

Identification of tag haplotypes for 5HTTLPR for different genome-wide SNP platforms

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Supplementary Table S1. LD values between SNPs included in the Illumina HumanHap610 quad and the 5HTTLPR (marker 8).

| Illumina HumanHap610 quad | | | | | Marker # | | | | | | | | | | | | | | | | | | | | | | | | | |
|---------------------------|---------------------------|----------|-----|---------|----------|------|-----|------|------|------|------|-----|-----|------|------|-----|------|------|------|------|------|-----|-----|------|-----|-----|------|------|-----|-----|
| Marker # | Marker | Position | MAF | Alleles | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | |
| 1 | rs4583306 | 25562841 | .40 | A:G | . | 1.00 | .97 | .98 | .99 | .99 | .98 | .46 | .86 | .86 | .86 | .83 | .83 | .74 | .85 | .85 | .85 | .85 | .84 | .89 | .80 | .81 | .78 | .92 | .73 | |
| 2 | rs140700 ^{a,b} | 25567515 | .09 | C:T | .07 | . | .95 | .95 | 1.00 | 1.00 | .95 | .58 | .64 | .65 | .65 | .60 | .64 | 1.00 | .65 | .64 | .64 | .60 | .62 | .19 | .24 | .22 | .18 | .18 | .30 | |
| 3 | rs6354 | 25574024 | .19 | T:G | .15 | .39 | . | 1.00 | .98 | 1.00 | 1.00 | .15 | .31 | .14 | .14 | .10 | .80 | .84 | .26 | .27 | .27 | .63 | .63 | .33 | .12 | .14 | .08 | .67 | .45 | |
| 4 | rs2020936 | 25574940 | .19 | A:G | .15 | .39 | .99 | . | .99 | 1.00 | 1.00 | .16 | .31 | .13 | .14 | .11 | .78 | .85 | .26 | .27 | .27 | .63 | .64 | .33 | .11 | .13 | .09 | .65 | .46 | |
| 5 | rs2066713 ^{a,b} | 25575791 | .40 | G:A | .44 | .07 | .15 | .16 | . | 1.00 | 1.00 | .53 | .40 | .48 | .48 | .39 | .84 | .61 | .55 | .54 | .54 | .32 | .50 | .15 | .57 | .58 | .48 | .36 | .72 | |
| 6 | rs4251417 | 25575984 | .08 | C:T | .14 | .01 | .02 | .02 | .06 | . | 1.00 | .85 | .93 | .91 | .91 | .63 | .52 | .89 | .85 | .85 | .85 | .92 | .85 | .82 | .94 | .94 | .93 | .93 | .85 | |
| 7 | rs8071667 ^{a,b} | 25576899 | .18 | C:T | .14 | .42 | .93 | .94 | .15 | .02 | . | .15 | .30 | .15 | .16 | .06 | .80 | .83 | .25 | .26 | .26 | .63 | .63 | .32 | .10 | .12 | .07 | .64 | .45 | |
| 8 | 5HTTLPR | 25586631 | .44 | L:S | .18 | .03 | .00 | .01 | .14 | .05 | .00 | . | .88 | .88 | .88 | .94 | .97 | .91 | .90 | .89 | .89 | .67 | .70 | .44 | .63 | .63 | .63 | .14 | .41 | |
| 9 | rs1487971 ^{a,b} | 25596879 | .37 | C:T | .29 | .07 | .04 | .04 | .14 | .05 | .03 | .36 | . | 1.00 | 1.00 | .03 | 1.00 | 1.00 | 1.00 | .97 | .97 | .94 | .94 | .16 | .77 | .77 | .77 | .17 | .82 | |
| 10 | rs7214248 ^{a,b} | 25598303 | .33 | G:A | .24 | .09 | .01 | .01 | .16 | .04 | .01 | .29 | .82 | . | 1.00 | .98 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | .97 | .98 | .07 | .78 | .77 | .77 | .21 | .82 | |
| 11 | rs1050565 ^{a,b} | 25600202 | .33 | T:C | .24 | .09 | .01 | .01 | .16 | .04 | .01 | .29 | .82 | 1.00 | . | .98 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | .97 | .98 | .07 | .78 | .77 | .77 | .21 | .82 | |
| 12 | rs6505167 | 25607179 | .12 | C:T | .06 | .01 | .01 | .01 | .03 | .01 | .00 | .09 | .00 | .06 | .06 | . | .93 | 1.00 | .98 | .93 | .93 | .17 | .85 | .43 | .80 | .78 | .02 | 1.00 | .87 | |
| 13 | rs11651241 ^{a,b} | 25613604 | .07 | C:A | .04 | .00 | .01 | .01 | .08 | .00 | .01 | .06 | .05 | .04 | .04 | .52 | . | 1.00 | 1.00 | 1.00 | 1.00 | .88 | .94 | .86 | .77 | .76 | .77 | 1.00 | .89 | |
| 14 | rs2129785 ^{a,b} | 25614656 | .10 | T:C | .10 | .01 | .02 | .02 | .03 | .63 | .02 | .07 | .07 | .06 | .06 | .02 | .01 | . | 1.00 | 1.00 | 1.00 | .97 | .96 | 1.00 | .93 | .93 | .93 | 1.00 | .93 | |
| 15 | rs7214014 | 25635520 | .45 | G:A | .38 | .05 | .02 | .02 | .25 | .05 | .02 | .50 | .73 | .60 | .60 | .16 | .10 | .09 | . | .99 | .99 | .75 | .95 | .42 | .77 | .77 | .77 | .07 | .83 | |
| 16 | rs11867581 ^{a,b} | 25646354 | .44 | A:G | .38 | .05 | .02 | .02 | .25 | .05 | .02 | .49 | .70 | .61 | .61 | .14 | .10 | .09 | .97 | . | 1.00 | .77 | .97 | .43 | .78 | .78 | .78 | .06 | .83 | |
| 17 | rs8073378 ^a | 25653889 | .44 | G:A | .38 | .05 | .02 | .02 | .25 | .05 | .02 | .49 | .70 | .61 | .61 | .14 | .10 | .09 | .97 | 1.00 | . | .76 | .97 | .43 | .78 | .78 | .78 | .06 | .83 | |
| 18 | rs3110454 ^{a,b} | 25675489 | .42 | C:T | .35 | .05 | .13 | .13 | .09 | .06 | .12 | .26 | .72 | .63 | .63 | .00 | .04 | .08 | .51 | .54 | .54 | . | .99 | .26 | .80 | .80 | .78 | .93 | .86 | |
| 19 | rs3110095 ^{a,b} | 25683136 | .50 | C:T | .45 | .04 | .10 | .10 | .17 | .07 | .09 | .37 | .54 | .48 | .48 | .10 | .07 | .11 | .74 | .77 | .77 | .73 | . | .94 | .79 | .79 | .79 | .91 | .87 | |
| 20 | rs3110093 | 25685518 | .18 | A:G | .11 | .02 | .10 | .10 | .01 | .01 | .10 | .03 | .00 | .00 | .00 | .12 | .28 | .02 | .05 | .05 | .05 | .05 | .02 | .19 | . | .90 | .89 | .84 | .97 | .71 |
| 21 | rs6505179 ^{a,b} | 25692986 | .33 | C:T | .21 | .01 | .00 | .00 | .24 | .04 | .00 | .15 | .49 | .60 | .60 | .04 | .02 | .05 | .36 | .38 | .38 | .43 | .31 | .08 | . | .99 | .99 | 1.00 | .97 | |
| 22 | rs4533339 | 25708371 | .33 | G:A | .21 | .01 | .00 | .00 | .24 | .04 | .00 | .15 | .49 | .59 | .60 | .04 | .02 | .05 | .36 | .37 | .38 | .43 | .31 | .08 | .98 | . | 1.00 | 1.00 | .97 | |
| 23 | rs8066222 | 25712980 | .37 | T:C | .24 | .01 | .00 | .00 | .20 | .05 | .00 | .18 | .58 | .49 | .49 | .00 | .03 | .06 | .42 | .44 | .44 | .49 | .37 | .09 | .82 | .83 | . | 1.00 | .95 | |
| 24 | rs887469 ^{a,b} | 25716700 | .09 | C:T | .06 | .03 | .19 | .19 | .01 | .01 | .19 | .00 | .01 | .01 | .01 | .01 | .01 | .01 | .00 | .00 | .00 | .12 | .09 | .46 | .05 | .05 | .06 | . | .63 | |
| 25 | rs3794794 ^{a,b} | 25744867 | .44 | A:C | .45 | .01 | .04 | .04 | .27 | .09 | .04 | .17 | .31 | .25 | .25 | .08 | .05 | .13 | .44 | .43 | .43 | .42 | .58 | .08 | .36 | .36 | .41 | .03 | . | |

Notes: N=1303 (those genotyped on Illumina 610 quad only); 5HTTLPR = length polymorphism repeat in the promoter region of the serotonin transporter gene; Alleles represent major and minor allele, respectively; D' values above the diagonal; r² values below the diagonal; warmer colours represent higher LD values; ^a SNP is included in Illumina Human317 array, ^b SNP is included in Illumina Human370 CNV quad; tagging analyses was based on a subset of 562,018 genome wide Illumina SNPs that survived stringent quality control (QC), the QC procedure is extensively described elsewhere¹⁻³.

Supplementary Table S2. LD values between SNPs included in the Affymetrix 6.0 and the 5HTTLPR (marker 7).

| Affymetrix 6.0 | | | | | Marker # | | | | | | | | | | | | | | | | | | | | |
|----------------|----------------|----------|-----|---------|----------|------|------|-----|------|------|-----|-----|------|------|------|-----|-----|------|------|------|------|------|------|------|------|
| Marker # | Marker | Position | MAF | Alleles | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
| 1 | rs140701 | 25562658 | .42 | C:T | . | 1.00 | .98 | .97 | .98 | .95 | .41 | .83 | .84 | .84 | .80 | .84 | .74 | .76 | .75 | .76 | .76 | .69 | .68 | .68 | .68 |
| 2 | rs4583306 | 25562841 | .42 | A:G | .99 | . | 1.00 | .97 | .98 | .98 | .41 | .83 | .84 | .84 | .80 | .83 | .74 | .76 | .75 | .75 | .76 | .69 | .68 | .68 | .68 |
| 3 | rs8076005 | 25571336 | .16 | A:G | .13 | .14 | . | .99 | 1.00 | .99 | .12 | .35 | .17 | .17 | .27 | .40 | .05 | .02 | .01 | .16 | .02 | .05 | .38 | .38 | .38 |
| 4 | rs11080122 | 25571461 | .16 | C:T | .13 | .13 | .98 | . | .98 | .99 | .10 | .37 | .18 | .18 | .28 | .42 | .03 | .00 | .01 | .17 | .00 | .03 | .40 | .40 | .40 |
| 5 | rs2020939 | 25574858 | .43 | G:A | .93 | .93 | .15 | .14 | . | 1.00 | .42 | .82 | .82 | .82 | .80 | .82 | .73 | .75 | .74 | .74 | .74 | .68 | .69 | .69 | .69 |
| 6 | rs2020936 | 25574940 | .16 | A:G | .13 | .13 | .99 | .98 | .15 | . | .12 | .35 | .17 | .17 | .27 | .40 | .05 | .02 | .01 | .16 | .02 | .05 | .38 | .38 | .38 |
| 7 | 5HTTLPR | 25586631 | .45 | L:S | .15 | .15 | .00 | .00 | .16 | .00 | . | .89 | .87 | .87 | .90 | .72 | .65 | .64 | .64 | .67 | .64 | .58 | .45 | .45 | .45 |
| 8 | rs7214991 | 25596486 | .37 | A:G | .29 | .28 | .04 | .05 | .29 | .04 | .37 | . | 1.00 | 1.00 | 1.00 | .79 | .75 | .75 | .75 | .77 | .75 | .72 | .85 | .84 | .84 |
| 9 | rs1050565 | 25600202 | .32 | T:C | .24 | .24 | .01 | .01 | .24 | .01 | .29 | .82 | . | 1.00 | 1.00 | .98 | .75 | .76 | .76 | .75 | .76 | .76 | .83 | .82 | .82 |
| 10 | rs17767256 | 25605169 | .32 | T:G | .24 | .24 | .01 | .01 | .24 | .01 | .28 | .82 | 1.00 | . | .99 | .97 | .75 | .76 | .76 | .75 | .76 | .76 | .83 | .82 | .82 |
| 11 | rs8072345 | 25628415 | .44 | C:T | .35 | .36 | .02 | .02 | .37 | .02 | .50 | .75 | .62 | .61 | . | .79 | .78 | .78 | .78 | .79 | .78 | .73 | .85 | .85 | .85 |
| 12 | rs3110452 | 25671878 | .37 | G:A | .29 | .29 | .05 | .06 | .29 | .05 | .24 | .63 | .78 | .78 | .47 | . | .79 | .80 | .79 | .65 | .79 | .75 | .85 | .85 | .85 |
| 13 | rs6505178 | 25688181 | .32 | C:G | .19 | .19 | .00 | .00 | .19 | .00 | .16 | .47 | .56 | .56 | .37 | .51 | . | .99 | 1.00 | 1.00 | .99 | .99 | .99 | .99 | .99 |
| 14 | rs8079175 | 25691408 | .32 | G:A | .20 | .20 | .00 | .00 | .20 | .00 | .15 | .47 | .57 | .57 | .37 | .52 | .97 | . | 1.00 | 1.00 | 1.00 | 1.00 | .99 | .99 | .99 |
| 15 | rs8068438 | 25692866 | .33 | A:G | .20 | .19 | .00 | .00 | .19 | .00 | .16 | .48 | .57 | .57 | .38 | .52 | .98 | .99 | . | 1.00 | 1.00 | .99 | .99 | .99 | .99 |
| 16 | rs9916613 | 25706579 | .36 | T:A | .23 | .23 | .01 | .01 | .23 | .01 | .20 | .58 | .47 | .48 | .46 | .42 | .84 | .84 | .86 | . | 1.00 | .96 | .99 | .99 | .99 |
| 17 | rs7215966 | 25711322 | .33 | G:A | .20 | .20 | .00 | .00 | .20 | .00 | .16 | .47 | .57 | .58 | .38 | .52 | .97 | 1.00 | .99 | .85 | . | 1.00 | .99 | .99 | .99 |
| 18 | rs8082357 | 25717438 | .33 | T:C | .17 | .17 | .00 | .00 | .17 | .00 | .14 | .45 | .54 | .55 | .35 | .48 | .93 | .95 | .95 | .82 | .96 | . | .99 | .99 | .99 |
| 19 | rs12952168 | 25723214 | .46 | G:C | .39 | .39 | .02 | .03 | .41 | .02 | .19 | .35 | .28 | .28 | .47 | .36 | .39 | .40 | .41 | .47 | .40 | .42 | . | 1.00 | 1.00 |
| 20 | rs12453652 | 25754986 | .46 | C:T | .39 | .38 | .02 | .03 | .41 | .02 | .19 | .35 | .27 | .28 | .47 | .36 | .40 | .40 | .41 | .48 | .40 | .42 | 1.00 | . | 1.00 |
| 21 | rs719601 | 25755541 | .46 | G:A | .39 | .38 | .02 | .03 | .41 | .02 | .19 | .35 | .27 | .28 | .47 | .36 | .40 | .40 | .41 | .48 | .40 | .42 | 1.00 | 1.00 | . |

Notes: N=479; 5HTTLPR = length polymorphism repeat in the promoter region of the serotonin transporter gene; Alleles represent major and minor allele, respectively; D' values above the diagonal; r² values below the diagonal; warmer colours represent higher LD values; tagging analyses was based on a subset of 646,601 genome wide Affymetrix 6.0 SNPs that survived stringent quality control (QC), the QC procedure is extensively described elsewhere¹.

Supplementary Table S3. LD values between SNPs included in the Illumina HumanHap610 quad and 5HTTLPR-rs25531(marker 8) for 5HTTLPR long long (LL) individuals only.

| Illumina HumanHap610 quad | | | | | Marker # | | | | | | | | | | | | | | | | | | | | | | | | |
|---------------------------|---------------------------|----------|-----|---------|----------|------|------|------|------|------|------|------|-----|------|------|-----|------|------|------|------|------|-----|------|------|-----|-----|------|------|-----|
| Marker # | Marker | Position | MAF | Alleles | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 |
| 1 | rs4583306 | 25562841 | .22 | A:G | .1 | 1.00 | 1.00 | 1.00 | .99 | .99 | 1.00 | .42 | .76 | .79 | .79 | .81 | .68 | .79 | .76 | .77 | .77 | .77 | .76 | .87 | .78 | .78 | .77 | 1.00 | .75 |
| 2 | rs140700 ^{a,b} | 25567515 | .14 | C:T | .05 | .1 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | .40 | .91 | .80 | .80 | .70 | .74 | 1.00 | 1.00 | .92 | .92 | .82 | .91 | .25 | .17 | .13 | .07 | .35 | .44 |
| 3 | rs6354 | 25574024 | .22 | T:G | .08 | .56 | .1 | .99 | .99 | 1.00 | .99 | .43 | .61 | .14 | .15 | .10 | .82 | .88 | .55 | .54 | .54 | .79 | .82 | .20 | .18 | .19 | .12 | .57 | .42 |
| 4 | rs2020936 | 25574940 | .22 | A:G | .08 | .57 | .98 | .1 | .99 | 1.00 | .99 | .42 | .60 | .12 | .12 | .12 | .80 | .88 | .55 | .55 | .54 | .79 | .82 | .20 | .19 | .20 | .12 | .55 | .41 |
| 5 | rs2066713 ^{a,b} | 25575791 | .45 | A:G | .34 | .20 | .35 | .35 | .1 | 1.00 | 1.00 | .48 | .26 | .33 | .33 | .12 | .77 | .68 | .63 | .58 | .58 | .21 | .54 | .04 | .45 | .46 | .31 | .40 | .58 |
| 6 | rs4251417 | 25575984 | .14 | C:T | .55 | .03 | .05 | .05 | .20 | .1 | 1.00 | 1.00 | .93 | .91 | .91 | .80 | .54 | .89 | .89 | .88 | .88 | .93 | .88 | .81 | .94 | .94 | .93 | .95 | .88 |
| 7 | rs8071667 ^{a,b} | 25576899 | .21 | C:T | .08 | .60 | .92 | .93 | .33 | .04 | .1 | .40 | .59 | .15 | .16 | .07 | .82 | .87 | .52 | .51 | .50 | .78 | .81 | .21 | .17 | .18 | .10 | .55 | .39 |
| 8 | 5HTTLPR-rs25531 | 25588472 | .11 | A:G | .01 | .13 | .08 | .08 | .04 | .02 | .08 | .1 | .80 | .65 | .66 | .82 | 1.00 | 1.00 | .68 | .54 | .54 | .60 | .35 | .55 | .51 | .53 | .57 | .56 | .22 |
| 9 | rs1487971 ^{a,b} | 25596879 | .37 | T:C | .28 | .08 | .06 | .06 | .05 | .24 | .06 | .05 | .1 | 1.00 | 1.00 | .35 | 1.00 | 1.00 | .99 | .90 | .91 | .88 | .84 | .34 | .91 | .91 | .91 | .34 | .65 |
| 10 | rs7214248 ^{a,b} | 25598303 | .45 | A:G | .21 | .09 | .01 | .00 | .11 | .16 | .01 | .05 | .71 | .1 | 1.00 | .97 | 1.00 | 1.00 | .99 | 1.00 | 1.00 | .95 | .98 | .28 | .92 | .91 | .68 | .38 | .66 |
| 11 | rs1050565 ^{a,b} | 25600202 | .45 | C:T | .21 | .09 | .01 | .00 | .10 | .16 | .01 | .05 | .71 | 1.00 | .1 | .97 | 1.00 | 1.00 | .99 | 1.00 | 1.00 | .95 | .98 | .28 | .92 | .92 | .69 | .38 | .66 |
| 12 | rs6505167 | 25607179 | .19 | C:T | .04 | .02 | .01 | .01 | .00 | .03 | .00 | .02 | .05 | .27 | .27 | .1 | .92 | 1.00 | 1.00 | .83 | .83 | .39 | .69 | .41 | .85 | .83 | .34 | 1.00 | .89 |
| 13 | rs11651241 ^{a,b} | 25613604 | .12 | C:A | .02 | .01 | .03 | .02 | .07 | .01 | .02 | .02 | .23 | .17 | .17 | .48 | .1 | 1.00 | 1.00 | 1.00 | 1.00 | .90 | 1.00 | .87 | .83 | .83 | .84 | 1.00 | .90 |
| 14 | rs2129785 ^{a,b} | 25614656 | .18 | T:C | .50 | .04 | .05 | .05 | .13 | .56 | .05 | .03 | .39 | .27 | .27 | .05 | .03 | .1 | 1.00 | 1.00 | 1.00 | .98 | .97 | 1.00 | .94 | .94 | .94 | 1.00 | .94 |
| 15 | rs7214014 | 25635520 | .25 | A:G | .48 | .05 | .03 | .03 | .16 | .38 | .02 | .02 | .56 | .39 | .39 | .08 | .05 | .68 | .1 | .99 | .99 | .78 | .86 | .50 | .93 | .93 | .94 | .02 | .76 |
| 16 | rs11867581 ^{a,b} | 25646354 | .26 | G:A | .47 | .05 | .03 | .03 | .15 | .35 | .02 | .01 | .49 | .43 | .43 | .06 | .05 | .64 | .92 | .1 | 1.00 | .80 | .94 | .52 | .95 | .95 | .95 | .04 | .71 |
| 17 | rs8073378 ^a | 25653889 | .26 | A:G | .47 | .05 | .03 | .03 | .15 | .35 | .02 | .01 | .49 | .43 | .43 | .06 | .05 | .64 | .92 | 1.00 | .1 | .80 | .95 | .52 | .95 | .95 | .95 | .03 | .71 |
| 18 | rs3110454 ^{a,b} | 25675489 | .36 | T:C | .30 | .06 | .10 | .10 | .03 | .25 | .09 | .03 | .72 | .60 | .60 | .07 | .20 | .39 | .36 | .40 | .41 | .1 | .98 | .25 | .96 | .95 | .92 | 1.00 | .73 |
| 19 | rs3110095 ^{a,b} | 25683136 | .24 | T:C | .53 | .04 | .06 | .06 | .11 | .40 | .05 | .01 | .37 | .35 | .36 | .04 | .04 | .70 | .69 | .77 | .78 | .54 | .1 | 1.00 | .97 | .97 | .98 | 1.00 | .88 |
| 20 | rs3110093 | 25685518 | .23 | A:G | .06 | .03 | .04 | .04 | .00 | .03 | .04 | .13 | .06 | .03 | .03 | .13 | .34 | .07 | .03 | .03 | .03 | .04 | .09 | .1 | .93 | .91 | .87 | .98 | .39 |
| 21 | rs6505179 ^{a,b} | 25692986 | .48 | C:T | .16 | .01 | .01 | .01 | .15 | .13 | .01 | .03 | .44 | .64 | .65 | .16 | .09 | .19 | .27 | .29 | .29 | .47 | .27 | .24 | .1 | .99 | .99 | 1.00 | .94 |
| 22 | rs4533339 | 25708371 | .48 | G:A | .16 | .00 | .01 | .01 | .16 | .13 | .01 | .03 | .45 | .64 | .64 | .15 | .09 | .19 | .27 | .29 | .30 | .46 | .27 | .23 | .98 | .1 | 1.00 | 1.00 | .94 |
| 23 | rs8066222 | 25712980 | .45 | C:T | .20 | .00 | .00 | .00 | .10 | .17 | .00 | .05 | .59 | .46 | .47 | .03 | .12 | .24 | .35 | .38 | .39 | .57 | .35 | .28 | .74 | .77 | .1 | 1.00 | .90 |
| 24 | rs887469 ^{a,b} | 25716700 | .10 | C:T | .03 | .08 | .13 | .12 | .02 | .02 | .12 | .28 | .01 | .01 | .01 | .03 | .02 | .03 | .00 | .00 | .00 | .06 | .03 | .35 | .10 | .10 | .13 | .1 | .05 |
| 25 | rs3794794 ^{a,b} | 25744867 | .27 | A:C | .43 | .01 | .02 | .02 | .16 | .34 | .02 | .02 | .27 | .19 | .20 | .07 | .04 | .55 | .52 | .49 | .49 | .35 | .65 | .02 | .30 | .30 | .36 | .00 | .1 |

Notes: N=434; 5HTTLPR-rs25531 = rs25531 on the long allele of the length polymorphism repeat in the promoter region of the serotonin transporter gene; Alleles represent major and minor allele, respectively; D' values above the diagonal; r² values below the diagonal; warmer colours represent higher LD values; ^a SNP is included in Illumina Human317 array, ^b SNP is included in Illumina Human370 CNV quad¹⁻³.

Supplementary Table S4. LD values between SNPs included in the Affymetrix 6.0 and HTTLPR-rs25531(marker7) for 5HTTLPR long long (LL) individuals only.

| Affymetrix 6.0 | | | | | Marker # | | | | | | | | | | | | | | | | | | | | |
|----------------|------------------------|----------|-----|---------|----------|------|------|------|------|------|-----|------|------|------|------|-----|-----|------|------|------|------|------|------|------|------|
| Marker # | Marker | Position | MAF | Alleles | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 |
| 1 | rs140701 | 25562658 | .22 | C:T | . | 1.00 | 1.00 | 1.00 | .98 | 1.00 | .02 | .73 | .69 | .69 | .71 | .67 | .55 | .61 | .58 | .65 | .58 | .58 | .62 | .62 | .62 |
| 2 | rs4583306 | 25562841 | .22 | A:G | 1.00 | . | 1.00 | 1.00 | .98 | 1.00 | .02 | .73 | .69 | .69 | .71 | .67 | .55 | .61 | .58 | .65 | .58 | .58 | .62 | .62 | .62 |
| 3 | rs8076005 | 25571336 | .19 | A:G | .07 | .07 | . | 1.00 | 1.00 | 1.00 | .32 | .90 | .16 | .16 | .68 | .22 | .16 | .18 | .15 | .28 | .17 | .17 | .20 | .21 | .21 |
| 4 | rs11080122 | 25571461 | .19 | C:T | .07 | .07 | 1.00 | . | 1.00 | 1.00 | .33 | 1.00 | .21 | .21 | 1.00 | .27 | .14 | .17 | .13 | .32 | .15 | .15 | .30 | .32 | .32 |
| 5 | rs2020939 | 25574858 | .22 | G:A | .96 | .96 | .07 | .07 | . | 1.00 | .02 | .70 | .66 | .66 | .71 | .63 | .51 | .57 | .54 | .62 | .54 | .54 | .62 | .62 | .62 |
| 6 | rs2020936 | 25574940 | .19 | A:G | .07 | .07 | 1.00 | 1.00 | .07 | . | .32 | .90 | .16 | .16 | .68 | .22 | .16 | .18 | .15 | .28 | .17 | .17 | .20 | .21 | .21 |
| 7 | 5HTTLPR-rs25531 | 25588472 | .14 | A:G | .00 | .00 | .08 | .08 | .00 | .08 | . | .21 | .39 | .39 | .06 | .28 | .82 | .73 | .75 | .80 | .74 | .74 | .42 | .44 | .44 |
| 8 | rs7214991 | 25596486 | .33 | G:A | .31 | .31 | .09 | .11 | .29 | .09 | .00 | . | 1.00 | 1.00 | 1.00 | .91 | .90 | .90 | .91 | .92 | .91 | .91 | .73 | .71 | .71 |
| 9 | rs1050565 | 25600202 | .41 | C:T | .20 | .20 | .00 | .01 | .18 | .00 | .02 | .72 | . | 1.00 | 1.00 | .96 | .91 | .91 | .91 | .66 | .91 | .91 | .69 | .67 | .67 |
| 10 | rs17767256 | 25605169 | .41 | G:T | .20 | .20 | .00 | .01 | .18 | .00 | .02 | .72 | 1.00 | . | 1.00 | .96 | .91 | .91 | .91 | .66 | .91 | .91 | .69 | .67 | .67 |
| 11 | rs8072345 | 25628415 | .21 | T:C | .47 | .47 | .03 | .06 | .47 | .03 | .00 | .55 | .39 | .39 | . | .90 | .91 | .91 | .91 | .93 | .91 | .91 | .89 | .89 | .89 |
| 12 | rs3110452 | 25671878 | .40 | A:G | .19 | .19 | .01 | .01 | .18 | .01 | .01 | .62 | .87 | .87 | .33 | . | .96 | .96 | .96 | .70 | .96 | .96 | .74 | .74 | .74 |
| 13 | rs6505178 | 25688181 | .48 | G:C | .09 | .09 | .01 | .01 | .08 | .01 | .11 | .42 | .59 | .59 | .23 | .64 | . | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| 14 | rs8079175 | 25691408 | .49 | A:G | .11 | .11 | .01 | .01 | .10 | .01 | .09 | .43 | .61 | .61 | .24 | .66 | .97 | . | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| 15 | rs8068438 | 25692866 | .48 | G:A | .10 | .10 | .01 | .00 | .09 | .01 | .10 | .44 | .61 | .61 | .24 | .66 | .97 | 1.00 | . | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| 16 | rs9916613 | 25706579 | .42 | A:T | .17 | .17 | .01 | .02 | .15 | .01 | .14 | .58 | .41 | .41 | .32 | .45 | .76 | .79 | .80 | . | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 |
| 17 | rs7215966 | 25711322 | .48 | A:G | .11 | .11 | .01 | .01 | .09 | .01 | .10 | .44 | .62 | .62 | .24 | .66 | .97 | 1.00 | 1.00 | .79 | . | 1.00 | 1.00 | 1.00 | 1.00 |
| 18 | rs8082357 | 25717438 | .48 | C:T | .11 | .11 | .01 | .01 | .09 | .01 | .10 | .44 | .62 | .62 | .24 | .66 | .97 | 1.00 | 1.00 | .79 | 1.00 | . | 1.00 | 1.00 | 1.00 |
| 19 | rs12952168 | 25723214 | .24 | G:C | .35 | .35 | .00 | .01 | .35 | .00 | .09 | .34 | .22 | .22 | .67 | .26 | .33 | .34 | .35 | .44 | .35 | .35 | . | 1.00 | 1.00 |
| 20 | rs12453652 | 25754986 | .24 | C:T | .34 | .34 | .00 | .01 | .34 | .00 | .10 | .33 | .21 | .21 | .66 | .27 | .34 | .35 | .35 | .44 | .35 | .35 | 1.00 | . | 1.00 |
| 21 | rs719601 | 25755541 | .24 | G:A | .34 | .34 | .00 | .01 | .34 | .00 | .10 | .33 | .21 | .21 | .66 | .27 | .34 | .35 | .35 | .44 | .35 | .35 | 1.00 | 1.00 | . |

Notes: N=144; 5HTTLPR-rs25531 = rs25531 on the long allele of the length polymorphism repeat in the promoter region of the serotonin transporter gene; Alleles represent major and minor allele, respectively; D' values above the diagonal; r² values below the diagonal; warmer colours represent higher LD values; tagging analyses was based on a subset of 646,601 genome wide Affymetrix 6.0 SNPs that survived stringent quality control (QC), the QC procedure is extensively described elsewhere¹.

Supplementary Table S5. Proxies for rs2129785 and rs11867581 whose haplotype tags SHTTLPR and the genotyping arrays on which they are found.

| SNP | Proxy | Distance | r ² | Arrays | Coordinate_HG18 | Major | Minor | MAF |
|------------|------------|----------|----------------|---|-----------------|-------|-------|------|
| rs2129785 | rs2129785 | 0 | 1 | I3,I5,I6,I6Q,IM,IMD,IC,ICQ,CYT,OQ,CM,IWQ,OE | 25614656 | T | C | .167 |
| rs2129785 | rs17767328 | 37736 | .883 | AxM,CM | 25652392 | G | A | .167 |
| rs11867581 | rs11867581 | 0 | 1 | I3,I5,I6,I6Q,IM,IMD,IC,ICQ,OQ,IWQ,OE | 25646354 | A | G | .425 |
| rs11867581 | rs8080300 | 1753 | 1 | None | 25648107 | C | G | .425 |
| rs11867581 | rs13341611 | 4075 | 1 | None | 25650429 | C | G | .425 |
| rs11867581 | rs6505171 | 7757 | 1 | None | 25654111 | G | A | .425 |
| rs11867581 | rs7342929 | 10026 | 1 | I1 | 25636328 | C | G | .425 |
| rs11867581 | rs7214014 | 10834 | 1 | I2,I5,I6,I6Q,IM,IMD,IWQ | 25635520 | G | A | .425 |
| rs11867581 | rs8072345 | 17939 | 1 | A6,IM,IMD,AxM | 25628415 | C | T | .425 |
| rs11867581 | rs3816828 | 23511 | 1 | IM,IMD,CYT | 25622843 | G | T | .425 |
| rs11867581 | rs6505173 | 23829 | 1 | I1,IM,IMD,CYT,OQ,OE | 25670183 | A | G | .425 |
| rs11867581 | rs6505165 | 47379 | 1 | IM,IMD | 25598975 | T | C | .425 |
| rs11867581 | rs8073378 | 7535 | .966 | I3,I5,I6,I6Q,IM,IMD,IC,ICQ,CYT,CM,IWQ | 25653889 | G | A | .417 |
| rs11867581 | rs6505169 | 16548 | .966 | IM | 25629806 | G | A | .417 |
| rs11867581 | rs7210085 | 33827 | .966 | IM,IMD | 25612527 | T | C | .417 |

Output from the SNAP (SNP Annotation and Proxy Search) website⁹. The MAF and r² estimates are based on 120 chromosomes.

MAF=minor allele frequency. Array acronyms: AX=Affymetrix Mapping50K XbaI; AH=Affymetrix Mapping50K HindIII; AG=Affymetrix 50K Human Gene Focused chip; AN=Affymetrix Mapping250K NspI; AS=Affymetrix Mapping250K StyI; A5=Affymetrix Affy 5.0; A6=Affymetrix Affy 6.0; AD=Affymetrix Affymetrix DMET plus; AxM=Affymetrix Affymetrix Axiom; I1=Illumina Human-1; I2=Illumina HumanHap240; I3=Illumina HumanHap300; IC=Illumina HumanHap370CNV (single); ICQ=Illumina HumanHap370CNV (quad); I5=Illumina HumanHap550; I6=Illumina HumanHap650; I6Q=Illumina HumanHap610 (quad); IM=Illumina Human1M; IMD=Illumina Human1M (duo); IBC=Illumina CARE iSelect Array; CYT=Illumina Cyto12; OQ=Illumina OmniQuad; CM=Illumina Cardio-MetaboChip; IWQ=Illumina 660W-Quad; OE=Illumina OmniExpress.

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