S1 Table. PCR primer pairs used in the preparation of the RNA FISH probes.

A. Human *XIST* probe[1].

Primer pair	Sequences, 5′–3′	Amplimer size
XIST-1F + XIST-1R	AATGCTGGTAAAGCCCACAC TCTGGGGACAAGAACCATTC	516 bp
XIST-2F + XIST-2R	GACACCATGGCTACCTGTGA TCCCATTACCCTTTGGATTG	492 bp
XIST-3F + XIST-3R	CAACGAGGAAGCAGGAGTCT CATTTGCTCCTGATCTGTGC	491 bp
XIST-4F + XIST-4R	ATGGAATGGGCAAAGTGGT CGTCTGGGATCCTATGCACT	477 bp
XIST-5F + XIST-5R	AGTGCATAGGATCCCAGACG TTGCAGTTGTCAATGGTCCT	511 bp
XIST-6F + XIST-6R	GTGTCACCAACCATGCTGTC GAGTAGAATCCCGCTTCCTTG	506 bp
XIST-7F + XIST-7R	TTCATAGTCCCAGGGAAAGGT AGGTCCCTGCATCATCTTTG	508 bp
XIST-8F + XIST-8R	GGTGTGAGCAGTTGGGATCT TGCAATTGTCCAGAGTCCTG	475 bp
XIST-9F + XIST-9R	GGGAGGTTCAGACCACACAG GCTGTGTGCTTTTCGTGTTG	509 bp
XIST-10F + XIST-10R	GGTTGGGTTATGCAGCAATC TTGTTGTATCGGGAGGCAGT	525 bp
XIST-11F + XIST-11R	AACACTGCGACAGAACTGGA TTGTGGGTTGTTGCACTCTC	501 bp
XIST-12F + XIST-12R	GACTTCCTCTGCCTGACCTG GGATACCTGCTGATTCCCTTC	514 bp

[1]Primer set from our previous publication, Souyris et al., Sci Immunol. 2018; 3:eaap8855.

B. Human *MSN* probe.

Primer pair	Sequences, 5′–3′	Amplimer size
MSN-1F + MSN-1R	GTCTGCAGTTGCCTGTCTGT GGCTCAGTCGGCTTGTAGAG	516 bp
MSN-2F + MSN-2R	CTTAGGGGCCAGGGTAACTC ACCTTATTCGGGCAGGAAAT	508 bp
MSN-3F + MSN-3R	TCCTCAAGCTGGTTCGTCTC AGCAGGAATTGCCATGATCT	529 bp
MSN-4F + MSN-4R	CCTTCCCTGAATACCAAGCA TGCCCTCTATGGGTCTGACT	575 bp
MSN-5F + MSN-5R	AGATTTTGGTCACCCCATGA TGAAACACGCACAGAGGAAG	571bp
MSN-6F + MSN-6R	GGAGGTGACTGCCACTTAGC GCAGTTTGCACACAAATCCA	546 bp
MSN-7F + MSN-7R	TCATAACTCCAGGGCAAACA GCAATGCTTTGGACACTCAA	533 bp
MSN-8F + MSN-8R	TGGGATGTGCTGTGCTAATC TGATCCCATGCTCCTGTTG	515 bp
MSN-9F + MSN-9R	GCCACATTATGCTGTGAGAGG CTGCATTTCAAGTGGCATTC	522 bp
MSN-10F + MSN-10R	TTCAAACTGGACCCCAAGTC TGGCTAGCAGGGACTCATCT	577 bp
MSN-11F + MSN-11R	GTGTTGTGGGGAGTGGTTG GATTGCATATGGGCTGGTCT	523 bp
MSN-12F + MSN-12R	AGATCAGGGGAAAGGCAATC TTCCCTCTCCAAGCCTAACA	513 bp
MSN-13F + MSN-13R	GGCAACAGCCTGTCTTAGGT CAGTTCAGTGATGCTTTCCA	523 bp
MSN-14F + MSN-14R	ATTTGGGAAAGGGTGGAGAT TTAATGGAGGCCAAGGCTAA	595 bp
MSN-15F + MSN-15R	GTGGGCCTGGTGAAAATCTA CAAATGCTGAAAGCCCTAGC	561bp
MSN-16F + MSN-16R	GAAGACCCTTGGATTGGTCA CCTTGTTTCACAAGCAAGCA	530 bp
MSN-17F + MSN-17R	CCAGGTGGTAGGAAAGTGGA GCCTGGCCTACAATAAATGC	584 bp
MSN-18F + MSN-18R	GGGTGAAGTGGTTAGGTTGC TTGGAAAATGGGCAGCTATC	510 bp
MSN-19F + MSN-19R	TTGTTCTGTGCGGAACTGAG AACCCCACATGCTTTGACAT	516 bp
MSN-20F + MSN-20R	GTTGGCCACTAATGGAGGTC TGACTATCTGCAAGGCCTCA	584 bp
MSN-21F + MSN-21R	TGGGGAGTGCTCATTAAGCTA TGGACTGTGGAAACACAAGC	504 bp
MSN-22F + MSN-22R	CTTGCCTTCTTGGCTTTGAG CTTCAGGCTCTGGTGACTCTG	596 bp

B. Human *MSN* probe.

Primer pair	Sequences, 5′–3′	Amplimer size
MSN-23F + MSN-23R	GGTTTGGATCAGCTCCAGTG CACCACCCATTCTAGGGAGA	566 bp
MSN-24F + MSN-24R	GGTAGGTGAGGGGAAACCAT GGATGGGGTAGCATTTCAAG	566 bp
MSN-25F + MSN-25R	TGCATGAGTACCCATTGAATC TGCAAATTTCCATGGAGTGA	584 bp
MSN-26F + MSN-26R	AGATGCCGACATCAGTTCTTG GGGGATACCAATCCTCTCTTG	596 bp
MSN-27F + MSN-27R	AGGAAGTGACCCAATGATGG CTGCCTGCTGTGGGAAGTAT	584 bp

C. Human *PGK1* probe.

Primer pair	Sequences, 5′–3′	Amplimer size
PGK1-1F + PGK1-1R	AGCCGACTTGTTCTCTCGTC GCCCAAGAGTCCAACGATAC	570 bp
PGK1-2F + PGK1-2R	AGGTCATTTTACTTTCCCTTCC AAACACCACTCTTGGATCCTGT	624 bp
PGK1-3F + PGK1-3R	GGTTCAAATGAGGGCTTGTG TTAAGCAGCTCCTCCAATCC	608 bp
PGK1-4F + PGK1-4R	GGAAGTTACATGGTTCCCTGA AACCATGTCCATCAATGCTTC	641 bp
PGK1-5F + PGK1-5R	GGCAAGAGCAGTTCCTGTGT CCCCTTCCTCTCTAAGGCTA	638 bp
PGK1-6F + PGK1-6R	AATAATCATGGCAGGCACAA CACAGGAACTAGCCCTGAAGA	559 bp
PGK1-7F + PGK1-7R	TGAACTGACAACCAGAATTCAA ATTTTGAACTTGGGACTGACTC	528 bp
PGK1-8F + PGK1-8R	TTCCAATCACTAGTGGCAGATG GACTCAAGCTGCTGGCTACC	608 bp
PGK1-9F + PGK1-9R	TGTTGTCATGTTTCCATCTGC ATCCCCTAGCTTGGAAAGTG	536 bp
PGK1-10F + PGK1-10R	GGTGCTCATTTAGCAATTTTGA GGGGAATGTGCAAAATAGATGT	559 bp
PGK1-11F + PGK1-11R	GGGGAATGTGCAAAATAGATGT GATGAGCTGGATCTTGTCTGC	506 bp

D. Human *CFP* probe.

Primer pair	Sequences, 5′–3′	Amplimer size
CFP-1F + CFP-1R	GGGCGGATACTGACTCTAGC TCATAGGGCAAACAGCACAG	546 bp
CFP-2F + CFP-2R	GACTGCACACTCGCTTTCAC GTAGCCCTCGGCATATAGCA	504 bp
CFP-3F + CFP-3R	CTAGCTTCTTTGCCCCTCCT TCATAGGGCAAACAGCACAG	502 bp
CFP-4F + CFP-4R	TGCCTTGTCCTGACATTCAA TCAACCTAGGTCCAGGAAGC	532 bp
CFP-5F + CFP-5R	TCCGTTCACAGTCTTGATGC TATTACAGGCGGGAGAGTCG	553 bp
CFP-6F + CFP-6R	ACTCGGCAAGGCAGATACC ATCCGACGGAACATGAAGTC	539 bp
CFP-7F + CFP-7R	CAAAGCAGGGAATCAGCAA GCTCTTGATTGAGGGCAGAG	555 bp
CFP-8F + CFP-8R	AATCGTGAACCCTGAGATGC ACCCCACGAACCTAAGGAGA	523 bp
CFP-9F + CFP-9R	CTCCTCACCAGGACAGCACT TGGTGATCTGGTGGGTTTCT	502 bp
CFP-10F + CFP-10R	CTAGAAACCAAGGGCTGCTG ACTGGAAGCATTGCAGGTG	587 bp
CFP-11F + CFP-11R	TTGAGAAACCCTGAGGTATGG CTGCCAGCCACAGGTGAG	534 bp

E. Human *TLR8* probe.

Primer pair	Sequences, 5′–3′	Amplimer size
TLR8-1F + TLR8-1R	TCGAACTTTAAGCCTCCAACA TCGAACTTTAAGCCTCCAACA	534 bp
TLR8-2F + TLR8-2R	TAAAGCGGCTTGCTATGATCT ACGGACCACCTGCTATGTCT	480 bp
TLR8-3F + TLR8-3R	ACGGACCACCTGCTATGTCT GGCTTGTCCTATGGTCTTGAGT	484 bp
TLR8-4F + TLR8-4R	CATTGTGCTGAAGCAGCTAAGT CTGAAATTGGATGCTGATGG	495 bp
TLR8-5F + TLR8-5R	TTCCAGGAAGACAGCTTTACG CCTCTCCCTGCCAAATACAG	471 bp
TLR8-6F + TLR8-6R	GGCATGGTCACACAGCACT GCCTCAACATCCGATTTCAA	488 bp
TLR8-7F + TLR8-7R	TCTTGCCCTTCCCATTTATGT GGCCCAAGGAGAATATGTCAG	487 bp
TLR8-8F + TLR8-8R	ACATTAAGCAGCAACATCACGA AGTAACACAGGAGAGTGCCTCA	487 bp
TLR8-9F + TLR8-9R	TGGGCAATAATGATTGAGCTT AATCCTCGTGCCTGAACTGT	535 bp
TLR8-10F + TLR8-10R	AAAACACCTGGCAAATACTGC CTCTGGCAAACCAGAGGGTA	494 bp
TLR8-11F + TLR8-11R	ATATCACAGACGGGGCATTC TTAATTGAAGCACCACCATCA	487 bp
TLR8-12F + TLR8-12R	CAAACTGCCAAGCTCCCTAC TCAGGGGCTGGAAATCATC	518 bp
TLR8-13F + TLR8-13R	AAGGGGAGTTATCCACAGCA TGACATGAGGAATGGCTGAA	550 bp
TLR8-14F + TLR8-14R	GCCACAATGTGCTGCTTATG TTCATTTGGGATGTGCTTCA	544 bp
TLR8-15F + TLR8-15R	GGAAAGCAAGTCCCTGGTAGA TCAAAGGGGTTTCCGTGTAG	510 bp
TLR8-16F + TLR8-16R	AACAATCAACAAATCCGCACT CGGCTCTCTTCAAGGTGGTA	480 bp
TLR8-17F + TLR8-17R	GATGTCATTTGTGCCAGTCCT TAGCCTCTGCAAAGCCAAGTA	504 bp

F. Human *TLR7* probe[1].

Primer pair	Sequences, 5′–3′	Amplimer size
TLR7-1F + TLR7-1R	TTATAAGGAAGTGGGGAGGAGA TCTTGCCAGCTGGTTTCAG	477 bp
TLR7-2F + TLR7-2R	TGCTCTGCTCTCTTCAACCAG TTTTCTTTGACAGCACTCAAGC	513 bp
TLR7-3F + TLR7-3R	AGAGCCCTATGGTCTTTGGTG CTGGAAACCTTGCCCTCA	487 bp
TLR7-4F + TLR7-4R	TCAGCAACTTCCCTTATTCACA GGATTTCCTGCTCTCCTGACT	503 bp
TLR7-5F + TLR7-5R	GCTTGGAGGAACAGCTGAGT AGACAGGACATATGGGAGCAG	482 bp
TLR7-6F + TLR7-6R	TCAGTTGGTAGCCCTGTAGCA TCAGGCCTAAAGGTAACACTGC	525 bp
TLR7-7F + TLR7-7R	ACGTGGTGCTAACCCCTAGAA TGCTGTCAGGGAAATCTATGGT	525 bp
TLR7-8F + TLR7-8R	TTCTCCCTCACCTGCTTGA AGGAATTTTTCCCTGAAGATCA	476 bp
TLR7-9F + TLR7-9R	TTTCACAGCCTCCATTTTCC TGCCAGTGGGTACAGGAAG	536 bp
TLR7-10F + TLR7-10R	GTGTACCAGGGCAGGTTTAGC ACCATCTAGCCCCAAGGAGT	513 bp
TLR7-11F + TLR7-11R	ACTCCTTGGGGCTAGATGGT CAGTTTTGGCCCAGGTAGAG	480 bp
TLR7-12F + TLR7-12R	CCTCCCGCCTAGCTTACAG GGGCACATGCTGAAGAGAGT	484 bp
TLR7-13F + TLR7-13R	AATGCTTTTGATGCGCTGA TTGAGCAGAAGCCAACTTCA	490 bp
TLR7-14F + TLR7-14R	AGTGAAGTTGGCTTCTGCTCA TGGTGGAGGAAGAGATGTCA	520 bp
TLR7-15F + TLR7-15R	ATCTCTTCCTCCACCAGCAG GGACATTTTCTGGGAAGCTG	493 bp
TLR7-16F + TLR7-16R	CAGCTTCCCAGAAAATGTCC TGGTAACCAGTCCCTTTCCTC	511 bp
TLR7-17F + TLR7-17R	CAAACTGGAAGACCCAAGAGA CAAAACACGCTTTTGGTGTG	502 bp

[1]Primer set from our previous publication, Souyris et al., Sci Immunol. 2018; 3:eaap8855.

S1 Data

TLR7 escape from XCI (monocytes, women)

Donor ID	Total cell count	Escape cell count	Percent escape	95% CI lower	95% CI upper
F620	55	3	5.5	0	11.3
F489	128	10	7.8	3.1	12.4
F441	85	27	31.8	21.5	41.3
F438	78	13	16.7	8.1	24.7
F431	67	15	22.4	12.1	32.1
F258	56	6	10.7	2.3	18.6
Summary			13.3	10.3	16.6

TLR8 escape from XCI (monocytes, women)

Donor ID	Total cell count	Escape cell count	Percent escape	95% CI lower	95% CI upper
F620	103	19	18.4	10.8	25.8
F489	75	10	13.3	5.5	20.9
F441	85	10	11.8	4.8	18.5
F438	107	27	25.2	16.7	33.2
F431	59	6	10.2	2.2	17.7
F258	86	29	33.7	23.3	43.3
Summary			17.5	14.2	20.9

TLR7 escape from XCI (monocytes, Klinefelter syndrome men)

Donor ID	Total cell count	Escape cell count	Percent escape	95% CI lower	95% CI upper
K2	53	6	11.3	2.5	19.7
K3	39	7	17.9	5.4	29.6
K4	49	6	12.2	2.7	21.2
K5	61	11	18.0	8.1	27.4
K11	62	9	14.5	5.4	23
Summary			13.3	9.1	17.7

TLR8 escape from XCI (monocytes, Klinefelter syndrome men)

Donor ID	Total cell count	Escape cell count	Percent escape	95% CI lower	95% CI upper
K2	95	29	30.5	20.9	39.5
K3	54	27	50.0	35.7	62.5
K4	105	36	34.3	24.9	43
K5	88	9	10.2	3.7	16.5
K11	90	8	8.9	2.8	14.6
Summary			22.7	18.8	26.7

TLR7 escape from XCI (CD4+ T cells, women)

Donor ID	Total cell count	Escape cell count	Percent escape	95% CI lower	95% CI upper
F438	71	8	11.3	3.7	18.4
F557	74	7	9.5	2.7	16
F595	62	5	8.1	1.1	14.6
F619	39	4	10.3	0.4	19.6
F689	53	3	5.7	0	11.7
Summary			7.7	4.5	11

TLR8 escape from XCI (CD4+ T cells, women)

Donor ID	Total cell count	Escape cell count	Percent escape	95% CI lower	95% CI upper
F438	85	6	7.1	1.5	12.4
F557	107	10	9.3	3.8	14.8
F595	109	22	20.2	12.4	27.5
F619	85	5	5.9	0.7	10.8
F689	90	4	4.4	0.1	8.6
Summary			7.9	5.5	10.5

S2 Data. RNA FISH analysis of CD14⁺ monocytes, signals on the Xi. Left, observed frequencies: cell counts cross-classified as 2×2 contingency tables depending on the presence of transcriptional foci for *TLR7* or *TLR8* on the Xi of monocytes from women and from men with Klinefelter syndrome. Right, the corresponding expected frequencies, computed under the null hypothesis of mutually independent transcription of the two genes in *cis* on the Xi. Donor IDs in red.

A. Women

Observed frequencies

F620	TLR7 +	TLR7 –
TLR8 +	0	19
TLR8 –	3	136

F489	TLR7 +	TLR7 –
TLR8 +	1	10
TLR8 –	6	186

F438	TLR7 +	TLR7 –
TLR8 +	1	26
TLR8 –	12	146

F431	TLR7 +	TLR7 –
TLR8 +	1	5
TLR8 –	14	106

F296	TLR7 +	TLR7 –
TLR8 +	1	10
TLR8 –	13	85

F258	TLR7 +	TLR7 –
TLR8 +	0	29
TLR8 –	6	107

Pooled data	TLR7 +	TLR7 –
TLR8 +	4	99
TLR8 –	54	766

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	0.4	18.6
TLR8 –	2.6	136.4

	TLR7 +	TLR7 –
TLR8 +	0.4	10.6
TLR8 –	6.6	185.4

	TLR7 +	TLR7 –
TLR8 +	1.9	25.1
TLR8 –	11.1	146.9

	TLR7 +	TLR7 –
TLR8 +	0.7	5.3
TLR8 –	14.3	105.7

	TLR7 +	TLR7 –
TLR8 +	1.4	9.6
TLR8 –	12.6	85.4

	TLR7 +	TLR7 –
TLR8 +	1.2	27.8
TLR8 –	4.8	108.2

	TLR7 +	TLR7 –
TLR8 +	6.5	96.5
TLR8 –	51.5	768.5

B. Men with Klinefelter syndrome

Observed frequencies

K2	TLR7 +	TLR7 –
TLR8 +	0	29
TLR8 –	6	113

K3	TLR7 +	TLR7 –
TLR8 +	1	27
TLR8 –	7	58

K4	TLR7 +	TLR7 –
TLR8 +	1	36
TLR8 –	5	112

K5	TLR7 +	TLR7 –
TLR8 +	0	9
TLR8 –	11	129

K11	TLR7 +	TLR7 –
TLR8 +	1	8
TLR8 –	9	134

Pooled data	TLR7 +	TLR7 –
TLR8 +	3	109
TLR8 –	38	546

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	1.2	27.8
TLR8 –	4.8	114.2

	TLR7 +	TLR7 –
TLR8 +	2.4	25.6
TLR8 –	5.6	59.4

	TLR7 +	TLR7 –
TLR8 +	1.4	35.6
TLR8 –	4.6	112.4

	TLR7 +	TLR7 –
TLR8 +	0.7	8.3
TLR8 –	10.3	129.7

	TLR7 +	TLR7 –
TLR8 +	0.6	8.4
TLR8 –	9.4	133.6

	TLR7 +	TLR7 –
TLR8 +	6.6	105.4
TLR8 –	34.4	549.6

S3 Data. RNA FISH analysis of CD14⁺ monocytes, total cells. Left, observed frequencies: cell counts cross-classified as 2×2 contingency tables depending on the presence of transcriptional foci for *TLR7* or *TLR8*, regardless of Xa markers (Any X plots). Right, the corresponding expected frequencies, computed under the null hypothesis of mutually independent transcription of the two genes. Donor IDs in red.

A. Normal men

Observed frequencies

M366	TLR7 +	TLR7 –
TLR8 +	5	77
TLR8 –	50	120

M387	TLR7 +	TLR7 –
TLR8 +	6	63
TLR8 –	60	160

M235	TLR7 +	TLR7 –
TLR8 +	4	73
TLR8 –	22	112

M525	TLR7 +	TLR7 –
TLR8 +	7	35
TLR8 –	68	190

M657	TLR7 +	TLR7 –
TLR8 +	7	50
TLR8 –	44	198

M660	TLR7 +	TLR7 –
TLR8 +	5	65
TLR8 –	34	133

M661	TLR7 +	TLR7 –
TLR8 +	7	66
TLR8 –	22	210

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	17.9	64.1
TLR8 –	37.1	132.9

	TLR7 +	TLR7 –
TLR8 +	15.8	53.2
TLR8 –	50.2	169.8

	TLR7 +	TLR7 –
TLR8 +	9.5	67.5
TLR8 –	16.5	117.5

	TLR7 +	TLR7 –
TLR8 +	10.5	31.5
TLR8 –	64.5	193.5

	TLR7 +	TLR7 –
TLR8 +	9.7	47.3
TLR8 –	41.3	200.7

	TLR7 +	TLR7 –
TLR8 +	11.5	58.5
TLR8 –	27.5	139.5

	TLR7 +	TLR7 –
TLR8 +	6.9	66.1
TLR8 –	22.1	209.9

B. Women

Observed frequencies

F489	TLR7 +	TLR7 –
TLR8 +	49	26
TLR8 –	79	280

F496	TLR7 +	TLR7 –
TLR8 +	52	46
TLR8 –	44	147

F620	TLR7 +	TLR7 –
TLR8 +	34	69
TLR8 –	21	143

F438	TLR7 +	TLR7 –
TLR8 +	43	64
TLR8 –	35	120

F258	TLR7 +	TLR7 –
TLR8 +	27	29
TLR8 –	59	105

F431	TLR7 +	TLR7 –
TLR8 +	33	26
TLR8 –	34	93

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	22.1	52.9
TLR8 –	105.9	253.1

	TLR7 +	TLR7 –
TLR8 +	32.6	65.4
TLR8 –	63.4	127.6

	TLR7 +	TLR7 –
TLR8 +	21.2	81.8
TLR8 –	33.8	130.2

	TLR7 +	TLR7 –
TLR8 +	31.9	75.1
TLR8 –	46.1	108.9

	TLR7 +	TLR7 –
TLR8 +	21.9	34.1
TLR8 –	64.1	99.9

	TLR7 +	TLR7 –
TLR8 +	21.3	37.7
TLR8 –	45.7	81.3

C. Men with Klinefelter syndrome

Observed frequencies

K2	TLR7 +	TLR7 –
TLR8 +	35	60
TLR8 –	18	152

K3	TLR7 +	TLR7 –
TLR8 +	27	79
TLR8 –	30	156

K4	TLR7 +	TLR7 –
TLR8 +	22	83
TLR8 –	27	202

K11	TLR7 +	TLR7 –
TLR8 +	36	54
TLR8 –	26	239

K5	TLR7 +	TLR7 –
TLR8 +	31	57
TLR8 –	30	182

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	19.0	76.0
TLR8 –	34.0	136.0

	TLR7 +	TLR7 –
TLR8 +	20.7	85.3
TLR8 –	36.3	149.7

	TLR7 +	TLR7 –
TLR8 +	15.4	89.6
TLR8 –	33.6	195.4

	TLR7 +	TLR7 –
TLR8 +	15.7	74.3
TLR8 –	46.3	218.7

	TLR7 +	TLR7 –
TLR8 +	17.9	70.1
TLR8 –	43.1	168.9

S4 Data. RNA FISH analysis of CD14⁺ monocytes, Xa-positive cells. Left, observed frequencies: cell counts cross-classified as 2×2 contingency tables depending on the presence of transcriptional foci for *TLR7* or *TLR8*. Only those cells positive for the Xa marker probe (Xa⁺) were counted. Right, the corresponding expected frequencies, computed under the assumption of mutually independent transcription of the two genes. Donor IDs in red.

A. Normal men

Observed frequencies

M848	TLR7 +	TLR7 –
TLR8 +	6	40
TLR8 –	21	36

M387	TLR7 +	TLR7 –
TLR8 +	4	44
TLR8 –	30	20

M331	TLR7 +	TLR7 –
TLR8 +	6	36
TLR8 –	37	33

M235	TLR7 +	TLR7 –
TLR8 +	5	54
TLR8 –	18	23

M660	TLR7 +	TLR7 –
TLR8 +	5	46
TLR8 –	52	27

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	12.1	33.9
TLR8 –	14.9	42.1

	TLR7 +	TLR7 –
TLR8 +	16.7	31.3
TLR8 –	17.3	32.7

	TLR7 +	TLR7 –
TLR8 +	16.1	25.9
TLR8 –	26.9	43.1

	TLR7 +	TLR7 –
TLR8 +	13.6	45.4
TLR8 –	9.4	31.6

	TLR7 +	TLR7 –
TLR8 +	22.4	28.6
TLR8 –	34.6	44.4

B. Women

Observed frequencies

F489	TLR7 +	TLR7 –
TLR8 +	34	15
TLR8 –	21	27

F620	TLR7 +	TLR7 –
TLR8 +	20	22
TLR8 –	10	48

F438	TLR7 +	TLR7 –
TLR8 +	34	46
TLR8 –	11	30

F258	TLR7 +	TLR7 –
TLR8 +	23	5
TLR8 –	14	11

F431	TLR7 +	TLR7 –
TLR8 +	32	16
TLR8 –	14	19

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	27.8	21.2
TLR8 –	27.2	20.8

	TLR7 +	TLR7 –
TLR8 +	12.6	29.4
TLR8 –	17.4	40.6

	TLR7 +	TLR7 –
TLR8 +	29.8	50.2
TLR8 –	15.2	25.8

	TLR7 +	TLR7 –
TLR8 +	19.5	8.5
TLR8 –	17.5	7.5

	TLR7 +	TLR7 –
TLR8 +	27.3	20.7
TLR8 –	18.7	14.3

C. Men with Klinefelter syndrome

Observed frequencies

K2	TLR7 +	TLR7 –
TLR8 +	33	26
TLR8 –	7	21

K3	TLR7 +	TLR7 –
TLR8 +	18	36
TLR8 –	21	15

K4	TLR7 +	TLR7 –
TLR8 +	16	38
TLR8 –	12	26

K11	TLR7 +	TLR7 –
TLR8 +	27	29
TLR8 –	13	21

K5	TLR7 +	TLR7 –
TLR8 +	18	41
TLR8 –	24	17

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	27.1	31.9
TLR8 –	12.9	15.1

	TLR7 +	TLR7 –
TLR8 +	23.4	30.6
TLR8 –	15.6	20.4

	TLR7 +	TLR7 –
TLR8 +	16.4	37.6
TLR8 –	11.6	26.4

	TLR7 +	TLR7 –
TLR8 +	24.9	31.1
TLR8 –	15.1	18.9

	TLR7 +	TLR7 –
TLR8 +	24.8	34.2
TLR8 –	17.2	23.8

S5 Data. Xa versus Xi comparison for patterns of *TLR7* and *TLR8* transcription. The 3×2 tables show *TLR7*$^{+}$ *TLR8*$^{+}$, *TLR7*$^{-}$ *TLR8*$^{+}$, and *TLR7*$^{+}$ *TLR8*$^{-}$ cell counts in the RNA FISH data for the Xa and the Xi of monocytes from female and Klinefelter syndrome male donors; p-values from Monte Carlo χ^2 tests with 10^6 replications. Donor IDs in red.

A. Women.

	Xa	Xi	p-value
F620			
TLR7+ TLR8+	20	0	0.00060
TLR7– TLR8+	22	19	
TLR7+ TLR8–	10	3	
F489			
TLR7+ TLR8+	34	1	0.0013
TLR7– TLR8+	15	10	
TLR7+ TLR8–	21	6	
F438			
TLR7+ TLR8+	34	1	0.000048
TLR7– TLR8+	46	26	
TLR7+ TLR8–	11	12	
F431			
TLR7+ TLR8+	32	1	0.000074
TLR7– TLR8+	16	5	
TLR7+ TLR8–	14	14	
F258			
TLR7+ TLR8+	23	0	0.000001
TLR7– TLR8+	5	29	
TLR7+ TLR8–	14	6	

B. Men with Klinefelter syndrome.

	Xa	Xi	p-value
K2			
TLR7+ TLR8+	33	0	0.000001
TLR7– TLR8+	26	29	
TLR7+ TLR8–	7	6	
K3			
TLR7+ TLR8+	18	1	0.0065
TLR7– TLR8+	36	27	
TLR7+ TLR8–	21	7	
K4			
TLR7+ TLR8+	16	1	0.0030
TLR7– TLR8+	38	36	
TLR7+ TLR8–	12	5	
K5			
TLR7+ TLR8+	18	0	0.021
TLR7– TLR8+	41	9	
TLR7+ TLR8–	24	11	
K11			
TLR7+ TLR8+	27	1	0.0051
TLR7– TLR8+	29	8	
TLR7+ TLR8–	13	9	

S6 Data. RNA FISH analysis of CD4⁺ T lymphocytes from women and normal men. Left, observed frequencies: cell counts cross-classified as 2×2 contingency tables depending on the presence of transcriptional foci for *TLR7* or *TLR8*. Right, expected frequencies, computed from the observed frequencies under the assumption of mutually independent transcription of the two genes. Donor IDs in red. The any X data (**A**, **C**) corresponds to cells scored regardless of the hybridization with the Xa marker probe. In the Xa⁺ data (**B**, **D**), only cells positive for the Xa marker probe were scored.

A. Women, any X

Observed frequencies

F438	TLR7 +	TLR7 –
TLR8 +	47	38
TLR8 –	24	207

F557	TLR7 +	TLR7 –
TLR8 +	54	53
TLR8 –	20	178

F595	TLR7 +	TLR7 –
TLR8 +	44	65
TLR8 –	18	198

F619	TLR7 +	TLR7 –
TLR8 +	19	66
TLR8 –	20	175

F689	TLR7 +	TLR7 –
TLR8 +	45	45
TLR8 –	8	210

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	19.1	65.9
TLR8 –	51.9	179.1

	TLR7 +	TLR7 –
TLR8 +	26.0	81.0
TLR8 –	48.0	150.0

	TLR7 +	TLR7 –
TLR8 +	20.8	88.2
TLR8 –	41.2	174.8

	TLR7 +	TLR7 –
TLR8 +	11.8	73.2
TLR8 –	27.2	167.8

	TLR7 +	TLR7 –
TLR8 +	15.5	74.5
TLR8 –	37.5	180.5

B. Women, Xa⁺

Observed frequencies

F438	TLR7 +	TLR7 –
TLR8 +	45	9
TLR8 –	19	27

F557	TLR7 +	TLR7 –
TLR8 +	41	19
TLR8 –	6	34

F595	TLR7 +	TLR7 –
TLR8 +	35	33
TLR8 –	13	20

F619	TLR7 +	TLR7 –
TLR8 +	18	38
TLR8 –	17	27

F689	TLR7 +	TLR7 –
TLR8 +	44	40
TLR8 –	8	15

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	34.6	19.4
TLR8 –	29.4	16.6

	TLR7 +	TLR7 –
TLR8 +	28.2	31.8
TLR8 –	18.8	21.2

	TLR7 +	TLR7 –
TLR8 +	32.3	35.7
TLR8 –	15.7	17.3

	TLR7 +	TLR7 –
TLR8 +	19.6	36.4
TLR8 –	15.4	28.6

	TLR7 +	TLR7 –
TLR8 +	40.8	43.2
TLR8 –	11.2	11.8

C. Normal men, any X

Observed frequencies

M347	TLR7 +	TLR7 –
TLR8 +	15	56
TLR8 –	66	200

M605	TLR7 +	TLR7 –
TLR8 +	6	81
TLR8 –	31	190

M712	TLR7 +	TLR7 –
TLR8 +	8	76
TLR8 –	31	240

M720	TLR7 +	TLR7 –
TLR8 +	8	56
TLR8 –	36	270

M700	TLR7 +	TLR7 –
TLR8 +	4	31
TLR8 –	59	218

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	17.1	53.9
TLR8 –	63.9	202.1

	TLR7 +	TLR7 –
TLR8 +	10.5	76.5
TLR8 –	26.5	194.5

	TLR7 +	TLR7 –
TLR8 +	9.2	74.8
TLR8 –	29.8	241.2

	TLR7 +	TLR7 –
TLR8 +	7.6	56.4
TLR8 –	36.4	269.6

	TLR7 +	TLR7 –
TLR8 +	7.1	27.9
TLR8 –	55.9	221.1

D. Normal men, Xa^{+}

Observed frequencies

M347	TLR7 +	TLR7 –
TLR8 +	11	16
TLR8 –	23	52

M605	TLR7 +	TLR7 –
TLR8 +	6	47
TLR8 –	13	34

M712	TLR7 +	TLR7 –
TLR8 +	6	36
TLR8 –	21	38

M720	TLR7 +	TLR7 –
TLR8 +	6	36
TLR8 –	20	38

M700	TLR7 +	TLR7 –
TLR8 +	4	31
TLR8 –	44	21

Expected frequencies

	TLR7 +	TLR7 –
TLR8 +	9	18
TLR8 –	25	50

	TLR7 +	TLR7 –
TLR8 +	10.1	42.9
TLR8 –	8.9	38.1

	TLR7 +	TLR7 –
TLR8 +	11.2	30.8
TLR8 –	15.8	43.2

	TLR7 +	TLR7 –
TLR8 +	10.9	31.1
TLR8 –	15.1	42.9

	TLR7 +	TLR7 –
TLR8 +	16.8	18.2
TLR8 –	31.2	33.8