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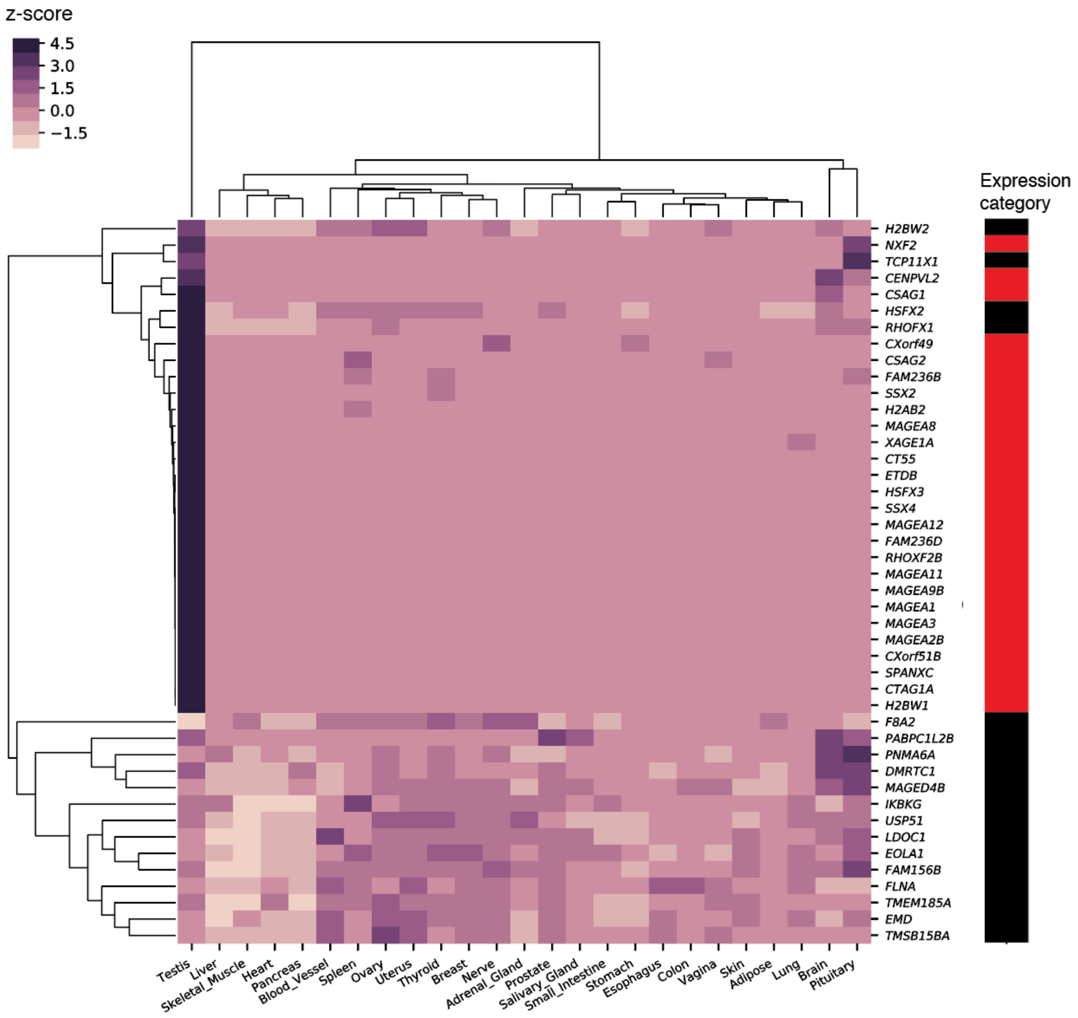
Supplemental Note 1: Treatment of human X-palindrome genes with conflicting annotations

There were three instances in which a gene in one arm of a palindrome was designated as protein-coding while the homologous sequence in the other arm was designated a pseudogene: *IKBKG* (protein-coding) and *IKBKGP1* (unprocessed pseudogene); *PNMA6A* (protein-coding) and *PNMA6B* (unprocessed pseudogene), and *AC236972.4* (protein-coding) and *AC152010.1* (processed pseudogene). We decided whether to include gene copies marked as pseudogenes in downstream analyses, i.e., whether their expression should be averaged with that of the corresponding protein-coding gene, as follows:

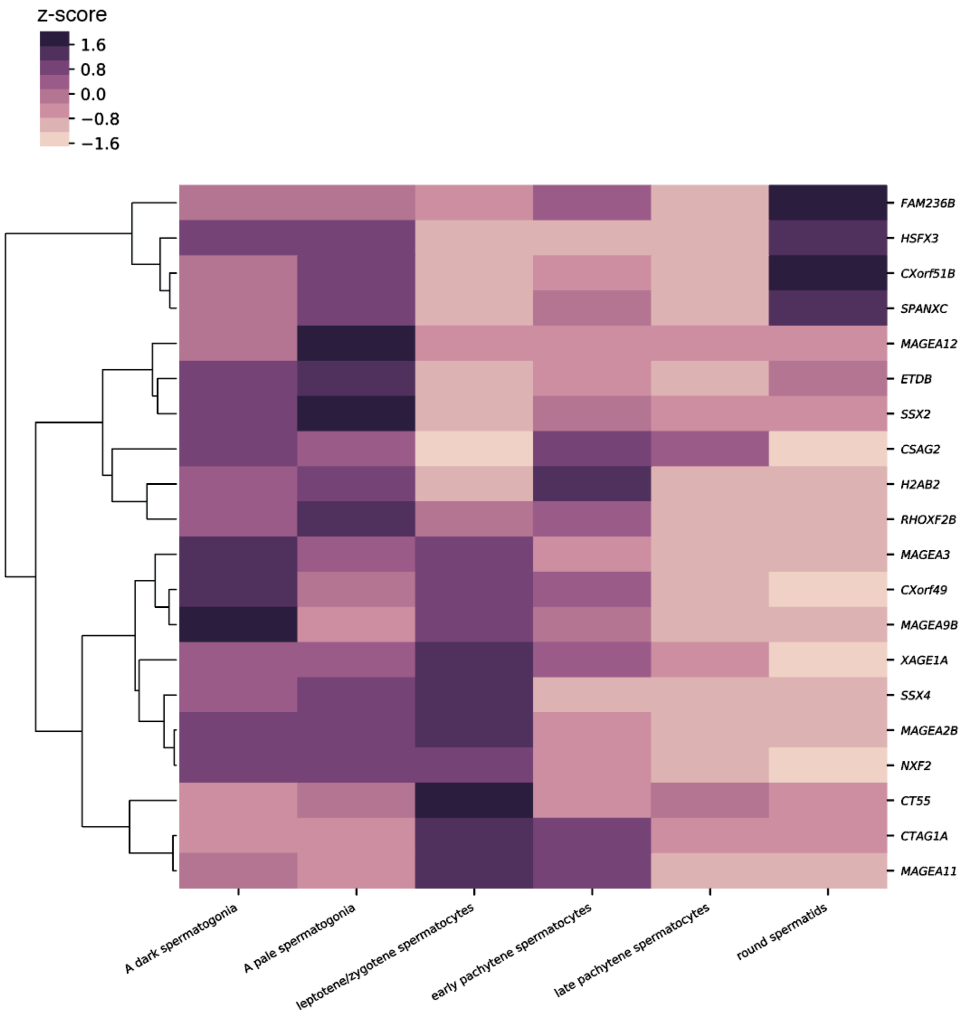
1) *PNMA6A* encodes a protein of 399 amino acids. *PNMA6A* and *PNMA6B* differ in their coding sequence by only a single missense substitution. The 3' UTR of *PNMA6B* is truncated, but the significance of this is unclear. Given that *PNMA6B* encodes an intact protein-coding sequence, we chose to include *PNMA6B* in downstream analyses.

2) *AC236972.4* encodes a protein of 2061 amino acids. *AC152010.1* has a nonsense substitution, but contains a downstream start codon that would lead to translation of the terminal 1253 amino acids of *AC236972.4.* Given that *AC152010.1* encodes a protein encompassing more than half the length of the original protein, we chose to include *AC152010.1* in downstream analyses.

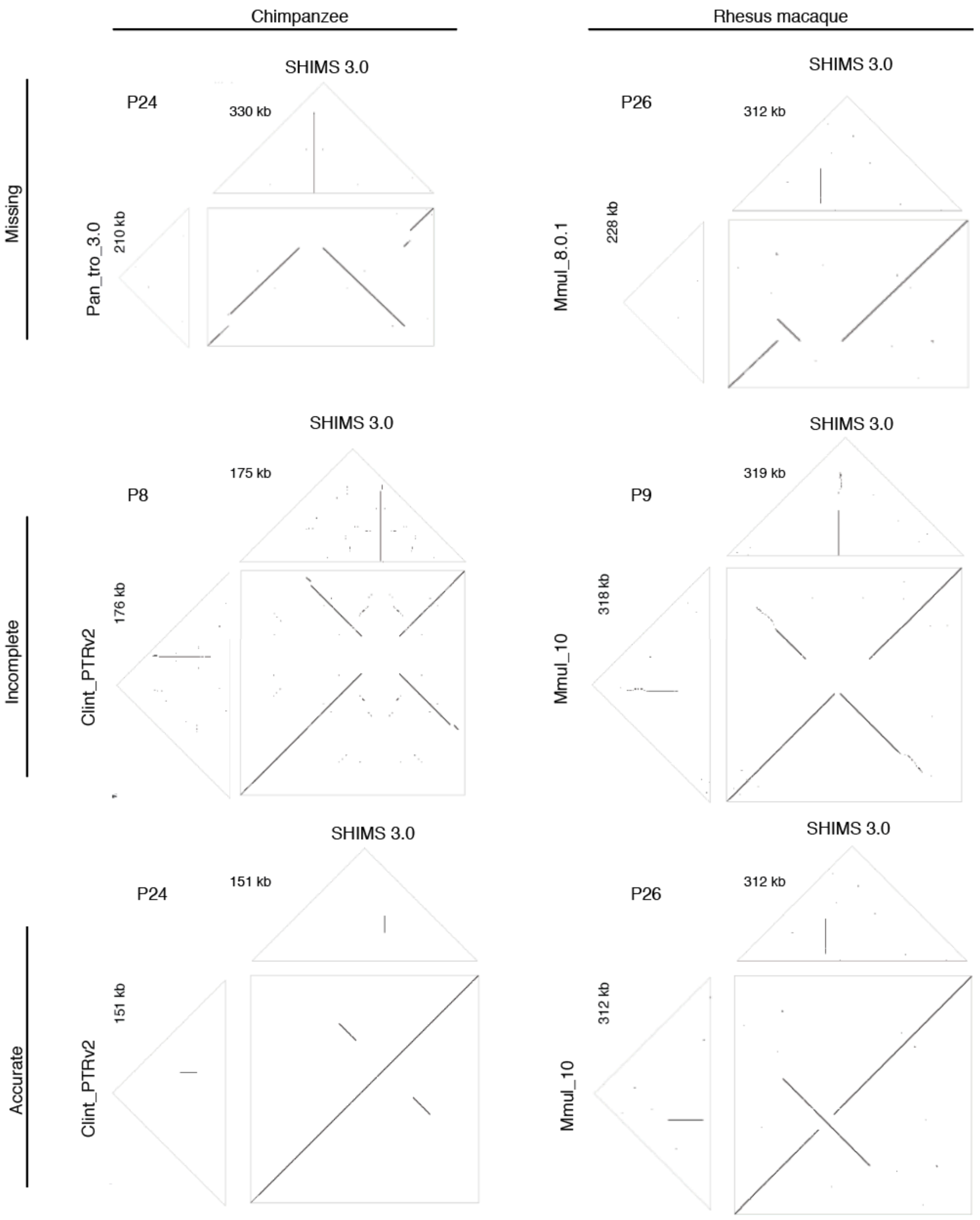
3) *IKBKG* encodes a protein of 419 amino acids. *IKBKGP1* is a well-characterized pseudogene lacking the promoter and first four exons of *IKBKG* (Aradhya et al. 2001); we therefore chose not to include it in downstream analyses.



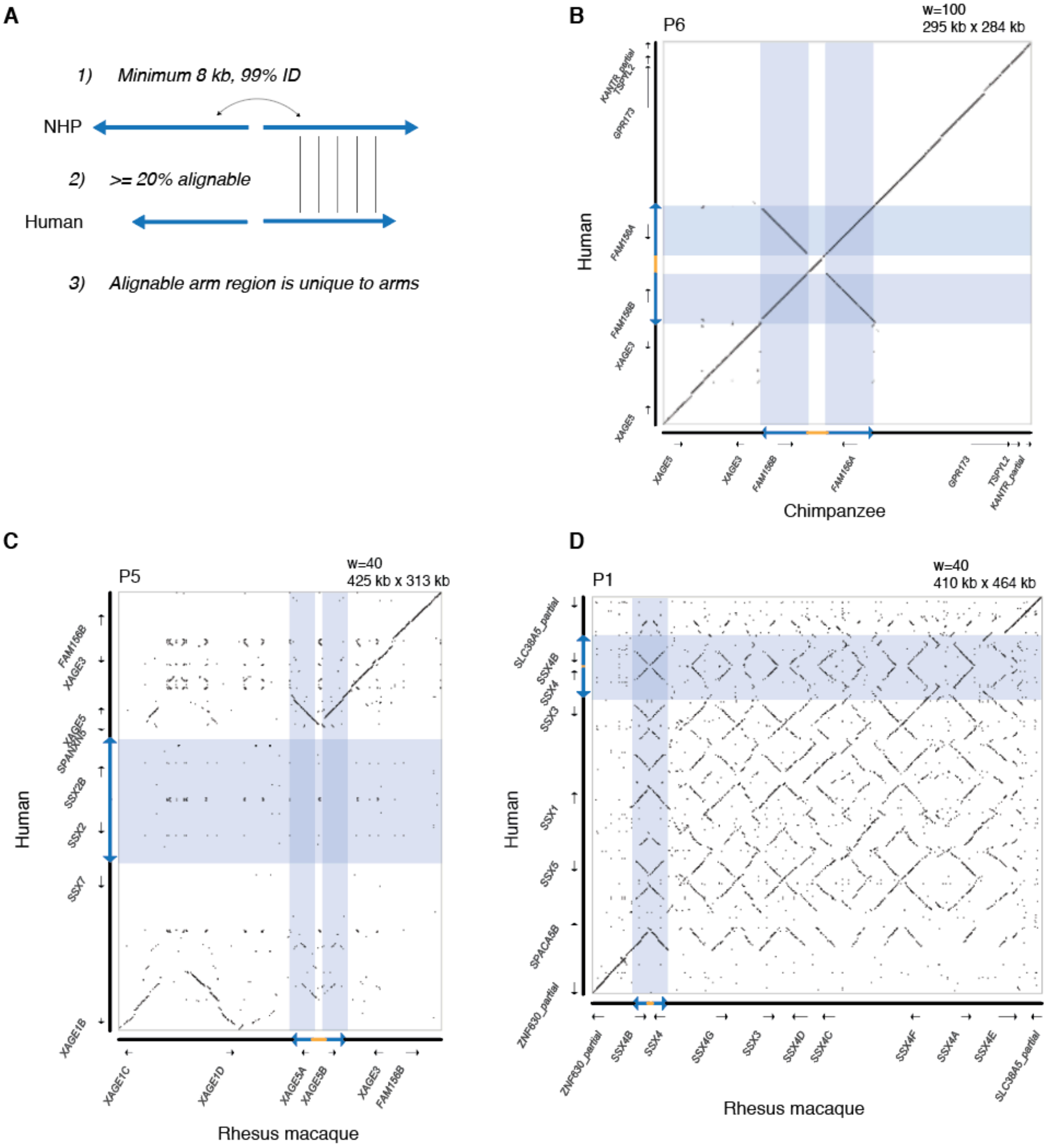
Supplemental Figure S1. Expression of human X-palindrome gene families. Heatmap shows z-score for each expressed gene (>2 TPM in at least one tissue) across 25 tissues from GTEx, with row and column order determined by hierarchical clustering. Expression category: Shows whether expression is testis-biased (red) or broad (black). Testis-biased: Minimum 2 TPM in testis, and testis accounts for >25% of log2 normalized expression summed across all tissues. Broad: All other expressed genes.



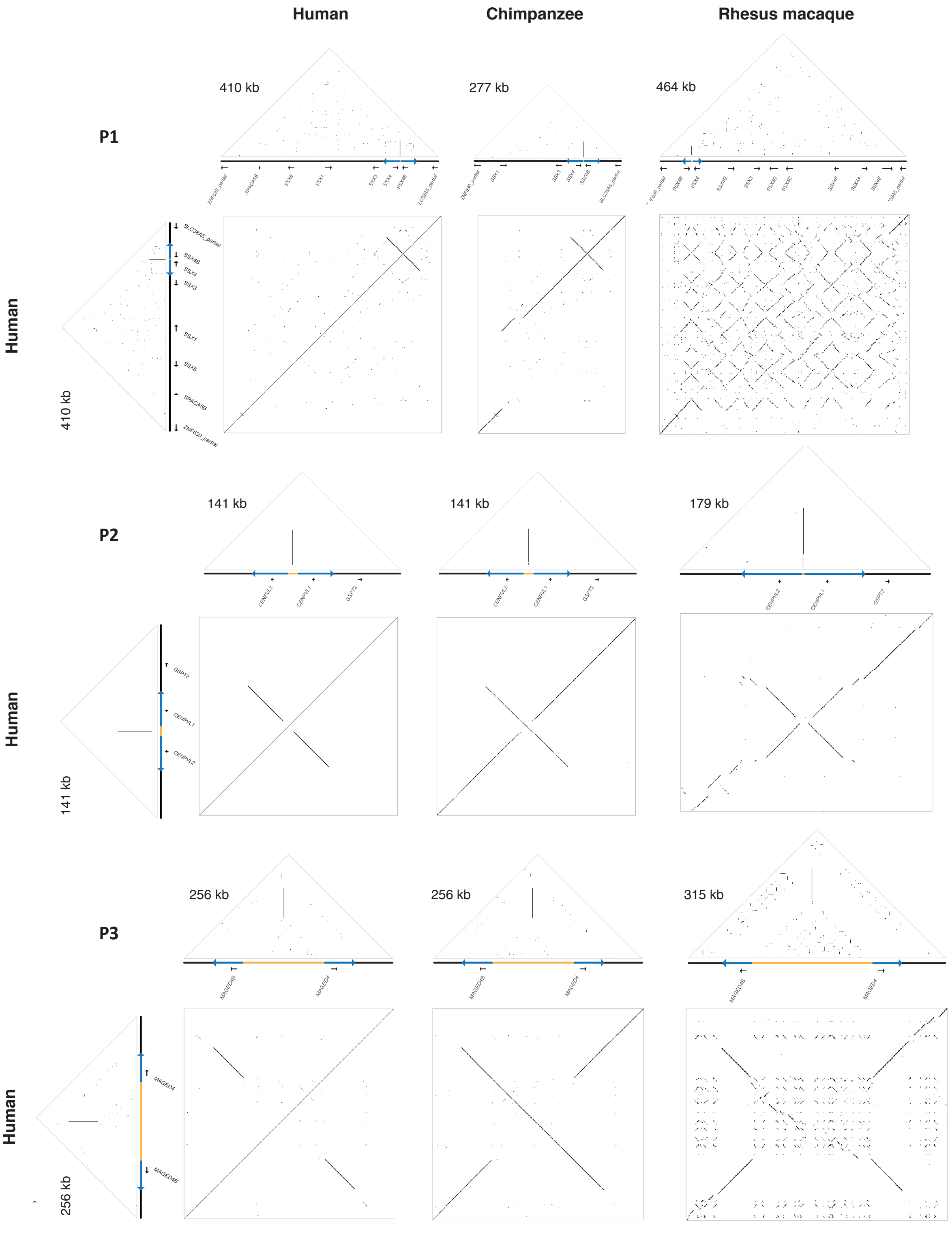
Supplemental Figure S2. Expression of human testis-biased X-palindrome gene families during spermatogenesis. Heatmap shows z-score for each expressed gene (>2 TPM in at least one spermatogenic stage) across six spermatogenic stages from Jan et al. 2017, with row order determined by hierarchical clustering.



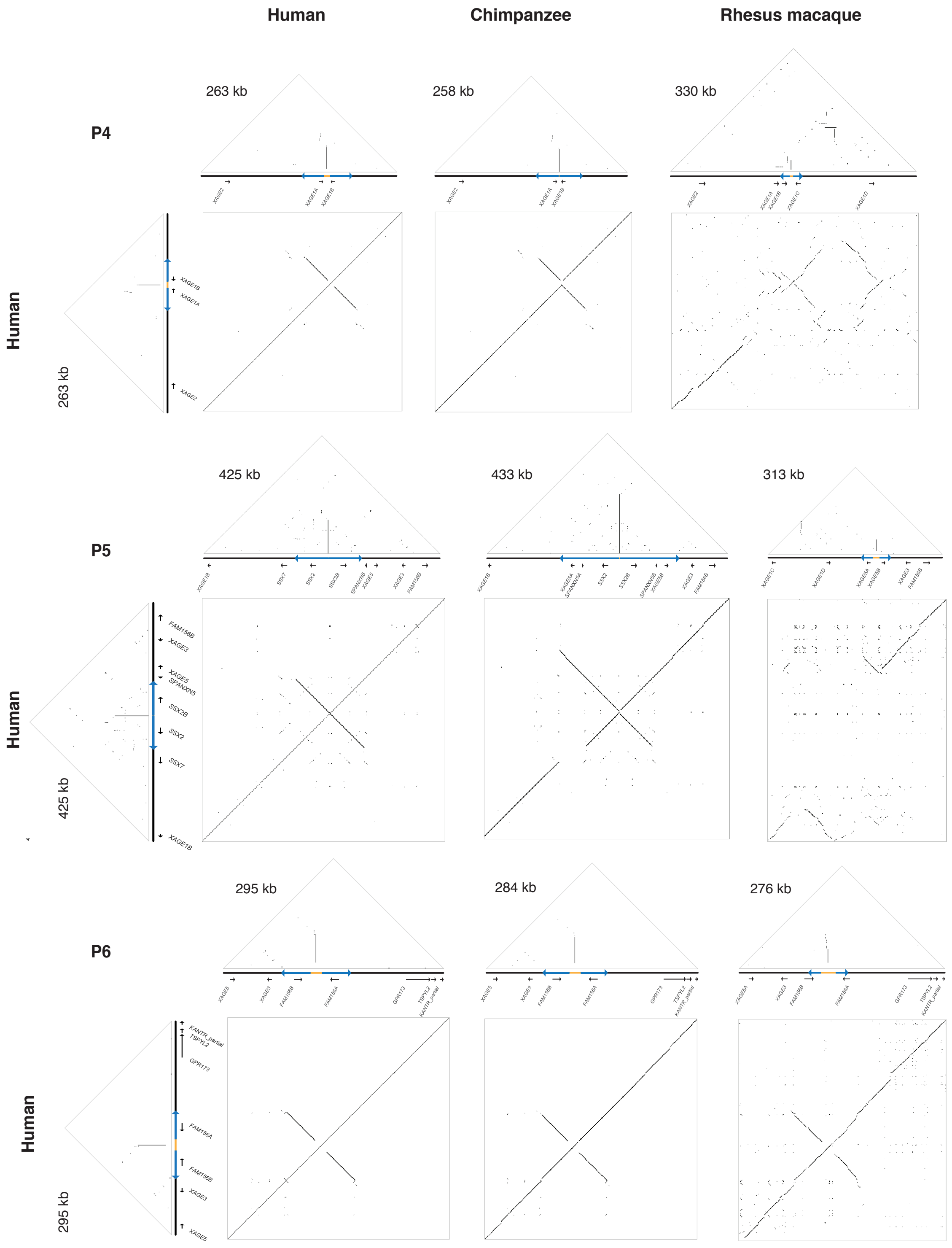
Supplemental Figure S3. Structural comparisons between palindromes in SHIMS 3.0 assemblies and existing X-Chromosome assemblies. Missing: No palindrome present in non-SHIMS 3.0 assembly. Incomplete: Part of palindrome present in non-SHIMS 3.0 assembly. Accurate: Full palindrome present in non-SHIMS 3.0 assembly. For accurate palindrome assemblies, note the presence in the square dot plot of an uninterrupted diagonal line and two arms that each map twice to the SHIMS 3.0 assembly. w=100 for all triangular and square dot plots.



Supplemental Figure S4. Definition of orthologous palindromes. a) Criteria for defining orthologous palindromes. NHP = non-human primate (chimpanzee or rhesus macaque). Human and NHP palindrome arms were aligned with ClustalW, and required to have at least 20% alignment between species. Palindromes were excluded if the alignable region between palindrome arms mapped equally well to flanking sequence using reciprocal BLAST hits (>10% positions in high-quality hits mapping outside of palindrome arms). b) Example of an orthologous palindrome. Human palindrome arms map exactly twice to chimpanzee palindrome arms, and vice versa. c, d) Examples of palindromes that are not orthologous. c) Human palindrome arms have no orthologous sequence in rhesus macaque. Rhesus macaque palindrome arms correspond to flanking sequence in human. d) Rhesus macaque palindrome arms correspond equally well to more than two positions in human, and vice versa. Note that the region with the strongest orthology to rhesus macaque palindrome arms corresponds to flanking sequence in human.



Supplemental Figure S5. Annotated square and triangular dot plots of primate X palindromes. w=100 for all triangle plots. w=100 for human vs. human square plots, human vs. chimpanzee square plots; w=40 for human vs. rhesus macaque square plots.



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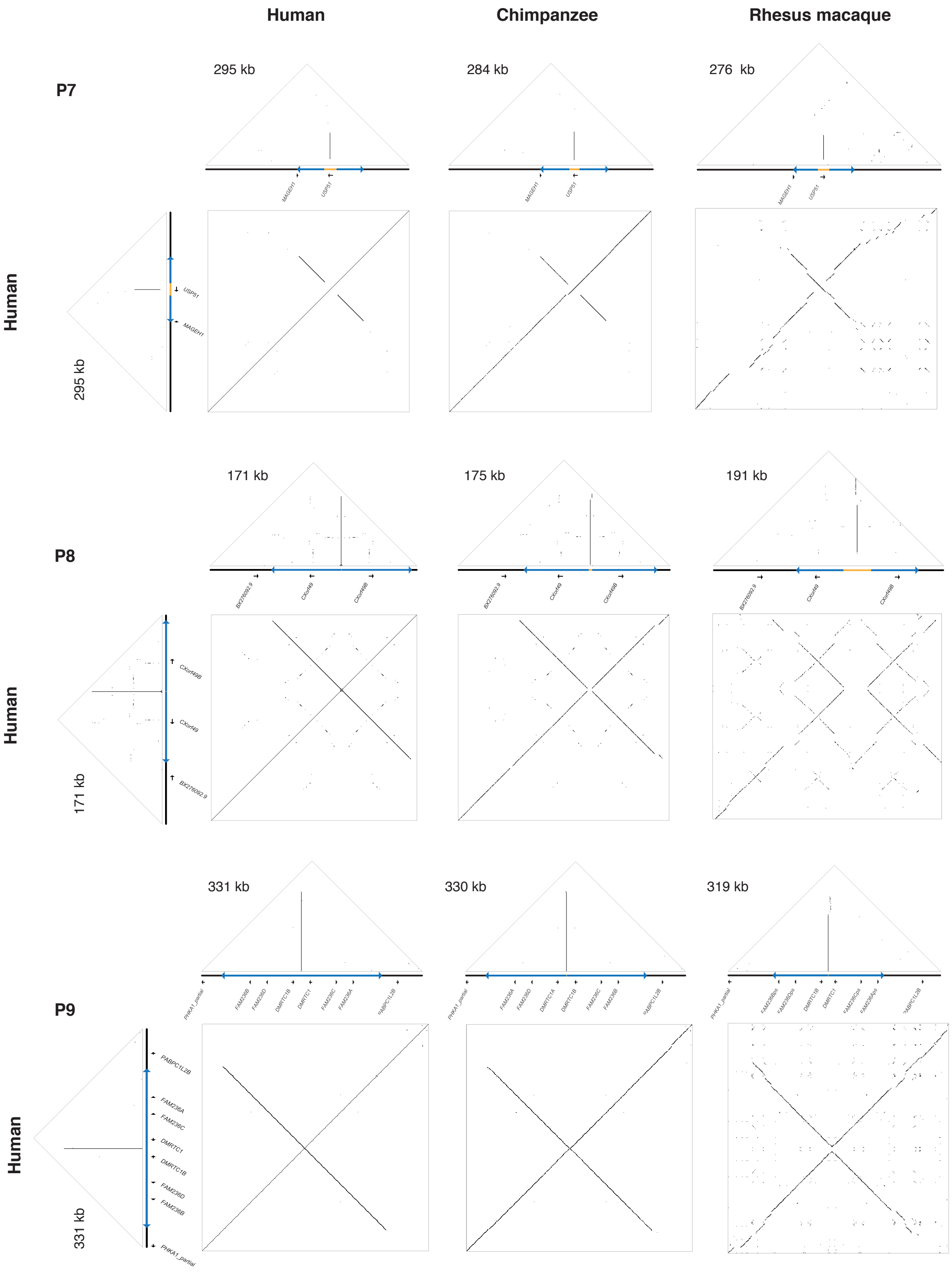

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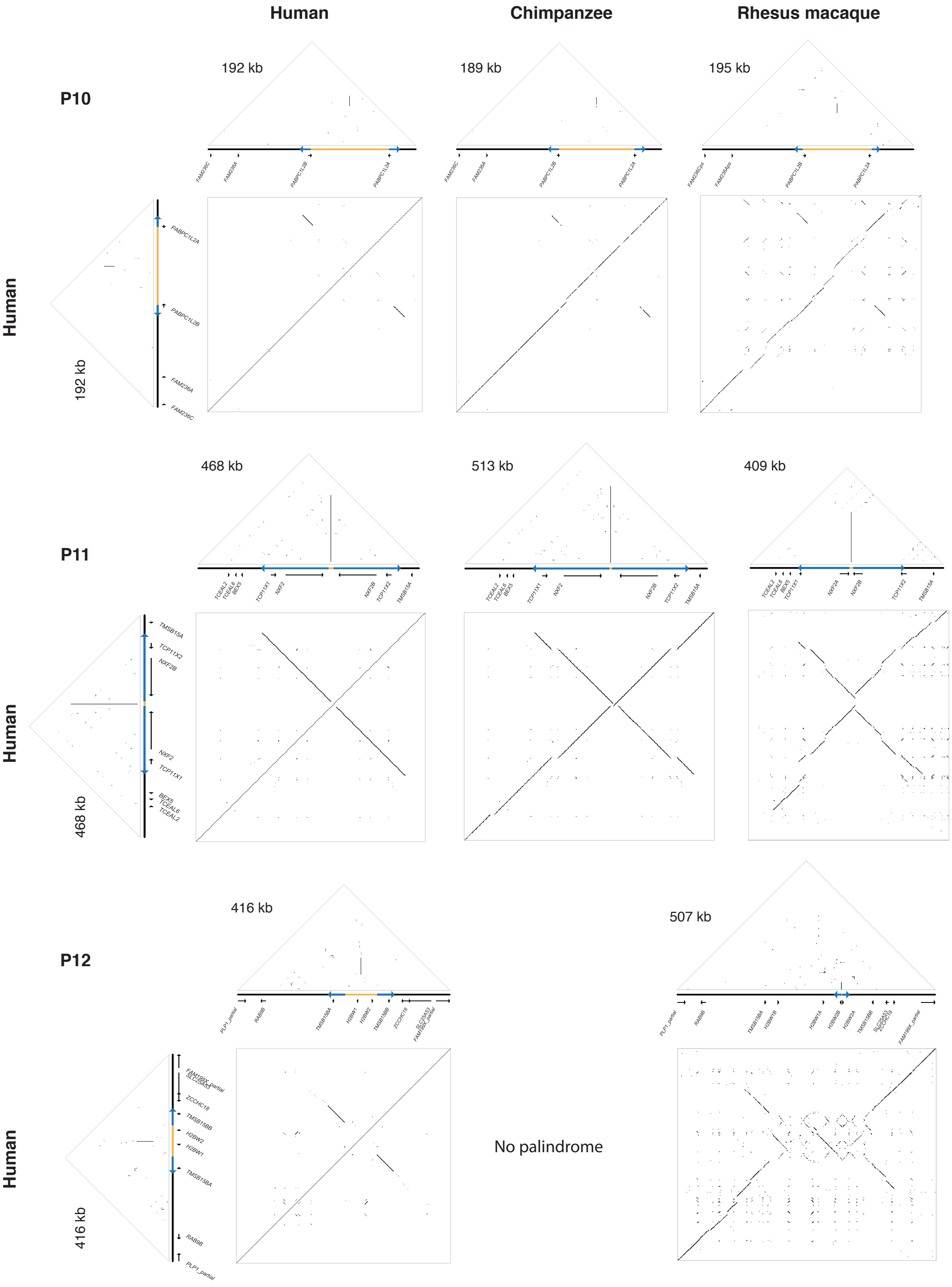

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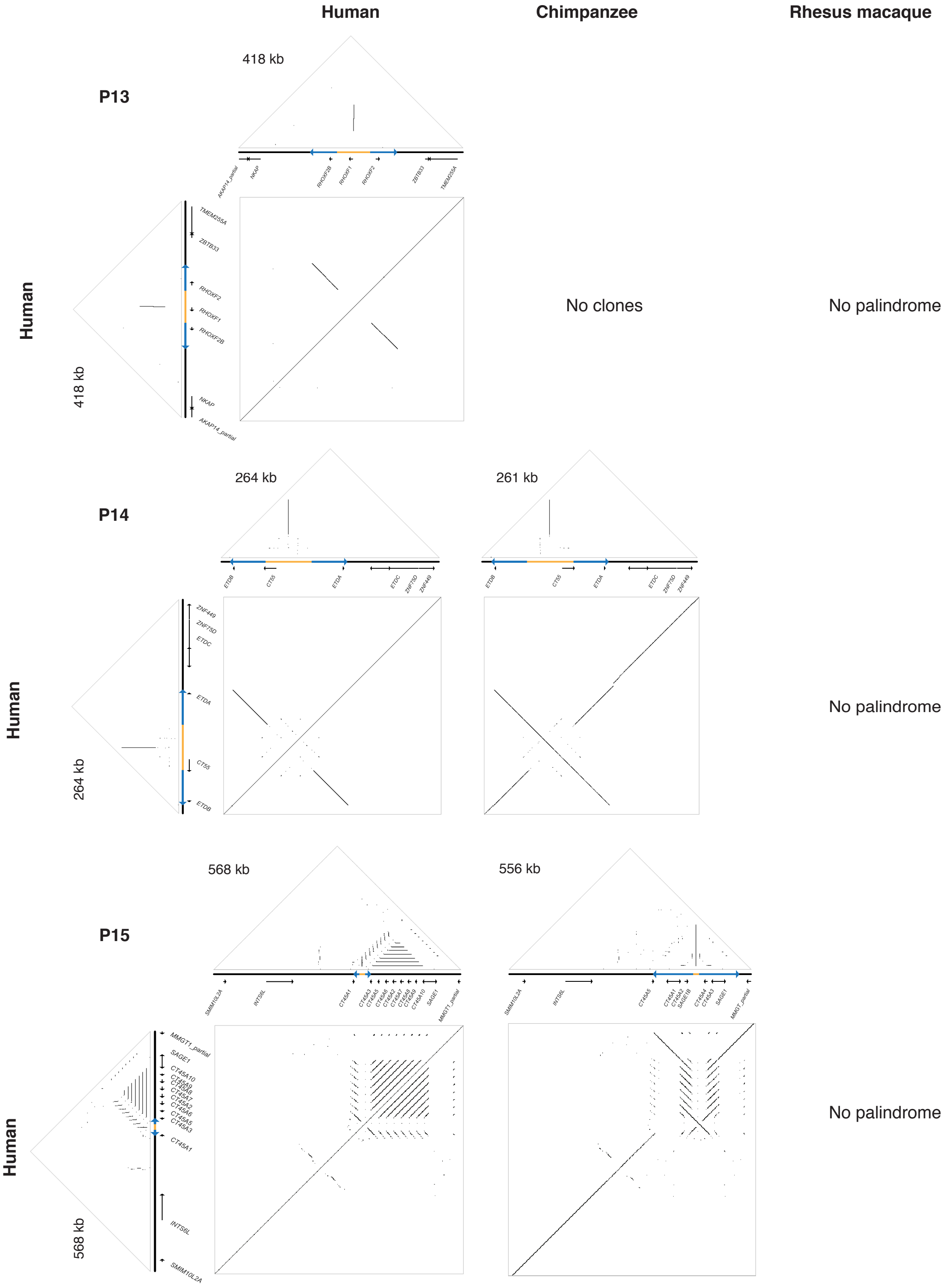

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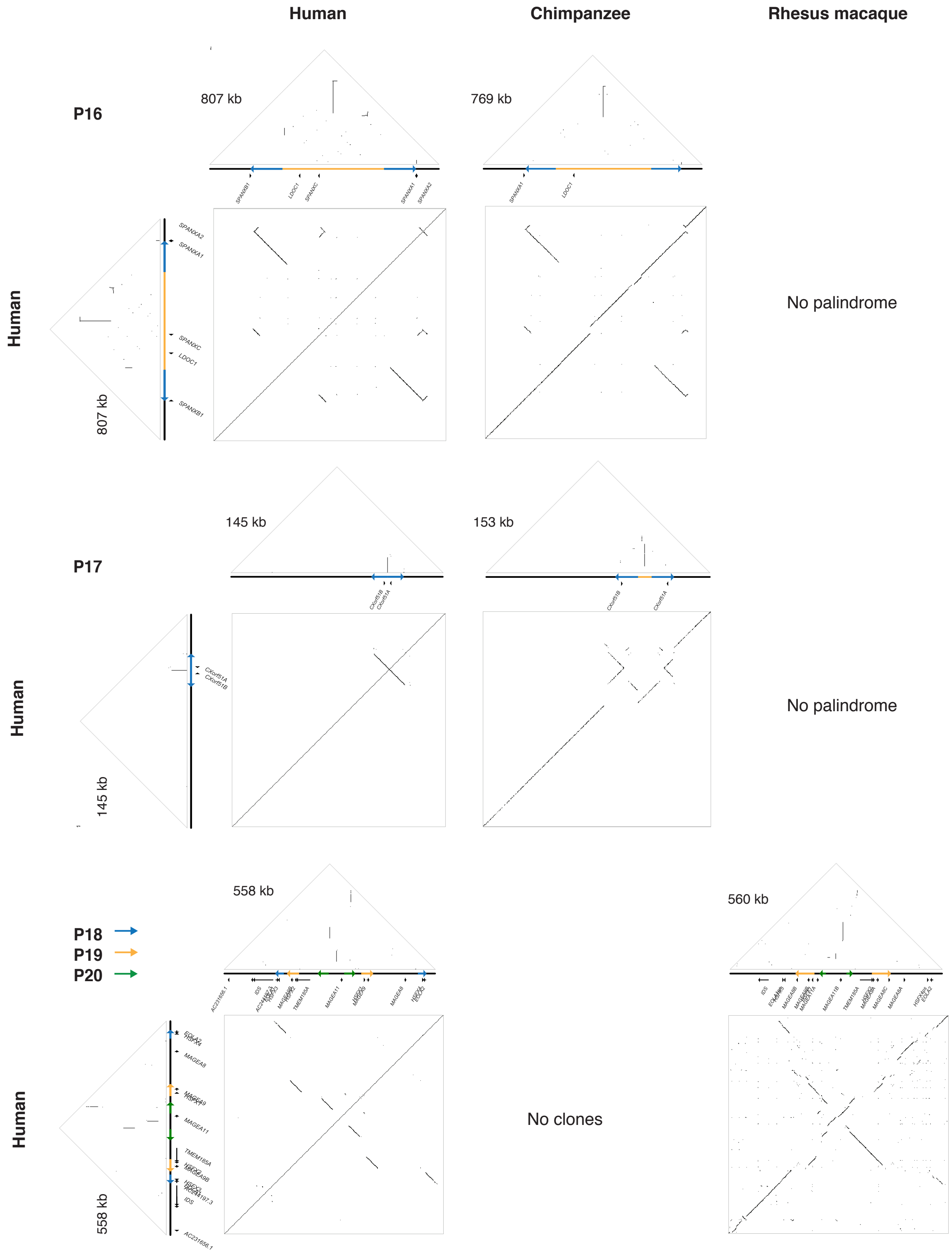

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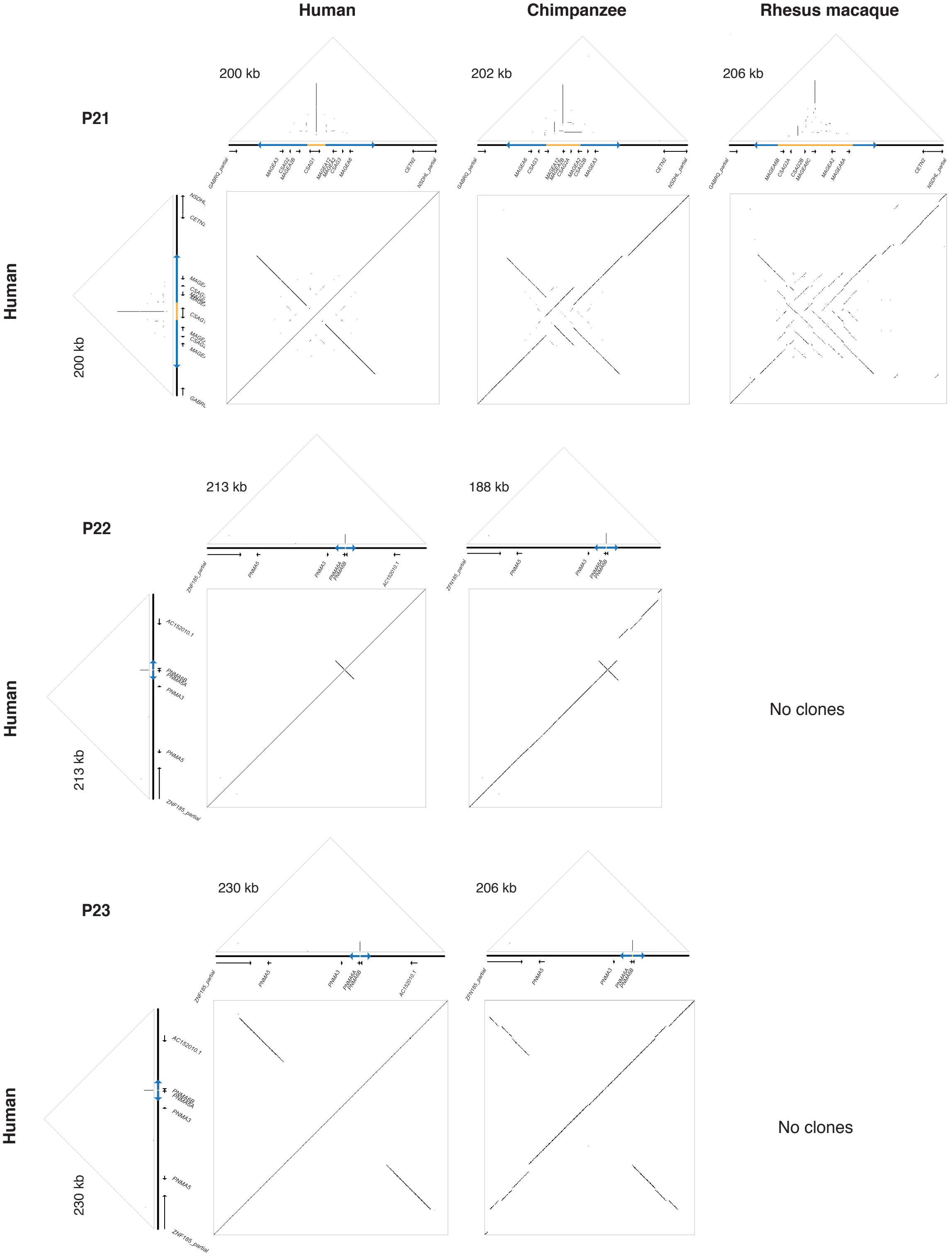

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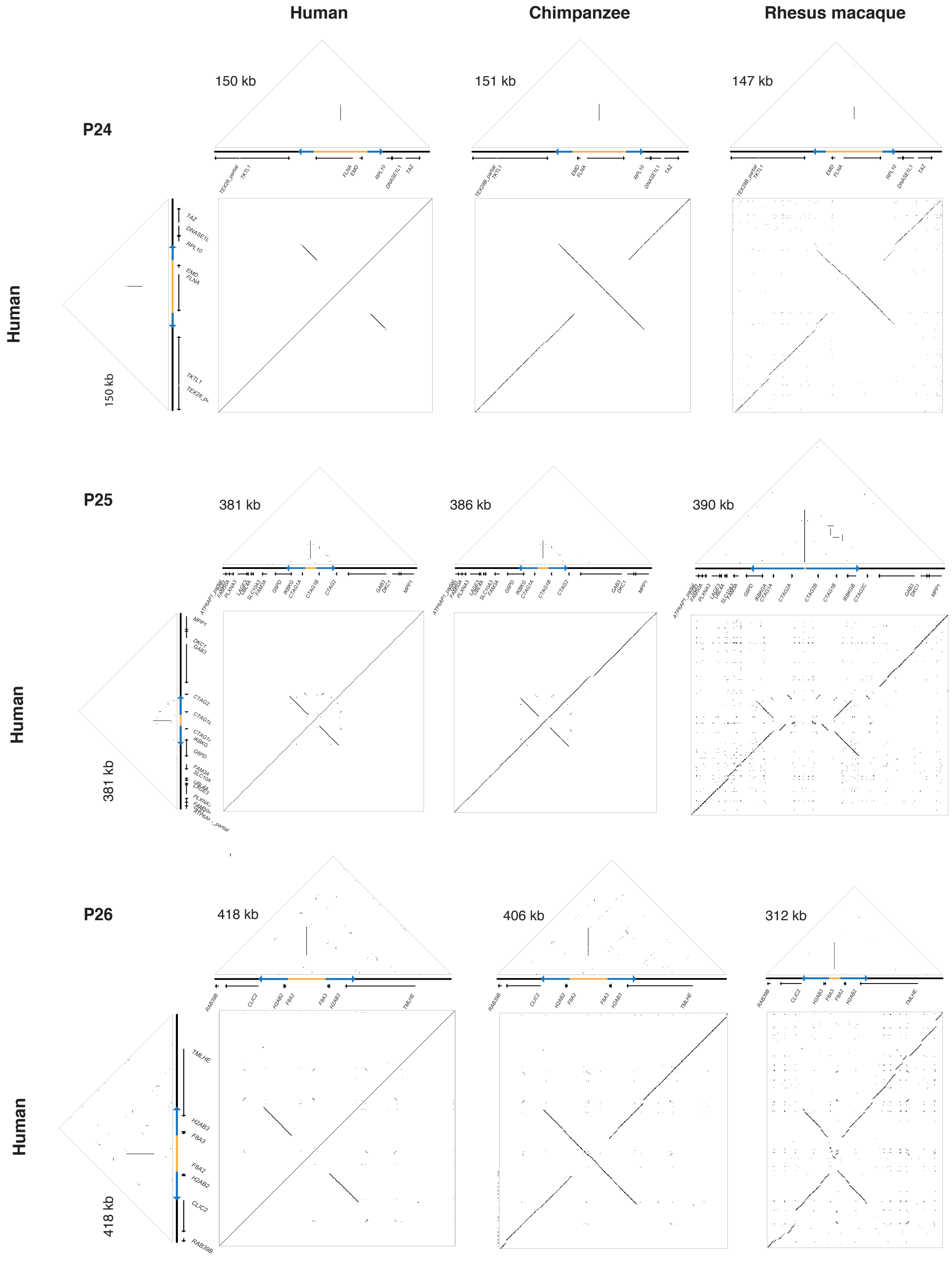

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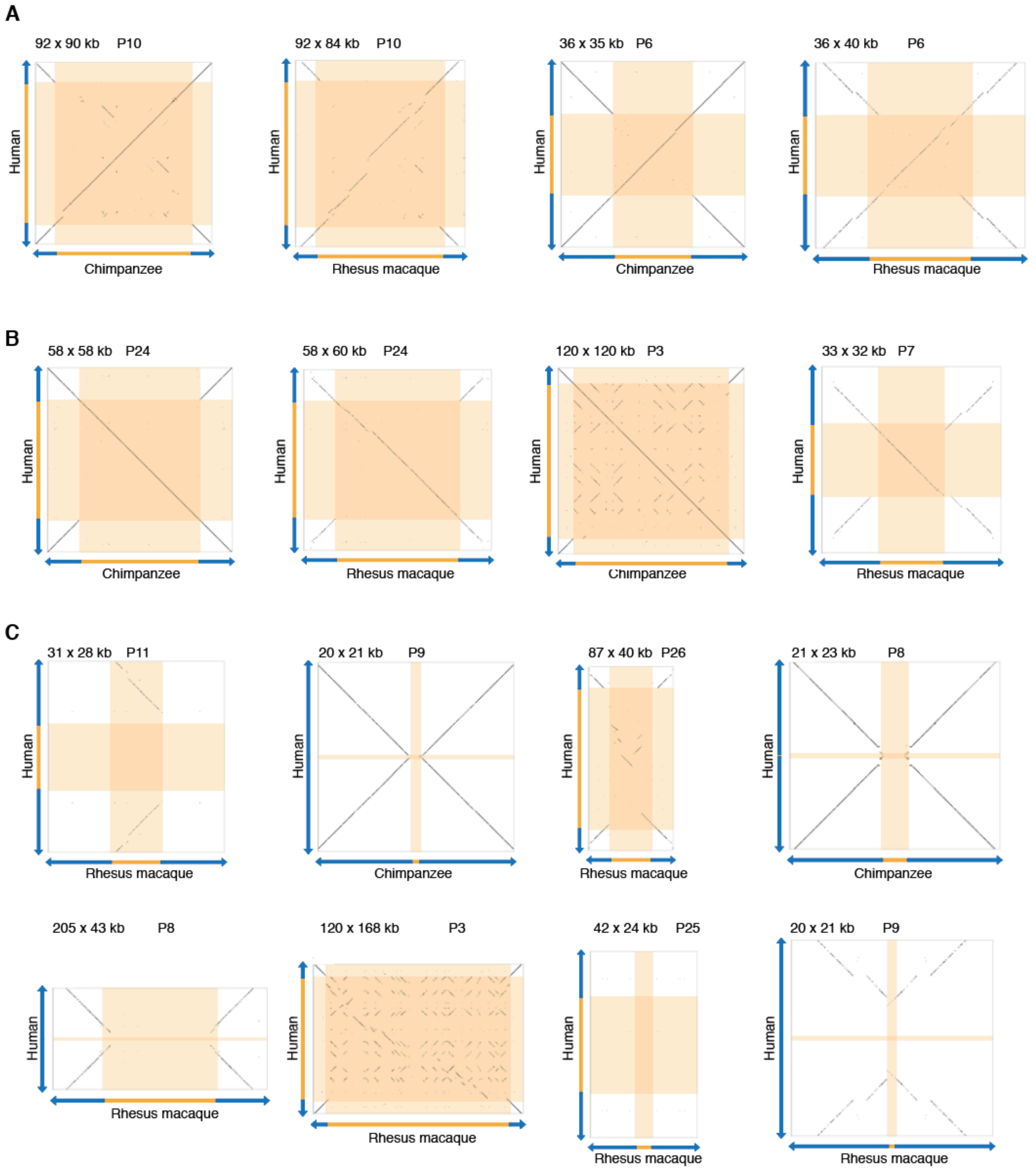
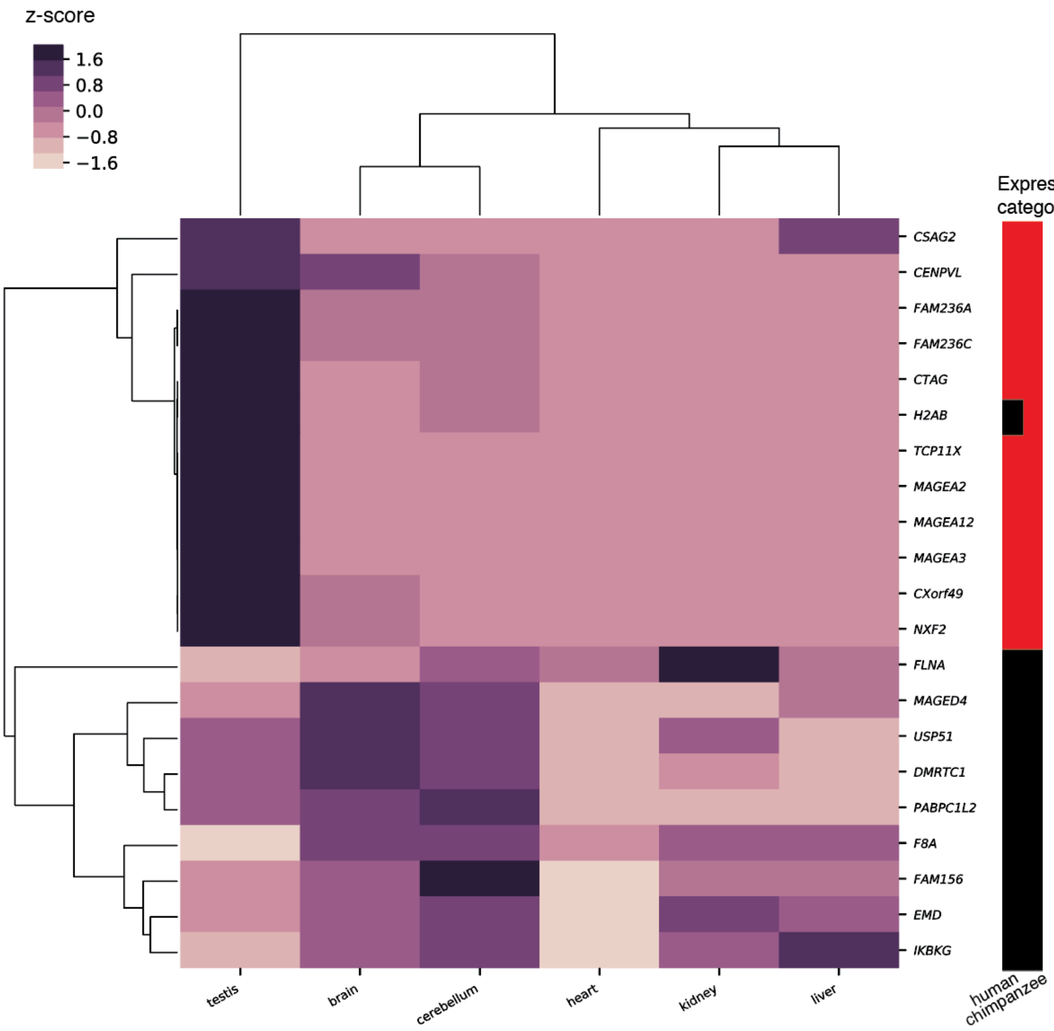
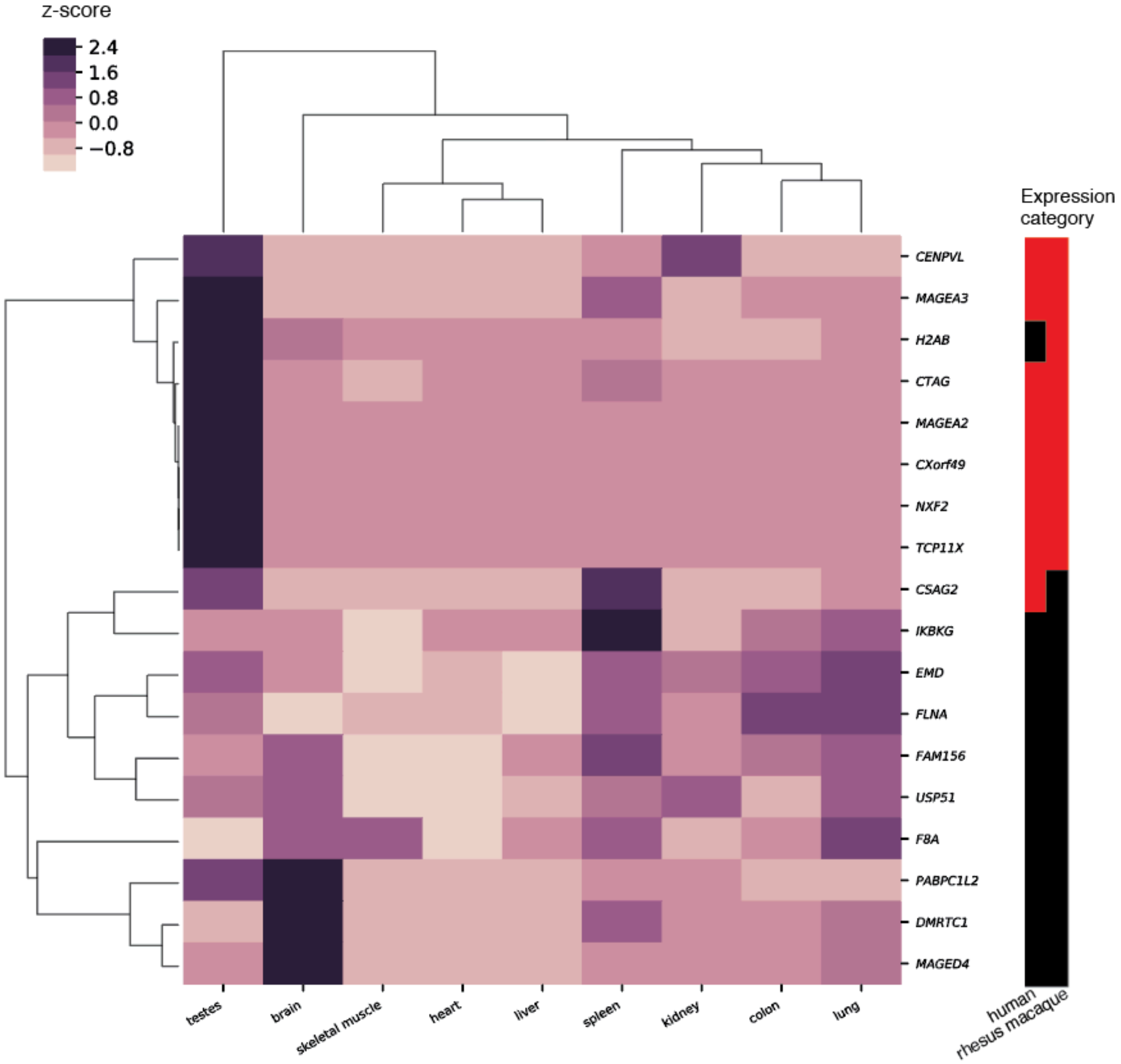


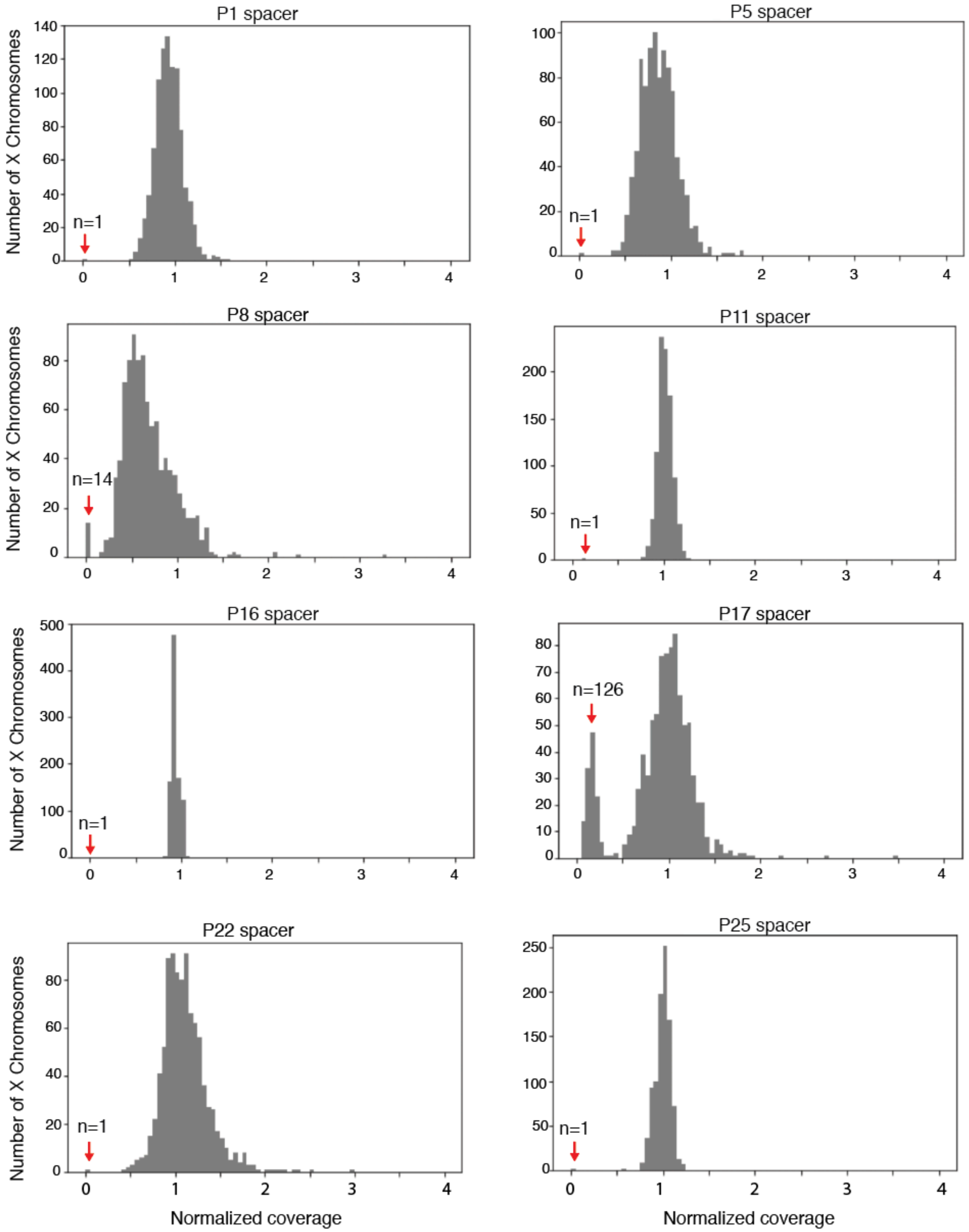
Supplemental Figure S6. Additional examples of spacer configurations in orthologous palindromes. All plots show the inner 10 kb of palindrome arms plus the spacer. w=40 for human vs. rhesus macaque comparisons; w=100 for human vs. chimpanzee comparisons. a) Human configuration, b) Inversions, c) Non-orthologous spacers.



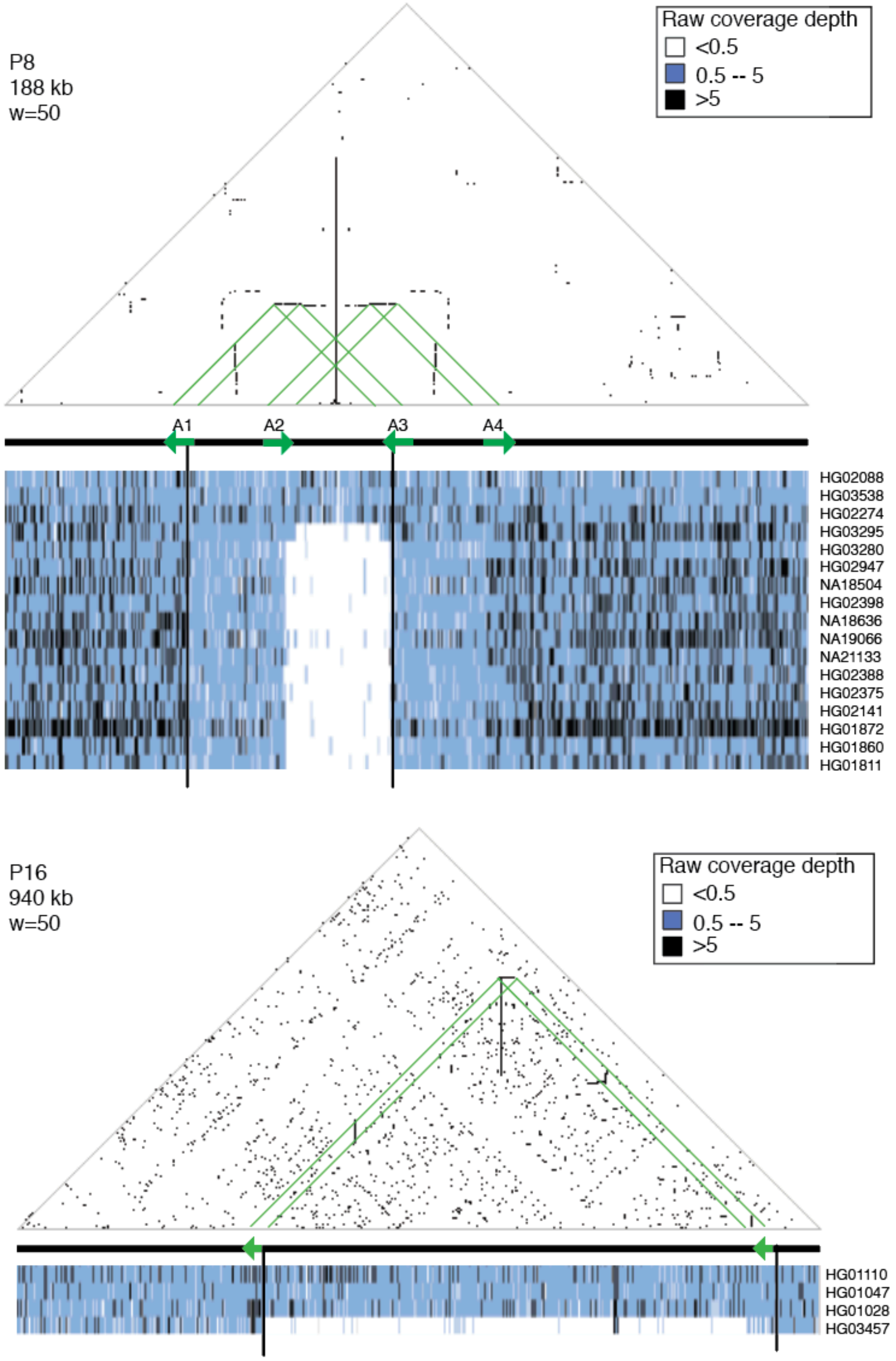
Supplemental Figure S7. Expression of gene families from palindromes shared by human, chimpanzee, and macaque in chimpanzee. Data from Brawand et al. 2011 was re-analyzed with kallisto. Each row shows averaged expression from one gene family. Row and column orders were determined by hierarchical clustering. Expression category: Shows whether expression is testis-biased (red) or broad (black) in the indicated species. Testis-biased: Minimum 2 TPM in testis, and testis accounts for >25% of log2 normalized expression summed across all tissues. Broad: All other expressed genes.



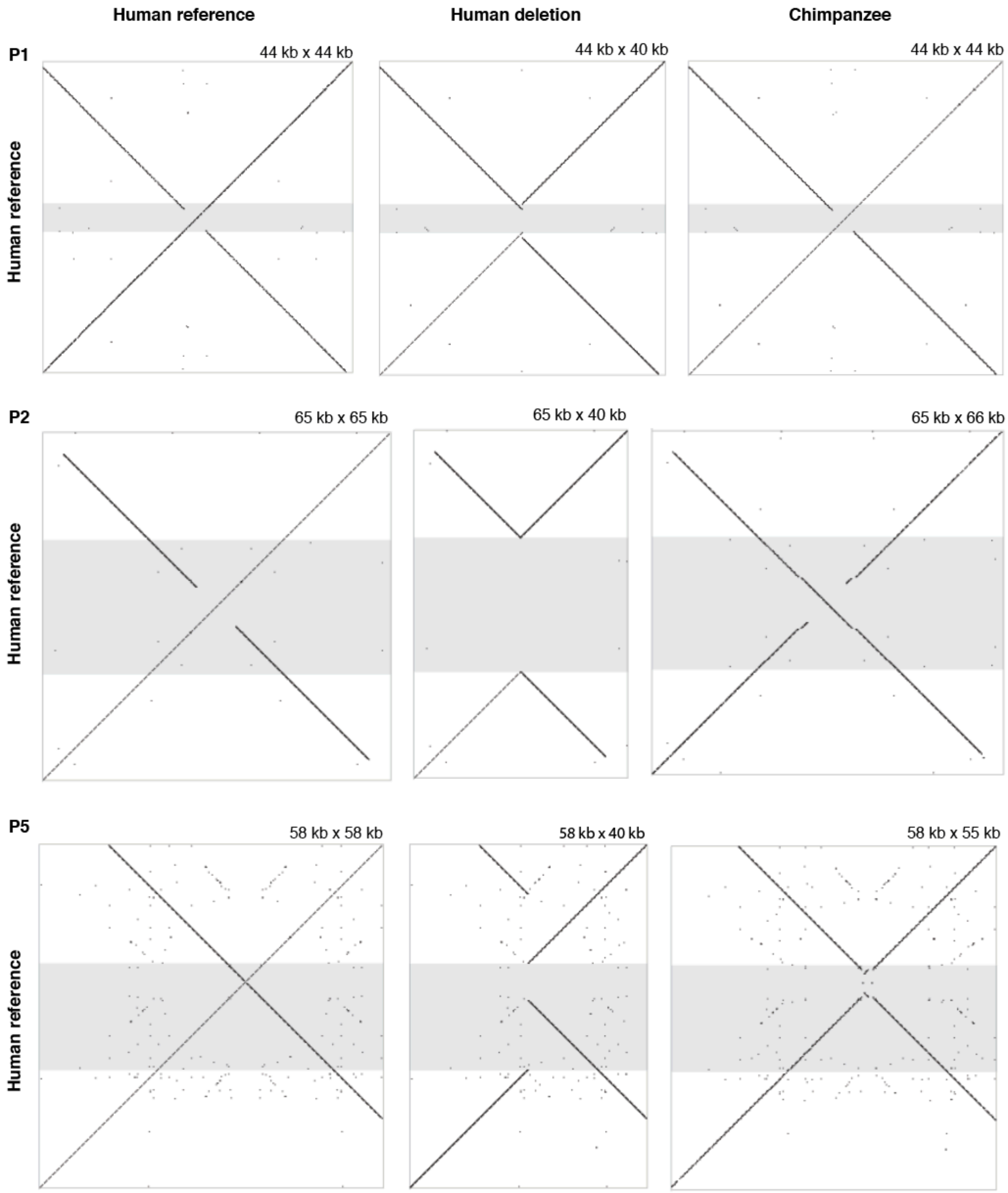
Supplemental Figure S8. Expression of gene families from palindromes shared by human, chimpanzee, and macaque in macaque. Data from Merkin et al. 2012 was re-analyzed with kallisto. Each row shows averaged expression from one gene family. Row and column orders were determined by hierarchical clustering. Expression category: Shows whether expression is testis-biased (red) or broad (black) in the indicated species. Testis-biased: Minimum 2 TPM in testis, and testis accounts for >25% of log2 normalized expression summed across all tissues. Broad: All other expressed genes.



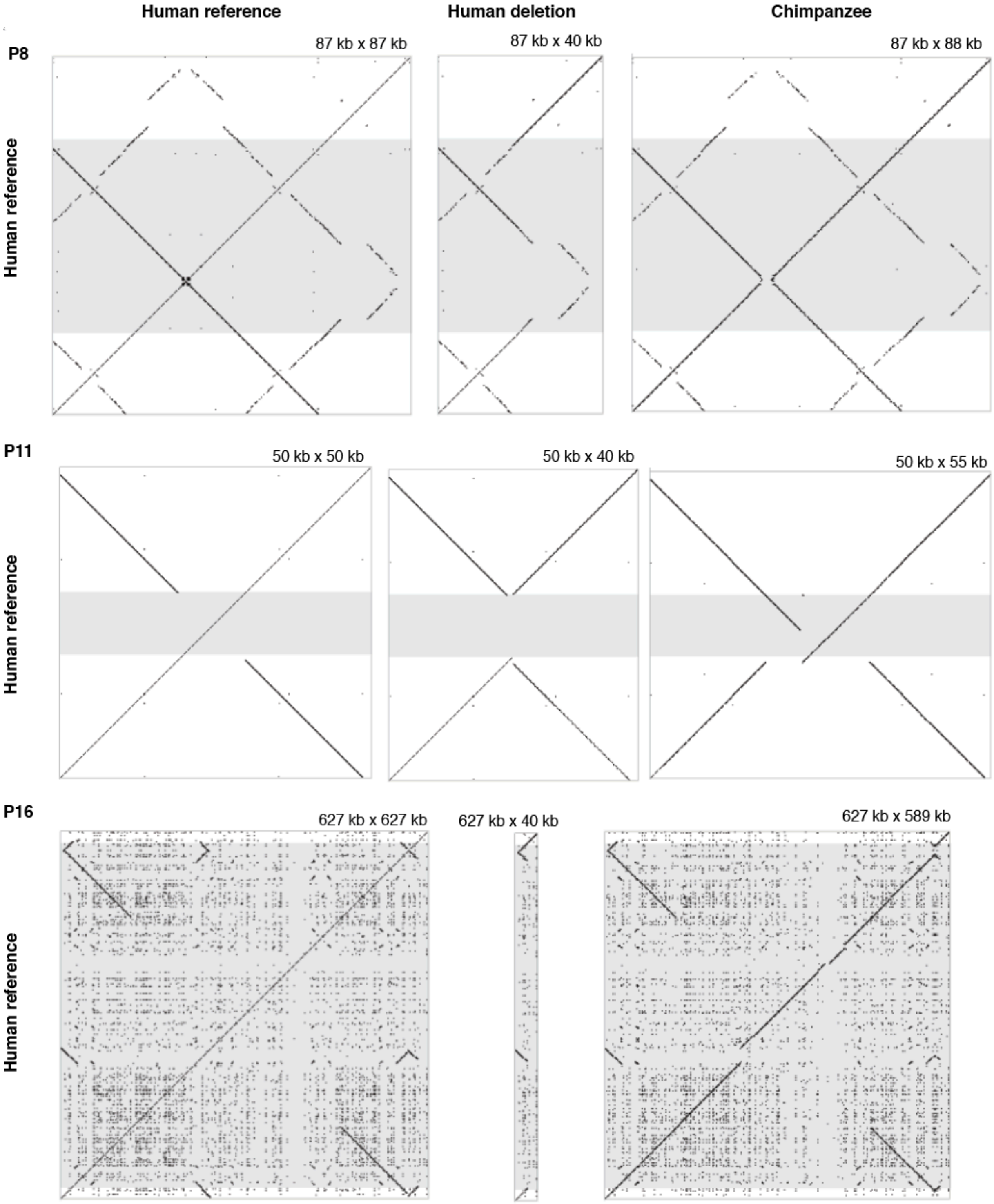
Supplemental Figure S9. Normalized coverage depths for eight palindrome spacers with at least one deletion in the 1000 Genomes dataset. Coverage depth for the ninth palindrome with spacer deletions, P2, is shown in Figure 6A.



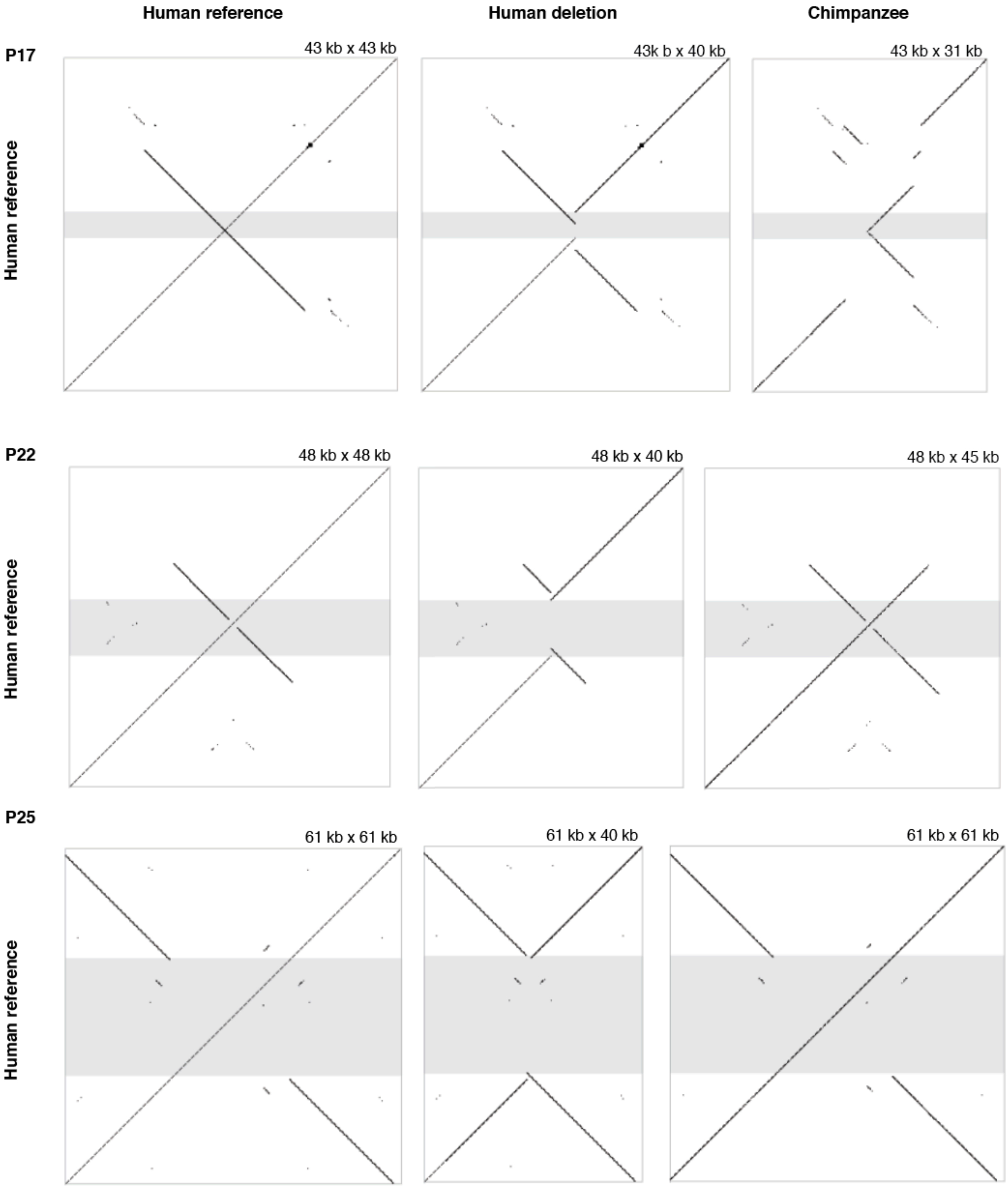
Supplemental Figure S10. Human spacer deletions with breakpoints within tandem repeats. Green arrows: Tandem repeats suspected to cause deletions through NAHR. In the case of P8, the deletion could have occurred with equal probability between arrows A1 & A3, or A2 & A4. Note that the suspected P8 deletion spans areas of no coverage (white) and reduced coverage (lighter blue, from approximately A1 to A2); the copy number of the lighter blue region is reduced from 2 to 1.



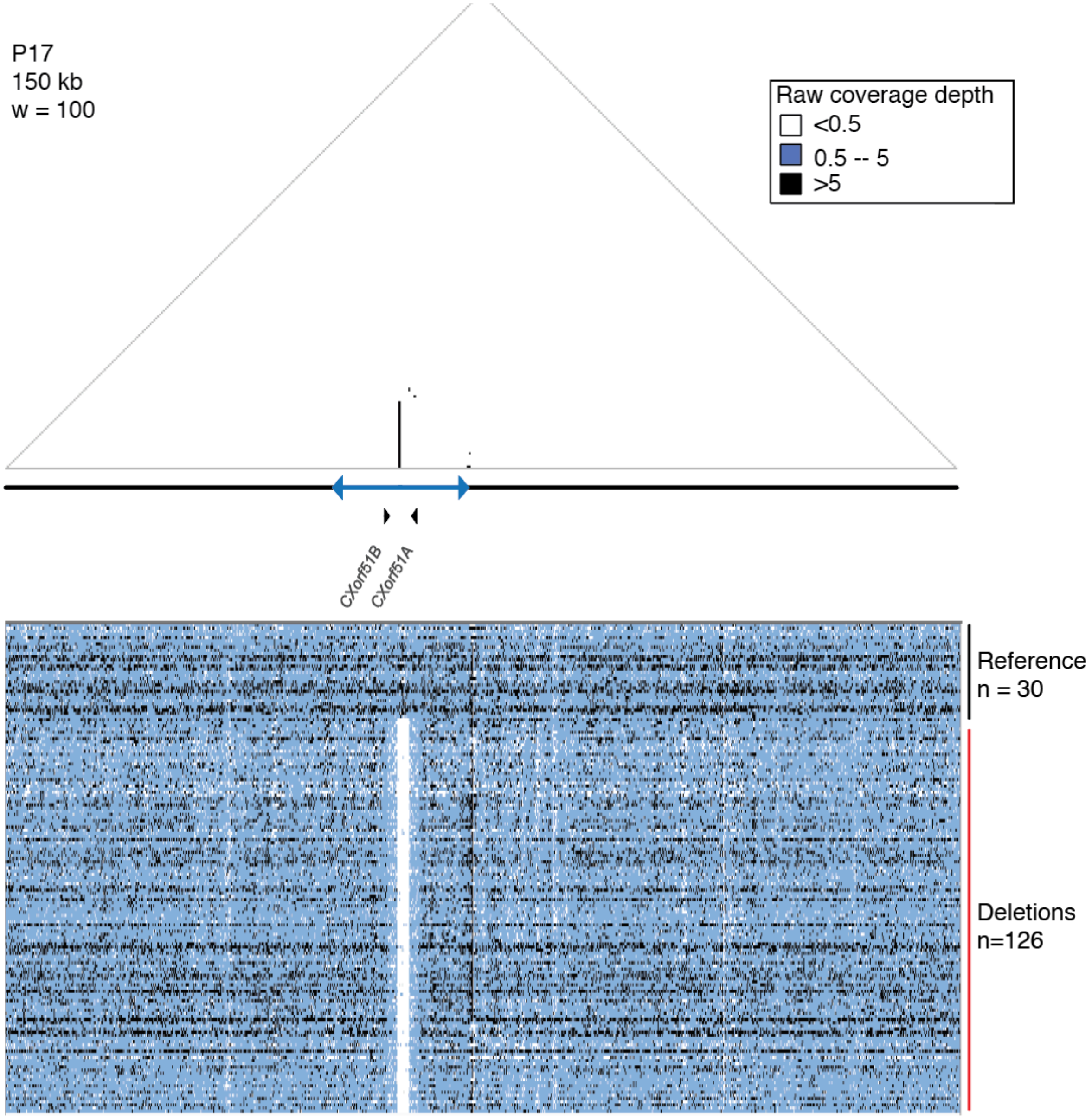
Supplemental Figure S11. Structural comparisons between human reference, human deletion, and chimpanzee for nine X palindromes with at least one spacer deletion. w=30 for all square dot plots. Position of the human X spacer deletion is highlighted in gray. For all nine palindromes, most or all of the of sequence absent in the human deletion is present in chimpanzee, confirming that the human structural polymorphism results from deletion rather than insertion.



Supplemental Figure S11. Structural comparisons between human reference, human deletion, and chimpanzee for nine X palindromes with at least one spacer deletion. w=30 for all square dot plots. Position of the human X spacer deletion is highlighted in gray. For all nine palindromes, most or all of the of sequence absent in the human deletion is present in chimpanzee, confirming that the human structural polymorphism results from deletion rather than insertion.



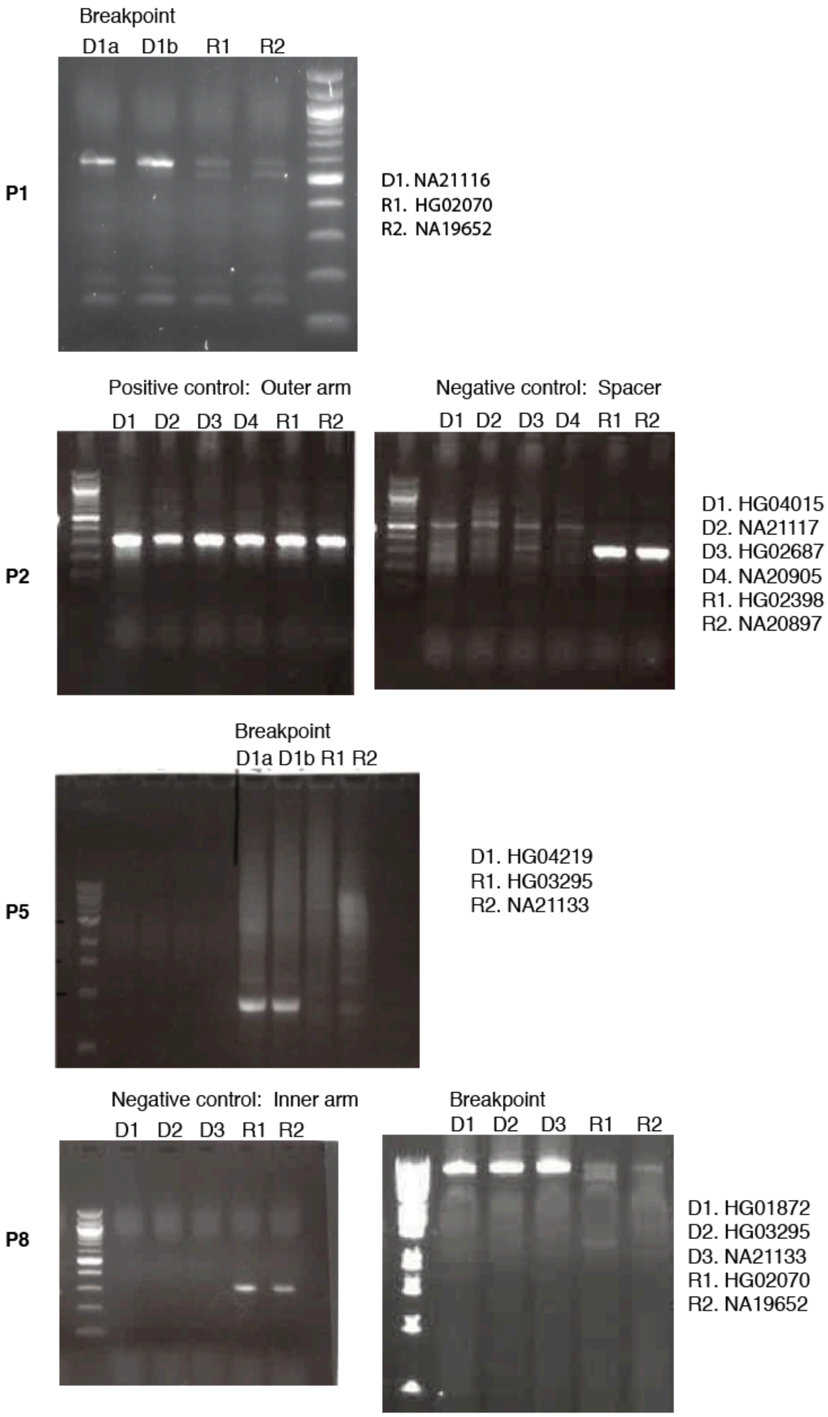
Supplemental Figure S11. Structural comparisons between human reference, human deletion, and chimpanzee for nine X palindromes with at least one spacer deletion. w=30 for all square dot plots. Position of the human X spacer deletion is highlighted in gray. For all nine palindromes, most or all of the of sequence absent in the human deletion is present in chimpanzee, confirming that the human structural polymorphism results from deletion rather than insertion.



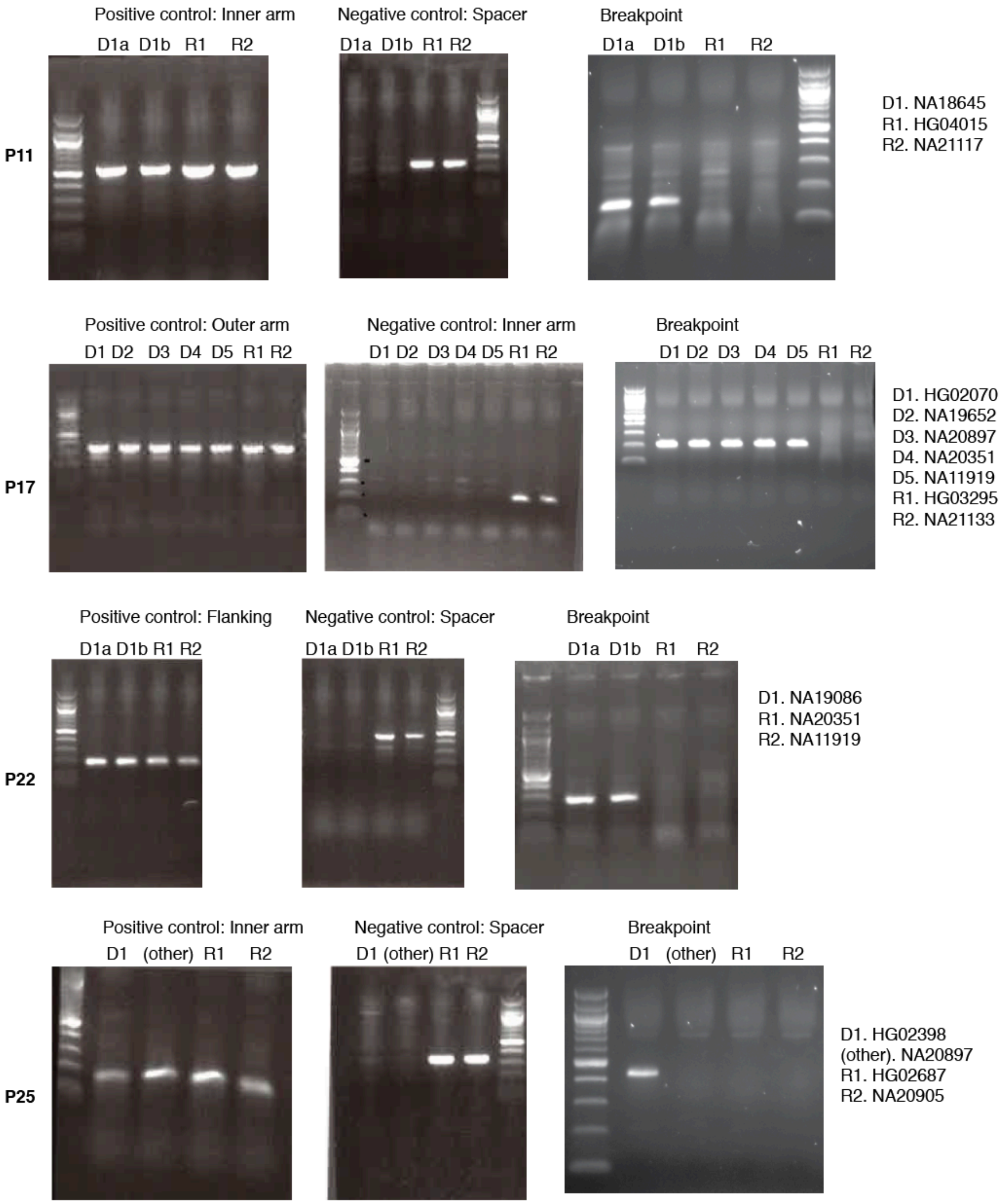
Supplemental Figure S12. Coverage depth for X Chromosomes with P17 spacer deletions. Tracks are shown for all 126 X Chromosomes with P17 spacer deletions, plus 30 randomly chosen X Chromosomes with the reference structure.

```
Proximal reference  GCTTTCTGTCACTATCTGTTTCTATTTTCTGGAGGTTTGTAAGAATGGAATCATAAGATATGTACTCTTT
                    . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
P17 deletion        GCTTTCTGTCACTATCTGTTTCTATTTTCTGGAGGCTCACTGGTCACCTTTGCCATACTGAATTGTCCC
                                                    . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
Distal reference    TCTGTTCGTCCACATCTTCATTAGGCTTCTGTGGCTCACTGGTCACCTTTGCCATACTGAATTGTCCC
```

Supplemental Figure S13. Junction for P17 spacer deletion. Proximal reference: chrX: 146811296-146811365. Distal reference: chrX: 146814668-146814736. Two base pairs (GG, purple) overlap between the breakpoints.



Supplemental Figure S14. Verification of human X-palindrome spacer deletions. PCR primers were designed based on deletion breakpoints from split reads or, in cases where reads spanning the breakpoint could not be found, based on the estimated deletion breakpoints from visualization of coverage depth. Positive control: Sequence expected to be present in both reference samples and deletion samples. Negative control: Sequence expected to be present in reference samples, and absent in deletion samples. Breakpoint: Sequence expected to be present in deletion samples, and absent in reference samples. D = deletion sample, R = reference sample.



Supplemental Figure S14. Verification of human X-palindrome spacer deletions. PCR primers were designed based on deletion breakpoints from split reads or, in cases where reads spanning the breakpoint could not be found, based on the estimated deletion breakpoints from visualization of coverage depth. Positive control: Sequence expected to be present in both reference samples and deletion samples. Negative control: Sequence expected to be present in reference samples, and absent in deletion samples. Breakpoint: Sequence expected to be present in deletion samples, and absent in reference samples. D = deletion sample, R = reference sample.

Supplemental Table 1: Coordinates of human X palindromes in hg38. Palindromes were identified using a kmer-based method (see Methods).

Palindrome	**Arm 1 coordinates**	**Spacer coordinates**	**Arm 2 coordinates**
P1	chrX: 48367308 - 48396305	chrX: 48396306 - 48399118	chrX: 48399119 - 48428123
P2	chrX: 51668115 - 51692963	chrX: 51692964 - 51700361	chrX: 51700362 - 51725226
P3	chrX: 52040713 - 52077110	chrX: 52077111 - 52176982	chrX: 52176983 - 52213380
P4	chrX: 52473449 - 52502219	chrX: 52502220 - 52510667	chrX: 52510668 - 52539437
P5	chrX: 52670289 - 52728969	chrX: 52728970 - 52729454	chrX: 52729455 - 52788214
P6	chrX: 52882200 - 52920138	chrX: 52920139 - 52935673	chrX: 52935674 - 52973611
P7	chrX: 55453561 - 55480141	chrX: 55480142 - 55493061	chrX: 55493062 - 55519639
P8	chrX: 71683199 - 71740534	chrX: 71740535 - 71741054	chrX: 71741055 - 71798363
P9	chrX: 72741066 - 72860190	chrX: 72860191 - 72860605	chrX: 72860606 - 72979767
P10	chrX: 72996086 - 73005278	chrX: 73005279 - 73077748	chrX: 73077749 - 73086935
P11	chrX: 102197589 - 102338170	chrX: 102338171 - 102348932	chrX: 102348933 - 102489526
P12	chrX: 103955950 - 103987907	chrX: 103987908 - 104050879	chrX: 104050880 - 104082911
P13	chrX: 120038201 - 120086776	chrX: 120086777 - 120149524	chrX: 120149525 - 120198163
P14	chrX: 135116122 - 135158129	chrX: 135158130 - 135214412	chrX: 135214413 - 135256414
P15	chrX: 135723708 - 135734732	chrX: 135734733 - 135748584	chrX: 135748585 - 135759685
P16	chrX: 141005250 - 141114518	chrX: 141114519 - 141472891	chrX: 141472892 - 141582141
P17	chrX: 146801856 - 146812219	chrX: 146812220 - 146812295	chrX: 146812296 - 146822659
P18	chrX: 149542167 - 149562176	chrX: 149562177 - 149917319	chrX: 149917320 - 149937339
P19	chrX: 149573130 - 149602230	chrX: 149602231 - 149767142	chrX: 149767143 - 149796257
P20	chrX: 149654519 - 149681126	chrX: 149681127 - 149722142	chrX: 149722143 - 149748749
P21	chrX: 152678580 - 152725390	chrX: 152725391 - 152743079	chrX: 152743080 - 152789894
P22	chrX: 153066010 - 153074417	chrX: 153074418 - 153075611	chrX: 153075612 - 153084043
P23	chrX: 153106025 - 153149489	chrX: 153149490 - 153250484	chrX: 153250485 - 153293919
P24	chrX: 154337197 - 154347246	chrX: 154347247 - 154384865	chrX: 154384866 - 154394951
P25	chrX: 154555880 - 154591327	chrX: 154591328 - 154613094	chrX: 154613095 - 154648556
P26	chrX: 155336691 - 155386727	chrX: 155386728 - 155453980	chrX: 155453981 - 155504550

Supplemental Table 2: Clones sequenced for this project. Some clones contained portions of multiple palindromes. “Finished”: Clone sequence was supported by complete Illumina coverage; “Prefinished”: Clone had at least one stretch of sequence supported by one or more nanopore reads, but no Illumina reads.

Clone	Palindrome	Status	# full length reads
CH250-106M20	P7	Prefinished	5
CH250-114J18	P9/P10	Prefinished	0
CH250-119L11	P16	Finished	0
CH250-120L20	P18/P19/P20	Prefinished	29
CH250-136N6	P3	Finished	12
CH250-137I15	P26	Prefinished	8
CH250-138B21	P12	Prefinished	2
CH250-149O24	P1	Prefinished	8
CH250-150I6	P15	Prefinished	0
CH250-163K20	P18/P19/P20	Prefinished	0
CH250-168E3	P21	Prefinished	3
CH250-174F12	P21	Prefinished	19
CH250-184A21	P18/P19/P20	Prefinished	3
CH250-191K20	P2	Finished	13
CH250-197O3	P6	Prefinished	6
CH250-214O8	P17	Finished	79
CH250-228D11	P11	Prefinished	3
CH250-234D7	P16	Finished	0
CH250-236O7	P8	Prefinished	1
CH250-240H14	P14	Finished	6
CH250-257F3	P1	Finished	4
CH250-257M3	P1	Prefinished	1
CH250-25I12	P13	Prefinished	3
CH250-273C12	P15	Prefinished	2
CH250-280C5	P16	Prefinished	6
CH250-300J22	P4/P5	Prefinished	20
CH250-312L23	P16	Finished	0
CH250-313D10	P13	Prefinished	11
CH250-318K15	P16	Finished	0
CH250-371L16	P9	Prefinished	4
CH250-396M7	P1	Prefinished	3
CH250-397P11	P15	Prefinished	23
CH250-398K19	P21	Prefinished	5
CH250-412K19	P5/P6	Prefinished	16

CH250-417G7	P26	Prefinished	2
CH250-420A18	P14	Finished	15
CH250-424H13	P25	Prefinished	23
CH250-436M9	P4/P5	Prefinished	0
CH250-440K2	P13	Prefinished	0
CH250-462M8	P21	Prefinished	4
CH250-486E21	P1	Prefinished	0
CH250-487N16	P26	Finished	2
CH250-491H11	P24	Prefinished	2
CH250-493M11	P25	Prefinished	2
CH250-498I16	P11	Prefinished	8
CH250-499B10	P1	Finished	8
CH250-503C21	P25	Prefinished	10
CH250-503N19	P25	Prefinished	2
CH250-504P11	P18/P19/P20	Prefinished	5
CH250-516N14	P12	Prefinished	0
CH250-530N5	P4/P5	Finished	5
CH250-540J3	P11	Prefinished	10
CH250-541H5	P3	Prefinished	0
CH250-547J16	P18/P19/P20	Prefinished	4
CH250-563M7	P3	Prefinished	22
CH250-57C9	P16	Finished	0
CH250-80G22	P9	Prefinished	6
CH250-87B7	P7	Prefinished	7
CH250-92B13	P12	Prefinished	1
CH250-94G2	P3	Prefinished	4
CH250-95D17	P1	Prefinished	2
CH251-130O9	P4/P5	Finished	0
CH251-160A4	P16	Prefinished	7
CH251-161L14	P7	Prefinished	2
CH251-172F20	P16	Finished	0
CH251-177B21	P2	Prefinished	21
CH251-183G21	P8	Prefinished	0
CH251-189G13	P16	Prefinished	0
CH251-239P10	P26	Prefinished	26
CH251-240O17	P5/P6	Prefinished	61
CH251-261H21	P15	Prefinished	4
CH251-277H18	P7	Prefinished	33
CH251-285D14	P26	Prefinished	1
CH251-292E19	P22/P23	Prefinished	8

CH251-316L7	P17	Prefinished	4
CH251-346A10	P25	Prefinished	12
CH251-34N14	P4/P5	Prefinished	3
CH251-385I8	P1	Prefinished	4
CH251-389B7	P14	Prefinished	20
CH251-397P16	P3	Prefinished	2
CH251-4M24	P11	Finished	21
CH251-504H5	P10	Finished	0
CH251-506D4	P6	Prefinished	0
CH251-50L15	P15	Prefinished	5
CH251-514B7	P8	Prefinished	3
CH251-542A6	P10	Prefinished	12
CH251-542D16	P12	Finished	17
CH251-542E16	P22	Prefinished	4
CH251-550E20	P12	Finished	0
CH251-565G15	P21	Prefinished	3
CH251-571K4	P15	Finished	23
CH251-58J24	P16	Finished	0
CH251-635P13	P11	Prefinished	15
CH251-639F23	P15	Prefinished	3
CH251-64D22	P16	Prefinished	4
CH251-651H9	P11	Prefinished	16
CH251-654E24	P16	Prefinished	25
CH251-657L4	P9/P10	Prefinished	17
CH251-658J15	P8	Prefinished	7
CH251-65E21	P24	Prefinished	1
CH251-671I19	P3	Prefinished	5
CH251-673E12	P16	Prefinished	2
CH251-677L24	P24/P25	Prefinished	8
CH251-702N4	P16	Finished	0
CH251-737G9	P9/P10	Prefinished	1
CH251-73C22	P2	Prefinished	0
CH251-83H5	P4	Finished	0

Supplemental Table S3: Status of palindromes identified in SHIMS 3.0 in other chimpanzee X assemblies. Missing: No palindrome present in non-SHIMS 3.0 assembly; Incomplete: Part of palindrome present in non-SHIMS 3.0 assembly; Accurate: Full palindrome present in non-SHIMS 3.0 assembly.

Palindrome	Pan_tro_3.0	Clint_PTRv2	Arm length (SHIMS 3.0)
P1	Accurate	Incomplete	28844
P2	Accurate	Accurate	25534
P3	Incomplete	Missing	36270
P4	Missing	Missing	29842
P5	Missing	Missing	105400
P6	Missing	Incomplete	34928
P7	Accurate	Missing	28530
P8	Missing	Incomplete	53154
P9	Missing	Incomplete	119578
P10	Missing	Accurate	9184
P11	Incomplete	Incomplete	160682
P14	Incomplete	Incomplete	41640
P15	Incomplete	Missing	90284
P16	Missing	Incomplete	102504
P17	Accurate	Accurate	14737
P21	Incomplete	Incomplete	37360
P22	Incomplete	Accurate	9934
P23	Missing	Incomplete	38530
P24	Missing	Accurate	11228
P25	Accurate	Missing	35368
P26	Accurate	Accurate	49024

Supplemental Table S4: Status of palindromes identified in SHIMS 3.0 in other rhesus macaque X assemblies. Missing: No palindrome present in non-SHIMS 3.0 assembly; Incomplete: Part of palindrome present in non-SHIMS 3.0 assembly; Accurate: Full palindrome present in non-SHIMS 3.0 assembly.

Palindrome	Mmul_8.0.1	Mmul_10	Arm length (SHIMS 3.0)
P1	Missing	Accurate	14749
P2	Incomplete	Accurate	42783
P3	Missing	Accurate	35266
P4	Missing	Accurate	11323
P5	Missing	Accurate	19290
P6	Missing	Accurate	15572
P7	Incomplete	Accurate	24490
P8	Incomplete	Missing	38496
P9	Incomplete	Incomplete	81971
P10	Accurate	Accurate	6574
P11	Incomplete	Missing	106186
P12	Missing	Accurate	12978
P18	Missing	Incomplete	47531
P19	Missing	Incomplete	14175
P21	Accurate	Accurate	21963
P24	Missing	Accurate	8398
P25	Missing	Missing	103488
P26	Missing	Accurate	46855

Supplemental Table S5: Conservation of X palindrome gene families. Values shown are the number of intact gene copies found in the given species. "Region" refers to the human region in which the gene family is found.

Gene	**Palindrome**	**Region**	**Human**	**Chimpanzee**	**Rhesus macaque**
CENPVL	P2	Arm	2	2	2
MAGED4	P3	Arm	2	2	2
FAM156	P6	Arm	2	2	2
USP51	P7	Spacer	1	1	1
CXorf49	P8	Arm	2	2	2
DMRTC1	P9	Arm	2	2	2
FAM236B	P9	Arm	2	2	0
FAM236D	P9	Arm	2	2	0
PABPC1L2	P10	Arm	2	2	2
NXF2	P11	Arm	2	2	2
TCP11X2	P11	Arm	2	2	2
MAGEA12	P21	Spacer	1	1	0
CSAG1	P21	Spacer	1	0	0
MAGEA2	P21	Arm	2	2	1
MAGEA3	P21	Arm	2	2	3
CSAG2	P21	Arm	2	3	2
FLNA	P24	Spacer	1	1	1
EMD	P24	Spacer	1	1	1
CTAG1	P25	Arm	2	2	4
IKBKG	P25	Arm	1	1	2
F8A	P26	Arm	2	2	2
H2AB	P26	Arm	2	2	2

Supplemental Table S6: Purifying selection on X palindrome genes. dN/dS values were calculated using the basic model in PAML (model=0,NSites=0).

2ΔL (observed vs. 1): Likelihood ratio test for observed dN/dS value versus null hypothesis (dN/dS = 1)

2ΔL (M1a vs. M2a): Likelihood ratio test for neutral evolution versus positive selection

Gene	**dN**	**dS**	**dN/dS**	**2ΔL (observed vs. 1)**	**2ΔL (M1a vs. M2a)**
PABPC1L2	0	0.0472	0.0001	16.94***	0
FLNA	0.0037	0.1483	0.02472	584.08***	0
IKBKG	0.0062	0.1403	0.04421	68.52***	0.18
F8A	0.0055	0.0832	0.06665	32.38***	0
MAGED4	0.0099	0.0695	0.14308	46.38***	0
CENPVL	0.0242	0.0998	0.24204	12.5***	0
FAM156	0.0202	0.0825	0.24445	10.56**	0
USP51	0.0125	0.039	0.31986	12.16***	0.64
H2AB	0.066	0.1925	0.34267	6.70**	0
EMD	0.0369	0.096	0.38423	7.68**	4.18*
NXF2	0.0334	0.0649	0.51501	7.28**	0
MAGEA2	0.063	0.1078	0.58423	3.84	0
MAGEA3	0.1432	0.2091	0.68475	4.12*	3.18
CXorf49	0.0725	0.1036	0.69933	3.06	0.86
CTAG1	0.1309	0.1751	0.74787	1.26	2.72
TCP11X	0.0406	0.0525	0.77242	0.6	0
DMRTC1	0.0165	0.0197	0.83446	0.08	0
CSAG2	0.0958	0.0866	1.10635	0.06	8.86**

*p<0.05
**p<0.01
***p<0.001

Supplemental Table S7: Rates of P17 spacer deletions in azoospermic and oligozoospermic men

Dataset	**# men**	**# P17 deletions**	**% P17 deletions**
1000 Genomes	944	126	13.3
dbGaP phs001023 (control)	292	54	18.5
dbGaP phs001023 (azoospermia)	286	47	16.5
Oligozoospermia	562	68	12.1

Supplemental Table S8: Chimpanzee clones used in this project that were previously sequenced and deposited in GenBank.

Clone	**Palindrome**
CH251-26J9	P1
CH251-17J20	P11
CH251-98I1	P12
CH251-55N11	P13
CH251-52P5	P21
CH251-498N14	P25
CH251-25B20	P26

Supplemental Table S9: PCR primers for gels shown in Supplemental Fig. 14.

Feature	**Forward primer (5' to 3')**	**Reverse primer (5' to 3')**	**Notes**
P1 breakpoint	CCTCCTCCGTGTTTTTCTGA	CACAAGACAGGTGCAAGGAA	
P2 outer arm	CCCTCATCAAAAGGTAGGGG	CTGGGTAAGGAGATGGGGAT	
P2 spacer	CGTGCGTGTGTACCATCTTT	AGCTGACTTACATGGAGGGG	
P5 breakpoint	AGAAGGAGTCTCACTTTTGTCGCCCAAG	GCCTCCCAAAGTGTCTTTGTTCAGTTCA	Long range PCR
P8 breakpoint	AGACTGGGTGTTGCGAACAGACAAAAAC	GGATTTGTCTGAGAACTCATTCTTGGCG	Long-range PCR
P8 inner arm	TCCCACTGCTCTGCATCC	CTGGAAGAAGATCTTTATCCTGC	
P11 breakpoint	AATCCACAGGGGACAGCTC	TGTGGGGATAGGAAGTGACA	
P11 inner arm	GCAGGAGTTGCTTCTGTTACTG	TTTGAGTTTGGCTTTCCTGG	
P11 spacer	TCTGTTGAATATGCTCCACACC	TAGTGCAAATTGCTTTCCAGTC	
P17 breakpoint	TCAAAGTTGAAGGGTGTGGC	TTTGGCAATTCTTCCCTGTC	
P17 inner arm	AAAGCAAGCTCCTAAGGATGTG	GGCATCATCCAAACAAGTGG	
P17 outer arm	ATTCGAATGCTGACTCCCAC	GGGAGCTGAACTGCTGTACC	
P22 breakpoint	AGTACCACACAGAGAGGGAGC	GAGGTCAGGCAAGGAAAGAG	
P22 flanking	AACCATGGTCCCAAAATTCA	TCAGCAGTCAACCAGCATTC	
P22 spacer	TGACCATGACTGTGGGAGAA	CAGCCCCTGCTCAAGACTAC	
P25 breakpoint	TCATAGGCTGTTGATGACGG	CGTGATCCCCAAAGGTTG	
P25 inner arm	CACTGTGTCCGGCAACATAC	TCTGTTCTGAGACCCTGTGC	
P25 spacer	TCACACGCTGGTAATTGCAT	CAGCCCTCAGAAGAATTTGC	

Supplemental Table S10: Chimpanzee and rhesus macaque clones sequenced for this project and deposited in GenBank

Clone	Accession
CH250-106M20	AC280444
CH250-114J18	AC280531
CH250-119L11	AC280481
CH250-120L20	AC280562
CH250-136N6	AC280430
CH250-137I15	AC280580
CH250-138B21	AC280536
CH250-149O24	AC280566
CH250-150I6	AC280452
CH250-163K20	AC280436
CH250-168E3	AC280520
CH250-174F12	AC280455
CH250-184A21	AC280508
CH250-191K20	AC280440
CH250-197O3	AC280457
CH250-214O8	AC280424
CH250-228D11	AC280538
CH250-234D7	AC280571
CH250-236O7	AC280541
CH250-240H14	AC280414
CH250-257F3	AC280575
CH250-257M3	AC280477
CH250-25I12	AC280437
CH250-273C12	AC280539
CH250-280C5	AC280451
CH250-300J22	AC280417
CH250-312L23	AC280517
CH250-313D10	AC280454
CH250-318K15	AC280486
CH250-371L16	AC280564
CH250-396M7	AC280543
CH250-397P11	AC280441
CH250-398K19	AC280504
CH250-412K19	AC280483
CH250-417G7	AC280442
CH250-420A18	AC280569
CH250-424H13	AC280467

CH250-436M9	AC280526
CH250-440K2	AC280563
CH250-462M8	AC280473
CH250-486E21	AC280527
CH250-487N16	AC280453
CH250-491H11	AC280464
CH250-493M11	AC280503
CH250-498I16	AC280468
CH250-499B10	AC280432
CH250-503C21	AC280489
CH250-503N19	AC280524
CH250-504P11	AC280429
CH250-516N14	AC280555
CH250-530N5	AC280476
CH250-540J3	AC280456
CH250-541H5	AC280425
CH250-547J16	AC280475
CH250-563M7	AC280492
CH250-57C9	AC280498
CH250-80G22	AC280568
CH250-87B7	AC280549
CH250-92B13	AC280534
CH250-94G2	AC280518
CH250-95D17	AC280449
CH251-130O9	AC280561
CH251-160A4	AC280458
CH251-161L14	AC280465
CH251-172F20	AC280557
CH251-177B21	AC280525
CH251-183G21	AC280578
CH251-189G13	AC280560
CH251-239P10	AC280533
CH251-240O17	AC280544
CH251-261H21	AC280545
CH251-277H18	AC280556
CH251-285D14	AC280499
CH251-292E19	AC280434
CH251-316L7	AC280500
CH251-346A10	AC280446
CH251-34N14	AC280480

CH251-385I8	AC280416
CH251-389B7	AC280426
CH251-397P16	AC280507
CH251-4M24	AC280567
CH251-504H5	AC280540
CH251-506D4	AC280415
CH251-50L15	AC280523
CH251-514B7	AC280488
CH251-542A6	AC280462
CH251-542D16	AC280579
CH251-542E16	AC280512
CH251-550E20	AC280495
CH251-565G15	AC280459
CH251-571K4	AC280521
CH251-58J24	AC280448
CH251-635P13	AC280558
CH251-639F23	AC280574
CH251-64D22	AC280469
CH251-651H9	AC280522
CH251-654E24	AC280553
CH251-657L4	AC280546
CH251-658J15	AC280445
CH251-65E21	AC280530
CH251-671I19	AC280576
CH251-673E12	AC280463
CH251-677L24	AC280565
CH251-702N4	AC280482
CH251-737G9	AC280491
CH251-73C22	AC280423
CH251-83H5	AC280548