

Supplementary Data: Table 1

ID Number	Coriell Order Number
N001	NA11197
N002	NA11198
N003	NA11199
N004	NA11200
N005	NA11201
N006	NA10975
N007	NA10976
N008	NA10978
N009	NA10979
N010	NA11776
N011	NA10965
N012	NA10966
N013	NA10967
N014	NA10968
N015	NA10969
N016	NA10970
N017	NA10971
N018	NA10972
N019	NA10973
N020	NA17392
N021	NA17393
N022	NA17394
N023	NA17395
N024	NA17396
E001	NA12560
E002	NA12547
E003	NA10845
E004	NA10853
E005	NA10860
E006	NA10830
E007	NA10842
E008	NA10851
E009	NA07349
E010	NA10857
E011	NA10858
E012	NA10848
E013	NA12548
E014	NA10844
E015	NA10854
E016	NA10861
E017	NA10831
E018	NA10843
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E020	NA07348
E021	NA10852
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E023	NA07019

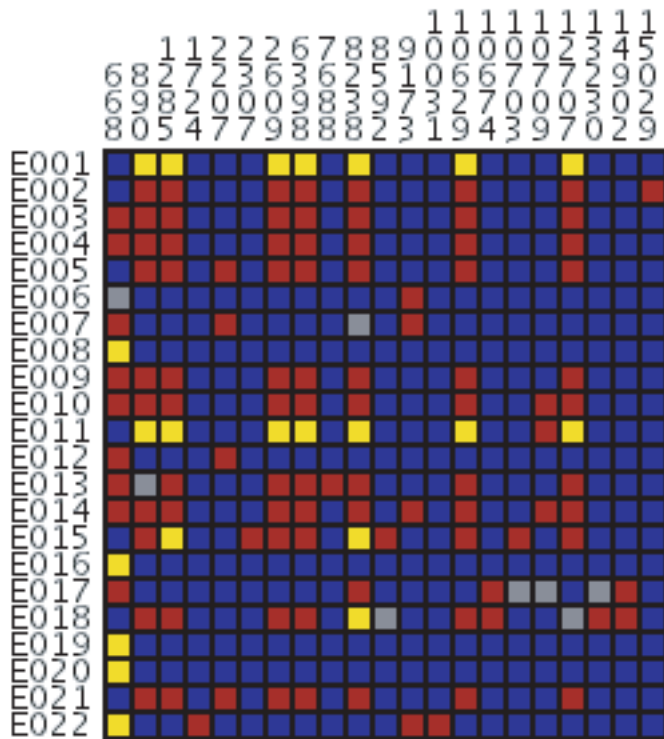
"N" samples represent Indigenous American Ancestry  
"E" samples represent European Ancestry

## Supplementary Data Table 2: Flanking Sequences in hGSTO1-1 polymorphisms

Site	hGSTO1-1 POLYMORPHISMS
668	...AAGCTAGCTTAGGGG (A/G) AGCAAAACAGGCTTC
890	...TTTGGATGTAATG (A/G) ACTGTTATCTCTGGA
1218	...CCATTATCTGAGGT (T/C) GATAATATCCAGGTT
1285	...ATCCTACAGGTGACG (A/G) TAGGGACAGAGGCC
1724	...TAGTGCTTGGTGAAT (C/T) TGCATTTTTACAAGA
1817	...CCTAGACCTGTCTTT (G/A) TCCCATACTGGGAA
2075	...AGCTGAACAGGAGCC (T/A) TTGGAGAGAACGCTC
2207	...GTCAGGGTCAGGGTC (A/G) GACGTGGAGCCCCGT
2307	...CTCCCGTGGGTGCA (A/G) CCCTGGCCAGCGAG
2609	..TCGGCAGCCCCGGC (GGC/*) GCATGTCGAGGCTG
6198	...ACACTTCTCAGGCTG (G/C) GCATGGTAGCTCAG
6398	...CTGCAGTGAGCTGCG (G/A) TCAAGCCACTGTACT
7062	...GAAGGATCTAGGCA (G/A) ACTCCTAAATTTGGG
7688	...CAGATTCTTCCCCT (T/C) CTCCTGTGCTGCTG
7964	...ATTACTTTGCCTCTC (C/G) GTTCATCATTGGTAA
8238	...CAAAGAAATGACTAA (C/A) AGATGTGTGTTTAGA
8592	...AGACACGAAGTCATC (A/G) ATACCAACCAAAAA
8963	...GAGAGGTGGCTTAT (G/A) TACATATGACCCTGC
9173	...GCCACTTAAGAAATA (A/C) ATTTTATAGAGGAGCA
9963	...TGTCCTTATCCCAAG (C/A) CTGTTTGTCCGCCT
9992	...CTCCCAATAATTCTA (T/C) GAGCCACTCAGTCTC
10031	...AAGTTGTGTTGGCC (G/A) GGCGTGGTGGCTCAA
10629	...ATAAAGAACTATG (A/C) TGGCCTAAAAGAAGA
10674	...TACCAAGCTAGAGG (AGG/*) TAATTTTCTCCTA
10703	...CCTAGCTATCATCAG (A/G) GTAAA [C/T] GATAACTAT
10709	TATCATCAG [A/G] GTAAA (C/T) GATAACTATATCTAC
11227	...TGTCCTTGGCCTTG (A/G) AATATTTTCATTCATG
12707	...GCAGACTGTGCATT (C/T) ATATTGAAAAGTTAA
13230	...ATTCTCTGGGTGTA (T/C) AGTGTATTGCATTT
14902	...ATGGCAGCCATGAAG (G/A) AAGATCCCACAGTCT
14987	...AGAACAGCCCTGAGG (C/T) CTGTGACTATGGGCT
15029	...AGGAGTCAGCAATAA (A/T) GCTAT [G/C] TCTGATATT
15035	CAGCAATAA [A/T] GCTAT (G/C) TCTGATATTTTCCTT

### Supplementary Data: Table 3: Flanking Sequences in hNP polymorphisms

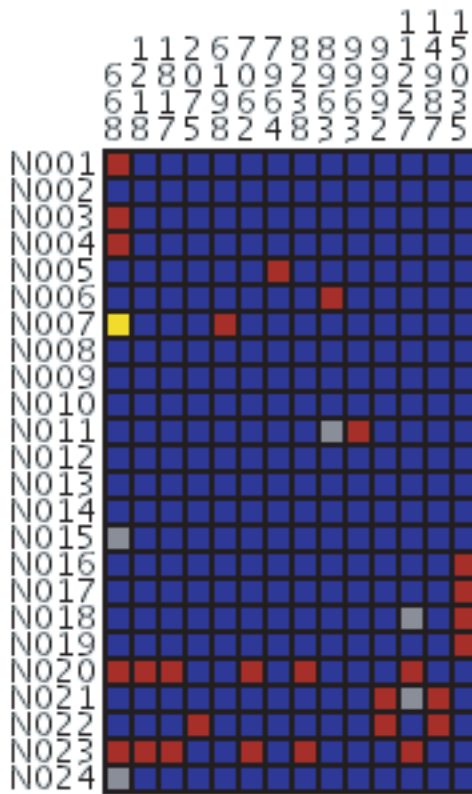
Site	hNP POLYMORPHISMS
208	.....ATTACTTTTAAATAG (C/T) CACACATGGCTAGTG
680	.....ATTGTGGAATATTTT (T/C) AATTTTCAGAGGAAA
1014	.....GGCTCAAACCCAGGC (A/G) GCAGAGATTGCATG
1088	.....AAACCCCTGTCTCAA (A/T) ATATAT[A/G]TATATATA
1095	.....GTCTCAA[A/T]ATATAT (A/G) TATATATAAGACAA
1671	.....ATATAAATTTTTTTT (T/A) AATTTTTTAATTA
1748	TTAAATGTAAATGT (AAATTTAAAGTA/*) AATTTAAAGTAAAA
2368	.....GGCAGAAGTTTAGG (G/A) CTGGGAAGAAGCTCTG
2544	.....GAACAGACCCGCGA (G/A) CCTGTCTCAGTTCAG
3207	.....CTAAGTGGAGACGGA (A/C) ATCAGTCACCGAAT
3253	.....GCTCACTCCCCAC (C/T) CCACGCCCTTGAAAA
3679	TCACACCTCATGCG (ACACCTCATGCG/*) CACCTCATTGCCACC
4008	.....GCCTATAAGATAGAT (G/A) GGGCCAATTTACATC
4303	.....AGCTAGGACTACAGG (G/C) GCCCGCCACCACGCC
4557	.....TGTGTGTGTGTGTGT (G/T) TTTTTATAGGGTCT
4594	.....GTCACAGGCTGGAG (T/A) GCCAGAATCTGTTTT
5328	.....GTGCCAGCTTCTCCG (T/G) CCTGTCTGCTCAGT
5483	.....ATGGCTTCTGTCTCA (C/T) ACTAAGCACCAGCT
5574	.....CAGATCTTTGACTAC (A/G) GTGAAATCCCAACT
5594	.....AATCCCAACTTTCC (C/T) CGAAGTACAGTACT
5703	.....ACTCCTTGACCTAGC (A/G) TTTCACTGAAGACAA
5766	.....GTCAGAGTACTTTA (G/A) GAGATGCCTCTAGCA
5802	.....CCATAAGAGACAGG (A/G) CATGTGTGTCTCAGT
6037	.....TTTTTAAACTCTTT (A/G) ACACAAGACTGGAAG
6272	.....TTATTACTGTTTTG (TTTTG/*) TTTGTTTTGTTTTT
6386	.....GCCGTCTATTAGAAG (A/T) GACTGCCAGATAAAA
6563	.....CAGTAGCCTCTTCTT (T/A) AAGAAGCCAGAGTAA
6586	.....CAGAGTAAGTATACT (A/G) TGAGCTTGCTTGCTG
6631	.....GTAATTAAGTTAGGG (C/A) AATAGATAAGAATAC
6688	.....AAGAGTCTATAATT (A/G) CTGCATTCACGTAC
6938	.....CCTGGCCTGTGATC (C/T) GCCTGTCTTGGGCTC
6986	.....CAGGTGTGAGACACC (G/A) CACCTGGCCTATTTT
7036	.....TTTACAGGGGTACAA (T/C) GCAGTTTTGTTATAT
7424	.....TATTTGTATAATTAT (G/T) AGTAATGCCTGGCTC
7717	.....TGGAAGGTAAGTCAG (A/G) GGGATAGGTCGGTT
8254	.....TATGAGGCAGAGGGC (T/A) CTCAGTACCTGGAAA
8477	.....CAGGCCTCATGGAG (A/T) GAGAGGATCTGATTT
8506	.....TTCAGGGAAGGGTGA (A/G) TTAAGTACTTATT
8538	.....AAATACAACCTGGT (A/G) GATTGGTGTAGCAT
8845	.....TGTCCTTGRACTCG (C/T) GACCTCAGGTAATCC
8883	.....TTGGCCTCCTAAGT (G/C) CTGGCATTACAGGCC
8912	.....CGGACGCACTGTGC (C/T) TGGCCAATGTGATGA
9293	.....TTTATTTTTGAGCC (G/A) AGGTCTTTTATGTT
9400	.....TGAACCACTGCACCC (G/A) GCCATCTTTGGATGT
9987	.....TCATTCCTGTCTTTT (C/T) TTACACAAGAGCTGG
10328	.....TGCTTCTCAGACAAG (C/T) AGTAGGAAGTACGAG
10461	.....CTTGATTGCCACTTC (C/T) GTCAGGCTGGTCTCG
10544	.....TGAATTAGTTCACCTG (G/A) TTAGCCTCTTCCTTA



Supplemental Figure 1

- Homozygote-Common Allele
- Homozygote-Rare Allele
- Heterozygote
- Undetermined

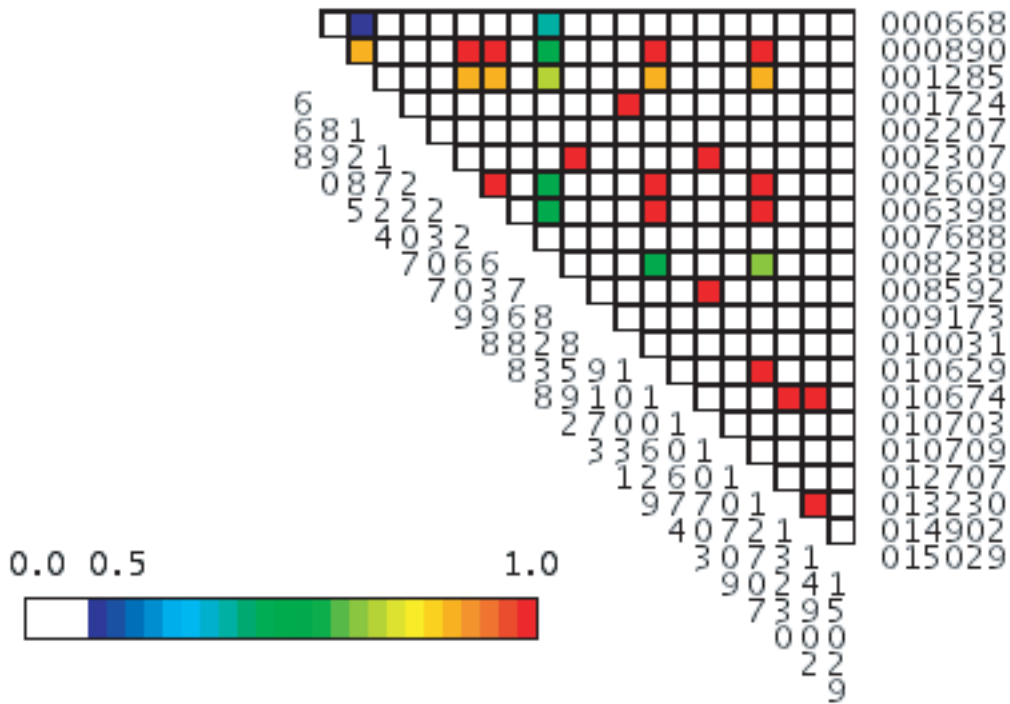
Supplementary Data Figure 1: Visual Genotype(Rieder et al. 1998) view of all genotypes in the EA group for hGSTO1-1. The colored box for each individual at a particular site indicates genotype. Legends for each genotype are shown in the figure.



Supplemental Figure 2

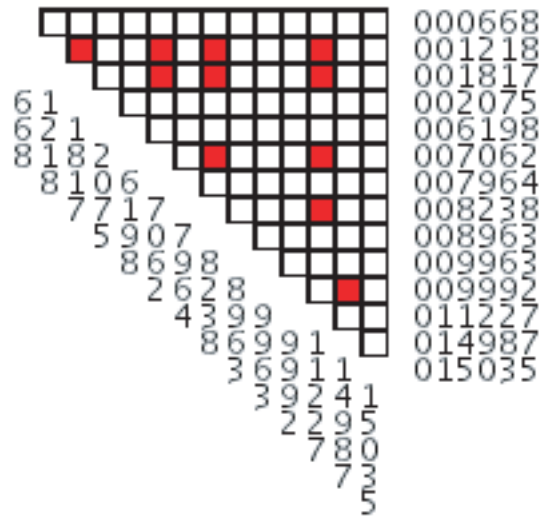
- Homozygote-Common Allele
- Homozygote-Rare Allele
- Heterozygote
- Undetermined

Supplementary Data Figure 2: Visual Genotype(Rieder et al. 1998) view of all genotypes in the IA group for hGSTO1-1. The colored box for each individual at a particular site indicates genotype. Legends for each genotype are shown in the figure.



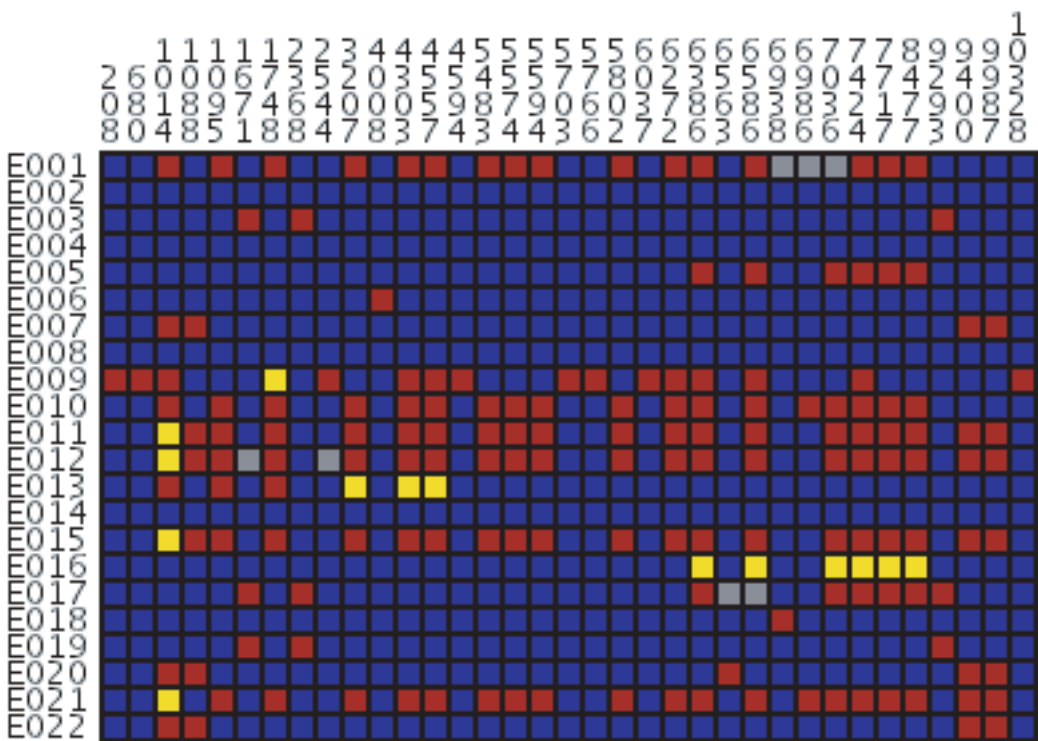
Supplemental Figure 3

Supplementary Data Figure 3: Pairwise linkage disequilibrium (LD), calculated as  $r^2$ , for hGSTO1-1 polymorphisms in the EA group. LD values are shown graphically, legends for value ranges are included in the figure. Graphic plots were generated using the UW-FHRC website.(UW-FHRC 2003)



### Supplemental Figure 4

Supplementary Data Figure 4: Pairwise linkage disequilibrium (LD), calculated as  $r^2$ , for hGSTO1-1 polymorphisms in the IA group. LD values are shown graphically, legends for value ranges are included in the figure. Graphic plots were generated using the UW-FHRC website.(UW-FHRC 2003)

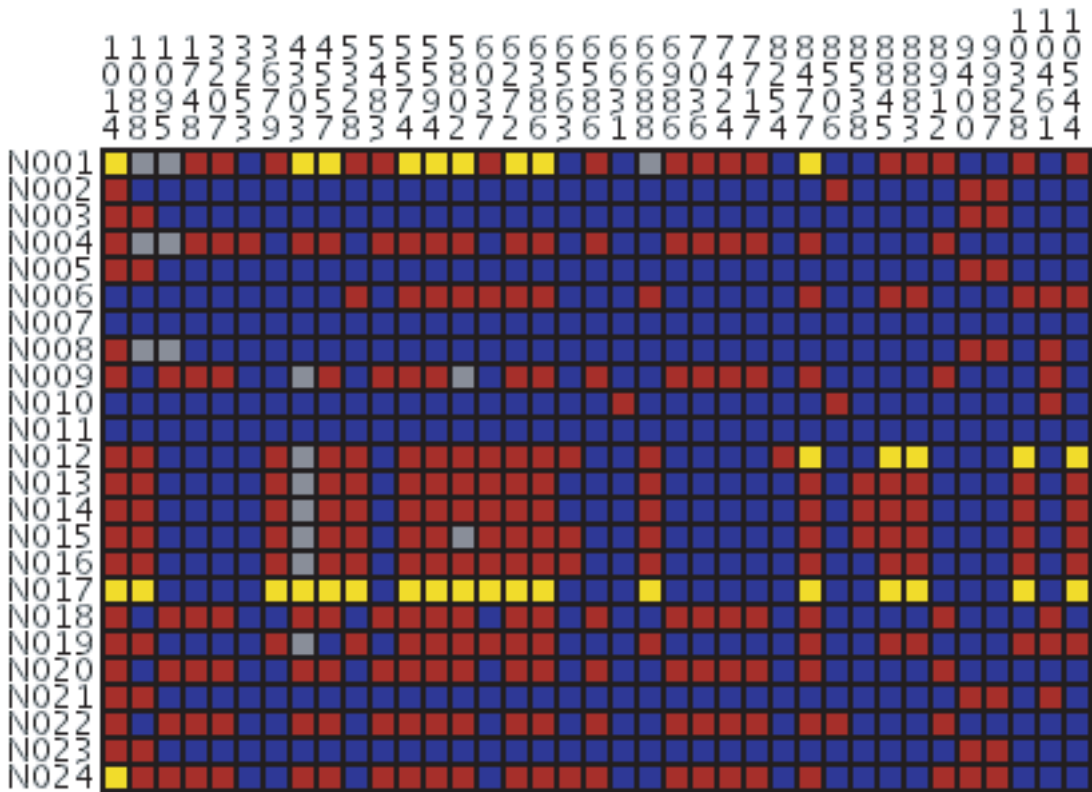


Supplemental Figure 5

- Homozygote-Common Allele
- Homozygote-Rare Allele
- Heterozygote
- Undetermined

Supplementary Data Figure 5: Visual Genotype(Rieder et al. 1998) view of all genotypes in the EA group for hNP. The colored box for each individual at a particular site indicates genotype. Legends for each genotype are shown in the figure.

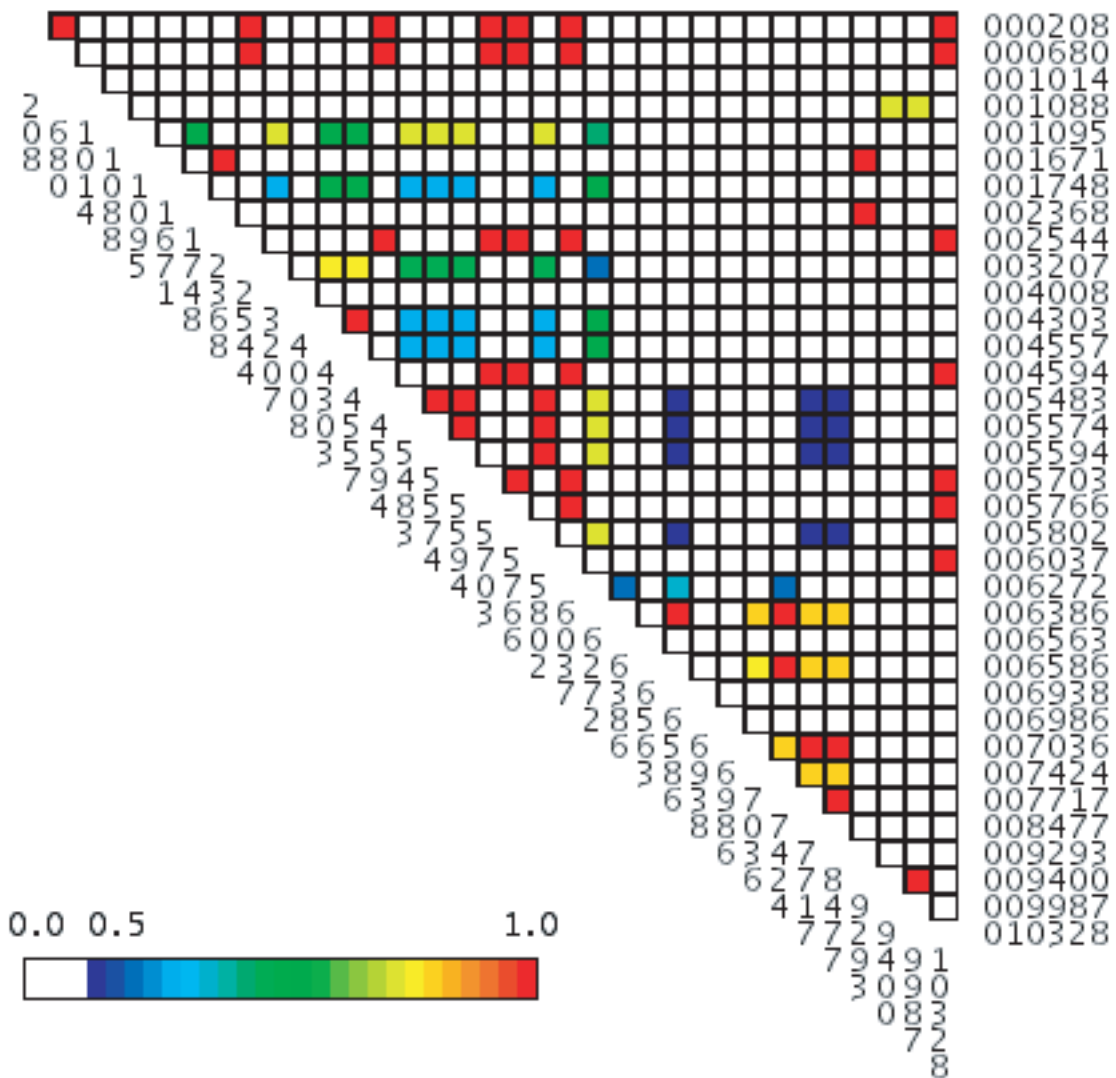




Supplemental Figure 6

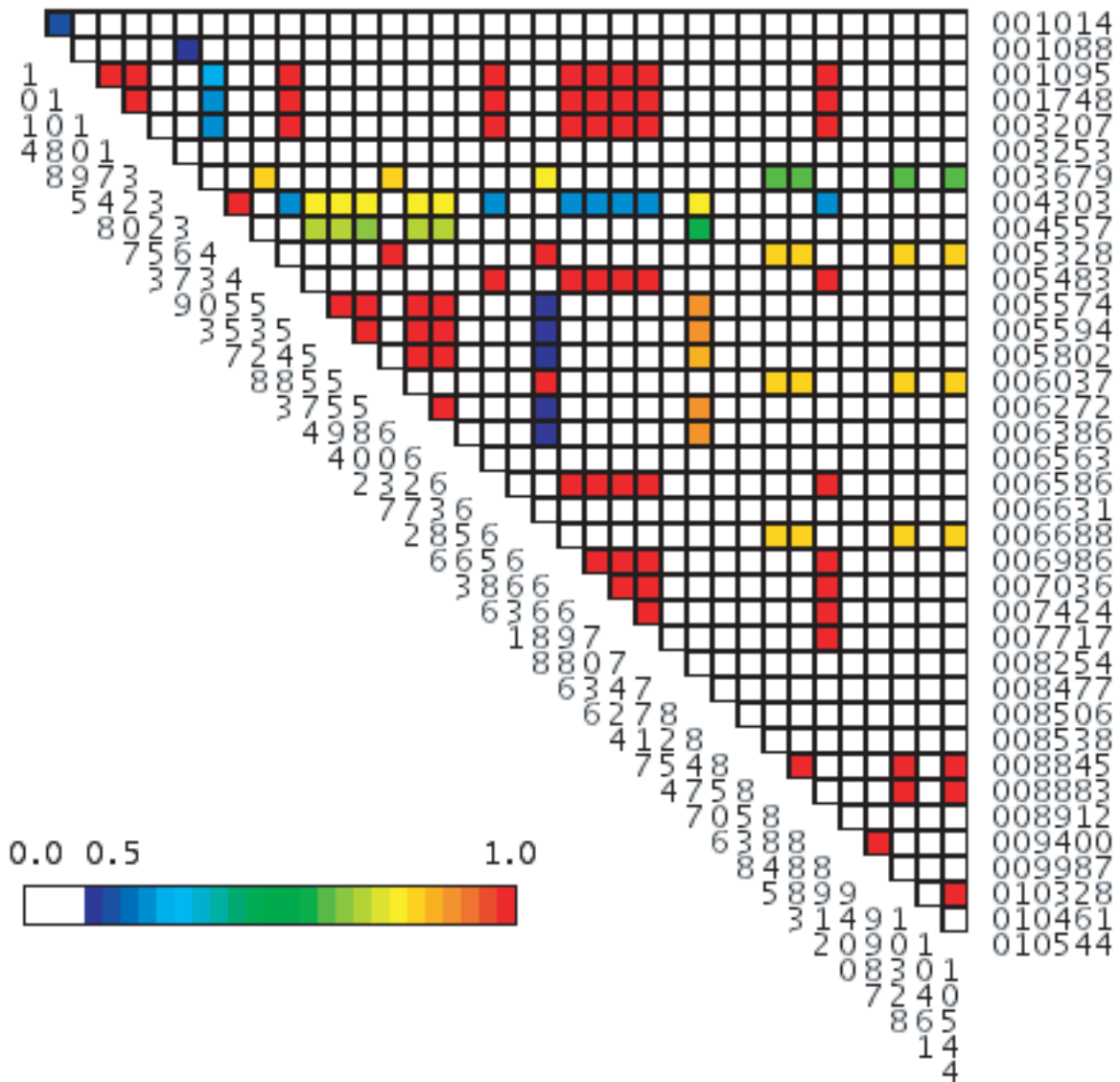
- Homozygote-Common Allele
- Homozygote-Rare Allele
- Heterozygote
- Undetermined

Supplementary Data Figure 6: Visual Genotype(Rieder et al. 1998) view of all genotypes in the IA group for hNP. The colored box for each individual at a particular site indicates genotype. Legends for each genotype are shown in the figure.



Supplemental Figure 7

Supplementary Data Figure 7: Pairwise linkage disequilibrium (LD), calculated as  $r^2$ , for hNP polymorphisms in the EA group. LD values are shown graphically, legends for value ranges are included in the figure. Graphic plots were generated using the UW-FHRC website.(UW-FHRC 2003)



Supplemental Figure 8

Supplementary Data Figure 8: Pairwise linkage disequilibrium (LD), calculated as  $r^2$ , for hNP polymorphisms in the IA group. LD values are shown graphically, legends for value ranges are included in the figure. Graphic plots were generated using the UW-FHRC website.(UW-FHRC 2003)