S1 Table: **Clinical correlations of the genes identified in the genome-wide differential screen**. Indicated are the correlation coefficient (r) R squared (R^2) and significance level (p) values obtained by simple regression analyses between the mRNA expression levels for each indicated gene and the clinical variables reflecting the immune-phenotype (CD8 T lymphocyte and subset counts) and the iron overload profile defined by estimated total body iron stores (TBIS). For each clinical variable are indicated the ranges of values in the total HH patient population analysed.

			CD8 T cell subsets		
		Total CD8 T lymphocytes (0,09-0,73x10^6/ml)	**naive + central memory (0,044-0,459x10^6/ml)**	**effector memory (0,060-0,403x10^6/ml)**	**TBIS (1,5-17,4g)**
mRNA expression levels	**CCR7**	*n.s.*	*r=+0,95 R^2=91% (p=0,0032)*	*n.s.*	*r=-0,78 R^2=61% (p=0,0129)*
	LEF1	*n.s.*	*r=+0,79 R^2=63% (p=0,0601)*	*n.s.*	*r=-0,70 R^2=48% (p=0,0379)*
	ACTN1	*n.s.*	*r=+0,87 R^2=75% (p=0,0249)*	*n.s.*	*r=-0,79 R^2=62% (p=0,0115)*
	NAT13	*r=-0,79 R^2=62% (p=0,0070)*	*n.s.*	*r=-0,91 R^2=84% (p=0,0108)*	*n.s.*
	P2YR8	*r=-0,86 R^2=74% (p=0,0015)*	*n.s.*	*r=-0,88 R^2=78% (p=0,0191)*	*n.s.*
	FOSL2	*r=-0,70 R^2=49% (p=0,0243)*	*n.s.*	*r=-0,81 R^2=65% (p=0,0525)*	*n.s.*

n.s.=not statistically significant