Supplementary Table S3. Expression Quantitative Trait Locus Relationships and High-Confidence Expression Quantitative Trait Locus Relationships in Each Integrated Set

	LD (r^2)	*AllCell_AllPop*	*LCL_CEU*	*LCL_YRI*	*LCL*	*Brain*	*Liver*	*Skin*	*Monocyte*
Unique exSNPs		548344	431758	23536	441971	9169	3588	84578	55943
Unique exGenes		15170	7869	2725	8918	1171	4295	2616	7186
Total unique eQTL relationships	0.8	240785	190902	17110	192093	1939	4914	14419	53656
HC unique eQTL relationships	0.8	18615	9585	257	9237	21	393	153	3562
HC unique exGenes	0.8	4252	2079	203	2245	16	393	91	857
Total unique eQTL relationships	0.5	169031	140831	14688	140481	1468	4803	6597	43065
HC unique eQTL relationships	0.5	8768	3990	208	3931	16	393	91	2923
HC unique exGenes	0.5	4252	2079	203	2245	16	393	91	857
Total unique eQTL relationships	0.3	133658	114892	12892	113989	1390	4750	3999	34118
HC unique eQTL relationships	0.3	5928	2802	203	2905	16	393	91	2282
HC unique exGenes	0.3	4252	2079	203	2245	16	393	91	857

LD(r^2) is the linkage disequilibrium threshold used for relating exSNPs. See text for dataset definitions.

eQTL, expression quantitative trait locus; LD, linkage disequilibrium.