Table S3. Detailed description of the identified X-box motifs and their conservation based on PhyloP scores calculated from 100 vertebrates.

Ensembl transcript					**RFX consensus (full site only)**							**X-box position**	**Conservation based on PhyloP100vert**					
Transcript ID	**Start of first exon**	**Strand orientation based on transcript**	**Location, strand**	**Sequence**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**Relative to first exon start site**	**Min**	**Max**	**Range**	**Mean**	**Variance**	**Standard deviation**
DYX1C1-002 NM_001033559	chr15:55790575	Forward	chr15:55790581..55790594 -	GCTTCC CT AGCAAC							x	-19 to -6	0,48	4,74	4,27	2,32	1,89	1,37
DCDC2-001 NM_016356	chr6:24358280	Forward	chr6:24360377..24360390, -	GTTGCT AT GGAAAC			x	x	x		x	-2110 to -2097	0,18	4,51	4,33	2,26	2,31	1,52
		Reverse	chr6:24360377..24360390, +	GTTTCC AT AGCAAC			x	x	x		x	-2110 to -2097	0,18	4,51	4,33	2,26	2,31	1,52
KIAA0319-001 NM_014809	chr6:24646383	Forward	chr6:24646440..24646453, -	GTCGCC GT GGTAAC	x	x					x	-70 to -57	-0,05	2,55	2,60	1,11	0,67	0,82
		Reverse	chr6:24646440..24646453, +	GTTACC AC GGCGAC						x		-70 to -57	-0,05	2,55	2,60	1,11	0,67	0,82
		Reverse	chr6:24648192..24648205, +	GCCTTT AA AGAAAC			x				x	-1822 to -1809	-1,28	0,85	2,13	-0,03	0,48	0,69
		Forward	chr6:24647258..24647271, -	ATAATT GA GGAAAC							x	-888 to -875	-0,84	1,94	2,78	0,15	0,41	0,64