 8	1535	2383	0.64	AT	38	1782	0.02	AA	164	496	3.02	AT	1603	129	12.42	TT	1311	682	1.92	AA	3076	1326	2.32	TT
pMC-G-MLH3delta7 4	1676	2507	0.67	AT	37	1792	0.02	AA	190	576	3.03	AT	2033	152	13.38	TT	1623	826	1.96	AA	3804	1483	2.57	TT
293T MutLa 1 (mCherry-MLH1 GFP-PMS2)	1478	2259	0.65	AT	46	1901	0.02	AA	155	485	3.13	AT	1399	112	12.49	TT	1057	504	2.10	AA	3391	1381	2.46	TT
pMC-G-MLH3WT 8	1037	1917	0.54	AT	37	1838	0.02	AA	179	582	3.25	AT	1624	110	14.76	TT	2280	1286	1.77	AA	3217	1251	2.57	TT
pMC-G-MLH3WT 12	1423	2209	0.64	AT	39	1653	0.02	AA	167	502	3.01	AT	1257	90	13.97	TT	919	436	2.11	AA	3095	1195	2.59	TT

[a] SNP locus 1, indicated are median fluorescence intensities (MFI) of the alleles 1 and 2, the ratio of both alleles and the corresponding genotype