

	(D)S-1a	(D)S-1b	(D)S-2a	(D)S-2b	(M)S3A	(M)S3B	(M)S3C	(M)S3D	(M)S3E	(M)S3F	(M)S3G	(M)S4A	(M)S4B	(M)S4C	(M)S4D	(Z)S4E	(M)S4F	(M)S4G	(M)S5A	(M)S5B	(D)S5c	(M)S6A	(M)S6B	(M)S6C	(M)S6D	(M)S7A	(V)SVA	(V)SVB					
(D)Sema-1a		47.0%																															
(D)Sema-1b			38.2%	39.0%	34.2%	32.5%	30.6%	33.1%	31.5%	32.6%	32.1%	34.7%	35.9%	35.9%	35.2%	34.5%	32.3%	31.2%	42.7%	42.6%	35.1%	38.8%	38.0%	39.9%	40.8%	26.1%	20.7%	26.7%		(D)Sema-1a			
(D)Sema-2a				34.6%	37.1%	32.1%	32.0%	29.5%	32.6%	29.7%	31.3%	32.4%	30.4%	33.0%	30.8%	32.7%	31.0%	31.3%	30.6%	36.9%	38.3%	32.8%	37.4%	35.6%	37.4%	39.8%	24.9%	18.5%	24.4%		(D)Sema-1b		
(D)Sema-2b					69.3%	34.1%	31.6%	33.1%	30.6%	29.9%	32.1%	29.6%	30.7%	29.6%	31.8%	33.3%	32.6%	28.7%	36.2%	36.4%	33.7%	34.2%	32.0%	33.5%	34.9%	24.2%	20.6%	24.6%		(D)Sema-2a			
(M)Sema3A						33.6%	30.1%	31.1%	31.9%	30.5%	33.5%	31.1%	30.7%	29.8%	32.2%	34.1%	32.3%	31.2%	30.2%	37.1%	37.3%	33.7%	33.5%	31.9%	31.6%	34.9%	24.7%	19.1%	22.5%		(D)Sema-2b		
(M)Sema3B							58.4%	51.4%	58.0%	51.0%	54.0%	50.3%	34.1%	34.7%	39.1%	41.7%	35.3%	34.8%	37.3%	33.5%	34.7%	28.5%	35.8%	33.0%	35.5%	36.6%	29.4%	20.0%	27.1%		(M)Sema3A		
(M)Sema3C								49.1%	51.4%	48.4%	50.8%	49.6%	32.8%	36.3%	38.2%	38.0%	37.0%	34.4%	35.1%	32.7%	34.4%	29.0%	35.1%	32.0%	34.3%	33.8%	30.8%	18.0%	26.1%		(M)Sema3B		
(M)Sema3D									48.8%	46.8%	60.7%	47.5%	32.4%	33.2%	34.2%	38.4%	33.7%	34.0%	30.9%	33.6%	33.1%	28.5%	34.2%	31.5%	31.4%	33.6%	27.8%	20.3%	25.6%		(M)Sema3C		
(M)Sema3E										49.3%	50.3%	48.1%	33.4%	34.4%	38.4%	39.0%	37.1%	35.0%	37.7%	33.0%	33.8%	30.3%	34.4%	30.2%	35.3%	36.1%	28.1%	19.4%	26.2%		(M)Sema3D		
(M)Sema3F											47.2%	53.8%	29.3%	34.1%	36.6%	36.1%	33.3%	32.4%	29.4%	33.7%	33.0%	24.7%	31.8%	31.3%	30.7%	33.8%	28.5%	19.0%	27.6%		(M)Sema3E		
(M)Sema3G												48.4%	33.2%	33.2%	35.0%	36.5%	32.5%	32.6%	34.6%	32.7%	33.6%	29.0%	32.4%	33.3%	32.4%	34.4%	27.8%	18.1%	26.8%		(M)Sema3F		
(M)Sema4A													32.0%	34.5%	36.8%	37.6%	36.5%	37.0%	35.1%	31.5%	32.0%	26.9%	33.3%	34.1%	35.0%	34.1%	28.4%	19.1%	25.7%		(M)Sema3G		
(M)Sema4B														40.8%	40.5%	42.1%	39.1%	36.3%	36.6%	33.8%	33.8%	29.4%	31.6%	31.3%	33.0%	31.4%	27.7%	18.0%	26.5%		(M)Sema4A		
(M)Sema4C															47.2%	45.5%	42.0%	43.2%	41.4%	33.2%	33.0%	26.9%	32.4%	34.6%	32.7%	32.6%	29.5%	18.6%	26.7%		(M)Sema4B		
(M)Sema4D																50.3%	44.4%	42.0%	49.2%	35.4%	33.9%	29.7%	34.2%	33.2%	34.4%	33.8%	27.0%	19.4%	26.6%		(M)Sema4C		
(Z)Sema4E																	49.2%	39.7%	43.2%	33.7%	33.8%	28.2%	34.1%	32.9%	34.2%	35.5%	29.3%	18.8%	27.5%		(M)Sema4D		
(M)Sema4F																		35.9%	38.3%	30.8%	31.9%	27.7%	34.6%	31.6%	31.9%	33.5%	29.0%	19.3%	24.0%		(Z)Sema4E		
(M)Sema4G																				37.4%	31.2%	32.3%	26.4%	32.4%	31.5%	32.7%	30.6%	28.3%	18.8%	26.7%		(M)Sema4F	
(M)Sema5A																					30.4%	28.5%	27.1%	31.2%	31.2%	31.1%	28.1%	26.5%	17.8%	25.9%		(M)Sema4G	
(M)Sema5B																						67.2%	38.0%	36.3%	38.3%	36.1%	27.4%	17.0%	26.5%		(M)Sema5A		
(D)Sema5c																							39.1%	35.5%	36.4%	37.7%	25.9%	16.8%	24.4%		(M)Sema5B		
(M)Sema6A																								29.4%	31.5%	32.4%	28.2%	21.9%	18.6%	20.0%		(D)Sema5c	
(M)Sema6B																									62.0%	51.4%	64.7%	26.0%	19.9%	24.1%		(M)Sema6A	
(M)Sema6C																										51.4%	55.1%	21.7%	16.9%	23.0%		(M)Sema6B	
(M)Sema6D																											55.8%	23.6%	19.1%	24.8%		(M)Sema6C	
(M)Sema7A																												24.9%	18.5%	23.5%		(M)Sema6D	
(V)SemaVA																													23.8%	48.9%		(M)Sema7A	
(V)SemaVB																														25.1%			(V)SemaVA
	(D)S-1a	(D)S-1b	(D)S-2a	(D)S-2b	(M)S3A	(M)S3B	(M)S3C	(M)S3D	(M)S3E	(M)S3F	(M)S3G	(M)S4A	(M)S4B	(M)S4C	(M)S4D	(Z)S4E	(M)S4F	(M)S4G	(M)S5A	(M)S5B	(D)S5c	(M)S6A	(M)S6B	(M)S6C	(M)S6D	(M)S7A	(V)SVA	(V)SVB		(V)SemaVB			

Suppl. Fig. 2. Percent identity of the semaphorin domain at the amino acid level for the different semaphorins. As indicated, Sema-1a, Sema-1b, Sema-2a, Sema-2b, and Sema5c are Drosophila (D) sequences. SemaVA and SemaVB are viral (V) sequences. Sema4E is a zebrafish (Z) sequence since it has not been identified in mammals. All other sequences are mouse (M). The amino acids used for the alignment of the sema domains were those defined as constituting the sema domain by the NCBI conserved domain search tool (as according to the SMART database). The percent identity was determined using the European Bioinformatics Institute EMBOSS Pairwise Alignment Algorithm using the Needle feature to align the whole length of both sequences (<http://www.ebi.ac.uk/emboss/align/>).