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Heterozygosities and allelic frequencies of 811 dinucleotide-repeat marker loci in the Taiwanese population

Received: 6 January 2004 / Accepted: 15 March 2004 / Published online: 19 May 2004
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Abstract To evaluate basic informativeness of commercially available microsatellite markers in the Taiwanese population, 190 unrelated Taiwanese children were genotyped using ABI PRISM Linkage Mapping Set-HD5. The average heterozygosity in Taiwanese was slightly lower than that in Caucasians among these 811 microsatellite markers. There were 50 marker loci with heterozygosities lower than 50%. Moreover, allelic distributions at many of the loci were significantly different in two ethnic groups. The results reported here represent a valuable database for disease genes mapping in the Taiwanese population. This database can be easily accessed at the Web site of Vita Genomics, Inc. (<http://www.vitagenomics.com/str.html>).

Keywords Microsatellite marker · Heterozygosity · Allele frequency · Taiwanese population

Introduction

Microsatellite markers, the short tandem repeats (STRs) evenly distributed in whole genome, are exploited widely for forensic medicine and used to search for identifying genes associated with diseases. The dinucleotide-repeat microsatellites are more useful than other STR markers because of their high heterozygosities and even distribution in the genome. Such markers can be analyzed by using a very small amount of DNA through amplification with polymerase chain reaction and subsequent

electrophoresis. In fact, the technology of analyzing microsatellite polymorphism is adapted to automation and high throughput. Due to their highly polymorphism traits, microsatellite markers have been heavily utilized in areas such as mapping disease loci using linkage analyses, loss of heterozygosity analyses, and association studies.

Genotypic information, including allelic frequency and heterozygosity, is available through various databases. However, most of these data were derived from analyses using Caucasian samples. The data obtained from Asian population currently available are: 358 dinucleotide-repeat marker loci validated in 32 normal Japanese individuals (Yamane-Tanaka et al. 1998), 406 microsatellite marker loci validated in 64 unrelated Japanese subjects (Ikari et al. 2002), and 285 autosomal microsatellite marker loci validated in Chinese Singaporeans (Tan et al. 2002). The significant differences of allelic distributions of certain markers have been found between Caucasians and Japanese (Yamane et al. 1997). Since allelic information often differs between ethnic groups and could drastically influence the statistical analysis, it is not certain that currently available information on Caucasians, Japanese, and Singaporeans could be applied to study the disease genes in other ethnic groups.

Theoretically, multiallelic markers always have more power to detect linkage disequilibrium than biallelic markers due to their multiple alleles and greater heterozygosity (Ott and Rabinowitz 1997; Chapman and Wijmsman 1998). Existing sets of microsatellite data, if sufficiently dense, may be useful for estimating the density of additional markers needed for screening a region for disease alleles in an association analysis (Schulze et al. 2002). Therefore, gathering information on additional markers in the Asian population is important for mapping disease genes in Asia by linkage analyses or association studies.

The STR genotyping laboratory was established in March 2002 by Vita Genomics, Inc. To date, we have completed several whole-genome screening projects and

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have built a comprehensive database for microsatellite markers. Here we report allelic distribution, allelic frequency, and heterozygosities of 811 dinucleotide-repeat markers among 190 Taiwanese subjects. The data indicate a high degree of genetic similarity between Taiwanese and Japanese. Our results represent an essential database for mapping genes associated with diseases not only in Taiwanese but also in Japanese populations.

Materials and methods

DNA preparation

Genomic DNAs were extracted from 190 unrelated Han-Chinese children living in Taiwan. We collected written informed consent from all subjects recruited. The informed-consent documents for all underage participants were signed by their guardians. DNA was isolated from blood samples using QIAamp DNA blood kit (QIAGEN, Valencia, CA, USA) according to the manufacturer's instructions. The isolated genomic DNA was quality checked by agarose gel electrophoresis analysis, quantity determined spectrophotometrically, and stored at -80°C .

Microsatellite genotyping

Genotyping was performed using the ABI PRISM Linkage Mapping Sets HD-5 (811 markers, 5 cM average resolution, version 2.5, Applied Biosystems, Foster City, CA, USA). Each marker set included a fluorescence-labeled forward primer and a tailing reverse primer. PCR amplifications were carried out according to the manufacturer's instructions, and the PCR products were separated on ABI 3700 DNA analyzers (Applied Biosystems). The use of GeneScan 500 LIZ (Applied Biosystems) as the internal-size standard assists polymorphic fragment length calling and allows more accurate allele calling and unambiguous comparison of data across experimental conditions. Genotypes were initially scored using GeneScan and Genotyper (Applied Biosystems) software and were then verified independently by three individuals.

Genotypic data derived from Caucasians for each marker were obtained from the Foundation Jean DAUSSET-CEPH (<http://www.cephb.fr/>). A control individual was derived from CEPH 1347-02. There are differences in the allele size of the STR markers between the CEPH database and our genotyping result because the pair primers of each locus had been redesigned by ABI and the mobility of PCR products were different among the variant sequencers (i.e., ABI373, 377, 3100, 3700, etc.). We corrected the differences comparing control data obtained from CEPH database and our genotyping data. Possible error in genotyping or allele calling was checked by comparing the expected number

against the observed number of heterozygosities by the Hardy-Weinberg (HW) equilibrium test utilizing the Popgene (version 1.31) program (<ftp://ftp.microsoft.com/Softlib/MSLFILES/HPGL.EXE>).

Results and discussion

Genotyping for all 811 markers was performed on 190 unrelated Han-Chinese children living in Taiwan. We experienced no ambiguous genotypes or unsuccessful amplifications. Based on the results of the chi-square test and likelihood ratio test in the Popgene program of the HW test, most loci we tested met the criteria of HW equilibrium. Nevertheless, there were 38 of 811 loci, or less than 5% of total markers tested, which did not meet HW equilibrium criteria. This could be due to the combination factors of random sampling, original genetic variations of the subjects, and the presence of low-frequency alleles. Heterozygosities were calculated at each of the autosomes and X-chromosome marker loci using 190 individuals and 64 females, respectively. Table 1 summarize heterozygosity of the 811 marker loci for the Taiwanese and Caucasian populations. In general, overall heterozygosities of the markers from Taiwanese contained higher similarity to those from Japanese than to those from Caucasians. Among these 811 markers, there were 400 markers identical to the ones used by Ikari et al. (2002). Between Taiwanese and Japanese, there were only two out of 400 loci with differences in heterozygosities greater than or equal to 20%. On the contrary, the differences between Taiwanese and Caucasians were much higher at the rate of 81 out of 811 markers when compared to the Caucasian data from the manufacture. The significant differences between Japanese and Caucasians have also been observed at the rate of 33 out of 400 markers. The level of heterozygosity in the Taiwanese population ranged from 0.13 (DXS8088) to 0.94 (D6S291). As shown in Table 2, 50 marker loci revealed heterozygosity lower than 50% compared to only five marker loci in Caucasians. The X chromosome has lower average heterozygosity in the Taiwanese population, as shown in Table 3. Although heterozygosity was higher overall in Caucasians, a few markers showed higher heterozygosity in Taiwanese. For example, at D6S291, we observed 94% heterozygosity in Taiwanese as compared to 73% reported in Caucasians.

In conclusion, we constructed a comprehensive database of allelic frequencies and heterozygosities of all 811 microsatellite markers evaluated in this study. We believe that our data provide a useful tool for mapping genes associated with diseases in the Taiwanese population. Moreover, data similarity of the 400 markers between Japanese and Taiwanese suggests a potentially powerful application of this database in the Japanese population. Data are freely available to all researchers and can be accessed at the Web site of Vita Genomics, Inc. (<http://www.vitagénomics.com/str.html>).

Table 1 Heterozygosities of the 811 tested short tandem repeat (STR) markers (part 1). *Chr* chromosome, *Het* heterozygosity, *Twn* Taiwanese, *Cau* Caucasian

Chr	Marker	Het	
		Twn	Cau
1	D1S468	81	76
	D1S2660	32	78
	D1S214	70	78
	D1S450	80	81
	D1S2667	81	82
	D1S434	65	61
	D1S507	83	78
	D1S2697	46	70
	D1S2644	77	80
	D1S199	80	83
	D1S2864	59	81
	D1S234	82	81
	D1S233	84	85
	D1S255	34	75
	D1S2892	84	88
	D1S2713	76	76
	D1S2797	75	74
	D1S2652	80	62
	D1S2890	71	81
	D1S2873	54	69
	D1S2737	73	75
	D1S2846	68	54
	D1S230	59	78
	D1S198	82	79
	D1S2841	83	78
	D1S500	78	62
	D1S207	80	84
	D1S2766	77	74
	D1S435	66	73
	D1S2868	65	76
	D1S2793	66	77
	D1S206	80	82
	D1S495	82	87
	D1S2726	68	75
	D1S252	77	81
	D1S498	74	82
	D1S2635	73	87
	D1S484	70	64
	D1S2878	80	84
	D1S196	58	74
	D1S452	60	75
	D1S218	82	83
	D1S2818	65	70
	D1S238	80	86
	D1S2877	67	71
	D1S412	74	70
	D1S413	68	76
	D1S249	70	87
	D1S2692	88	86
	D1S245	55	81
	D1S425	54	81
	D1S227	60	69
	D1S213	84	86
	D1S2833	83	82
	D1S2709	60	72
	D1S2800	74	77
	D1S2850	74	64
	D1S2670	79	83
	D1S2785	86	76
	D1S304	59	60
	D1S2842	65	76
	D1S423	65	60
	D1S2836	71	79

Table 1 (Continued)

Chr	Marker	Het	
		Twn	Cau
2	D2S323	59	57
	D2S319	72	73
	D2S2166	58	85
	D2S2211	68	74
	D2S162	81	75
	D2S168	75	82
	D2S149	83	74
	D2S305	78	72
	D2S2150	66	78
	D2S165	86	85
	D2S352	65	83
	D2S367	87	86
	D2S2163	76	76
	D2S2259	60	79
	D2S391	70	79
	D2S2369	53	69
	D2S337	85	88
	D2S2368	84	83
	D2S303	74	65
	D2S2110	75	79
	D2S286	80	66
	D2S2333	83	82
	D2S388	73	78
	D2S2216	65	76
	D2S2264	62	77
	D2S293	78	84
	D2S160	74	78
	D2S347	68	80
	D2S2271	69	83
	D2S112	71	71
	D2S151	79	82
	D2S2241	71	77
	D2S142	71	76
	D2S306	70	70
	D2S2330	79	81
	D2S335	84	79
	D2S2188	75	67
	D2S364	75	80
	D2S118	77	79
	D2S117	85	82
	D2S2358	63	81
	D2S325	74	82
	D2S2321	58	76
	D2S2361	75	76
	D2S2382	47	81
	D2S163	78	80
	D2S126	82	82
	D2S133	81	69
	D2S2354	56	81
	D2S362	64	77
	D2S396	89	83
	D2S2344	77	78
	D2S206	82	80
	D2S2202	55	68
	D2S338	85	81
	D2S2285	65	64
	D2S125	83	82
	D2S140	75	78
3	D3S1270	57	75
	D3S1297	74	82
	D3S3630	81	82
	D3S3706	47	64
	D3S1304	80	80
	D3S3728	63	68
	D3S1597	73	80

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
	D3S1263	89	86
	D3S2338	77	86
	D3S3659	78	65
	D3S1266	71	73
	D3S1609	55	64
	D3S3567	57	70
	D3S1277	68	82
	D3S3521	80	83
	D3S3685	82	89
	D3S1581	77	88
	D3S1289	80	81
	D3S1300	83	82
	D3S1600	73	72
	D3S1285	74	73
	D3S3697	69	88
	D3S1566	85	84
	D3S3681	81	83
	D3S1276	50	72
	D3S3634	72	78
	D3S1603	66	71
	D3S1271	63	73
	D3S3574	77	85
	D3S2496	64	77
	D3S1278	77	87
	D3S1558	46	78
	D3S1267	76	88
	D3S3606	87	82
	D3S1292	89	85
	D3S3637	88	90
	D3S1309	78	76
	D3S1569	76	80
	D3S1593	77	77
	D3S1555	71	79
	D3S1279	76	85
	D3S3668	82	83
	D3S1614	74	83
	D3S3725	85	84
	D3S1565	76	64
	D3S3715	63	79
	D3S3609	86	87
	D3S3592	77	80
	D3S1262	71	80
	D3S3686	70	80
	D3S1580	81	84
	D3S1601	80	85
	D3S2748	76	74
	D3S1265	77	86
4	D4S2936	65	83
	D4S412	71	77
	D4S3023	79	69
	D4S2935	64	62
	D4S403	61	77
	D4S419	65	77
	D4S2994	53	82
	D4S3022	89	88
	D4S391	81	85
	D4S2912	79	67
	D4S1587	72	74
	D4S405	73	86
	D4S2971	74	80
	D4S428	81	76
	D4S1592	83	72
	D4S398	79	82
	D4S3004	63	80
	D4S392	79	82

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
	D4S3042	79	84
	D4S2964	73	76
	D4S1534	81	77
	D4S2460	57	72
	D4S414	78	89
	D4S2986	69	80
	D4S1572	81	84
	D4S406	68	87
	D4S402	72	91
	D4S1615	57	74
	D4S1575	28	65
	D4S1579	32	65
	D4S424	66	83
	D4S1586	70	77
	D4S2962	76	82
	D4S413	60	85
	D4S3046	71	76
	D4S2952	67	58
	D4S1597	28	76
	D4S1595	71	72
	D4S1539	41	68
	D4S415	75	80
	D4S2920	70	68
	D4S1535	78	77
	D4S2924	75	72
	D4S3051	71	51
	D4S426	69	76
	D4S2930	75	80
5	D5S1981	65	73
	D5S417	72	75
	D5S2088	67	83
	D5S406	67	79
	D5S1953	45	77
	D5S630	86	89
	D5S416	69	77
	D5S2031	59	75
	D5S419	85	81
	D5S1993	74	78
	D5S674	75	78
	D5S426	77	80
	D5S2021	62	58
	D5S418	83	80
	D5S407	85	86
	D5S1969	85	86
	D5S427	62	84
	D5S647	76	82
	D5S424	60	76
	D5S672	65	63
	D5S641	83	77
	D5S428	72	76
	D5S618	84	80
	D5S644	80	85
	D5S495	77	82
	D5S433	67	86
	D5S2084	64	71
	D5S2027	60	78
	D5S2055	79	84
	D5S471	73	76
	D5S2115	70	76
	D5S2011	81	86
	D5S436	69	83
	D5S2090	62	83
	D5S410	52	79
	D5S2049	60	77
	D5S422	81	84

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
6	D5S2040	80	78
	D5S2050	72	71
	D5S400	84	82
	D5S1960	72	80
	D5S2073	85	79
	D5S408	78	73
	D6S1617	82	86
	D6S1574	73	84
	D6S309	78	83
	D6S470	67	80
	D6S1721	65	78
	D6S259	81	74
	D6S289	79	79
	D6S422	64	77
	D6S1660	66	77
	D6S276	77	83
	D6S291	94	73
	D6S1610	78	84
	D6S1575	84	82
	D6S1549	64	62
	D6S282	86	88
	D6S1650	69	80
	D6S452	78	85
	D6S272	76	73
	D6S1573	78	79
	D6S257	86	87
	D6S460	80	81
	D6S1609	78	81
	D6S462	52	68
	D6S300	66	77
	D6S1671	87	89
	D6S434	75	86
	D6S1698	81	82
	D6S287	63	85
	D6S262	77	82
	D6S1656	71	74
	D6S270	71	77
	D6S292	83	83
	D6S1569	65	79
	D6S308	64	75
D6S1654	71	82	
D6S441	80	86	
D6S1577	70	87	
D6S1581	57	72	
D6S305	79	84	
D6S1599	88	70	
D6S1719	81	75	
D6S264	48	70	
D6S1697	34	55	
D6S446	45	62	
D6S281	82	68	
7	D7S531	72	77
	D7S517	78	83
	D7S641	68	72
	D7S513	91	83
	D7S2464	58	66
	D7S664	56	71
	D7S2557	69	74
	D7S507	86	89
	D7S493	68	88
	D7S516	74	76
	D7S2496	88	71
	D7S2252	79	87
	D7S484	78	74
	D7S510	75	77

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
8	D7S691	63	74
	D7S2427	67	81
	D7S519	73	81
	D7S506	83	88
	D7S502	87	84
	D7S2476	53	64
	D7S1870	63	75
	D7S669	85	80
	D7S630	77	73
	D7S657	83	81
	D7S515	75	82
	D7S2459	69	77
	D7S486	78	81
	D7S530	66	78
	D7S640	88	85
	D7S2560	76	86
	D7S684	84	81
	D7S2513	80	74
	D7S661	82	75
	D7S636	93	90
	D7S483	81	83
	D7S798	75	84
	D7S2465	80	83
	D7S2423	44	72
	D8S264	85	83
	D8S277	81	73
	D8S503	54	74
	D8S520	71	78
	D8S550	75	87
	D8S552	76	79
	D8S1827	56	67
	D8S549	49	63
	D8S258	68	70
	D8S1734	60	67
	D8S1771	62	75
	D8S1820	30	74
	D8S1769	61	83
	D8S505	78	79
	D8S532	76	84
	D8S285	74	78
D8S260	81	81	
D8S543	69	75	
D8S1705	76	84	
D8S275	50	76	
D8S270	69	79	
D8S1778	83	87	
D8S1762	71	77	
D8S1784	72	67	
D8S1779	75	76	
D8S514	70	77	
D8S1799	80	84	
D8S1720	66	81	
D8S284	83	83	
D8S256	77	84	
D8S272	80	81	
D8S1837	80	80	
D8S1743	45	82	
D8S1836	82	84	
9	D9S1858	69	58
	D9S1779	52	64
	D9S288	84	84
	D9S1810	38	78
	D9S286	80	88
	D9S168	66	76
	D9S269	56	75

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
	D9S285	59	78
	D9S157	78	84
	D9S171	31	79
	D9S259	43	68
	D9S169	80	84
	D9S161	54	78
	D9S1853	64	64
	D9S1817	82	88
	D9S1874	85	83
	D9S273	61	74
	D9S175	72	85
	D9S1834	55	70
	D9S1674	81	73
	D9S1843	70	81
	D9S167	82	87
	D9S1812	69	68
	D9S283	70	80
	D9S1796	81	79
	D9S1781	80	79
	D9S287	67	67
	D9S1690	74	78
	D9S271	67	65
	D9S1677	88	81
	D9S289	81	75
	D9S1776	71	84
	D9S1682	63	68
	D9S290	69	83
	D9S164	82	80
	D9S1818	68	72
	D9S1826	79	69
	D9S158	48	69
	D9S1838	78	83
10	D10S249	77	75
	D10S1745	76	85
	D10S591	57	71
	D10S189	75	73
	D10S1649	78	84
	D10S547	49	74
	D10S570	77	81
	D10S191	84	82
	D10S1653	78	78
	D10S548	63	70
	D10S197	76	75
	D10S213	79	83
	D10S208	79	80
	D10S1780	72	66
	D10S578	62	66
	D10S196	68	79
	D10S1790	68	84
	D10S1652	66	78
	D10S581	84	80
	D10S210	81	79
	D10S537	79	83
	D10S580	60	73
	D10S1730	45	83
	D10S1686	72	86
	D10S1765	79	84
	D10S185	77	77
	D10S1709	76	74
	D10S192	84	78
	D10S597	50	64
	D10S1693	76	80
	D10S587	80	80
	D10S1656	79	75
	D10S575	75	63

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
	D10S217	84	82
	D10S1655	57	68
	D10S1651	59	80
	D10S212	28	72
11	D11S1363	69	59
	D11S4046	77	86
	D11S4146	81	70
	D11S1760	85	75
	D11S1338	71	74
	D11S4149	52	77
	D11S4116	82	80
	D11S902	81	80
	D11S4190	80	82
	D11S915	81	81
	D11S904	74	83
	D11S914	57	71
	D11S935	73	73
	D11S4102	62	77
	D11S905	79	75
	D11S4191	89	87
	D11S987	82	82
	D11S4162	52	64
	D11S1314	82	78
	D11S4207	83	89
	D11S937	83	88
	D11S901	66	82
	D11S4147	65	81
	D11S4175	85	89
	D11S917	65	80
	D11S898	33	85
	D11S4090	83	83
	D11S908	43	76
	D11S4127	72	71
	D11S925	79	84
	D11S4094	70	80
	D11S4151	53	79
	D11S912	78	80
	D11S4126	63	59
	D11S1320	44	68
	D11S968	62	81
12	D12S352	78	73
	D12S1725	74	79
	D12S99	83	84
	D12S336	74	82
	D12S1697	78	83
	D12S358	78	76
	D12S364	84	87
	D12S310	63	69
	D12S1682	82	78
	D12S1617	84	80
	D12S1640	70	54
	D12S345	85	87
	D12S1663	53	78
	D12S85	81	69
	D12S368	61	81
	D12S83	83	82
	D12S313	79	79
	D12S326	69	80
	D12S1708	61	72
	D12S351	74	75
	D12S346	73	84
	D12S78	82	92
	D12S1613	59	62
	D12S1583	77	88
	D12S1646	81	96

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
13	D12S79	60	72
	D12S1718	40	44
	D12S86	72	90
	D12S304	72	56
	D12S324	64	69
	D12S1675	74	74
	D12S1659	52	79
	D12S367	74	76
	D12S1723	79	67
	D12S1638	66	69
	D13S1236	85	67
	D13S175	71	76
	D13S1243	72	78
	D13S1304	66	73
	D13S217	78	68
	D13S289	68	67
	D13S171	64	73
	D13S219	73	64
	D13S218	64	66
	D13S263	78	84
	D13S153	90	81
	D13S1320	39	76
	D13S1296	85	86
	D13S156	78	80
	D13S1306	79	85
	D13S170	85	90
	D13S265	61	70
	D13S1241	81	82
	D13S159	77	90
	D13S158	76	82
	D13S1322	28	63
	D13S173	74	82
	D13S1265	83	80
D13S285	86	81	
D13S293	59	50	
D14S261	64	75	
D14S1023	74	82	
D14S283	78	81	
D14S990	77	85	
D14S972	67	75	
D14S275	53	70	
D14S1040	68	73	
D14S70	74	75	
D14S75	83	78	
D14S288	88	83	
D14S276	76	76	
D14S980	87	87	
D14S274	52	72	
D14S63	73	76	
D14S258	65	79	
D14S1036	71	79	
D14S74	75	79	
D14S1037	63	82	
D14S68	79	91	
D14S1044	63	65	
D14S280	71	68	
D14S1050	75	81	
D14S1054	74	76	
D14S65	76	79	
D14S985	73	76	
D14S1051	20	32	
D14S292	72	73	
D14S1007	73	77	
D15S128	80	79	
D15S986	78	71	

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
16	D15S975	77	45
	D15S1002	78	79
	D15S1019	64	59
	D15S165	31	80
	D15S1007	82	87
	D15S1040	77	77
	D15S118	67	76
	D15S1012	58	72
	D15S994	70	73
	D15S978	83	83
	D15S1016	83	88
	D15S117	71	79
	D15S1033	78	70
	D15S1036	72	80
	D15S153	81	87
	D15S988	74	80
	D15S131	77	84
	D15S205	87	88
	D15S979	82	85
	D15S127	80	87
	D15S130	77	71
	D15S1014	73	73
	D15S212	78	71
	D15S120	75	75
	D16S521	61	71
	D16S3027	83	88
	D16S423	84	75
	D16S418	80	83
	D16S404	75	82
	D16S3075	82	80
	D16S3102	74	69
	D16S500	77	80
	D16S3103	44	82
D16S3041	83	82	
D16S3046	74	74	
D16S403	74	86	
D16S3068	71	78	
D16S3100	69	67	
D16S3136	59	70	
D16S415	70	74	
D16S3034	58	65	
D16S3140	82	82	
D16S3057	75	73	
D16S514	68	82	
D16S503	56	81	
D16S3066	62	80	
D16S515	85	80	
D16S3049	69	77	
D16S516	60	73	
D16S3040	74	74	
D16S505	86	76	
D16S3091	83	74	
D16S520	80	84	
D17S849	75	67	
D17S831	87	82	
D17S1828	77	80	
D17S1876	51	84	
D17S938	84	76	
D17S1791	60	85	
D17S1852	81	87	
D17S799	68	68	
D17S921	67	72	
D17S1857	44	64	
D17S1824	79	83	
D17S798	55	80	

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
18	D17S927	74	77
	D17S1868	82	73
	D17S1795	49	72
	D17S787	80	81
	D17S957	50	45
	D17S944	42	75
	D17S1816	83	83
	D17S949	80	80
	D17S1862	88	83
	D17S1807	83	86
	D17S785	74	83
	D17S1847	76	66
	D17S836	71	63
	D17S784	63	77
	D17S928	83	76
	D18S59	81	82
	D18S476	57	76
	D18S63	68	80
	D18S1132	81	67
	D18S452	79	83
	D18S464	59	65
	D18S1150	60	71
	D18S53	80	80
	D18S453	73	82
	D18S1107	74	72
	D18S478	61	64
	D18S56	72	75
	D18S1102	76	79
	D18S468	74	80
	D18S450	71	79
	D18S474	80	82
	D18S1127	86	87
D18S1129	78	85	
D18S64	80	75	
D18S1147	85	85	
D18S68	81	80	
D18S465	75	78	
D18S61	82	88	
D18S469	60	65	
D18S1161	75	83	
D18S462	69	70	
D18S70	81	84	
19	D19S886	69	64
	D19S209	80	78
	D19S894	83	77
	D19S216	59	76
	D19S884	82	86
	D19S865	84	89
	D19S221	83	87
	D19S226	87	86
	D19S566	76	87
	D19S931	64	78
	D19S414	61	78
	D19S220	87	87
	D19S420	76	79
	D19S903	80	79
	D19S902	84	80
	D19S904	50	65
	D19S571	42	83
	D19S888	75	82
	D19S921	80	78
	D19S572	85	81
D19S418	55	66	
D19S210	62	75	
20	D20S117	85	85
	D20S906	31	78

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
21	D20S842	87	86
	D20S889	77	84
	D20S882	75	72
	D20S846	77	78
	D20S115	52	67
	D20S851	82	74
	D20S186	86	86
	D20S898	51	81
	D20S112	73	82
	D20S912	75	81
	D20S871	83	89
	D20S195	76	81
	D20S107	77	80
	D20S861	62	67
	D20S119	76	83
	D20S178	75	83
	D20S891	85	85
	D20S887	83	83
	D20S196	87	81
	D20S902	73	76
	D20S100	75	77
	D20S171	78	78
	D20S173	65	67
	D21S1911	68	69
	D21S1904	78	53
	D21S1256	63	65
	D21S1899	66	86
	D21S1884	72	59
	D21S1922	36	65
	D21S1914	80	86
	D21S263	83	75
	D21S1919	79	82
D21S1255	62	80	
D21S1252	79	80	
D21S266	84	59	
D22S420	73	77	
D22S539	56	58	
D22S1174	80	74	
D22S315	81	78	
D22S1154	53	73	
D22S1163	65	75	
D22S280	77	82	
D22S277	86	85	
D22S283	82	89	
D22S423	81	82	
D22S274	79	77	
D22S1170	72	64	
D22S1169	73	79	
X	DXS1060	85	84
	DXS1223	52	75
	DXS8051	84	88
	DXS7108	62	75
	DXS1224	55	61
	DXS987	80	83
	DXS8019	87	80
	DXS7593	77	70
	DXS1226	84	84
	DXS1061	65	73
	DXS1214	75	79
	DXS8090	71	81
	DXS8102	42	65
	DXS1068	65	79
	DXS8015	50	74
	DXS993	68	79
22	DXS8080	42	68
	DXS8083	43	74

Table 1 (Continued)

Chr	Marker	Het	
		TwN	Cau
	DXS1055	68	72
	DXS1039	68	61
	DXS991	78	80
	DXS1216	46	61
	DXS986	89	77
	DXS1196	72	79
	DXS1217	51	62
	DXS990	65	74
	DXS8077	86	60
	DXS8020	67	78
	DXS1106	27	67
	DXS1059	67	72
	DXS8088	13	62
	DXS8055	21	65
	DXS8064	37	56
	DXS8067	73	70
	DXS1001	81	82
	DXS8009	73	52
	DXS1047	82	81
	DXS1062	75	74
	DXS984	32	72
	DXS1205	74	72
	DXS1227	54	73
	DXS8106	69	69
	DXS8043	76	80
	DXS8091	55	78
	DXS8045	60	49
	DXS998	44	57
	DXS8069	68	62
	DXS1073	64	80

Table 2 Comparison of heterozygosities at 811 test loci between Taiwanese and Caucasians. *ABI* Applied Biosystems, Inc., Foster City, CA, USA

Observed heterozygosity (%)	No. of markers in each category among Taiwanese tested	No. of markers in each category in <i>ABI</i> (Caucasian)
11–20	1	0
21–30	7	0
31–40	14	1
41–50	28	4
51–60	76	19
61–70	168	103
71–80	302	320
81–90	212	356
91–100	3	8

Table 3 Comparison of averaged ethnic heterozygosities between autosome and sex chromosome. *VITA* Vita Genomics, Inc., Wugu Shiang, Taiwan, *ABI* Applied Biosystems, Inc., Foster City, CA, USA

	Taiwanese (<i>VITA</i>)	Caucasian (<i>ABI</i>)
CH 1–22	0.72	0.77
CH X	0.63	0.72

Acknowledgments We thank Dr. Ellson Chen for advice, Julia Kuei-Ting Yu for administrative support, and Arthur Fen and Peter Chen for IT support. This study was funded by an internal research grant at Vita Genomics, Inc.

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