Table S1. The time-line of the pull-down method

Day	Task	time
1	Harvest lymphoblastoid cells or blood drawing	30 min
	↓	
	Extraction of total RNA	45 min
	↓	
	cDNA synthesis by reverse transcription	110 min
	↓	
	The process of the pull-down method (details in Methods)	125 min
	01. Preparation of the annealing mixture containing cDNA (100 ng) and biotinylated RNA probe (100 pmol)	5 min
	↓	
	02. Heart-denaturation at 95 ^{o}C for 5 min	5 min
	↓	
	03. Annealing at room temperature	30 min
	↓	
	04. Add streptavidin-resin to the mixture	5 min
	↓	
	05. Incubation at 37 ^{o}C with gentle agitation	60 min
	↓	
	06. Wash the resin with wash buffer followed by centrifugation 3 times	10 min
	↓	
	07. Elution and collection of cDNA fragments from the resin by 5 mM biotin solution	10 min
	↓	
	SNP typing by the TaqMan SNP Genotyping assay	120 min
	Examination of trinucleotide repeat sequences by PCR and gel electrophoresis	

Table S2. CTG oligonucleotides used in this study

Name	5' - sequence -3'
(CTG)10	GGCCTAAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAAAAGCATG
(CTG)12	GGCCTAAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAAAAGCATG
(CTG)14	GGCCTAAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAAAAGCATG
(CTG)16	GGCCTAAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAAAAGCATG
(CTG)18	GGCCTAAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAAAAGCATG
(CTG)20	GGCCTAAAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAAAAGCATG

The CTG repeat sequences are underlined.

Table S3. Genotype of the cSNPs in the *HTT* gene in HD patients and healthy individuals

SNP ID	Exon	Alleles	Heterozygosity[a]	HD patients						Healthy individuals	
				C0142	C0160	C0166	C0221	C0222	HD995	N0001	N0002
rs363099	29	C/T	0.333	C/T	T/T	C/C	C/T	T/T	T/T	C/C	C/T
rs362331	50	C/T	0.494	C/T	C/C	C/T	C/C	C/C	C/C	T/T	C/T
rs362273	57	A/G	0.370	A/G	G/G	A/A	A/G	G/G	G/G	A/A	A/G
rs362272	61	A/G	0.374	A/G	A/A	G/G	A/G	A/A	A/A	G/G	A/G

[a] The heterozygosities are derived from the NCBI Entrez dbSNP database: http://www.ncbi.nlm.nih.gov/snp.

Table S4. Synthetic siRNA sequences targeting cSNP sites (1/2)

SNP ID (alleles)	siRNA name		5' - sequence - 3'[b]
rs363099 (C/T)	siRNAs targeting the C-allele		
	siRs099_C9	ss[a]	GGGUUUCUCCGCUCAGCCUUU
		as	AGGCUGAGCGGAGAAACCCUU
	siRs099_C10	ss	AGGGUUUCUCCGCUCAGCCUU
		as	GGCUGAGCGGAGAAACCCUUU
	siRs099_C11	ss	GAGGGUUUCUCCGCUCAGCUU
		as	GCUGAGCGGAGAAACCCUCUU
	siRs099_C12	ss	GGAGGGUUUCUCCGCUCAGUU
		as	CUGAGCGGAGAAACCCUCCUU
	siRNAs targeting the T-allele		
	siRs099_T9	ss	GGGUUUCUUCGCUCAGCCUUU
		as	AGGCUGAGCGAAGAAACCCUU
	siRs099_T10	ss	AGGGUUUCUUCGCUCAGCCUU
		as	GGCUGAGCGAAGAAACCCUUU
	siRs099_T11	ss	GAGGGUUUCUUCGCUCAGCUU
		as	GCUGAGCGAAGAAACCCUCUU
	siRs099_T12	ss	GGAGGGUUUCUUCGCUCAGUU
		as	CUGAGCGAAGAAACCCUCCUU
rs362331 (C/T)	siRNAs targeting the C-allele		
	siRs331_C8	ss	CCCUCAUCCACUGUGUGCAUU
		as	UGCACACAGUGGAUGAGGGUU
	siRs331_C9	ss	CCCUCAUCCACUGUGUGCAUU
		as	UGCACACAGUGGAUGAGGGUU
	siRs331_C10	ss	UCCCUCAUCCACUGUGUGCUU
		as	GCACACAGUGGAUGAGGGAUU
	siRs331_C11	ss	CUCCCUCAUCCACUGUGUGUU
		as	CACACAGUGGAUGAGGGAGUU
	siRs331_C12	ss	GCUCCCUCAUCCACUGUGUUU
		as	ACACAGUGGAUGAGGGAGCUU
	siRNAs targeting the T-allele		
	siRs331_T8	ss	CCCUCAUUCACUGUGUGCAUU
		as	UGCACACAGUGAAUGAGGGUU
	siRs331_T9	ss	CCCUCAUCUACUGUGUGCAUU
		as	UGCACACAGUAGAUGAGGGUU
	siRs331_T10	ss	UCCCUCAUCUACUGUGUGCUU
		as	GCACACAGUAGAUGAGGGAUU
	siRs331_T11	ss	CUCCCUCAUCUACUGUGUGUU
		as	CACACAGUAGAUGAGGGAGUU
	siRs331_T12	ss	GCUCCCUCAUCUACUGUGUUU
		as	ACACAGUAGAUGAGGGAGCUU

Table S4. Synthetic siRNA sequences targeting cSNP sites (2/2)

SNP ID (alleles)	siRNA name		5' - sequence - 3'[b]
rs362273 (A/G)	siRNAs targeting the A-allele		
	siRs273_A8	ss	UGCUGCUACAGAUCAACCCUU
		as	GGGUUGAUCUGUAGCAGCAUU
	siRs273_A9	ss	CUGCUGCUACAGAUCAACCUU
		as	GGUUGAUCUGUAGCAGCAGUU
	siRs273_A10	ss	GCUGCUGCUACAGAUCAACUU
		as	GUUGAUCUGUAGCAGCAGCUU
	siRs273_A11	ss	AGCUGCUGCUACAGAUCAAUU
		as	UUGAUCUGUAGCAGCAGCUUU
	siRs273_A12	ss	AAGCUGCUGCUACAGAUCAUU
		as	UGAUCUGUAGCAGCAGCUUUU
	siRNAs targeting the G-allele		
	siRs273_G8	ss	UGCUGCUGCAGAUCAACCCUU
		as	GGGUUGAUCUGCAGCAGCAUU
	siRs273_G9	ss	CUGCUGCUGCAGAUCAACCUU
		as	GGUUGAUCUGCAGCAGCAGUU
	siRs273_G10	ss	GCUGCUGCUGCAGAUCAACUU
		as	GUUGAUCUGCAGCAGCAGCUU
	siRs273_G11	ss	AGCUGCUGCUGCAGAUCAAUU
		as	UUGAUCUGCAGCAGCAGCUUU
	siRs273_G12	ss	AAGCUGCUGCUGCAGAUCAUU
		as	UGAUCUGCAGCAGCAGCUUUU
rs362272 (A/G)	siRNAs targeting the A-allele		
	siRs272_A8	ss	GCACGGCAUCCUCUAUGUGUU
		as	CACAUAGAGGAUGCCGUGCUU
	siRs272_A9	ss	UGCACGGCAUCCUCUAUGUUU
		as	ACAUAGAGGAUGCCGUGCAUU
	siRs272_A10	ss	CUGCACGGCAUCCUCUAUGUU
		as	CAUAGAGGAUGCCGUGCAGUU
	siRs272_A11	ss	CCUGCACGGCAUCCUCUAUUU
		as	AUAGAGGAUGCCGUGCAGGUU
	siRs272_A12	ss	CCCUGCACGGCAUCCUCUAUU
		as	UAGAGGAUGCCGUGCAGGGUU
	siRNAs targeting the G-allele		
	siRs272_G8	ss	GCACGGCGUCCUCUAUGUGUU
		as	CACAUAGAGGACGCCGUGCUU
	siRs272_G9	ss	UGCACGGCGUCCUCUAUGUUU
		as	ACAUAGAGGACGCCGUGCAUU
	siRs272_G10	ss	CUGCACGGCGUCCUCUAUGUU
		as	CAUAGAGGACGCCGUGCAGUU
	siRs272_G11	ss	CCUGCACGGCGUCCUCUAUUU
		as	AUAGAGGACGCCGUGCAGGUU
	siRs272_G12	ss	CCCUGCACGGCGUCCUCUAUU
		as	UAGAGGACGCCGUGCAGGGUU

[a] ss: sense-strand, as: antisense-strand.

[b] The nucleotides corresponding to the SNP sites are underlined.

Table S5. Mismatched siRNA sequences

SNP ID (alleles)	SNP position	Mismatched position	siRNA name		5' - sequence - 3'[b]
rs363099 (C/T)					
siRNAs targeting the C-allele	9	13	siRs099_C9(A13)	ss[a]	GGGUUUCUCCGCaCAGCCUUU
				as	AGGCUGuGCGGAGAAACCCUU
	9	14	siRs099_C9(G14)	ss	GGGUUUCUCCGCUgAGCCUUU
				as	AGGCUcAGCGGAGAAACCCUU
	9	15	siRs099_C9(U15)	ss	GGGUUUCUCCGCUCuGCCUUU
				as	AGGCaGAGCGGAGAAACCCUU
	9	16	siRs099_C9(U16)	ss	GGGUUUCUCCGCUCAuCCUUU
				as	AGGaUGAGCGGAGAAACCCUU
rs362331 (C/T)					
siRNAs targeting the C-allele	9	14	siRs331_C9(A14)	ss	CCCUCAUCCACUGaGUGCAUU
				as	UGCACuCAGUGGAUGAGGGUU
	9	15	siRs331_C9(C15)	ss	CCCUCAUCCACUGUcUGCAUU
				as	UGCAgACAGUGGAUGAGGGUU
	11	14	siRs331_C11(A14)	ss	CUCCCUCAUCCACaGUGUGUU
				as	CACACuGUGGAUGAGGGAGUU
	11	15	siRs331_C11(C15)	ss	CUCCCUCAUCCACUcUGUGUU
				as	CACAgAGUGGAUGAGGGAGUU

[a] ss: sense-strand, as: antisense-strand.

[b] The nucleotides corresponding to the SNP sites and mismatched nucleotides are underlined and represented in small letters, respectively.

Table S6. IC50 values of the siRNAs examined in Fig. S6

		IC50 (nM)		IC50 (nM)	
SNP ID	siRNA name	Target allele (*Renilla Luc.*)	Non-target allele (*Photinus Luc.*)	Target allele (*Photinus Luc.*)	Non-target allele (*Renilla Luc.*)
rs363099					
	siRs099_T10	0.21 ± 0.081	>20	0.18 ± 0.107	>20
	siRs099_C9	0.20 ± 0.077	0.86 ± 0.171	0.12 ± 0.063	0.26 ± 0.055
	siRs099_C9(G14)	0.29 ± 0.048	>20	0.25 ± 0.043	>20
rs362331					
	siRs331_T9	0.07 ± 0.015	0.52 ± 0.431	0.05 ± 0.007	0.57 ± 0.125
	siRs331_T10	0.12 ± 0.032	7.63 ± 2.663	0.15 ± 0.074	0.98 ± 0.157
	siRs331_C9	0.48 ± 0.151	0.94 ± 1.685	0.18 ± 0.033	0.38 ± 0.044
	siRs331_C9(A14)	0.28 ± 0.066	8.19 ± 1.131	0.11 ± 0.032	>20
	siRs331_C9(C15)	0.14 ± 0.080	>20	0.08 ± 0.033	>20
rs362273					
	siRs273_G9	0.27 ± 0.032	>20	0.19 ± 0.048	>20
	siRs273_A9	0.26 ± 0.031	>20	0.38 ± 0.092	>20
rs362272					
	siRs272_G12	0.43 ± 0.141	>20	0.46 ± 0.148	>20
	siRs272_A9	0.53 ± 0.219	>20	0.71 ± 0.483	>20

Averaged IC50 values (mean ± S.D., n=4) are indicated.

Data fallen short of the half-maximal inhibition at the highest concentration of siRNA (20nM) is indicated by '>20'.

Table S7. Synthetic DNA oligonucleotides used in construction of reporter alleles

SNP ID (alleles, heterozygosity[a], exon)	Sequence name[b]	5' - sequence - 3' [c]
rs363099 (C/T, 0.333, exon 29)		
C-allele	rs363099(C)-ss	ctagcatgcGTTTGGAGGGTTTCTCCGCTCAGCCTTGGATa
	rs363099(C)-as	ggcctATCCAAGGCTGAGCGGAGAAACCCTCCAAACgcatg
T-allele	rs363099(T)-ss	ctagcatgcGTTTGGAGGGTTTCTTCGCTCAGCCTTGGATa
	rs363099(T)-as	ggcctATCCAAGGCTGAGCGAAGAAACCCTCCAAACgcatg
rs362331 (C/T, 0.494, exon 50)		
C-allele	rs362331(C)-ss	ctagcatgcGCCTGCTCCCTCATCCACTGTGTGCACTTCAa
	rs362331(C)-as	ggcctTGAAGTGCACACAGTGGATGAGGGAGCAGGCgcatg
T-allele	rs362331(T)-ss	ctagcatgcGCCTGCTCCCTCATCTACTGTGTGCACTTCAa
	rs362331(T)-as	ggcctTGAAGTGCACACAGTAGATGAGGGAGCAGGCgcatg
rs362273 (A/G, 0.370, exon 57)		
A-allele	rs362273(A)-ss	ctagcatgcCGAGAAGCTGCTGCTACAGATCAACCCCGAGa
	rs362273(A)-as	ggcctCTCGGGGTTGATCTGTAGCAGCAGCTTCTCGgcatg
G-allele	rs362273(G)-ss	ctagcatgcCGAGAAGCTGCTGCTGCAGATCAACCCCGAGa
	rs362273(G)-as	ggcctCTCGGGGTTGATCTGCAGCAGCAGCTTCTCGgcatg
rs362272 (A/G, 0.374, exon 61)		
A-allele	rs362272(A)-ss	ctagcatgcGGAGCCCTGCACGGCATCCTCTATGTGCTGGa
	rs362272(A)-as	ggcctCCAGCACATAGAGGATGCCGTGCAGGGCTCCgcatg
G-allele	rs362272(G)-ss	ctagcatgcGGAGCCCTGCACGGCGTCCTCTATGTGCTGGa
	rs362272(G)-as	ggcctCCAGCACATAGAGGACGCCGTGCAGGGCTCCgcatg

[a] Heterozygosities are derived from the NCBI SNP database: http://www.ncbi.nlm.nih.gov/snp.

[b] 'ss' and 'as' fixed to the names represent the sense- and anti-sense strand sequences, respectively.

[c] SNP sites and linker sequences are underlined and represented in small letters, respectively.